

Table S2

>2617922370 Ga0073689_1972 glucose-1-phosphate thymidyl transferase [pelotomaculum Ga0073689_197]

VKALI LSGGKGTRLRPLTYTTAKQLI PVANKPI LEFVVGQVCQAGI HDI G
MI I SPETGEQVKGAI GDGKRWGARI TYI PQDKPAGLAHAVKTAKPFLGDD
PFLMFLGDNLI QGGVGRI VEEFVSSRVGAMI QLKEVADPRQFGVAVLDEN
NRVVRLEVKPQDPPGNLALVGI YLFSPAVHGAI DRI KPSWRGELEI TDAI
QEMLESGCAVEARI LEGWWLDTGKKDDI LEANRVVLDEYARPTVEGDVDQ
DSSVYGRVQI GRGI EI RNSI I RGPVVVG DGVKI KDSFVGPYALGNESVL
DSVSI EHSVVLNCCLRDVERI EDSL I GNNTRVSGKKDRHRAVRLFLGDD
SEVLV

>2617922369 Ga0073689_1971 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_197]

MI PVVLVFSGAI LFLAGAHRVPAPDRRFLFVLALWALLARLLFI VATHSF
DTPFI SYI KTSDAI YYEYI GKLI ARAWQEGRNI VI PSDNYGYFYWNGLI Y
FLVGFKPD I RVLNSVTAVCTGFNLYFI SLKLSGSKAAKTSFALAVFFPS
SI LWSSNLNKDSL I FLI TLI VKQSLELMEKFTPGKVL SVALLLMPLVSL
RFYVGI LLAI CI ALSYI FTATKFLWQRLAYALVI FLI AGI TLOQMGYGF
LGADYVLSQSI ETI GEHQKAAAYGGAAYAEDVVFDSYAAALKYLPTGVFY
FLFAPLPWQAMGPLRFI TI PEMFLYFLYVYFLAGARSLWRARRGDCLFL
LI VI ALFGLI YSLGSANI GGLYRVRLQVI MVAFLVI SAGMQRSWVLNRI I
NRLSGRRPLLE

>2617922368 Ga0073689_1964 ABC transporter [pelotomaculum Ga0073689 : Ga0073689_196]

LKI VNLOQVYFESADGMVKA VDDVDSLVSGETVGFLETGSGKTVLGLAV
I GLLPRNI KLKGVWYREKNLLSMTTEEGMRGVRGREI AMI MONPLSSLNP
SLTVGEQRTSTQVSDNKRPRSQERRDMTGHTSPQKI PGI CLSLCSSTVS
FQ

>2617922367 Ga0073689_1963 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_196]

LASLPANI DPHEI EKTLNKMFSPWLRNTAAKAGYVQRNRKI DPATLFWI
LVLGFGVGQRTLASLRRAYETAAAETLVPSAFYYRFNKGLI AFLKDCLA
HGI ADLADHTSLTSDKLOGFKDI I VADGTVI KLHDKLDKQFPGARHKA
LKI HTAI AK

>2617922364 Ga0073689_1954 DNA replication protein DnaC [pelotomaculum Ga0073689 : Ga0073689_195]

GI MVEREWLAKKNARI QRLNLSASLGLNACI EDI DYSADRTI DKKTI QTL
STCMFMEQKLNI VI SGKTGSGKSYAACALGNNACRHGYTVKYFRI PELL
EI QDVKNENRYAKFMTQLQNI KLLI LDDI GLKSYTLEESRDI LEI AESRY
NKGSMVLAGOI AHTQWYDLFPDPTI ADAI MDRVI HNAYI LALDSKKSMA
VMAEKAAKNMKMTDS

>2617922363 Ga0073689_1953 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_195]

MFI RWKGRYAYLERRYTGKDGKVKQSQSKYLGENYLMMLLEKMMMAAGEI SEY
EFKLAGYAPEGTLKTTTSGALTI SDEASCLLNHRI AI FFNSWQPGLV
AKDEYGWYLKDDNGNKVGLHPGTVKRLI LQNVLSWL

>2617922362 Ga0073689_1952 Protein of unknown function (DUF1670) [pelotomaculum Ga0073689 : Ga0073689_195]

MENAVQERI QAKTRDNQLFEVFNHFEFSPKTAEEAI NTVKEI YELHRFD
PDLLCETSQVI RQVVS I KAKHGPRRLREL PKVTVKLTADTGAEDQEVFRKH
GAPGLREVQI CRMAEEALDQGGVLTQEDLADI I QMDI RTVRRTI RQLQER
SVRVQTRGLYHDI GPSI SYKAWI VGLHLEYKTYSEI ARTTRHSTASI KRY
IMDFARVSI SKRI KEYQEERQVVLPI KGNKLDMPGNHPQTNY

>2617922361 Ga0073689_1951 Protein of unknown function (DUF1670) [pelotomaculum Ga0073689 : Ga0073689_195]

MYEKKVATPDI ARQVNHSQEAVDRYI KDYER I RFLVRRGMDI AEI SHLTG
RGKQVVKQHLEI I KHHYPELFETGQAPDRCPDTCTGCSPKTQ

>2617922360 Ga0073689_1944 Transposase IS116/IS110/IS902 family protein [pelotomaculum Ga0073689 : Ga0073689_194]

VI KTLOSEVKKLDKLI EEHMKA I PQTLSLKG I GPVYSAGI LAEVEI TR
FKNHKS LAKFAGLVWNEKQSGEWAEDI KRI RSGNKYLRYYLVEAANLI R
MHDREYADFYSAKYAEARTHKKRALVLTARKLVRLVYALLRFPNDEFG

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>2617922359 Ga0073689_1943 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_194] MLKAREI LKLKHEVGLSLREI GKSCNCGKSTVSEVLERAAGI TWPI EL KATTLI ALPTRGTEKNSS
>2617922358 Ga0073689_1942 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_194] MHDVPVQKNVGAEKSI ATAAPLLLLSRLWPFI I FLVI AI AGLFI VKWNPYY HKALVASSKHFI GASI LSGNAPVPPAPSWGAAWNYAAVYFKSVWQAVLLG LI LASMVEALLPGEWLQRF LGPGRYRSTALGGMAAI PSMMCTCCAAPLAV GMRKRSVSVGAALAYWLGPNVLPATLVFMGFI LSWQLVALRLI FGI VI V FGVAYI ANRLAGEETVAEPLSATWKASADKGNWLVRLHSFWRLALDSLP I YLLMVLLLGALRAWLFPVAVSPDWANSFWVI TGFALAGTLFI I PTAAEI P I VQTMLSFGGLGI GPAAALLVTLPTI SLPSLFI LRNAFPARVLVFI SI AVV VLGI LSGLLASLLFPA
>2617922357 Ga0073689_1941 putative membrane protein [pelotomaculum Ga0073689 : Ga0073689_194] MMGFGFGGTFGSLVWGLSMLI TMLLPVI I I VGMVYLGLSLWDRKKNNSTK ETVLQDPLKI LKKRYASGEI SEEEFGRVKEELLKG
>2617922354 Ga0073689_1925 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_192] MAGEI I VGLTI LLLVALSVRERMLQHMSREKDWSAI GEAKSSPFSQALAN LVGVAGGI YLTLM I MVTFMELQVPERI QVCGFSMEPLAAVSI LMALAQPY LHRVI NAWRRI
>2617922353 Ga0073689_1924 sporulation protein, YlmC/YmxH family [pelotomaculum Ga0073689 : Ga0073689_192] MRMCDLVGKEI VNI YNGARLGVVGESDMAI DI ESGEI LSI I LPRKNNFIN LWVDKQQLVI PWEAVRKI GLEVI I VELDQTSPHYRRYSI
>2617922352 Ga0073689_1923 Molecular chaperone IbpA, HSP20 family [pelotomaculum Ga0073689 : Ga0073689_192] MYVSSLNPSQVVMNQGYQTGATAFPVSI RPGLQGNVTYAFNPLFGQSA AWSLNPSTVGMAVNPLLNQSLALSWNPMMASAAMAPWSPI MSAAGI SAFN PTLSTAMAQNNLPGSGI SAWSPMI NPAQAMNAVLNPVSMGI NTI QSTSGL AQMVRDLHETNSDVVAAELPNVSLNDLNLTVTDDSLSI SATAFAGNRST SLFRTVALPTSI KSEQVEATYANGI LEI RAPKSDVVTRRKVKVNLA
>2617922351 Ga0073689_1922 Serine dehydrogenase proteinase [pelotomaculum Ga0073689 : Ga0073689_192] MARQKRVELI KKI SELRGSEVLCYI TGDRENVNTRI APDVTQVFYRHLE I GECQOI DLFLYTRGGDVLTPWRLVHLI REYTPRFTVLVPFRCYSGTLL CLGADEI VMGKMGELGPI DPSVVNAFNPQDPNPAARI PVNI EDVYSYLA LAGEKAGVCSNDQVKAFATMLAERI HPLALGNVHRNYMLI RSLAKKLLAM YQQPLREGSI EHI VDNLTEKLYAHNHMI SRREAAKEI NLAI I FPDNI LEP LI WALYQDFAELALADPFNPVAVQLRGARSEFEVI SGYVESI HGADAFI F SGVVERREFPEAGQI NVSI LNQGWKTI V
>2617922350 Ga0073689_1921 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_192] LEDKRSDLKGERVSFHYRTNETKYLLTEGSGYPLAEYNFSNLAAQRGTG MVPENRPKTANVVPRTDPTGLTREV
>2617922349 Ga0073689_1915 Small, acid-soluble spore protein, alpha/beta type [pelotomaculum Ga0073689 : Ga0073689_191] LEKDLAVI NNDYPDLMKTI GQGLMPKELERYVAPALÉDFRNEMAAELGLP DYENVDKGELPSRMNGNVGGSMTKKMVRFAEAVLAWNYQRLALKEKN
>2617922348 Ga0073689_1914 Plasmid stabilization system protein ParE [pelotomaculum Ga0073689 : Ga0073689_191] VKFKI RI NPMAI DDVREI KDHI AGDNPGAAI KI SNAI YTG I ERLADFP GVSLSAKI NVKTNRYRFLVCGVYLI FYKI EGEFVSVYRVLNGMRNYLPI LF GKELPKD
>2617922347 Ga0073689_1913 prevent-host-death family protein [pelotomaculum Ga0073689 : Ga0073689_191]

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MPNI KPVSDLRNYNDVLRSCQI GEPVFLTKNGRGYVLLDI QEYERQQAV
I KLLSKLFEADMI KRGEWKSLLDDKKVLEV

>2617922346 Ga0073689_1912 Signal transduction histidine kinase [pelotomaculum Ga0073689 : Ga0073689_191]

VRNHLLAQTRTLRQEADTLARALSSQSLEKERLGRLLKKATLRLAGRL
LSGNHAVVNAQGVVVASDLENGLAPGSRLODVLPGI FSAEALQORGETGVW
RNREFMAAAAPI EGVGGKVI VMI RMDSLREI RRELFVLMARSLALAVPLA
LLAAFLLAGRI ARPLRLLQERARQLSRREFGRPVEVRTGDEI EDLGRDFN
LMAQRLAEYDAAQKCFLOASHLKTPLTNI QGYAEGI KDGVTFTGEEVDQ
GLTVI I KESRRLKKI VEELI YLSRLETVEEFYSFGPVELTAVLQEVLETL
RPAALERGI ELALNAPEELCLRGDREKLLRLFMNI VMNAVSFARSVELA
VKTGRERNLTLI SCWDDGPGFPPEQI HHVFERFYKGPGRGSTGLGLAI VKA
I AEGHGGRTAQNAPEGGARLEVELPLGGMTCCCK

>2617922345 Ga0073689_1911 two-component system, OmpR family, response regulator ResD [pelotomaculum Ga0073689 : Ga0073689_191]

VQTI FVVDDDPNI LRLI KQYLLKEGFRVEAFASMDGVEEGLANTAPDLFV
LDI MLPGEDGLAFCCRRLAERNI PVI FVSARGEEMDRI LGLEMGGDDYLA
KPFSPRELVARVKAVLRRAGAFKPGEEAI EVKGLEI I PSRREALVNGRK
LDFTPKEYNLVALLARSPGQVFSREQLLDRI WGI DYVVDI RAVDDLKRV
RRKLREKAASVGI ATWVGYYGYKLKI

>2617922344 Ga0073689_1903 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_190]

TDVLKDLGWEMPVDFI KLQYLPDNRELNTTWEAGKKLGAAI LAHPGK

>2617922343 Ga0073689_1902 S-layer homology domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_190]

LRKLVI I SLVLLFSLYAGI AAVSAQPLNTEDLLGVFPESPELTQPVTRSA
FAAMLVKAANLPAVDQRAYQAKDVPESWFAPAMATLAGEGI MAGYPGGA
MRPEQPLTGVEAAALVSRTLGLYGTLDLDEFAGPLAPGHWGSSLYNWLVDQ
GLI SGGSDPENPLTVNNAALFLVRVFGSDPQALAI VEKSGQAQADI KAMR
SKI DMDMAI KPKTSAAGEFPMKGTGKTDMEVVMPTI HQVNRWQFTASG
KREI PEMVVEQYI VDGKMYTKVI DPVSGEAQWMMRMEGALPDMKALVEE
SMKAGKMG I PDELKPYFHYQLLGVKDKNGQKVHEI GYYGCI DDLDAFMKA
ALPESLRDTLGGPELEKSLGGAGKMI KSI FYWGREEVGAGDYLPVSSEMK
I VI SFSDQFQGEAMPVELAEMHI KVREYSFGDQI KI ELPPEALQAKEI PV
QETGSGGGGGGGKGTQGESSRQAPVN

>2617922342 Ga0073689_1901 CoA-substrate-specific enzyme activase, putative [pelotomaculum Ga0073689 : Ga0073689_190]

MI TVGI DVGSI TTKVVLLNDTTWQSLLLPTGCSPRETGRFVFEQI LNGAN
LTPADI HYVVGTYGRI SLPFI DKAI TEI TCHARGAHLVNGTDMVI DI G
GQDSKVI MVDEQGGVTDFAAMNDKCAAGTGRFLQVMAAVLGTDVSELANLA
RGAEPVQI SSMCTVFAESEVVSLLAQGVAKERI I AGI HRSVASRVAAMVE

>2617922341 Ga0073689_1893 ATPase, P-type (transporting), HAD superfamily, subfamily 1C [pelotomaculum Ga0073689 : Ga0073689_189]

LGCLVI SDKVRPEVRGLVPKLYRLGLQKVVMLTGDSRAVAAQVARVSGI R
DFEAGLLPEQKLOHI KSLQNHICYKAMVGDGI NDAPSLAAADI GI AMRAM
GTDVAI ESADI ALMSDDI TKI PYALEAGKATLTKI NYNHELCSYR

>2617922340 Ga0073689_1892 Transposase DDE domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_189]

LDDTKVAHPFGKKLPFLCWLDSSTRNHI WCMNLI STYAVLKNLDLEYPLF
WRFWRKTENQNDKQTKLELAREMLDLRTTCHEQLWVAMDRWFLCKNFFN
WLVEHNFDWVTKAKKNTVLYCRYFDPTSRKEKYKKVNPKELLRTVYKQLS
ALSKGGVI SI PDVYNKLSYETTNRKGKPMRRWRYVSI AAVASTYRKEPVI
VDGI LREEDESATYRDAYLLI SNRYDTPEEVAAYVVKRWRI EVFYRTVKQ
ELGLTNRHSRSEASHFAHMELLFTAETLLCYARWECNKEGAEALSCEM
VGYLFNASHRI CCYEQQI QVYFDI TGDRTSRFI EKFWPPHPFLWLWNWCY
LPVTA

>2617922339 Ga0073689_1891 His Kinase A (phospho-acceptor) domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_189]

ANVSHELRTPLSI MQGYTEALI DGMAESEADQKYLGN I HEEI LRLRLV
TEI LDLRRI EAGRLEMEMKEVSLPDI AGSVVNKLQALAEERKI SLLQDFP
PGPPAAYADPDRLEQVFI NLLDNALRVTPDGGKVEI AI RDLKEMLQVSI R

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DTGPGI PLEEQPLI WERFYKVDKSRTTRI GGGTGLGLAI VKEI VEAHGGS
EI I SKPGE GSI FVFTI PKKS

>2617922338 Ga0073689_1882 succinyl -CoA reductase [pelotomaculum Ga0073689 : Ga0073689_188]

MFIEQI VSI NPATREEI GKI NVTTREEI KQI VSNKNSFKQWSFFSFEKR
GSYLKKLAVELKKNSQDI ARLI TMEMGRPI KESLSEVMI SARFLNYFADN
TEYFMVSEPI KDLGNKI ARI I YEPI GI VAAI KPWNMSI QTPI WAI APALM
TGSVVI LKPSSENSLLVAKELEKMTSFCGFPQGVLSFVYGSKDTGRYLLDE
DI DMVSFTGSVSAGKEVASI VANRFI KMSLELGGKDAMVFPDCDLDFAA
MAAVYGSTTNCGQFCAAVERVYI HEQI YEPMVEKI VNFTKSI RVGNGLRE
DVMGPLVKNQQFDLVLGQI NDAI KKGAKVLCGG SAYESGELSKGFFVKP
TVMNVNHSMDI I KYETFGPVI CLMSFKDEDEAI ALANDSMYGLGASVI T
QNI ELAERVASRLDVGMMVI NEPLMSMASCPWI ARKQSGI GNELGELGVK
EFLKPKLI SSQYKENDSKRKWWYPY

>2617922337 Ga0073689_1881 Winged helix-turn helix [pelotomaculum Ga0073689 : Ga0073689_188]

VRHLDKKHLPDPLAKNGFFKESDSTQVKYEMLRNATTKKSVVEVCQEFN
FSRKAFYNAKERFNEDGLVGLI DRLPGRGRHKVDSEMEETI VRI KREHM
NDPKFKVPQVFOALKEEYTERCLPVNI STKTVERVLI DHGLHTPRSKKNQ
GVRKKNRE

>2617922336 Ga0073689_1872 D-alanyl -D-alanine carboxypeptidase (penicillin-binding protein 5/6) [pelotomaculum Ga0073689 : Ga0073689_187]

MCHCFRRSALLLPAAVMALSLI SLYPAVARPAEYDAPGAPAI TADAAVL
MDACTGQI LYDKNAGORRAPASTTKI MTAI LALEGGRLGQLVTVSPRAAS
VGEASLDLRAWELTLEELI YGALLHSGNDACVAI AEHI TGTESNFVLLM
NQKAKMI GARDTCFI NTNGLPAAGHYTTAHD LAVI TRYALNNPTFKRI VS
TRSKMI GGQGDYLNNTNRLLWSYAWADGVKTGTTNEAGNCLVASATRED
ROLI SVVLHGDDRWNDSVKLLDYGFTAFDYI RVLDEGEACETI TVKEGAG
KEVQAVASAE LGAVI PKNRPKYLEKMVEI DRDLTAPI RKGQWLQVTVLV
KGKVVGTANLVADRDMEKKT I YGDLRRI I R

>2617922335 Ga0073689_1871 Predicted Zn-dependent peptidase [pelotomaculum Ga0073689 : Ga0073689_187]

MYQKVALNNNVHI LTEEVPVRSVAVGFVWDVGSRDENPEI NGI SHFI EH
LMFKGTRRRRTAKDI AEALDAVGGQLNAFTTKEYTCYYARVLDEHFDLAVD
LLSDMLFESKFNARDI DRERNVI I EEI KMYEDAPDELVHDI FAGSMWQGH
ALGRTI I GTA EVI TGLSRERI LDFYETYYRPGKMVAVAGNVRHEEVNK
LOPI LEEKGGMVPVREMI TPAPHRGI TCRNKETEQVHLCVGTPLSLNHE
RI YVFOI VNTI LGGGLSSRLFQEI REQKGLVYSVSYHSSYHDSGLFCVY
AGLSKQNVDEVLDI LKQVRDI QLNGVKEEELQRAKDQLKGNLYLSLENV
NTRMSRLGKSQLYLGKVI PPEGI VAKVNVKTAAEVQELAREMLRPDLFSL
AAI GPWEDCGNLERALGQLLNG

>2617922334 Ga0073689_1865 IstB-like ATP binding protein [pelotomaculum Ga0073689 : Ga0073689_186]

LNQNEPEI I RLAKMKWPVVENYKKHKADNSFEENLLTLRLENEQRDK
AI TRQRI RQAGFPI I KTLDTFEFNQTMPLHLKQEQVLELALCDFI RNRTN
VVAI GNSGTGKTHI VTALGMEAI RKGYSVRFRRACD

>2617922333 Ga0073689_1864 Integrase core domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_186]

MQFDWGDMSAVI AGSKTVSVFCAVLPSGALCAFVYPDKSTLSFLHGH
QAFEFAGGVARRCI YDNLRTAVKKGSGKNAVKQDSFI RLEAHYGF EAVFC
NAAAGWEKSNVENAVAI VRR I AFTPMRVDSEALQSHVTNRCLHYAQTH
TI CGHEHSI RDALEQERKM LLLPLPEVRLDTGFTFTALVHPDLTVHHDGAR
YSVPRHLVGKEVTLCLSPFHLTVFHNGREVYKHDRSMKKQDHRVLEHYL
EI LERKPRAVEQAI PVKRG I MPQECKEFLRLCREPEAKQQLVQI LLLGRQ
VERERLLWVI QQANTRNPSLSLVKLYLELEEPGPPRDDLAVQHKSLAAY
DDLLOEGGSTI EPE

>2617922332 Ga0073689_1863 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_186]

LTI DWGTYRKVRQLFLVEGQSI RAI SRQLHMSRKTVRKYCRGGVLPDVRK
VTERPAPLFLKVESEI I HLL EENKTLPKKQRLNAR

>2617922331 Ga0073689_1862 chromosome partitioning protein, ParB family

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[pelotomaculum Ga0073689 : Ga0073689_186]

MVKAERLI TOVDTAHVKDNOVL SLSVNRQDVERCAWVI RQYGLLTPPVVG
DFPDGTRLVLSGCEFLALREMGVSSVEAVAPVLEEQDSSRLSLLLSSL
RKSPNALSEGLLVAQLLKTGQYTQSQVGELLGKSVSWVNKRVS LI TRLHP
AVRELVTLRQLCPHSAQE I ARLPEE I QHPFATKVVOEGLPKSAVEVLVET
YHKEGCPDSFKEQMLEQPRHALEKVADI RKVKTI RNCTGKDI SPSTQTLR
NDLVLLLR CI SDAQRQLGI LDYPALLOQRSLLVRSRDASLRFASLLDACL
ETMNVSPGENRKGGANP

>2617922330 Ga0073689_1861 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_186]

MVLHYRDI QVECPVQLDGKKPAGI I FPAFKLPYRKYPVFVYLYAVALYLA
GESMRKAARKTAKEFGVPKFSHSTVSRITLDALTLKI NELTAI VSPPESET
SOAGDGADCAAPADQPSL VVRPRWREPRKQAAPHLFSVLSSLLSSPESGS
KLAYRYFTEYGRFLL

>2617922329 Ga0073689_1854 Transposase [pelotomaculum Ga0073689 : Ga0073689_185]

MTI DWD TYRNV RQLFLVEGQSI RAI ARQLHMSRKT V RKYCHGGVLPDVRK
VTD RPAPLFRQVEGEI TRILLEENKTFPKKQRLNARNI WEYLQSEKGI AIS
QSTVRKYVRELKERHPEVFLPLDHEPGDAMQFDWGDMSAVI AGAKTVVSV
FCAALPHSGAI FAFVYPDKSTLSFLHGH I QAFESAGGVARHCI YDNLKTA
VRKGS GKNVVKQESFI RLEAHYGFEAVFCNVAAGWEKANVENAVAI I RRI
AFTPMRVD SF EALQSHVTNRCLYYARTHTI CGHEHSI RDALEQERKMML
PLPEVRLDTGFTCTALVHPDLTVHHEGARYSVPRHLVGKEVTLCLSPFHL
TVFHQGREVYKHDRAMKKQDHRVLEHYLEI LERKPRAVEQAI PI KRGI M
PEECKEFLRLCREPEAKQQLVQI LLLGRQVDRARLLWAI QQANNTSPNI
SLVKLYLELEEPGPPRDDLEVQHKSLTAYDDLLOEGVKPGLYKARTAGDS
ME

>2617922328 Ga0073689_1853 chromosome partitioning protein, ParB family [pelotomaculum Ga0073689 : Ga0073689_185]

MERAERLI TOVETACVKDNOVL SLSVNRQDVERCARVI RQYGLLTPPVVG
DFPDGTRLVLSGCEFLALREMG I RSVEAVAPVLEEQDGSRLSLLLASL
RKSPNALSEGI LVAQLLKTGQYTQSQVGEMLGKSVSWVNKRI SLI TRLHP
AVRELVTLRQLCPHSAQE I ARLPGKI QHAFATKVVOEGLPKSAVEVLVET
YNK TGCPDSLKEQMLERPRHALEKVM DL RKVKTI RNCQAKEVSPCAQTLR
NDLI LLLRCI SDAQRQLGGLDHPALLQHQS I LARSRDASLRFASLLDTYL
EAVDVSPGKSLTGGVSP

>2617922327 Ga0073689_1852 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_185]

MNI TLI QAEYKPFETI FCPLTPEEFELRQVGVAKKKRI YHMELYYRDI
QVECPVQLNGKKPAGI I LPTWKLPYHKYPVFVYLYAVALYLSGESMRKAA
RKTGEKFGVPKFSHSTVSRITLNTLTLKI GELI TI CPLKSESPKAQDSSNY
AAPATSPGQPALVVRPRWADARKKAAPPLFKALASLFSSPQTGNI LAYRY
FTQYGRLLL

>2617922326 Ga0073689_1851 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_185]

MI WPAI KLPHRKYPVYVYLYAAALYLSSNLSMRNVAAKVRNI FGLDKFSH
STVSRITLKKLAGI VEDLFR LMAADI PKYDDLSCMNI FVPRRGWDNTRQDK
YRRL LHI VFPVLDKSQTREYGSLLNYKYFND

>2617922325 Ga0073689_1844 transcriptional regulator, Card family [pelotomaculum Ga0073689 : Ga0073689_184]

LFKI GDKVVYPMHGAGVI EAI EEKEVLGERRQYI LRLPVGDMKVM I PI S
NGAGVGLREVI DREGVQRFHI LRQSSAMSPNWNRRYRANLEKI KSGNI
YEVAEVVRNLI KRDREKGLSSGERKM LENARQI LI SELVLATELGEDKAO
SLLDSAFA

>2617922324 Ga0073689_1843 diadenylate cyclase [pelotomaculum Ga0073689 : Ga0073689_184]

VKEEKVEDKLLKVLRTVAPGTPLREGLNI LRAKSGGLI VI GDTPEVMEI
TEGGFI I NADFTPANLYELAKMDGAI I LSGDVKKI LAANTQLVPSQNVPS
SETGI RHRTAERVARQDTLVI AI SQRRGI I TTYKGTLYVLRDLGVI LT
KANQAI QTEKYRTVLD RVMVSLSVLEFEQAVTLFDVAKAI QRVEMVLRV
VKEI ERYI SELGVEGRLI SMQMEELLANVENQGLLVI QDYATI I GEKSPA
SI LGVI GSWPAEDI LDLSLI ARALGYPGSASI LDQHVSPRGYRI LEKLPR
LPLPVI DNLVKTFESLDKI LVATI EELDEVEGI GEI RARSI KKGLNRYRE

NLLQERRG

>2617922323 Ga0073689_1842 DNA repair protein RadA/Sms [pelotomaculum Ga0073689 : Ga0073689_184]

MRVKSKECCRECGHQSARWLGRCPGCGAWNSFVEELAGRAAARPALPGGE
GPLPVTEVPVLAERFPTDI GEMDRVLGGGVVPGSLLLVGDPGI GKSTL
LLQVAHRLSQRPLVLYVSGEESVRQVRLRADRLGTI SPGLLLVSETDMDV
VESYLKELAPPVAI I DSI QTMFKSDLASAPGSVGQVRECAAAQLMRLAKTT
GI SI FLVGHVTKEGALAGPRVLEHMDTVLYLEGDRRHFFRI LRGVKNRF
GSTNEI GI FEMRSGLEEVTNPSALFLNRRSRAAVPGSAVVAGLEGTRPL
LVEI QALVSPAGYGMPPRMTAGVDYNRVALI AAVLEKREGLNLSGHDLYV
NAVGGVKLDEPAVDLAI ACALVSSFRDVPVDSGMACAGEI GLTGELRPVT
GMEKRI REAFKLGFFSFLLSGQSAPSAGETKCVLTADTLADALELALKG

>2617922322 Ga0073689_1841 C-terminal, D2-small domain-containing protein, of ClpB protein [pelotomaculum Ga0073689 : Ga0073689_184]

VSRAVRRARAGLKDPKRPI GSF I FLGPTGVGKTELAKALAEVLFGTEEAM
VRVDMSEYMEKFSVSRLVGAPPGYVGYEEGGQLTEAVRRRPFTVLLDEI
EKAHPEVFNI LLQVMEDGRLTDAKGRTVDFRNTVI I MTSNVGLQTI KREA
TLGFRAGDRKETDYEDMKRRI TEDLRRTFRPEFLNRI DETI I FHPLNPGH
I REI VSLMLREVAGRMRENDVEI EVFEPVKDLLAKEGFDEAYGARPLRRV
I LRLVEDRLSEEFKGAFFHSGDRVLLDDETGEI KVQKI

>2617922320 Ga0073689_1834 transcriptional regulator CtsR [pelotomaculum Ga0073689 : Ga0073689_183]

MSNI SNLI EGYLKKLLADSPHDYVEI QRSELALRFKCVPSQI NYVLSTRF
STGHGYI VESRRGGGGYI RI VKI PLDRRAELVSDI CDLI GDTI SQADAEG
LI KRLKEEKLI TRREVWMRAAMDRDI LRLGLSGRGLRAMVLKAMVTAV
LRD

>2617922319 Ga0073689_1833 Protein-arginine kinase activator protein McsA [pelotomaculum Ga0073689 : Ga0073689_183]

MLCERCGQRPVTVHLEI TNGHKQDVHLCEVCAGEI QPQGFKLVPOLYLH
NLLAGLLKHEQGHGNYNQETETSI KKCEKCGMAEKQFI KRGLLGCQDCYRY
FEERLLPLLRI HGNTIRHI GKVPDRTGGRFRLAKEI ENMKSLLWEAVNRE
EFERAAQLRDHI RRLKLTLEEGGEA

>2617922318 Ga0073689_1832 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_183]

MMAI KETVNKAYSRRWMKADGPESDVVSSSRVRVARNLAGI PFPQLLNAEK
AAEVI HAVRLAVENKEAWEMTGELEI SALSELSPVDRQI LVDKHLI SPDL
LNNFQNKAVVLRDDEVI SI MVNEEDHLRI QCLLPGLQLKEAWDI VNAVDD
GLEKTLEYAFSEKLYLTSCPTNVGTGVRASVMLHPLGLKLTNQLGGI LG
VI GKLGLTVRGLYEGGTNALGDLFQI SNQI TLGQPEGEI I NNLI SVTRQI
LAQEKTAGRVI YKDRREAI EDRVYRAYGI LKYARI LSSEAMRFLSRLRL
GLGLKI TPEI PLRLLNELMVKI SPAFLMKTAGREMSSYERDVFRAGLI RK
EFEI PR

>2617922317 Ga0073689_1831 UvrB/uvrC motif-containing protein [pelotomaculum Ga0073689 : Ga0073689_183]

MFGRFTEAOKVLRYAQEEAKNAAYPFVGTEHLLGLI REGEVAAKI LA
AAGLDADKVRAAVAQVVEPGKGPVPGPAFTPRAKRALELSI DEARRMGH
SYVGTEHLLGLI REGEVAAQLLNAFGADYRKVRAMVAHLQGGQAEAGE
KAPGRAKGGETPTLNQFGRDLTVLAGEDKLDPVVGRDKEI ERVI QVLSRR
TKNNPVLI GEPGVGKTAI AEGLAQRI TAGNVPEVLANKRVVTLDMGSLVA
GTKYRGEFEERLKKI I EEI RRAGNI VMFI DELHTLVGAGAAEGAI DAANI
LKPALARGELOCI GATTLDEYRKYI EKDAALERRFQPI TVAEPTEETI Q
I LRGLRDKYEAHHRVRI TDDALEAAAKLSSRYI TDRFLPKAI DLVDEAG
SRVRLQAFTPPPDLKEREKLEELQKEKEAAVNGQEFKAAELRDREOKL
RAELDRLRESWKQKGGTELVVDEENI AHI VSSWTGI PVKKLAEETERL
LKMEEVHLHRRVVGQDEAI R

>2617922316 Ga0073689_1827 DDE superfamily endonuclease [pelotomaculum Ga0073689 : Ga0073689_182]

VVFI GYASDRGYGLVNYQLFMPEKWFSEYESLRKKCCVPDDVTFTKPE
MAGEMLKAEAFNSGLVKAKWI GCDSLFGASKTFDLSLPQECRYFADI HRPT
LVWRDRPEVALPEYSGRGPFLCETPPHNVRADRPSTFYI GNAPAFKKNR
TGLDATSGPKTDHRLI RQ

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>2617922315 Ga0073689_1826 putative transposase [pelotomaculum Ga0073689 : Ga0073689_182]
MAEYRKGGHTI YDI KYHFVWI TKYRYQVLKGLI AQQLRELLRQGCECRNM
V I I KGAI KPDHVHLI SCSPQLSPSKI VQYLKGRSSRLI QEEFPQLKKRY
WG

>2617922314 Ga0073689_1825 5' -methyl thioadenosine phosphorylase [pelotomaculum Ga0073689 : Ga0073689_182]
MVVTEI PRAGFAVI GGSSTFSI NFPEDLKRDDVRVLSPGMTFTTPYGESP
LFKLF I LDDKTVLTLKMHGWRSGVARADASRQVFWLRETGVKRI LAEGG
VGS I NRLLRPRDLI VPTDYLD F SMRKDVGLDSSYLLI MRQPVCPHI RKEL
VRAAESGAVGRVDFDRGVYAVTDGRHFESPAEVEALYRLGADI VGQSMCPE
VYLAREI GACYGRI DMVVNYAEGVLKEWDYREMSAI FYYEPARI GNI LLN
TLKRLEAVQTCRCPELRKPTLLQEK

>2617922313 Ga0073689_1824
2-polyprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinol methylase
[pelotomaculum Ga0073689 : Ga0073689_182]
VKS YKGLAAVYDHLVSGVDFEGWVDYLEQI MERFGYRADTVADLACGTGN
I TLPLAGRGYRATGLDLSP EMLAVAREKAAARNLTI EFLCADMRDFRLSR
PADLVI CFHDGLNYL TEYNDLI KTFNCVGLNLKPSGFFVFDLNAVRLWLSG
TGPEVTMAEEELMLI WESVYHEKEDI WEARLTGFVREREGEMYRKFKFKEV
HREKAYRPAEVEAALKSANLKLASYDAFTFNHI HEKSRRHFYVAKRIS

>2617922312 Ga0073689_1823 Adenylate kinase [pelotomaculum Ga0073689 : Ga0073689_182]
VKLLI MGPPGAGKGTQAEMLVKLQI THI STGDMFRAAI KEGTEMGKKAK
EYMDKGELVPDSVVVG MVKERLSQPD CAGGFLLDGFPRTVAQAEALDETL
KTMEI KLDGVI NI AVPREKLMARLTGRR I CRSCGASYHI LFNPSKVEGRC
DTCGGELYQRSDNEVAVGNRLDI YEAQTQPLI DYYSKQGLLKN I NGDQE
I KKVLAIDLAI I GK

>2617922311 Ga0073689_1822 SsrA-binding protein [pelotomaculum Ga0073689 : Ga0073689_182]
MAI KTVTENRKARHEYHI LETYEAGLALTGTEVKS LRVGKANLQDSFARV
ENAELMLYNMHI SPYDQGNRFNHEPKRTRRLLMHKQEI MRLLGKTREKGL
SLI PLKVYFKNGLAKLELALAKGKKLHDDRREDI AARDARREI DRAMKERS
RF

>2617922309 Ga0073689_1815 Mu transposase, C-terminal [pelotomaculum Ga0073689 : Ga0073689_181]
MNNDQDLERÄLFYRGM I HPLDDSLSPGEKSALRKQI LSKTYDI PHSSRT
TI CERTLRQYLKWYREGGFSALMOCKRKDKGDVRAI SEEV LKKA FSLKEE
LPTRSI REI I EMLELSGEVAPDSVKHSTLSRLVAQHTGQLRPPTSGKTFR
RYQKENVNDTWQSDVKHCI YLPDPQTPKEYI KTYLI AFLDDKSRRVCGKI
YWAENGANVEDCFRKALI QMGVPLCFYTDNSKI YKTKRLQTI CAELGSQ
KYCLPYPPQSKGKLEKFNAYVDRSFEPEARHLKI QTLEELNQYFEVWLTE
NYNHKVHAEI RRTPLEAHQSEQARLRYVTPEELRKI FI QRQVRKADNAAT
VSLGGNLYRVEGFLARKKVELRYDAKDLSCVEVYNGQQYSNAEPLI I RA
NWWDGETESATGAPKQQDETAGDKTVQTSLSQSCYRRNMSKSSKTKPI VS
I TPNSI KRRMNP MYESYFGFSKTPFI RDI DVKQLYLHADFQELKGRLOYA
I ENRLF AAVTGEVGS KTTAI RAVVEE I NPVSHKI I YI SQSDMSPKAFYN
EI LEQI DMTPSYFKPESKRKVNKAMLELYQHG

>2617922308 Ga0073689_1814 peptide/nickel transport system permease protein
[pelotomaculum Ga0073689 : Ga0073689_181]
MQI YLLKRFFYLLPVLLGVSLI TFGLI NLAPGDPAELI LRVGGVEPTREA
VEALREELGLNDPVYI QYGRWLWHAHLDLSKSFRTGQPVAAENLDRFPA
TLELTCAAMALVVL FALPLGI LAALYRHALADHLTRFGALVGASMPGFWL
GLMLI YLSAVKLRLLPVMGRGGI NHLVLPVAVTLAFGMAATYARLLRASML
EVLGQDFI RVARAKGLAEKWVI GRHALKNALLPVVTMLGLSFGHLLGVFN
NEKLPHYKSANFSQRI AGEI SS

>2617922307 Ga0073689_1813 Adenosylcobinamide dihydrolyase [pelotomaculum Ga0073689 : Ga0073689_181]
MVL DGLCI TTELA VFSGHL CRQLLARHLPRRGKRDFLSPLRPRNGKNFDG
AMATGTTTDAI VI ACTGRGRLLPYAGAATDLGFLVGRTVYRAVAQGI RDY
LAANGHEKLERTPGGVLLN

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>2617922306 Ga0073689_1812 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_181]

MKSKTKTI AQCLLALSQWNGGTDHLDRLANLLAGRQRTADTGKGSFENS
VYSMMWAYI ALGEAGKMSCI DNAAAKAHI LSKQGADGSWGETWGTEYYPD
FMSTTQAI RALTYI PDAAGDQVQTAINNGLA

>2617922305 Ga0073689_1811 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_181]

LAKI LREGTSYTORDDVVELLGEFSAFKDRVEKKFKELARELEGKANEHDL
WVNLVLLSSDYAEVVKHKHQEPLQKIS

>2617922304 Ga0073689_1805 Group II intron, maturase-specific domain [pelotomaculum Ga0073689 : Ga0073689_180]

KDKI RELTPRNHGMSLKEMI KRLNPVLRGWANYFRAANCKKLFAQLMEWIR

>2617922303 Ga0073689_1804 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_180]

MCYGNAGVPKPEREDEI LRFAEYWKI RTGHYPRELVDLSQLTTYSNLQKL
NECDI SFI TLRRTTKMI AGLYATPPSQWRVNLPALTRQYRNPRVLESR
AQLKGYNGSLRLAI TDLGHEEPTLLL TNQFNASAVQLI TRYAQRMLI EN
GI ADAI NFFHI DSLSSMVGLKVDFDLQLTLMAASLYRVMAQRI GREYRRA
TAKTLFRKLFVSGQVI I TDSEI I VELTRRAHNPLLVEAGLTDKI VI VPW
LOGKSLHI GLG

>2617922302 Ga0073689_1803 tryptophanyl-tRNA synthetase [pelotomaculum Ga0073689 : Ga0073689_180]

MRVLSGI QPSGSLHLGNYFGMMKRMVEYQKNNELFCFLVNYHALTSVFDG
EQLRRQTFEACDFLALGLYPDKSVFWQSDVPEVTELTWLLSNVTGMGL
LERCHSYKDKTAGI PSSHGLFAYPVLMAADI LLYGGEKVPVKGDKQKQHL
EVARDI AI HFNNTYGETFVAPEPDI DEDVAVPGTDGQKMSKSYGNTI EI
FADEKSLRDKI MRI KTDSTPVDQPKPI EGNVLFDLTYTLFLDERGKETLKE
RFLTPGLKYGEI KKEI FGI WDYFAPYREEREKLARDKRYVVTMRRGAA
KARQVAAVYLD RARRNVGLDYWNE

>2617922301 Ga0073689_1802 Zn-dependent protease (includes SpoIVFB) [pelotomaculum Ga0073689 : Ga0073689_180]

VFNLPSLHSMVLMPLAI VLGLTFHEFAHGWAADRLGDRTARNLGRLLTI NP
VAHVDPLGLLLLFLAGFGWAKPVPVNPYNFRGDMSRGMLLVSLAGPATNM
I LAVASAVVLGVFAGFRLPYFREI MLYMI QI NVVLAVFNLI PI PPLDGSK
I LAGLFPGRQNWLYQLETYGAII LI I FIFTGVI GYVFKI LVYPVVKLLLS
FASLI SYLYFK

>2617922300 Ga0073689_1801 tRNA nucleotidyl transferase (CCA-adding enzyme) [pelotomaculum Ga0073689 : Ga0073689_180]

VEI I THTNTDLDALASMVAQKLYPSAVMVFPGLSRNVEEFMALHKDA
LNVKAVRDI EPELVETVVLVDTKSPGRLARLAELLEKSGVEVHI YDHHPR
GEGDASGKVEVEMVGATTTLLVEKI REHGLELTSMEATI LALGI YEDTG
SLVFSSTTPRDAEAVAYLLARGANLAVVADFLGRPLTEDQRALLKELLVS
AERYQI NGI KFLI ARGNMDEFVGGALLTHKLADFALHDAVFTVVMEDR
I HVARSSVPEVNVKEI LGVLGGGGHPAAASATI KKAHVDEVTEQLLEAI
RSNVRSPVTTADI MSSPVKTI TPDTVI EEAGRVMLRYGHTGLPVVEGERV
LGVI SRRDVEKAVHHGLGHAPVKGFMSNLVTVGPDVPVSAVRELM EHD
I GRLPVLKNGKLVGI VSRTDVLRTLHGDVQSRHQKVYTGHCYEI SYKNI L
ELMHRGLPAEQMKI LERTGEMASDMEYRVYGAGGI VRDLI LGMECLDI DL
VVEGDGI ELARALGREYGGVRRI HPKFHTATVLPNGQQVDVATARVEFY
QYPAAMPQVETSSLHQDLVYRRDFTI NAMAVSLNKDDFGDVVDFFGAREDL
ERGLI RVLHNL SFVEDPTRLRGVRFENRYQMNLEHQTLKLAKEAI RNKM
LTRVSAERVWEEKHI LLEPRPGLALSRLMELQLWEFLFPGVDHFNI RQV
I VEMPRSVKTLRSWDLAEPGEPWMVYLLAVLHRTDWDSAVRI CRRYHLGR
HQEKVAAAALGGWRSAMEDLRNPDGI TMSELARQLMSI PREYVPLI LTYL
TENASRRRFROVFTAI YYDRPSI NGKDLRAMGYKPGPAFKRALNAVWQAR
LDGLVTRTQEELDYVREYLAGYEGAI SSV

>2617922299 Ga0073689_1797 protein of unknown function (DUF2383) [pelotomaculum Ga0073689 : Ga0073689_179]

LNTLDKLQDALQGEMMQSMYNMHMMDI ANPEVRQLFTQMRDAKMQNVTO
LQOEI QKMMQOGKTS

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>2617922298 Ga0073689_1796 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_179]

VLTDQERMNNALKEMLFHEESMAKKYAQLGQEI TDPKMQMLKGMEMAAR
NNYGTLSQKMTSLGI V

>2617922297 Ga0073689_1795 Uncharacterized membrane protein YcaP, DUF421 family [pelotomaculum Ga0073689 : Ga0073689_179]

MEDLASI FGSMQKLSSTGFI I RTLAVGVI LYFASRFLPRRSGGQYSGYDF
AFFWMMGGLVASPLFDSKI SFDSVLI AAGTI YALHYLI SYI MVKSRTMSR
I I GGMAI PLVMGGKI LRQNMKALFPI ELLLSGI RQADAPSLAELEVAVL
ETNGHI SVLKKPNFQPVTPKDLKI ATVEAGLPVLLI NEGRVI VENLRKLG
YTREWLDGELHXYGI LNI ADI YMASLDGTGQLYYSVQTD A

>2617922296 Ga0073689_1794 Uncharacterized membrane protein YcaP, DUF421 family [pelotomaculum Ga0073689 : Ga0073689_179]

MEWQAVFNGAKEI PLWGFVAVRATLLYFALI I GI RWMGHREVS I LAGHNYL
VAAGI MSAAVRMVAEASLTAALLI VFVYSGVNVLYSYLDI KWPRAI DR
KPMI LI ENGQI NKKNLMDTHVTI DNLLGQLRLKGAHNLSI NYAVLEPTG
KI SVI KKSATLPVTRQMMNLPAKFDALPTLLVHDGQVDEENLNLGLDLN
WLKTKLAKEGFGRFEDVFLAALQPDGTI YVSA

>2617922295 Ga0073689_1793 putative copper resistance protein D [pelotomaculum Ga0073689 : Ga0073689_179]

MEKI LHSI SGSLHI LAAVTWI GSMI YSMFAMAPALKHLGTPRANAI NMI A
AGRFSPLTWASLVVLI I TGI YAVSGNVDKLSPLFGQPAGNVLFVKLLLLVA
ALI VI LLFQI YSLSPQMKKI I NPATPKDQENTLEMARADNRANFWSWTHL
I VGI TVI I LAVI LSELLQK

>2617922294 Ga0073689_1792 geranylgeranyl reductase family [pelotomaculum Ga0073689 : Ga0073689_179]

MPHDVI VVGAGPAGSSAAYHLAAAGRKVLVLEKDNFPRYKPCGGGI SLKA
VPLLDGFWQSTVESI PRAI LFSYHPERQFRVEVEKPLVYMVMRDRFDALL
ADRAERAGAEI KYGLPVEEVSVERGGVTVKTDGNSYRASYVLGADGAAS
KVAKSLNLMKGRLFGAAVAVEI QLEQGAPARHDEVI KVDGCAVPMGYGWV
FPKAGRVSAAGVTYRKGVNQLNQFADQYLTQEGLANGVI LRQGHLLPADGG
KKNAPTAAHRAAGLLGDAAGLADPLTGEGI YYALKSGALAAGAI I QKDNPQ
VTALYRERI RQSI FPELSAAGRLAALFFRFTGI VFKLLQI NPGLARHFTD
AMFGDINSYRKFI AEHKFLKVI RETSVN

>2617922293 Ga0073689_1791 cyclopropane-fatty-acyl-phospholipid synthase [pelotomaculum Ga0073689 : Ga0073689_179]

MQKALLDEMFSRLPEGAI TVQYWDGTNKQYGEQNSLFAI HLMRPLSGLKA
AKDPVLALGEAYMDGVI EVDGDLTEVI RWAFSNQNMPLPASPSGKLARRVL
AKI NKPASLAQKKDQVQFHYDLGNDFYALWLDETMSYSCAYFHSPEDTLT
QAQLQKI DHTLKKLELKPGETLLDI GSGWGWI I RAAQEYGI KAMGI TLS
EEQLKETKRRI AELDLDQKVEVELMDYRVLAESGRTFDKI VSGMFEHV
QANYPOFMLTLKLLKEGGLTLLHTI THTKGGPVNSWI EKYI FPGGYI PS
LREVI WLLPDYDFHVI DLESRLMHYAMTLDRWAEGFEKHVDEVREMYGDR
FVRMWRLYLRSAAASFQVSGLNVHQI LFSRGLKNNLPLTRRHLYT

>2617922292 Ga0073689_1787 Protein of unknown function (DUF3732) [pelotomaculum Ga0073689 : Ga0073689_178]

MKLVI LKLI I WPKDTKKSPRI LDFKPASI NLVTGASKSGKSAVLEI I DYC
LASSDCSI PKFGPI RRSSWYGLLVDTSSEGEKLI ARKDPDDQNSTDEFYL
SEGRSI EI PSLI TKNTNRDI I KAMLARLAKLPQVDSDFAEATGSGYKKGKPS
FGDMKAFMFQPOPI VANKYTMFYKTDKEEHARKLREVFPVLVLGVVDADTL
I I QHRLREVRI LESRRRKLESI KMALRDFAGEVRGRI VAVELGLI EGD
SNSVNDVDI DVLLMLRKDI VSNWYENLLAFQSKDYAI SSERFSFLKAKES
SLASQLTALKI RLTLRELTMARSI SESNI SRERDLSSI SWLTEKLNDP
YVCPPI CGNHPI SFNDELENLRAI HRSVESLWDGI QVI PPMLDAEEVQVRK
EI SSI GEELRQVQFELDTLTKETDKKKLVKQQRAI FI GRLEEFDFQKTI
DDGSNLVDEI KELEDEEKDLLKLVDFSVLAERKESALFLI SKFAQLYGNL
MELETGDDLI QLDTSKLSI KVI SKNGQSAWMWEI GSGANWLGYHVSTLSA
LHEFFVNRLSPYPVNLVLVDQPSQTHFPDDEDEESEFEFFDAVRRRAVTF
SSAI DRTNGALQVI VSDHAGSRVVENI LNANI VERWRKGRKLI PWHWDEQ
LLLDLKGSKADFALEDLLESI VKPRI SDHFGLFDESTI I QLLI NSAVFTE
LGI KFNLKI KGTFEVEVPDSI SGLVDHNLNVHI EKG

>2617922291 Ga0073689_1786 hypothetical protein [pelotomaculum Ga0073689 :

Table S2

Ga0073689_178]

MKTAVFHEFEI MQNSVLGAHVLWAFADGFSSVDKNYKNELTLWHLI TVLP
LVFHEVSRRAI NKRRVSSGLRAI LDRDPEI DVAQNEAI FNLASRI KNLQE
RSFRSLNRAI ALGFI EI TEGYFI PSKRLKLPREMNLETKQI I KSSQKLG
WAGQLSI FEYLTILGVKP

>2617922290 Ga0073689_1785 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_178]

MYLVENNLPITI I KEDFDREVRALI RRI KVAPLTSI ASPVLDPNLQDFE
I AGFVEQLDWI ESETLI REAI I HYI QARDTRI KWTGDVSEESLDMYF
EDLI SRWRRVQROTARRSWATLEI QGQECLEDTLSEDTI LDGEPMPKAI S
CGNFHVLADFAPNKQPTI GWHPKFMELANKKKR

>2617922289 Ga0073689_1784 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_178]

METRKNHSAYGQALGYI YQFDRATYRLLSSGI SVVAVGI EHVDDVSVHFE
DGQTI REQDKLTTVAKYSPLSDNSI ALWKTLLHI WAEFFGANLSLLDI TEF
HLI TNGKVSDESI ASRLGRAI EMEDCI KI AEELTSKANNLRENLAGYGKT
I SNLSI ESLARI I SRI FVFDNVSPKFGGI WPQFNLCVI SQI LRKLAFILK
LVVG

>2617922288 Ga0073689_1783 protein of unknown function (DUF1413) [pelotomaculum Ga0073689 : Ga0073689_178]

MPDVNELLNFAI QETENLNQDEVFLI RDLFKGYEWNRI SRSQRLLLGLTF
LNYVNTSKDFI QAI EKTSSGQKYRI KI NNGQLYVAT

>2617922287 Ga0073689_1782 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_178]

VKNQEYYGQLFEPYPDVVTLDDEFAMLGGI GETTARKI LHGKHI KYFFIR
SAYKI PKVWVI EYVLSDHYAQYRQELKVQV

>2617922286 Ga0073689_1781 Phage integrase, N-terminal SAM-like domain [pelotomaculum Ga0073689 : Ga0073689_178]

MAKKKVATVKKELPGTWQEQALQDFLFWKQAQGLSERTLTDRKHVSQFFN
RYPKAYNSKNLKSAVLEYMAQPVKPAFNLRLI NLKAFFDWC I KEGI LTE
NPLVDFKRRKAEGRVVNI EEEKLARLLTLPNWI RYDLREP KTI PMLPK

>2617922285 Ga0073689_1776 translation elongation factor 2 (EF-2/EF-G) [pelotomaculum Ga0073689 : Ga0073689_177]

LKNYQTGOI RNLGVVAHGGAGKTSLEAVLFNTGVLSRLGRVEDGTTVSD
YHPEETTKQI TI HTSLVPCEWNGVKI NLLDTPGFSDFI GEVKGALRVADA
AI FVVSADVGVQHEVI WDLADGYELPRI I FI NKMDRENANFEKVLDDL
KTKFKASFVPQI PI GDFDTFTGVVDVI NEKAYTGDGKGEETAI PSDLAG
EI ARYREQLI EAAAEGDDMTMKYLEGEELTREEI KDGLKKS I DRGKVI P
VLGSATKNI GI AQLLDVVVNYLPAPAEESGPMVALVFKTI ADPYVGKMN
FLRVFKGTLKSDTVVLNSTKEKNEKI GNVLYVRGKNTVQTDTPCGDLAV
VVKLQDTGTGDTLCKDKPAVLEGI DFPVPTFTVAI APKSKNDEKLGDA
I SKI LEEDPTI RVEKNTETKQTLTGMGELHLNI MVEKLKRKYGVDDVMN
DPKVPRYETI KSKVEVEGKHKKQSGGRGQYGHVWI RFEPNPEEDFVFTEE
I FGGSVPRQYFPAVEKGLREAMVEGLAGYPTTGI KATLYDGSYHTVDSS
ELAFKI AASLAFKKGAAQAKPVLLPEI MSVEVVVPDNFMGDI I SDFNTRR
GRVLGTESGKNTVI KAMVPLAEMYRYAI DLKSMTQGRGSFTMEFSNYEE
VPARQAEI I KKAKAAAEAEK

>2617922283 Ga0073689_1774 D-alanine-D-alanine ligase [pelotomaculum Ga0073689 : Ga0073689_177]

MAPKVGVLMGGRSAEREVSLRTGEAI YNALKTGYPAVKI DVGFDVVEKI
KEEKI ELAFLALHGKYGEDGTI QGMLEMLDI PYTGSGLLASALSI DK I AT
KKI LLLLEGLPAPRYMLVERGEAEVVGLEVKAGQI EREMGLPVVVKAPTQG
STI GI SFVHKEDLVPALAYRYDPVALVEQFI EGVEVTASVLGNDNPV
ALPLI EI VSATGVYDYESKYTPGLSNHI I PPRI PGEQQKAAKELAVRTFK
ALGCRGLARI DFI I DRRGNPYVLEVNTI PGMTNTSLFPDAAARAAGI EFPE
LVDKI VKLVQEKI

>2617922282 Ga0073689_1773 deoxyribose-phosphate aldolase [pelotomaculum Ga0073689 : Ga0073689_177]

MNKTNSEPI I SKQELAGLI DHTLLKPEATPADI KKLCAQAGEFGFAAVCV
NPCYVNI ACTELAGSGTGVCAVVGFPPLGANDPAVKAAEVA AVRAGASEV
DVVI NI GYLKGRLLTAQVQADLGGVVRAARQVRPEMVVKVI LETCLLSDE

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KAEACRLAVTAGADFKTSTGFNKGATVSDVALLKRSVGPGRVKAAGG
IRDLATALAMI RAGADRLGTSSGVAI I SEI KDS

>2617922281 Ga0073689_1772 transposase [pelotomaculum Ga0073689 : Ga0073689_177]
MAI TGKRYDKDFKI GAVKMFEEKGRKTSSVATDLGI SYDTLLRWI KEFSA
DPEYSFRGSGRLRPDEEEI RRLKRENQDLREENAI LKKAAGI FANPRK

>2617922280 Ga0073689_1771 HTH-like domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_177]
MCQVMKVSRSYYAWI KRPPSQRRQDNEELLKAI RRSHLRNRKLYGVRR
HADVKEQFGCGKNRVHRLMKANGI QSI RPRKYKATTNSKHNLPAENLLN
QNFOATAPNTVWSDI SYGTPS

>2617922279 Ga0073689_17610 Methyltransferase domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_176]
MSSYLEAI AALNGSLHPGGFSHTLEI LRRFSI SPEDI VLDI GCGTGRTA
CHI AAAYGAHVAFALDNSGKMLAKAKARAARDGVEVHFI HGDI LDMPFRDE
VADLVFI ESVALI FLPVPSALKECFRVLKRNGI LVDVELLAAESLPPTAAE
QI KAI CGLPQI PTFQEWI GHFKNVGFARAVVRQNRFPGLI DNLKEI LYKD
PHQAVSSELMTNWELSRI LSQYGLI MRNRRLHGFNGFI AQKG

>2617922278 Ga0073689_1769 voltage-gated potassium channel [pelotomaculum
Ga0073689 : Ga0073689_176]
LLSLRPI I SAVLALI LLI SAGI YCLVKLEDKNFFDALWLMVI SI TTVGYG
DVVPSTTTGRVI TMSVI I I GVGLLTYVLSTVFVGVLGHLRDI WGKKRMM
KEI SRLRNHI VVCGAGRVGKEVVAGLLQEKQRFVVI EKDFARLEELRSEG
GVLFI AGDATEDKVLLSAQAPWARGVI TTLAEDAGNLLI AI ACKEFNPEV
RI VARANRPESI VRLKRAGADTVVCPSAI AGNRMTLASLKPASVAFVQTL
VEDREI NLNLEELI LSKNSSLVGKELKDSEI RENFGVMVLAVRRGEESI I
NPGPGKFLPEDLLI LCGPAEGLTRLEKVAAGEEV

>2617922277 Ga0073689_1768 Mannosyl transferase (PIG-V) [pelotomaculum Ga0073689
: Ga0073689_176]
LKRVAIYI LNKLLI VFLI WLAREVLGPI LPAAVEGRHPNVVLDLFLHWD
AGWFLRVVGGYDFDSAPFFPLPLMI RLLTYI TGNGVVAGFLI SNTAFF
I ACYLLYRMVRESYGGIEI ATTTVFI MLFFPTAI FFTSI YSEAPFLAFTLG
AFHFARRGRWFPVFLGACAALTRNVGVVLFFAFLYMQYRDNGRRLELKG
ALPLLFI PASLTI FMAVLWKYAGDPLAFHSLNSEYWGYPHFTYPGAGQF
LNLSLFFKDSQFYSLFESGMAFLFLYLVI RSFKYI EDRSLI FLVLGFLI
PFSSVDNLPLGMPRI I VLFPGYI TLARLLHKNDLVQVYSI I SVFVFSV
I SVMFI VGRWIS

>2617922276 Ga0073689_1767 Putative flippase GtrA (transmembrane translocase of
bactoprenol-linked glucose) [pelotomaculum Ga0073689 : Ga0073689_176]
MFTENVLQLCKFAAVGCMNTLI DWAVYFTI LKI FPAESTLFYAAAKGFSY
FCGI I NSFFLNRCWTFKSGPATCEGVRFVKFAAVNALGLI NSASI YVFL
TLDLNHTVALFFATSI VFVFNFTLSKLWVFRKGMVAKTTGG

>2617922275 Ga0073689_1766 Glycosyl transferase involved in cell wall biosynthesis
[pelotomaculum Ga0073689 : Ga0073689_176]
MKKYPI TI FFPCYNEEQNVERTREALAVASGI SDDYEI I I VNDGSKDRT
AEI ADRLAGENPAVRVI HHEVNKGYGAAALQSGFKNATKELVFYTDGDGQF
RLEEI TNLLPLI EQYDI VSGYRLKRRDPFMRKVNAFLWGALVNTLFKI KV
SDVDSAFKLYRRKI FDEI TLTSQALI DTEI LAKARAKGYTI SEGVNHY
PRSAGEQTGAKFSVI LKAFKELFELRNSFSKV

>2617922274 Ga0073689_1765 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_176]
MEWLSRI ALALVI VGALNWLLVGLFEWDLVTALFGGDTLRASSGFSRFI Y
ALIGI AGLYAI TFFFKENAAVRNEDK

>2617922273 Ga0073689_1764 4Fe-4S di cluster domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_176]
MLKKRQI VKI DEDKCTGCGLCVTPCAEGAI KMDVGKARVLSEELCDGAGF
CLGVCPVGALTI EEREAVPFSEEAVEEHMRSQPAAYLEQSCFNCGNSEEK
VALLPCRKGKSLWVCTRCLPALI HG

>2617922272 Ga0073689_1763 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_176]

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MDPRKKDRLQTPETI TSSAEDESSTCSEAEENSCPKSGVSKSGDSASC

>2617922271 Ga0073689_1762 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_176]

MSYQEKGYNSDYRVNI LNNGTI I SI EI TCCGKHI GEMRFKDSESI KCPFC
GTVHSVTI QHNHFHI RPTKPALDEAEPKYSCL

>2617922270 Ga0073689_1761 Peptidase S24-like [pelotomaculum Ga0073689 : Ga0073689_176]

MVGEGI CPGNLVLI HROSGVDFNGQI I CALVNGENTLKI FFKDGEGKI RL
RAANPI YPDI VLDGEGALVVQGVYAGVFKFPAGPGNDLSSSAAGDQPPVN
T

>2617922269 Ga0073689_17511 ABC-2 type transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_175]

MQTDVAI SVNGLEKYYKTLKVLKKI HFTI KRGS I FALLGSNGAGKTTTI K
I LTTLLKPKDGSAQI CGFDVVRQSDQVRGVI SLTGQNAAVDNVLTGRENL
RLI GKLRHLPDANKKADALLKSFGLLLEAADRRVATYSGGMRRRLDLAMGL
LGTSPSVFLDEPTTGLDPQSRI TMWKI I KDLTHSGI TVFLTTOYLEEADQ
LADQ

>2617922268 Ga0073689_17510 Polymer-forming protein [pelotomaculum Ga0073689 : Ga0073689_175]

MHKPDSPDLQGDNLQTI QSPGHFKRTGQPEAVSAKGEREKNQODLRI NGA
GAI SDGCYRQVSI NGAGAI SGGKYRRVSI KGAGAI SGDVECESFTCRGSA
SI NGS LTAQSKI FGVTDLTGVLQ TENLDARGEVKI KGQCNTROLKVEGV
LTI SEHLAAEEVKLRGSLQVDGDCNAETFI GEGNFI I GQMLNVEKI EI SL
HGDCQAKEI GGGSI RVTRRKHI LEPLDKLFHRLI NHPHGLTAEVI EGDEL
YLQSTRAKVVRGKKVYLGSGCEI ELVEYSESCELAEDARVKERKQG

>2617922267 Ga0073689_1759 Protein of unknown function (DUF4004) [pelotomaculum Ga0073689 : Ga0073689_175]

MSKELI SKKDLLALTGI SYGQLYRWKRKGLI PERWFI RKSTYTGOETFFP
KEMI LERI EKI RHLKEDI SLDELAELFSPHPVRDTFSSEELLRRNTVTPM
VLDFVQQQGTTPPWI FSQALYMHVLEQLFTTGEI SREEGAMVLQLLTEH
YPAFSEQSCDLI FLRKMGI ATCCLAPTATPI TFEKSARVI FRLNLAQHVE
I LKGLV

>2617922266 Ga0073689_1758 DNA-binding transcriptional regulator, MerR family [pelotomaculum Ga0073689 : Ga0073689_175]

VEYTI NKI ARLAGVTLGTLRYYNKI SLLTPSARTDAGYRLYSDDEVRLQ
QI LFFI KLDFPLAKI RETLNNPAFDRKEALRMQADFLEKRADWSRRLVTA
TQAGL

>2617922265 Ga0073689_1757 prevent-host-death family protein [pelotomaculum Ga0073689 : Ga0073689_175]

MDTI NMI DYSQNNNI KKGLP EMHI KPSTTI RQDYNGFSKLCHELDEPVVL
TRNGEADLVMSYESFRRMEARI KLQSKLLVAEKQI TEGAQLLEHNEVI A
RI RGKI NAEKA

>2617922264 Ga0073689_1756 toxin ParE1/3/4 [pelotomaculum Ga0073689 : Ga0073689_175]

MPKKHKI KYTPAAVDDMDEI FSYI SQDNI I SAEMI LENI NERI AKLAEFP
NMGSVLSDEEYTI I KRGYRFVVHPYLVFYRI I DNTVI I HRI LHGRRDYL
RALFD

>2617922263 Ga0073689_1755 DNA-binding transcriptional regulator, MarR family [pelotomaculum Ga0073689 : Ga0073689_175]

LSGDKNGGFDI EKSLGFLAKCHQKAFQI FREKLVPHNLTPPQFAVLAFI
WKKDGQSQI QLGTVLEMDRTTI SGVI DRLESQGLVNRHRHPEDRRVFMH
LTEAGRELEHTLPRLSLEANA EVAANLSAKEKETLLFLLKKMRGE

>2617922262 Ga0073689_1754 Uncharacterized conserved protein, DUF169 family [pelotomaculum Ga0073689 : Ga0073689_175]

MKMKSKI AEAVSLRYSVAI VFTGEKTEGALQFKEGRWGCVVAMLGAAAK
GRTAVFDRKTYGCI GGGTGLGFGNTYVNFPGGI EYFLSTGNKEFCESSEM
KHVVRNMPALSHGEAYKKTPELAKSFVDSLPCYDVPTTEYVVFKEPLEELSP
GEKPEVVVFLATPDQI SALVVLANYARHGGDNVI APFSAGCHSI FI I PFN
ERNSENPRGVI GLTDVSARKHVDKDI LSFSVPYKMFLEMEGNVEESFLTR

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DEWLKVRKRNN

>2617922261 Ga0073689_1753 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_175]
MLTAALI DRLTHHAHI LNMNGTSFRLKQRLQKKDVTSDGAI SNSKEEMEA
P

>2617922260 Ga0073689_1752 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_175]
MLNKKPPLFRVDSKRPYRNEPGI TCRCGKEFNDLEDLI I SLDDAGFTFYC
ETCPEI VPRLNPNQYFFPYA

>2617922259 Ga0073689_1751 Transposase DDE domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_175]
MNPI YQEVFLSHLNPI ELLPGFI KKI REI I GQVAYFTI VFDRGFFKGALF
QELQSMQVRVFI TLAKGYKKI I EQLEAI PATHFKELCDGKAVVDTFLHI T
DCDSPLRTI VI KLLDTGKLI GI LTNDQKTHDSELI LRYARRWRI ENLFKD
TNSFLHLNHLPGI DQVKI DALLTI KFI AYSLFNQLRNQLGGYRSMTPE
MFDNLFNKKAYI QLI GGRLVVRFGYFPGQETI I EFRNLQDKLI CNKI DP
QI PWFSGAKMQFLFEDKDGNTRI RS

>2617922258 Ga0073689_1747 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_174]
PGQAVRMMAEAGFHHGREYTVTVALI VLEEI GLLVNRGGEDFLKVGLLPA
PPEKKDLLDAQTYKRLLLLAKEESI TWMRKLLNEPI HRLLDI REGVL

>2617922257 Ga0073689_1746 adenine phosphoribosyl transferase [pelotomaculum Ga0073689 : Ga0073689_174]
MDLRSKI REI PDFPREGI NYKDVSTLLLDGRAYRQVVQELARLCKHKQAD
LI VCPKARGLMI GAPLAYVLGTGLVTLSPKPGKLPGEVFTWHYDFEFGGEA
I EI NREAI EPGMRVLVADELLATGGTAATAI KLI GELGGEVVGTVFLI EL
TGLGGRVKLQDYDTI SLLQYNY

>2617922256 Ga0073689_1745 GTP pyrophosphokinase [pelotomaculum Ga0073689 : Ga0073689_174]
METHAFI TSAEQSSQPGRAKPEDRGGTLKFQDRDTGSPLDELLRKI KI Y
NOKADLSVI FAAYKYAEKAHVEQRRFSGEPFI VHPLEVAKI LAEELDQ
TLVAGLLHDVVEDTGVTLEDI KERFGGEVALMVDGVTCLGQLEFKSKEEQ
QAENLRKMFLAMAKDI RVI LI KLADRLHNLRTLKYHPVLKQVEI AKETLE
I FAPLAHRLGI YRI KWELEDLAFRFKEPENYFGLAEKI SKTRVKREEYI R
SVI STLMSKLAAMGI EADI KGRPKHLYSI YEKMI EQQKDLNEI YDVM
CLLKTVRDCYATLGI VHTMWTP I PGRFKDYI AMPKSNMYQSLHTTVVGPQ
GEPLI QI RTREMHRTAEYGI AAHWRYKEGGRGDREFDKKLSWLRQLEW
QHDLRDAREFMESLKI DLFADTVFVSPKGDVVELPAGSVPLDFAYRI HT
DVGHRCVGARVNGRI VPLEYKLKNGDI VEI LTAKNSGPSRDWNLVKT
SN AKTKI ROWFKKEOREENI LKGKENLEREAKKQGVVDVLI KGEKLLEI GKK
FNLLNLDDLYAAVGDGVVTAGNI LTRLKI EETKTEKKGLLAEEVQI LKAE
VRPAAWWGKPTRGI RVKGI DNLLI RLAHCCNPVPGDPVI GYI TRGRGVS
I HRSDCRNI VSYMRDEKERMVEVAWDKDFREPFOVKLEI NGMDRAGLLSDV
MAVLLEMKI SANWVTARGKKDRAAVI ELVLEI RGLEQLDYI VDKI SRI KD
VYDVKRVSFSG

>2617922255 Ga0073689_1744 D-tyrosyl-tRNA(Tyr) deacylase [pelotomaculum Ga0073689 : Ga0073689_174]
MRVVVQVRTRSSVTVEGRVVGETGPGLVLLGVGCDDTVDDAVYLAGKLA
NLRI FEDEQGMNLSVL DAGGMVLAVSQFTLYGDCRKGRPAFSDASPPE
EARRLYEI FVRELEKLGKLVATGI FREHMMVEI I NDGPVTLLLDSKKNF

>2617922254 Ga0073689_1743 Glyoxylase, beta-lactamase superfamily II [pelotomaculum Ga0073689 : Ga0073689_174]
VI FEGFPVGA I EANCYLI GCEETKEGAVVDPGAEGRKVLKKVEGLGLKI R
YI I LTHGHADHI GALAEVQATGAEVLI HSADADMLTNARSNLSAYVGPL
MTFEGSHRLLQDGD I I KVGNI SI EVI HTPGHTRGGI CLKCGPDVI I TGDT
LFAGSVGRSDFPGGSHTQLVASI KSKLLKFPDPTRI YPGHGPESTI GEEK
HYNPFLR

>2617922253 Ga0073689_1742 histidyl-tRNA synthetase [pelotomaculum Ga0073689 : Ga0073689_174]
MLTMRPRGTSDI LPGEVKKWQRLESFRKI CREYGYDEI RTP I FEHTELF

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LRGVGDTTDDI VEKEMYTFTDRGDRSI TLRPEGTAPAVRAYLEDKLYAGPO
PVKLFYI GPMFRYDRPQAGRFRQFHQFGVEVFGAHDPAVD AVMAMAMDF
YGRGLGLSLELHI NSVGCPNCRPELRRQLQDFFRLYVENLCKNCRDRFAK
NPLRI LDCKEARCGEI GSGAPTTI GCLCGDCAGHFELVRKHLDLLHI PYI
VNQRLVRGLDYYTHTAFEI MAPDI GAQSSI GGGGRYNGLVETCGGHPTPG
I GYALGMERI I LAMERQGLAMPGTAGPAVFVVTAGREAEQAFSLLFRLR
SAGI PADKDYLNRSMSQMKFAGKTGAGYVLI LGEEELRRDI VLARDMTT
GEQESVKTNDVVEYLEKRI HQEGPCDD

>2617922252 Ga0073689_1741 aspartyl -tRNA synthetase [pel otomacul um Ga0073689 : Ga0073689_174]

MI EFMNGLKRSHNCGELRI GHTGAEVVLMGWVQRRRDHGGLI FI DLRDRS
GLVQVVFSPDLHKEAFLKAGAVRNEYVLAVRGAVRERPEGTVPNPATGE
VEVLAHELOVLNQAKTPPFYI EDGI DVDENLRLRYRLDLRRPEMQUEALI
LRHRVAKTVRDFLDEKGFLEI ETPMLTKSTPEGARDYLVP SRVNPCKFYA
LPQSPQLFKQI L MVAGMDRYFOI VRCFRDEDLRADROPEFTQI DI EMSFV
DVDDVLELMEEMVSRLCKETAGLEI PRPFSRLSYREAMERFGSDKPDTRF
GLELKDI SDI AAGCGFKVFSSVVAAGGRVKGI NAKGCCGYFSRKEI DELTA
YAAI YKAKGLAYFI VTGDGVKSVI VKFFSEQELAAI MERLEAEPGDMLLF
VADKPGVVADALGALRLHLGERLGLI PQD

>2617922251 Ga0073689_1736 Uncharacterized protein YqfA, UPF0365 family [pel otomacul um Ga0073689 : Ga0073689_173]

LNAAFI ASLLLI VFVI I GVAVI FSFI PVGLWI SAMAAGVRVGI FTLI GMR
FRRVPPAQI VNPLI KADKAGLNI TVNQLEAHYLAGGNVDRVNNALI AAER
AAI PLPFERAAAI DLAGRDVFQAVQMSVNPKVLETPLVSAVAKDGI EVKV
I ARVTVRANI DRLVGGAGEETI LARVGEGVTTVGSADSHKHVLENPDLI
SRTVLSKGLDAGTAFEI LSI DI ADVDVGRNI GAQLQTDQAEADKRI AQAK
AEERRAMAVAREQEMKASVQEMRAKVVEAESQVPLAMADALRQKGLGVM
YYNLQNLADTQMRDALSKMGENKEGPGPVVPTK

>2617922250 Ga0073689_1735 hypothetical protein [pel otomacul um Ga0073689 : Ga0073689_173]

MEFFWLLI FMVI VFRVLRLLSERYGNNGKFEGPWGGPFGGERPWKRAPN
DEKNESRPKLN I PEYLTRRSGEPAAGEI APGGEKPQPAVLEDVTVVI KPA
AVEKKEPLPLEEHLAGKAVLPGCPRDEQGAAPREHRRRAGAGPLDGLVC
PGEMI KGVVWSEI LGPRGGKGGRCLSVYKLKKP

>2617922249 Ga0073689_1734 hypothetical protein [pel otomacul um Ga0073689 : Ga0073689_173]

LKTFKQVFSPEWLRETAARVGYVQRNRKI DPVTFWFVVVLGFGVGVQRTL
ASLRRAYETASAE TLVPSSFYRFNKGLI AFLKECLAYGI ADLVSHVSLT
LSDKLGFKDLI VADGTVI RLHDKLAEQFPGTRGKAEPKI HTATGI TGND
MGLSMVKAI TRPPANYTDRPRGRRPI SSHR

>2617922248 Ga0073689_1733 Cu⁺-exporting ATPase [pel otomacul um Ga0073689 : Ga0073689_173]

MSGNSAPGSEPPLOKEGKSAKVS LKI KGMSCAACAARVEKGLSRMVGVAS
ARVNFAAESAAVDYDPLVKPGDLVEKI KQLGYDVPSERL EL SI SGMSCA
ACSARI EKKLKATPGVLA AVVN LATEKAPI EYNPAEVSAA DLI NAVI LLG
YDARRAGEESPDREREEREI RQVSLFVFS AVFSAPLLI GMLGMLAPF
EHYFPKLLHNALFQFF ATPVQLVAGYHFYRDSYI ALKNRSANMSVLVAL
GTSAA YI YSTVATFWGHR LGLHHVYFESSAVLLTLI PLGKMLEARAKGRT
SEALKKLAGLOAKTARVFRGGSEVDVPVEEVVTGDLVVVRPGEKI PVDGI
VREG RSTVDESMLTGESI PVDKKEGDQVI GATI NKLGTGFKFEATRVGRDT
ALAQI I RVVEEAQGS KAPI QRLADVI SGYFVPVVI GI AVATFLGWYFFGD
PGNVTRAI LNFTAVLVI ACPCALGLATPTSI MVGTGKGA EYGI LI KGEH
LERAH RVNAV I LDKTGTI THGEPVLTEI VPAPEFAGREEYLLKLAGAAEK
GSEHPLARAVVKKAGNNFEDMGEI TSFQAI PGRGVEAEI SGRAVLI GARR
LMRERGI ELAPGFENVI EELEGRGKTVM LMAVDGLMAAALAVADTVKETS
KEAVAYLRNMGTQAWMLTGDNARTAAAI AREVGI DENRVMAQVLP GD KAR
KVRELREKGLVVG MVGDGI NDAPALAEADVGF AI GSGTDVAI EAADI VLV
RGDLRSVADSI ALSRATI RNI RQNLFWALI YNI I GI PVAALGFLNPVVAG
AAMAFSSVS VVSNALRI KRFKPERLKNVQKS

>2617922247 Ga0073689_1732 hypothetical protein [pel otomacul um Ga0073689 : Ga0073689_173]

MSHERVLKVVDCEAVCEGTLTAVLSMVDVQSRVMQI HLLHDCADI CTLT
AKYI ARYSSFAKHI AHLCAHI CEVCGKHCLMHPDPQSQHCGRVCLDCAKE

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CRAFSGMMTTPMSSPDLSYPDSGCAGI PGMYSPEKKKDEKK

>2617922246 Ga0073689_1731 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_173]

YEERACEQLYRVRPVADGLI NSFI FII FAFSFTPRPTS RDWRSFGAFSAF
I MALFTEMYGFPLTI YLLSGWLGSRYPG LGRVFP

>2617922245 Ga0073689_1727 N-terminal half of MaoC dehydratase [pelotomaculum Ga0073689 : Ga0073689_172]

MPQAVVPTI RWEDLWPGWEAPPTYWAVTPMELVMFSSAI GCDDPVYRDEE
AAKKAGFKTI I AHPGFVNNWHFECAL

>2617922244 Ga0073689_1726 adenine deaminase [pelotomaculum Ga0073689 : Ga0073689_172]

MSMPALKKLRGLI DVAAGRREASI YLEGGMLVNNI SGEI YPANI AI YDDK
I AYGASKKMGASTTVI DAKGFYI CPALI EPHFHPNVGYNPASLAEVAL
CRGI TTI VCDSI FFHTRLGAQGLLKI I KSLENLPI RLFWTARI FYQGATE
TDTNFSETSLRKLFRDPHI I KIGE I ARWPLI VDGNESLLEKI CLAREYNI
GVEGHTAGCSYDRLNAI AASGTESCHEAI TAEAAERLRLGLWTMLRNSS
LRPDLPELI QVI TLMRLHTGRI LFTTDGPSPSFI AREGLLDGMLRLAVKA
GVNPVTALQI ATI NPATYLG I EKEVGS I TPGRHADI LLLPDLENFNPHMV
FFNGKVVAAGKLSVPLTPPDWKEAGLHLNLSPLRELVSVPFLFGVPADK
PKVFPVI NFI SSVI TKQDCLEPHGGFLERKEDMLYCALI DRYGKWVVN
GFI RGLGLVEALATTGTSAFNI LVFGQNRSSMARAAA EVVEMNGGI ALI E
DGQVSFRMPLELGLMSSSPFAVI ADKTNELEKKALKFGYPYNDFI YTLA
FLTSDFLPELRI TTSGI VNI KSRQI LFPAQEI NQLFDKPRA

>2617922243 Ga0073689_1725 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_172]

MPKI VGN I MVQKRGVSLGLLDYMP LNDGDI FQVQLEGDKVI LVPMKLI
PAEQAWFWAEWQKGEREA EEDKAAGR VKSFDNVDDLLEDLDK

>2617922242 Ga0073689_1724 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_172]

MRFQRTERFKRMYKKLDLEQQNAI KKALGLMSDNI NHPSLRVKRI QGVKG
I WEASATMGLRI TFDWEGDTI I LRNCGAHDKTLKNP

>2617922241 Ga0073689_1723 putative pyruvate formate lyase activating enzyme [pelotomaculum Ga0073689 : Ga0073689_172]

MGRGSYLKLAAGELAKRAERAVAMLADCTVCAQQCRVNR LAGELGVCRRG
RRAAVSSHGPHFGEEAPLVGTRGSGAI FFTHCNLNC LFCQNCGI SQEGEG
DEDSPEELAGMMSLQKRCCHNI NLVSPSHFVPQFLEALDVAAAKGLNVP
I VYNTGGYDSPATLDLLDGVVDI YMPDI KFGEDGAGRKYAGAAGYFSVLK
EAVKKMHGQVGDVLDERGI AVRGLLVRLHVLPGNLARTEKVAEFLAEEI
SANTFVNI MDQYYPAYKAFDHP ELNRR I TREEYREALKKAREAGLKRI YT
G

>2617922240 Ga0073689_1722 Protein of unknown function, DUF488 [pelotomaculum Ga0073689 : Ga0073689_172]

LGNDKRKI LCTI GFSKKS MR RFVELLQGAGAQRVLDVRLNNTSQLAGFAK
RDDLEFMLS LVGNI CCLWPDQAI YRRKRDTQARGADDY LNCFSAGDT

>2617922239 Ga0073689_1721 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_172]

MMNLNCGLI GLPMVGKTTI FNLLTGAGAETSNFLTGKTETNVGAARVPDS
RVDFLSGLYRPRKTHAQI QFSDVPGLVRGSSQKG VGNQFLNAI RNVDL
LVHVVRAFVNPDVPHVDDSI EPLRDI ETI AMELLFADLEI VEKRI QRI KS
GKKI KKENLLELAVMEKCLN ALENEVSI GRLELSGEERLT LKNYSFLTEK
PLLLGVNTDEEQFKTSY PGKGELEAHAAARGLPAL EICGKI ELEI GQLP
AEDREMFLADL GVAQSGVDR LARAAYDYLGLI SFFT VGEDEVKAWTI CRG
TDARRAAGKI HSDI ERGFI KAEVVKYSDMESLGSMAKVKEKGLFRLEGKE
YI VEDGDVI NFRFNV

>2617922238 Ga0073689_1719 Methyl -accepting chemotaxis protein [pelotomaculum Ga0073689 : Ga0073689_171]

MKTKMNL YLI AMYLGGLP LMLAGVLI SGI LSPWQVGQALTSPWCLSWI AV
NVGMMLI YFNYYI WPKI DQRQTSGI TKQFFYVQLLFYSTYASVGPI SGLF
NKEWSSAGLLVAGFSLFSLFSFGLPFLI KAQLTLEASVAEPYFAKI GS
LSLP I RGKLGLSFSVLVASVAAMTGAI GVAQVTPQTSI TVTKI LLVMPVV

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IISSLI SVYYLVQSLTETLEPLRKELNKADQQQVNLSI RLPVI ATDETGE
I AYYFNRLMERLGOVMERTROSANRVDVYARELSGI NESAI AAVNKTAVK
TLKMSEFI VKI NDFVESVMNTSEKAAAAGLSNAKSI SENFLAQTENNI AV
SRASESLDELGSTVEKI GDI NFVELVADQSHLLSKKI GQSSGGTQTGD
FRTLVS EIQHRAQSVSSAARGLAGLFKSVQVYTRQASNALKKDQETVLNG
FNAARGTVQSLGLI VELKNLSI VVKEGLDYI KLVSDDLLNI YSI TEEQN
VLLKRYTAAAEALNNVFGEMQEI LANLKT

>2617922237 Ga0073689_1718 NAD⁺ synthase (glutamine-hydrolyzing) [pelotomaculum
Ga0073689 : Ga0073689_171]

LLKVALAQMEVI PGRPDNLNTRTMLEMI AEARRREARM I FPEMAVPGYLL
GDTWEQRAFLQDCESHGRI I EASAGLCVLFGNVAVDWNKTGDDGRVRKY
NAFFVAMDGRHLHGGENFPHTFRI KTLHPNYREFDDTRHFYSLRKLAL ELG
ERVENLLQPVCLNI DGVP I KLGC I LCEGWNDDYAVKPI AVI HRNGPVDL
FVNI STSPFTLGKNNKRNRFVSRHAATTGVPLI YVNNVGI QNNGKT VYTF
DGYSTVYNGKGEI EYCAPFSRELKLLDLKDKGNSHEAVPAPDDRGVD
SI YQALHYGTSSFLNSI GMERVVI GSGGI DSAVSACLYSKI LEPENVLL
VNMPSI YSSQTRGLAHLAFNLGCMYTVI PI QEVVDYTVRQI RETPVTN
LKNGSRFHLVSSSFVQENI QARDSARVLAGLAAAFGGGFTCNANKSEMT
VGYSTLYGDLAGFLAALGDLWKHQVYTLAEYLNEHI YRMEVVPREI ELV
PSAELSPEQEVKDGKGDPI VYPYHDYLFRAFMEHWNRPED I LSWYLED
VLGERI GCRPGLVKQLFPGSREFI ADLERWWKLYTGMATAKRI QAPPVLA
VSRRVYGFHDHREAQNRTYFTARYLEMKEDI LKNGK

>2617922236 Ga0073689_1717 protein of unknown function (DUF4338) [pelotomaculum
Ga0073689 : Ga0073689_171]

MASHYYLGFHSLTGKTLKYVALLNGQWVALI GWGAAALCKGHRDK

>2617922235 Ga0073689_1716 cobalt/nickel transport system permease protein
[pelotomaculum Ga0073689 : Ga0073689_171]

LHI PDGFLDAKTAI ATYALSAGALGYI KKTGKELNDRQI PTMGVLAIFI
FAAQMVNFPI FGGTSGHLLGAALATI LLGPWCSALI STVLI I QCLFFQD
GGLTALGGNI FNMAVVGTLVALGI YQLI RLAPGGKGEMI GI FTAAWASV
VAAAFFATVELALSGTFPFKI ALGAMLGWHVVI GEGLI TAATVSFVRK
MGFGGVQQQGQAEKEVY

>2617922234 Ga0073689_1715 cobalt/nickel transport protein [pelotomaculum
Ga0073689 : Ga0073689_171]

VKKPAI I FLLVVLVVAFLSPFASPNDGLDRVAQDLGAEKSEGREAI Q
SPVPDYKFPGI ENEAVATSLAGI AGTI LTLGVALGLKAVSKRNKTTG

>2617922233 Ga0073689_1714 formylmethanofuran dehydrogenase, subunit E
[pelotomaculum Ga0073689 : Ga0073689_171]

MCMEKTDWERA I EFHGHSCPGLAI GYRVAKI ALKELDSLRSAD EELVAI V
ENDACGVDAVQALTGCSLGKGNLI FRDHGKQVYTLACRNSGRAVRI AVR
PARRSAPEFGELRKKVFGGI ATEEEQRFYQKLQHERI QQI LELPEEDFCE
VRHVNLA PPPKARI FNSHPCAECGEPVMEPRARVKDGKI VCI PCAESYSR
GW

>2617922232 Ga0073689_1713 pyrophosphatase PpaX [pelotomaculum Ga0073689 :
Ga0073689_171]

MVKTALFDLDGTLI DSLPLI KATYQRFVETMEI PWDDGRVMESI GLPLI R
I AEQFAGNQADCFYKLYLKYQENHGDYI KLFPGTFDALNKI KSKGYTI G
I VTSKRRETAEEAI ESTHI EPLI SALI AFEDVKAHKPEPEPV LKAMNFLT
AAPEKTVYVGD SWYDI MAGKSAGVATVGVTWGMADRLKLQEHKPNRI I DC
WDELFHVI S

>2617922231 Ga0073689_1712 DNA-binding transcriptional regulator, MarR family
[pelotomaculum Ga0073689 : Ga0073689_171]

MLMYAGDNLVLSLGERMLVSRANI TGLVDRLERDGLVYREADPODRR
SLRAKI TPKAVSLLQRVAPVHGFEFTAGVLSALDRRDKETLI ELLEKLQSG
LSKF

>2617922230 Ga0073689_1711 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_171]

MKCARCGEDLAADDKFDFYQGI LCEDCYI GAVQPPRSCDPAAVSSAVATR
QQLGQKGTEGLTKLQDI YRFVKEKGRVPREELAPAFNMPQWEMEKQI AV
LRHCELLRGFKEGDKVYI TLM

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>2617922229 Ga0073689_1708 Fe-S-cluster-containing dehydrogenase component [pelotomaculum Ga0073689 : Ga0073689_170]

MAKIKKKIKTIKVDADKCNCRACEVICSASFHATPKYSSNNPARSRIQVISHRLKDIWLPVFAGEYTPAECMGRDKYVIDGKEYDECFCRAACPSRDAFKEPDSGLPLKCDMCEDDPPQEKPLCVQVCLNDVLIYEEREEEEEEVNLG
GIEMGLKPLVDKYGLDKLADTLARI

>2617922228 Ga0073689_1707 aldehyde: ferredoxin oxidoreductase [pelotomaculum Ga0073689 : Ga0073689_170]

MRYAETGYNLEIDLATGNIKVVETDPKLMELYLGGLGTNVKIHWDRVPPEVKAADPENLLIFSNGLLCGTPAFSANRTLATFISPQTDLLAYPMMGGFWAAELKYAGYDKVIRGKSPKLIYIWIHNDKVEIRDASHLKGKGALETQDLIRDELKEPRAQVAAGLAGENRCFTASIEQSRSSASRGGGAVMGDKNIKAI
I
AVRGTGDVYLARGAEFMEHMKGVTEYINFRNANPLPGVMTILSGIGSPQEMKHTDEKWHTEFSAWGNARTRRKDFWTKEIEESWKKSQLSAVKRLISCFNCPQQCGALITYQDVPRYMMKCFSKLTYIMAAKVDDLNTFTWRI
CQRAFEYGLDSFSTPQILAFAVELYEAGILTDAFAGCPSDKEGRFFWLLDRVARREGIDVLADGTWYAARKIGKGAEKYDHNTIKKHEQMNIKLGMLDPLYLMLFSTNEKISIPQIEGNWPPQAPFPSREDRESFVKDWPQLPDEKFKQYFLDWEP
RGENANPPYYPTPEISSEIVDWMEMLHNI
DDALGLCAGMASFCLKPPYHIH
NYPKLI
SAATGMDLDEDGLKKIVNRSRNLHRAFNNRRGLRRADEKPPEDH
WKRRFPELEEKLLTTYKFKGWNVDGIPTKERLHELDLNYVAEDLEKRGILKDGQD

>2617922227 Ga0073689_1705 4Fe-4S binding domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_170]

MKLRGVIGLELVKLKIDQKEIGVPVGTTLNAAEQIGIYIPRLCHDPDLSALGACRLCVVEIEGMRNLASCVTAAAPGMVVRTNSPAVVEARRTVLELL
IANHPLDCLTCEKTGDCKLAEYCYEYGVKESPIGEKHSYAPDDSNPFI
VRDPDKCICGKCI
RACAEITGKDNLDFAIRGFNTKVATFGDTSYLESDCVFCGNCVSVCPGTGALMEKQMRKARRWELQKVKTTCPCGTCGCFELCVKDGKVVGVVSNPDSVNGRALCVKGRFGWDFI
YSRRRLTTPILIKRNGEFIPASWDEALDLIAARLGDIKEKYGPDSFAALSSARCTNEENYLLQKFTRVVMGTNNMDHCART

>2617922225 Ga0073689_1703 formate dehydrogenase, alpha subunit [pelotomaculum Ga0073689 : Ga0073689_170]

LVGTNTTEAHPVIGYKMRQAARRGAKLIVVDPRRIELAEAEADYWLRLQPGTDIPLNLGLMHI
IK
KEGLYDKTFISERTENFEALKETVEKYTPDYVFRILTGVVDDLYAVARLYAKTDKAMIFYTLGITEHICGTNNVMSIANLAMLTGHLGRPGTGVNPI
RGQNNVQACDMGALPNVYPGYQVRVTDPAQAQAKFQAAGVSLPAEVGLMIPDMFDEANAGELKAMYILGENPVLTPNSNHIRSGLDKLEFLVVQELFLTETA
EYADVALPAASFAETDGTFTNTERRVQVRKAI
EPLPGLANWQIMALGEKMGYPLRYRNPEEIFGEIASLTPSYAGISYARLEEKGLQWPCPTCDHCGTPYLHAQCFVRGKGLFQAI
DHI
PPAELPDREYPFLLS
TGRI
LYHYNVTTTPYSAGIQSLWSEERAENVPPDAARLGLDSGSKVKVTSRRGEVVTQIVQTDVRVPPGVVWMSFHYKESPTNVLTSHAVDPI
TKTGEYKVC
AI
KIEKI

>2617922224 Ga0073689_1702 Probable molybdopterine binding domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_170]

MREVPI
TEAVGLTLCHDITKI
VPGREKCRAFRKGHVI
RSEDVPLLRDLGKEHI
YVWEPEPGLVHEDEAALRLARHAAGPGLSWDEPNQGVNLI
ATRDGL
LKVSADRLALVNNLEGVAFATLHNNRVVAKDQVAGTRI
PLTI
QRGILE
EAESFCSRPAPLIEVKPFQPFVWGVVTTGSEVYEGRI
RDGFCGVI
RRKTV
PLGGRLLGQVIVPDDPDYIALEIRRLVTEGAELVLVTGGMSVDPDDVTPAGI
RATGAEVVFGAPVLPMSFMFLAYLGHVPVCGLPVCVMFNRRTIFDLILPRLFAGERLSRGGITALGHGGLCQECDCRYPACSFSGKTT

>2617922223 Ga0073689_1701 MoeA N-terminal region (domain I and II) [pelotomaculum Ga0073689 : Ga0073689_170]

LLSNIQVEKAQELLLGFAVPLPGETVPLLQALDRI
LYRDLFAGWDLPPGP
RAALDGYAVREEDLGRCENYTITERLNGEVPAPHLPGPRASGVVTGGPV
PDGTGAVVPRELTRVECDRLLLTAEISPGDNI
RQSGEDFQAGELLARRGF
RVDPLGILGILAAFGQSEAPVYRRPRI
AIFSPGSEI
PCQVTPGAGQVRDS
NGPLLAAL

>2617922222 Ga0073689_1696 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_169]

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MTREYGTSA RTFKSALI WAVADSDTALKEEARKALAWEDI QSEKDELQLD
 EAQKRQLAENLKKAAQRLKECVWRSYKNVALLGKDNAVRVVDLGLVHSSA
 ADTMVALI LNRLRODGDVEEGI SPNFLVRNWPPAFHEWSTKSVRD AFFAS
 PQFPRLLNPESI KETI ARGVSGEI I GYVGKSGAGGYDPFYFSGSLAVSDI
 EFSDDMYI I TAE EARKHI EPPTLASVEI SPRNVVI EPGKKQAF TARGLDQ
 HGREI ALTDPAWRATGSGI DRDGVFHAGQDEGSFVI I ATAGTVSGQARVS
 I AKRGI I PTPPEPPRPPQGI TKLLWSGEVPHQKWMNFYTKVLT KFTGGNG
 LKI AI NI QVEPDGGI SQQKI EETKVALRELGLSDDVEVY

>2617922221 Ga0073689_1695 Protein of unknown function (DUF499) [pelotomaculum
 Ga0073689 : Ga0073689_169]

MALKPWNKVTPREDLREGKPLDAAEFVHLDQVRDGRAPKDYQQPERFF
 ERTYLTQNLTAAGVI RRLSGI RTETSAI FNMTTQFGGGKTHALTLLYH
 LAKNGPSANNWVGVDKLLARAGVRSVPQAATAI FVGTEFDSLVRGGNDG
 TPI RKTWPGEI AYQLAGEQGLALVVEHEKQMI APAGDMLRRLLPKGKPC
 I LFDLMNYVSRNRKSGLAAQLYNFLQNLSELARGEDNVVLAVSI PASEL
 EMTAEDQSDYDRLLKLLDRLGKAVI MAAGAETSEI I RRRLFEWDPRVTP
 DGRVLLTRDALQVCNEYADWVVDHRQQTGPWFPI DHAREFAATYPFHPV
 VLSVFDKRWALPRFQQTGRGI LRLALWVSRAYQEGFKGAHRDPLI GLGT
 APLGDPLFRAAVFEQLGEPRLEGAVTADI CGKKDSFAVRDLKEAVDTI KK
 ARLHRKVATAI FFESNGGQLRGEATVPEI RLAVAEPNLDI GNVETALET
 ESSCFFLSVERNRYRFLSPNLNKLADRRANI QPEKI DERVKSEVQKVF
 TEANNI KPVIYFPEKSSQI PDRAALSGRTVTGGSFYAG

>2617922220 Ga0073689_1694 Adenine-specific DNA methylase, contains a Zn-ribbon
 domain [pelotomaculum Ga0073689 : Ga0073689_169]

LKRLI EVDLP I KRI SAHARREKSI RHGHI STLHI WWARRPLAACRAVLCA
 ALWPD PADPLCPESFRKTARDLMKKWAKEYLGLLGAESYRRFVGFQKKPG
 RLEDNEELRKALLDFI ADFANWDNSTRAEYLET SRALTMAAHESLDGLPG
 TRPLVVDPFAGGSI PLEALRVGTDAFASDLNPNVAVLLNKVVLEYI PKHG
 RRLAE EVRKWGEWI KKEAEKELAEFYKDPDGATPI AYLWARTI I CEGPG
 CGAEVPLMRSLWLAKKGRSVALRMAPDPAVKRVDFEVI HNAKEKDVAGG
 TVRRGSATCPVCGYTTPVASVRRQLKERRGGATDARLYCVVTRPEQQGR
 FYRLPNERDI EVSLKATDELERRKQI LKESLSLVPEETLPI MSGVFNAPI
 YGHNTWGSFLTTPROALALTTLRLTRKASNKAESGCGSTELALAI RALLA
 LSVDRVAVRCTAQCI WDVTTQCI MQI FNQGQSI PVRFEFAEMTPMTDEGS
 GWWNTLLYYDKVI DHGAKI KSPGHVEQASAHHLPLNDVATAYI TDPPIY
 NAVPYADLSDFFYWLRRALKEDYKDFFAMELSPKDDEI CEMAGWDPERY
 PHKDSFFFEREMCKALSEGRI LQPNGI GI I VFANKSTSGWEAFLQAMI D
 AGWI I TGSWPI DTEMKQRLRAQNSAALGSSI WLVC RPREEQDGLRTNNI
 GDWRDVLQELPKRI REMWPRLAAGVVGADAI FSCLGPALAI FSRYSVE
 KASGEQVTLKEYLEQVWAAVAKEALNMI FEGADASGFEEDSRLTAMWLWT
 LSTGTNGNSKTGLADNDDEESDDEENVSSSKQVFGGYI LEYDAA

>2617922219 Ga0073689_1693 Predicted nuclease, contains PIN domain, potential
 toxin-antitoxin system component [pelotomaculum Ga0073689 : Ga0073689_169]

MSTLLI DEDMPSTGKVLKTAGFTI I DVRDAGLRGFPDHAI LAFARDNK
 ATI I TADVGFGSLVYLSNVEHFGI I I LRLPVETPVRKI NETLVNALLRI P
 PDEVAGSI I VI DRQKI RI RRRK

>2617922218 Ga0073689_1692 Uncharacterized conserved protein, DUF433 family
 [pelotomaculum Ga0073689 : Ga0073689_169]

MQEI SPGI I VDPEI RGGKPI KGTRI PVDLLVGKLAGGAAYEEI MQEYDL
 TREDI FAALKYAAKLLSEEQVKVI

>2617922217 Ga0073689_1691 protein of unknown function (DUF3883) [pelotomaculum
 Ga0073689 : Ga0073689_169]

LSGCRKTCGAVFFDLHCGI PSRLDVFSAAI RDGRGHTLHRI FVVQTDI N
 GTLSVRQPTI FLDLI PTTNGKAVPDDAGLPGRDLVEQVLI EKALQPFLAE
 NI AQRGEEI ETI SRHLEI SLNELI QRONI RMAELLESQQAEEQNPLLAAN
 I KTTEDRLDELFGCLERRREELEQERHCSI AGI QHHGRAWI LPHPERTSP
 GI SPMVRDEI EQI AVQAVI AYEKARGWHI ESVEKENRGFDLI SRKPHPE
 DPKTAVEVRFI EVKGRAAI GEVALTANEYKTADRLKKDYWLYVVFNCVSL
 PEI YPI QDPARLGWEPI MRI EHYFLGTEQI LALNR

>2617922216 Ga0073689_1689 diguanylate cyclase (GGDEF) domain-containing protein
 [pelotomaculum Ga0073689 : Ga0073689_168]

MVLYGI QGDI TERKEAEEQMKYLSLHDPLTGLYNRAYFEQEMRRLDKGRR
 VVPAGVVMCDVDGLKLI NDTLGHSAGDQLLKI AAGVLRNSFREEDTVARV

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GGDEFVALLSDCNRAAVENACRRLREVI DGYNAAANPVFPLSMSVGFAFRC
NLTKSMDDLKFEADNDMYREKLYRROSSRNAI VQALAKMLVARGFI TEGH
AERLODLI ESLAAAI GLPSPKI SNLRLLAQFHD I GKVG I AERTLFKRDPL
TPEEI TEMQRHCEI GHRI AHSAPDLLPI ADLI LKHHEWWNGQGYPLGLKG
EEI PLECRI LAI ADAYDAMTNVRPFRRAKTRRKAI AELRRCSGTQFDPLL
VEKFI GI I EKSTEI KPSESD

>2617922214 Ga0073689_1687 Site-specific recombinase XerD [pelotomaculum
Ga0073689 : Ga0073689_168]
MVTGHLREKNGYFQMI LTYKDMNGKRQTKSVSTGLPLKGNKKRAETLLWK
TRQEFNPDTAMSDKNMLFADFLKKWLQEV I NRVDADTYALYAYDAKTFVI
PYFKDTAVTVAKI KPGDI EGYQYERTEKNAI KTALLOQYHEVI REALAYA
VELELI RDNPADQVNPI TGEVRI LFTDFLLEWLEMTKHNVEMTTYASYAM
CI KSCI I PYFKDFRLTLKDVTPKHI QDYYQYELNEKGVSACTVI HRHANI
RKALQYAFKVGLI AFNPADRI ERPKTTKFVGS I YDAGELEALFAI VKNKP
I ELAVI LGAFYGLRRSEI VGLKWDI DFEKKTLLTI KHTVTEVRVDGKAI I
VEKDRTKTKSSHRTLPLVEPFELLRRLKAEQERNQQVCGKAYCREYI GY
I YVNELGERI KPGYVTQNFALMLKNHGLKKI RFHDLRHSCASLLYANGVS
LKEI QEWLGHSDI STTSNI YTHLDFSSKVASANAI I GVYPS

>2617922213 Ga0073689_1686 Helix-turn-helix domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_168]
MSKTGKNNKRLLPFPVI TAASGGDI DAI NKVLKHYEGYI I ALSTRRLYD
EYGNHLFLDEELRRI LETRLI TKI LTRVA

>2617922212 Ga0073689_1685 RNA polymerase sigma factor, sigma-70 family
[pelotomaculum Ga0073689 : Ga0073689_168]
LAKLFVTDEYFKDAYI FHVLGHD I TVSDEQI AEALNALPADRRDI I LLAY
FRDMADKEI AERLNLVRRTVAYRRTSTLQELKKFMEENFYE

>2617922211 Ga0073689_1684 ABC-2 family transporter protein [pelotomaculum
Ga0073689 : Ga0073689_168]
MTNI LKSDLYRFGKSKLFYGI AAFTFI I AFLLI MLMRQDI RLGI SI FGDL
TAFKQI DDI I RI GI AYQKGLGI LVAVLI SVFI GOEYQWQTWQQKWMTSKN
RI FI YLSKTALSSAVSAI FLI FOI VALLSSGOI QEMLTPNYAGMMI SGV
FI YAALGSVI CLLSMLVKSSTASI I VCLGYVLFSETLVSVI KNLSSFSNT
AARLVEWGAQHSI YGMSSI VSGASVSTGLAI TI LI NSLAI MLLSTSI GLV
I FRKYEL

>2617922210 Ga0073689_1683 ABC-2 type transport system ATP-binding protein
[pelotomaculum Ga0073689 : Ga0073689_168]
LNHYI LTAEHI QKKYNGNTVLRDVS I HI KKGEI YGLTGKNGSGKTTLFRI
LTGLI PGYNGTVSVGEVGVQSKVSAVI NSPALFLNLSAFENMKAQAFLL
GMCDDSR I EQALKTVGLEDCRNKLVRDFSQGMTQRLKLG MALL ENPDI LI
LDEPVNGLDPDGI AELRELLHLNHAGGMTI LI SSHI LSELEQVATCFGI
LQDGEI VKEVFI QDI LQRGTTLEKLYMQSTKGGKH

>2617922209 Ga0073689_1682 Putative zinc-finger [pelotomaculum Ga0073689 :
Ga0073689_168]
MKVSCFI I KDLLPLYHDGVCNSDSRTMVEEHLAYCDSCAELOAMEDALF
LNKTEQNLNEAEAVKKLSKRWKKGMI KSLLKGI LLTI LVI ALI AFVLYCF
MDI RFVSKPY

>2617922208 Ga0073689_1681 RNA polymerase sigma-70 factor, ECF subfamily
[pelotomaculum Ga0073689 : Ga0073689_168]
VADFGFI YTEYFTGVYKYVLTLCRNEAI AEEVTQETFFKAMRHI DQFNGS
CKLYVWLCOI AKNTYFSLSKQKRMALDI DADFPDTASDLEKDYFDKETA
RRLHI LLHNLNEPYKEVFTLRVFGELPFSQI GVLFGKTDSWARLI FYRAK
KQLQEAMK

>2617922207 Ga0073689_1677 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_167]
VFFKMSKSYLKLAKKFQGRSYDSMVAHTAI VFI RYI I LALESRNGEDPRT
I GNLFYI CCDELODI SLVEALQRI FSLMEQFLQEQLQLAEAEI RKLI DYI
I SNLPSFFKERLAVCYCES

>2617922206 Ga0073689_1676 Predicted ATPase [pelotomaculum Ga0073689 :
Ga0073689_167]
MFLRAI KI TGEGDKNSYPMNI PAFRGI KI I SVTRPVTFPI GENGSGKSTL

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LEAVADLCDFPFGGSRNHLFDYQATESNLKEYI RLSWLPKATDGFFLRA
ETFYHMASYI DELAKKEPSVLSYGGRSLEQSHGEAFFALFKHRFGRRG
FYLLDEPEAALSPSRQMAFLRLLRQMEQTGKAQFLI ATHSPVLLAYPGST
I YSLDHSPLQRVEYEDTEHYRLTRDFLNDKRFFRYLFED

>2617922205 Ga0073689_1675 membrane fusion protein, cobalt-zinc-cadmium efflux system [pelotomaculum Ga0073689 : Ga0073689_167]
LKGVEMLGKGLALLAAI LAVLLI AAGCGKKQADPAVEAGPVAVSAARAV
MGVLENGTLVSGKLEAGQSADI VPKAPGKVAHVHVDVGSRVSDGQVLVTL
ENKDLAERVAQARAGVAQAEAAVAQAEAGYQAARAALANARDQFQVAEAN
YRRAGELLAAGAI PRATFESQYDLPYKQAKQALEGTLPAQVEQARAGMGQ
ARAGLDAARAQLGLAGQAYEDSFI RAPFAGVVTARRVNPGEAANTPIIT
LVNLDRVEVKATVGERI I NQLKQGQKVWVKVSAVSGQPI EGVVTSI ALAV
DPATKAFP I KVEI DNPENVLKPGMFAEVQLPASGQEQLLASREAVI KEGE
KNFWWLI KDGRAEQREVQVGESDGKI AVTSGLSEGEELVTAGQEKLQEG
AAVAVQQN

>2617922204 Ga0073689_1674 hydrophobic/amphiphilic exporter-1, HAE1 family [pelotomaculum Ga0073689 : Ga0073689_167]
MKI TDTSI RRPMLVAVLVTVLLLLGGVSLSLRLAI DLWPEMNLPVAAVTE
YPGAGPEEVEQQVTKPLESVLATVSDLSLQSTSNMGTSTVI VMFKWGT
MNYAALQI REKVDI I RSMPLSGAKAPMTFKMDPNMMP I I QLALSADDP
LKQLTDDVI QPRLERAAGVASVWSAGGMEREI HVLVDPAQLAGFGLTLNG
I TOALQAENMNVSAGVLEGRKDLLVRVTGEFKDLEQVRQVVVGAPGGTP
VHLEDVARVEDGQKKVTQFSRVDGKPGLSVFI QKQSGANTVQVAREVRKA
LDGLKQELPGVEFRTVLDQSEYI EQSI NHVVKEI LVGGFLAMLVMWI FLR
NLRSTLI I STAIPI SI I GTFVLI YFNNMTLNL I TMGGLALGVGLI VDDAI
VVLENI YRHRQMGSYLDAARTATDEVGGAVI ASTLTTI AVFLPVI FVKG
LAAQLFAPLALTVSFAI FTSLLVSLTVTPLMASRWLNLEEEEPVGRPAGG
AAVPVAEAREEAAEGPTVPVETAGGAGI PATEGTADNPAEPPAGKTPTG
GSAARRRFRRLYRI SERWFNGLNDNYRRLLEWSLGHRRRVLI I VAVLFI
LSLAAFPVMGVFEFMPMTDQGVNI TVEMPRGTAEETNRVATRI EKMARA
PYVESI FTGVGFTGTQGMWGESNTDVAQI TLDLVDKKQRAVTAEOVAEDL
RQRFKDI PGTDI KVSQAQEGGGMDTGAPVSI QLRGDDMDTLTRLGNQVV
DLI ROVPGAREVNSSLQGRPEI QVLVHRDRAASYGLSPAEVASTVRTAI
DGTVAATKYRTGGEEVDI RVQVANGEVSRLPDLFNLT I LSPAGAQVPLSQV
AEI KETRGPHTI SREDQTRYVAI TAQLAGRDLGSVMKDI QGKI AGLALPS
GYAVEYGGEQKQMAETFGDLSMALLAVVLVYLVVMVAQFESALYPFI I MF
SVPVTMVGVSFSLLI SGRAFSVPAFI GVI MLVGI VVKNAI VFVDYVNI LR
RRGMRREAI LKAGPTRLRPI LMTALTAI LAMLPALTTLGEGSEGOAPMA
TVVAGGLAFSTLI TLVLVPI I YTI LDDWKDRWQAWRNKKRDGRVHNGAVR
QAAGNQGS

>2617922203 Ga0073689_1673 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_167]
VETYGKKRKVSFLCLDLI WKPVKAKVRFVLVVDGTEKFI LMCSDLLLDPV
MI TTAYVYRLKI EVCLKMLKLLVGNFCYHFWSKARPI RDRRGHSNLDSVT
DERSRANI VKAVRAI EAFMNFCCI ATGI LQLLALKYKQI I WKGYRGWLRT
STSEVPSEETVMSVI QESFFHNFHDFRNTAI YAI I MAKKRKVFTKRYRDA
A

>2617922202 Ga0073689_1672 HB1, ASXL, restriction endonuclease HTH domain [pelotomaculum Ga0073689 : Ga0073689_167]
MDDFYRFLDYQORI AEMTLEEI KKTRNRPVKTPRTYKLRI VETI LKKAGK
PLHI SEI I RI AERDYDVTLERDSLSSYLAKKI NQGLFVRTAPNTFTLS

>2617922201 Ga0073689_1671 transcriptional regulator, AbrB family [pelotomaculum Ga0073689 : Ga0073689_167]
VKATGI VRR I DDLGRVVI PKET RRTMRI REGDPLEI FTDREGEVI LKKYS
PI GELGEFASEYADSLNEALGHI SCI ADKDSI I AVAGSPKKQLLNKQI SP
DVEKVMADRKMAVFSEPRFLT I DEDI SYN SAVI API VAEGDAVGAVI I AA
KEPGVQMGDLETKLAETAAGFLAKQMES

>2617922200 Ga0073689_1668 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_166]
MATQMDPI RATRHLEKWI NFYGMDDRNSWPPEDYTYVKKACKAI QLAI DV
LRENDAYETSI RKA AAVLDEWPTI HSMDDPDVWDPMDFFPVQNALEAI I F
ASTFLKKQQAGRSS

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>2617922199 Ga0073689_1667 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_166]

MTKI FSLGKNCRAYLKRYGKKRPQLKFTCEKEGCNSQVLHENGRIYRMAA
LKHHQFKI SI YRWRCPCGETLSVLPDFLVPWGHFVTPVREAALKRKKHG
ESLKQI AKGLVSVKAGGVSI DTI KRWWTRHLQKAGDAAQWVAGELI QAGV
NEDLLRFYI LKVMASYAVAG

>2617922198 Ga0073689_1666 amino-acid N-acetyl transferase [pelotomaculum Ga0073689 : Ga0073689_166]

MKFRKAKI TDVEPI HTLI TYAERGLMLARSRAMLYESLREFTI AEDRDR
VVGAGSLHI VWEDLAEI RALAVAPEYCKRG TGRLVNMFL EESRELAI PR
VFALTYQQE FFEKCGFKVVPKDSLPSKVWKECVNCPKFPSC E E I AVI I DI
YPFLSI N

>2617922197 Ga0073689_1665 P-loop protein of unknown function (DUF2791) [pelotomaculum Ga0073689 : Ga0073689_166]

MERFEARQVI ECLRSVSSRYLSGI FSYGREVALERVGRELNRVQSEGA
QALVVKGNFGNGKTHFLNI I ARKAEEMNF AVSFI PLSKETPFDKLDRLYR
RAAAGLFLPGYPQPGFAPLLES LKPGSGQAEEM LDFAGRN LHPKLEAVLR
NYLEGSGEAYNQYI LAGDLAGDFVPNAQLKSI HRLNFRALSLPSFKVKE
NAFDYFRFLSRLI RAGGYAGWVI LFDEFEQLMYLGI AARTNAYLNAARFM
SPSFGLTATYTVFSASSNLWSELI WKQKNSDYDNVPQRLTAKERQHEI PT
VREVFASFLKDNFLD TL SAFDI RRMLQAVRDH HALAYS RPAPADI DQAT
AGLPGDRPLRTVI RAVVEYLDQYLYGGNPEI TVGAPEEI LPNEPPEKNG
PV

>2617922196 Ga0073689_1664 P-loop protein of unknown function (DUF2791) [pelotomaculum Ga0073689 : Ga0073689_166]

VDPAVREEALQNL LRGFPPRDREALDAI TVGTREGI WNFWRDCYLDYI A
SGGSKVKFLT GKP GSKTHVLL LLL EEARRLGYVTVFADARQVRLNKFDS
I YQVVLEAI EPGDLVAA YCGAVVEGLGYHPGQVPPEQDFFNWAQARGRAA
DTLRREI QERLDVLFQDRKI NYNFALAF TQLCADNLGSRR LAPDQKDI LI
NWLKGRSLPARTLKPLKI FTRI DKYNARYMMASFLHLLRLCSRRGLCVAV
DNLNALLERGPEGRTLYGKSARNEVYESLRQLVDDFAGFEGVFFVFAGRN
DLI YDEKGGFKSYEALWMRI QNEVSGTRPNKFADLLNQDALVKEFFT VET
CLELODKLNGLFGPGSGLRRED FQC LLENVGI I SPLQRVVEAI VNQY GAG
GDLDEI

>2617922195 Ga0073689_1663 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_166]

MPATLDDFLDHSLQEDFKNLNNVHRSI LNVVRRI KTASAEGNLETLOQSL
ARYEELLDRQENLQGFKEKLPSFDVQYYLQEDFH HGFLEALAGEGLAVE
AEYPVYEVLPFKVRVLPEKELI TI DDHI YRNLRPDVLRHLKKGLDRLNA
ASFDAORFLQSLADAYDTETARQVAKTKI DLSEQEVLLKD VYNTLT PMPH
QKRDPVQRFADLHRVLKSGRMNAPDGRRLWLGNVRNRKQALTVLDAQG
QPQRYGVI KFYREG

>2617922194 Ga0073689_1662 acetyl transferase [pelotomaculum Ga0073689 : Ga0073689_166]

MLSVDYINKLVAPCSVALVGVT SRTGRGSNNPLEI LI ETGYRGTI YPCNR
RGEDI LGI TTYQSVLELPEVPDLAI I CAPRNAVP ELFAQCAEKGI NLVI I
VAQGFSDGDEEGKQMRKLFSLAKSRGI RI I GPNTLGVI NNDFR FCTSM
RFI NRPAPVGI LCQSGI FVVA AAEVYTGAGI CI DTGNTT D VDFGDLI GHL
AADSRLKVI NLHLEGVKEGGKLMLEARKAATQK PMLVLKTGRSKAGARVA
GSH TGSMAGEDRVADAAFRQCGLI RADNVEELNDFNKTFLT FDDI GGRI
AVMSI SGGAGI I SADACAA YGMELATLSDRSVATLQSMNPSWLKPANPVD
I WPAAMLAGYHQVCREI LRVLLEDPNVD AVI CI TASFLEE QEDFLDI SGL
VREEARAGSGKPVVAW TYGARS RDI YI KKFEQEGNVVAYPTLERAVKSLSV
LYRYHHTI RKKVGQRENDMSVHPATDTADARQI LSVATGEI LMPDALKLL
EAYGI PTAPWRYFQSAEEALLAAGKVGYPVLVKG VGLCLSHKTEAGVVKL
GI SDPGELAAACLEMETSI SGLNGFV VQKEMAGGTEVLVGFKRDPQFGPV
LAFGSGGVFTEVLDDVSLRVAPLDREDACEMI RETKVYRI LSGYRGKPRA
DEDALAGCI LRLAKLAMDFPALTGFDI NPLMAGPDGVVALDARAASR

>2617922193 Ga0073689_1661 Transposase IS200 like [pelotomaculum Ga0073689 : Ga0073689_166]

LRKLCKYKGT E I I EAKACSDHI HMCLAI PPKYSVANI I GYLFRKI PPGI P
GNKVGMSVTLOVKLI GGFAGCKDFLPDPKNEPSLEEEAGQYI TSHGYP

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>2617922192 Ga0073689_1658 penicillin-binding protein 2 [pelotomaculum Ga0073689 : Ga0073689_165]

VDTLRRKRLVRI FFI FWLCFLGLMVRLWVI QI KDGYNYSQALAQGSRWV
SLEEAPRGGI LDRNLVPLTGEKEEDRVVLFPMVADKDEVARDLAGLLGV
DYPMTGYLEGGPCLLPYRVGPAQSAAI KERGWPGVMVLPVQFRYGDRPL
AAQTI GHLGRI SSREEFSALAGRGGKI YRYDDMVGKTGLEKYEEQVLKGV
RPQRAVRVFADAGGRLLGGPEFRVEEDVDRERRDLVLT I DSRI QLAVED
IMDRRVARGAVVI VEAGSGDI LALASRPGFNPARPEQYLGGMEERFFDH
CI ALYQPGSI FKVVVAAAALEEGLVGPESRFTCHGERDDLI HCWKAEGHG
EIDFSRAFADSCNPFAETGLKLGASRLI EYAGRLGLANQSI TGYPAPRD
PRQDHNLI GAPHNLVNSSVGQGPVLVTPVQVAAMLNTI VSGGVYREPRLA
REVHKKSGEVVRAYPLDPGKRAI SSETAEKLRVLLESVDHGVGREAGVP
VYGSAGKTGSAQI GNGSVNAWFAGYAPRSNPRYVTVLVEKGASGGESAA
PVFREI MERI LQ

>2617922191 Ga0073689_1657 DNA-binding transcriptional regulator, XRE-family HTH domain [pelotomaculum Ga0073689 : Ga0073689_165]

MI VRGEQI RTLREERGYTLQDLARRANLSLSYLSEI ERGSKRPSLTKI DK
LAAALNVARTRLI EGDLTDSGLSLGDKI RMMRAEKNMSLQELAQKAGI SL
SYLSEI ERSTVYPALSTMKRVAEGLAVPPAALMGHEGTLGHKLKALREEY
GLTQACLASLAGVTAGLI GOI EOGKVQPSLKTLEKLADVMGI TPCYFI ME
PGAVDQMLSLMNPRLRELLMHPNVQSVLSLI YNLNEKELQFVLNFI QLFK
KSELS

>2617922190 Ga0073689_1656 4Fe-4S dicluster domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_165]

VLELAVFVI KDI CNGCGMCVEACPNGAMSVRLKVATVDPEKCEDCEECVF
TCPVGAI TAGDSNTNKQR

>2617922189 Ga0073689_1655 putative regulatory protein, FmdB family [pelotomaculum Ga0073689 : Ga0073689_165]

MPTYDFQCSWCNHHKFSVLT I AEKDKVVCPKCRSKEI HQLFTGCGVSLRG
SKCDI GDAKSRLRG

>2617922188 Ga0073689_1654 thioredoxin [pelotomaculum Ga0073689 : Ga0073689_165]

VALSFTEENFESEVLKSTVPVLVDFWAPWCGPCRSMAPI I DDLAKEFEGK
VKVGKLNVDENKNLAGNLGVMSI PTLI FFKDGKKI DQFVGYTAKSTLVKK
IDSLVEDS

>2617922187 Ga0073689_1653 Methyltransferase domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_165]

MPLPNNAEI AVNTPETI PGGPGFYI DEEQAGNI KENYTNVPRLRDI GRW
YVTDVFRAVSESLPSGSKI LDAGAGECAYKKYFSHCKYVSVDLAI GEENW
NYHNLDI APLDNLPFDDASFDAL LCTQVLEHLEHPRAAVKELFRVLRSG
GRLFSTVPMAGHEHQAPYDFFRYTSYGLQSI CENAGFREI GI TPLGGMFS
RWAYEFPGMI TLFPGAGI RSGRI NI KGLLLLLPVRLVCLLAI RI TQMFFLG
IDRLDKVKNFPLGWSLVAWK

>2617922186 Ga0073689_1652 NDP-sugar epimerase, includes UDP-GlcNAc-inverting 4,6-dehydratase FlA1 and capsular polysaccharide biosynthesis protein EpsC [pelotomaculum Ga0073689 : Ga0073689_165]

LTAKAKAKPVL I GAGVAGGVVAEI LAKSPNREFEPVGFVDDDPGKQKRT
VHGLPVLTGREDI PAI VKRHD I GEI I I AI PSAPGQVI SQI VEI CHKSKAR
LKI LPGFYDLI TGRI KTSKI RDVEMDDL GREPVTLDVEKI AGYLTGRTV
LI TGAGGSI GSELSRQVARFSLKELI LLGRGEGSI YEI ETELRENFPDLA
I GAEI GDI KDHSLI NRI FGRHGPDVVFHAAAHKHVSMEQCPDEAVKNNI
I GTKRVAEAAAYRAGAGTFI LI SSDKAANPASVMGATKRVAEMVI KNMNNR
GATRFAAVRFGNVLGSRGSVI PLFKRQI ARGGPVTI THPDMVRYFMTTVE
AAQLVI EAGALTRGGEI FVLDMGRPVR I LDLAENLI RLSGYEPGKDI QFR
FTGARPGKELVEQLFEDGEI I PTKHKRI FTI AGRHREPARI DALFNALE
DPDFSYPDDEI I ALLQTVLPKFKK

>2617922185 Ga0073689_1651 UDP-N-acetyl -D-glucosamine dehydrogenase [pelotomaculum Ga0073689 : Ga0073689_165]

MPLLNGRGEQLAGVLKEKLSNRSAMVAVI GLGYVGLPMAVEQAKTGFSVA
GI DRDAKKVEQVNSGRSYI RDVPDEDLRDMVKGKKLTAHHDFDPVGEADV
I I I CVPTPLQSMRQPDLSFVLSAAREVAGRLKPGQLVSLESTTFPGTTRE
VVLPLESGGLTVGEDFFLAFSPERVDPGNKHYI TRDI SKVVGVTARCL
DVACSFYQGSMKRVVPVSSPAAAE MTKI FENTYRAVNI ALVNEFMI LCDR

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MGLDI WEVVDAATKPFQI QTFYPGPGVGGHCI PVDPFYLAWRARDYDFH
TRFI DLAGEI NI QASEYVYVQKLI ELLNKHKKCLNGAKI LVLGVAYKKDVE
DI RESPAKLI I SLLRRSQAGVFYYPYVPRFRLSEKDEVCLSVTLTEEV
VAGADCVLI LTDHTCVDYQWVDHVGLVLDARNATRDVGRGREKI TKI

>2617922184 Ga0073689_1647 heat shock protein Hsp20 [pelotomaculum Ga0073689 : Ga0073689_164]

MALVKWEPFRELQGLQSI NRLFDDNFRFWGLPERTLGQAWSFPVDI KDT
PEAVLI KALPGLDKGDI KI CFNDNLLTI QGERKKEEKEERENYVRVERS
YGSFSRTFSVDAPVKQDQI KARYQDGI LEI TLPKEEDSGKKEVTI PI EG

>2617922183 ClpA ATP-dependent Clp protease ATP-binding subunit ClpB [pelotomaculum Ga0073689 : Ga0073689_164]

MRLDKLTLKTQEFETAQRLMAEHSQQQMEGVHLLLGLLQEEGI VKPI L
RKLEI DAAKLKQQVQAAVERLPRVRGAGGVYVSRELSEI VDLAWKEAERL
KDEYLSTEH I LLGMVAQKDGEAGKI LSHGVTQDRVYKI LVDI RGAQRVT
DQNPEDKYQALGRFTRDLTDLAHKGKLDPI GRDEE I RRVVQVLSRRTKN
NPVLI GEPGVGKTAI VEGLAQRI VSGDVPENLKNRLLSLDMGALI AGSK
YRGEFEDRLKAVLKEI SESQGEI VLF I DELHTLVGAGAAEGAVDAANMLK
PALARGELRCVGATTLDYRKH I EKDAALERRFQPVYVGEPNVEDTI AI L
RGLKEKEYVHHGVRI KDAALVAAAMLSHRYI SERFLPKAI DLVDEAASR
LRI EI DSMPTI EI DEI DRRVRQLEI ERQALAKEQDQASRERLQKMEELAA
LGSKMEELKEHWRKEKELI QSI REI KEKI EETRLAEQAAERDADLGKVAE
LRYGVPELNLKRLQONNEKLAELOKDHKMLKEEVDEEDI AQVVAKWGTI P
VSRMLEGEVQKLLKMEELLQERVVGQDRAVKAVSDAI RRARAGVADPNRP
MGSFI FLGPTGVGKTELARALAHFLFNDERAMLRFDMSYMEKHTVSRLI
GAPPGYVGYDEGGQLTEAVRRRPYAVI LFDEI EKAHPDVFNI LLQLLDDG
RLTDGHGRTVDFRNTVVI MTSNLGNHYFRELNGGARAALAEARVMDELKAA
FRPEFLNRI DEVVI FNNLGKEE I I KI VDI QLALLKQRLAKLGLSLEVAPE
AKALLAEFGFDPVYGARPLKRV I QRLENPLSVHI LEGKHTRGDHI LVTA
DPVTNTLI FQ

>2617922182 Ga0073689_1645 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_164]

LKNTGERLLQELMENRTEHVLELI ERLSSEKLKI I I NKVNKLLNKKD

>2617922181 Ga0073689_1644 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_164]

MAAKVYFTDMRAGHNKSLLDKLEKLFDRAGFAEI I EPKDLVAI KLHFGER
GNTGYI RPOFI RRI VKRVKELGGI PFLTDANTLYVGSRSNAVDHLQTAVE
NGFDYAVVDAPLI I ADGLTGKEYI SVEI NRKNFKEVKI GAAAYHANALI A
VTHFKGHEMTGFGGVLKNVGMGLGSRSGKQMMHSDVLPSPDPKCKGCEL
CSRWCPTVAI GVRDGVSVVDESKCI GCGETVTCPVQAI GI NWKTEPDI I
QEKI AEYVEGVLKNKNGKNGFI SFI TNVSPDCDCYGWTDASLVRDI GI LA
SRDPVALDQACVDMVNQAALLPENRLEGKGEVQDKFRALYPDI DWNRLQA
YAEI GLGARRYELVKVY

>2617922180 Ga0073689_1643 purine-binding chemotaxis protein CheW [pelotomaculum Ga0073689 : Ga0073689_164]

MGLARVLSNLKRPEI PGPSI ALGGCNPVI QTEKGAI VMSKMEKDLTGRED
QVVVFQLSEQTYGI DI ASVYEI I RMEKI TRVPRTPDFVEGVI NLRGRI I P
VI DLCKRFNLDPSEKTGSSRI I I VDVGNTVGM I VDAVSEVI RVPVGS I E
PPPAMI HGI DAAYLKG I AI LDSRLI I LLNLEKMLYEHEKSELQGFVETA

>2617922179 Ga0073689_1642 two-component system, chemotaxis family, sensor kinase CheA [pelotomaculum Ga0073689 : Ga0073689_164]

MFSDEE I SVFLDELEEKI QVLNENI LI LEREGGLEAI QEI FRAAHTI KG
SSAVMGYENMASLTHEMENLFDQMRKGLLPVTGQLVDALFTALDTLHALR
DEI LGKNVSVDI GOAVAGLRQCQETCSAAPSADETRPTSSGDGARVPTP
GNSPGVLEAI DEEVI REAYLI GYQAYRVRVELDSGCQMKSVRAFLVFEVF
QQMGEVI KSEPAEEI QEGNFDTGFRVLLTGEDPDRVRNLLMTVSEVAG
VGVEKI VLPAGETGGDKQAPAREAGPAGVERGVGAGPGGRTEHTEVKAVQ
TVRVDVQRLDSLMLVGLVI DRTRLNRFAEI FEGRFGAGSSEMVDTLNE
I SNHLGQVTGDLQEQI MKARMLPVAQVFNRFPRMVRDLAQKLGEI DFI V
EGHETELDRNVI EI I GDPLI HLI RNALDHGI EGPEEREKLGKPRRGVLKL
KASYMENHI I I TVADDGRGI DPVRLRDKALGKGLLDEEMARRMPDREALN
LI FTPGFSTAGEVSGLSGRGVGMDI VRNQI ENI SGTVDI SSTVGVGTTFT
I NLPLTMAI I RALMVGLRDEQFAFLANVVETI SVRAGEI KRVKQSEVI L
VRGHI LPLVRLSRVFGLEGGGKERLFI VVLGVGEKKVGI I VDKLLGELE

Table S2

I VI KSLGDYLGKAPCI SGATI LGDGQVALI VDVRSLVREI GVEEAVYAAG

>2617922178 Ga0073689_1641 Response regulator receiver domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_164]

MPPVKVLVVDSDVLMRLI TRMLAGYPDQ VPGTAVNGSDALAKAAALKP
DVI TMDVEMPVMDGLTALRRI MRENPLPVI MFSTLTALGTRATI EALAAG
AVDFVTKPASPAQLGPLVEELVGKI RVAAAVPPRRLLVRRPLPTPRSAGGT
PSPGPAPLANGGAAGTAPGGRGAARPEGI PAGKKPAAGEGTDREI PPAEE
GTAAGLTPAGGRA

>2617922177 Ga0073689_16314 Ubi quinone/menaquinone biosynthesis C-methylase Ubi E [pelotomaculum Ga0073689 : Ga0073689_163]

VDTEI I KKRYNRTAKFYDYMDRMI SESLRQEVLLGGVVRGKI LEVGVGTGK
NLPLYPPGSDVTGI DFSPEMLKRARARAERLGLRNVKLI EMDAQKMDFPD
HTFDTVVATCVFCSVPDPVKGFQEI KRVCKPDGQVI LLEHVRSENPVLGK
IMDVLNPLAVNLTGANI NRDTVANVQKGGKLSQVKNVKGNI VKLI QARP

>2617922176 Ga0073689_16313 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_163]

VKKRFWFLAAVGI LVVALAAPAAFGAI TGGGQSGQNGQDNQAGQQNQAFV
DQMFQDWHQKWMQDQARDGRI SSDQAQAWQDHF SYMRDFHSKNGFGMMGSM
MGGDGVYGMGKYNGAGGYGGMMGNYPGPAQSN

>2617922175 Ga0073689_16312 Protein of unknown function (DUF2933) [pelotomaculum Ga0073689 : Ga0073689_163]

MEKWYLLFFLLCPLMHLLMMRGHGHGNGNKGKDAVNE

>2617922174 Ga0073689_16311 Cysteine-rich secretory protein family protein [pelotomaculum Ga0073689 : Ga0073689_163]

VTSDLNADEKLMFDLVNQERVKAGLPAYTLDMRLVNLARLKSQDMVQNNY
FDHVSITYGTPEMEKNAGI SARVMGAENI AKAATAQRAFELFMGSAGHK
ANI LNSLHDAI DIGI VSTPSGVVVTQMFIGN

>2617922173 Ga0073689_16310 Protein of unknown function (DUF2680) [pelotomaculum Ga0073689 : Ga0073689_163]

MKKRYVVLALVGLALAVLVPAAFAAVSGDQAAPWFNRMFDSHKQWVDQ
AVQNGQMTPEQGQAWGQHFQDKAFHQQNGYGCPCFGGGMMGNRNGGMM
GGTRGQSQNGPSDNGSN

>2617922172 Ga0073689_1639 Predicted permease [pelotomaculum Ga0073689 : Ga0073689_163]

MGEGLFCNCRNRNYRGYKRAVSPEWAENLWVI AGFALAGTMFI IPTAAE
IPI IQSMMSFGLGVGPAAALLVTLPAVSLPSLYI VRNAFPARVLVMTFA
VALLGVLSGVLAALVY

>2617922171 Ga0073689_1638 putative membrane protein [pelotomaculum Ga0073689 : Ga0073689_163]

MMGFQGGTFFGSLWGLSMLLSMLLP I AVI VGAAYLVI NLLERRKTASVG
ETGLPDPLTI LKSRYAKGEI SKEEYYSMKEDLVRG

>2617922170 Ga0073689_1637 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_163]

VEHKTWWLALLGLTAVGFI LGMAVNPLRGPAAKPQGYVPGPMDNRGMMN
YMATPDHAGPMADMMSSPETRDNMTRVMSSPQMKGAMVELMQDPQMKQAM
ANMMQDTRMQQAMAEVMADPKVRQGMMLNMMATPGMMGVI NDMTKDSRLRP
AMSEALEAVR

>2617922169 Ga0073689_1636 protein of unknown function (DUF1540) [pelotomaculum Ga0073689 : Ga0073689_163]

LSKVTKCGI EECMHNNNAMECHADGI EVKSSTMDRKVNMSSENTCCDTFKPK
K

>2617922168 Ga0073689_1635 Cu⁺⁺-exporting ATPase [pelotomaculum Ga0073689 : Ga0073689_163]

MADANVNVADREPAGLKTMTVKVAGMSCAACVARI ERTLSKTPGVVSARV
NFAEETATVDYRPETTNPKDI LDRI KEAGYRPVTGRTELKLSGMSCAACA
ARI EKGLNKLPGVTRAAVNFATEKAVVEFNPAEI DVPQI KKAVIDI GYKA
SEVDDRTTADLEREEREREI RRQKSLVI FSGVLSAPLVVYMLAMVLNLQE
AI PAFFLNPYFQFALATPVQFVAGANFYKEAYTALRGRNANMSVLVALGT

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TAAYLYSVVGTFFANRI GMVEI YYETGAI I I TLVLLGKTLETI AKGRTSE
AI KKL I GLQAKNARVVRGGEVEI PI EDVQAGDLVVVRPGEKI PVDGI VK
EGYSTVDESMLTGESVPVDKKAGDEVI GATLNKLGTFKFEATKVGKDTAL
AQI I KI VEEAQGSKAPI QRMADVI SAYFVPAVVGALVTFFAWYYYGAPG
DFTRSLLSFTAVLVI ACPCALGLATPTSI MVGTGKGAENGI LI KSGEYLE
KAHKLTAI I LDKTGTI TKGEPALDLPAPDYRGYEKELLQLAGRAEKSS
EHPLAQAI VI HAKENGAALNDPDHFEAI PGHGVAEI DGSRI LLGTRKLM
QENGVDI SGLTADVERLEEEGKTAMLMAVDGKPAAI I GVADTI KESSKEA
I ARLKEMGLEVWMLTGDNRRTAEAI ARQVGVEKVLAEVLPEDKAKQVEKL
RGQGVVGMVGDGI NDAPALVTADVGF AI GTGTDVAI EAADI TLMRGDLR
GVAAAI RLSRATI KNI KQNLFWALVYNTVGI PVAALGFLNPVI AGAAMAF
SSVSVANALRLRRFKAGI A

>2617922167 Ga0073689_1634 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_163]
MEI LKDYAPWLI LGALMFFMMRRGCCGGHAGQDEKSGDNHGGGQEKSSP
PKRGCH

>2617922166 Ga0073689_1633 phage shock protein A (PspA) family protein
[pelotomaculum Ga0073689 : Ga0073689_163]
MPKNQI KTDWNLSLRFVMTFPLAALTWPSRWCFSGPVPARPDGAGYRP
OLOEMEEQAKRALAAGREDLAAGVLERKQAVQSQTTLLEGQI ATSVKEQE
KLAATEARLSAKLEAFRTKREVKAQYSAAEQVKI GEAVTGI SEEMADV
GMALERAREKTENMRARAAA DELTKRGLLEDPLEPGDPI NRELDKI TAA
QNVQVELHRLKKEMQQEGAR

>2617922165 Ga0073689_1632 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_163]
LI I RI LNEGQYELDGEQLSRLDELDRMTEAVACGNEPFFQKTLDEMI DA
VRNGGARLPDDALTESHLVLPPTTLSEARRLFSGI DGTGAGTI

>2617922164 Ga0073689_1631 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_163]
MLANI PKEI VDFAVYFSGI SKFYCWMI PGGLVLWPKYI YSVHGI I LGGLI
DFI I AGVLGVGLTYFLTLMEKRYLF

>2617922163 Ga0073689_1629 phenylalanyl-tRNA synthetase, alpha subunit
[pelotomaculum Ga0073689 : Ga0073689_162]
LI DKLQKLGEAEARRALAAAGNLEELNEI RI RYLGGKGELTRVLRGMGGLS
AEERPRVGQAANEVRTSI EEELVARTAAKETVKEQRLREEGI DVTLPGA
PVLRGGKHPLTLVREEI EEI FLGLGYSI AEGPEVETDYNNFEALNLPKDH
PARDMQDTFFI SGEI LLRTHTSPVQVRTMEKTVPELPVKI I VPGKVYRRD
DDATHSPMFHQVEGLTVDRRI TFSDLKGTLDLFAREMFGPRTKTRFRPSY
FPFTEPSAEVDI SCVMCGGGSCRVCSHTGWLEI LGAGMVHPRVLEI SGYN
SEETTGFAGMGVERI AMLKYGI DDMRLLFENDLRFLOQF

>2617922162 Ga0073689_1628 phenylalanyl-tRNA synthetase beta subunit
[pelotomaculum Ga0073689 : Ga0073689_162]
VRVSXKWLREFVDI DI TPRELADRLTLAGI AVEGVTEGKGI EKVI TGRI
ETI SRHPNADKLVTSTVNTGMEKLQI I TAATNVREGDVI PVAVEGARLAG
GLVI KRAKLRGVESRGMCSGRELG DPKI MPADQAHGI MI LPPGTPLGK
DAKELLGLDDFI MELDLTPNRGDCLSMTGVAAREVAALLGRPLRPVQPAFS
ELAEI TGQVRVDI EAGDLCRRFVGRLI KNVRVGRSPLWMQYRLRAAGI R
PI SNI VDVNTNYVMFELGQPMHAFDYDI LKDGI I VRRAREGEKI VSLDGV
ERELTPEMLCI TDPSGPVAI AGVMGGLATEVTEKTTTVLLESAYFNPVSV
RRTSKALGLRSEASLRFEGKI DI GGCDRASARAAQLI AEI GAGEVVAEAV
DNYAPVQEKTI SLRPERATYVLGVDI SRDETSGI LTDLQFKVQDAGAEL
LVGVPTYRVDI NLEI DLI EEI ARMHGYHRAPGTLPYGPSTRGFRTRQSF
TARLRDL MAGAGLYEVVTSYFTHPRVFD RMNPLDSPLRNTVKI QNPLSE
EHSVMTI MLPGLLEI LARNYSRRVQNGAVFEI GRVFHPGDEGCLPEERP
VLSAAMGRTAGGWNTRPREMDYYYLKGVLLENLFAGLGTEPVTFRSLTAN
PSFHPGRTASLAAGEMDFGI GELHPEVLEHFELPERVVAFEI DLAALFA
ASRRPARYSPLPKFPGI DRDLAI VVRQDVPAADI I ETI RDAGGALLRSVS
LFDI YWGEQVPGCRSMAFSLKFLADDRTLTDAEAGERI EAI AGALAKRF
GSELRG

>2617922161 Ga0073689_1626 tungstate/molybdate binding protein [pelotomaculum
Ga0073689 : Ga0073689_162]
MKLVKKLALPVFI VLLAFAAGCSGATGPNNTNNNQATNDGKTAKELSGKV

Table S2

II FHAGSLSVPFQMEKEFERLHPGVDVQREAAGSRECAKKVTDLGKPAD
II ASADYAVI DDLLI PGFADWNALFAKNEMVI MYSGHISKYKDEI NGESWP
EI LLRDGVQYGHSDPNADPCGYRALMVWQLAEKHQI PDLYQKLAQKCPA
RNI RPKETDLLAMVESGALDYLFY YRSVAQQHNMPFVELPAPI NLSDI NQ
ADFYKQATVDTTGKKPGEVI TOVGMPY VYGVMTMLKNAPDKENAI EFLRFL
LAKDKGLKI LNDNGQPVEDPLI I KGKEAI PPELKEI TG

>2617922160 Ga0073689_1625 tungstate/molybdate transport system permease protein
[pelotomaculum Ga0073689 : Ga0073689_162]
MNLRI DKLYLTSAFLGLLI I LFIMYPI TNLLI TTDGRI LLQTLMDREVVS
AI WTSI FTATVTTLI VFVFGVPFAYFLARNEFQGRKRI VESI I DIPIVI PH
TVAGI I LLTI FSRQSWTGRLLNMG I GVI GTRI GI VAAMLFVSMPLLI NA
AKDAFLSI SPKLENVSRITLGANHLQTFMLI TFSI GWRAI LTGMI LTWARS
I SEFGAVVI LTYHPMI APTLI FDRFNSFGLDYSKPVSAI LI VI SLGI FIA
LRVI AKRGVQDC

>2617922159 Ga0073689_1624 molybdate/tungstate transport system ATP-binding
protein [pelotomaculum Ga0073689 : Ga0073689_162]
LLEI RDLTVHLPGFALHNI NLSLNKGEFFALLGPTGSGKTVFLETI AGI K
TPSRGKI FFHGRDVTNLKPEQRNI SI VYQDYALFPHLNVQQNI RYGLRFR
KKGSGQSEKFNLSI EMLGI GHLLKRYPGNLSGGEKQRTVLARALI VEPD
I LLLDEPFSA LDANTKETVQSEKTLHGVLKTTTLMVTHNFSEVFLAER
VAI I KEGTVQQVGS I QDVFKTPRSKFVAFVGMKNI FSLRQI NGKVTLGD
LLELDLQEPGGPDLSKQKNTGNGDGEYFI GLRPEDI VVGKQNLQTDYQI Q
GTVTAVSNNGVYSEVRVAGRLNFTAYLTPNRYFELGLRENKPVCLGDR
ENI NFFVAARAPSNN

>2617922158 Ga0073689_1623 cell division protein ZapA [pelotomaculum Ga0073689 :
Ga0073689_162]
MAGQENRVEVEI FGEYYTLKGDSSPGQMLALAKLVNRKMRQLAERNPRLT
RTQAAVLAAALNI AEELKKLQEEYDNLVRLLEPEKK

>2617922157 Ga0073689_1622 DNA polymerase (family 10) [pelotomaculum Ga0073689 :
Ga0073689_162]
LLKRDGESEAAKFRSQQFQVLSAWSGRAGHLNTGATPLPVGNTQESNVTK
EPSLCLHLSQFHFNKETGFVVRNI EMACI FOELADLLEFKGEDFFKVRA
YRNAARVLAGLDKPLEE I REKGGLGKI PSI GKN I AAKI NEI LSTGRLLKH
EELLREI PPGLLEI MTLPGI GPKRAAMLQOKLNVTSLEELAGAARAGRVR
GLPGMGGKTENDI I RNI EMRKDQGGRVLLATARELAGELAAYLETLPEVA
RI GAGGSLRRWRETVDI DLVAAAEPGPVI DAAAI HPRI GEVLERAGEW
ARLLTNWGI RVDLEVVPQSFQAALFRSTGSRAHLRRLQEALREKKGLDF
DPAEPGVFREEEDLFASLDLPFI LPELREDRGEVEAALAGGLPRLI ELAD
I KGD LHI HTKWS DGLASI KEMADRAREKGYQYMAVTDHSQSLKI ARGLSL
DRLREQQAEI RSLNENLEDFHI FTGI EVDI LPKGDLDCPDEI LKEVDLVV
ASVHSAFKQDRDRTMTARI I KAVENKNVDI I GHLTGRLI NHREGYALDVER
VLEAAAGCGTI LEI NSSPDRDLNDVNARRAKEMGI KTAVSTDAHDLRRM
DEMI YGVSVARRAWLGPEDVVNTMPAGELARFLKRR

>2617922156 Ga0073689_1621 DNA-3-methyladenine glycosylase [pelotomaculum
Ga0073689 : Ga0073689_162]
MPRRKI DLDQI TGGASI LPRSFYARDTVTVARELLGKI LVHDSSTEG I AAG
RI VETEAYLQGDPAHASRGMTPRNRVMFGPPGHAYVYFI YGMYYCFNAV
SAPEGVGEAVLVRALEPVAGLGLMRSRRGRERPAELCGGPARLVQAMGI A
RRHNDADLT

>2617922155 Ga0073689_16113 IS66 C-terminal element [pelotomaculum Ga0073689 :
Ga0073689_161]
VKKQRQQTLPKSTFGQAI TYCLNQWENLNNFLLDGRLEI DNNRAERSI KP
FVI GRKNFLFSNTPRGAKGSAI I YSI I ETAKENHLKPFNYLT YL FERLPN
VDMGDHTVI DSLLPWSTVLPDNCMP I KDYTSTLPI KSI M

>2617922154 Ga0073689_16112 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_161]
VKKRKWLALVGVAGI MTMLTVFAPVPPASANDRVRLLVNGREI QSDVPPR
I I GDRVMVSVK

>2617922153 Ga0073689_16111 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_161]
MSI I KMI FAAI LI I HGLI HLMGFGKAFQLAEI NQLTQTI HKPI GVLWLI S

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ALLFI I AA AVFLLRKDWMMVAVPALALSQLLI I I YWPDACYGTI ANVVI
LVGI VI CGGTWSFNAMVKNELEAFI PPVSSGKEI VTKEMLGDLPPAVQKW
LDSSNVI GKEI VYSAHLQOI GEMRTAPDGKWWPVKAGQWFKTEKPGFVWV
ADVKAAPGI HLAGRDKYENGEGHMLI KLLSLI NVADAKGKETSQGAMLRV
LAEI I WFPSAALNDYI QWEQI DSTTAKATMTYGGI TAPGLFKFDANGDVV
SFEAKRYYNRKGVATLEDWFI QI EPNGYKEFEGVRI PARSSVTWKLKEGD
FTWYKLEI TDI YYNRI RLHPGPSYYDI LKAG

>2617922152 Ga0073689_16110 tRNA (cmo5U34)-methyl transferase [pelotomaculum
Ga0073689 : Ga0073689_161]

MTGFDKTRWSEKDYAYKYLEEADI YVI DRQRLLAI LKSFYNHFLGDKKQN
KVLDLGCGDGI LTNELLKI DGS SATLVDSGSEMLNKAKERLVGFRNI RF
I RASFQELLSTDI KLDPYRFTVSSLAI HHLTKDEKESFFNYI YSHLENGG
YFI NI DVI LSPTEALEGWYLRWQEWI TEKKTL SALEGDYSYI I HNYQES
GHYNKLDLTGQLDVLRGAGFKNVDCFYKYGVFSI YGGKK

>2617922151 Ga0073689_1619 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_161]

MNVLTIVDTDI LI DAARQI SETVDCLAQI ERQSVLAVSVI TEGHTEFPV
RMI EYGVF

>2617922150 Ga0073689_1618 RNA polymerase sigma-70 factor, ECF subfamily
[pelotomaculum Ga0073689 : Ga0073689_161]

VKTGNGNRKGAGDSFEELYDRHFDVNRVLYRYI NSVWDADDLTA AVFLK
ALENYHKYRGDAPI AVWLFRI AHNAYVDYLRGRRRERVFSDGEMALLEAPP
AGPEEEELLRDEEARQLRDMWLWLAPEQRDVVSLRYAGELKFGQI ALVLGK
TESAVRMI HHRALKALRVFYLSNGEGVEGFARG

>2617922149 Ga0073689_1617 TolB protein [pelotomaculum Ga0073689 :
Ga0073689_161]

LREDSSHGKVPDKI TPLDAQRSKRTNRMEADDI WGGSPGELLI HMRKV
REAVPVNTRLREELRARLARTRAEQAGEGAVPAGGAVAAAGEGAMTQSP
SWQEAGRGWAKFWWLFP AALLLAVVYWLWWSAAAPKLL EAGPAREI SRFW
LEDGPLDFACAPGGRGI TARGGALLLLDQYGNQTGTVRPPAGQSYASPA
LSRSGDKLALVRRHDAGGGEI TTAAMPVI PLEPGAAPRVEEALAGAETLL
AVEEGKSPAGLTPSPDGQTLAYSLGVPGGGEEVYLLAKGREPVPLGAGRN
PAWSPDGSRLVVERTGASGQPELWLI KPGDGSAVRLVEGQRPWGPGRYL
AFVRVTNTERALTYSPDGSPFLTVRORQGEI RAI NLGRKGELPADQMEGK
MLSSDRLLLLAPDTPPGNELNWLRRLEMEGVREPRITLLLEQANNYQNVSF
SPDGETLLVARRDGGTVALAQAGLREI STRRGEQ

>2617922148 Ga0073689_1616 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_161]

MRGKRCLYCGVFI CAI LAVAVI AAALPSSAAA AAVEMKAWPGLGGLFRMDQ
PLELLI TVENSGPGFKGSI TVGPDVEQPEGLRPLARHVLDDVI PAEGSA
QFRMVI PGELAARKPVVELAAGGAPLAEDQVEGVAVGGGRVFLTLGEDI A
GGGLQGWLAETPGAQVNLKYI SPGELPEESLLLGVADVI MLNPAGASSLN
EEQVRALKEWVELGGSVLVFDGAGAGEGGNFADVSPVRVTGGKVVDGKLA
GLRSGGPLEVAAGELVAGRALAVENGVPVLARRALGGGGVVYCGAAPRNL
GGESRGVWSTLLSGAVPEQVYKDRASGRTYGLGAGPAGQLVSPSSYI PRL
AGPPVPLLAALWL VYTA AVGPLLYFLLRRGDRRDWAWALVPAGALVAAGG
FYLLAPAGRMQGYLTQTLATVEI LSPELA AVRAGATVVAARGGDLTVHHA
GDMFTGPTGYSPKENQAPVLVQRDDGKTTVSFGGVPYSSLRQLYAYGLR
RDPGRI EGKFLAGKDI KGD LNNKTGLDLRDCRLVLGGRVI RI GDLPAGD
TVHI DETTEGPGFTPGREMLLNELGGNTGVPNRPDPFFQERAMI SESLY
GGPGRTAGI QFI GWHDGAPGI FEVAGKPGRVEDYGLVMVKQAI GMEAAPG
RFRLPPGFI KPRPGETGFAS TGGPDAKVI YSERVNLVYDI DEAGLNADFK
I GALEFQYAGGQFTAPVEI YNHRDGKWEQLPDGGGKI GAEELSRVLSGSE
VRLRVAGESRGYPVWPGLAVEGVMS

>2617922147 Ga0073689_1615 ABC-2 type transport system ATP-binding protein
[pelotomaculum Ga0073689 : Ga0073689_161]

MIKFVGVSKNFGATRALDNFSLEI GGGVVYGLI GPNGAGKTTAMNI LATL
LPPDAGTATVDGLDVVREAGEVRGRI GYMPDFFGVYDGLRAAEYLEFFAA
AQHVPAERRSRLARTLLELVNLPDKADVVDALSRGMKQRLALARCLVHD
PGALI LDEPASGLDPRARAEMKEI I RHLKHLNKTVLI SSHI LPELAEI CD
EVAI MAAGRLVVS GTVAEI TAVSRGARQI RVEVLERAELADFLATRPV
GETLVDGPEVRFFFGGSPAEOAGLLQAVI SGGWPVVEFGEVRRNLEEAFM
AVTGGEVDGFDGN

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>2617922146 Ga0073689_1614 ABC-2 family transporter protein [pelotomaculum Ga0073689 : Ga0073689_161]
 LTEI NPVLLKELRQRFRTGKTAWLLALYLLVI GAFVLGFMYNLRNSPGM
 FQGRSRDLFI ML SVTQLVLLGFVVPGLTAGVI SGERERQTLNVLLTTRL
 TTRQI I WSKLVSSSAFVALLVI ATLPLYSI VFMYGGI APGQVLGVFGFY
 VTMFLFASI GVACSTFFQRTGVSTVTAYGLAFALAAGAGFLAVFLYNLNO
 LQHRGNWRPETWSPAFMAWVVEFLQDI NPVFVLLLEI LGESGI PTGVDFGP
 PYWAI YAAVYLVGTI LLLCWSARLLSPGGKRRRHLSGRSWGTK

>2617922145 Ga0073689_1613 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_161]
 MNSGFRVGVDFGHI TSFHRDREEGI ELAESPDAQAVTREEAANKFTGL
 LEMELQYLERLPSYGPFKPEGEARPALVYVPAGLTAAI DALTGKPLAEFM
 PSLPRSQRLTQEGEQLI VKTPEEAGKLLTDVFGI DLAGMQFHGSVDVS
 PFGNRESKQKDYSWNTMPQKGGDGRPDGQMRHAHMTI DAGTGQVI GFNY
 QDESGRGQKGTASLEAAQETAVQLLQKYLPEGPVEMEMRVRYQDVEEMI P
 AWVDKSKLKEHERPRPVI SFTFNRVHQGVPMMDRAYSAQVDALTGKI VGF
 YTGKSVSSI TKPDVALPDNRNVVSPEAAKAEFLQQHPLKLVYI WPEYFNQ
 KAPAPWLVIYI LGPGAGYFVDAFTGKTVTTRNE

>2617922144 Ga0073689_1612 prevent-host-death family protein [pelotomaculum Ga0073689 : Ga0073689_161]
 MPNI RPSSDLRNKYNEI SEFCHKYSEPVFI TKNQGD LAVMSI ETFERLV
 GKFEYKLLDEGMEAMKTGKVMPAADVFRKI ENGLDG

>2617922143 Ga0073689_1611 addiction module toxin, RelE/StbE family [pelotomaculum Ga0073689 : Ga0073689_161]
 MKSYKVLLTQPAANDLRSI TCYI ANELKEPTVVKLTGKI KEAVMSLAGL
 PTRHALVADERLAVQGI RKLMDVSYI VFYI VDEKAALVTTVRI LHSPTFD
 F

>2617922142 Ga0073689_16012 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_160]
 MRQNSNCTSC EEAKNGCEDKSKCELERLPENDFSRI KNVI AVMSGKGGV
 GKSSVTS

>2617922141 Ga0073689_16011 Predicted Fe-Mo cluster-binding protein, NiFX family [pelotomaculum Ga0073689 : Ga0073689_160]
 MKIAI TCWGSRVSP LFDTRKI VI I ETDASGI QNSGEVDI SPVNPFSRAG
 FLQDMGVEVLI CGGI SECYLQMAALKI KVI PWI SGEVDKI I SEYI KTL

>2617922140 Ga0073689_16010 PAS domain S-box-containing protein [pelotomaculum Ga0073689 : Ga0073689_160]
 MNKKGLDEMNTI I LDSI TDGVFTVDREWRVTFFNRAAEEVTGVSGEMAVG
 RYCWEVFRANI CETECALROTLETGNPVFNKAVYI VNAAGKRI PISI CTS
 VLKDSQKQVI GGVETFRDL SVVEELRKELYGRYTFADI I SKNHLMQQI FN
 I LPDVAESESTVLI EGPTGSGKELVAKAI HNLSHRREKPF I AVNCASLPD
 TLLESELF GYEAGFTDARKSKPGRFARAQGGTI LLDEI GDI SPALQVKL
 LRVLQEREYEPLGATRPVKSDI RVLAAATNKDI TKLVEQGSFRRDLYRI N
 VMKLTLPPLNRRKEDI PLLAEHFI NRFNTLREKDI SGI SEEALAI LMQHD
 FPGNVRELENI I EHAFI LCKEGLI MPRHLPGQLQSAKAPPLAAGCTLHEI
 EARVI FEALARNGWKRI AAARELGI DKTTLWRKLRKLRQESGFNFG

>2617922139 Ga0073689_1609 CO dehydrogenase/acetyl-CoA synthase complex beta subunit [pelotomaculum Ga0073689 : Ga0073689_160]
 VI DEFKGQWRSFNEFCYKNSQRNI EVVNFYTI MEYPMTSCGCFECI LAMV
 PECNGFMVVNREHGGMTPSGMTFSTLAGAI GGGAQMPGFVGI GKSYLSSP
 KFLVADGGLARLVWMPKALKEQLRPQLEEAEEAGLGKDFVDKI AGETIG
 VSGEEI LPFLEEKGHPTLTMESLI

>2617922138 Ga0073689_1608 carbon-monoxide dehydrogenase, catalytic subunit [pelotomaculum Ga0073689 : Ga0073689_160]
 MPRFRDNTLTHRPSAKAPRVDPKNI KRSVDPVLEMI DVAREN NVI TAF
 DRVLAQQPQCQFGYKGI CCRFCMMGPCRI KSDEGPASRG I CGANEWTI VA
 RSVGLMI LTGCASHAQHGNHI AHVLHMI AEGHAPDYTI KDPEKLARI CKK
 VGI DTEGKDNLALAKELAEVALEDFKRLKGEGEATWI TKMVTNDRNELYR
 SHMVMPHGI HATI SDLVTOAHVGMNDP VNLVFSAVRVGLADLAGKWI AT
 DLSDI I FGTPKPVVSEANMGVLDPKKVNI I VHGHNP LLSEMI VQAARELE

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SEARVTGATGI QLSGI CCTGNEVLMRQGVPI I TSFASQELAI CTGAVDAM
VMDVQCI MPGLNTVAQCYGTRLI TTSDI VKI PGSAHI DYQEARAMENAKD
VVRQAI GAYKERGI RPVHI PDVKNKVAGWSLEVI FDLFRTVNPDRGLR
NQPARLEPARSQGRDRRVQGPVAVV

>2617922137 Ga0073689_1607 acetyl -CoA acetyl transferases [pel otomacul um
Ga0073689 : Ga0073689_160]

MYSKAFI PYRGYYSSPFARWQGSLOENSI ELGAKTAKRWLETKNLDPKI
FDYLYLGKSVGQLHTFYAAPWAAALMGAADI PGCHVPQACSTSTTCVSQA
AAGI ETGLYQNVFCLMTDRLSNAPHTI WPNPLGPGGEVI SENWAMDNFNR
DPWGGVPMI QTAENVVKKAGGI TREDCDALTLRRYEQYRDALANDREFQK
RYMFPVEYRKGKGTALLEADEGVTPPTREGLVKLKPVI EGGVHTFGAQT
FPADGNCGI I VTRGKARELSVGSNVEI QVLSYG FARAPKAHMAMAVVPA
ARMALEKAGLEI KDI KATKTHNPFAANDLYLANEMNI DVMKFNNYGSLLI
FGHPQGP TAGRSI I ELI EELVI LGGGYGLFTGCAAGDTGAALVVKVS

>2617922136 Ga0073689_1606 Enoyl -CoA hydratase/i somerese [pel otomacul um
Ga0073689 : Ga0073689_160]

MKKPPI AVI NGLALGGLELAMTCDFLAADKVEFGLLEVTGLI I PGNGG
RQWRHAAPAAADWRRSRNL

>2617922135 Ga0073689_1605 hypotheti cal protei n [pel otomacul um Ga0073689 :
Ga0073689_160]

MVFI I NI LLLKMTLTWFCDVYTCI LRMLCI KEQKLLTLKLF

>2617922134 Ga0073689_1604 hypotheti cal protei n [pel otomacul um Ga0073689 :
Ga0073689_160]

LI SKAPQFLRGHI YVCPGMGVVYEVSVSNGEGSSCSLRQSVLSLLI GAV
MRTCGSVNYFV

>2617922133 Ga0073689_1603 tungsten-dependent benzoyl -CoA reductase-rel ated
protei n bamF [pel otomacul um Ga0073689 : Ga0073689_160]

MSAGRDFKPRI VGFLCNWCCYGGADLAGVSRFQYPPYI RVI RLMCSGRVD
LAHVLRAFSNGTDGVFI GGCHLNDCHYNTGNYDALSM TQLCRKLLERI G
I NPERLRLEWVSAGEI RFADI MNEFGNKVKKLGLPGSSEGI DKNELRSG
I EAVTKLI PYI KLVKRGKLLALHVPDEEEYNELYTSDEI DRLI REAPSYYI
DPDKCRACMI CARRCPVEAI I SVKNQI HVI DQEKCI KCGTCFEACPSRFG
AVTKI TGGPVPPPI PKGERI I I RKSKEKAEI S

>2617922132 Ga0073689_1602 tungsten-dependent benzoyl -CoA reductase-rel ated
protei n bamE [pel otomacul um Ga0073689 : Ga0073689_160]

MKKELERI EGHVLKSLADGNFGDVM I VGGGI SGI QGALDLATAGFKVYLV
DKAPTI GGHMAQLDKTFPTNDSCSMCI ESPKFVECNRHPNI EI MTYTEVGS
VEGEAGDFKVTLI KKPRYI VESKCTGCTTCVEYCPVKYPDQYNQEI SKNK
AI HI YFSQAI PLVTYI DESCLYLKEKKCTI CQSVCKNEAI DFNQTAEKVE
VKVGAI VLAPGFEPDPLREDYGYGKFENVVTSLDYERLLCATGPYEGE
I LRASDKKHPHI AWI HCVGSRQVI PGGNSYCSAVCCTYTQKQVI LTKDH
DAEAECAL FHNDI RSYGKDFERFYQRAEKLPGVRFI RSYVSI GKEI PESK
NLTI RYSTPGDGVEEEFDI VVLSVGLVPPADFKGLADKFGI ELNAHGFC
KTNPANPMETSRPGI FI SGAFQGPVDI PESVVTASGAGSQCGALLAYRRG
DLAKERVYPPERDVFGECPKGVFVCHCGANI GRVVDVPSTVKYALTLPN
VVHAEGLFI CSTDAAQKI ADSI REKGLNRVVAACTPRTHEPLFRDTLR
EGGI NQYFFDFANI REHCSWVHSKEKEEATRKA KDLI RMSVARARHLEPL
QEFDLPVNKAALVVGGLAGMTSALS I ANQGHEVYLVEKEPDLGGLARRI
HYTLEGLDVQAYLRDVI RKVYQHTLI HVTYDATI TGVSQYVGNFVTRVRS
EGRDMEI KHGA AVI ATGAEVYKPT EYLYGQDDRMTHLELEE QI AKRGER
ALNARSLVMI QCVGCRQEDRNYCSRVC CGESI KNALRLKEI NPGMDI YI L
FRDI RTYGFKEDYYREASKEVRFI RYKPHDKPQVEAGEDEEGRPVLRVT
VTDPLVGGKLDLADLLVLAAAVI PSAGSQAI SQLFKLALSPDGFFQEAH
VKLRPVDFAAEGVYLCGI AHYPKPI PETI GQAYGAAGRALTLLSHDTVVA
SGSVCEVDEKKCI GCGACI SACKYGAI EFRDTRQGKKATVI AVLCKGDGL
CNSKCPTGAI SLKHYADEQVFRQI DALFSEA

>2617922131 Ga0073689_1601 hypotheti cal protei n [pel otomacul um Ga0073689 :
Ga0073689_160]

MI VKYLN DLQERFF TWCDHAVQNF I EREGTMLQWRPRKNPDGSYDLVFK
VAARDKTGSI FTVPI PMEFHELLEREYFI NHPPDEPV

>2617922130 Ga0073689_15913 Predi cted dehydrogenase [pel otomacul um Ga0073689 :

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Ga0073689_159]

MQKLKVGII GAGMAFERLHYPAYQHLADRYEII AVCDLDREKARDWADRL
HLSQGSVYTDFOEMLAGADLDVVDI MVPI ELNFI VTEAVAKSLAGRRKGI
I CEKPLAPTLAQALPARDLAQYNI PI MI AENYRYNQEI DI I RDLVRTGR
I GEVYFYI QNRVVDFFPGDMLQDKFPAKEWROHPEFPGGAI ADTGVHDLA
LRHI FGPI DRLQAFGRLOPSGFAPYAVVNVNLLFKSGVTGQFSFFCAGRE
MQRPLTGLRI FGARGMI YLEERDAGTI NLA FNDRTERI PYKAQKGYNE
LLNFYNALTGVEPI SVTPMEFGLKTVQDI LLSI REERI VPVDEAASYE
PVYGRSPAGQENI LQ

>2617922129 Ga0073689_15912 Choline dehydrogenase [pelotomaculum Ga0073689 : Ga0073689_159]

MPKNLDFVKHNCDDHRLHDLNKRKYAKEADI CI VGAGAAGGVLAYEL
AKAGFKVVVI EAGPFWNPQTDFADEL SMQNLAWNDRVLVAGSNPLAMGH
NNSGRGVGGGTVHFTGVFYRFHESDFRVKTL DGVADDWPI TYQDLEPYD
RI EKEI AVSGPRFFPWGPFQGPYPYPEREPI SANA EVFRRGCEKLG I RSA
VAPLAI LSAPFDGRPPCI NRGFCNQGCPLNAKFSTLI HHI PKAI KHGA EV
LSDCMVTRVDVDTGKVTGVT FVHDGKEHCQEARLVI LSNFCVETPRLLL
HSACSRFPDGLANSSGMVGKALMTHSGHDVYCKFPDEVRI YKGTPVLAVS
QEFYETDKSRGFVRGYTLNSHGSRLGLAKNLASKAGI WGKKLYDI MRDY
NFYAQVTVVGEI LPDNNNTVTL SDEKDEYGMPPVPVTF SYGENDNRLI AH
GVRKAQEI MEAAGGGPAFI I PDTGHLMGACRMGNPATSVVDGFCRSHDI
PNLYI CGASVFTSGGCNPTETVMAI AARTADHI I HEAPKGEL

>2617922128 Ga0073689_15911 Gluconate 2-dehydrogenase subunit 3 [pelotomaculum Ga0073689 : Ga0073689_159]

MQENRTRYPHYVDVLEKEHWDHTREI VLKRLGPFPENKFLKEREAAMI F
AVARHI VYDERKEI LDYVVHLDVLSPLGESQRKVGAPQKTLVRRGL
KAI DKLSQKQYGAPFLEI GAQRQLDVL TSLHLGKALPLDEWQNVPOKELF
KKLATEI VSAYYSHPLVWSEI GYGGPAYPRGYI RVEMGLSDPWEAVRNAE
KS

>2617922127 Ga0073689_15910 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_159]

VWI GWPI DRV I LLFTGI AFLMI SLOVTMFHYRQNFHWAMYGPVVAGPVL
GVLA VLLAFYNLP LLRGVLAVLFFAGLALGVTGSVLHVYGVGQVRVGGYQQ
SQNFLI GPPLTL PAMVAAMSVLGLI ALYWR

>2617922126 Ga0073689_1599 pyruvate oxidase [pelotomaculum Ga0073689 : Ga0073689_159]

MDQTVAQI I LKAFAAWGVKNVYGVSGDAI LPFFDALGKQGEI KFYSAA TE
QGASFMACGEARVTGKPGVCLATEGPGALNLANGVADAYRDGVPMI I TG
QVETAGLSTI ARQYFDQQQLFAPI TGFTTLLTRPESVLEVFKTAMEKAAG
DNTPCHI SI PKDI FSSPARDFS I PGLGRPLPPGVSGSVEEALNI I GGCRK
PVI I TGRAAVPFKDVVFQLAARTGAGI I PAQGAGGI YPGAESLVLGGLGE
AHI PPLLNRADCI LL I GAAPYEHKFI PPAI KLVQI DTRPQNLDHRLRPFP
LTGDMALI LNKLLLEGLSNAGPDAGWQEEI KI CRAARLKMI EGEASLTGKP
I PPRKTVSVLNGVLPEDAVI TVDTGEFMHWFDRGFI AKDRQQVI I SGYWR
CMGCCLPFGLGARAAPFGRKVVL TGDGGFI MTMQEI I TAVRYSLPVTVI
I FNNGAYSLEKHRMQAGMDPFGVEVKAPDFAAI AAACGAEGI RVEEPEM
LREALARAMALDRPVVI DI I SSEEKPTFV

>2617922124 Ga0073689_1597 RNA polymerase, sigma-24 subunit, RpoE [pelotomaculum Ga0073689 : Ga0073689_159]

MQPADKI LI EKSKNGDLEAFEI LVRRYESKVYTVAYRFLGNHADASDFAQ
EAFRLRYQALPGFRGDSSFMWLYRI TANVCRDEI RRRQRRHVSLDGGGA
ETGGVQAGFTGYGCI LSPEEAFERKEFSEMVOQCLNELSEEHLRI LVMRE
IQGMSYEEI AAVLQCSMGTVKSRLSRARQAFKEKFSGRRELFARGSRLAK

>2617922123 Ga0073689_1596 Putative zinc-finger [pelotomaculum Ga0073689 : Ga0073689_159]

MQCREVKELLSPCLDGVLPPEEVDVTTHLAVCTDCREEWYALCEMVDLF
RSLPEI APHNGFSAGVI DKI TSYRKMKKESGAVLLI GNLARRPWTRMLAL
AAGVVLVFGI TALI YGI TGRWGFQDQFSAPYRAI HRNAGQSASGDADNI D
DTGGAGPAVNRTVEI ANNNQSSGRGPAAGDPPAGVNPAGVNPSSGKARM
KOPASKAVYKDESSDNDNSAAHGTDNKNMSRTDTPAAERVGEEAQLFSVP
VRMAI PRMTSVKEGSTSQQDAFSSI PVSSKNPQKVI RI VSLGLAATNPA
RVKEQI AAVASENGSLLPSDPGGEI TI KLPASRFQALNLLREMGNVTL
RHEGDEDTVTEKYFSYESSLKEI AEEQRLLA EAASAGPDKAAEVQARLDR

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VRENMKQQEKLFDNLSGRVEYATIKINLE

>2617922122 Ga0073689_1595 peptidoglycan-N-acetylmuramic acid deacetylase
[pelotomaculum Ga0073689 : Ga0073689_159]

VEKWKNNKKVYLAVLVVFLGI SGYALKNHLDAAAGREAGGPDQTAVSETST
EAGTPSVSETAYGAAGTGHTGTGDGKGGAENVKDGKPSGATTATGDLSNT
RRGWGLKRNSDHRQPEMPSGI SNTLKKYGAYWI GGPDEKVVYLTFDEGYE
NGYTPKI LDALKANDVKAFFVTGHYLSQPDLVRRMVEEGHI VGNHTET
HPSLPDVSNEQI KKELOQSVVEERYGEVTVRKDMKYL RPPKGEYSERTLAVT
RELGYHNI FWSMALVDWVPMPPGGPQESHQSVMDNLHNGAVI LLHAVSKDN
TEAMDRI LKDI KARGYTFKTLDDL VKS

>2617922121 Ga0073689_1594 RNA polymerase, sigma subunit, ECF family
[pelotomaculum Ga0073689 : Ga0073689_159]

VVADEI LVKKAQGGDTAAYGELVRRYQDRI YGLALKMFSREDAGDAAQET
FVRAFRLSGFNQASFATWLYRI ATNVCLDQLRRRGRERORLLPLETGD
DEGARLRDNSPGPEERLLDRERAGALKQAVRELDPGYRTALALHHYQGLS
YSQVAAAMGLPEKTVATRI HRAKKMLREKLLGGEDGALPEGKKEAGRVP
RRMSAL

>2617922120 Ga0073689_1593 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_159]

MAEVSRI SAASGAEEERGGAPARGRLKPPRSSARLELLQDLAVAAVSL
LLFWNAGAWLGGGKMLAAGKSVTGAAVAYSRTDTTVVERFTETTGEYTRK
IFFEEW

>2617922119 Ga0073689_1592 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_159]

MKCVNHPEVETDTLCAVCKASVCPECRVTLRDQDYCRSCLEEMAGKVNTG
VYKQI SAFWALALSLFPGAGYMYLGLMNRGLQI MVVFFGAI FVAGMTHI D
EILPLVLPVWFYSI FDTLQLTRQMRGLRVEDKPLLDTGHTNWQRLLG
YALI GLGALALLNNFLPYI FNYWMTSKLI TPLII I AIGVFI LYRSLGRGR
HNDGEGND

>2617922118 Ga0073689_1591 Domain of unknown function (DUF4098) [pelotomaculum
Ga0073689 : Ga0073689_159]

MTAKGMTKAGPI TLAVGLI AGGGVLLLLYNLGTVKNLDWVWKLWPLLLVGV
GLEFYI KRALI REEEVHFHLPISI LLI LVLI LSSGVLYAVTGVGRSLLDGI
PFHQFKPAYTRTWEADPVAVKAGERLVI KNARVGVEI TPAPDNMLRVKAV
VRGPDTPGAGAQAGGANPEVKREGEVSVTVPETGGWFNDTVVTDLEVAV
PDGLDVRVENTAGRVEARNAGI NLTVAGNTGSI ETEDVGGNLEVRNNTGR
I EIRNPGGDVMAGTNTGSI ELTSRPLAGKYALESNTGRVGLRLPGDSDL
TIEAESRTGRI TVHDLPPDRGSRDAGENI EKAAGVDVKDKFSYTLGSGK
GRADLRSGTGAVNI TVR

>2617922117 Ga0073689_15814 Fumarate reductase flavoprotein C-term
[pelotomaculum Ga0073689 : Ga0073689_158]

WLQEPVEVDYATLRRELETLMGQKVGVPVRSGQGLKEALNFFDHWSFLYRH
RVENADQMEVKNMLQVGELVAEALARRESRGGHYRVDYDPDTHPRWQKHM
IFRR

>2617922116 Ga0073689_15813 putative N6-adenine-specific DNA methylase
[pelotomaculum Ga0073689 : Ga0073689_158]

MSRI ELI ATATFGLEAVVAREVKELGYEDMMVENARVVFAADEAAI CRSN
LWLRTADRVLVKMGEFQALTFEELFERTSALPWPDPWLPENAAFPVEGKSV
KSRLHSVPDQAI VKKAVVEKMKQYKQWFEETGSRYTI EVALLKDVAT
LTI DTSGAGLHKGYYRRLGSPAPLKETLAAAMVLLSFWRPERTLVDPFCG
SGAIPI EAALI GLNI APGLRREFAAEGWPNVSKNLWAKAREEAGDLVTPG
RSLRI LGTDI DHEVLGLARYHARRAGVEDKI HFQSLPVAELRSKYKYGCI
ICNPPYGERLGERROVERLYREMGVVFRLDTSFYI LTSHPDFERLFG
GADKKRKLNGRI QCNNYQFYGPPPPRPHQTDDG

>2617922115 Ga0073689_15812 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_158]

MAPHLLRDGALLLI HETMALTYTCPLI RRTKTLRKDFI DTVARCWRELLQ
DPRI RDLVKMDSRDREREGPYPSVVMWGRGGGGP

>2617922114 Ga0073689_15811 Predicted amidohydrolase [pelotomaculum Ga0073689 :
Ga0073689_158]

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MKETRVALVQMMAKTGLVDENMKKI EWFTNEAARQEVDI I CFPELCVQGY
NREMARLI AASI PGEI SGAVGRMARQAGLTVLVGVAERSKTGEPYI THLV
AFPDGSI QKYRKTHLGKSEI PYFTPGDEFVVLSCATARFSI QI CWDLHFP
EMSTI LSLRGAEI I FAPHASPTI VGDRRDI WLKYL SARAYDNAVFVAACN
LVGDSGHGGSFCGGAMVI DPKGNVMAEAFNGREMLVVDLPTLLNTI RN
KEAKTMRNSFYLAGRRPELYGDLVKNP

>2617922113 Ga0073689_15810 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_158]

VDLNTHTWVVTGSVAEGLKNI SFKARLWI FFTAALAMI FISGCSI WKGEK
TTYKPLEI KAEDFAI FLFESSEEI YRANVKNPDMWAGLREQAQRDKDYAP
HYNWLYDITYGRWDERRRDQLKQI MADYHPQPMSERLI QNGKQAAGLDEI I
RFI KEDRFFGKNRNTLVDFYSWYGANYALPHYERI KPLLQRKANI VGGRV
EKDFNI VGFMEKETGI KLKEKPDAL ELQLNMRI I GASGFSRDRDSI YTVQ
WNSAPGKI WMSMFHEFGHPFFRTFTGKWSFKRLAGKLLKDEKL TARFKED
VPYTWEGWVEENLVEGFARYLNMRKGI AMDVGEGI YI FDADFARALLEGF
DPQKTSLEDFTI KFLKRKYNL

>2617922112 Ga0073689_1589 nicotinate-nucleotide pyrophosphorylase [carboxylating] [pelotomaculum Ga0073689 : Ga0073689_158]

LQMEKLVENCLNEDI GFGDLTTNSI VPPDATSNGYI VAREEGVVAGLPLA
EMVFRRLDPSI EFRAGARDGEWVDPGRVLGAGVAGSARAI LTGERLALNFL
QRLSGI ATATALLARLI AGEKARI VDRKTTTPGLRMLEKYAVRAGGGRNH
RFGLYDVTI KDNHI KMAGGI KAAVAAARRTAPHTAKI EVEVEDLAGVQE
ALAAARVDI I MLDNMDPVAMREAVELVAGRALVEASGGI GEENI RAVAAAG
VDLI SVGALTHSVKSLDI SLDI KEI KPRSATGDVFPTHSA

>2617922111 Ga0073689_1588 BirA family transcriptional regulator, biotin operon repressor / biotin-[acetyl-CoA-carboxylase] ligase [pelotomaculum Ga0073689 : Ga0073689_158]

LKKAI LRLLEKQPEYVSAGEE CKSLNVTTRTAVWKHI QVLREDGYE I DAR
PRAGYLLTGVPDKLLPEE I RDGLTI RFI GRKVFIYDRVSSTNDLARELAR
KGAGDGSLLVAAEQTGGKGRIGRGWFSAPYKGI WFSLI LYPPVNPFDASQ
I TMLAAVALASAI RDVTGVAAGI KWPNDLLVNGRKI CGI LTELSEAEMDRI
NHLVVGVI NANLDPEDFPGEVWNTATSLKI EAGRPI SRVGLLQAALAEF
EKWYTVWLTGGFAPVLAKWKEMSVSLHCPVRI HTLNKAWDGWAEDVDEG
ALLLRLPDGKLQRLVSSEVSLRLVNFSQGEQLF

>2617922110 Ga0073689_1587 competence protein ComFB [pelotomaculum Ga0073689 : Ga0073689_158]

MEYLVNEAFEEI LRFDKSYRGCRRLDTMAVALNKLPAHYI TAEGEVL
LRAVSLMQQFKVDVI KAVAESLELI LKHPRHKE

>2617922109 Ga0073689_1586 type III pantothenate kinase [pelotomaculum Ga0073689 : Ga0073689_158]

MI LVFVDGNTNI VLGVEDKQLVANWRLSTNRYRTPDEYGVLLKELFVFS
GLEMKSI SALVI STVVPPLSI TLDRCRKYFNLSPLVVGPGI KTGLSLRY
ENPREVGADRI VNAVAGLERYGGPLVI VDFGTATTFCAL SARGEYLGGA I
APGI GI STEALFARAAKLPRVEVTKPPSI I GKNTVNSMQAGI FYGFVGQV
DEI VRRMKKELGENTKVI ATGGLANLVAQESVTI DRVDPLLTNLGLRLI Y
ERNAQR

>2617922108 Ga0073689_1585 tRNA-U20-dihydrouridine synthase [pelotomaculum Ga0073689 : Ga0073689_158]

MRI GSVQLENRVI SAPMAGI TDRAYRI LAKEAGCGLVCTEMVSDQALLYG
NLKTCGLLDI TGEAGPVSMQI FGSNI KYMAGAAEI VESRGA I DI NMGC
PTPKI VKNGEAALMKEPAKAAAMVRVAVVVRVVPVTVKVRKWDENSVN
AVELARLVVDAGAAAVTVHGRTRSQFYTGADRG I AAVKRAVDVPVI GN
GDI WTPEDALAMLEQTGCDGVI GRASLGNPWI FSRTSHFLKTSSELLPGP
DPAEKVAMALRHLDLLVEI KGERVAVWEMRKHAAYWMKGLRGAARLRERV
NTARTGNELRKI I QLVLE

>2617922107 Ga0073689_1584 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_158]

LELI RLSEKI I SRRKI DHSI DEI LALRSKGLSQTEVAARLGVDRTLVCRL
ENLGEI RKGRSLAVVGFP I LNKEELQDALEQEGVDFVI LMTEAERWEYI R
QKSGVELFNSI MKLI AKAHSFDQVLVI GSSQRI KI FEAVLNKEVVGFEI G
ESPI QEDKFVDVEKI VRLI RAI KG

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>2617922106 Ga0073689_1583 Predicted amino acid dehydrogenase [pelotomaculum Ga0073689 : Ga0073689_158]

LQNFAPMI HPMHAGDVARKFKFARFVPDRVLERAFAMLPMSMKVSHI TGI R
SPYGGAEWFWACPLTARLMTALPREYVLNKI IQGGRVAEKLGAKE LGLG
AFTKVVGDAGI TI AKHLRI PVTGTNSYTVATAI EAVGEAARLMGRDLKKS
SVVVLGATGSI GRVCALI LAREALSMTLVARNEKKLEELAVKI LYDTGLA
VKVTSKSKSALRSGDI VI TVTSAVDTVVEPEDI KPGAVVCDVARPRDVSS
RVAEVRDDVLVI EGGVVEVPDVEFDLNFVGFPPKTAYACMAEAMVLALEN
RYESYTLGRELTI KQVEEI AALAKKHGFKLAGFRSFGRAVTMQEI DEI RN
RANSPPLI PAVAK

>2617922105 Ga0073689_1582 transcription elongation factor GreA [pelotomaculum Ga0073689 : Ga0073689_158]

MKEKEVI LTVDDLKLEDELGQLKSVKRREVAERI KQAI EFGDI SENSEY
EDAKNEQAFI EGRI LLEKMLRNAKI IDENLGTVEVSI GSTVKKLDLEY
GDEFEYTVVGSVEADPGASKI SNESPVGKAI LGQTKGNVVEVTVAGQLK
YQI LDI LR

>2617922104 Ga0073689_1581 lysyl-tRNA synthetase, class II [pelotomaculum Ga0073689 : Ga0073689_158]

MSEQKKKKAEI ADSKAPSGKPEEDLNEMMLVRREKLAAMREKGVPEYGG
FERTHTARYI LDNFDLENKPVVAGRI ISRRGMGKATFAHI QDATGRVQ
I YVRLNNVEPEAYDLFGKLDI GDI IGVKGNVFKTRMGEI TVSVEELKVL
KSLRPLPEKWHGLKDVELRYRQRYVDLI VNPEVKEVFETRRI RVI RKF
LDRRGFWVEVTPMMQI I AGGAAARPFI THHNALGI NLFLRI APELYLKRL
LVGGFEKVYEI NRNFRNEGI STKHNPFTMLELYQAYADYNDMMDLTEEL
I SSVAEVLGATKI ECGVEI DLSPPWDRI PMLEAVKLHSGLDFTI KTA
EEARRAVKEAQLELELEPADSWGAVLNKVFEVVEPRLI QPI FVMYPVE
I SPLAKRKADDPELTFRFELFI YGRETANAFSELNDPI DQRRERFLKQVEK
RRAGDEEAHMMDEYI NALYGMPPAGGLGI GIDRLVMLLTDASIR DVI
LFPLMKPRE

>2617922103 Ga0073689_15713 Tetratricopeptide repeat-containing protein [pelotomaculum Ga0073689 : Ga0073689_157]

MTEINGQGRLEQARSLLTANRLKEAEAVLKGLI CEEPRNAEAFNLLGAVW
ERRGGLLEEAGLLYRVALVI NPAYAPARHNLNRLVRMPPELGGI DLSHGRH
ESESHSI EKDGGKSSGATGTGKKLTDKGSN

>2617922102 Ga0073689_15712 NADH-FMN oxidoreductase RutF, flavin reductase (DIM6/NTAB) family [pelotomaculum Ga0073689 : Ga0073689_157]

MI TI QKVTRGPSTVLPVPAVLVTSQLEGSEPN I TI AWTGI MNSEPPV
YI GVRPVGRHSYRLI MESGEYVI NI PSAEQAKVVDYCGTVSGKDVNKFKE
TGLTPLPASRVKAPLI AQCPVNVECGVRQVSLGSHDVI AEVLAVHYNE
DI LNEKGRPDLDKI KPYGYCFNEYRMLTEKLGFMFGYSKKG

>2617922101 Ga0073689_15711 hydroxymethyl pyrimidine synthase [pelotomaculum Ga0073689 : Ga0073689_157]

LYTTTQMDAARKGI VTKEMEAVACKERMGI KLRELVAEGKVVI LANKNH
ASLAPCGI GRGLKTKVNVNLGVSKDCCNI ETELEKVRRAI ELQADAI MDL
SCYGKTEEFRRRLVEMSPAAGTVPVYDAVGFDYDKELKDI TAGEFLGVVE
KHARDGVDFMTI HAGI NRETAARFKKSPRLTNI VSRGGSLLFAWMELNGR
ENPFYEEYEDLLDI CRKYDVTI SLGDACRPGSI KDATDASQI QELI VLGE
LTKRAWAKDVQVMI EGPGHMALDEI VPNNLLEKKLCYGAFFYVLGPLVTD
VAPGYDHI TSAI GGAI AAANGADFLCYVTPAEHLRLPTLEDMEKI I AAR
I AAHAADI TKGVPGARQWDEMSEARRNLDSRMFELALDPEKARRYRKE
SRPENEDSCTMCGKMCVARNMNKVLAGAEP

>2617922100 Ga0073689_15710 thiamine-phosphate di-phosphorylase [pelotomaculum Ga0073689 : Ga0073689_157]

MAEKRGLAGLLAADI YGI TAEYSWGRSNI EVVARI DAGLRVI QYREKD
KSARQKYDECLKI REMTAAAGVTFI VNDHPDLALLVEADGVHLGQDDLPP
EKVRELVGEGMLI GLSTHSSAQALAAVKAGVDYI GVGPI FATMTKKDVCD
PVGLEYLEYVTQNI RLPFVAI GGI KEHNI AAVSRQGRCI ALVTEI VGAG
DI GAKVRALRAVLSQREDKN

>2617922099 Ga0073689_1579 sulfur carrier protein ThiS adenyl transferase [pelotomaculum Ga0073689 : Ga0073689_157]

MNDFEKAMAETLGVANLARI QEVKVGI AGAGGLGSNCALFLARSGFKKFR
I VDFDVVEYSNLNRQFYFASQVGRRKVDALKENLLMI NPSLSI EALPEKI

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EQSNSKDLFNCCDVVEALDRAEFKRMVVEAYLDAGKLLVAASGLAGWGR
SDQI KVHRI KENFYLVGDLVSEAGPLPALAPGVNVAAAKQADVI LSCFL
GERG

>2617922098 Ga0073689_1578 tyrosine lyase Thi H [pel otomacul um Ga0073689 : Ga0073689_157]

MLSFYEARRRYDNFDFESFFERVTDRI KRI I VKNRLGKLDYLALLSPRA
EQYLEEMAQRAHRLTVQHFGRI FLYTPLYLANVCVQCVCYCGFAHNTL
KRKKLSPAEVAEEARI I AATGLKHI LI LTGESRKESPVSYI KECVEVLKE
YFTSI SI EVYPLEEEEEYTRLVSAGVDGFTMYQEYDEEVYDELHPAGPKR
NYRFRLEAPERACRAGI RTVNVGALLGLHDWRTEAFFTGHLADYLQNVYP
DVDVSI SPPRMRPQLGGFLPRVSVSDKNLVQYI LAFRLFMPRGGI TI STR
ERSELDRDLI LLGATKMSAGSCTAVGGRSNHDSI GQFEI SDERGVAEMAQ
MI YARGYQPVYKDWQLI

>2617922097 Ga0073689_1577 thiazole-phosphate synthase [pel otomacul um Ga0073689 : Ga0073689_157]

VEDVFKI GGRELTSRLFLGTGKFSSNKLI PEVAKASGAQVVTVALRRVDL
DYEEENI AAYVPKDCI LMPNTSGARDAREAVRI ARLARAAGCGDWVKI EV
I NDNRYLLPDNYETI KATEI LAAEGFLVLPYI SPDLMAARRLVEAGAAV
MPLGAPI GSNRGLRTKELI RI LI EEI PLPI I VDAGI GRPSEAAEAMEMGT
AAVLVNTAVATAGDPVAMARAFGLAVEAGRLAHLAGPGETLEYARASSPL
TGFLSD

>2617922096 Ga0073689_1576 sulfur carrier protein [pel otomacul um Ga0073689 : Ga0073689_157]

LLTVVLNGKPEEFPSGMTI AELVTOKGLNPEI VI I EYNYELVDREAWAGT
VLKENDRLEI LRFVGGG

>2617922095 Ga0073689_1574 AAA domain-containing protein [pel otomacul um Ga0073689 : Ga0073689_157]

LTEL RVDGFGI LNLHLTGEDLSHNI TVI HGLNEAGKSTLLEFI RAVLFG
FKAGAGRGGEPLRGGRPGGYLVFTGEDGRVYRVERVLGRGQKATVTLPD
GSAGDEAVLKSAVLHNI SPLVFRNVFAFGVDEMRRLEELREGEI GAYVYV
AGAGVRADRLAGLNLRLQEEMGALFKPGGSKPEI NRLLKELEEI NAAI RR
LOREPEHYEELGRELAGLKEKREGLERRKRQDEARRNWLEKVLGARESWI
RLAEARRCLEQMPAPSLPENGEKLRFLDSLEAGVKRSLLEERLEREA
GRLRELKRQEDDLVSELKMPRSPVPLWLPAALAVVLAVFTAVAFSADTA
PGLFSLAADA AVLALVTTAVRRGAADLKSRGRLEENLNELKRRI REAGE
EVERLSSQAASLSGELKKA AVATLGNPDFTAEEI SATRRALVVELRRGEE
WRRVEERLRERI QACRRELEI I AGSPRAVDLERDLAEREDGDI KGELGR
LTDRLEEAKKVI RETGELI GELEGRLRAMEKGEELAAGLQEREMKLSTLA
GRAREWQVRALCLRLHLAKDRHERTRQPTVLRQASRYLAPMTGGKYTG
I APVGRADMLEVETPEGARAAAGSLSRGAASQLYLAVRLALARQYGGAGL
PVFLDDI LVDFDPERLKGAVRVLGELGRDRQVLLFTCHDHVLAALGECPD
GFLI RLGDGLKLDI

>2617922094 Ga0073689_1573 DNA repair exonuclease SbcCD nuclease subunit [pel otomacul um Ga0073689 : Ga0073689_157]

LSGGFTFVHTADLHLDLSQFRGLEQAFNLGEKVPEGVLRRLRNCTFEAFER
I VDLCI ERKADFLLLAGDVYDAADKSLRAQI RFREGLARLASAGI ATFFV
HGNHDHCAGWRAGLEFSNTVHVFSREVEFRPFVRNGREI ARI YGI SYPG
RMVVENYADRFKRNKDAPFAVALLHCNV DGI AGHENYAPCRLSDLLNRGF
DYWALGHVHSLVLNPEGPCVAYPGCPQGRRPGEGERGCLVVNVSDSGK
VSLEFVPVGPVRWEAL ELSI EGLGSDQGLVNRLGGLRGMRKETGGKPVV
VRI TLTGRGALHRYLNRPSYI ADLI REVRDLLPRGEEDFI YLESI RAATG
VEVDLDELARSDTLGLDGLLAGRARGDGLRTELRRALAPLLEHPGAGK
HLEPPGEEELDRLLERAGEMAVDLLME

>2617922093 Ga0073689_1572 hypothetical protein [pel otomacul um Ga0073689 : Ga0073689_157]

MGEKDERGKVYQFTPRKGPKLTKMKYVAPEKKELLKERARAKMDKRNFI
GVGI LLI LVAVLTFFKLR

>2617922092 Ga0073689_1571 hypothetical protein [pel otomacul um Ga0073689 : Ga0073689_157]

LTNRLADEKSPYLLQHKDNPVVWYPWGGEAFKKAKREDKPVFLSI GYSTC
HWCHVMERESFEDEEVARVLNGGFI SI KVDREERPDI DHI YTTVCQAMTG
QGWPLTVI MTPDKKPFAGTYFPKKGKGMPLLDI LERVGEI WKEDRE

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RVLEAGEQI TGAVRSRSGVSPGDGLAEGTLKKAYEQFRGRFDRQYGGFGL
APKFPTPHNLAFLLRYWKRTGEKDALTIVEKTLAAI YRGGI YDHVGYGFS
RYSTDKRWLVPHFEEKMLYDNALLALAYI EAHQATGKEFYARVAKEI FTYV
LRDMTAPESGFYSAEDADSEGVGKFYVWTPGEVREI LGERDGEI YCRLY
DITPDGNFEGRSI PNLINNTTLEGVAAEFGMAPGELENLAAGMGQKLFNAR
ERRVRPHKDDKI LSWNGLMI AALARGAAVFDEMSYRDAAVRAVDFLYRQ
LQRGDGRFLARYREGEAAYPAYLDDYAFWGLLELYGATFDATRLERAG
ALVRQAVDLFWDKKEGGFFFTGADAEELI ARPKEVYDGALPSGNSVMLVN
LLRLARLTGDESLDGI AGKLVEAFGGEVAAHPQGYTHFLMGVDFQLGPPR
EVVI AGQPGDPGVERMLRAARRKFLPDTVVVFHPI GDTGGKI EKLAPFLE
GQTALDGRATAYVCQNYSCRAPVTDYQQFI NSLS

>2617922091 Ga0073689_15613 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_156]
LASLPANI DPHEI EKTLNKMFSPEWLRNTAAKVGIVQSRKI DPATLFWI
LVLGFG

>2617922090 Ga0073689_15612 pyruvate, water dikinase [pelotomaculum Ga0073689 : Ga0073689_156]

VPEGFCVTTTEAYKRAI GHNQKCNALLEQLSALKVEDRERI VVVGKI RKV
IEGI EAGDI AEEI FRHLAKLGEENAYAVRSSATAEDLPLASFAGQQDTY
LNI RGKDAI LOHI SKCWA SLFTDRAVI YRMQNGFDHRKVYLSVVI QRMVF
PEMSGI LFTADPVT SNRKALSI DAGFGLGEALVSGLVNADI YKVREGRI F
DKKI STKKLAVYALEEGGTEEREI EPGRQNMQMTMTDEQI QLERMGRKI E
EYFGCPQDVVEWCLGEGHTSDPHGRAPMI GVSPFRCKHSSDHI DWTKREVC
PLSFFI VQSRPI TTLFPVPENDGQTRVYMSI GHQMMTDAI KPLGMSFFQ
LLSGDFPMHKAGGRFLWEVTHDLASPI GRKI VLNTAGMSDPLLKNALLSL
IRRKDFMDSLPRGKRSI SMRTEGLSWAMLI QALKI YRKNDAI I QDLI AR
NEASVRDLRQRI TCVSGDELFAFI I EDHKQLKEI MYDPRGFGVI VVGVLV
SGWI NKKMEKWLGEKSAADTSLQSVPNNTVTSEMGLALLDVADVVRHYPV
I EYFEHASDETFEFLAKLEGGDAVSHSLQAYLEKYGMRCPEI DI TRPR
WSEQPTALI SAI LSNI KNFGPNASSVKFEQGRLEAEQKEQELLNRLEQLP
GGKQKAKKTKKMI SVLRNFI GYREYPKYGFI QRYWVYKQALLKEVANLAQ
KGVIREKEDI YYLSFEFEFREVI RTNRLDYSI I TGRKEEYEVYEKLKPPRV
MTSEGEVI SGEYNTGNVPKALAGI PVSSGI I EGRARVVLKMTDANI EDG
DI LVTAFDTDPSTPLFVSI KGLVTEVGGMLMTHGAVI AREYGLPAVSVEN
ATRLI RDGQRI RVNGTEGYVEVL

>2617922089 Ga0073689_15611 PEP-utilising enzyme, mobile domain [pelotomaculum Ga0073689 : Ga0073689_156]
VLVAPSTDPGWTPFLFRASAI VMETGGFLSHGSI VAREYGI PAVVNI PNA
MKVI RDKRI I TVDGDEGKI LLMPNPVKQ

>2617922088 Ga0073689_15610 putative ABC transport system permease protein [pelotomaculum Ga0073689 : Ga0073689_156]

LNLYAALTVAWRSLANKLRSI LTMLGII I GVAAVI IMI SI GQGASAQVT
SRI ASMGSNLLQVMPAASFPGVVRGAGGQVNSLTMGDAEAI GELPLVQNV
PEARSQVTASSGSQTWTTSLVGTMSGMQAI KGWQMTAGAFFSNDDVDRAA
LVAVLGQTVVDNLLPAGSNPI GTSVTLNNLRFESI I GVLPPQAGFGGDQD
DVI YI PI TTAQRRFLGQGV I PDSVRMI NVQAQDATSLNAVQEEI TSLRR
RHHLGAGQNDDFRI QDMTAI LETVEATTASMTLLLSGI AAVSLLVGGI GI
MNI MLVSVTERTREI GI RMAVGATRGAI LTQFLVEAMI LSLVGGLI GVI G
GI TGSRI VAMLANWSP I LNPMAI LLAMGFATLVGI FFGYYPARKAANADP
I VALRFE

>2617922087 Ga0073689_1569 putative ABC transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_156]

MAFPVI QLKEVKRVYSPGLNQVMALRGI NLTI NEGEMVAI MGASGSGKST
LMHI LGCLDRPSSGQYLFNDQDVTGMPDQLAGVRNRKI GFI FQGFNLLS
RMPAWENVCLPMYYAGI SRTVMI LKAMDMLARVGLAGREEHRPSQLSGGQ
QQRVAI ARALVNEPYI I LADEPTGALDTRTSI EI I SLLQQLHQEKNLTI V
I VTHELEI AAYCRRVLRLRDSI I EDRLVEKPRLALELAALPQEEGDLN

>2617922086 Ga0073689_1568 HlyD family secretion protein [pelotomaculum Ga0073689 : Ga0073689_156]

MESSTVTAGEGFFKNRI KGI FPGNRKI I WPTVI FLLLI I AAGWYWWARGH
QKAPHYMTLTGEGSI VDAVSASGKI EALHSI GLSFKNPGTI KEI YVKEG
QSVKAGQLLALQDATDLELQVROAQANLDNALAKLQALQAEPLTTDVAQA
EAGVEQTQAEYDNAQDTLRRNQSLFDAGALPEVDLNSARKAEVTAAGNLK

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KARAALEDLMDGSRPEDI AAARAQVESTRTQVELARNNOAATEI KAPWDG
 I VTNVNGQVGQVRGVSNTSATEPSNSFI FLI SPELQLRVQVNEADI HKVKV
 GODVEFTVNSLPDRTI KGRVTAI APQAQTVSNI QLYDVLVNPBGDGGTPLK
 AGESASVTI VVSRKDNVMTI PRAAI AYARGYLSQTAQAGGPGTPSGRTL
 SGGNQGGRI VQGTGGAATGASAGKTTGSGENLATI LVLEKGQAPROQVVT
 GAGDERNI EVVSGLTGTEQVVVGTGSPGGAAGSGNQGNTRSALQPRGMMI
 TR

>2617922085 Ga0073689_1567 two-component system, OmpR family, sensor histidine kinase ResE [pelotomaculum Ga0073689 : Ga0073689_156]

MFKNLF SKLMVSYLVI TLI TLFTVGI AI SQLFANYFYTSKERELALRGYR
 MARFVAANLEKGQTQPLDSTFKMVVTSWDI QLEAI SKENLLQGESGFRGP
 PQMWLTAEAEERVLRGVEVSKRGFSQRFEQAMLSVTVPVQTNGVVGALV
 LSAPVSGLTATVNAVRLLI LYAAAGAVVLSVLLGYWLSRSI SRPLSQMSA
 VTREMARGNFRQLVEVTSGDEVGRLAEDFNHLAGSLEQTI SALSREKGI
 ENI LTNMTEGVLAVNGPGRVI LANOAVSRTLGVKPAEI LDRRLSEVPCCP
 GLAGLFSAVI ESGKPRSAEFETNGGKAFVLAHLAPLREAGGGSYGAVGV
 QDI TELRKLELLRRDFVANVSHELRTPLTSI QGFLEALLDGTI SESQAKE
 RYLKVI HGETLRLNRLI HELLDLALI ESGKVRWDI NPI DVSSLVSRVLLK
 LKPQMEQRQVVVEPGVPGNLPMLGNEDRVEQVLTNLVENAVRYSPPGSA
 I TVRAAELEGTI TVEVADRGPGI PPEDLPYI WERFHRVEKSRSLGGTG
 LGLAI VKQI I VAHGGRVNVRSEAVRGSTFSFTLGAAPVED

>2617922084 Ga0073689_1566 two-component system, OmpR family, response regulator ResD [pelotomaculum Ga0073689 : Ga0073689_156]

MAADTI LVVDDEELVQELI RLYLEKEGYRVI GARDGEEALAKL RAYGPGL
 VI LDI MLPKMDGWAVCREI RKNMTTPI I MLTAKVEEFDRVLGLGLGADDY
 VCKPFSPVELVARI KAVLRRSALAGRADAKI LSYPGMI VDYSSHRVEVDG
 REVTLTPKEFELLWFLAGHPGRLYSREQLLQNVWDYDYLGDPRTVDTHI K
 RLREKLEAGAKKRYI RTVWGLGYKFEVAE

>2617922083 Ga0073689_1565 prevent-host-death family protein [pelotomaculum Ga0073689 : Ga0073689_156]

MPNI RPI SDLRNNANEI SEFCHRRERKPVFI TKNVGDMVMMSI EEYERQQ
 ALI ELYEKLAEEAEI ANGAAGEDFFEVARKL RASVYGKV

>2617922082 Ga0073689_1564 addiction module toxin, RelE/StbE family [pelotomaculum Ga0073689 : Ga0073689_156]

MEKYRLLI FPSARRDLQDI I DYVNELSQDAALKLYDGI VEGI SSLSKMPE
 RRP LLKNPVLVRGYRTL I VHNLYLVFYVVKSNRVEI RRI LYGRROYEFLF
 VTG

>2617922081 Ga0073689_1563 RNA polymerase sigma-70 factor, ECF subfamily [pelotomaculum Ga0073689 : Ga0073689_156]

VTAVDEI NKAAGDPKSI ERI CSATWEPLYRFVYFKVQNRREEADI TQET
 YVKLTLYLRGHKAPGENFLGFMKT I ALNVLRDRWRQKKRRGKPVSFEEI N
 PWWTAGVDHQRDVARRLQI ENALAKLSEDQRAVLDLRI I KGYSVAETAKL
 VGKTEATVRSQFRALQALARI LDDI D

>2617922080 Ga0073689_1562 Outer membrane lipoprotein-sorting protein [pelotomaculum Ga0073689 : Ga0073689_156]

MNNPENI LSDYI DALNAEQEPEKHARGAADTTELEKLLAAVRLRLTREPA
 LPDPGYPKRLTNAVADQI RKNKSAGLYRPF EKNSKPAGRI SKMAAGRARR
 RWLLPSVAAMI AGLLLFAVLTSWTGLFN RDVAYAMEKAVAQLTNYHGVLE
 MRSKNAAGEEWM I RRVELWSEGEKYAVRQDDGALTVNNGERKWQVRPQSK
 EVALLPLI PDPARNGFDLRDEAKRARRYPHTVAGPEMI AGRQTTKLEI SP
 PGGLTYYLWI DETNL PVQLQTAMQNALQTTFTFVSFEPNTRI DPGI FAY
 QPPEGYQVMEEDPGQLVTMVEESAAI SRLTPLLPQEAPARI FAFKDRVVL
 DYGD TTI VETAAGGSFEPAPNSALGI AAGGPLEVWQERLRWRQDGI EVQV
 EGPRRLELARI AADLALPDAGKNLVNKARVKVPVDLEI VKASQQQVDRG
 SSPWQLDPLQVALTFVNLKVSPEGI QGEPKI PVSSFKLEANNGVEAVVEV
 AGGPI KOVYLQRLVRQDETGI WSVAGYDPR

>2617922079 Ga0073689_1561 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_156]

LLKKLAPI I FCLCLI VTAGCTTDRRTEPGPPKEPPAGTVMNDFHALTQKD
 SRVEEVANFI KNNI SSVSKEDASKMVDNFEKI QKKNLPRFEDMFASDDVQ
 RKI NSEYKAI I AQSDI KDAGLKELLVKTKNSGYKVETAEGSYFPI I DYEF
 YKNFSSHVTSMDKDYI EI MAEESDKAPAKDAALVI GWDEVI KRALNQEKF

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INTYKDSMKI SDVKQLYKKYVFTFTMYGLNNTPLFSYNSKTMVPAKEVYL
AVVADTGGSEFLKTLSGFLDLI QNNNYKLTSEAKEYREDVVKKLG

>2617922078 Ga0073689_15521 tRNA 2-thiouridine synthesizing protein A
[pelotomaculum Ga0073689 : Ga0073689_155]
MEEI KSNETLDARGLSCMPALKAKKALQKLLPGQI LELLGTDPGSRNDL
PNWCKRSGNEYLGEKQENGFNRFYI RKK

>2617922077 Ga0073689_15520 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_155]
VTLCCKTNQEKELGI CI SSDRHLHHLI GI VLAAQRAGKEVI TFFTHKGVLL
TOEPEFMKLAGKAKHTLCYVGWKANGLEGKSVPGMNETGFATQFRHAEIM
EEVDRLVL

>2617922076 Ga0073689_15519 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_155]
LCFEETEQQKVAI LI RNKEDQWEGLRSSLGLALEKNHVTMVVLDHEVELT
GEYEENLEMLVEMDGEFYNSLVNVEKYGFKPVTI EELGNKCLKEMNWVI A
F

>2617922075 Ga0073689_15518 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_155]
MKI LHI FRSPPTPEVLKLVAVLSERNEAAEFPLYQEDVDYDSLVR LI FSH
DKVI SWW

>2617922074 Ga0073689_15517 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_155]
MRVGI VVLMVLSLI LGMVI GREI EFGVARQPERVSPVSPDVGLSAEMMRK
GEESFGRSRYGEAREYFHKAI LTDPASI NSWSWYDLALI YTI AEQFKNHG
EI VESTAPASESTAAPLSEQVQEPDEKTSEQTTRAKATPKSVPATAPAK
APKAI SNPSGI I EEPVNKASAPESAPAAKVQPAPAPTSLPPASGVKSPK
EKEGC

>2617922073 Ga0073689_15516 Rhodanese-related sulfurtransferase [pelotomaculum
Ga0073689 : Ga0073689_155]
MKKVMLI AGCLLI VLMLASVAMATGSQVKLI VNGKEI TCDQPP I ENGR T
LVPI RAAAEALGAGVDWDQDNFTVNI TTALPAADGDEYLRGLNDPAAAK
PSI HSNFI KAGDLQAI LDDDKDGDLCDYRAAHSGGDQI ANDPLVLDLRGK
TDYEAGHVP GALWI ASAENI GKSENI ALKEALSKHVAAGGKSEI VAYCF
TSHTAGLACGVLAGKFNVKNMRFYSI GWEGTKQADAPI YGQREDKDGK
PVSYPQK

>2617922072 Ga0073689_15515 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_155]
VTRI CSATYI LYSFYGVDKRGGVAGCGI VVSGRPI SSP I VTGPAVVVNKY
VI NLEAI KHLVARGTLFSVFRNAHETLFRHQWPALTGGMLLGLFSI LVVA
WDRPWGI VGGI RNWADWLFYGLGLFPDRPENPLLFSSSVLDI GLLLGAF A
SALI AQEFAFRPPILLEI YKGF FGGALMGVGA AFARGCNI GGFYSPLI NL
SANGFPMFTGLAMGAFFGLKYLLWELEKFPKPAI SPMSEQNWNVNGKI I
QPYLGVLVFTGLI VAAFLYSGTAYTI PGGLLLFGAAGFI I LQRCRFCFAR
AFRDPFMTGDASMVKALALSI VI GAI GVG I LKWTGFRSESLWVTPVFWWG
SLAGGFVFGTGMVI AGGCGSGALWRAAEGQLKLWAALI TFALVNSLVTVL
LKNTGWQQKLGKAVFI PDVLGWSGSI LLI ALFAFVWYLAVTWNEETNRFT
FGL

>2617922071 Ga0073689_15514 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_155]
MERFKKFMGRELDLEKVKDTGR LAASGI ECAYLPDPLEDFDEVEFRTGFG
NDI I VI TVAVELGKVKRI MI SMADEKNPDMVRSLTGSQLEGFLAEKCETL
VGFFEYVTG

>2617922070 Ga0073689_15513 long-chain acyl-CoA synthetase [pelotomaculum
Ga0073689 : Ga0073689_155]
LI VSDI HKRDGRDPSCPALSYHDRVTSYAELENNVEHYARFFLSRRLNRG
DRAAVALPNCPEFI YSYLGI VRAGGVVLPLNLLQTPQELLYI LRDSGARF
LVTNPAI GLQLKQLPGLPLTLI I LDEETQREI AAARPAVFPEVGSDAVCA
FLYTS GTTGQPKAAML THEDLLSNVRSMDEASRLGRDENFLAVLPMFHSF
GWTVCVLLPLYLGC AI TI LDSFKPKEMLOVLSEGI TVFCGVPSMFLVLL
KARQEAAFPRLKFAI SGGDSI AEETMRDFEKI FNFPI VEGYGLSEASPVV

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SI NPLYGVRKI KSI GLPLPGI EVKVVDGDLRELPAEI GELVVRGPNVMK
 GYYNREEETNESLRGGWLHTGDLAYRDEEDGYFFI AGRKKELI I TAGFNVY
 PREVEEALMSHPSVAEAAVI GVPHPLKGEVVKAFI VP EEGRMPDKQELFQ
 HLKGRLAGYKI PEEYVI TGDLP RGVGGKVLKRLK

>2617922069 Ga0073689_15512 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_155]

MGDI VCI EKRNEAYATEAAI EPEI QTGAGRGPEAPGSRAI VPTI DI YTAR
 I I YNLTQRMVEEVVDRRVSLLLEKRI EDRDREVMRTI RRMQARMVMEQNKV
 HQPWWRKLFARKNDAGK

>2617922068 Ga0073689_15511 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_155]

MRLI AGMPDTRQVGFLVDTLRNGGFDRKDMI I SDLADAAEQRRDDPGEI A
 G

>2617922067 Ga0073689_15510 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_155]

VKTERDGLWEADAFVDGI KGLEPGKRG I VAVEVPKHGADRLRAMMEQSG
 AVEI IQD

>2617922066 Ga0073689_1559 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_155]

MGGGETASPEDCETARRLGGLI AREGWVLLNGGRPAGI MEASARGAKENG
 GLTVGVLPDSSSRFACRFI DI PI VTGMGNARNHI NVLSSDVVVALPGRAG
 TI SEI ALALKNGKKVLLNFNPGE LFDHYMAEGLLCTAAGPEEI RI I KE
 LQCEVLARG

>2617922065 Ga0073689_1558 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_155]

MRNSSGLSPDESALKI PVGDI SFTEVAI GDLPLFI VI TSQVFDVDLPVKE
 FPGEEFEAYLHRYAREKFTDPVKREKFI KKHLLNNA LYMDDEI KGDTAWQ
 FNGEVHFQONARRCGFI LKTQSKQFYMFQTS LGI DLPSQFAAYQTLTYGK
 VEEKYLPLFVTGEGRERLMLMI GEDVYVPVLEALGLAGLAGI KETR

>2617922064 Ga0073689_1557 Major Facilitator Superfamily protein [pelotomaculum Ga0073689 : Ga0073689_155]

LQNPQPFVWSRDFTLHWL TNFLMALGFYFLLPTMPVFAVKALGADKSQVG
 YI I GI YTL SAVAI RPFAGYALDSAGRKKVFLWALGFFALFVFSYPAGRQP
 AFPTLAAPAARLCLGGHHHRRRRHCGRHSPSRQAG

>2617922063 Ga0073689_1556 Major Facilitator Superfamily protein [pelotomaculum Ga0073689 : Ga0073689_155]

MTLAMALGPMLGLWLMGDTRYDRLFFGAGLLAALAFFTATLVRHPRQLT
 RRPLSWGAFI ENRVAPCI ATFFLT TVYGGI VSFI TLYSDEI GI ANGGLF
 FLAYAAAMSVTRPLAGRI MDRRG PAPVI MAGFI FLI AGFLI LWAI RDLTG
 FTAAAI LI GI GNGNI WPTMQTMVI NMVEPQRRGVVNSTYFSALDLGI GAG
 SI SLGWLAQGT SI GAMYLASALI LLI PLAYLSLYVLKDYSNKVAGDAS

>2617922062 Ga0073689_1555 mRNA interferase MazF [pelotomaculum Ga0073689 : Ga0073689_155]

MTEKKPSRGEI WFDLNPARGHEQAGKRPALVVSVDLFNSGPAGLI I VLP
 I TAKRKG I PFHVEI HPPEGGLKEKSF I KCEDI RSI SKERLLSRI GAVSLA
 TI EAVEDRI RI LLNL

>2617922061 Ga0073689_1554 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_155]

MSATVRI SQVSWQTLKLI AAQAGEPMQSVLDKAI EAYRRQFFLQKANEAY
 AALRENAETWQEEVKEREAWDI TLGDGLRGDD

>2617922060 Ga0073689_1553 Methyltransferase domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_155]

LNQLFDEKASSYDSWYETDAGR VVDRI EREALYSYMEPRAGMKVLDVGC
 TGI YALDLAGKGLDI TGVDI SVPMLEQARAKAAETGLEASFLEADACKLP
 FNDDSFDAVLSVTALEFVPDLAAALREAFRVLKTGGRLVVG LI GRDSAWW
 RLYDEKSRREPDNI FNHARFYTLDELLAAMPGRNVQKAVLFVPPDFDFS
 REECVLSMEAAAARTNNRTDGGFI CAASVK

>2617922059 Ga0073689_1552 hypothetical protein [pelotomaculum Ga0073689 :

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Ga0073689_155]

MTYNDPI I EDVRNVREKLFKKYDFDLKKFLKHI REEDKRHPESI AKDI KP
YKLPNLSKPF>2617922058 Ga0073689_1551 Predicted ATPase of the ABC class [pelotomaculum
Ga0073689 : Ga0073689_155]GVYDHI PGDGREYVI TRHDAVKI RAEDGRRVEKVDI CPFI NNLPFGRDTS
AFSTEDASGSTSQAANI I EAI ETGTSLLLLEDTSATNFM RDARMQALV
AKDKEPI TPFVDKVRQLYRDMGVSTVLMGGSGDYFDVADLVI MMEEYRP
FVVTGRAREI AGEMPTRRQPEGGAFGRI KQRVPLKQGRPERGHRTRVD
AKGLHTI VFGDTAI NLGFLEQLVDASQTRAVADLLLHLSRHYVDGQRPVP
QLI RAVYKELAEKGLDVI SSFHGQHPGDYAMPRAQEVAGAI NRLRTLVR>2617922057 Ga0073689_15415 Sensor_kinase_Spo0B-type, alpha-helical domain
[pelotomaculum Ga0073689 : Ga0073689_154]VNLPKLLELI QTORHNFNLHLOVI SGLLQLNKADRVREYI GRVSLEMAQY
AKTARVI VPEVTAALLI GFNEASMSQI GLELTVESSLAECVPGPVLGEA
LEHSMDCAI MAMAFSGTEDRRRLNVI FSENGENHVCRLLFSETPPPAGMDH
FTKELASVENLLEPYGGRI NLETAGGSMEI FLMFPRKEPQIG>2617922056 Ga0073689_15414 Large subunit ribosomal protein L27 [pelotomaculum
Ga0073689 : Ga0073689_154]LAHKKGVGSSRNGRDSQPKMLGVKRDGQFVLGSI LVRQRGTKI HPGRN
VGRGGDDTLFATVDGVVSFERNGRDKKI VSVNPAAEVG>2617922055 Ga0073689_15413 Large subunit ribosomal protein L21 [pelotomaculum
Ga0073689 : Ga0073689_154]LYAI I ETGGKQYRVQEGDTLYI EKLPAEVGETVELDRVLT VVKDGD LKVG
TPLVEGARVVLKVI RHGRGKKI I VFYKPKKNYRRKQGHROPFTQVTVKK
IEA>2617922054 Ga0073689_15412 ribonuclease G [pelotomaculum Ga0073689 :
Ga0073689_154]MLKEI VVNVGEEETRVAVLEDRVPVEI YI ERSI NQRLVGNI FKGRVENVL
PGMQAAAFVNI GLEKNAFLYVEDALPARSPDNGQGGSALGANI GDI LKQG
QELLVQI VKEPI GTKGPRVTTHI TLPGRYLVLMPTVDYI GI SRRI DSEKE
RDRCLKDLAARVKPEGMGVI VRTVAEGVEEDEFQDVNLLAKLWRKI LSRA
AHGPAPNLVHRDLELVQRI LRDAFTEDVDRLTLDSRYEYKVLDDLTD
PRLKLKVFLDERENVFEDYGI EQEI EKVI KRKVWLKCGGYLVI DQAEALT
AVDVNTGKYVGTNLEDTVLKTNLEAAREI ARQLRLRNI GGI VI VDFI DM
VEEAHRQEVHLALEEEI RKDKTKTNI LGI TQLGLVEMTRKKVRPSLAEVL
QKPCPYCEGRGKVLSEETLGI HFKNQI YNVARQTSQTI LVEANPVVAAR
LI GSGGASLRDLEGKTGKSLYI RGSASHHI ESVTI RPLQDNEEI QARTLP
VKPGEVLEVKVEEPHI TNVNDGI ARVNGFI LDI EGAGALVGETI PVEVSK
VYRTYAKARPVRT>2617922053 Ga0073689_15411 radical SAM-linked protein [pelotomaculum Ga0073689
: Ga0073689_154]MPRYRMMYAKERPARYI SHLDLLRAFERAVRRAGLPVAFSRGFNPHPKI A
FAAPLGVGTAGEAEFADMELTADI PASGVAAALSKVLPEGLRLI EVRPAP
EQAPALMAVVDRTYRAEARLERSVDSGDLARAI TAFLARPEI SVERKNK
AGEKKMYDI RPGI FAMSGRLDDDI I I I EAEKLTGSSGNVRI EEVLDAFTE
FI CLPVRGRFVLSRTGLYAGGKKGKRTLW>2617922052 Ga0073689_15410 radical SAM family uncharacterized protein
[pelotomaculum Ga0073689 : Ga0073689_154]MDVLDQI LPLVQKPARYAGGEWNAVRKDWERVALKVAFAFPDVEVGMSH
LGLOI LYGI VNSRADALMERVFAPWPDMECKMQEGLPLFTCESRRPVVD
FDI VAFTLQYEMSFSNI LYMLDLAGI PLRADQRGEEYPLVI AGGPCAFNP
EPLADFI DLFI VGEFEFVNEFLDFFLDGRKRGLPRADFLDGAARLPGVY
VPSLYRVSYREDSVFVKI QPVREGLPEKI TKRVVRDI DRAPFTRPVVPS
TEVVHDI MVEVLRGCTRGCRFCQAGVLYRPVREKKPETVLRQASELVN
TGGEI SLTSLTSDYTPVRSVI RALMDEHARRGVSVSLPSLRVDNFSVE
LAKEVQVRVRRSSLTFAPEAGTQRLRDVI NKGVTEDLLKTVGAAAFREGWQ
AI KLYFMI GLPTETDELDGI ARLARAVLAMGRGAGVPRGRLRVTVSVSS
FVPKAHTAFQWEPQAPPAELKRKQAYLAERLRERGLVFNYHDAGVSSMEA
AFARGDRLGNVLLKAFELGCKFDGWSEHFGLERWLEAFRLTGLDTSWYA
CRRYDNDPLPDWHI DPGVSKKYLVEEHRRALAGRTTGDCRTGSCPGCGL
CPGLEVEPVFAGGERDAQV

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>2617922051 Ga0073689_1549 stage IV sporulation protein FB [pelotomaculum Ga0073689 : Ga0073689_154]

LKVGCVSGVEI HLNNAFLALLGLFFVAGVLGKGLI AFTVVLLHELAHVTV
ARRLGVHVSDVELLPFGGVSHMGSEVVFNPAREI CVAAAGPATNLLLLGL
GI AMKNYGLWDDDLGSSFFI QCNLMVFANLLPALPLDGGRVFRAWLARRA
GFRLATYRAAWWGQFWGAADVFGGAAGLAAGVSGLDVI I TGVFLFYAATR
EKSMAPYHFI RHLAQKKEELAAAGI LPGQPLVSLDTVRLGEVI RAFVPQR
FHMVLLLLDRHWQYRGVI SEVQI VDALLNHGVDVPVSSVDKI K

>2617922050 Ga0073689_1548 Peptidase family M23 [pelotomaculum Ga0073689 : Ga0073689_154]

LKGTDFKPGGAFKQEDWI SNYRQPPQWKPKLGGGRRNNFYRI GVALLI FM
AFLALRETGNPWGVAARENLKQVLTTEWNYQPVEKVVQYGLQLANVDWP
LFSSSQPVFSKSRKAATGGGLPLPVSGKVVRGYGMVLDPI DNMERFHPGI
DI AAPVGSAVRAVGDTVKKAGDSPVLGKYI LI EHEPGSFALYGQLARAT
VTEGQTVQAGQI I GEVGSAGDI TGGGLHFEI RENNKLVDPLTRLQI NH

>2617922049 Ga0073689_1547 rod shape determining protein RodA [pelotomaculum Ga0073689 : Ga0073689_154]

MFKQVRLLRKLDHTLI AVL TMI I LFCLTVMYSATKETDLLEYGSGYYHVI
ROLFWVFLGLGAMLFMLGI QYEDLAKHLKALYVLNLI MLGAVLFVGHSA
GAQRWLPLPGPFKFQPFSEFSKLI I I I CFAAFLVQREGKLSRLKDLI PCFVF
I GVPMLLI LKQPDLTSLVFMAL MFGMLFAAGARPLLLI GLMVGGLSVI S
LWI GAHFWVEANGPVYI AGHEI SNI WI PLKDYQLKRLTTFNPNWQDWHGE
GYHI I QSQI AI GQGGFWGRGLFQGSQTHGDFLPI QETDFI FSVVGEELGF
I GAVALLFLFFI VLYRYI LI AVNAKDSFGTLLAAGVI SMVTFHVMVNVGM
TTGI MPVVG I PLPMFSYGGSSMI TNLAAMGMLLNI NMRRQKI LF

>2617922048 Ga0073689_1546 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_154]

LASI I EFLLALVFTHKNLYQTM I MI NKEVPFAKDTVYRI LNNTKDRLGQL
QLKLGTKI I NNHLTS

>2617922047 Ga0073689_1545 MoxR-like ATPase [pelotomaculum Ga0073689 : Ga0073689_154]

MAI KLPRFKGTGDYLASGELQNSVNI AI ALGRPLLI KGEPGTGKTM LAKS
I AEDLGLRLI VVNI KSTTKAQEGLYVYDTVQRLYDSQFGDHDVSDI RQYI
KLKGLGEAFTSDDPVVLLI DEI DKADMEFPNDLLWELDI MNFFI PETGET
I AAKHRPI VI I TSNAEKELPDAFLRRCVFHYI AFPDREMAEI VRVHHPD
LEERLLGQALEAFYTLREVSGLLKKPGTSEL LDWVQALALGGI EPGRI AR
ELPFLGVLLKKNQDFD TTLRRLHDRGAGRQAVQSRKLNW

>2617922046 Ga0073689_1544 perosamine synthetase [pelotomaculum Ga0073689 : Ga0073689_154]

LHVPLSSPDI GPRRELVNEVI ASNI LSI GPRVKQFERMVAQYLGVKEAV
AVNSGTGGGLHLAVRALGI GEGDEVI TSPFSFVASSNCLLYERAQPV LVDI
DPLTLNI DPGGI EAGI TPRTKAI LPVHVFGRPADMEAI LEI AGRYNLAVI
EDACEAI GARYNGKMAGSGGDAGVFAFYPNKQI TTGEGGI I CTNSAELAG
LCRSMRNQGRSDGDKWLEHCRLGYNYRLDELSAALGVAQMERI DEI LARR
EEVALAYNARLERLAGVTAPDWEPI KI SWFVYVI RLDPAI DRDRVMAFL
REKGVDCRPYFPPI HLPFYRKDFGYREGDFPHAERAASSTLALPFFNNL
TEQQMDYVI ETLAGAI AAAG

>2617922045 Ga0073689_1543 Predicted dehydrogenase [pelotomaculum Ga0073689 : Ga0073689_154]

MTGVRFGI AGCGRI AGAHVEEI LASPRAELVAVCDI DPAALDRFTRRHGV
EGHRDYAELLARKDVDVVVI CTPGGLHAGMGI MAARAGKHVLVEKPLALT
MEDADMLI DTCEREGVI LSVVLQNRFKPPFQLLKTAVAEGRFGLSHAGV
TVRWNRDEAYYLNPNWRGRKAGDGGVMMNQAI HSI DMLQWLMGRVESLFA
YTATRYRPI EAEDVGVAVLKFESGALGVI EAASTVYPVNLEESI AVFGER
GTAVI GGVKAGEI KTWRFSGAGDGGGGDELSPVGCDAAAGLI TGHGAVL
QDMI KAVERGGTPAVDGREGRKSLEI VTGI YRSAGAGRPVSLPLI

>2617922044 Ga0073689_1542 Capsular polysaccharide biosynthesis protein [pelotomaculum Ga0073689 : Ga0073689_154]

LEYVRLGEI LKRRFLVL TALI LAMTAGGLVCLVSPARYQAKAVLI LDRT
GPESGVFQPDYNSLMMYRLARTYSELAASEPVLRLKLSAALDQKLSPGEL
GRMVKVRKVKDLELLLEV L VADTSPDRAAYI ANKLAEI LRQEERDTWKMSN

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LRLI APAVPDRRPVGPDLPLAVFTAGLAGLFI SVI LAAVDYRTGREES

>2617922043 Ga0073689_1541 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_154]

SPPLAGEMVNGDFSQGRGTGWAGPDVVVKAGADGNKYGSAKYGWNFYQYV
PVQPGGKYI LSAQSRKGNAAGEARMAYFFYDAAGKQLASGDI LYKHRGAG
WEQVPARTVTAPAGAAKI LI KLLVNGGSGAHDFDNVSI KKL

>2617922042 Ga0073689_15321 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_153]

FFDAYDAGRSLEEKLVPI ASEALDEALRGLSEKEI KQLKVLLNKI FTNI D
D

>2617922041 Ga0073689_15320 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_153]

VSI I KNERI KQYI DTVLQQI DYEEAREEI RVVLESYFNELVEFNNTKTDS
EEGVI RKAI KDMGDPMLGKELAWLEALFTFDF

>2617922040 Ga0073689_15319 drug resistance transporter, EmrB/QacA subfamily [pelotomaculum Ga0073689 : Ga0073689_153]

LDRVKEVMDKTGDVRKYVLTAAL LASFLTPFMGSSI NLAVPTI GREFQLE
ALKLNWI VTSFLLSSAVFLLPLGRAADLYGRKKI FLAGI I VFSALSLASG
LAGSGDMLLLFRVLHGI GGAMI FGTGMAI VTSVFPPQERGVKLVGNVASV
YTGLSLGPVLGGFLTHQFGWRYI FYFNFLGLLVVI AI TVWKLKGEWRDDR
GGGFDPGTGAVLYTLGMAALMSGLATVKSFSYAPWVWMLLGLALLAWFVRHE
LRFRLFLLNMNLFRLNLAFAFSNLAALI NYLATFAVGFLLSLYLQVVRGI D
AQAGFI LLSQPVLMALLSPPAGRLSDRVEPRLLASLGMGLTMLGLLI FT
AI NQTTAPGVI VANLVL I GVGFALFSSPNTNAVMSSVEKRYGI ASATLS
TMRLVGQAMSMALVTLFFALYLGKMAVSPENAPLLLKSMRLSFFVFAVLS
AAGVLASLARGQI RGTEKNNQA

>2617922039 Ga0073689_15318 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_153]

VEPGRRAVTEVI LLERI PEGKI TVKI VRFI I I LSLI ALVSGCVAGKREPS
NTQNEPAVSMQAI TEYLENNVI PLPPPTGVRTFAAYDLFGVSENGNEK
KAYLWALI TTYGVDPNI GI GPRSGSSLPLALI LKEENGSTTVVGHROPGD
GAYYWPDKVEI FPKEYHEKI LNYQKSGKI KELEQSI KENVNNYLMSVGLK
NTP

>2617922038 Ga0073689_15317 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_153]

LWTTAQPNNI LFCRGTEWDKGGGKQNLVPGQKI RMRTAGREARALTTG
TVDTADYAPLLSLGGKDLFFLRLNRYDRGSLYYLSTDGGREVELI RGLNG
SPGYGYNYYPEWLKI HWKK

>2617922037 Ga0073689_15316 WD40-like Beta Propeller Repeat [pelotomaculum Ga0073689 : Ga0073689_153]

VI SLPRSHEQPLLI DRI TLEGKRFNLYTLEKARESEGYI RSATKFKWSP
DGRYLAFYLNMSGSLSADGVI RVLDLQHPEQLLDLGGGLRYAQWLAW
PDSSQLAYI RGGGREATTNKRHLVDMRDGGKI TDCGLTGQVDT

>2617922036 Ga0073689_15315 WD40-like Beta Propeller Repeat [pelotomaculum Ga0073689 : Ga0073689_153]

MDRKRLGAI WLI LLLLEVLPLVSPVFADGDEVTLTVDGKKLNLDLPPVLQ
NDRVLAPVRNLAEALRAQVDWDPVTASVMVVKGSKTI KMSAGSREVL I NG
KQI FVGEPPQI VQDRFFVPVSATVSTLGAAFEWVGETRTVAI TTPLPPP
PERVSQLHFPALVAFTNAGHLWI LDGGKTGAAPVQVTREGKTEI LGWSPD
GQWLAWPQRADEDEYSAPPYLWVVKADGTGSFQVDRRPVLGTPAWSPQTN
SLAYSTTGPGGGYAPDGNLKI ASI ENGRRRPLQRFCLTTAACSMI SSGRR
TGGAW

>2617922035 Ga0073689_15314 Fic/DOC family protein [pelotomaculum Ga0073689 : Ga0073689_153]

MDQYDRAVELWQSYKI ASAADLDKYLDSFRI LFAFHSGKI ENEEI TYHDT
REI FENGRVVDYTNPRALFEQQNQKLCYELLKEKI VKKEPLSI DLVKEI
HKVLTSGTYDERRYI ENEERPGEFKRHDYI TGVHEVGSATEDVENDLTEL
I AEVNAYEGRDVLKAAAYFHARFEYI HPFADGNRVRGRTLMNYLMTTHNH
PPLI VYNEDKRMFYFECLOKYDQAEADLNPLYEFLKYETEKTWGKALALADG
RKPERKGLSDFTQSM

Table S2

>2617922034 Ga0073689_15313 looped-hinge helix DNA binding domain-containing protein, AbrB family [pelotomaculum Ga0073689 : Ga0073689_153]
MI RAKLTSKGQI TI PVAVRHKLDLQPGDELLFEFDRDDEVKLRAFKRKRL
TELYASLPVKRSFPNKEQVREEVAAEMARRI LKKGKDQ

>2617922033 Ga0073689_15312 Predicted nucleic-acid-binding protein, contains PIN domain [pelotomaculum Ga0073689 : Ga0073689_153]
MVYIWI DANVI LRFI TGDPPEMAEKVLELMARAEKGAAALRLSHI VATEV
VWVLSSFYKYSKGEI AETMI TFI NADGI CPDNPDLI QALKDMADNNVDF
I DAYLAAI ARTRSEAVCSFDSDFVKLNVSLVI PPGTEKFNG

>2617922032 Ga0073689_15311 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_153]
VSYEFYYNSPLEVPESELLTEI NLPEKRLDFI YGLQDQENEYI LHLDFQL
RHERDLPLRMHI YNLGLTAI PESLDI AEFI AWHNLGGP

>2617922031 Ga0073689_15310 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_153]
LTASNQKPV I SKVI YLERREYRNSPGEYVVS YRVKRENVFSYEA I KLWDH
TEE I I KGELKELAPLLI LLTRAKSEAVLAKTRELI LSGENEKYKADALSL
AI TVAARYFSKEHGLGRAKSENGI E

>2617922030 Ga0073689_1539 Major Facilitator Superfamily protein [pelotomaculum Ga0073689 : Ga0073689_153]
LSLSSMSGLFRNRI VQAI LLSAI FLQI GI WVRNFSVLLYV VEMTRGDAFA
VSMVSVAEFAP I FVFSFLGGTFADRWRPKQTMVWCDLFS AVSI FAVLLTI
I FGSWKAVFFTTLFS AI LSQFSQPAGLKL FKI YVP AEQI QTGMSI YQTI F
AVFMVFGPVLGTFVYQ I FGI QVAI AI TGTAFLMSAAALLFLLPNRDI SAD
EI THSALLQEMADGI RYLFSKKVLTLLGACFVAAGLGLGLI QPLGVFLVT
ERLGLGKESLQWLVT FNGI GMI I GGVLA VSFARSVAPHKLLTLGMFVDSI
GI AVSGI STTPWLTLTAQFC SGLVFPCI SI GI NTMI LQNTESRYVGRI NG
I LSP LFTGAMVVTMG MAGLLKNSFPLVAI YEVAGI LFI VGMMFI LPLYRQ
PVTRE

>2617922029 Ga0073689_1538 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_153]
MI LSAQLKHI DFREQQI ALLDREI AERMHSSEEDLELLDAI TRI GLKSAQ
EI LAAI GI DMSRFP TESLI SSWAYLSGI DPPPVQKVDEEAFYAYSL

>2617922028 Ga0073689_1537 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_153]
VPRKKS FPLRI DPKLYEVLERWAADEF RSVNAHI EFLLR EAARRAKRLPT
VTEDSTGNEKPEYANGPMFNTTWDNLAI KGTLFSCLL

>2617922027 Ga0073689_1536 SPFH domain / Band 7 family protein [pelotomaculum Ga0073689 : Ga0073689_153]
LTFFGRYMGSVRDNGI WLTA PLTVRKKVSLRVN FNCKTLKVNDI YGNPV
EI AAVVVFRVI DSARAVFDVDDYEKFVEAQSETALRHVATKYPYDNFDEQ
GYI SLRGNT EEVAGELARELQDRMALAGVEVMEARLTHLAYATEI ASAML
ORQAAAAI VSAROKI VEGAVGMAQMAI KQLQRDGVVELNEERKAAMI NNL
MVAI VSDRAAQPVFNTGSLY

>2617922026 Ga0073689_1535 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_153]
MLREASI VQDWI NEGMEKGEI KALQDAI LDI LEERFGLLRKNI GKKI KAI
DDPALLKSFFSRSQTHLLLAGGQFSYASALPFPAGESH

>2617922025 Ga0073689_1534 asparaginyl-tRNA synthetase [pelotomaculum Ga0073689 : Ga0073689_153]
METTSI KELFRRPESFLNKRI RI NGWVRTVRSSKKFGFI ELNDGTF FASF
QVVYDENLANFKEMSGLI TGSAI RVEGELVESPGAKQPFELKAESI AI EG
PSSPDYPLQKKRHTFEYLRTI AHLRPRTNTFS AVFRMRSVAAAYAI HKFFQ
ERGFVYVHTPI I TGSDAEGAGEMFRVTTLD FNQTSWDDRG MVDFTKDFFG
KETNLTVSGQLEAETYAMAFSRVYTFGPTFRAENSNTPRHAAEFWMI EPE
I AFADLRDDMDLAEDMLKYVI NYMLENTPGEMQFFNSFI DKTLLERLLESV
VRSEFGHI TYSEAI DI LI KSQE QFEYPI AWGVDLQTEHERYI TEKHF NKP
VFVTDYPKEI KAFYMRMND DGR TVAAMDLLAPGVGEI I GGSQREERYDYL
EKKMDELGLNKEDYWWYLDI RKYGGVRHAGFGLGFERLLMYLTGMNNI RD

VI PFPRTPKNAWF

>2617922024 Ga0073689_1533 isocitrate dehydrogenase (NADP) [pelotomaculum Ga0073689 : Ga0073689_153]

LVAEKIQMKVPLVEMDGDDEMTRI I WOQLKDI LLTPYI DLKTVYFDLGLKK
RDETDDRITVEAAEATKKYGVAVKCATI TPNAQRLKEYNLKQMWKSPNGT
I RAI LDGTVFRTPI I I KNI KPFVKTWERPI TI ARHAYGDVYKGVEMKI PG
KGEAELVFTSKDQVSREVI HFDGPGI VMAMHNLDKSI ESFARACFNIA
LDQKQDLWFATKDI SKKYDHTFKDI FQDI YAGEYREKFSAGI EFFYTL
I DDAVARVI RSPGGFI WACKNYDGDVMSDMVATAFGSLAMMTSVLVSPGG
YYEFEAAHGTVTRHYYYQYLGEEETSTNPVATLFAWTGALRKRGELDGAGD
LAQFATKLEQAALDTI EAGI MTKDLALLAEGEKRVVNTROFLQEVNTRLT

>2617922023 Ga0073689_1532 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_153]

VKTSRYNLYSEHLVKKFGEKVYKLPVNLPGTCPNRDGRVGRGGCI FCDEA
GSGFECLPDTI PVRQQVVENKTFLNRNFKAKKFI VYFQSFTNTYI PFDRF
RENVLADEEDVVGSLI STRPDCVNDRYLDFLI GI KREKGLNI NI ELGL
QTVNYHTLTRVNRGHTLAEFI DAALRVKRHGFETCVHLI LNLPWDNMADV
VENAKVLSVLGVEYVKLHSLYVVRGTVQGDYQGEFEI I SMDEYVERVA
VFLAYLDPAI VVQRLVGKGPKESSLFSNWGVSWWLLKQRI EQYLEKHDI Y
QGGKFDYLNKAVREFL

>2617922022 Ga0073689_1531 carbonic anhydrase [pelotomaculum Ga0073689 : Ga0073689_153]

APKAADTASQAALYKRPEVVASASEAKQLLI DGNGRFTSSKLAGKDMGST
KREELAAKGQKPFVAVVTCSDSRVPPELI FDOGLGDLFVI RVAGNVFDPV
AVGSVEYAVEHLGTPLVVVMGHEKCGAVKATADGGEAPGSLGSI AAKI KP
SVEKAKAAGATGNDLYEKATDENI KAAI ADLEKSPI VKHLKESGKLTVAG
AKYHLGSGEVTFTDVK

>2617922021 Ga0073689_15215 Fructose-1,6-bisphosphatase [pelotomaculum Ga0073689 : Ga0073689_152]

MGRRI TLTI I KADVGGFVSHSSVHPELMETAQGI LAGSALLTDFHVTGVG
DDI NLI MTHEGGKDNQEVHQLAWDTFSACTRI AKKLLKLYGAGODLLADAF
SGNI KGLGPGVAEI EFEERTSEPMI VMADKTEPGAWNLPVYKMFADPSY
DLARQKANEI ASYMRMGPFKSHRLHLEEMEYTTMPEVSKHLKDRFEKLR

>2617922020 Ga0073689_15214 nicotinate-nucleotide-dimethylbenzoyl phosphate transferase [pelotomaculum Ga0073689 : Ga0073689_152]

MLLGKTI KEI NGLDNVAMEQAQKRLDSLI KPPGSLGI LEEMAVRLAGI TG
NPRPQI KDKVVI I MAGDHGVVAEGVSVAPQEI TYQMLPTFLSGVAGI GVL
AKHAGARVLVVDVGAVPVEFPGLRRKVRAGTSNI AAGPAMTREEAVKA
LEVGI EVALAEI DRGAGLLATGDMGI GNTTPSSAI LAAFNGYTAVEVAGR
GTLVNDEVLKI KAGTI ARALEI NRPNPKDALDVLAKVGGLEI AGLAGVI L
GAAARRVPVLI DGF I TSAAALVAYKLQPKAREFMI ASHLSSEEQAHRMLME
QLGLSPMI HMRMLRGEGTGAALTMHLVEAATRI I GEMASFEELSMVNLLDD
DKI LKQ

>2617922019 Ga0073689_15213 competence protein ComEC [pelotomaculum Ga0073689 : Ga0073689_152]

MNRALVLFVTFYI TGVLFGEFTKFKASI AFALAVLCLLATVAGNI LAWRE
NRRI FLVLFLLGLALSRLGVEESKTPLI NYAGQVALVGLVAAEPDVRE
DKVFYLFQAREMVKGDEHRPVSGLVRLSVQGSNRVYNYGDVLRVNGLLI Q
PEPAGNPGAFNYRTYLERQGI WVVLMKSEADVQKI GAGSANPVLNAAW
VKEKLSAVATHSLAPSNDAL NGI VFGTQGLI DRDTRQAFVTGTGVVHI LS
VSGLHVGLVLGGLVGLRLRLKLPPGLTAPLTPVLI FYALMTGAVPAVLR
ATI MALLFLWGHHLGRDRDWPPTTLALAALVI LLLNPLQI YHPGFQLSFAA
TWGI LYLGPLLGDFAGI FKGLPSGMVRPLVQGLAVPLAAQLATVPLVAW
YYNLVSPVAI PANLLAVPLVGLI LFLGVFAAALGLFWLPLAGLVNVSTDA
AI ELFLALVKFFQGLPGAVI YLATPPVLLAAAWYGGLLAVTGLRPGGWRN
ANFRRI KGWAAAGVALTVLLLI WWPWPAGGRLSVHFI DVGQGDVSVLVRT
PTGKNMLI DTGGRRDEFQGTSGMGDQVVPYLRKI GVHRLDVLVVTHPHE
DHCGGAAYLAENFPVGLAVVSPTGNTAGRARTEAGEEAAAGGQGGREDS
GEI PPAYTELMTKMAGMGVPVKAAGDTRLRLDGKVG I EVLSPEKTTGET
KPDLLNNSVVLKLTGRRSFLFTGDVETEAQGELLRREADLRADVLMKMPH
HGSRLLLPELVEHVHPEMVVI SVGAHNTFGHPAQTTLDI LDQAGAKI YRT
DQDGAVI VETDGNLSLKVRMGKGRAKPQTFP

Table S2

>2617922018 Ga0073689_15212 Transglycosylase SLT domain-containing protein [pelotomaculum Ga0073689_152]

MDFNPLI RMLLM EYLAGALTGAKRGRESEDGGEFAAFLTAALAGGVLPKPP
FHPGGATGGI SMNSLRPVPQQWCGGRAASAPGMHGGDGRKAAPAEGL
ELI EKAAGKYGVDPALVKSVI QAESGFDPKAVSLAGAMGLMQLMPGTADS
LGI QNPYDPAQNI DGGVRYLKQMLERYGGDVTLLAAYNAGPGAVDRTGG
IPGYRETRNYVQNVLRNRVNYVV

>2617922017 Ga0073689_15211 competence protein ComEA [pelotomaculum Ga0073689_152]

MVQLDRKQQWVI ALLVAVI LFGAGYRLAQVKERAANEDRPSLEAAGEDKA
GDLYVHVAGAVLKPQVYKLPGRARI I DAVNMAGPTGEADLSLQLAAPAP
DGKTI YVPLKSAAVQAGPTASGGPAGAPASAPAGAGRNI FAPQAGAAGAA
AAPDLVNI NTADASQLDTLPGI GPALAQRI I QYREI NGPFKNI EDLKNVR
GI GDKNFANLKGKI I VQ

>2617922016 Ga0073689_15210 Uncharacterized membrane protein YcaP, DUF421 family [pelotomaculum Ga0073689_152]

MVWEYI YRTLFI YLLVLAVI RMMGKREI GQLSPDFVVTI I I AELAAMP
EATDI PLWHSVLPLVVLGI LEVLVSYASLFNQTLRGI I CGHPQVI I KNGT
I LRGEMRKARYNLDDLMAQMREKGI VDPDDVEYAVLETSGKLSVI LKSQH
RPVTPADLGI ATTYEGLPTVLVMDGNI MKNLNLKEADLDEKWLLEVLKERE
I TPRKVLLAI LSTDGRLFI NKK

>2617922015 Ga0073689_1529 leucyl-tRNA synthetase [pelotomaculum Ga0073689_152]

LKGKYNFKEI EEKWQTRWAGHNLYI VPDFS DRPKYYCLEMFPYPSGKLHM
GHVRNYSI GDVVARFKTMQGFHVLHPMGWDAFGLPAENAAI KHGGI HPAD
WTMNNI YNMRAQLKQLGI SYDWNREI ATCHPDYRWTQWLFLQLFHHGLA
YKYYAAVNWCPDCATVLANEQVRDGECECKALVEKRELAQWFFKI TDYA
DRLLKDLELLTGWPEKVKI MQENWI GRSDGAEI DFKVDGMNEVI TVYTTR
PDTVFGVTCI VLAPHEPLVEKLI AGAGREEEI REFI RKVRNLSEI DRI ST
EVEKI GLPTGAYCVNPLTGDKVPVLI ANYVLLLEYGTGCVMGVPAHDQRDF
EFARKYNFPI KVVI QPPGEELDPVTMTAEYEEEGVLVNSGRFNGLLNKEA
I KVI TNHLAERGQGRFRMTYRLRDWLI SRQRYWGAPI PVVYCDRCGVVPV
PEADLPVMLPMDI EFKPTGRSPLAECPDFVNTTTCPGCGGPGKRETDMDT
FMCSWYYYRYTSPRDVEGPWNKVKVDHWLPVDQYI GGVEHAI LHLLYSR
FFTALYDMDLVSNQEPFTNLLTQGMVLKDGVKMSKSKGNI VSPEDI VAR
YGADTARLFI LFAAPPERDLEWSDQGVGECYRFLNRVWRLVAPLVDTLKN
APVGAGGNLVGNREMRATHNTI KKVTEI GNRNFNTAVSAI MELVNA
LYQYKEVPETDRDPAPVLKEAVESLLLLLAPFAPHI AEEI WEATGHKESI H
WQPWPSYDPEAI VEDEI TI VI QI NGRVRDRMLMVTAGLTAQEMQERVLEEP
KVLKLTGEGKKI VKI I PVPGLVNI VVK

>2617922013 Ga0073689_1526 ribosome-associated protein [pelotomaculum Ga0073689_152]

LSLNPOEVVNI AVQAAEDKKAWDVTVLDI REVSVI ADYFVI CSGRSSTHV
QAI AENI QEKLGEKGLPVLRRREGFRECGWVLLDYGDVVHVHFREAERQFY
NLERLWGDARVVGIL

>2617922012 Ga0073689_1525 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) [pelotomaculum Ga0073689_152]

MARTLYVGNLPWATKAEDLADAFSAHGEVLSSRVI TDRETGRSRGFGFVE
VRDEDAENMI AAMNGAELNGRVI TVNEAKPREERP

>2617922011 Ga0073689_1524 nicotinate-nucleotide adenyl transferase [pelotomaculum Ga0073689_152]

LFMSNEI GKVSRLGI MGGTFDPI HYGHLVTAEGTRYELGLEKVI FI PAGR
PPHKDYHMTGPWLRYTMTCLAVTSNPFFQVSALEVERPGPSYTI DTVQE
FTRLFTGAQI YFI TGADAVLEI LTWKS VKRLLSTCRFI AATRPGYHLMEL
WEKLDKLSLELKKNI I FMEVPALAI SSTDI RRRVREGRP I KYLLPESVEE
YI I KNNLYGQ

>2617922010 Ga0073689_1523 hypothetical protein [pelotomaculum Ga0073689_152]

LNLDOKQARFLI AAKSFLNKEKMARPEI NI FDHEVPKSEI VKI SKLSEAE
VEEVADSLNKCGLI HVQI CDGKFDCCKVASLSFDQLDCFLTDMVRRK

>2617922009 Ga0073689_1522 glutamate 5-kinase [pelotomaculum Ga0073689_152]

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Ga0073689_152]

MEENKRGFESFKRI VVKVGSSSSVAHTTGKPNLFQI ETLVRQLADLYNRGK
EVI LVTSGAI GTGAGKLGLARRPKTI PEKQAAAAGQGMLMHI YGKI FAE
YGVTVGQVLL TREDFADRRRFLNARNALHAMLQFGVI PVVNENDTVAVEE
I KLGDNNDLSALVACLVDALLI LLSDI DGLFTADPRKEPDATLI RDVME
I TPEI ESLAGGAGSKLGTGGMATKLQAARMVMHSGVVTVI ARADEKDI I L
RI I SGEDTGTVFWSANKLENKKRWI AYSSAVCGKI FI DGGAVRALAGQG
KSLLPSCI TGVEGAFEMGNTVSI I ASDGREI GRGI VYYSSDEI NKI KGAQ
TKDI ARI LGYKDYDEVVHRNNLVLDI

>2617922008 Ga0073689_1521 GTP-binding protein [pelotomaculum Ga0073689 : Ga0073689_152]

IMFYDKAKI FVKGGDGGNGCVAI RREKYVPEGGPWGGDGGRGDDVFRAD
EGLRTLVDTRYKRYHKAERGRHGEGRNMHGASGDDLTVRVPVGTVVRDAC
AGELI TDLVRDGGQEVVARGGRGGRGNARFATPLNKAPKI AEKGEPGEDR
WLELELKLADVGLVGFNPAGKSTLI SMVSAARPKI ANYPFTTI TPNLGV
VRVVDGRSFMADI PGLI EGAHAGAGLGHEFLRHVDRTLLVHVLDTAGS
EGRDPVEDFRVTNLELTLYNLALGQRPQI I AANKMDLKGAAENLERLKEA
CGEYEI FPI SATTGSGLVLI YRVAGLLEEI PDEALLPDEAAEPVVHRA
GPRFTVSREEGI FLVGGKEI ERHVAMTDLENEEAVERLQRI I RRMGVEDA
LREAGI REGDTVKI GKLEFEFI E

>2617922007 Ga0073689_15115 Elongation factor Tu GTP binding domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_151]
MAKQKFERTKPHVNI GTI GHVDHGKTTLTAI TMVLATVGKAAVKKYDEI
DNAPEERERGI TI NTAHVEYETEK

>2617922006 Ga0073689_15114 translation elongation factor 2 (EF-2/EF-G) [pelotomaculum Ga0073689 : Ga0073689_151]

VARQFPLEKNRNI GI MAHI DAGKTTTTTERI LFYTGRVHKI GEVHDGAATM
DWMVQEQERGI TI TSAATSCHWSDCQI NI I DTPGHVDFTVEVERSLRVLD
GAVAVFCSVGGVEPQSETVWRQADKYGVPRI AYI NKMDRVGADFYRGMKM
I KDLRGANPVAVQMPVGVDSFRGVVDLVRNKAI I YTDGLGARSEETEI P
PELVEEAGVLRDLRLEVAELDEDLMMKYLENETLTDEEI REGLRKATLA
VKI I PVLGSSSFKNKGVPQLLDAI VDYLPAPTDVAAI RGTAPETGVVEI R
AAGDDEPFSSALAFKI MADTFVGKLTFFRVYSGRLKSGSYVYNSTKRRER
I GRI LRMHANHREDI EEVYSGDI VAAVGLKVTGTGDTLCDEKRPI LLESM
EFPEPVI QVAI EPKTKADQEKMI ALQKLAEEDPTFRVNADPETGOTLI S
GMGELHLEI I VDRMLREFKVEANVGRPVAYKETI RKKI KAEGKFI RQSG
GRGQYGHVLEI EPLEPGSGYQFTNKI I GGVVPREYI PAVDAGVKEAMEN
GVLAGFPVI DAGVTLVDGSYHDVDSSEMAFKI AGSI GFKNAAGKAGPVLL
EPVMKVEVVNDEYMGDVI GDLNSRRGRI EEMESRGNTRVI HAFVPLAEM
FGYATDLRSRTQGRMYTMQFSHYAQVPDNI AEGI I ARRVR

>2617922005 Ga0073689_15113 SSU ribosomal protein S7P [pelotomaculum Ga0073689 : Ga0073689_151]

VPRRGA I PKREVLDQPVYRNKVLTKLI NQI MLDGKKSVAEAVVYGAMDI V
KEKTGKNPLEVFETAMKNI MPVLEVKARRVGGANYQVPVEVRHRRQTLA
I RWLTNFSRARAGRTMEEKLANE I MDAAAGTGGSVKKREDTHKMAEANKA
FAHYRW

>2617922004 rpsL SSU ribosomal protein S12P [pelotomaculum Ga0073689 : Ga0073689_151]

MPTI SQLI RKGREEAVKKSTAPALKECPQKRGVCTRVTYTTTPKKPNSALR
KVARVRLTNSI EVTSYI PGI GHNLQEHSSVVLVRGGVRKDLPGVRYHI VRG
ALDSAGVQNRNRGRSKYGSKRPKK

>2617922003 Ga0073689_15111 large subunit ribosomal protein L7A [pelotomaculum Ga0073689 : Ga0073689_151]

MAYDHLLSARKKTVGAKQTMKAI ERGQAKVVYVAQNADRHVVEPI LQI CA
SKGI PVI HVDSMQALGKACGI DVGCSAAVTEE

>2617922002 Ga0073689_15110 DNA-directed RNA polymerase subunit beta' [pelotomaculum Ga0073689 : Ga0073689_151]

LLDLNNFDRI RI GLASPEQI RDWSSGEVKKPETI NYRTLKPERDGLFCER
I FGPTRDWECHCGKYKRVRYKGVVCDRCGVEVTRSKVRRERLGH I ELAAP
VSHI WYFKGI PSRMGLLLDMSPRALEKVLVYFVSYI VTDPGDTGLI KKQLL
TETEFREYRDKHGTETFKAGMGAEAI KKLLEE I ELEEMARELRQELKEVAG
QRKVRAI RRLLEVVEAFRKSNGRPEWMI LDVVPVI PPELRPMVQLDGGRF A

Table S2

TSDLNDLYRRVI NRNNRLKRLLDLGAPDI I VRNEKRMLOEAVDALI DNGR
RGRPVTGPGNRPLKSLSDMLKGQGRFRQNLGKRVDSYGRSVI VVGPEL
QI RQCGLPKEMALLEFKPFVMKRLVNDGFAHNI KSAKRMVERVRPEVWDV
LEEVI SEHPVLLNRAPTLHRLGI QAFEPVLVEGRAI QI HPMVCTAYNADF
DGDQMAVHVPLSAEQAARLLMLSANNI LNP KDGRPVAI PTQDMVLGGY
YLTOEREGDLGETKAFANPEEAVMAYNNKVI SLHARI KVRMGDAGLLETT
VGRLI FNEVI PPELGYNNRVVDKKI LSRI VDDCYRKLGSATTKLDDGI K
KLGFTFATRAGVTI GI RDI TI PEKKKEI LEEAEQQVQKVEQQYRRGLI TE
DERYRKVI GI WNDATKGVTDALI ESLDRFNPVYMMANSARGNI QQI RQL
AGMRGLMADPSGRI I DLPI KANFREGLTVLEYFI STHGARKGLADTALRT
ADSGYLTRRLVDVAQDVI VREI DCGTDQGI EVMEI KDGTVEI EKI QDRI I
GRVSMEDVKHPETGEVLAHAGLKI TEQEAERI VAVGI KKVKI RSVLTCRS
RYGVC I KCYGRNLATGRVVDI GEAVGI I AAQSI GEPGTQLTMRFTHTGGV
AGDDI TOGLPRVEELFEARRPKQAVI AEADGAVEVREVKGRREI EVI TD
EGEKAVYQAPYGARMKVKDGRVFAGDELTEGSVNPHDLLKI KGVQGVQV
YLLQEVQRYRLQGVDI NDKHI EVMI RQMLRKVKVDESGETDLLPGGLI D
I FEFEDENDRVI AEGGEPATAKAVLLGI TKASLATDSFLSAASFQETTRV
LTEAAI KGKLDPLLGLKENVI I GKLVPAGTGMSRYRNI SI I VDDDRDDEE
GAEDLDI MYREGMV

>2617922001 Ga0073689_1519 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_151]
MQMVVLYGEKAYYGEGI SLMKQYRLHRGLRPNEFRYPDD

>2617922000 Ga0073689_1518 DNA-directed RNA polymerase subunit beta
[pelotomaculum Ga0073689 : Ga0073689_151]
MAYPEKVGAGGRYSFGKLGEI LELPNLI EVQRNSYDWFLKEGLREVFRDI
SPI QDFTGNLVLEFLDYTLGEPKYSVEECKERDVTYAAPLRVKVRLI NKE
TGEVKEQEVFMGDFPLMTEKGTFI I NGAERVI VSQLVRSPGVYFAGSI DP
SGKNLYNATI I PNRGAWLEFETDVNDHI FVRI DRTRKI PATVLI RALGYS
SNAMVAALFNEDENI QDTLARDNTDTEEEALVEI YKRLRPGEPTVDSAR
ALLEALFFDPKRYDLANVGRIYKI QKKLKHGI LYRYSEGEKVSAGDQAEED
VI SPETGEVLLTAGKI LNANDLMRLREAGLEPCKSVLYGRGEVELDPYLK
KKVPRQREFI RELTREDI VETMRYLLGLMNGECQVDDI DHLGNRRRLRSVG
ELLQNFRI GLSRMERVVRRMTI QDQDVI TPOVLI NI RPVVAI KEFFG
SSQLSQFMDQTNPLAELTHKRRLSALGPGGLSRERAGFEVRDVBHSHYGR
MCPI ETPEGPNI GLI GSLSTYARI NPFGEI ETPYRKVDKESKRVTDEI VY
LTADEEDGI VI AQANAPLDEEDGRFREPRVNARSPEI VVVPADRVYMDVS
PKQVFSI ATALI PFLEHDDANRALMGANMQRQAVPLLKAQAPLVGTGI EH
KAARDSGVVVI AKEPGTVERVTANNI EI RTSRGI I ERHKLLKFSRSNQT
CI NQKPI VRKGDRVEAGQI I ADGPSTDNGELALGRNI LVAFMPWEGYNYE
DAI LVSEKAVKEDYFTSI HI EEECDARDTKLGPEEI TRDI PNI GEEI LK
DLDDRG I RVGAEVRPGDI LVGKVTPKGETELTAEERLLRAI FGEKAREV
RDTSLRVPHGEAGKI VDVKVFSDAGDELPPGVNQLVRVYI AQKRKI SEG
DKMAGRHHGNGKVI ARI LPEEDMPFLEDGTPI EI VLNPLGVPSRMNI QVL
ESHLGWAAAAAGYRVATPVFNGASEKDI LEFLRKAGKPEDGKTI LRDGR
TEHFDNPVTVGYYVMLKLAHLVDDKI HARSTGPYSLVTQQPLGGKAQFGG
QRFGEVWALEAYGAAYTLQEI LTVKSDDVGRVKTYEAI VKGENVPEP
GVPEFSKVL I KELQSLGLDI KVLSEDDQEI EI KEAEEI TETAKEI DI
QEEEPPEMDDDEFDGDAGDEEGLNEDFLDEDFDLDD

>2617921999 Ga0073689_1517 LSU ribosomal protein L12P [pelotomaculum Ga0073689 :
Ga0073689_151]
MSKVQEVLETVKGMTVLELSELVKAEEEEFGVSAAAPVAVAAVPGAGAAA
APDAAEEEQTEFDVI LTAI GDKKVVNI KVVREI TALGLKEAKDLVDSAPK
PVKEKVSKEEAIAI KAKLTEVGASVEI K

>2617921998 Ga0073689_1516 LSU ribosomal protein L10P [pelotomaculum Ga0073689 :
Ga0073689_151]
LENVPLSRAEKETI VRELKEKFEKSTVAI LSDYRGLNVAEVTLRRLRE
AGCEFKVAKNTLTGLVAKQI GLEDLEPYLEGQVAI AFGKDPVTPARI LSD
FI REAKKMEI KAGVLEGKVI DADGVKVLADLPPREVLLARVLGGMQAPLY
SFAGVLQGTLSFVYALEAVRKQRAGEA

>2617921997 rplA large subunit ribosomal protein L1 [pelotomaculum Ga0073689 :
Ga0073689_151]
MPKYGKKMADALKEVDRGVLYEPAEAFELVKKVAPAKFDETVAVRLGV
DPRHADQQVRGAVVLPHGTGKTRTVLVFAKGDVKVEAEEAGANFI GAEDM
VARI QQEGWLGFDDVAI ATPDMMGMVGKLGRI LGPRGLMPNPKTGTVTFDV

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ARAVKDVKAGKI EYRVDKAGI I HAPI GKVSFSTEKLLLENLRI LVDTLI RV
KPAAAKGTYLKGI SVSSTMGPPI KVNTQKVT

>2617921996 rplK LSU ribosomal protein L11P [pelotomaculum Ga0073689 : Ga0073689_151]

LAKKVAAI VKLQVPAGKATPAPPVGPALGQHGUNI MAFVKEYNERTAAQT
GLI I PVEI TVYEDRSFTFVTKTPPAVLLKKAAGLETASGEPNKKKVAQL
PRSRVREI AELKMPDLNAADVEAAMRMVEGTARSMGI DI VEG

>2617921995 Ga0073689_1513 transcription anti termination protein nusG [pelotomaculum Ga0073689 : Ga0073689_151]

MEKKWYVVHTYSGYENKVKANLEKRI ESMNMEEKI FRI LVPMEDEVEI KD
GKKKI SKRKVFPGYVLVEMFMTDDSWYVVRNTPGVTGFGVSGSKPI PLND
NEAAQI I TOMGVEGPRARVDLTEGESVRVVTGPFENFI GKI EEI NLEKNK
I RVMI SMFGRETPVELEFTQVEKI S

>2617921994 Ga0073689_1512 preprotein translocase subunit SecE [pelotomaculum Ga0073689 : Ga0073689_151]

MAVTKKEENNKKDPPGKKVI AKKDTVKKDTGKKELAVKKDKVNRI EQVQKF
FRGAYSELKKVHWPTRETTI YTAVVLVAVVVVGAMI WAFDSALSAVLGL
I LQR

>2617921993 rpmG LSU ribosomal protein L33P [pelotomaculum Ga0073689 : Ga0073689_151]

MRVGVTLACTECKRRNYTTTNNKKNDPNRI EMKKYCRFCHTHTMHKETR

>2617921992 Ga0073689_15015 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_150]

MALKVVVADDDDPVCKLLKLLNVQKSLATFSRQVI PERRYLRYLRLCKER
LCLLLW

>2617921991 Ga0073689_15014 Fe-S oxidoreductase [pelotomaculum Ga0073689 : Ga0073689_150]

VEEAVNYFLEVRDAI TEMGGNDI NI CMQCGTCSGTCPWGRLEEKSPFNI R
RMI YMGRMGLEGFETDDI LYACTTCNHCVTRCPRGVKI I DVVRAMRSVTA
ETGGI PKNLKAVVSGI NSQGNPWSQEQEKRAEWAKGLNI AEFTPDTEYLL
YACCTSAVDGRSQI ARSI AELLQKAEVSFGI I GNEEQCCGEATRKI GAE
AEFAMLAANI NLFQKGKVKI I TTSPHCFOAFTRDYPEFGGEFEVYHYT
QI LDSLVKEGKLSFSKTAGQKVI YHEPCYLGRHNKI FDAPRQLLGAVPQL
ETMEFEKAKDDSLCCGGGGGRI WMETKAGQRFSDI KVKEASKKANLLVT
ACPYCVMMEDSVKNLNKDEEI AVKDI SEI LKESL

>2617921990 Ga0073689_15013 soluble lytic murein transglycosylase [pelotomaculum Ga0073689 : Ga0073689_150]

LAAAFHRKANKGMFGRRLI LALI LVVI LLNLDGI GRI LYPFPYREMSFFY
ARSYNVDPFLLAAI MKAESGFNSRAVSEKAGKGLMQI MPETGRWI ARQTG
DPDFQPDHLFEPETNI KFGAWYLADLEKEFGSNTVLALAAYNNGRGNVRE
WLTSKNLSGDKSDI DQI PFPETSHYVKKVLLYRELYSRLYGRGGD

>2617921989 Ga0073689_15012 dephospho-CoA kinase [pelotomaculum Ga0073689 : Ga0073689_150]

MLI I GLTGNI GSGKSTVARHLES LGAKVI DADRVAREVVLPGAPALREI V
ETFGPGVLKDDGTLDKRLGATVFADPAARARLNGI THPRI NEAI RRQI T
EYSTHADSCDYGGVLVI EAALMI EVGLHQNVDEVVVKTDDEEDQI RRLAR
RDDLTPEEARLRLATQLTQAEKLKHACRVI DNSGDSAETI KQVDRHWADF
LQEH I QKTGGI

>2617921988 Ga0073689_15011 putative sporulation protein YtaF [pelotomaculum Ga0073689 : Ga0073689_150]

LELLSYI FFALALNLD SFGAGVAYGARQI KVPPLSLVI I SLI SVTAI VI S
MLGGQALLKFI PVSLSHRLGGFLLLLI GFWVLMETHRSKGQAGGKDGRGK
SNGRVFEI HI RPLGLVVQVLREPTRADLDSSGVI SPKEALI LGSALAMDA
LGAGFAVSM LGFSI ATTAVVVG LGHFLLTYLGLLAGRTI TSRVGRQLTAL
PGCI LI LLGLLKI Y

>2617921987 Ga0073689_15010 DNA-(apurinic or apyrimidinic site) lyase [pelotomaculum Ga0073689 : Ga0073689_150]

MNKMPELPEVETVKRTLSPKLI GQKFTGVQI FLPKI I KTPEPAQFI DFI K
GRKI I KI DRRGKYLLFDLSGGLTLVVHLRMTGSLVYSEKDGPPARHTHVI

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FHLDNGGNLHFADMRQFGGLWLAPTGSLGNLTGLKDLGVEPLGGFLFTKEF
LKKEFRRRRI RI KPILLDDQTFI TGMGNI YTDEALHRAGI NPERPATTLTP
GEI ARLYHAI QDVLREGI ANRGTTVRDFI DGDGRPGKYQELLRVYNREGK
PCPHCGRKI VRKKVGRSSYYCPACQKN

>2617921986 Ga0073689_1509 DNA polymerase I [pelotomaculum Ga0073689 : Ga0073689_150]

MNMFTAPMI I I DGNSLTHRAFHAI PPLSTSQGLLTNAVYGFTNMLLKI LA
EEEPGLI TVAFDKGLTFRHEHYEDYKAHRAATPDDLRPQFPI LKDVLRRA
MRI QVFEFEGYEADDLI GALSAAEQAGI RSI I VTGDRDALQLVSPLTRV
RLTKKGVSELEEYDEGKVDWRYGI SPQQYNDFKGLTGDASDNI PGI PGI G
EKTASRLREYGSLEEVLTHI GEI PGRI GELVKTYRHOAEMSKQLATI HR
DVPVEI DLERCWQGPDPYRELLEI FNKLEFRSLI KSI YRDNKLDTGEEKI
KGLGGENRTARRTLPEPAMETCPVTYQRLDTGDALKNFVKTAQRAGQVSL
DLSRNSRGGI AAVGFAI EKDKAYYAGPRQSDAGHQEVSNTFPDKALDALK
TI CENPDI KKYCHNGKELFQLLHRHGI GLNHLAFDTMI ASYLLNPASPNI
DLEDVSLEHLGAVLPGGEEGLPARALCVTQLTRSLDQKLKLFQDRLFYD
I ELPLI QVLAEME I EGVAVDKQLEAMSRELGRSI KNLAGEI YRLAGHEF
NI NSPKQLSKI LFEELKLPVI KKTGTGYSTDAEVLDELAMSHEI VAKVLE
YRQLMKLKSTYTDGLAALI SPETGRLHTTFHQNVATGRLSSAEPNLQNI
PI RLEVGRLI RKVFI PRRKENMLLTADYSQI ELRI LAHI SSDRVLI NAFK
SGEDI HTRTASEVFGVPPEEVTREMRGRKAVNFGI VYGLSDFGLARDI K
VSRQEARRYI DNYFARYTGKTYI DRI I REAREKGYVTLLNRRRYLPDL
FSPNRTVRGFGERTAMNTP I QGSAADI I KLAMVNI HRELAEHGLGAKMI L
QVHDELI FDTPV E I NQLKELVRRYMENALALDVPLVVDI KVGPNWYDVK
KV

>2617921985 Ga0073689_1508 carboxyl-terminal processing protease [pelotomaculum Ga0073689 : Ga0073689_150]

LRKRI PPVLLLVFVLSLWI SVPASGAESPAPGPTI KEI LNYVQTEHI SS
PDPGTLTRGAI EGLI DTLDPPYTEYLPGEELFEFNRLDGDYVGVGI QLE
PGEVYPVVNTI ENAPARDAGVKPGDLLI KVEGVDVAGEPLGKVVQRI RG
LEGTTVRLTLRROGAGDFE I GLDRANI NMPTVSGFLDGGTGYI GI SSFG
AYTAGEFREVLQAI RRGADKLI LDLRDNPGGLLQGAQVI I SCFVEPGKL
AVSVAYRGGDRQEHYTDGAPI ARNMPVVI LVNRNSASAAEI LTGALQDYG
AAVLAGEPTYGKGTQAVI PLKAGGALKLTI ARYHTPKDRVI DGTGLDPD
I QVLTPLDLQAAAERYLEQPEKNTI TVKTGKSEALVNGKTVFLRQAI QR
SGVTYLPPLRFVLEALGYRVDWQAQEGSI KI I GYNTMAAI NPEGGS I SVGG
RPVPGGEPLLFEDGAAYI SI STL SLLNI GVKI EDGKI TI EK

>2617921984 Ga0073689_1507 DNA adenine methylase [pelotomaculum Ga0073689 : Ga0073689_150]

MCKTYHATRTATKPKPPVKWAGGKGQLI PQFEPLLPKNAYRLYI EPFVGG
GALFFHLLPSKVI LI DNNKEI I NFYLAVRDYLEQLI QDLKKHEI TAEYYY
RVRALDAEI LSPVERASRFLYLNKTAYNGLWRVNSSGKHNVPFGRYKNPR
I VNEQNLRLVSKALKQAEI HDDFSRVLECAAPGSFI YLDPPYQPLSETS
SFTSYTQGSFANDQRRLLAAVFRELDGKGCI VMLSNSDTPFI REI YSGYE
VKVQARRAI NCRADKRGPI NELVVRNYS

>2617921983 Ga0073689_1506 SEC-C motif [pelotomaculum Ga0073689 : Ga0073689_150]

MPGNERSCPCGSGKSYEKCCGKNNVLFSLDQVRWRAGQDLRRRLGEFAD
QPSFTWDAARAQDLYLGCLDAQLADRDDDFTMERCFEWF I FDYKLSSGRT
VI ETFRDDNSHI LSSREASLVDRWARTRI SLYEVTGVI PDEGLYI KDLIG
QREFKVRDI NAAAEI VTGNI LLMRVLKVGEYEFSTSGLALPGHYKEPLL
ERI HRDRQDYFTGKKAGARGWI VYLQERAHRI NAWVMELGLSGARGEKEP
AGRSLEPCRVI LSVENWQEAALNSLRSDTCRMI RELKDCSGVFRQATAAI
LGRHRRLDGPAQPPMPAEASDECAVKTGEAVLSPVI GHLVLTQQFI I I T
AGLPKLLSKCKKTLMEFLKGAVAESPAGRQRRPYTSDGAALTEDRQKI AG
GEDNYPWPEPEHAASVWVWAGLDALGYNPKQKQKALKLWYDYCSKEKP
SVRKAASVAAATVI YTFTRVEMENGLKQQDLAGRYGVASSTI SARFRQLCR
ALELVAYDKRYSTKKPPSAGLWEYHPLFRGLPES

>2617921982 Ga0073689_1505 membrane protein DedA, SNARE-associated domain [pelotomaculum Ga0073689 : Ga0073689_150]

MFOETI YMSKELKVRIFYQGGFLTELI EDAI KI I TNAI ATMGYWGI GI G
MAI ESANI PLPSEVI LPYGGYLVSTGRLEFYRAVLAVGTGGTAGSALSYY
LGLRGGRPFLVKYGRYFGFSMKHLELAERWFDYGEATVFFTRLMPI VRT
FI SLPAGI AGMNFKKFLVYTFGLSLPWSLLLT I YI GLKMGQNWTAI KPWFH
RLDVVVALGI LAVI I YLWRRRRRNGLYSRN

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>2617921981 Ga0073689_1504 N-acetyl muramoyl -L-alanine amidase [pelotomaculum Ga0073689 : Ga0073689_150]

MRPDSACAVRGDEYKGGAPMSSHNFAIRI TNISKVVSEAGDLFSRVVIE
SYGSFQYKAATRDGAVVLEVGAAAPNMPEGPVEI NDGLVRQVSLTKTGPGA
AVVEI SLEHPADYKI EVVEGI PVRTTVI LERSYLSKI FGGRKI VDPGHG
GDDWGGRGVPVNLLEKNVLPVANNLRKLFEQAGARVVLTRAVDERI APED
RIKI ALVEKADLFI SI HTHVDQDCKVGGPAVLVYGPSCPGGPVVAELVREA
LNKKLKLKDRGVGESRDYAVLGAI PAIEVEVVAI TNWVEEGLLRSPVHK
KAAEGI FNGVKNYFANI GRG

>2617921980 Ga0073689_1503 F420-O: Gamma-glutamyl ligase [pelotomaculum Ga0073689 : Ga0073689_150]

VIIGRIPIRTHIVTEQDDIVDVVKRYTGEI AGPGDI IVAESVVAI TQGR
AILEKVRPGALARFLCRFPKGDSLATPHAMQLAI GETGTLRI LLGAAA
AALGRI I GRRGDFYRVAGRNLALI DDVAGTMWPFERYI I LGPKEPRKI VE
RI REATGAGAVI ADVNDTGNVDI LAASKEVDLKKLVKYLKDNPFGNDDQQ
TPI VVLKTASKKQ

>2617921979 Ga0073689_1502 sporulation lipoprotein, YhcN/YiaJ family [pelotomaculum Ga0073689 : Ga0073689_150]

LKRPAASLPTLAALLI AAFLLAAGCAALKKPAPENPPGTQVPAPAAPSGQP
MPDTAELNRMASSLADTAAKEPGVNRATTVI AGTTAYVGVDQKAGAEGK
ETERI KRNVSNAVKKAEPRLTAVFVSSDADTVTRLRRI ADGI AAGQPVSA
FDSELAIE AKRLSPTAR

>2617921978 Ga0073689_1501 D-alanyl-D-alanine carboxypeptidase [pelotomaculum Ga0073689 : Ga0073689_150]

MRAALKARTI VLLVLVFSLI LPHAAAAAPQGVTAADAVLMDVETGQVYFA
KNSTRRAAPASLTKI MTVLVALEYGKLDDVTVGGGAASVSMGSI I DLRK
GEKI TLAELLKAALVCSANDSTVAI AEHVGGSHAGFI KLMNAKATALGLF
GTRYVNTNGYHHPNHYTTAYDLAVLTRYALGHPRFNLVQTRETTVRWVD
PPQREEKLQNSNRLLFNGYEGI DGVKTGTTPMAG

>2617921977 Ga0073689_14921 exonuclease RecJ [pelotomaculum Ga0073689 : Ga0073689_149]

MFFTAPLTLPNPAASAI I LLSMKNI PKSNHKKI WRVKKPVPSLNRI LARKL
GI SPVTAQLLI NRG IYTVEEGRAFLDSELARLHPPLLLKDLKAVNRVLK
AAGAGEKI LVYGDYDADGI TATALLVQVFRRLGADVDDYI PHRLAEGYGL
HOAVLQKTRGKTALVTVDCGI SAVAEAVWAGENGLDI I TDHHEPPEE
I PRAFAVI NPKRPGCDYPFKELAGVGVALKLAQAI MEAAGMGSTWQEYL
DLVCLGTI ADI VPI RGENRI LVKHGLPALAATGNPGLRALMAVSGTKKED
LGPREVAFGVLPRLNAAGRVGSPLLAARLLLTDDGGLARELALELDGRNQ
ARQEI EAAVLEELGLLKEDPGLAEARVLVLASENWHPGVTGI VAARLVE
RFYRPALLI ALEGPLGKGSARSI PEFNI YGALNHCRELLLAYGGHAMAAG
LSI EAGRVADFREKI NAYAGEI LGDKQLI POLVLDGI I DLSRVSEDLARE
I DLLRPFGHANPRPLLGCCLKTPVLESRGVGREAAHLKLRLRGRNNI LDGI
GFRLGAYAEVVATAEMVDLAFVPGI NEYNGRRSVQLEI KDLGTPARLDVR
ELESRGVSDPVVEYANSSGTLVENLEELFTPEYVLETI ARI KTGNRPPGA
FDEGKI TNVELVDHRGSGDRPGRLAGLVFPGEPTMVI TSCGYQTI ELAHI
LRLAGLPGKGKAAFCGCLSRETKVALAAGFEVGEI TTVVATPAMAGLFE
RCARQVLLYNLPFGPETVNSALDVLEPGGRLGLLFNPADMQENLAVWKAL
APDREYLACFYRLRRVRNGGDEVSL

>2617921976 Ga0073689_14920 Gas vesicle protein [pelotomaculum Ga0073689 : Ga0073689_149]

MGI RHSVQASSLAEVVDRI LTKGI VIDAIVRVALVGI ELLAI EARVVI AS
VETWLMYAEAVGLTKEPI PA

>2617921975 Ga0073689_14919 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_149]

VSLETSMQSWCNFTSSCTARADNI RILKNYSQEVVKKHKDYRKEI I TAR
FLENKKMVLGLVDRYLKDRRKASEI LASMRKI V

>2617921974 Ga0073689_14918 Gas vesicle synthesis protein Gvp0 [pelotomaculum Ga0073689 : Ga0073689_149]

MVI KKVI NTVDQFFNEELEKPGKI I GVI KEDDYWKVKI EVPEEVEYMRKR
AQDDLMAI YEVHVDNNFEVTSFDRI ALRERDSLTCHPVEQNADEN

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>2617921973 Ga0073689_14917 gas vesicle protein GvpN [pelotomaculum Ga0073689 : Ga0073689_149]

MLEKQMLI YENKNFVETEYLKKI SERAAI YLKSGLPVHFCGPAGVGKTSL
ALRI AKNLDRPYSFLFGNDFNTSDLI GGNYGRRRKTVDNFI HNVYTV
EDFQLKWLDROLVKACREGHTLI YDEFSRTRPTVNNI FLSI LEEGI LFLP
SFELETQYVKVHPEFRLI FTSNPNDYAGI HQTQNALEDNMTI WLTEMDH
ETEVAI TVNNSGLDEKTAFAKVVSLVREYRTGLVSSSCSVRSSI KIAKSL
KGDNI LSNTGLTI SI FSDI LFSEI GQTDSDRNKLKNQI SLLVEKYF

>2617921972 Ga0073689_14916 Gas vesicle synthesis protein GvpL/GvpF [pelotomaculum Ga0073689 : Ga0073689_149]

MKI FSGLYTYCI I EMNQEADPGVKLPKDAFLVRYRNI AAI VSSVPKSNWQ
PTKNNI RRHQKI I SQI QESFELLPLRFGI VFKNSEI QKMLQEKYQEI TI
LFHKI HDRVELGLRVFWNHTAFLNEVANRKVEKLKKEYDSGKKDRYLI AL
EVGKI VEAVALQKREEYI KTI FEPLSNLAEDSLLSPVAGEKMFVNAFLI
KKELI TNFDEAVKKI SDKYKDKFTFKYSGPWPYPYSFVTVSL

>2617921971 Ga0073689_14915 Gas vesicle protein G [pelotomaculum Ga0073689 : Ga0073689_149]

MFLI DDI LLAPAKGLWFI FKEI HKQVMDEYCNEEKI YKELARLQYYLDI G
EI DEETYNRLNELI RQLQEI EEEKESLAEWDDNQE

>2617921970 Ga0073689_14914 cation diffusion facilitator family transporter [pelotomaculum Ga0073689 : Ga0073689_149]

LNDKI RAARLSI ASNTVLTGLGLGI GVMNSASVI SEAI HSGLDLVAALI
AFFSI REASKPADERHNYGHGKFENLAGI I EAMLI LGAAALI VVNAYPKL
YGEAEI HSLGLGAGVMGVSAAALNFFVSRKLMRVARKTESPALAADAWHLR
ADVYTSGLGVFAGI VAI KVTGLTI LDPLI AMAVALLI VKAALELI GDSMRS
I LDVRLPEPEERAVREVLAHSNWFVEFHQLRTRKAGSHRYI DLHLVVPK
NNAI NEVHTLCDRLEEDI CSRLKNTHVLI HTEPCGLSCEDCNQVAEEQKR
AAKCEPACGDRSQCGKEPVSPHGE

>2617921969 Ga0073689_14913 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_149]

MMI PVKVKEI AYDI MMNPVLLI DEEELKALPI WVGPFEAHAI ALALQGV
SLERPLTHDLLKSI CDRLEARLSMVVI NDI KDGTYFAELHMMWRNDRELVI
DSRPSDAI ALALRTGTPI YLTKVAEGSLSI KDLI SEEQSQELKDLLESS
RPDDI KKSLLH

>2617921968 Ga0073689_14912 Nucleotide-binding universal stress protein, UspA family [pelotomaculum Ga0073689 : Ga0073689_149]

LNRKI LVASDGSNALRAAEFAAGLAGLSTESKVTVLVNDMLENMKYYS
PLRSPVI FEEVEVFFRDKSQDTLDRTLAVFEKYRCRVDGVI RVGNPAREI
VDFAREGGFGQI VI GSRGMGRLLGI VLGSVSSKVVLADCPVTVVK

>2617921967 Ga0073689_14911 transcriptional regulator, TraR/DksA family [pelotomaculum Ga0073689 : Ga0073689_149]

MQEEI LLKFKQRLLSEREHLTRRVEAMDGEGLGVSLSDSI SELSTYDNHP
ADI GSEVFERSKDFALRENAMI TI TAI DDALEKI KNGVYGTCDVCGKEI A
PERLEAMPTTTI CRDCKEAEKI PHRENDRPVEEYVLGKPFARTFVDASG
DI MYDGEDAWQEVARYSETTDEWSRGGSYGYSEFDI VEDRGSVEEVDNI
PYEVGDDGVFYKNFRGADDESAPAEKI DVGI EHSEEPNNRGMPGAGG

>2617921966 Ga0073689_14910 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_149]

MECESQNSLLRALRDRVADLAVKMEKMKLAEYI QLLDNPWRLMYI NFI AG
LARGVGI AIGFTI LGAI VLYFLKI LVI LNLPIWGGFI AEI VRMVQLKVG

>2617921965 Ga0073689_1499 preprotein translocase subunit SecF [pelotomaculum Ga0073689 : Ga0073689_149]

LRLRDRKPFHFI KLRKI WYTI SILI I LPGI VSLFLHGLNLGLDFSGGSLL
DLRFNQSTTVEQVRGALREFGLEESSI QRSDTDFI I RTRELTEENARV
I QSLDGKLGTVTVQSRVGPVI GRELI MKALGALAAASVLMVI YI TWRF
EFRQGI AAI I ALLHDTLVVLGVFSI FQFEVDI AFVAAI LTI I GYSI NDTI
VI FDR I RENMLNKKKGAELEDVNNASLWQTMARSI NTVLTVI FI LVALFF
LGGTTI HNMVLALLVGI I SGAYSSVCNASPI WFDLQKFERRGGTRAARA

>2617921964 Ga0073689_1498 preprotein translocase subunit SecD [pelotomaculum Ga0073689 : Ga0073689_149]

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MKWDKI LKLAGI I LVVA AVAVLAVKPVFPGVNWLPFTNLI KQGLDLKGGV
HVVLEAKDTPESPVTPESVKRAMAI I ENRVNAFGVAEPI I QQQGSRR I V
ELAGVSDPD EAVRNLI KTAYLVFKTEDGNTVLTGRQLKDAVESKDPSGQ
VQVNLEFQPDGAKTFADVTAA NVGKRI AI LLDGNVLQAPVVREPI PNGKA
QI TGYESLEEAHNI AI LLRSGALPVKLDVMEKRTVGPTLGADSLNKS I KA
GI VGLAAVLI FMAVYYRLPGLVADLALVI YALLVLMVFAALHVTMTLPGI
AGFLLSLGI AV DANVI I FERLKEELWTGKSLRS I DSGFKRAFVAI LDSN
VTTLI AAVVLYYFGYFGMGPI KGFAVTL SI GI LASMFTAI TI TRWLLHLV
AGSNLVRNVKMYGA

>2617921963 Ga0073689_1497 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_149]

MI TLEDI KKDPVVDSFI RKG NKYLGVMGFTEHSYRHVNLVSSI AKNI LER
LGYPQRQVELAAI AGYMHDI GNVVSRNDHGI SGAVI AYP I LLQMGMPDE
I ATVI SAI ANHEEQYGHAVNSVAAA I VADKSDVHRSVRNPDFATFDI H
DRVNYAVEHSFLWVADDKRAI TMELTI DI DI CPVMEYFEI FLSRMI MCRR
AATFLKCNFELVVNGAKLL

>2617921962 Ga0073689_1496 preprotein translocase subunit YajC [pelotomaculum Ga0073689 : Ga0073689_149]

MTNPNQLMSLLYI VALFAI LYFLMI RPQQQRQKKHQEMLKSLKVDDRVI T
VGGI YGAI VKI KDNSI I LRVADNVRI EFLKSAVSQVTSKEEGEKGE

>2617921961 Ga0073689_1495 tRNA-guanine transglycosylase [pelotomaculum Ga0073689 : Ga0073689_149]

MAI SFTVTRKDKTCRARLGLLQTPHGTVETPI FMPVGTQATVKTMTPEEV
SEAGGRMI LSNTYHLYLRPGHELI REAGGLHRFMHWDGPI LTDSGGFQVF
SLGPLRKVSEDGVTFRSHI DGSEHFFSPEKAMEVQMALGSDI AMAFDECA
PYPCSREYAAALERTTRWARRSLAVHRRREDQGVFGI VQGGVFPDLRERS
AGELVELDFPGYAI GGLSVGEPKELMCEI LDHTVPLLPEEKPRYLMGVGS
PDYLVGVARGVDMFDCVLPTRI ARNGAVL TRRGKLVVRNAEYARDFTPL
DPDCDCYTCRHSRAYI RHLI KAGEVLGI RLTTI HNLRFVLRMLMEEI REA
I KRRNI LEYRDKFLKSYQEG

>2617921960 Ga0073689_1494 S-adenosylmethionine--tRNA
ribosyl transferase-isomerase [pelotomaculum Ga0073689 : Ga0073689_149]

LKLSDFNYFLPEELI AQEPAERDI SRLMI VHRDGALEHRLFKDLVDYL
NPGDALVI NDRVI PARLMTGKEGTGARI EVLLLKQLDATRWEALVKPGR
RAPMGTKI RFGEGSLECLVTGGTGYGGRVVDVFCFAGPFEEVLDRVGMPL
PPYI KRPLLDQHRYQTI YARQAGSAAAPTAGLHFTPELLNRI GEMGVKVV
PVLLHVGLGTFRSVKVEDI RHHMHAEYIEI SEDSSTAI ADTRTGGGRI I
AVGTTTI RCLESAAEEGGRVRPGSGWTEI FI YPGYRFKVI DGLVTNFHLP
KSTLLMLVSALAGREKI LAAYAEAVRLRYRFFSFGDAMLI I

>2617921959 Ga0073689_1493 stage II sporulation protein D [pelotomaculum Ga0073689 : Ga0073689_149]

LKLD CFFKI FPAYMVAVWI ALSPLAVASAATAPGTI RVALVREADSLEFK
VTGNYQLVDQSTGKEI AKLERGDNWLVKLQGNKI ELRVQDQTYGPFKGPV
LVRELSFSATI TGASGSGTERHSI DGLMAI GATGKVVSLSPSGNPSVTA
TGTSALSGDGGGTNLVSLTGDAETRRYRGNMEFRVEDGKLA AVNELNI ED
YLRGVVPAEI PASWPAEALKAQAVAAARNYALQRAEVTGRSYNVTSDQYS
QVYKGYDAESPATNRAVEETRGVVM LDRGNLVTAFFHASSGGYTENSEDV
WKYPLPYI KSKTDPFDKNDRHYNWQVDYAEQLAQQLQKAGYNFKEVNDI
EELARTASGKRVEKI AVEGEDPDGKPLRVEI FNADSVRLALGLKSALFTM
QKDYDKDKNL TGVS I SGSGWGHGLGMSQWGALGMAEQGYSYQDI LKYYYI
GI TLAGDYGRPAVPVRSSGGNAQAWLGN

>2617921958 Ga0073689_1492 Protein of unknown function (DUF2905) [pelotomaculum Ga0073689 : Ga0073689_149]

MWESLGKMLLFFGI FLAVTGGLMLLGGKLFGLGRLP GDI YI QRENFSFYF
PVVTSI VLSLLTI I LNLI RR

>2617921957 Ga0073689_1491 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_149]

VLSI KI LLHI CCAPCSI YPVDFLREKGM EI YGYFFNPNI HPYTEFVRRRE
TLERYAAETGLKI I FDEEYRLEEF I QAVAYRESHRRCVYAMRLEQTARV
AKRGGFDCFSATLLVSPHQHNL I RDI GLAVGDKHGVFPFYADYRSGYRE
ATARSRELGM YRQQYCGCI YSEKERYRPAKKGDI LLDVGVFG

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>2617921956 Ga0073689_14818 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_148]
MKGGIRGEKPLISEFGRPNVLAATQDCCLVLGVGYDCSQIR

>2617921955 Ga0073689_14817 mobilisation protein (MobC) [pelotomaculum Ga0073689 : Ga0073689_148]
MRKRGIRIQVWLNKEENTRLHTSAKKAGLSQEGYLRSLISGYVPKELPPP
DYFSMTRELHAI GSNLNQIAAKANAI GHI DKTLFQYEANRLRKAVQDI ME
AVTAPERRT

>2617921954 Ga0073689_14816 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_148]
MDKETQLINRINRNFM DYRAKMLKLDGQKIFEKAEELAAAYTQAHWYLI VD
HRYEPEELDYFLLFQNPLEVVDQYQNEVRSANDVLELVVNVNSCDKQEAL
ADYPLMKKHGEPEER

>2617921953 Ga0073689_14815 Relaxase/Mobilisation nuclease domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_148]
MATTAIWDVTDRLDRVIDYAANPEKTENPDFSSPDFQGLHKVLDYTQQDA
KTEKQFYVTSLNCDPATACQMGRTKRQYQKQDGLAFHGYQAFAPGEAT
PETAHAIGVKLAKELWGDRFEVVVSTHLDKRHLHNHFVLSVSFKDGKRY
YDNNATYALMRQASDRLCREHALSVIENPQRGKSKHYAEWKAGREGKPTW
RGLIREVDQAI AAAMTFTQFI AALRKQGYEVKTGVKHMVVRPLGKERFI
RLKTLGDDYTEEAINRRI LQNRAPQRPPLPEPKRKRRTFKGSLKTAKKI
TGLOALYFHYLYKMGILPKPRASSKRTHFLLREDLRHLEEI TAQTRLLCK
NHI SSSEQLFTYRSTVEQNMA SLAARKSLYNRI RRCGDEEQATAYKEQI
AGLTRQISQLRKEVKLCAGILSRSGEMREKLSRI KQEEIQQRKEAKAYEQ
RSRRRGSSRQHDS

>2617921952 Ga0073689_14814 Protein of unknown function (DUF3801) [pelotomaculum Ga0073689 : Ga0073689_148]
MNSEAAAADQVVMNTLKGIEVMARISGEGAKNLAVYLYAVLTGQKKTRGK
TRLEGMLRSGKELKVFVAVRNEDLQKFTQEAKEYGILYCALRDKRDTDGM
CDIMVRAEDASKINRI VERFKLATVDTASIKSEIQKSRAAKQEDKAPAEKE
TPAEKSADDFLDELLAKPDQPEPDQERSNNPNPTDPTAATAAEKSPSEP
TYERSGKAAGGTSEPERKSVRQELKEIREAHREQAEPKREQSKEQSKSTG
QPAKSGQKSKAKKSKPKER

>2617921951 Ga0073689_14813 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_148]
MSNFDDLFRQEQGQSPPI SDQPFDEAWAQKKQEORETVYAMIDETATAV
ARDGDTFQKYLDVQSRFDYVSNSALLILAQKPEATRIDFDTWKEQGAY
IRKKESGFYIIEPGEYQQRQDGSTGISYNPKKMFDSQTGNSRKREIPVY
PDERTRI KALLAHAPVPVRI SDTLPSGVNLYQPDTRI QIRRGLDANHI
FRALAQELAQAE LDKGDGSYNRSEHG FHAYCAS YMLCKQYGVETDGFYHF
EGVPQMLETLEPQEI RAELTVIREAAGEISGRMNRMNLNQRQQRQEPER

>2617921950 Ga0073689_14812 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_148]
MKEEERVLTDDEYEGVVVNALNELRNDLIKEERPTDTVDELLLLKTI DAP
TKKQKRRNHDEAR

>2617921949 Ga0073689_14811 Type IV secretory system Conjugative DNA transfer [pelotomaculum Ga0073689 : Ga0073689_148]
MKRAETARSNLI LWAVFLIPVWVAALLTAPSLSGGLPEILENLTAAMNHP
FHI QWVDNSPKCVLLFVAAYGMGIGI YLSTKRNYRPREEHGSARWGGA
A VDKKYRDKDPQKNKILTONVRI GLDGRRHRRNLNLVLVGGSGSGKTRFYA
KPNVMQANTSFVILDPKGGTTRS

>2617921947 Ga0073689_1489 group II intron reverse transcriptase/maturase [pelotomaculum Ga0073689 : Ga0073689_148]
MATSERTLKKQKIRNNEYGTQELFDDLYEKSQSGHMFHLMELVESEN
ILLAYRNI KKNKGSNTRGTNSTNIVDIGAKEPAALVSYVRKRLTDFKPHS
VRRVEIPKPDGRMRPLGIPTEIDRLIQQCQKVLEPICEAKFHKHSYGR
F PNRGTHHAVARAMFLSNI SGFRFVVDIDIKSFFDNVSHGKLLKQLWTMGI
RDKRLLSVLSKMLKAEIQGIGIPKKGVPQGGILSPLLSNVVLNEDWWIS
SQWETYPELRRYRSRPNYKKGKGLKSVYIVRYADDFKLFCKKRSADNLF
IATCMWLQERLGLIEISEKSRVVNLKKQYSEFLGFKMKLRRKSNKWWIKS
HMTNKALNKCKDSIRTOIHKLGREPNQWSVMNFNAAILGYHNYYKCASN

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YLDFDRI AFDVRKTLI CRI KSHRSRTGLKSKAFEQYYGKFTGKI FNLCLG
ALFPI NGI KTVPPMCFPSDI CNYTEAGRAKI HSLQKAI DPTYLQQLMQSP
I KGKSAELNDNRI SLYVAQRGKCAI TGEVLELGNMDVHHI I PMHMQGDDR
YANLVLLTSDAHKLLHATQGETI QKYLLKLQNYTI HFQRLNKM RKHAGLS
EI STNR

>2617921945 Ga0073689_1487 Type IV secretory system Conjugative DNA transfer
[pelotomaculum Ga0073689 : Ga0073689_148]

MHLSHCYNPFTYLQDDKDVLLKLVNLI RNTTPKGSNTNDPFWERSETALL
EALI LYLLYEAPEDERNFPMVMEI AAAEVREEDETYQSPLELDERLAM
REPEHLAVKQYNI FKLAAGKTAKSI LI SLGVRLEKFNLSI AGI TTVDEM
ELPAI GEKKTALFAVI PDNDSSFNI VGMLYTQLFQSLMYLADYKHGGRL
PVHVFVMDFAFANLPDFDKLLSTMRSREI SVSI I LQNLALQKALFKD
TWESI VGNCEFLYLGGNEQSTHKYVSELLGKETI DLNTYQSGRGHGSY
STNFQLSGRELLTPDEVRLDNRVALLFI RGEHAVMDDKYDI LKHPGVKL
TVDGGGHPFRHGTTEHALDWQAVALEGGDYELLSEEELESLSPS

>2617921944 Ga0073689_1486 TrbC/VI RB2 family protein [pelotomaculum Ga0073689 :
Ga0073689_148]

MKMSEKTKRVFAI CCALVLPALFATPAYAADDPLQVNNLSEFI FGLI RA
I GLI LLGFGI VOI GLSLKSHDPSQRANGFLTLAGGVI I TFAKEI LNI I TG
G

>2617921943 Ga0073689_1485 TnsA endonuclease C terminal [pelotomaculum Ga0073689
: Ga0073689_148]

MSKRSRVWNQGVYEKYLREGRGRGDGPYKPI RI QDFASKGVVSRVKGR
TTGRVHHLSMNNELAYFYLLDWSNDVLDI REQYPLLDLGCAI NAAAQAGI
NYPTNRVSGYPYVMTCDFLI TTHGLKARTVKLSSELTNARTVEKLEI ER
RYWAANGVDWKLVTENEI SYRKSNI EWI YSAQDFGALQVESDVLNAKD
LI RQLFYSEFESI VEI AQSVEDKFHLGKGI GLLLFKSLVLDKEI YI DLNE
RLNLNAKKVAVTVTA

>2617921942 Ga0073689_1484 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_148]

MYI KPGKYLHFKGNEYEVI GTATHSETLEEVVI YRALYDDGGLWARPAAM
WNEI VEHNGCHVKRFTHI DEVVQEAPTGI HNYSAPTEKVELFMSLFAGR
DVYAKRWENAKKGSAGYVPCQNEWSPKSGGGKMKCGECPNQNFVKF
DAGAVEKHLKGQLTAGVYPMFPDETCTFLAFDFDGDYSPEDLRRDVTAI
REACTEKGI SMAVERSRSGKI HWMFFAENI PTGI ARKFGSSLI THAMS
KHHELSFKTYDRMI PNQDTLPKGGFNL I ALPLQKI PREQNSAFVDENF
NAYADOWNYLYNVKKYTLLEEI ESFI KQLSPSGELGDLRRDSEEEKPWESK
RPEQKLTRDFDPMVKI VRANMLYVDKSGI SSPALNALKRLAAFRNPEFY
KAQAMRLSTFDKPRI I SCSDETGHYLCPLRGLEDGVWELLEDNGVRI QFN
DESNRGRKI DVEFKGELRGEQQQAADVLLMHNNGI LSATTAFGKTVI GAR
CI ANRKVNTLI LVHRTNLLAQWVERLNEFLI I NEEPI I ELTPKGRKRKKT
VI GRI GGGKNPNSGVI DVAVMQSLVSGDEVRELVRDYGMVI VDECHVSA
FSFEQI LKTVNAKYI YGLTATPTRODGHPI I YMHCGKI RYRVDAKEQAA
ARPFEHVI PRFTRFQKPAHQDESKWTI TDI YNDI QNNELRNSLI LQDVA
VAVEQGRNPI I LTERTEHVKYLVSQLKPRI KNI ALTGGETQKKSRETLQ
TVADI AKDESFLVATGKYVGEFGDMPRLDTLFLAMPI SWKGTLLQYAGR
LHRLYEGKNEQVYDYVDVHVAMLEKMYQKRLRGYATI GYKAKGTPQPLE
EVHSI FDSHTFFPVYSADI LAARSEI LI VSPFVTKRRI LSALNYMTAANA
KVTVVTKPLENYAEKDKAKI VECI ELLTQHG I TVKTKDRI HQKFAI MDQR
VWYGS I NFLSYGTSEESVMRI ENVDI AGELLRSI

>2617921941 Ga0073689_1483 Mu transposase, C-terminal [pelotomaculum Ga0073689 :
Ga0073689_148]

MRNLLI NSI LKTAESGHLI RI LWI SSELKSI CLFNTDTMAMPYFVDRADL
QNQLNEGALTI QSDPYLP I LSEEHLAKDKDFRDVWTKMQSLVLEPDI
I YDRTLRLGQLI QEKVDEI GFTKRI I YKYLRLAYWLHGKTKNAFLPNYQNCG
GSGKDRNSGASKRGRPRKYGESSGRNVDDDETKRI FEKAI KKYHNRHEYT
LKDAYDLMI KEHYTEFVTQPDGTMKAELLPEI PTI GQFRYWGKKHDT
KEKI SKRKGAKYALDHRAI LGKSDYGI MGPGAKYQI DATI GDI YLVSRF
NRADI VGRPVI YFVI DTFSRMVAGMYVGLEGPSWAGAMMAI ANAASDKVK
YCAEYGI EI SDSEWPCRHPVNAI LDDRGEMESKSVETLI NALNVRVENAP
PYRADMKGI VEQYFRTVNNKAVAFPLPGHI KPDI SERGGRDYRLDAKLDI H
QLTKI LI QCI LQHNHHFLDGYERTADMI ADNVEPI PI KLWNWGI AHCSG
ALRSFPEETVKLCMLPTGTASVTAKGI RFKGLYYLCERAAVEHWFETARA
KGSYKVDVSFDPNRMSAI YVREPDGSFDSFLAEWQDKYVDMCLDEI RYL

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QESEKLLRRQNAAKEMASKADLSAAI DSVI AEAEEMARQTVVPKSKLART
KNI RENRRAEKERSRRDEAFSLGDNEVPQTKSEAQEKPAAI SPTLAMI QQ
QLEERLNEK

>2617921940 Ga0073689_1482 AAA domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_148]
MKNKPVKACYLPQMI EEEYKGNPLI EALPPI YSSYEAAKLLTVDPGYNEGE
REFDAQYRFHCI GRLFRYFQPLDTHI DI EQRVSRAI RQGYI SKNPI TPDY
AARLVQGAVALI REKSGQNAVYSLNSTAFGFTVI MSGVGKTTAMEKVLSL
YPQOI LHTQYKGKPLFLTQLTWAKI DCPFDGSLKGLCLSFAYVDRI LGT
SYSKKFSSDRMTVDAALPRMAQI ATTHCLGLLVI DEI QHLSQAKSGGSDK
MLNFFVTLVNTI GVPVVL I GTTKAMSVLQSEFRQARRGSGQGDLLWDRI K
NDLSWEI MLRAMWKNOWI RNQTPLTDELKDI LYDESGI I DI AVKLYAMA
QMKA I ADGTETI TAGAI REVAAEKRLRLVKPMLEALRSGNMKKLLMYEDI K
PI NVEDYLAQSGRI AGGNI PLGQNEI LSLTEQAVLRLLLEMDI SSKVAR
AVKKA I GKS VSGQPLAAVVKAFKI ALNMESEKNPTDI DEQDDDLRKAAG
ESPYENLKKSGFI AESADEF

>2617921939 Ga0073689_1481 Tni Q protein [pelotomaculum Ga0073689 :
Ga0073689_148]
MSFDESPLCFFPTYPDEI FYSVLCRYHI RSGNPAFVSTAKTI WGKKI SA
NLYLPQSLGKVALRI PPETGLTAEYFATYNTI YPFLKPFLSKERGLQVLK
LLKNEAQSEI MAYQLCGLPRSKSPKWRYLRYCEDCWREDI RLYGEPYWHR
LHLLPGVLMCPVHGKPI RNSVI FQKDI SSKFHTASFVTSNEPAPSFSDN
AAKRLMNI AVDAAWI MQNGHALPFSESTMEI YDQLLQVKGYRCLSGRRMK
SOLL DKEI CEFYQGELELLELVGSQGVVPWSEVMHKRNSLLYPVYYLLL
I RFLAGSAEDFFTKQHGVAHPYGTGPWPCRNVPVCPYYLKDVI SELLPLVQ
FASRHQATFTCPHCGFAYRRSRERPKSKQYSGQI DTVDYGWLWMDTFKKM
MKSGAPI MHI TEKLHCGFHTVKRLGVELGFLPESQLPKKKPNI YYKRKV
PEPTPKPTSQSYRYEQWLQAMKDNPDSSRSFLI KRYPEI YKWLKNDVDW
YEVNAPKSKRYTMFERADSDDDSLKARAAVVYLKSFPGRPVWI NRHSVE
KYGGLNNLYKNLAKGYLPKTOAYLDEALETDEEWRKRKI QWAVKELYDAG
KNLLLPOVQI KASI SHKLFTPLETFTTRDCI EQLQK

>2617921938 Ga0073689_14722 non-canonical purine NTP pyrophosphatase, RdgB/HAM1
family [pelotomaculum Ga0073689 : Ga0073689_147]
VHSARFAGEEKDDRANNQKLELLAGVPEERRTARFRCVMSVVVPGGRI Y
TAEGTCEGRI ALEPRGSGGFGYDPLFYLPYEGKTMALDLETNKI SHRG
RALAVALDI LAELKRTVDEE

>2617921937 Ga0073689_14721 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_147]
LRVI VFSDSHSVLDYALRALRETGEVDLI LHAGDHYRDAFRLAAETGLPV
RAVAGNCDRPGEGPVEELLEADSRI LLTHGHLGGGPKQWEAWLLRRAGE
RGAGAVVYGHTHAAKVACEGGI LI FNP GSI TAPRDRGRPSYGI LEI SGNG
I I PSVHRI

>2617921934 Ga0073689_14718 Uncharacterized 2Fe-2 and 4Fe-4S clusters-containing
protein, contains DUF4445 domain [pelotomaculum Ga0073689 : Ga0073689_147]
MASDNSKNMVI LEERTTAEI QLDPLTKKFFLQLEPPSLSNQADTDRLRE
ALRTVTGRVAVPLPLMRVI GDI CREKEWMVTPTI GPWGGGPGLLGLEPGD
TTQRHFGLAVDI GTTTVVVYLI DMVNGNVLGSAADYNGQVSFGEDI LTRI
YLAATAGGLDQMGEAVI GTLNALI AELTEKHNVVNGEI SAVVVGGNSTMI
HLLGLDPSRI CREPYTPVVNNPGMI PAGEI GLAVNPLAVLYCLPSVGSY
VGGDVI AGVLVSGMHRSDKI SLLVDI GTNGEMVVGNGEVLVACAGAAGPA
LEGGVARAGMRAEPGVVEAVTI EPGTLKVHYRTVGGEPARGI CGSGLI DC
LAEFLLNGI I DRSGHFRNGRASFTI VPAGESATGEDI VVSQMDI NFMRT
KGAVNAALETLLLEGVGVGLADLDRFYAAGAFGQHLNLES AVTVGLYPDLP
REKMI RLGNSSGEGARQVLLSNRKRLEAEI AGRI TYFELNANQQFMNKF
VSSKFLPHTNLDYFPTVKARLAERGLLSQ

>2617921933 Ga0073689_14717 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_147]
MLLSPFRFNSLAFFEHPFLKKRKELWSQGRADVDDTQVAKGLFKETFI GR
LESLRNEQVNI EFEVSERLKKKALGVVLSRVGADFVELSPANPQLPFTVL
SYHPGLPLPVVEFARGVI I RDI NRI VSVEKA

>2617921932 Ga0073689_14716 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_147]

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LEKKNLEHHSI NEI EKNGEPPVCAAPEEI QTALI GMPSSFDI VSSDPDGR
I TGI DVVDLPRWAEFEI I TELPAADAVARI SGI PGSEDTGLHVMSI VATD
NDGNRI VSPLKVNVPKEGFKDEQPGVF

>2617921931 Ga0073689_14715 CDP-glucose 4,6-dehydratase [pelotomaculum Ga0073689 : Ga0073689_147]

MSYWRGKNVFTGCTGLLGTHLCELLI NQEATLI GLVRDYVPRSRLFTQO
LKQKMLVNGDVENYRLLERAI NEYEVDTVFHLAAQTI VGI ANKNPLSTF
NANI RGVWNLLACRRNPGVQRI I VASSDKAYGEHEHLPYKEDALLOGRH
PYDVSKSCADLI AQMYNYTYDLPVCVTRCGNFYGPGLNFNRLVPGTI RS
ALRDERPVI RCDGTYI RDYLYVKDGAAYLHLAQKMGEMPI KGEAFNFSN
GLQI TVI ELVQKI LSLMGCSHLQPD I KNEASKEI QRQYLSTEKAGKI LGW
QPKYPLEQSLTETI EWYRDQLSGGMR

>2617921930 Ga0073689_14714 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_147]

VKFCLLSTEPYHPDQGVYTV EQDNI NI WATI MGGTVYNGPLFDQGDYGL
DYDYFNDFDLVMVALRQETI EVGI KVKRRSKVKVAVFLDGEIDRYTTHTP
RDLQAKMVVELLNI VDAVAVLHDESI PLLKAMSTRPVGLVGLPFPLERVRE
LCPPVPKREEI ELGSTI RSVFTHNRNALVNLAALSEI GMPGAVDI REPEE
MEYVRR I RKYVPI PQI RFRNDLGWDHYI I QASYSLGLHLDYRYTWGRF
PI ECAAVRMPCVAPPSLYTQKI LFPGLCVPYHDI EGTVALMKKLASDI NF
YEETVSYAQSQFELFSYEQCKRRLVDLI G

>2617921929 Ga0073689_14713 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_147]

LKFCLVSLTPLSDLGKI FTDEVNRI TQWATVMKGTHYNGLAFDI NHYGL
PYEFFSEFDLVMVAVRHELI EVGI KI KRQSTAQVLVFLDGEMEYFTSYLL
GELQAKFVELLNI ADAVGVTHEYDI PI VQALTSRPVGLVGVFPPLKRVRE
ELCPQVEKELAI HVGCGTGKSFNRNGI VNLAALSEI GLPGVVDVWSMEDI
EYVRSMKKYMPI PPI YFSHTLRWEDFI SQLNKSMI GLHLDYRQI WGRFAL
DCAAVRMPC I APDNFYTQKRLFPGLCVNHQDI DGVVRLVGELLKSNSFYE
EVI AHAEQLSFFDNEGAKKRLNLG

>2617921928 Ga0073689_14712 Glycosyl transferase involved in cell wall biosynthesis [pelotomaculum Ga0073689 : Ga0073689_147]

MRVDQI TPAI RDGEDI SKAVLV LQKI I GDLGCETI FTETRPKEPRAKVL
ELSSLGNERENI I YHMYMGSOI SKTLVDLKA KRKVL FYHGI I PPEYFENH
PARI HLLNGYEELKTLRDQFAVAI TTTKFHERELQKAGYGQTMVLP LLVD
LNEYDQEPD SHLMNEYDDNFTNI L FVGRI TPNKKLEDTI LVFNYYHKKLN
PKSRLFLVGSFSDHASYCQKLLTLI KELEI KNVFLTGRVSFKLLAYYRL
SKVFLCMSEYKGFSTPLI EAMYLKVPVI AFARSAVPEVLGGAGYLI DDKN
VRETAKLLDRI VI DQAEREEI I SRQWERTAFSPERVFPLYRKAI MEAFG
YKTPEDSSKKI GSSHRHAFFTPLAGPVFPDYGNGLSALMQI RKGWRR

>2617921927 Ga0073689_14711 glucose-1-phosphate cytidyl transferase [pelotomaculum Ga0073689 : Ga0073689_147]

LNPKVVI LCGGKMRLREETENPKPLVSVGKYPI LWHI MKQYSHYGFND
FI LCLGYKGELI KEYFLNYKNHCSDI QFNLDGDKTVLQDGPVDNWN I
FANTGMEITNTGGRVKKI EKYI NEGYFFLT YGDGLSDVNI R KLEEFLEKG
KAGVI TGI RPOSKYGOI TI DHDCI VTGFREKPLLNDYI NGGFCVFHKRI F
NYMDENCVLEQEI FEI LVNRRELAVYKHEGFWKCMDTYKDYTELNEMWVQ
GNSPWSAYQEEQNV I

>2617921926 Ga0073689_14710 CDP-6-deoxy-D-xyl o-4-hexul ose-3-dehydrase [pelotomaculum Ga0073689 : Ga0073689_147]

MSFKAGDI LQTEGGFVLVAASGTGGYYVWLMAPSPADSLYGLEETDLVL
EKSLEI PLGVDLDCQLMI KKEDI HGKAGEVTRPCLEKLWRSDFSRRAGQF
YQLFHLVLPFEPGKTWVSCSGKVYDEREMANLI DASLDFWLTTGRYASIF
EEKLANFLGVRYCCLTNSGSSANLLAI SSLTSTKL GKQRLRPGDEVI TVA
AGFP TTVAPI VQNR LVPVFDVDELETYNVDVEQLETAVSPKTGAI I LAHT
LGNPFNLDVATEI ARKHNLWLI EDNCDALGSTYKGRYTGTFGDLASLSFY
PAHHI TMGEGGAVLTSAPLLKRVI ESFRDWGRDCWCPGKDNTCGCRFAW
RLGELPDGYDHKYTYSHLGYNLKMTDLQAAVGVAQLAKLI DFAGI RRKNF
RDLYAGLRKYEDVLI LPKNTENADPCWFGFPLTVRTGAPFTRRQLVQYLE
DRRI RTRLLFAGNI I KQPAFQGVRYRVAGELENTDLI MERTFWI GVYPGL
GQKEI NYVLNVFNRFMRVI

>2617921925 Ga0073689_1479 virgini amycin A acetyl transferase [pelotomaculum

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Ga0073689 : Ga0073689_147]

MGVI I GEHSLMLMPVHLLI FSPDAVI LMGKFSGLSVGAKI LGGGEHFQKNV
AVVSLKSVHLQEI GEYAKDVYTKGPTI I GNDVVVMANALI I SGVKI GDGA
I VGAGAVVTKDVPPYAVVAGNPARI I KYRFVEEQI KALLRI RWWDWPI EE
I REFKECFYAGVDTFI SKSFEMRKEGRL

>2617921924 Ga0073689_1478 Protoporphyrinogen oxidase [pelotomaculum Ga0073689 : Ga0073689_147]

MYSVVTLGAGPTGLSFSSHFHKTNI YEKEATWGGRCRSHVVDGFI FDEG
PHSSFTKDDYVRELFAGSVEGRFNEI FPRI LNRYGPYWL RHPVQTNLNL
PVDLVI DCI VNFVKAQAGAGTPKNYQWLI GRFGEKFARTFPYAYTRKY
WTVEPEQMTTEWI KQRI YRPDLGEVLRGALSDEFYNNHYI SNVRYPGTGG
FQSFLKDLQEGAKI NYGFELTEI DVKKKKI TFGNGFERFYEVLVSSI PLP
ALVRCI RDCPAEI REAAARLACTSVI LVNLGVKRENLANCHWFYI YDEKI
LPCRHHFSPQSYANAPSGSGSLQAEVYYSRFKPLGI SPENVLEKTI QDL
I SI GVVAKDDKI TLAAYQDI KHAQVLYHGQHAENRRRAVL DYLENKDI HCI
GRYGEWAYLWSDQSI LNKRLAERLLRNMG

>2617921923 Ga0073689_1477 Nucleoside-diphosphate-sugar epimerase [pelotomaculum Ga0073689 : Ga0073689_147]

MKMLVTGATGFGVSGCLTRRLVEMEYDVHVI RSGSNKWRI EDLLGRVTRH
EVDLRDADVVOKAVTQI GPAL I CHLATYGGFASQKEPSVI MESNLMTAN
LLEACEKTGFTCFI NTGSSSEYGLKSRPMSESDI LDPVGDYGVSKAAATL
LCRARAFEGKLPVVTLRFLSPYGPWDDPQRLI PYVI KSFLRGKAPELSTP
KSVRDFI YI DDVLDVFFKVMKASVSGGEI FNVGTGVQHSVGEVSMVGGI
I ENGI EPVWGRVTSAPRAEPDSWVANI RKAGI KLGWFPSTSLRAGLNKTV
WFRKNLELYP

>2617921922 Ga0073689_1476 acetolactate synthase-1/2/3 large subunit [pelotomaculum Ga0073689 : Ga0073689_147]

MKLSDYVI DFLVNEGVS HVFELAGGVI THLLDSI YSRHDLQCPVHHEQA
AAFAAEAYSRI NGNLGLAMATSGPGALNLVTGI GSCYFDSVPCLFI TGQV
NTYEEKFGKAVRQLGFQETDI VNVVKLLTKYAEVLADAEQI RYHLEKAVY
LARSGRPGPVLLDLPNI QRARI EPEKLKGFNSNEEFKRI HAMSFCKTME
I DEVI NLMSKAARPI LAGGGVRTAKATGELL SLVERTGI PVVTSMLGLD
AI SFDNPACFDMI GAYGNRYNLI LANCDFLLI LGSRLDTRQTGRPDTF
ARAARKVHVDLPAELNEKVKVDVAI NCDVKEFLAKI NARLEGYVKADLT
PWYELI KRYREKYPTLSQTNKAENI DPNRFMFLSGYCSEGI I CVDVGQ
NQMWAAQSFRI KKKQRMFLFSGMGAMGFALPAALGAADPGARVVVI AG
DGGI QVNI QELDTI VNHHLVKI FVMNNRCLGMVRQFQDLYFGNRRQSTV
TGYSCLDLRKVATAYGMPYSYKI DSLTTARDVVETVLKTEGPAFVEVKLEQ
NACVDPKLVVNRPI EDMSPHLDRTELKEI MLI DLVEEMEVP

>2617921921 Ga0073689_1475 purine-nucleoside phosphorylase [pelotomaculum Ga0073689 : Ga0073689_147]

MGKQLLQNRGFEKELNGYI TQGSVSTNSDI AYSGI KSAQMLSTPTSI AEI
SQVVI I ASPRSPVRFSFFARKLLDEAVENVS NVRAEVNFI SAFGTVI PPG
I TI TI RGRDI SENVWNYEYEGYAEASFGTI AAQVVI RLEPPESGTSGLLVD
DLALVAEVTTPAHLPAPI VLP

>2617921920 Ga0073689_1474 cysteine desulfurase family protein [pelotomaculum Ga0073689 : Ga0073689_147]

LI YFDSAATSWPKPVEWEMERCI KFGANPGRSGHRMAVEAGRLVDEA
RELLASLFNI GNPDR I VFTLNATEALNLTKGLLEPDDHVI TSSMEHNSV
TRPLYVLOGRGVEVTKVPGAGDGS I RVQDVEAAI KPNTRAI VI THASNVT
GTLMPVAEI GOLAKKRGLRFVVDAAQTAGVFEI DVAFMGI HLLAFPGHKG
LYGPTGTGGLYI AEGLDLTPLKEGGTGSKSELPGQDLMPEYSGTLNS
VGI AGLAAGLKFI RREGRERI RRHEMELTGRFLEGVKGVKGI RVYGPVEL
YARAPVVSFSLDGKSGQVGTMLDQQYQI ACRAGLHCAPDAHRTLGTLGQ
KLVRFSFSYFNNEREVDYAI RALAEI AAMPPEKFKAENKSCGC

>2617921919 Ga0073689_1473 protein of unknown function (DUF4338) [pelotomaculum Ga0073689 : Ga0073689_147]

MRMLKSPVLPEDSSCI YFMLARLQSTFTPPRQGT CYLAANWRYI GETAG
LGREPRRQKSHPVVKLMFVYPLVREWRSELCAPTPVADGEFDA

>2617921918 Ga0073689_1472 CoA-substrate-specific enzyme activase, putative [pelotomaculum Ga0073689 : Ga0073689_147]

MKAYLGI DVGSVSI NI VVLDEAGEVLTSLYLRTRGRPI EVI QEGLKAAA

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SI PKGVEI AGVGTGSGRYLAGVMVGADVVKNEI TAHAVAASMLI PEVQT
VLEI GGQDSKI I I LRNGI VTDFAMNTVCAAGTGSFLDQQAARLNI PI TQF
GELALRSETPVRI AGRCTVFAESDMI HKQQMGHSI PNI I RGLCEALVRNY
LNNVGKGKEI LPPMI FQGGVAANAGI KAAFERALGI PVQI PKHFSVMGAI
GAAQLAREETVKTSTTRFKGFKVTGLPYRTGSFECDGCSNACEVVEI YEE
NKVI GRWGSRCWKDLV

>2617921917 Ga0073689_1471 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_147]

GNEVRMI VFEPRLHPFNFI KNVI ALNRTRVSI KGI I AHI KRAWHKLQTL
DNTEKLSHVVRPRELNRGTTTRVYRKVLEWI DQAYTTEQI I KAEAAALEA
LRSI PRDPDREVLKVGI VGEI YVLLPAGNLEMEETLGNLGEVERSMFL
TGWTRDNTWTETTHGMTVKEAATPYLPELVGGHGRDSI GNTI LCAKRGFD
GMI QLAPFTCI PEI VARTI LPRVSRDYRI PVLTFFLDEQTGKAGMTTRLE
AFVDLMRRKKQSSRFLTG

>2617921916 Ga0073689_14619 non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family [pelotomaculum Ga0073689 : Ga0073689_146]

LKLVLATNNRGKI REI TELLAPHGI ETMSLNEFPEI GEI EEDGDTFRENA
VKKATVTCERTGLAALADDSGLEVDCLGGAPGVHSARFAGEE

>2617921915 Ga0073689_14618 RNase PH [pelotomaculum Ga0073689 : Ga0073689_146]

MERVDGRKPDQLRPVRI TRNYNKAEGSVLI EVGDTRVI CTATVEDKTPA
FLRGEGKGWI TAEYGLPRATGVRTAREAAARGKI GGRTYEI QRLI GRSLR
SVVDLGMGLGERTVWLDGDVI QADGGTRTASI TGSFVALVDALNRLKENGL
LERMPVTDFI AATSVGRLRDGVI LDLCYEEDSAAEVDMMNI VMTASGRFVE
I QGTGEESSTROEMDOMI ELAAQGI SRLI SCQREALGAAGAGI GEGRAG

>2617921914 Ga0073689_14617 Ribonuclease BN, tRNA processing enzyme [pelotomaculum Ga0073689 : Ga0073689_146]

LEI I VLGCWAPYPRAGGACSGYLVRAAGLNI LLEAGNGSLRLMSLI DFR
RLDAVI VSHLHHDHYLDLFLPLRHALEGARRDGSRADPLKLLVPAAPAAEF
NLLAGYRKAAFAAVPI ESLPEERMAGGFTVRRLELDGLTCWFLSTRHSLPG
YSVAVEGAGRLVFSGDTARTKGLAALAEGADFLCEASGLDSDAGYLKDA
HLTARQAGEVAGEARAGRLLVTHFWPEYDPAELALAGEGFGGPVEPVRE
GETYRVSGDI FLDHVI K

>2617921913 Ga0073689_14616 CoA-substrate-specific enzyme activase, putative [pelotomaculum Ga0073689 : Ga0073689_146]

MFI GLDLGSRNVKVAI MDEDRSLRLQKFDTMKFYREHGRKEDGQLVVNFA
SLGLPAAFEAVTATGYGHQTVHVKGARVI PEI KAHVLGAI YLTGLADFTL
LDLGGQDSKVALVRKGRVLDFLTNDKCAASTGRYLENMAAVLNI SLEELG
RHHRSADLTSTCAI FGESELI GKVVEGYSI PALAAGVNHSI FKRI RPML
AKLSSDTI VFTGGVAYNGALRQI I REETGAAVVVPENPEYAGAVGCCVDA
AGL

>2617921912 Ga0073689_14615 Benzoyl-CoA reductase/2-hydroxyglutaryl-CoA dehydratase subunit, BcrC/BadD/HgdB [pelotomaculum Ga0073689 : Ga0073689_146]

LPVGI TTTVPVEVI YAAGWAPVDLNNVFI TDENPRVLVEEAELAGYPRN
LCAWI KGI YSI VLKRRDI RTI I AVTQGDSCNTHALMETLQLAGVEVVPFA
YPYDRDPDLLRLOMEKMMSFFGVSWRRVRETKERLDRVRGKVWELDRLTW
EENRVGGWENHLYQVSCSDFNGNPEKFGTEVAGFLEEARTAPAREGELRL
GYI GVPPI VDDLYDYLEERGARVVFNETQRQFTMPFNTDDPVEQYRLTY
PYGI FYRLEDI CREAARRKLDGI I HYAQSFQFRQI EDLI VREKLDLPVLT
LEGDKPNRLDARTRMLDVFLLI LR

>2617921911 Ga0073689_14614 glutamate racemase [pelotomaculum Ga0073689 : Ga0073689_146]

LSKHGPI GLFDSGI GGLSVAMEI YRQLPAESTI YYGDTAHVPYGPERSAGE
LI RFADRI VSFLEGRGGKYI I FACNTSSSVSLPLLQGRHAVPMI GLI EPG
VTEALRKTVNRRVGI ATEATI KSGAYQRELKRLGRDVHLFVRAAPRLVP
LVEVGKTESGEAAVVREYVKPLQEAGI DTLI LGCTHYPFLARFMAAELG
PAVRLVDPASATVRLAGEEMLRLGLAVPDTVATEHRFFVSGDPEAFRAAV
LRCLGRDI GPVVKAEI

>2617921910 Ga0073689_14613 N-acetyl muramoyl-L-alanine amidase [pelotomaculum Ga0073689 : Ga0073689_146]

LEGSAGWYRVQLATGATGWI AGWLVI EYSAAPVVPSP PPVAPPAAANP
GGGSEGGKLAVVTGSVVNVRSRPGTANGI TGQVLQGDKLSVAGQSGDWLR

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VQLPGGGTGWVAGWLVSSELPPAPARPPRPPEPPGQVNQPPAGPGGSGG
 I SRGGDRTPDNNRPKALSLEVKETNGKTS AVI KADAPFDYTSFPLSGPD
 RL VVDLKGVAI GDL PDKTSVNSKTVSQVRAGYYQKNPDI TRLVFELKGGGA
 QYVASLSGDRKVLTVQTYI PDI SG SYKGKVI TVDAGHGGPDPGAMGANGT
 KEKDVTLDI ARRTAKLLEARGAKVVMARSGDYEVGLYERTDKANYARADI
 FVSI HI NAHPDRNFGGTTTTYI YRSNGDP SRTARI RESDRLARHVQNELLK
 TLGLRDVGVR SANFAVLRTSNMPAI LVEVAFI SNAAEKMMSTDDFRNKA
 AEAVVKG I GLYFSERRTAVNGSNI

>2617921909 Ga0073689_14612 SH3 domain-containing protein [pelotomaculum
 Ga0073689 : Ga0073689_146]
 MKLKSQ LCFALSAVVALTLFLSVCLAYPQSSAAAGETAMVAVDVLNVRDG
 PGTGYGVI TQVGLNERLPVLESSGDWHRVRHAAGGTGWVAGWLVNI ETAA
 APLSPPANPGEPRPAGRQPL

>2617921908 Ga0073689_14611 Amino acid transporter [pelotomaculum Ga0073689 :
 Ga0073689_146]
 LQLKRVLT LRTI VATSAGLTASSSFVA AVQVAGYVLGDTAWI A I LVGGV
 LCF LAAACFSELNGLLP TAAAGI RLYFSRAFNDQVSLTVSI LYMLVVI I GV
 VGAESYVLSRALNEAFPAVPPYAWI VMLLLLVTGMNI RGI KI AGVFQDLI
 TYGLVASLLLI GLI ALYKFD FQLSAPLAPGGAAGI I NAVAVGVFLFVGFE
 WVTPLAEEVTRVKQI SKGMMI ALGI LSVTYAVFTVAMTAVAPKEALAASA
 APQMLFARAALGETGAAWMLAVSLAASVTTFNAGLI SVSRFMYASAREHV
 LPAVFSKVS LRFFTPWAAI LTLFFVSLVVAGVTLWTHRYLVLVEMAAAME
 SI VYALVGLAVI SLRRMPGEP RP YLI KGGWLVPASTALVFAI LAAAVFA
 ADPWVLLDMAVAFLACL VYVNTAVPYLKKKHQSHRPAARRRPARAAGEAE
 GK

>2617921907 Ga0073689_14610 Alkyl sulfatase C-terminal [pelotomaculum Ga0073689
 : Ga0073689_146]
 LAAHREI TESLKAFTDNYNKNERLKI MNRDWD R VVVVRATDVESQHTLTV
 QEGV VSLKEGPSDNPD LTVI SDSETLADI FYGDI TPTEPYNNGI LRI MGS
 EDDI I RLDFI SLLI WGE

>2617921906 Ga0073689_1469 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_146]
 MELI ESADLAGYLKGVLFLKR VVS VSLGSSRRDHKVLVELLEE QFEI ARM
 GTDGD FNRALELLKELDGKVD AI GLGGI DVYLFVRQKRYAI ADGLKLMEA
 VKVTPVVDGSG LKNTLEREVVRI LAGETGLLKKGAKVLMVSSVDRFGMAE
 ALEEMGCDMTFGDLI FTAGI PYP I KTMEEL E I ANRLLPEI TRMPFHMI Y
 PTGKKQESQDEEKVRKFAPYYHEAEVVAGDFHLI RRFMPAGLNGQTI LTN
 TTTRDDLDLFLREKGAGFLVTTTPEYEGRSFGTNVMEAVLMAI LSKPRAEV
 TTGDYLDLLRKL NFRPRI LNLKD

>2617921905 Ga0073689_1468 phosphoenolpyruvate--protein phosphotransferase
 [pelotomaculum Ga0073689 : Ga0073689_146]
 VLKGVAA SPGI VI GKAFVYHPGKLFF EK VQI GPESVEKEVARFEQALAKV
 QQELSRMYARTVSEVGRGRASGFI QLEMLEEPTLKEEVI SRI KGGVNAE
 AAVSEVFS DYGG LFRVLRDPYLR ELVEDLQDI DYRI KRHLLGASDSLKMG
 LDKESVVLARDLSPSEI I QLGRSRMLGLATEGGGRTSHTTI MTRSLGI PA
 VVGLGPFLSSVRDGD I VI VDGSQGVMI VNPDEKTLAEYQRREANHRAYKQ
 ELQGLQGLPAETGDGQNVLLLANI EHPAEVDWALSNGAQGI GLFRTEYLF
 MGRDEYPDEEEQYQDYKKVVEVMGGKPVI I RTMDVSGDNTVFRLPALREA
 NPFLGWRGI RFSLDL KELFKTQLKAI LRSGVHGDVKVMFPMI SNLMELRR
 AREI LEEAKGELKVEEKAFDPGMKVG I LVEVPSVAVTADLFAPEMDFFSI
 GTNDLI QYTMAVDRANEKVSSLYQSLHPAVLR LI RQVVEEGRRARKEVAI
 CGEMAGEPLATVLLVGLGLRVLSSGSGI LPEI KKRVRAVTMVKAREI AEK
 ALQFATSGEVKKYMESEMKALNLYL

>2617921904 Ga0073689_1467 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_146]
 MQLPPGKR SI LSSFPSSGQARKAVEALKNAGLAEVQLDRVSRYGVEI DAH
 YNNPI NRAETQGTLYSRNAKMDDNTRVLLAAAPSASGYGCDDHGVAG
 GKAFLVTVVADEEQVDRAVETI KQHGGEV

>2617921903 Ga0073689_1466 Spore germination protein YaaH [pelotomaculum
 Ga0073689 : Ga0073689_146]
 MAFYPYYFENN WYYYVMEPRALSNIQI HGGEI TFLVPFWFGVTGEGTLVDQ
 SDAETTALARRLGLPVLAI VHNYASRQYGPLI HRLLTTENLRRALVANI L

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DLTGTGKFAGVNI DFQFI PPEDRPFMTTFMAELYRALKPHGFLITI SVPP
ELRDDPAHPFSGAFSYPDLTRHSDQVYVLAYDEHVAEPGPI ASI GFVRQV
LTYALSVI PRLNI RLGMVYGRDWTGVELPEEMSYDEAVTRAARHGVT
QYDAMAQEPITYEENGVGHVWFEDARSFAAKLELI FKEGI PGVGVWRL
GLEDPRI WSLLRGMRSFP

>2617921902 Ga0073689_1465 Protein of unknown function (DUF2892) [pelotomaculum
Ga0073689 : Ga0073689_146]
LDLDWKKNLGNTDRVI RAVI GLLLLALAYGKTLTGWWAAAAVTFALFQFV
EAAFAY

>2617921901 Ga0073689_1464 penicillin-binding protein 2A [pelotomaculum
Ga0073689 : Ga0073689_146]
MFKSWQGPYKAAI LI FTPFLVFAVAFLI WPHLYAGRVLAGFSGAGAGAAA
PGQTTFLYDHNGNVTSEVHGEI NRVPVPLEKI PEHVQKAFVAVEDERFYR
HHGVDPRAI VRAVFSFYTAGRVTEGASTI TQQLMKLNFLSPEQTLRRKVK
EAALAVEFERRFTKDEI LEFYLNRVYFGEAGYGVQSAKVYFNKDSRELN
LAEGALLAGLVQAPSAYDPYI NQEGALRRRNVLKEMVEQGV GKDTGVK
ASKEVLNLRREGSGPGDTKNHSYFI DRVI DEAVAAGVEEKLFGGLRI HTT
LEPEI QKKAEEI FKRPDLPDREVEAALVLVENETGAVKALVGGROYEAR
RGFNRAATQLVRQPSAFKPVAVYAPAFETGYGPDSAVSDTPFKSGNYEPH
NSDRSYGQI NVRTALQSRNVAAVRLNLI GI DRGYEMARKLGFELVEE
DRCLPLALGGLTRGVSPLOMAGAYAAFANHGI FTKPYTI RYI EDAEGKVI
YRHEGAPVMKASTAETMKDVLRTVVAYGTGHRADI RGVEVAGKTGTTEL
PDTPVFRGLRGNKDAWFVGFTPRFTAAMWGYDEKMDMGRHYLTSYGGNQ
PAEI FRLVMAGVMGVDDRPVPGKTTAPDQEEQDDTGRQADDKQVI KE
AGGRREQPEERDGGNOGRQDVEKQGGKSGGQNPDPKPVQEGPGRPEAE
PAGTESREKETTRPVKGEQGGNMNQTDAGR

>2617921900 Ga0073689_1463 protein of unknown function (DUF4309) [pelotomaculum
Ga0073689 : Ga0073689_146]
MNKGGKI I AVI FLALLVAAI VSGCSKASNGGVTNPPSQPTAPQTPVPT
GENPPAQENDPQKQLLNEI MQSARQKVI NCEFTAGKTVFEDVEKKWGKP
GKVDYVPEAGGRFATYPDRGFVFGI NKGEQVFDI RSYDSRLKEI PLSKVK
EVLGPPDMERNYAGEDI I GYKAGTEFKI RLI FPEVTGQNPDPKLDHI SVF
YPRGTVNYMSENTGLEW

>2617921899 Ga0073689_1462 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_146]
LLKKTKI LMLLCVLCI GVAYSANAASQLSAKQLLLNKLQSSAPDLETE
LNNTSSGSASFVKNKLSGTLVSDVEPLEKLAGAKLKLDYELNSPEKKFGA
DYDLVVNKNFAKGNLFI DDNKLI STTEI LALI KETDPDFRDI DVKDLPQY
VYFTDNELVKMWDALI NSKGQGI LPEFKELLI YVVEAVPEKYFTTSLGNH
KVSFSLDKQGMEDVI FSVLQKI KNEKERFATLAANFVAASDPTQDPEKI K
MAI LMALEESI QNGDFPDTPAEVQKLAKAI TLEELTYEI SLLPSGHSRFI
MTNFDGNLDLTGRI KVDHFTGGKKNSSGTYKVNVTAGKQKKNVKVNGQ
LNGKVTQTGVNTKENDLI KLNVTDFSGTNTLLDLQANAKARVDKNVNI
NI PVLNETNSVNI EQFI KDSPKVSFFERVRLLI SMLPC

>2617921898 Ga0073689_1461 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_146]
FFDAYLLTNQFNASAVQLI TRYAQRMLI ENGI ADAI NFFHI DSLSSMVGL
KVDFDLQLTLMAASLYRMAQRI GREYRRATAKTLFRKLFDVSGQFI I TD
SEI I VELTRRAHNPLLVEAGLTDKI VI VPWLQKSLHI GLG

>2617921897 Ga0073689_14515 CoA: oxalate CoA-transferase [pelotomaculum Ga0073689
: Ga0073689_145]
MREALSDVKVLDLADGI AGAYCAKLLADFGAEVI KVEAPGGSRMRDYGPF
LNDEPHPEKSGFFFYLNNTNKKSVTLNLENGTGAGI CRQLARDVDVVESF
DPGVMSLGLSYEVL SGLNAGLI MTSI TWFGQNGPYKDYKGTNI VAEGMG
GAMYTARHTRWPKGSPAVLGGAQAEYRCGLLGFI ATTAALI NRLNTKKGT
RI DLSI TESVASSLTGI SADYSYMGLSRTTVPWAVHGYPTQENYPCKDGW
VNI LPGI GGVMMI ATLI GKPELKEDPLFAKAGVRLAQPEKFAELCI PWFK
EHGKWEI AKEAQKLRFMAFSPTLSPCELLEDEQLKAREVFARVEHPVMGEV
TYFGAPAKLSQTPWKAGRPLI GEHNEEVYGR LGYAREECVKLRECGI I

>2617921896 Ga0073689_14514 Crotonobetainyl -CoA: carnitine CoA-transferase Cai B
[pelotomaculum Ga0073689 : Ga0073689_145]
MAQKLLEGI RVI DLTLYAGPMGTRLLADMGAEEVI KIESAQRPMFTRMT

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SY PENNPPEKA WDLGGYFHV LNAGKKGI TLNLGNEK GREVFKKLVA VSDV
VMENFSPKVM DKGWLG YDELKKI KPDLI MVSMSGLGHY GPMRDVYMYMTG
MENMSGLTHI TGLPEQPPLFTNYAYGDWMLGVTGASAMLVALYHRQKTGE
GOYI DVAGREAI SSHI GEVI MDCTLNDR I ASRTGNHSFSKALQGCYRCKG
VDEWVNI AVENDDWEAF CNAI GNPVWAKDERFANVI GROKNODEL DKKLI
EEWTGKYNHDE VVEI LQAGVPAGAVCSLKEVYLN DHFI ERGLFEI I DHG
EGVGKRPVLKOMP AKFSGAESYI PKRAPRFAEDNEYVFC DLLGMSKEELA
KLEEEKI VEKI PKFPPGRPV RKDLI EKQAGEGAGCFEANYLEELRKRF GD
DI GR

>2617921895 Ga0073689_14513 Acyl dehydratase [pel otomacul um Ga0073689 : Ga0073689_145]

MQGDTI CRSKKRRVTKACI DEEVRREVSGNEEKGVLAEGRI TPELI KEME
GKKGLALRVEKYLN NVDTVTKMAI RSFADGVGDWNPLWRNDEYAKNTSYKG
I TAPPMFVYSI LPAAPQFGWRGI GGFNAQNELQFFRPVRPGQHI NVT SRY
KDFEI KELKDGKKRI YEYEEQTYENEKGELVCI FNQMN I RVERATMRKST
EKKI SKEKKGP ELPHPWTD AELAKI EEEI LAEELRGKEARFWEDVQEGEE
LKPVI KGPI GLSDMVAFFLGGATPVRPMGHELAVRDKKEHGAWYFRDPDT
YAI EPVYAVHYNNHAAKSQTGI AWPYDVG I QRNCWQGHLLTNWMGDDGWL
KMTRVQYRGFVYLS DVI RVGGKVVKKYI DGEGEPCVEI ETYAI NQRGQNT
MPGI AVVVLPSRESEYWPVRKRVD

>2617921894 Ga0073689_14512 3-hydroxybutyryl -CoA dehydrogenase [pel otomacul um Ga0073689 : Ga0073689_145]

MDI KTVGVLGSGVMNGI TQTVAGAGYNNV MRDVEDRFVEGGMKNI DKTL
SKSVEKGKMTADQKAI MGRI KGTTRMEDLKDVDFVI EAVI EDI GVKKSV
FTELDEVTRK DVI LSSNTSSLSTEI ASATKRDPKVVG MHFFNPAPLMRL
VEVI RGMKTGDETVAI TI DFSKKLGKEPVEVKVDI PGFLVNRLMMPYI I E
AI KLYEMGI ATKEDI DKA VKLGLNYPMPGFELMDFTGI DI HLHVASYFYQ
ELPKELKWDPPLTLKNI VRAGNLGKKTGNWYSYTK

>2617921893 Ga0073689_14511 enoyl -CoA hydratase [pel otomacul um Ga0073689 : Ga0073689_145]

MFEDI I YKKEEGI ATI TLNRPPMNP MRYKTYFEI ERAVYDVWADSDVKVL
I FEGAGDRAFSAGDI NAFYELGGTVENVREYVI HCENAMRSI KTL EKPT
I AAI KGFCLGGGLELASACDFRI ATEDVKFGNAEI NVGLMPGTGGTAELA
RLVGPARAKEI TMLGRMYSAQDGLNMGLFNKVVPREKLMDEAMALAKELM
SKPQTALRLI KTI MNLT LNMDDRSARV VETEFFNLVYMAKDAQEGLKATI
EKRKPEFKGEALVESI KGLLDEKKI I N

>2617921892 Ga0073689_14510 acetyl -CoA synthetase [pel otomacul um Ga0073689 : Ga0073689_145]

MKTI LDEYKSYEEAREKYKWSQRWQI FDGNEESFNI ANECVSRHPRNDLG
I RI LFDDGKKEI YTFGQFSDSVAQFANYLKNNGI EFGDAVAVLLPPCFQF
YVGMFGTFRKGA I VI PCSPHFGPEAI TYRLEKGGAKALLTTRDKASLLED
EVCKLNLQVI FAEDLLQAMEKEPKEFESTTSANDLAMYQFSSGTTGAPK
AVNYRHGAI TVSAPFI KFAQGI KPDDSYFCPSSPAWGHGI WYGTI APLI F
GVAVGTYSYTGKFNPDRC LQALQDFEVTNVAI SSHYRLMI NSPNVDKYK
I RLKRLTYTGPEMSKDFYAI QEKWGVTPHGQYGTTEVGPLTSDFAAFDN
WKVKPGSLGKPSI GSYVSVI DEDGNEVSPNAVGMQMAI KRGDKWI RVGDMV
YKDEEGYFWYI SRADDVI I SSGYTI GPLEVESALMKHEAVEECAVVGSPD
KDRGVI VKAFI KCKDGYTPSESLGKEI QEFVKNKLSKHEFPREI EFI DEL
PKTADGKVRRLVREQEI EKKKDQLKF

>2617921891 Ga0073689_1459 acetyl transferase [pel otomacul um Ga0073689 : Ga0073689_145]

MLALDI YYS GAPDFLI AGDI LV RRI TI LSGVCKYLLNI QLI KLKGDNI MI
SGLGKI FNPDSI AI VGASEI PGKAGERRTRSLI EGGFKGKI YPVNPKRER
I FSLKAYPGLKNI DGDVDL VMTI VPVNAI SSVVSESAEK GAKGVI I I TAG
FGETGEHGGKVEQDI VDI AHTVDLRI I GPNC SG I FSSEKEMNLLGI PSI K
RGPFSVVAQSGNVI DSLTHYARL KDI GFSKI I SVGNAI DVG FVEYLEFLR
DDQYTKVI LLYMEEI KNGAKFLEFAREVSKKKPI VAI KVGRT EAGKRAAS
THTGSI AGNEFI TEAAFNQAGI I RAYSVDEMFDI AKTLVSLPRPKGNRVA
VLSEGGGDNAI TVDNAVTQGLGVNI LSEETQDKLKPFI LKGLKPI NPVDY
GGTAEENPHQI I PACCGVCMEDEGVDAI I I TGCFGGFKEI I APHVEEY EK
EASKKLI ELVNKYKPV LNTSFANEKI ESLRI LEQGGI PVI ESSERVAK
CASVLVRAAENQVRFGRRPVKKKPSKTAVQVLI NQVI KERSNLLI ES
RTI LEQYGI TI PPAQLVSSSREAVEKAEGFGYPVVLKVI SPDI I HKSDAG
VVKI NLKTPAEVESAFNEVMEGAKRVVAQI KGVLVLPMM PQGEECI I GMV

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RDKSFGPVLMMFGLGGI FTEI LKDFSI RI LPLDRNDI DEMI SSI RGFPLLC
GARGRTKKDLAALNHI LQKVADI AVDYPEI EEI DLNPVVVYESGAYVLDS
RMI VRR

>2617921890 Ga0073689_1458 enoyl-CoA hydratase [pelotomaculum Ga0073689 : Ga0073689_145]

MKFETI I YEQRDNVALI TLNRPOVLNAMNHQMWKELSQLDKVEKNDEI K
VMVI TGVTTTEKGKKTFTSTGADLKDSEKRTPEEYRSYLDLSLQEVSLRI I KF
PKPTI AAI NGYAMGSGYELALACDI RI ADEDAI I GSPEARVSSAVTGGAT
RLI I ELI GMGKAKELLFTSECI TGSEAERI GLVKNKAVPSEKLMKVFEMA
GTI AQNSSYSVRLI KESLDMARTNNPEEMMDVEVEACLKTVFHSRRKAI
KDFESRKA

>2617921889 Ga0073689_1457 KamA family protein [pelotomaculum Ga0073689 : Ga0073689_145]

VKVKYI NKI SDVPQLSSEEVRELEKVARFRFPFRANTYYLGLI NWEDKADP
VRRMI I PI NEELESEGWGA I DPSKEVDYTVLGLQHKYKDTALFLLSDI C
GGQCRYCFRKRFLFMGDRDREI LKDYRSALQYI REHSEVNNVLLTGGDPLS
LETSALKGALSALREI RHVEVI RI GTKMPVYNPFRVI DDAELPKVI KEFS
APERRLYFMLHFSHPNEI TKEAI EAVSI LI GSGAVLCNQNPLLRGVNDVP
SVLAELYRKLSYI GVTPYYTFQVRPAI GNKPYAVPLVQAYQI FQEAGKNI
SGTAKRAKFVMSHALGKI EVVGLDDRYVYMRFRAPNPVDNGNFI I ARRN
DQAYWFDDFEQVSFA

>2617921888 Ga0073689_1456 FAD/FMN-containing dehydrogenase [pelotomaculum Ga0073689 : Ga0073689_145]

LSI KECLQNVASVSDNAKDI SDHSKDFSLVPPSEPEAVVYPKNVDEI AGA
VVALNKI GVPI YPVSSKVHFNNGTI PRRGGVSMDLTGMNSI DKLDQENHW
AHLEAGVTWEQYANALKEI GARTTMPLLPAAERSVMDWLEREAATI PLF
EYSAQLAGMWWVWGNGEKFATGSSSSNTFGQPGNYAGGVNPQPGTI DFW
RFLEGGQGTMG I VSKAVVKYELI PKI EKTFFLTAEKKLEE I DPLYDI LH
RRVGYECLLVNMMVLASMLGENAKQI ADLRKLPPTYTVLLI I GGLLRPE
EMLAYQEEYLNNTTFKEKFPAADLKTLAGAPGLEEKLPGLMRNPWPKEKT
YWKHNYKGACQDLVFMTTI DRVSKFNDVVMPLAAGKGYPVEDI GVIY QPV
ENGRACQLTYSFYNNKAEAAKI LDLYQAAI PAVYEAGAYFTQPYEWI AQF
VYPKAPYTRYLMRVKKMFDPNMI LSPGKLCF

>2617921887 Ga0073689_1455 heterodisulfide reductase subunit D [pelotomaculum Ga0073689 : Ga0073689_145]

MTMKLDLNMENYAWETRCMGCFAFKYGDWI YVPSQHDFSWI CPEWQYGO
FDNWGACGRTRI VNGLLYGD I EYEDPNVLENAYKCFNCGACDMACKRNLD
LEI LMMNQSLKVALVDRGI GMPAHKQI TARI ERTGNYFGSEQSERQDWL
NGDI KVAKKADVLFFVGCTASFVDKEVAQASARLMSKAGVRFMVLEEETC
CGNLLFNFTGQLEKFKKGAKI NLEKI RATGAKTVVCCCADCLRNKVEYPK
ALDMGTNELGFEVLHI SELAATLVKEGKLKAKKEMPMKVTYHDACSLGRM
SEPWI AWEGI RTGGDI SPKGWQGLNPPREWRRGKGCYEPPRDLLRGI PG
VELVEMLRHHNNAYHSGEQGGVKEAFPEVALFAADWRVKEAGLTGASAI V
TPCVHSKEMLAGAVMRVKNKI QGVYHI I ELVDQVYGR

>2617921886 Ga0073689_1454 FAD binding domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_145]

MLSVVEAQAKLKELRQNPYWEMPDEAYKEI EAVVGPDKVSREKAVRQAY
VGRGYARELI WFSGQAYPPCCVVQPETTEEVAI VKI CNKYNLPFNPCSS
QWAYNANPRFRPDQVQI DLQRMQTFEFDKKNMCTRVGAGVRYGHFQQKCF
ENDSYFLNTGGGCSSCVVANHLVWGCSPLNRYRTGNSERRTMASTWVTPEG
DI VHLGWSWAGREPSLESFGWGDGI GPNLNGVLRGHI GWFGAMGI VTEMTI
KVFPFVEDAANVMVPEGI SPHSTVAFKKPRI AWQNYKLPTREAL EEV MFE
FSYAI GAAI TKVPVFWRYVAKAQNKEDFWERWSGMTKEEMDGFHMARAL
I I GFTNEKQLEYEQAVMDDI MKEKGGVATRTKPSDESWFKNADVPGMWWW
TSGYSSCEAGTESLRCTYETGKKLGKTL EEKYVPPFMAEYGDPGWFQSSD
FGHSSYLEFLVYMNVDRCDPMSKDYP EYVAKMI PWYFEETPKI DAETGF
LDFFPASCHGI LFQGPFFSDYQI WDRFLEEDPNCVSNPPAPYDPEYFT
EMLPPFMLTESRQMLRTV KRGKSM LRRGRF

>2617921885 Ga0073689_1453 Predicted site-specific integrase-resolvase [pelotomaculum Ga0073689 : Ga0073689_145]

MKLYSI REFAEKLGVSVSTLRVWDRDGKLI ALRTPTNKRRYTEEMLHHAL
GLKDVREPOKNVLYARVFSKERLPDENLV DHLKNFSAAQGMVI DEI LTD
I GGLNLCERKNFLELCDMVI RNEVKTI I VSHKDQLI RFEFEFFEKLFARF

Table S2

GCKLLVMNRAEESSSSRELAEDLI GTVQQFAAKI YGQRSCKTRMLCKTI K
DSLTDI LNN

>2617921884 Ga0073689_1452 tungsten-dependent benzoyl-CoA reductase subunit bamB
[pelotomaculum Ga0073689 : Ga0073689_145]

VRYGETGYNLEI DLSRGN I ERVETDPRLTELHLGGLGTNTKI LWDRVPAD
VEPFSPDNLLI FSAGLLVGTPAPGANRTI I SAYSPQTLMLMGFSI MGGYFA
PELKYSGYDKI I FRGKSPSLVYI WI HNDKVEI RDAHLRGKGAVETQELI
KAELNELNAKVAI GLAGENRVYTASI EEGRSSASRLGLGAI MGDKGI KA
I AVRGT KDI NI ARPAEFI ELCNEVMKYI QFRNENPVPNVMTI LQGLGSPQ
EMLHTDEKWHTEFVWGNARVRRKDFWNKEI EERWKSQVQLNVRKRLI SCY
NCPI KCGAI I SVPGLSTYMMKCFSKLTYAMAAFVDDLDFGFRI AQQATEY
GVDGFSTPQMMFAVELKEAGI LTDADFEGCPSDNQGRFYWLLDRI VRRE
GI GDI LANGTYWAAKQI KGAEAFAHNTI KKHEQLPLKLGMLNPI YYLMY
CTGEKANI TOI EGQFPQSPFMTVEEREEFVKDWFQVPDEKFKQYLMDWEP
RGERSFPYYPTVDMCVDI VDWOEMMHYI DDAVGVCAGLSSFPLKPPYHI H
NYPKLI SAATGI NLDEEGLKEI YRRNRNLLRAVNVRRGLRRADEKPPEDH
WKKRFPELEENLMDAYYKFKGWNNDGI PTKENLEKLDLAYI AEDLEQRGI
IQNGQE

>2617921883 Ga0073689_1451 Fe-S-cluster-containing dehydrogenase component
[pelotomaculum Ga0073689 : Ga0073689_145]

MAKNKKI VKTI KI DVDKCNCRACEMI CSAFHASPKYSSNNPARARI RMI
RDPI RDVYVPVYAGEYTAECMGRDKYVI DGKEYDECFCRAACPSRDAF
KEPDSGLPLKCDMCEDDPPQEKPLCVQWCI NNALI YEEREEVEEEVNLD
ELEVGLESVDKYGLQKLVDTTVRM

>2617921882 Ga0073689_14416 Phosphoglucosyltransferase/phosphomannomutase, C-terminal
domain [pelotomaculum Ga0073689 : Ga0073689_144]

SLEELAGQMERLPQLLENVPVADKKMVMSSPLLVGAI EAEEKRLAGTGRV
LVRPSGTEPLVRVMAEGRDMGQLRDI I NRLVNMI KELK

>2617921880 Ga0073689_14414 glutamine--fructose-6-phosphate transaminase
[pelotomaculum Ga0073689 : Ga0073689_144]

MCGI VGYI GPQEA VPI LI EGLTKLEYRGYDSAGVAVPEGDCCLKVI KKEGK
LAALREKLNCGNCANVGI GHTRWATHGRPSDENAHPTDCSGKFAVVHN
GI I ENYLGLREWLQSLGHVFRSETDTEVLPHLVEHFYNGDLVEAVGKAVE
RLEGSYAMAVVSSHEPDKVVAVRODSPLVVGLGSGENFLASDI PAI LKHT
RCAHI LADGEMAVLEAGRVVRMDRRGNEAHKEVMEVKWEAEQAEKGGYDH
FMLKEI HEQPKALRDTLSGRI SADGSRVVLDEVKI SPEEARGLKRLYI AA
CGTAYHAGLVGKYI I EKLVRLPVEVDI ASEFRYRHPI I EPGTLVMVI SQS
GETADTLAALREARROGARVI AVTNVVGSSVSREADDDVI YTWAGPEI AVA
STKAYTTQLAAMYLFALYLAAERGAPEEI WEI LLGMKKLAGKAQSI LD
NTSELKDFAREFACCKDLFYI GRGLDYAVALGSLKLKEI SYI HAEAYAA
GELKHGTLALI EEKVPVVALATQEVLF EKMSNI QEVNARGASVVAMAME
GLKEVEKVAGRVVYI PKTHPLLTP I LTVI PLQLLAYHTAVARGCDVDKPR
NLAKSVTV

>2617921879 Ga0073689_14413 ATP-dependent DNA helicase, RecQ-like (EC 3.6.1.-)
[pelotomaculum Ga0073689 : Ga0073689_144]

MVINKAREI LKRRYGSTFKKGQEKI I DSI LRGHDTLGVMPTGGGKSVCF
QI PALLFPGLTLVFSPLI SLMKDQVDALAGLGI PGTFI NSSLRQEKVEDR
LSQASRGRFKLLYVAPERLESGRFLTLMRSLPVSLVAVDEAHCVSQWGH
FROSYLGI SGFI EGLPKRPAAVAFTATATEEVRADI I KLLHLRDPQVFI T
GFDRENLSFSVVRGENKRDFLLGFLENRRGQSGI I YAATRKEVDNLNDLL
QKKGFPAGKYHAGLSDEERTTAQEKFLYDEVVMVATNAFGMGI KSDVR
FVVHYNMPKNI EAYYQEAAGRDRDEPGECVI LFSPQDI HVQKFLI EQSQ
LAQEGKTSEYKRLQAMVDYCHTPNCLRRYI LRYFGEENVSEECGNCGNCS
DNRELADI TI DAQKVFSCI LRMKEQFGVTLVAEVLKGSDDSKKVRQYGF
LSTYGLMKERTLQI TDMI NVLI ADGYI SLSEGQYPVAKLRLKAYPVKKG
QEKVWQKVRKREKAAAAGDPLFELLRLRLKEI AQREKVPPYI I FADSTLR
EMSERHPPDQKSMLSI KGVGQAKLERYGGFLDLI KEYCAERGI PMGOAG
PSARKEREKLP SHI ATLNI YRECRSVGETARKRDLKPVTVDHLVRCGL
EGHEI DWDEFI PREYEELI LQKI KVHGAELRPI KDELPEEVDYLAI KAV
LCKYRLYRRGTHQN

>2617921878 Ga0073689_14412 Ubi quinone/menaquinone biosynthesis C-methylase UbiE
[pelotomaculum Ga0073689 : Ga0073689_144]

MSDDVREFVRQKYARAI TLKTGCCGESRGSACCREPLNDVNL I TGGLYR

Table S2

PDEV DGLPGDAVAASF GCGNPTALADL REGEV VLDL GSGAGFDVLLSARR
VGP G GKAYGLDMTDEMLAEARANQARAGLENVEFLKGHI EDI PLPDQSV D
VI I SNCVI NLSGNKDRV LREAHRI LKPGGRFAVSDI VLTRSLPPKVQDDL
MAWAGCVAGALGEE EYREKLAKAGFTDI EVQI TRVYDLTSPLAGAI VPGL
SPAELSELNGAI VSAFI RARKP

>2617921877 Ga0073689_14411 PGAP1-like protein [pelotomaculum Ga0073689 : Ga0073689_144]

LFI KAFWVVF LTFLLFI TPLSYEPLVNLQDPVKHGQFKNVHFVFI NGL
GCRSNGSCY GDMGFENI RRS LGELGYSYDDRFLLYSYKGGRMVDGRWCP
EKYSPGDT SQPI FFSVNMLRELVEKYSAHPDAAFI LVGHSLGGRVALDF
I TKAPPKI REKI KGI TLNSPLL GAGKNVPPAI IAALEVVD SI WADPAVR
QLLYETEYRRELNL YRRETI RELRDEGVRI ATFSFYRDFVPPLTACVMD
ENNKPCTEGFI I NPVSFSI KDLSGHMRI LERPEI VNYI YFI YQK

>2617921876 Ga0073689_14410 Nucleotide-binding universal stress protein, UspA family [pelotomaculum Ga0073689 : Ga0073689_144]

VFKKI LVAFDNGI KAQKALETAMEI AGNNQAEI FI VTSVKI PEVI SASVL
DRSLLQLEDKTRKHFEKI LDETA AKVKEKGLSVQTAI LHGGSGEAI I KF
AEKEGV DLI TI GSHNRGPVERFLLGLGSVS NYVVNHAKCPVLI TKA

>2617921875 Ga0073689_1449 cold-shock DNA-binding protein family [pelotomaculum Ga0073689 : Ga0073689_144]

LI GKVKWFNADKGF GFI ETEEGKDV FVHFSSI QSEGFKSLDEGQTVEFDI
I PGNRGPQAANVVKL

>2617921874 Ga0073689_1448 MarR family protein [pelotomaculum Ga0073689 : Ga0073689_144]

MGQLARHGGMSVKELS QKVGLSHSTVSGI VDRLERKGLAARVQDSGTDGL
PK

>2617921873 Ga0073689_1447 ATP-binding cassette, subfamily B [pelotomaculum Ga0073689 : Ga0073689_144]

MI KLFRFLKPF AFSVA AVLALVFLQSLADLYLPTLMSDI VDI GI VKGDTQ
YI LRVGGLMLLFAAVSAI CMI TASFLSAKI AAGSGRNLRSEVFSRVEGYS
LHEFDQMG TASLI TRTTNDI TQI QQVLI MMMRMMI SAPMMCI GGI I MAVS
KDAVLSLVFVVLPVLAGAI LLI FHKGVP LFKAMQDNLDKLN RVLREGLT
GI RVVRAFNRLDHERERFI GANS DLTGTAI KVNKLMAALMPLMMLVMNLS
TI AVVWFGGI RVDLGDMQVGDMMAFI QYAMQI MFSLVMI SFMFI MI PRAE
ASAARI NEALGVVPEI KDADKI KNADSKRGFVEFI NVTFSYPGAEQPAI S
NI SFSAGPGEI TAI I GGTGSGKSTLI NLI PRFYD VDTGSVLI DGVDVREM
SQESLR AKI GLVPQKAALFTGTI AENI RYGKEGATDE D VRRAAETAQATE
FI NKMKGDFNSVI AQGGANI SGGQKQRLSI ARALVRRPEI YI FDDTLSAL
DYKTDARLRAALRKETAGATVLI VAQRVSTVMDADRI I VMDQGGI AGAGS
HRELMNTCEVYREI VSSQLSGEEI A

>2617921872 Ga0073689_1446 ATP-binding cassette, subfamily B [pelotomaculum Ga0073689 : Ga0073689_144]

MRDEHRELKPAGRPGGPGGGPGGGFGRGPLGGQMGPVQKARDFKGTI KR
LLGYLKPRRFRLLTVFAMAVLSTI FSI VSPKI LGKATTKLFEGVMMKYNH
VPGAGVDFEYI ARI LLLLI GLYFFSAFFGYLQYI MAGVAQLTVFDI RND
VNDKLVRLPLKFFDSRTHGDI LSRVTNDVDNI SSTLQQSLTQFI SSLVTI
AGI LI MMLTI SPLMTLI ALVTLPLSFI VTAVI AGRSQKYFAAQKELGI L
NGHVEDMYTGHQI VKAFGRERESI AKFNEI NERLYHAGWKAQFI SGVI FP
LMNFI SNI GYVLVCVAGGI LVMKKT I EI GDVQAFI QYTRQFTHPI I QTAN
I ANI I QSTVASAERVFELLDEAEI PDREDAKKI ESPKGEVRFQNVRFY
KEDVTLMENMNI DVKPGRTVAVVGPTGAGKTTLVNLLMRFYEVNAGKI TV
DGVDI RDLKRGDLRAMFGMV LQDTWLFNGTI RDNI AYGRAGATEEEI VRA
AEAAHADHFI RPLPDGYNTI LNEEASNI SQGQKQLLTI ARAI LADPAVLI
LDEATSNVDTRTEI LI QKAMKELMRGRTSFVI AHRLSTI RDADLI LVMNN
GSI I ETGSHDELLAKGGFYADLYQSQFTGANVEEDEYAKSAKDAKRLGRA
VYPVACEI D

>2617921871 Ga0073689_1445 DNA-binding transcriptional regulator, XRE family [pelotomaculum Ga0073689 : Ga0073689_144]

MKLDKKLKTTDL LSLAGI STTTLAKLSKDQPVSM EVMSRI CSALFCDI GD
VMEI VPNQNEG

>2617921870 Ga0073689_1444 Putative inner membrane protein (DUF1819)

Table S2

[pelotomaculum Ga0073689 : Ga0073689_144]

MAWKKPYTSSI KDMPLFAEMRRTAQLLCEGNSRDDI I KLSMKSNI YQLE
 KEKRRRDLPLRMLKRLGTI DMPLLRVLADGCDDDAKLI AFLALI KSDRLL
 FEFMREYVADKFOAGQMEI NDRDFLDFI ERKAQNSDTVAGWTSNNLVRVR
 NTFKNI LCQAGLAKRSGKSLLI QKPVCDQOI YNLAGGENEI FAKAMLLEV

>2617921869 Ga0073689_1443 protein of unknown function (DUF1788) [pelotomaculum
 Ga0073689 : Ga0073689_144]

MMMTLNKRLDLI EPKI LEKSFRGTGRGTANEI NFWI FDYDPADEMAVRAHV
 SYLEQRVNNQYDDVRI VRFDLYKLI LDVLRKKNYLDKVMQMEQAKTSHAI
 I NPI KKTLLRLTLDGDLI VGKI TESI VPERDI I FLTGVGKAWPI I RSHTVL
 NNLHSKI DRNPLVMFFPGDYTNELRLFGEI TDDNYRAFKLI AR

>2617921868 Ga0073689_1442 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_144]

MKI QDMFKKDI GROI QGVVKI GODSTEMI TMELDEYVVTKELNRYFDEFF
 DSYRKGTTTTRTDKMGVWI SGFFGSGKSHFLKI LSYLLSNKTYDGKKAI SF
 FEGKI ADSRI MADMQMASNTSADVI LFNI DAEADADSKTNKDAI VKVFMK
 VFNKMQGFCGSMPIW ADLERQMSKDGVDYDSFRARFKELSGNEWENARDDF
 YFEEDNI VQALADTTKMSI DAARSWYSKSEGNYSLDI NTFARRVREYI EA
 KSKATGKKHFVI FLCDEI GOYI GSDSGLMLNLQTVVENLGTECGQAWVI
 ATSQQDI DSI TRVDRDNFSKI I GRFDTRLSSLSSANVDEVI KKRLLAKTDA
 AADKLRLLYADKAAI LKNLI TFSPDTPEKKLYSSPGDFMDVYPFI PYQFN
 LLQAVFTGI RTHGASGKHLSEGERSLNNAFQEAAMQFSGFDDGI LI PFNA
 FYKTI ETFLDHN I RAVI I KAAESAERTD GALQPYDVEVLKVLFMVKYI AN
 VLPANLENI TTI MLQNI DQDKI EAKKKVDASLRRLLEEKLI I KNGDQFI F
 LTNEEQDI NREI REI KI DTSEI I EKVGGDI FSALFGLNKKYRYNDRYDFS
 FNTI I DDRPRGAQKEEI GI RMLTPMYALGSATEI ELKTMMSMRERNVI VTL
 PSDMSFI EEMEQALQI ETYI RRNAGKTSTDI VEDI KTTKAREGKQRADRC
 RELI VEALKRAD I YVYGKLDI KEKQPSEI NDAFKALVEGI YTKQNYI T
 KPFYTSDSLREI LTAQDTQI TLEGMEPTPNHLAVTEMSDVI TRSSYKNI
 PI TMRSLI DI FGKI PYGWKDMDI AGI VLTFLFKQEI RLELGGESI AGTDV
 NVI NYVTKREYLERI LI KTRVKI PPALLANAKNLAKDVFGRSVPNDEG
 LMARI KELASVELTRHPENPGI KQLLDEYGNAGYPGQAVLESGKKLFK
 EI ERI KDI KAFYDFLSDEKESLLDYEEEDVQDI KKFFKNQKVI FDKALQI L
 TLYEGNRSYVLDPETI KLVEAI EHI TRLPSPYSEI HKLPELMEQFMTCFV
 NLLEEECQPI RADI ETDRAAALSDLERRSCKESFSDKVRADFAALLERLS
 HANNI YEVI AMRTESDRMKQRFI QSFDEEEARI AARQASAGEDAAPPPPA
 RKTKTVSLKKLFHGTQVSSKDDI DKLLDHLRAKLEAQLEENTTI KI I

>2617921867 Ga0073689_1441 Type II restriction/modification system, DNA
 methylase subunit YeeA [pelotomaculum Ga0073689 : Ga0073689_144]

MDKAKI KNYAVARQKLI EAVRQKAYQLYI FEDGVLPDEAYHKLRSQDI
 FLTPEQSRARERLCAYLALLGNELDNEKAYQHLLI EEVAYTWFNRLI ALRF
 MEANDYLPSGI RI LSSVDEGRAEPDAMREAERLPYVNQDKI AEYRAATGI
 DASEKLYKYI LI SQCNALSDI LPMFEKI DDYTELLLPDALYRKGGVAHD
 LVHSI DEDDFRDQVQI I GWLYQYYI SEKKDEVFAGLKKN I KIKETI PAA
 TQLFTPEWI VRYMVENS LG RVI VDSGQKAVGSGEGRVSGQWTVDSI EKL
 KAGWKYYI EEAQOTDEVRQQLLTNHCSLPTALSI ENVKVI DPCMGSGHI L
 VYAFDVLQYI YASQGYAEREI PNLI LQNNLYGLDI DGRAAQLAYFALMMK
 ARSYNRRFFRQESI PQPHVHAVI ESDGARRHHLDYI GHGMSEAERQACKD
 DLGWL I GLFADAREYGS I LKI NRTLDYDRLRRFVKDVP SGQLDMYSTGI D
 RTERI LLEI LSVAEI MTQKYDVVVTNPPYMGLLGMEPKLSAYLKKEYPDS
 KSDMSTVFMERTLDI CKPNGFMAMI NI PVWMFLSSYEKL RVKLLKSNTI I
 NMLHFGRGVFGSDFGTAFVFERERI FG YI ATYRKLFPKQGA VDSVEQKE
 KWFFENI GSYI AKQENFARI PGMPVAYWVS NFGI FDAKKLSYRFLSGGRN
 KTHNNEKFVRYWVEVNNYQKWQHYANGGEFRK WYGNNYYVI DWSDSA KNL
 YRLLGGLYNERFWNKEGI CWSLI TSSKSSFRI KEKDFHYSSGSPTI FDYK
 HDNHN YI LGFLNTAVASY I LGI MNPTI NTSVGDVLLLPI I ESKERPSI EQ
 I VNQNI YI SRTD WDSFETSWDFRVHPI VRFKMADNEKPTTRI SSAFKAW E
 TFAEQFNK LKANEEELNRI FI EI YGLQDELTPVEDKDVTI RKADLSRN
 I RSFI SYAVGCMFG RYSLDEPGLVFAGGRFDRARYKTF LPEDDNI LPI GA
 SDYFDDDI VVRFVDFVRVYGDAAALDENLNF I ANALYPNGGGS AKEKI RR
 YFLNDFYKDHVKTYQKRPI YWLFDSGKKN GFKALI YLHRYDKFTVARVRT
 DYHLPLQRKYESI GRLGMLSGI TENAREKAAYRKEI ETLOKRI EECRVY
 DQVVAHI AHQAI ELDLDDGVRVNYAKFQGV EVPKDNKTVKMDLLAKI

>2617921866 Ga0073689_14325 tRNA-splicing ligase RtcB [pelotomaculum Ga0073689 :
 Ga0073689_143]

Table S2

VELVGEGKNRYRLARRGGMVRDGVVYVNEHLLPMVKKDKSLOQLANAACL
PGVVGRVYGMPI HEGFGLPI GGVMASADGVI SAGAVGMDI NCGVRLLT
TAVLASELRAPFLRLSI DRI EEEVPTGI GKKGNRKETTGAFFEEVYTGS
RGLVERGYGLPDDI KNTTEEGCFPGAGPGVVSREAFKRGAAQLGTLGGGN
HFI ELQVVVEVYDRAAGESFGLVPGLLAVMVHTGSRGFGHQI CNDYTKI L
LSAAGKYGI ELPDRGLACAPVDSREGRDYAAMACAVNFAFANRQLI SHD
I RRAFSDVFSCAPEKLGLKLVYDVAHNI AKWEEHGGQKTLVHRKGATRAL
PPGHPGNPAVYRRTGHPVLI PGSMGAASYVLTGTEKAAESFYSANHGAGR
ALSRTAAAKEI SREQFEASMGGLVYNSRNYKDLLDEAPGAYKDI DQVET
LAAI GMTRKVARLRPLAVI KGKD

>2617921865 Ga0073689_14324 GntR family transcriptional regulator [pelotomaculum
Ga0073689 : Ga0073689_143]
MWFRVEPGRGVPI YI QLMEQI RRAVAGGI LSPEEQLPPVRDLSQLSI NP
NTI SRAYQELEREGVYTMGRGTFVAGPASTLTDQERRRRLDQAVEKLL
VDAYHLGCTPGEVLAIVKRRVEDNQSQGG

>2617921864 Ga0073689_14323 ABC-2 type transport system ATP-binding protein
[pelotomaculum Ga0073689 : Ga0073689_143]
MTVYDSAI LTQGLTKTFRGKPALDGVLEVPGRGVFALLGPNGAGKTTMM
KLLLNLLRPDAGKI QAFGLNVLTDVAVRRRVGYQSETQRLYWWARVEEV
I GLCRSLYPRWNRDRVERYCRLFELPPRARI GELSKGKLTLLALVMVAVGP
DPELLLLDELTTGLDPLRRRQALKLLVEE I AGEECTI VFSSHQLQDVERI
ADRTGFLMRGKLLLSRPLEQLLAEKKVRALFSGSPADLQQWPGVRR I E
REGSRLLI SLSGHLDEI LDRLKTVDGI AFEVLDQTLEDI FVEYSGGEKSD
KEERTND

>2617921863 Ga0073689_14322 ABC-2 family transporter protein [pelotomaculum
Ga0073689 : Ga0073689_143]
MI NYALLRWEMRRFRWWYGGSLFFGI GLVMLTDI NTVFHWERHPFFTFG
MFI ALFWGMGLFAREFREGGTMEFLLARPVSQQFLNTLALAGGAPFI LL
MI SPLLYSI I LSPWVSGI SFFRLAALNLLAATWVSGVYLFGI LLGLYTY
HSNSRYPRYLQAFI I SFFVAI I I NLDVTRKNEWLNPDLLI HNHPWVSL
LSLALGYLFYHLGRMLERMDI

>2617921862 Ga0073689_14321 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_143]
VTI I YEGAMRSCHVLI RAVMKKKLFAFLVLLI SFI LI KOARTMNDPGHV
SI RRPLNI GGVSKPRCAVEKVVVARDEDGDI YDLDDI VLGARKDLQAKP
LYKDAYYAGGYPPDNEGCTDVI WRAMQNAGYDLKGMMDRDI KEHTGDYP
RVGGMPEPNI DFRRVPNQEVFFKKYAGKLATEI KPWDPENLKQWQGGDI V
VFGPPYDHVGVSDVRREDGVPLLI HNAGPRTREDEGLLTWPSP I KYHFR
YPKNG

>2617921861 Ga0073689_14320 protein of unknown function (DUF4372) [pelotomaculum
Ga0073689 : Ga0073689_143]
MDKDTTKSTFNEVLNQLPFEEFCSLVKQI GADRYI KKLFTTKLLCVMSI A
QI AQI KSI RPLAG

>2617921860 Ga0073689_14319 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_143]
MKMKNKDDFKFLVEYAI KAPSGHNTQPKFENTENGI TI HPDFKRALPVVD
AENYELI YI SLGCALENLVI VASQNGYQYSVQNPDPKSSI NVQFMKVETN
I KPDDLLEYI AI ROATKSKYI HKNI LSSDLKQLGSCFNFDGVSLTLLNGK
ENFEKLI PLI I EANNLOFSNKDFVNELVSWCRFSKSEAERTKDGI WSATM
GMPGLGRFI GRVI MKNFVTAKSEAKRLRDLLKHTQGLAI FI TDANNVASW
VKI GRAFQRFGLTATKLG I RHAHLNMPCEEI DVRYKLAKELNI ENKHPLL
LI RYGYAEKMPYSYRRQFSDI VI TP

>2617921859 Ga0073689_14318 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_143]
MNDERLKALQKLSAI DI MPRQQLTGYQNRLVGLKSCFALTRLETVRAGFK
RAWQEHDIYATI I AVAGKI SQNI LQEDPRLLMWYDQAVTRSEKCFSTPFR
KRFI Y

>2617921858 Ga0073689_14317 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_143]
LI LESLQAFNSPGKLKNYCYDAPEVSGHREGLRTLEEI EFLQELVSSLGT
TTAYI STAEAI LPAGHEWTGMRVVREDI LEQI TEPAGRGAADFRQQTQR

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KLSGLKKAYLQAYLGLHTRARLGVNNEDEKRNSSGS

>2617921857 Ga0073689_14316 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_143]

MDIREWEFLDAFEKRMQI VAAVDSI VNRGNRKI DLERLFEPGQLDNIIFS
VLVFI VTAHEFCFCFLYRLLVRQLLAGLLVDRGLTPTVI CESAGCQAEDA
MIYRDIYYKLLSLNTKNRE

>2617921856 Ga0073689_14315 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_143]

LAADVNSSLEAVAKI SAKI RDLVDEI NNKNGPVEDRELMLMAAYLHHFYT
GLESMFERI SDELDGGVGRRGNYHREVLRSMTI DIGGVRPRVI SPELAEE
LDDYRKFRHLFRHAYAAELRWKKMGHLALNI TAIYNLVEINI KGFATFLV
NLASRL

>2617921855 Ga0073689_14314 Predicted nucleotidyl transferase [pelotomaculum Ga0073689 : Ga0073689_143]

MMI GEKELAGYLAGHLKKI AREEEELARLAGRARKNAAKI TGELVKRYGL
SKVYLFGSLACGDFKWNDSI DLAVEGLPEELLLKAYGLAEELAAPLKVDL
VLLETALPSLRECI LREGEI LYDLQGKKDRPPEKI GRRCKQQP

>2617921854 Ga0073689_14313 DNA topoisomerase-3 [pelotomaculum Ga0073689 : Ga0073689_143]

MKSLVLAEKPSVARDLSGI LGTFTKRDGYLENDKYVVSVAI GHLVGLADP
EDYNPGLKKWSFDLPI I PDKYALKALPGTI KQFKI LKTLLSRPDI GLI I
NSCDAGREGELI FRYI YALSGSKKPFKRLWLSETTPEAVKKAFASLRPGE
DLDLHLALAAGARSRADWLI GINATRAFTVKHNDLLSVGRVQTPTLALI VS
RESEI KNFTPAYWELYAVFEKEDGQTYTGKWFKEDLDRFDSADAAGQVE
DRVKDKPGVVEKVEQDI SEPPPLLYNLNDLQKDANKKYGLSAAKTLEVA
QSLYETKKLI TYPRTDSRHLLTI ELAATI PKRLSALSGLSVYADLAAGAKA
AGI PGKRYVDNSKVTDHALLI PTDVRAGI NTLSPERKI YDLVARRFLAI
FFPAALYKQTRVVTGAGGETFI TTGRVELQPGWKVYAAPEGGNPVRKTK
KQGEAGPDPEEGEDTPENI PLPQLLRGEKVMVI DTKVVEKQTRPPKRFTE
ATLLAAMEGAGKLLDDEDLKNAMKGHGLGTPATRAAI IERLI KVNYI ERK
QKSLVPTPKGEKLI SLAPDI I KSPMTANWEKTLSDI ESGRADPKAFI AG
I VDLTRQTVELARAQEPSAPARTGVKGGKEPLGRCPLCGRDVVDVFPKSYG
CAGYREGCKFAI WKEI AGKKI TPAQAGALLKKGRTGI LKGFKSKEKKSFD
AALALNKGKVMFQFERGGEKKE

>2617921853 Ga0073689_14312 addiction module toxin, RelE/StbE family [pelotomaculum Ga0073689 : Ga0073689_143]

MPKNRI SITGAEEQDLAEI VDYI ANDNPAAALKLAETI EQSI LQLEEFPL
TGTPKNRRLSRRGYRI LI VESYLVFYVLPENGALERI I SGKRDKFL
L

>2617921852 Ga0073689_14311 Antitoxin Phd_YefM, type II toxin-antitoxin system [pelotomaculum Ga0073689 : Ga0073689_143]

MPVI RPVSDLRNKTPETI EEICI KEKKPVFI TKNGNGHLVI MSQQLFEEQQ
ALLDLYDKLDEAEEQSRAGKRRPFREVMVDLRSRI HAKESN

>2617921851 Ga0073689_14310 signal peptidase I [pelotomaculum Ga0073689 : Ga0073689_143]

MLPTLKVEDRLI I DKVSFKLNGI RRGEI VVFHAPPASRLDVVMI KGVIGL
PGETVSI KKGVVYI NGKPLTESYEKMTKTI YCLYQI HDI I MTKI

>2617921850 Ga0073689_1439 DNA-damage-inducible protein J [pelotomaculum Ga0073689 : Ga0073689_143]

MAETTNLNI RIDKELKEQAEKFFNELGLNMTTAFNI FVRQSLRQGGI PFK
ITLNTDAFYSPANMKI LRQSI RDAEEGKLTAHELFE

>2617921849 Ga0073689_1438 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_143]

MSII I PESGMKFGPYEETNVFHVESRLYKLLGEYVKTI EFILCNSDREI
YLI EAKSSSPQPSNQEDFDEFI LEI HEKFAHSI DLLFAI LLKRMLDDSGE
VPSCI YDANSQVDI KLI LVI NGHKI DWLSPI NDAI NQKLRRQI KTNWLEF
VVMNEQLAYENQLI QA

>2617921848 Ga0073689_1437 AAA domain-containing protein, putative AbiEii toxin, Type IV TA system [pelotomaculum Ga0073689 : Ga0073689_143]

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MSI TKLYLKNFTVFDKLN I EFSKGI NVFI GDNGTGKTHI LKLLYSACQAA
QAKTTAI DFSQKI VRVFRPDDLSI HRLVKRSVGSNNNAVI KVSSERHTLSL
EFNSKHTMNI LVKGNETWEKQFAGLTSTFI PAKEI LSNSRNLI QAI DKGNI
VDFDDTYKDI I SAASVDI SRGPESATKKKYLNSLQEI TTGTVKVKNEEFY
LKPGTQSLLEFQLVAEGI RKI ALLWQLI KNGTLESGSI LFWDEPEANI NP
KNI PAI VDMLLNLKSDGVQI FI ATHDYFFAKYLQVRKVSNDVLFHALHR
KDDI VEHESENEFSLLENNSI I SQSI ELYKEEVKKVMG

>2617921847 Ga0073689_1436 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_143]

MRFVYFVRVYGDAAALDENLNI ADALYPNSGGSAKENI RRYFLNDLYKD
HVKTQYKRPI YWLFDSGNKDGFKALI YLHQYDKFTVARVRTDYPHPLQRK
YESEI GRLEMLSGI TGNAREKAAAYRKEI ETLOKMI EYRVYDQVVAHI AH
QTI ELDLDDGVKANYAKFQGVKPDNGRI VKMDLLAKI

>2617921846 Ga0073689_1435 Virulence protein RhuM family protein [pelotomaculum Ga0073689 : Ga0073689_143]

MSTAQWPVGGANRLGRRSLEMHEDI AKQDYI LTPGRYVGI EEQEDDGEPF
EEKMARLTGELSEMFKRSHELEEEI RKRLGAI GYDMTFDNSEI I I CQTGD
GRTKI DVRMEDEAVWLTSQMAELFQTTKQNI SLHNKQRLATLNRMVSAF
FDLAELRAMQHOPMYMRDWVVELDDFAKRYGKGI LPNAVCVLCPRGVW

>2617921845 Ga0073689_1434 ATP-dependent Lon protease [pelotomaculum Ga0073689 : Ga0073689_143]

MFEENSKSMNTLLQEFAGKI VRKDLTKKI KEGANVPVYVLEYLLGMYCA
TDDEAGI EEGVQRVKDI LADNFVRPDEAEKI KSKI REMGSYTVI DKAEAK
LDPYSDTYRAVFSNLNLKNVI VADSYI KQYEKLLSGGI WCI LRMNYNRLE
ARYDEYDSDAPKGGKRNKVSPFEI EELTPI QLPHEMEMQEFFDGRKQFAKE
EWI DVLLRSTGMEPTQFENRTKWHLLARMI PLVENNYNLCCELGPRGTGKS
HI YKEI SPNSI LI SGGQTTVANLFYNMANKTI GLVGMWDCVAFDEVAGI S
FKDKDGI QI MKDFMASGGSFARGKEEKANASMVFGNI NQSV DVLI KTSH
LFEPFPAAMAYDSAFFDRMHYYLPGWEI PKMRPEFLTNEYGFI TDYLAEF
FREMRRKSYGDTI ERYFRFGGDLNQRDVI AVRKTVSGMI KLLYPHGEFSK
EDVAEI LEYALEGRRRVKEQLKKI GGMEFYDVHFSYLDNETFEEHFVSV
EQSGSKLI PEGQKPGHVYTVSHGDTGMLGVFKLETEVVGNGKFEVTGV
GYDREARENKTAQNYFKANKKLI SGSI SI DTSNFLMHI ADCQGVGTTSE
LALCAFVALCGASLRKPVQSQCMLGNMSI GGTI SKVAELANTLQVCFDA
GAKKI LLPLSSAADI ATPSDLFQKQTSFYTSPEDAVFKALGI E

>2617921844 Ga0073689_1433 TIGR02687 family protein [pelotomaculum Ga0073689 : Ga0073689_143]

MNLTEVKKSLERQFARELSQGSVRNI VFWDYDEEGVFAGDI DSLALEGVKI
I KLYDNNMFAVKLYI EETDTTGNLLVYSPLPRPANRENWLTDTI KYSQTF
STDETSQNLNLFKI DSALRHVAERYKLFFRNSERCKRFEGYHLAPYTETK
I DI GVL SALCKLPAPNLDNVVRLTI ELANGESAVYDSI AKFGNMDALWA
LI QKSYGYHFPEQSLEKLI LLLCTHLAHSI NGNLPKEWRTYVSANSNCF
VFVDNFMKNSQLWEAYNKLAGFVAERLNLSGRTSKWSI DEI VDCDTFEF
DRSI I SRLCENI GQGAGEYERYRKVI HSRKNRRYYYPQFEI EYDVLLYTCE
YLELAQRHAGLSGLTVAKLFDEYTKTLTKLDSSYRHFLGYDKLAERDGF
GPLFEKVDNSYTNWYLNELSMKWALWDGERAWQAPGVTSQQGFYDKYVR
RFVAGNERLI VVI SDGLRYESAVALSAI LNREQKGSSELDVMLGVI PSYT
ALGMASLLPHKDI AI TDKADI EI DCI STKGTDNRGKI LKLVKESVVTY
EHVMGMTKQKMAEFSGVKLI YI YHNTI DARGDNAATEHEVFEATEKCFR
ELSGLVRLRNNI SAI NI LI TADHGYI YRRTPLAGRDKTPKEDAAAI EAK
RRFI LTKENI DMQGTQVFSMDYLTKDKSDI RAVI PRATNCFKI QGAGSCY
VHGGI NLQEVVI PVI RFKSDKNLPRSMGAKKVSGLTNL SRKI TSVI THF
TFFQNEPVGEKLLPLRVYTAFFADEAGNRI SNENI I I AESTSDKPDERTYK
EKFTLKDI PYDKSKYYLVLKDEDEI VNSEYLRI PFI I DLI FGGS I QF

>2617921843 Ga0073689_1432 toxin YoeB [pelotomaculum Ga0073689 : Ga0073689_143]
MEKLWTDKAWEDLYWQTQDKKTLKRI NQLVKDI ESNGYDGI GKPEPLRG
DMSGWWSRRI DDTNRLVYRI TDGKI I I AYCRTHYGDK

>2617921842 Ga0073689_1431 DNA-damage-inducible protein J [pelotomaculum Ga0073689 : Ga0073689_143]

MAETTNLNI RI DRELKEQAEKFFNELGLNMTTAFNI FVRQSLRQGGI PFE
I TLKTDAFYSPANMKI LRQSI QDAEEGKLTAEHLI ED

>2617921841 Ga0073689_14219 hypothetical protein [pelotomaculum Ga0073689 :

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Ga0073689_142]

LI FVTTQPLQRI KEI NREKRPFYLLSAGRKSFYAI APVMI GYVLKAI DI D
KDPLLLFNI SGKPI THGTFLT PFSI YCNKLI I

>2617921840 Ga0073689_14218 two component transcriptional regulator, LytTR family [pelotomaculum Ga0073689 : Ga0073689_142]
MPGSTLKI LI ADDDELI CNFLSNI LSTFEGVAVAGKTNDGSKLLELLKDT
GPDVAVFLDI QMPGLDGLSEVP LLKROQPGVFI VFI TAHTHYAAEAFDLDA
VDYLI KPLNRERI GRALEKLMRFKAMQAAGGKSFRPPAGSGGGSKTTLDS
NTRLTVKSGHGM I I NTDSI FFI EKAGKKCVI HTDSGRHETPEQLYCI EQ
RLEPDRFFRCHKSYI I NI NYVEKVL PYADRAYEVI FHNYPKVTMRREKF
EEFRLMI EK

>2617921839 Ga0073689_14217 Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase [pelotomaculum Ga0073689 : Ga0073689_142]
MKKGI NTA VLLALFOI I LLVAI FMLYI LOYPVQHAQTSKHLI LCFFAGS
I AFNFFI VTRMVKVCEKEAHL SAREDMARSFASI AESI KAQNQDFKFI K
EI SRLLOEGRWEDLSGYLENI GNKI TVSNDVLKVDNAI I GALLKAKAAEA
DVKHI RLDI DI CASLAGLDVKAVDLARI TGNLVDNAF DAVLPLDETEKI V
SVKI HRS GPFLQLEVCNPGPAI DPGMLGKI FEPGYTSKGMHSGGLGHI V
KTLAEKLMGTVRVFSKTDGTRFVLTLPGV

>2617921838 Ga0073689_14216 Sensor_kinase_Spo0B-type, alpha-helical domain [pelotomaculum Ga0073689 : Ga0073689_142]
LLGTGLATLLHYGLFLYNF I LAMI VFLALALTNGYDI KQNRRI LLLG
TILGSASLVFLHLPQTFRI VLQWAFI FCI I KLFFGFTAKKSVLVTLSI LT
VAFVAEGTTSFVLHFI I GVTPADYLASF TLRVCPLAYI TPLAI LTYI SY
RRRWQI FKENARI NI PVGTFLLPI QI LLI CI VTNELFFAMDFEPSTRKL
TAVI FALLTI SLFLSLFI WRFLHFARREAVVAAQQKLAEEI NRETDVLR
YQNHDFI NHI QI I TALLAERRKEELATYVKAI LTNDVHFTSRQPVSE

>2617921837 Ga0073689_14215 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_142]
VREAPWPALGWGLLLVTPLA VLLLI TVVGI PLSLTLI MAYTLLLHAAK
I I I GDAAGRLLARRFGWEKRAHDI FPFSI GYAALI LLGKI PVVGFFI NI V
VI CMTMGAVFLAI YRWRQSVQPALI E

>2617921836 Ga0073689_14214 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_142]
MEENKEALLERARSGDRAALAE LALARGPEVYRLALYLLHLGTDSATLRA

>2617921835 Ga0073689_14213 NADH dehydrogenase [pelotomaculum Ga0073689 : Ga0073689_142]
MENTELNVVTGAFGYTRRYI TSRLAMGKKVKTI TGCPGRPNPFGDRVSA
APFNFENPGELTRSLRGATTLV TYWVRFPHGEV TYDLAVENTKI LI KAA
RKAGVPRFVYI SI TNASTNSPLPYFMGKGLLEKAI I DSGLSYAI I RPTVI
FGREDI LI NNI AWLLRRFPVFAVPGRGDYRLQPVFVEDVAELAVSAALKD
RNI I MDAAGPEI YTFDELVRLI AETVGSKARI VHLPPGQVLFI SKQI GRI
I NDVVLTRDEVAGL MANLLVSQDAPTGEKAFSDWLKENS SVGA EYASEL
AKHYPRRR

>2617921834 Ga0073689_14212 Secreted protein containing C-terminal beta-propeller domain [pelotomaculum Ga0073689 : Ga0073689_142]
VKRFLALVI LLALAVI LI PWLQPGVNAAPGHS AVFVI GRDSYVNDGRTVS
MDAVPFLHHDRA YVPVRYLGNALGI GERDI EWEGATRSVI LSPDGATVRL
VVDSDKLSVDGEERTMDVTPLLREGRVFLPARWVAEALGYEVKWDGGARA
VLVGPPGNI PAPPAGMSGLPVVG DYENLKNLLAQAAQGEWALT LNDAKA
AAQGVRESLRAGAAA PGGGAGAADYSKTNVQVAGVDEADI VKTDGSYI Y
QVNGRRI VI ARAYPAGEMLVSTLGFAAKDFSPREMYVDDRYLVVI GQSP
GYGDGPI RPMLLEGGKMI EI MPPYRQGTVKAI I YDI SDKSSPRQI REVELS
GSYVSSRKI GPAFYLVANRSI YYHPGGEMEDPGPYRD TAAGGEFSTI DY
SQI RYFPGFVRPDYLI VAGVNLDRSDERAQVSAYLGSGENI YASTENLYV
VVTDYRYGI MEVRPGPPPGPTPADGNKTRI YKFAMNNGRLTYAAAGEVPG
AI LNQFSMDEHNGYFRI ATTRGEVWQTGQYTSRNNI YVLDDRLTTVGRVE
DI APGERI YSVRFLGDRAYMVTFTVDPLFVI GLRDRHPEI LGALKI PG
YSDYLHPYGENHI LGFGKDTVEVGQKGGDGATGSMAYTGMKMALFDVSD
VNHPVEMFKEVI GDRGTDSELLRNH KALLFSREKNLLAFPVRVMEVDGNG
EKPAAGFPEYGRFQFQGAYVYSI DLANGFTLRGKI THLTDEDYLKAGNYW
YDSEKNI ERI LYI DDTI YTL SKRFI KANNLADLKEMNTLKI K

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>2617921833 Ga0073689_14211 oligoendopeptidase F [pelotomaculum Ga0073689 : Ga0073689_142]

LNMI I REVL FMEGKGGLPARREI PDKYKWRLEDI YTSNELWERDFQQVWE
MTGEVEVYRGKLGQSAOTLLKVLQLODRLOELNEKVFTYARMRREDNAH
PVYQALTD RADSLNTRVQTAL SFI VPEI LALPADI LERFRREEPGLALYN
FALDELLRQKDHTLSAEEEQI VARVGEVAQAPANI FKMI NNADI TFPSI L
DEEGRDVEI THGRYI QLMESGDRRVRREAFSALYGVYRK LKNTLAVTLAA
SVKKDLFYARVRKFPSALHVS L FADNI YPEVYENLI QMVRRNLGSMHRYM
ALRKKI LGLDELHMYDLYNPLVKEI RWEI PYPRAVVMVREGLAPLGAPYG
ETLAGGVDAGWVDI YENRGKTS GAYSWGPGYGVHPYVLLN YRDNLHN VFTL
AHELGHAMHSYYSYREQPYVYAHYKI FTAEVASTVNESLLMDYLLKTVTQ
RDKKLYLLNHYLEQFRTTVFROT MFAEFEKI I HAKAEAGEALTPELLCSV
YQQLNVDYHGP EMVVDGDI DLEWARI PHFYAAFYVYKYATG FSAATALTR
RI LAEGESAVAGYLD FLKKGDSYPLNLLKAAGV DMAAPQPVQEALDLFT
LLLDRL EALAARK

>2617921832 Ga0073689_14210 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_142]

LFI NFYYQLKSEGVPSLNEW MALMEALAKGLSFSSLTGFYHLARAMLVK
SEAHYDRYDLAF AKYFEGI ETGDEI I KHALEWLTRSLPPLRVPPGERSPF
ADWDLNELRRQLEERLKKQDGEHHGGSRWI GTGGTSPFGHSGYHPAGLRI
GGKSVNRS AVKVA AERRYDRDQDI TGVRQFEVALRKLRQFSTRTEGPK
DQLDL DGTI DATCKNGGALKLVQRPRRNTMKVVLLMDSGGSMNPYI QI C
GRLFTAANRTTHFKEMRFYFFHNCI YDYI YTSPI LVRQH AVKTEELLKTL
NPDYRLI I VGDASMAPSELTMI GGAI DWGVENDEPGMVWLERLTHHFPFS
AWLNPI PASHWEI MEGSYTI KLVRSI FPMFELTPEGLEQAVKKLKARR

>2617921831 Ga0073689_1429 MoxR-like ATPase [pelotomaculum Ga0073689 : Ga0073689_142]

MAI KLPRFKGTGDY LASGELQNSVNI AI ALGRPLLI KGEPGTGKTM LAKS
I AEDLGLSLI VVNI KSTTKAQEGLYVYDTVQRLYDSQFGDHDVSDI RQYI
KLKGLGEAFTSDDPVVLLI DEI DKADMEFPNDLLWELDI MNFFI PETGET
IAAKHRPI MI I TSNAEKELPDAFLRRCVFHYI AFPDREMM AEI VRVHHPD
LEERLLGQALEAFYTLREVSGLLKKPGTSEL LDWVQALALGGI EPGRI AR
ELPFLGVLLKKNQDFD TTLRRLH DRGAGRQA AFSRKVNW

>2617921830 Ga0073689_1428 Cd²⁺/Zn²⁺-exporting ATPase [pelotomaculum Ga0073689 : Ga0073689_142]

VAGLPGVEEARLNF GAAKLTVRGCTDSGRI I EEGKKHGVTAA ME GAPTAK
VFRLSGLTCADCAARLEKNVASLPGVESAH LNF GAATLNVTGDVAVHLV
DEARGEVTA VVAAGAPEQALSFWEKNRR AVI SAI SGLFLLAGWLADLLL
QLPGI STGLYLAAML SGGFGTARKAAASLRRLDFNMNVLM TVAVTGAALI
GEWGE GAVVAFLYSVSEALESYTI DRARQSI RSLMEI APGTATI RREDRE
VELPVEEV R PGDVLVVRPGEKI AMDGRVLSGRSAVDQAAI TGESVPVEKV
AGDEVFAGTLNQYGVLDVEVTKLVNDTTI ARI I NMVEEAQARRAPAQAFV
DRFAKY YTPVVI ALAAGI TVFPPLFLGQPWSPWVYRGLALLV VACPCALV
VSTPVAI VSAI GNAARNGVLI KGGVYLEEAGSLAAVALDKTGTLT TGTGA
VTDI I TVDDKMDERELLSLAASVEKMSEHPLAAAVVRKAGEAGLELAPVT
GFEALVGRGARADLGDREVI I GNPGLFKELRMDPASLAEDVQRLQSEGKT
AMLVGVDGRTAGVLAVADTMREAAGD TVREL RAMGI EKVI MLTGDNPAAA
ESI ARRTGVDEFMAELLPRDKVAAVQELRGKYGRVGMVGDGVNDAPALAA
ATVGI AMGGAGTDTALETADI VLMADDLSRLPFTI GLSRTALKVI KQNI A
FSVVI KLA AVL LVFPGWLT LWLAI LADMGASVLVT LNGI RLAGFNPGK

>2617921829 Ga0073689_1427 cadmium-sensing regulator, CadC [pelotomaculum Ga0073689 : Ga0073689_142]

LPAGRENDVCEVFCFDREKVDRLREKVGI TRGLSLLFKALADDTRVKI AY
ALSREELCVCDVAGI I GSNVATASHHLRLLRNMGLARQRKEGKFVYYS LA
DGH I GELI TLALRHVGEDKGELRKG

>2617921828 Ga0073689_1426 Pyridoxamine 5'-phosphate oxidase [pelotomaculum Ga0073689 : Ga0073689_142]

MSKI I GDTLPPEVVELFNKELTTVI VSTVTPEGFP HAMPVHLLVAPDGRT
VRMALVKAHQTTNI KDNGKSFI TVLDGPD LAVGI RGVARVVREPMEGNA
AMCMI EFNVEQVKS DTTPTVVVTEGVRTKHRSPKTAEFFRVMFDEMYKG

>2617921827 Ga0073689_1424 glutamate 2,3-aminomutase [pelotomaculum Ga0073689 : Ga0073689_142]

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MSIPI TERWRFSEEEKRTI ALMRAAELKKKI DDYLEEKDSI KTGF DLQDM
I GLNRI NLMAYFNATEENWNDWRWQI SHRI SDAAVLAELFGFNGRQCEQV
GKVGRRYRWAI SPYYASLMEWGADYDPI GLQSVSPFEEMDDSGHADPMAE
EFTSPAPCI TRRYPDRLI I NVTNKCAMYCRHCQRRRNI GDVDSHKPHQSL
VAALDYI RKHEEI RDVLI TGGDALLNDKKI DWLLGELDKI EHVEI KRLG
TRVI VTLPORI TPELCAVLKKHPPVYI NTQFNHPREI TPESKWACDMLI E
AGVVLGNQAVLLKGI NNHPHVMKKLNQALLKI RVRPYI FHAKAVKGTRH
FI TTVDEGMAI MEKLRGYTSGLAVPTYI I NAPNGYGKTPVLPSYVLGHED
GKVRRLRTWENRVLDSFLPGVE

>2617921826 Ga0073689_1423 possible tyrosine transporter P-protein (TC
2.A.45.2.1) [pelotomaculum Ga0073689 : Ga0073689_142]
MAWEYENI LNCSPSPYGRGLGETPRPSPVKEGTI ESI FKGGI KLQHET
QVI VATAVFLI TYAVI VSEKVHRTVAAFVGAALVVMLGI I KPEKAVHAI D
FNTI GLLVGMVVI VGI TRRTGVFEYLAVKAAKGSERGEPLKI I AALS LVTA
VLSALLDNVTTVLLI VPVTF AI AROLELSPI PFLI AEI I ASNI GGTATLI
GDPPNI MI GSATGLGFMDVFVNLTPVI VVVYVLT I FCI QLI YRKKLAAQP
ELQANI MQLNERDEI KDPVLLRKCLTVMSLVVLGFVLHQYVHLESSVI AL
SGASLLLLVTREDPEHALNVVEWPVI FFFI GLFVVVGAL EEVGVI EAVAK
WSLEVTGGNMAPTAMLI LWLSAI ASAFVDNI PFVATMI PLI QDMGR LGGI
ADLNLFWWSLSL GACLGNGTVI GASANVVVI GMAEKRGAI SFI GFMKI
AFPLMLMSI LVSTGYLLFWYYFHTMTAMAVTLGFGVLALLLRPVTRMLT
RESAPRAARENPA MDGTDVRNI

>2617921825 Ga0073689_1422 solute carrier family 13 (sodium-dependent
dicarboxylate transporter), member 2/3/5 [pelotomaculum Ga0073689 :
Ga0073689_142]
MSMEFKRVFFI LLGAALLFLFYLLPQFSPA I DPAGKVFELPKAGQSALGL
FLLAGI WWVFEVI PI GVTSLAI GLLQPLFGI RPAKEAFRDFMDPTVMFI L
GSLLVGLTFSKCGLTRKI AYKMLVI VGEDTRKI ALGCFI I TALLAHVMAH
TAVAA TMFPI LLAVMAL YGGERPTKFGKFLFI GMAYTAGAGSI ATMLGG
ARNPAAVGFFKEFTGGDI SFMQFSAHMLPLGWVCVFLFWAMLMI YRPEK
TKI PGLRETAGDLYKQLGPVTKQELFVMAVVALALLALI LQSAVPAMKTL
DRSVPMLAAGLLFFI TRI LTVQDLEKMLPWN I VLLFSGAMSI GFALWQTG
AAQWLAVSWLSMI QNAPWLLFVMGI AAMVAI MTNFI MNVAI AI VLPVAL
VI AQYLGVPNLLI VFSSVAAAGMPLLLLI GAAPNAI AYESKQFSTGEFFM
AGIPGTI LMLI VI AIFI YTYWPLI GLSPLI R

>2617921824 Ga0073689_1421 Transposase [pelotomaculum Ga0073689 : Ga0073689_142]
MASI I KKKFKGQVYVYAAKSKRVNGKPRI VWQYLGKVGDI VEAVSSANT
LPSPKSAKI YRFGAEAAALLEMAKRLGVKDI I NKHAGGLTDALELGEYI LI
YAI NCCI KPGARTPEWLAGAVLRRHLNI NPKLLTEKRYREVAGLLTKDVL
GKI QADLAGRI YNEFGI GTRCLI YHDI EPPGI PAARSPRSEKNFTRI GLL
VSSDFFI PLFYEI YQNGFDGLTSDEKYTCTLTERLRS LGRPENEI AVVKH
I CCAPGKI NNGOSGI SCHI LGTLPKEDNKDLLGI PLERFHALGTNRRNKV
MAYRCSKDI SGENTTVLVFSEKEMREQEALTFNLQKCI NELVELKTCF
QLRRNDEGGRKTNLSPVKKRVEE I LNKPLLKSMVDVSLACDKKGRVDLSY
VVKKNP LTPAQERDLGKRI I FATNNSWDNEDI YSAFTGKWI LEDALNAMK
KSDSRSFKTARGGEECLRLDV FCTVLGLSLLTLLQRELHRYGI TGSIPET
LQI LSGI REVAVI YTRDDQVRVKKKEYI TI TQLDQKQKEI FQRLRLDQYAA
GNRLYNTGKND

>2617921823 Ga0073689_14128 SOS-response transcriptional repressor, LexA
[pelotomaculum Ga0073689 : Ga0073689_141]
MSEDLTPKQVAI LAVI KKS I RQKGYPSPVREI GQAVGLSSSSTVHG YLKK
LEEKGYLRRDATKPRAMEVL DGLEGEKVDFVNVPLLGRVAAGLPLLAVEN
REGI FPLPTHFTNGE FFM LAVRGDSMI EAGI LNGDMVVVRRQNDANNGD
I

>2617921821 Ga0073689_14126 Uncharacterized protein, contains ferredoxin domain
[pelotomaculum Ga0073689 : Ga0073689_141]
LKDTMLLVAGLMELSARTAPKSLGQDFVRTKVVAGADLAVLADAMDRYGR
EKGAVNFD RDAENI RRS DALLLLALDKPTPAGLNCGACGQSRCADLKPVA
GPEFMGPLCAWRI LDLGI ALGSAAKTAGI LNADNRVMYRPGVVAKKI GLL
DGD LVVG I PLSASAKNI YFDRPEKK

>2617921820 Ga0073689_14125 S-layer homology domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_141]
LRRKWPGGFFLRNI I LVALMI SLLVPAWADAYQVTGKAGGEEI I TRGAVL

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QTI GMNTGEGPLNVYI LKVDLSDPYI KVDTI I GSDGT FNKNQSVLEMAKR
SGAVAAI NGDFFQMKDSGRPI GLAYKGGNLVSPALRNDMYGFGLTKDKT
PLLEI FQFSGQVVAGNGKTFPLSGI NKPAYLLMPDTSSDI DALTLYNSFW
GPVSRGKLPGLGVEAVVKNVVRQVLTQDQEVPI PPDGYVLMGHGEAA
KFI TENLPAGSKVSYTYAVTPOGDKLFAAVGGQALLVEEGHLPAYFTQNI
SGKHARTAAI SRDGKTLYLVAVEKQAAKDGAALSLGMSQEELAEFLI SI
GVWRVNLDDGGSTTLAARHQGYFDPSLI NRPOGGSQORSVPDAI GVFSTA
PRGNLKGVLVSGPSVLVAGMAGRFVKGAYDEYYNPI TVDSTKVSWSAAP
AVGEFKGGVLTPEKGGI VTVQAEEMGGAGGTATVKVVGLESLAGLLVNPAS
VTI KPGRSVQLTAQVKKEGETFDLAGQDVQWTVASLGRI MDGKFI AVN
NPASGEI KAAFQGLSATVPVTI KPSWSEI RLTPQEAEMLMDDRI KI RFP
AGSVTEPATI KSAYADNPADLPSCGLPLGAI DI GPTDGOAARPAVPWRLS
WQYGPDAVTSRPFALMMWDTALNNWRQLPTGI VEDGSAKAVSARVWDFGKI
VLVDDHRPAPSFKDTDGHWRWVI NLLAMRDVVKGYPDGTFGPDQGVTRA
QFVSLLAALRWPAPPEGGTAFKDNVPAWARPAVAAVSRGVI AGYPDGAF
KPDARI TRGEMAVMI NRALGLGESEAEELKYADAASI PGFARSAGVGTAA
GLMQDGGNFRPGDGATRAETAMAVYRVLNWWWK

>2617921819 Ga0073689_14124 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_141]
LKYCARRSFGALELVHERSNVKYYNQATEHLLPFTQRI TAGFWLNFLEQA
GVI PDSKLYFI SRTPVPTLLSSK

>2617921818 Ga0073689_14123 Endonuclease, Uma2 family (restriction endonuclease
fold) [pelotomaculum Ga0073689 : Ga0073689_141]
MPDLLQPVAFSMLDFPKRKFSYEDYKLDDDNKYELVEGELI VVPRPRPR
HQRVLNKL VYAFEGFLQKNPVGEFYTDLDVHLGDAVVAPDLLYI SKDRAQ
I VGEI NI QGAPDLVVEVLSPATAKYDKKEKGRLYFNCGVKEFWLVPEDR
LVEVYRAGETNWEWGVFDAEDI LTTPLLPGFQLVLENVLM

>2617921817 Ga0073689_14122 nitrogen regulatory protein P-II family
[pelotomaculum Ga0073689 : Ga0073689_141]
VKKI EAVI RPEKLEEVKDALGKYGI HGMTVSQVVGCGLQKGRVGVYRGHE
YSI NLLPKLKI EI VAKDHHVEDVVG I CKTARTGAI GDGKI FI FAVENAV
RI RTGESGDDAL

>2617921816 Ga0073689_14121 ammonium transporter (TC 1.A.11) [pelotomaculum
Ga0073689 : Ga0073689_141]
METGI QELASGI DTVWVLLCAALVFFMEGGFAFLEAGFI RAKNSMNI VMK
VFTDSTVGMLSYWAVGFI MYGLDRAGLFGATGFFI EGD LGHI QLRI PI Y
AYWLFQAAAFAMAMASI VSGAVAERMKFGPYI I Y TALATGLI YPVAGHWVW
GVDGWLGKMGMLDFAGSAVVHAVGGWSALA AVLVLGPRTGKY NEDGTMNV
LPAHNMHLAFLGTFI LWFGWFGFNP GSSLSGLDMNI ARI ALTTNLA AAAAG
GATGTLFTMF KYGKADPSMAMNGALAGLAAI TAGTAFVSPAAAVI I GGVA
GVLVVLAVGFFDRI KADDPVGA I AVHGVNGTWGALAVGLFAQKGGLFYGG
GTGLLAVQALGVL SVSVFAFGATYLVFSALKKTVGI RVSAREEFEGLDLN
EHGI PAYTGLVATPL YDVEENPAHALAGANARGTLHVTPQPVTTGGKR

>2617921815 Ga0073689_14120 ammonium transporter [pelotomaculum Ga0073689 :
Ga0073689_141]
MSRFLRTI STSFVFLMTLPALAWAGEAAEAAGPAI DTGDTSWVLASTALV
MLMTLPGLALFYGGLSRKKNVLSTI MYSF FAMVVI SI QWALAGYSLAFGP
DI SHVI GNLDWLGLNGVGQDPNPDYSATI PHQAFMI FQMMFAVI TPALI S
GAFAERMRFPAFLAFLVLWGTLYYDPVAHWVWGV DGLRN LGALDFAGGT
VVHI LSGVSGLVVALVI GKRGYGGEPMI PHNLPFTVLGAALLWFGWFGF
NAGSALGANGLAASAFM VTHLATAAAAFSWVVAEWVHHGKPTTLGAASGA
VAGLVAI TPAAGFVEPMPAI I I GLI AGVVCYLAVAVAKALGYDDALDAF
GVHGVGGTWGALATGLFATKAVNPAGNGLFYGNPEQMVAQLI GVAASWA
MAAVGT FVI LKVVNVFCKLRAADSEQEAGLDNTQHGEDAYS DVLVLAGSPL
GGGNPTAYAVGGA VKTAL

>2617921814 Ga0073689_14119 nitrogen regulatory protein P-II family
[pelotomaculum Ga0073689 : Ga0073689_141]
LTKI ECI LRPGKLEDVKDALNKFGI HGMTVTQVI GCGLQKGRKEVYRGTE
YSI NLLPKI KVEI VTKDKYVVDVVKI I RETARSGEI GDGKI FTYKI DNAV
RI RTGETGEDAI

>2617921813 Ga0073689_14118 Winged helix-turn-helix DNA-binding [pelotomaculum
Ga0073689 : Ga0073689_141]

Table S2

MQSLDNI DLAI LKMLQENALASYQDI ATRTCI SRVTVNERVRKLMESGVI

>2617921812 Ga0073689_14117 AsnC family protein [pelotomaculum Ga0073689 : Ga0073689_141]
LNTAQGSEAYRTI EELROLPEVEEI YVVTGRYDYLLKVRALDNEDLQRI L
FDKI DHVYGFERRAETMVLSSPVEKCGI DLGCVI GNI QGFPQG

>2617921811 Ga0073689_14116 Acetyltransferase (GNAT) family protein [pelotomaculum Ga0073689 : Ga0073689_141]
MLTI SKAGKEDI DQMCLLLWELFELEKDFTPDRDKQKKGLALI LDNPRYG
ALLLLKRDREVLGMANLLFTI STAMGTRVI LLEDFI I KKAERRKGLGRYF
I EGI KDLARKEGYGRI TLLADKDNRPAREFYNSLGFQI SNMDCWRYMMK

>2617921810 Ga0073689_14115 Putative restriction endonuclease [pelotomaculum Ga0073689 : Ga0073689_141]
MTPAPSAKHQRI VGELFRQI ANYLLNKPCEVFI APFDVRLPKGSEKEEDI
ETVVQPDIT I VCDQSKLDENGYKGSPPMI I EVI SPRTVKKDLKEKLYLYE
SVGVREYWI VHPI DKTVM I FKLESSPQAVVLAGEGMRAPMGYGYGYGK
PGI FTEEDSVKAGI FDDL I ELETVFKE

>2617921809 Ga0073689_14114 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_141]
LPRTQDEDEGKDGRLVVKI RLDFKGAGRPGRFLFGGKPTDKAAEEAREH
QVTI FRNVPI HGI QI MDI DVSTEVYTVYDEATNSETAYAPLVLT I KADCL
ENVI RLI SREDFRKI EVLDPAYI SLGHSDI ERLLFKVHDEI KEFKSRLER
KYNLK

>2617921808 Ga0073689_14113 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_141]
MSVRTPLEARLERI LI RLVAATAALVMI AQFLLADDPQKHTTGPARPYLK
NPERFPYSPVVT LQLKNYSSLPLAGVLVNGEPRGEFRDRYVTVYVREGDL
LEV DGV CYNRPLEI EVLDVSKEVI RPSAGTKLRVEGGI GVLGRVCLADR

>2617921807 Ga0073689_14112 HutP protein [pelotomaculum Ga0073689 : Ga0073689_141]
MI LYGSRKVARVAI EMALTESREQEKEYKLRFKGEI RTAAVDYGGDFI S
SVNKI I ERAVVASKREGVI REVHADEGAVAGATREALSQVI PKAI GFNVG
GKI GI ARKDDHI SVAVFFGVGLLHLDEVAVGLGHRAVQS

>2617921806 Ga0073689_14111 chorismate mutase [pelotomaculum Ga0073689 : Ga0073689_141]
MGNTVVIRGI RGAI TVERNTAEI VAATRELLEVI I RENDLDPENI ASAFF
TVTADLDAEFPAASAREMGWKYVPLLCTTEI NVPGRLDRCI RVLVHVNTE
KTQREL RHI YLGKAVQLRVDLLPQ

>2617921805 Ga0073689_14110 4Fe-4S di cluster domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_141]
MPRI LRADQMKKCI GYSCMLACARTVHRDFSPFKSAI QI RSVGGGLQSRL
VADI CRGCKEPPCAAACNCGALTTPRPGGVRFNKEKCLSCGKCVNACI I G
VLRFDREENRPI VCVQCGSCI RYCPHEVLSMEEAPSDV

>2617921804 Ga0073689_1419 Aldehyde ferredoxin oxidoreductase, N-terminal domain [pelotomaculum Ga0073689 : Ga0073689_141]
LFHSWVASAWQPGFFNEYI DYAKDALDPAQPVLSCGPLSTI FPMATKVL
AVFRSTLTGEWGESYAGMRLALAMRLSGYQAVVI RGRAGRPTFLAI GPNG
VQFKDASALWGLPADEAGRI LCQLVPGRGFRSCI RI GSAGERQVAFANVN
LGTYRHFGRGLGAVFSKLLKAVVI YGYRGEPI PNPKRYREVYERLYRA
AVQTDVMEKYHGLGTSVNVTTNLNGLALPTRNLKESAFENAAERRKKVSS
QG

>2617921803 Ga0073689_1418 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_141]
LDYTLI SSHMAFDI DEI VEMLEEYTD EYVLL EHYEDQLLDSSI I FLEDV
EVDYDPGEFGRFFKQKYLKDELEDEEFSYLLRNNFATGLFLNGSMYEI EV
QNARI VCLVGGRGELI LRTGSESYVFSPLFKLMI DPAKI PALLDI I GVL
RKNHVEMTEDKI NSETFSMI SGVCLMSMEKI NELPVNNYELNLSHDEMLL
FGLALNLASENDDEI KALTRSI MEQI KMYFPEI EHI SPESFEPpprmgq
LLDFKKPDQNGKKGGKED

Table S2

>2617921802 Ga0073689_1417 NAD⁺ synthase [pelotomaculum Ga0073689 : Ga0073689_141]

LEVRKRAEKI VKWLGVMLENAEARGFVVGLSGGI DSSVTAALCKRTCPDY
TQGVIMPCHSDPRDALDAQLVADAFNI PVEKVVLLDI FELFVQKLTGEKY
DKTQKDL SI ANI KPRLRMTTLYFFASRCKSLVVGTSNKSEFKVGYFTKYG
DGGVDLLPI ANLVKSEVRDLARYLGVPQRI I DKAPSAGLWAGHDDEVEMG
FTYDELDRCI LTGECSLRAKAI I EEMAKRSEHKKI LPLMPPV

>2617921801 Ga0073689_1416 DNA-binding regulatory protein, YebC/PmpR family [pelotomaculum Ga0073689 : Ga0073689_141]

MSGHSHKWTI KRKKAKVDAQRGKI FTRLAREI I VAARQGGGDLEGNMRLK
AAVQRAKEANI PNENI MRAI QKGTGELGGSNYEEVVYEGYGPGGVAVMLE
IMTDNRNRTAGEI RHI FSRNGGSLGESGVAMMFQEKGLI VVEREDNKVD
EDDLMLVALDSGADDFKTEDDSYEI TCVPGELQVRDALEQAGI RI ALAE
ATMVPOSTVNLEGKEAEQMMKLVDALDHDDVQNVYANFEI ND

>2617921800 Ga0073689_1415 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_141]

MLTGKDRLI TVFI I LLFVCTAAAGFLYSSGLLNPPERKPAAVFRPPGDYF
NPRVSAETMVI KYREYI CGDLEKVSEEMAPGELQCLDKKALAGRFPAAEG
WTVNFNGPGVLT I TGKSDEFCTVHRSYRHLGVYHGLVAI YEGPLGFNDQV
LRVESI PLES LDAEFKI KLEQAMDFDKMALPSAERLREELEFSSDEALNA
ALENLDENG

>2617921799 Ga0073689_1414 Holliday junction endonuclease RuvC [pelotomaculum Ga0073689 : Ga0073689_141]

LLIMGVDPGTAI TGFGLVKYSNRFSLVECGCI RTAPGVLLARRLQVLF
ELNDI I GRYKPEHFAVEELFFNKNTRTALAVGHARGVAI LTAANAGLPVF
EYTPLOVKQSVVGFGRAAKTQVQFMVKTI LALPVAPAPDDVADALAVAI C
HAHLYKWERMLK

>2617921798 Ga0073689_1413 Holliday junction DNA helicase subunit RuvA [pelotomaculum Ga0073689 : Ga0073689_141]

MI AFVKGNLADVRAGAVVI EAGGI GYKVQVPLSLLHSLPAKGGEVMLHTH
LAVREDAFTLYGFREPGELEDFI KLLSVSGVGPRVALAI LTI FPPGELGR
I I AGGDTASLTRAPGVGKKTAGRI I LELKDKVAAPVPEQENAGGRTEFDA
VEALEALGYSAREARKAVRDALKNSGEKPPVTELVKNALRLLARN

>2617921797 Ga0073689_1412 Holliday junction DNA helicase subunit RuvB [pelotomaculum Ga0073689 : Ga0073689_141]

MEDRLI AATVRPEDFENDLGLRPRRLEEYI GQDKVKETI AI FI QAALGRG
EALDHVLLFGPPGLGKTTLANI I ANEMGVNI RTTSGPAI ERTGDAAI LT
NLARGDI LFI DEVHRLSRTVEEVLYPAMEDFALDI VI GKGPGARSLRLDL
PRFTLVGATTRAGLLTSPLRDRFGVI SRLDYYQPEDLVQI I I RAARI LGV
EI TREGALEI AGRSRGTPRVANRLKRVRDYAQVRANGAI TLEVAVSALL
FLEVDPLGLDQTDNRNLLTI I QKFGGGPVGLDTLAAATSEPETVEDVYE
PYLI QLGMLARTPRGRVATPRAFHHLGLKVAGKEPEQETLW

>2617921796 Ga0073689_1411 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_141]

MRI ESLCI KNYKI FKDI FI KNI PNMVVYLNAMRDLFTRYVTYWHLI PGN

>2617921795 Ga0073689_14022 K⁺-transporting ATPase ATPase A chain [pelotomaculum Ga0073689 : Ga0073689_140]

MNQVDI LQLI LYLI LVI LLAVPLGSYAMVYQRETTLLDPLVPLERLI Y
RLAGVEAGREMNRQYAGALLAFNFLGMALLLLLQLVQALPFNPQGFGA
VKWDLAFNTAAGFMTNTNMQAYGGESTMSYFTQAGLTVQNFVSAATGMA
VVI ALVRGLARRTAQTI GNFWVDLTRSVLWI LLPI SLVGALVLVSQGV I Q
NLSPYFTVTTLEGARQTI AMGPVASQEI I KELGTNGGGFFNANSAHPFEN
PAPFTNLVEMLA I LVI PAGLTLTFGRMVGDARQGRAVLAAMLVLFVLM LG
SCYAAETTGNPQVAAAGVSGPSAMEGKEVRFGI ANSALFTTVTTAASCGA
VNNMHDSLTPGLGLAPLLQMLLGEVVLGGVGAGLYGMLAFVI VTVFI VGL
MVGRTPEYLGGKI ESREMKMATLAI LI PGVTI LALSALAASTGVRLLSSVA
NPGPHGLSEI LYAFASGTGNNGSAFAGLNANTVFYNLTVGLAMLI GRFGV
I LPMLAI AGSMAAKKTAPAGPGTFQTTGALFAGLLAGTALVVGALTFS
PALGPVVEHLQMLAGKAF

>2617921794 Ga0073689_14021 K⁺-transporting ATPase ATPase B chain [pelotomaculum Ga0073689 : Ga0073689_140]

Table S2

MSI RHKSTYAGRLEEKDAGLPVRLGGADEI KQKGGFDRPI LRQAVKDAF
VKLDPRTLWRSPVMFVVEI TAVLTTFI I RDAAAGRTAGLWFLNQI AVWL
WI TVLFANFAEALAEGRGKAQAVLRKTRSETMAKKLAGGRVERI AAPEL
RKGDVVLVEAGDVI PGDGEVVEGI ASVDES AVTGESAPVI RESGGDRSSV
TGGRMLSDWI KVRI TANPGETF LDKMI HLVEGARROKTPNEI ALNI LLL
GLSI VFLAAVATLEPFAYSGTTVSI LVLASLLVCLI PTTI GGLLSAI GI
AGMDRLLKRNVLAMSGRAVEAAGDVGVL LDKTGTI TLGNRMAVEFI PAP
GVGARTLADAAQLSSLADETPEGRSI VVLAKEKYGLREREMAGLQAGFVP
FSASTRMSGVDFAGREI RKGAVDAI EKHLMEKGGAI PAELRAAVEEI AKK
GGTPLVVAEGDQALGVI HLKDVVKGGI RDRFAQLRRMGI RTVMI TGDNPL
TAAAI AAAGVDDFLAEATPETKLLI REYQAGGRLVAMTGDGANDAPAL
AQSDVGVAMNSGTQVAKEAGNMVDLDSNPTKLI EVVEI GKQLLMTRGALT
TFSVANDVAKYFAI I PALFAATYPQLGVLNI MALATPQSAVLSAVI FNAL
I I VALVPLALRGVTYRPLGADAVLRRNLLI YGLGGLLAPFAGI KLI DMAL
AALGLA

>2617921793 Ga0073689_14020 K⁺-transporting ATPase ATPase C chain [pel otomacul um
Ga0073689 : Ga0073689_140]
MAKTLGGAFLLLI MTVLTGVL YPLAVTGLAQVI FPRQANGSVVYRDGAP
AGSALI GQNFSSPRYFHGRPSAAGPDGYDAAASAGSNLGPTNQKLLDSVA
ENAAKVVREENG LAPAAPLPADLI TASASGLDPHI TPASAYLQAPRVA KAR
QLPEDRVGAL VESHI EGRQLGLLGEPRVNVFLNLMALDEL R

>2617921792 Ga0073689_14019 CBS domain-containing protein [pel otomacul um
Ga0073689 : Ga0073689_140]
LNI AFFLLPKREV VYLSRSTMRQAMERMEHHRYTAVPLVDEEGRYSGTI
TEGDL LWKLNTPGFCLKDAEKI LLKDI PRHVKNQWVNI NTEI EDLI SLA
VKQNFVPVDDQEI F I GI VRRREI VEYCLRFF

>2617921791 Ga0073689_14018 two-component system, OmpR family, sensor histidine
kinase KdpD [pel otomacul um Ga0073689 : Ga0073689_140]
MEKDKRPDPDVLLAGI QREGRGKLT VFLGAAAGVGKTYAMLEYARERLAE
GVDVVAGWVETHGRAETEALLQGLHAVPPRRMVYRGKEFMEMDL DALLAR
KPELALVDELAHTNVP GSRHARRYQDVEELLAAGI SVYTTLNI QHLET LN
DVVAGI TGVTVRETV PDRFI EEASQI QLVDI PPEELI QRLKDGKVYVPGQ
AEEAMRRFFRPGNI NALRELALRYTAKRVD RQVESYMRQHGI AGPWPTGE
RVMVCVSPSPFSARLI RI ARMAEGLRSEWLAVYVDTPRRFPVREEEKDR
LARNLR LAEELGAETI NLSGNDVAEELLELAGKRNI SQI I I GKPLHSRLW
ELLHGSVVDKVI RQSHGI SVHVI PGEAKPARERRPAQRPPQRPAS PASL
FPYVWTLMMAGL TALAAALRDVLGLVNI AMLYLVPVLLSAVRWGTGTAV
AAALTGVAAFDFFLVPPVLSFTVADI RYVLT FVI FLAVAVFTGHL SRSR
RQVVHSRRREARVSALYSLSREI AAVAELEPV LQGI VKKVAATI EGQVVL
LLPEKGGKLALQASSETGENSFFNDNEYAVAAWVFERGLKAGRRTDTLGA
ASGLYLPLRTDNEI HGV LGLRSED PDTYFEPEQLRLLEAFAGLASVAVAR
VLLAERAREAQTLAESERLRTALFNSLSHDLRTPLASI I GAATG LLENDE
VYTPGARWELLOSI LQALRMSRFVHNLLDMARLEGLVQPKKDWCDI QD
I VGVAVGR LDESLKGRPLRI NI EPGLPLVRADFVLI EQVLVNLLDNALKY
SGPGAGI GI DARRRGGEME I SVSDHGQAI PAEDLERI FDKFYRLQSPRLV
SGTGLGLAI CKGFVEAHGGKI WAANNPAGGVMTFTLPLENDLPGAVAAA
GGGKENG E

>2617921790 Ga0073689_14017 two-component system, OmpR family, KDP operon
response regulator KdpE [pel otomacul um Ga0073689 : Ga0073689_140]
MESNGARI LVI DDESQI LKLLRVALTSHGYEVAEATGRQALAEAAVFRP
DMI I LDLGLPDM DGLEVI GRLREWTGAPI I I LSARERENDKI LALDAGAD
DYLTKPFGMGELLARI RAALRHAAGTADEPVLR LGLDVLVDLAHRRTAGE
GEVKLTPT EYELI KNLALHAGKVLTHRQLRAVWGPSCENDI HYLRVFI G
QLRRKI EADPSRPRHI I TEPGVGYRLF

>2617921789 Ga0073689_14016 cytochrome c-type biogenesis protein [pel otomacul um
Ga0073689 : Ga0073689_140]
LENPQTLNI FI AFAFGLLSFLSPCVLP LLLPGYLSCVAGFDQAKPGASLRS
RALRNGMGFV LGSLLFVAMGAAAGGFGQWLSAYREVL MRLAGGFI FI MG
LHI SEI LPI KLLFRQWRGKG TGSSTGLARSFLLGLSFAAGWTPCVGPVLA
SI LLMAGSTETAARGAVLLAFYAAGLALPFLLAALGI ESI HKWLGRARYI
LPYVNAVSGLLMAVGI LLLTGI WPRLARLFY

>2617921788 Ga0073689_14015 Peroxi redoxin [pel otomacul um Ga0073689 :
Ga0073689_140]

Table S2

MNPRI LAVLVAVVLLAGALWYAVAGGKTTGPDEKKEDAKMI AGEVMVTPP
PGSGRTVPPGRVPPEFLI SLDGRNLLLED FRGKYVFI NFWNSWCPPCREE
MPDLNRLYLDYRDKNVEFLFI NI TVQEKTPQVEEFMKDLHLQLPVYLDL
RGEVASTCGVRSI PSTLVLDPPGGKVYARPGPLTYEQAEKLVK

>2617921787 Ga0073689_14014 Thioredoxin domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_140]
VEDITKI AKASVLLPPGLI I NGKLKVS GKVPGKEEVKRYI AEER

>2617921786 Ga0073689_14013 transcriptional regulator, ArsR family
[pelotomaculum Ga0073689 : Ga0073689_140]
MNDKI TRTKAEI LKALAHPTRI NI LESLRGDERCVCEI I DEVNVEQSNVS
OHLAVLKKMGI VNRKDGRLVI YQVKHKEI FOI LSLLDSMMSSQMEETMA
MLDGLKQKRAGFR

>2617921785 Ga0073689_14012 two-component system, LytT family, sensor kinase
[pelotomaculum Ga0073689 : Ga0073689_140]
MRSLNGI TCGI LLRWGLPQLVTLVI LI NSSLWEI I FCMLI ANAI STFLV
VDYMQKHGKVKVKGDLHI DPTLQI ANETLPHLRRLNEETARKTAEI I R
KI SEVSAVAI TDRERVLAYLGE GSDHHKAGGPI I THATKQAVVTGELMI I
RDKKGLSCPKKDCPLQAAVI APLKCKGKVAGTVKLYQASQGDLPQSVI KL
AVAMAQLLGLQMLAE LDRQAQLVTKAELD ALHAQI NPHFLFNTLNTI I T
YSRTNPETARRLLI RLAVFFRHAFKRHGHFNTLREELEYVNTYLVLEKAR
FREKLRI KREI DPALLNYHVPVLTLOPLI ENAVKHGI QPKVGP GTVHI MA
RLFNKEI LFI I RDDGVGI SREKMSKVLFPFGSGNGVGLSNVHERLKSFL
GEDYGLRI VSEVDKGTSVYARVPLRMTTSEKGAAGEAQI VNSR

>2617921784 Ga0073689_14011 two component transcriptional regulator, LytTR
family [pelotomaculum Ga0073689 : Ga0073689_140]
VKLKSLI VDDDEYPARQELRFALGGFDDVEI VGEATNAKEALTLI KALDYQ
VLFLDI SMPGMSGLELGA AI QELPKKPHI I FI TAYDEYAVSAFEVNAV DY
I LKPVDPKRLRKAI DKVI KLTQEA AVSEVATCHDGR TAREVDPRAGQNVH
SOI KI DRI PAEKOGKTI LVTESDI FYAFI EQDYVYI KTFSDKLFTRTLK
ELEARNLPQMFFRTHRCYL VNLHKVKEI VPFFNGTYTLI VEDKERSEVPV
SRAQAKKLRI LGF

>2617921783 Ga0073689_14010 hol o-[acyl -carrier-protein] synthase [pelotomaculum
Ga0073689 : Ga0073689_140]
MFHDQQPAAGI I GI GADI I EI HRI KRAVERGGRRFLERVFTPAERDFCNA
RRDRYACYAARFAAKEAVLKAMGTGLSGCRWVDVEVARRGGGRPEI LLHG
TAAKLGRKGI ATVLI SLSHGLEHAVAFAVAAGEEV

>2617921782 Ga0073689_1409 NAD(P)H-hydrate epimerase [pelotomaculum Ga0073689 :
Ga0073689_140]
MRVVTAKEMKVLDRAMEEYGI ASI VLMENAGRQVVEVI RGVLEVRVDKV
I TI FI GKGNNGDGLVI ARHLLNMGA EVKVLALADVAE I TGDAAVNLEI W
OKMGQKI YSLHSDGI NVVRLALMNTDLI VDAI YGTGFRGKMGEKVGR I V
EVLNGSGKPI VAVDI PSGLEADTGRVNGPCI QAAHTVT FGLPKLGLI LEP
GVDYAGQLHVADI SI PAVLVERSAPRRYLLTRELVKEWLP SRPTNAHKGN
FGRVLV VAGSRGMTGAACLAGEGALKAGAGLVTVAA PETLNDI MEAKLTE
VI TVPLPDTGMGVLSRGAKQHI LSLLEGTDVLAVGPGLSTVPEVATMVRE
LLSSVRVPCVLDADALNALAGAGDI LRKVQAPVVI TPHPGEMARLLGVTA
KEI QGDRLTYAVKAANI WNVVALLKGARTVVAAPDGAVYI NPTGNPGMAT
GGSGDVL TGMVAALI AOGLEPARAAAAGAFI HGLAGDLAAGEKGMGLVA
GDVLSALPAATRELTLYP

>2617921781 Ga0073689_1408 alanine racemase (EC 5.1.1.1) [pelotomaculum
Ga0073689 : Ga0073689_140]
VSAYPVWAEI DLGAI AHNVKEI RRVAVPTAKVMAVVKANGYGHGAVEVSR
TALANGAEWLGVARVAEGVALREAGI EAQVLI LGYI HPEQFGEAVRHRLS
QTVYTRDMARALADA AVREGVLARVHFKVDTGMGRI GWPAGPGVVREI LE
LARLPHLKVEGI FTHFAAADVADKTYTLEQFHKFM EVVDEL RKNGLFPL
RHAANSAAVMELPETHLDLVRAGI I I YGLYPSDEVDRGRI DL RPAMSLKA
RVAYVKKALAGCKVSYGCTFTTGRPTVI ATLPLGYADGYSRLLSSKGEAL
LHGRRAPVVGRCMDQVMVDAGHI PGVRVGDDAVLI GRQGDEEI SADEVA
SKLGTI NYEVT CMI SHRVPVYI

>2617921780 Ga0073689_1407 phospholipase C [pelotomaculum Ga0073689 :
Ga0073689_140]

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MGPASWNAVKYLLAAGTPI QRI VSGKGETHLFCNRQAVKI LKKDGKI AYA
HLFNYYLEVI NRGVLWADKGWKNFAHYFDPVDGQGLGPWPDARLECRYLF
EKALKYWRRGNGKKSSFFFLGAAHLVQDLCVPHHAKGI AFCGHQEYENWV
RENCDFDSVDLTGQYNMASHPGEWVEANAKVARFYFPYVSDVSSLT SYRM
ATGVLLPLAQRSTAGFFAFFLDYVNTQTLAQR

>2617921779 Ga0073689_1406 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_140]
MRFQI SVNQLFAPSLLGACATSTTG YRCI PSDI I I RI I RQEKQVFSWGT
P

>2617921778 Ga0073689_1405 8-amino-7-oxononanoate synthase [pelotomaculum
Ga0073689 : Ga0073689_140]
LFSSNNYLG LATHPRVKAAA I AAVKI WGTGSGGSRLTTGNFNLHRQLEKR
I ARFKRSEDAI I FNTGYMANLGVI SALVGRKDLVI SDQLNHVSI VDGCR
SRAMVRI YNHNDTLDLDR I LLERTSFSRCLI VTDGVFSMDGDI APLPQLF
ELAQEHQAI LMVDDAHATGV LGDRGAGTVEYFGLEKQGI I QMGTL SKALG
SEGGYVAGSTSLI DFLRNRRARSI YSTALSPPIV AAALAALDVLEEEPHL
RWQLHANVQFLYRGLKDMGFVLPTRSAI I PLI VGDHAKAMVLSATLAEI
GVFI PAI RPPTVPEGTSRLRI TLMATHTRDHI QFALDAFQKAGKKLGLF

>2617921777 Ga0073689_1404 sporulation protein YunB [pelotomaculum Ga0073689 :
Ga0073689_140]
LFKKRRRFKPYLPLVTFSLI LFGI FLLI DLTLRI VFFNI AEVRAI QLATD
AVHRA LQQEVADGNLQYQDFI SI HKDSQGHVALMQANTVKVNKVAADTTM
AVQKTMEELKWQSF SI PMGQVLGI PLLANYGPKVSYHI LPVGTVRVNVVD
KFESAGI NQTRHMI YLNFDTNVRI VI PSKSGEAVVATQVPLAESI I VGVV
PNTFI TLS DGI LRSGLTK

>2617921776 Ga0073689_1403 tyrosyl-tRNA synthetase [pelotomaculum Ga0073689 :
Ga0073689_140]
VLTLDKQLET I KRGAVEI VPENELVDKLR SI ESGRPLTI KLGLDPTAPD
I HLGHTVV LQKMRQFQDL SHQVLI LGDFTARI GDPTGKSETRKQLTEEQ
VLANARTYERQI FKI LDRERTRVFN SHWLAPLTFAQVI ELAAKYTVARM
LERDDFAKRFKECLPI SI HEFFYPLVOGYDSVALKADVELGGTDQRFNLL
MGR TLQKEYGQEPQVALMMP I LEGLDGVHKMSKSLGNYI GVDDPPREMYG
KTMSLSDELMI RYFELVTAAPFEEI RAI ETGLKSGAMHPRDVKMRLAREI
VTQYHGPGAARTAE EEFKKI FOQKDLPEI PDFYLSPDML EDGAI WLPRL
LVS AKMAGGTSEARRLI QQGGVKVNGEKLDDPGFNI KPASGMI I QVGKRK
FTRI I F

>2617921775 Ga0073689_1402 D-amino peptidase [pelotomaculum Ga0073689 :
Ga0073689_140]
MVEKAFTI FI AADI EGI TGYVNWPEKPPEETWSREQMTAEVNAAI KGALK
SGAKSVI VSDI HWRKQNI MPDKLLGGASLI RGTKRTRMMWDCVERS DLFV
LVGFHAGCGVAGAVLSHTMDTRI TRLRI NSSEANEAFI SAAAAGYGVVPV
GLATGDRALI DEVKKFLPDI ETVAVKEGMGNCAALNLHPEAALERI EQVA
EKA AKKGLEGGFKPFSVN EPVEMALEVCWPGYADALCLI PGVKRLSSREV
AYTGDWPGAFGI LSLFVNWVSNLPGI F

>2617921774 Ga0073689_1401 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_140]
TELGS DYFSKQI NKKLERRLI RRLEELGYKVTLEI VNPSA

>2617921773 Ga0073689_13934 Penicillin-binding protein 5, C-terminal domain
[pelotomaculum Ga0073689 : Ga0073689_139]
TGGTAPAVEAERDLEVR LDPDDL PKLEKRV DVEGTVAAPVKKGRKLGR
AVYVLRGQELGRVDLVAGADVL RKGWSRQLW DKVFD

>2617921771 Ga0073689_13932 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_139]
MSI ML SRKNFPEKPD AQI KI NI SKLANELEI LI EKEVLLDKDAEKI LRHA
CNI YVESLFDKFVSNKFKKI VSI Q

>2617921770 Ga0073689_13931 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_139]
MKEAAVLMKPVGVMMDSVRKMVKLSMPEDLSEEEKPEKKSQAVI LLDLA
SRATLLHDDLQEPFACFEVQHFEI RPMKSKFFRRWLR YQYFRETGKSPN
NEAVSQALGVLEGRGPPCLTCTL

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>2617921769 Ga0073689_13930 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_139]
MSAYEQI QSTAENAI QELETEI I DLEEKI EAHKLRI QYAQVQI QSLKRFL
YPEESSFDTPKTTROAKKNGKVHVVEVDSGREMI S

>2617921768 Ga0073689_13929 LexA DNA binding domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_139]
MTDRQWEI YEDVRDYTRTGGYPPTI REI EEMVGLSSSSTVYDHLKKI KSK
GYI TFEPGCPHALRVVK

>2617921767 Ga0073689_13928 LexA DNA binding domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_139]
MVGPFVKHTRLSKQI LLDAL KQYTERHGYSPIT RELAEI TGAGAGTVHKH
LNELI YGGYVKVEQPQRRVFRVVKDYD

>2617921766 Ga0073689_13927 cation: H⁺ antiporter [pelotomaculum Ga0073689 : Ga0073689_139]
MTMGVI MLI AGLLAI LAGAKI FTNGVEWL GKRLNLSEGA VGSVLAAVGTAL
LPETMVPLI AI LFAPTGNAHEVGI GAI LGAPFMLSTLAFGVVGVS KMVYC
RGE GGC I DVKRSI LARDLKYFLGFYSLALAASFI PSHALKAPVALALVA
GYGYYVKKTLGDGDNLAEMDLPPLYLWRKASPAPVPVI LGQI GLSLVLI A
VGAHYFVDALGSLATAVMVPALI LSLI I TPVATELPEKFNSVI WVKGGKD
TLAMGNI TGAMVFQSTI I PAI GI LLTPWSLSFLAAASAGLALLSSLI VYF
FAMKQKKLKAGVMFYPAAI YGLFLLLV I SML

>2617921765 Ga0073689_13926 putative sporulation protein YtxC [pelotomaculum Ga0073689 : Ga0073689_139]
VAQI I SI GATRHI DLLKARLGRELKVFEGDGLNVDLEESPSGKFTFLACH
VAGNGECSYTEGDTRVI FKRFLAEI I SDI I LNHWEDNLI RDI I RENYFYF
GNEEKKLI YDYVLRHI NREDGDCRNTI YQLSRKSRI LQKVLEYLRHNDI
I I DGFI RFRLKEYI SELREAADRAVDLMDREYREFI QLLKYFVEI QEP
GI EAVHVL I KAGGNFKLFDKKMQPVKSDYLEGFI I DLADSEI NYEDLLI S
ALI TMAPKNI TLHCTSGAGPGAMLETI RNVFDGRVKECPGCDLCVASLKV

>2617921764 Ga0073689_13924 threonyl -tRNA synthetase [pelotomaculum Ga0073689 : Ga0073689_139]
MSGNNNI TVTLPDGSAREYPAGI TI LDI AKSI SPSLTKMALAAKVDDKLE
DLGRPLERDAAVLF LTFDDEEGR LVYRHSTAHVMAQAVQRLFPGVKLAI G
PSI ADGFYYDFDTPPEPFTPEDLAKI EKEMEKI I KADLPFERFEPARAEAL
ERFGKAGQDYKVELI EDLP PGTP LSCYRQGEFTDLCMGPHVPSTGR LKAV
KLMSLAGAYWRGSEKNMLQRI YGTSF PKKSMLDEYLFRL EEA KRDRHK
LGAELDLFSI HDEGP GF PFFHPKGMVLRNELEKFWREEHKKRGYQEI HTP
VI LSRALWEQSGHWEHYRENMYFTKI DEG DYAVKPMNCPGGI LVYKSRLH
SYRDLPI RLAE LGLVHRHEL SGALHGLMRVRCFTQDDAHI FMLPSQVKEE
I I GVI GMVDDFYKVF GFFPYHVELSTRPEKAMGPDEI WELATGALRDALEA
GGLEYKVNEDGAFYGPKI DFHLED SLCRTWQCGTI QLDFLMPEKFDLTY
VGEDGRKHRPVI HRVI FGSI ERFI GI L TEHFAGAFPAWLAPVQARVLP I
TDRHAEYARRVVD SLDEKGI RVELDARNEKI GYKI REAQRKI PYMLVTG
DKEAENGAVAVRQRTKGDLGAMPPDEFAEMLLEE I RMKAY

>2617921763 Ga0073689_13923 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_139]
MLRYDI FYNKI NYEPAHNI LGESDQTVVVI LAGTYENFYEELKWI I KRL

>2617921762 Ga0073689_13922 RNase HII [pelotomaculum Ga0073689 : Ga0073689_139]
LDLSSLSVAEVKKLACGPGGVAEELLAMADDPRAGVREI HRRLRRAEAA
LEAERKRLAKMFI YEEDLWARGHTTVAGVDEAGRGPLAGPVVAAAVI LPG
KVPLLDLKD SKKLTAVRREALAGQI KEVALAWAVGMSTVEEI YNENI HRA
GLLAMRRRAVLGLKKRPACVLVDGFRI HGLDLPQKTLVGGDGLSGSI AAAS
I LAKVTRDHLMDSYHELYPEYGFNRHKG YGTPEHMRALASFGPCPI HRAG
FQPVKGLLEAPSGADGDRLTSS

>2617921761 Ga0073689_13921 NADH-quinone oxidoreductase subunit A [pelotomaculum Ga0073689 : Ga0073689_139]
MLSDWGA VI I FLI VGI LFGVGGI VTSFLI HPRRKTVQKATTYECGMDTI G
PTWI QFRTSYFLYALLFI FVETI YLFPWAVKFKSLGLFAFI EMI I FLF
I LVVGLWYAWKEGALEWK

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>2617921760 Ga0073689_13920 NADH-quinone oxidoreductase subunit B [pelotomaculum Ga0073689 : Ga0073689_139]
 MEVTENPHPI EDMTNDLAI I DQVKHLVYFAPLEKLLNI GRAHSLWPLGFG
 LACCAI EGLMAPMMPRFDQARFGYEAIRNSPRQSDVMVAGTVTHKAAPF
 VVRLYEOMSEPKWVMAVGSCAI SGGPFVDSYHVVPGVDKLI PVDVFVPGC
 PPRPEAVLEAWLMI KQKI LTPKVVSQIRG

>2617921759 Ga0073689_13919 NADH-quinone oxidoreductase subunit C [pelotomaculum Ga0073689 : Ga0073689_139]
 VADCKVPTTEI EALQSKFSGMEVLENQSI I I PADNLI TFMTELKENLDFA
 MDYLTNLTAVDYQDRFEAVYNLVSITHGTYTLMVKVRI SDKEKPEVPSLCP
 LWKGANWQEREI YDLMI VFTGYPGHPTRI LLDECFKGHPLRKDFEWEGG
 REA

>2617921758 Ga0073689_13918 NADH-quinone oxidoreductase subunit D [pelotomaculum Ga0073689 : Ga0073689_139]
 MKTQTYSLNLGPQHPSTHGVRFI VLELDGEVVVKA EAVPGYLHRGI EKLA
 EARTYTQVI PYTDRMDYLASMLMNWGYVQTVKLMGI EVPERAEYI RVI V
 GELSR I ASHMMAI GAYGGDLGALTAFTYTFRDREYI LDLLEMVSGSRLTF
 SFFRI GGVADDFPEEFYPAI KKFLAELPGMCDEYDGLI TGNEI FQARTKH
 VGI I TPEMGI NYSLSGPTLRGSGVNYDLRKVRPYSVYDRDFDI PLGKNG
 DCFDRFRLRVEEI ROCKRI I EQALEQI PEGPI LAKVPKVI KPPAGDAYAE
 VESSKGVYGCYVSDGSPKPYRVHFRPSFI NLGYLEKLCEGWKI ADVI A
 I LGSIDI VLGDVDC

>2617921757 Ga0073689_13917 NADH dehydrogenase subunit H (EC 1.6.5.3)
 [pelotomaculum Ga0073689 : Ga0073689_139]
 MGENI FTNLAGLLRSI DAAGVPSLLNDI TLMI VKMLAI LLFI LVNAMYL
 VYMERRI SAVI QSRLGPNRVGPQGLLQPFADMLKMLGKEI PLPRNI DLVV
 FLLMPMI AFAPPFLI YAVLPFGENMVAI DMNI GLFYLVAVASLSTI I LWA
 AGWASNNKYSLVGGMRVAQMVSVELPLALSLLGVMI TGTMMNNEI VNA
 QKHVWFI FTQPLAFI YLI AGI AETNRTPFCLVEGESEI I AGPFTEYGG
 GWGTFAI AEYASVMVSSSLCTVMFLGGWLAPFGWTFI PSWLWFFLKMYVM
 I FI FMVVRWTPRI RVDQLMGFGWKVLVPLTLANI FI TGVGMYI YRAI GW

>2617921756 Ga0073689_13916 NADH-quinone oxidoreductase subunit I [pelotomaculum Ga0073689 : Ga0073689_139]
 MFGQGLLKGLQI TWKRMLGKKQTVQYPDEKLEMFPRYHGRFQLDVKCI A
 CGMCANACPKNVI QMEKKKVGNGKQYLTKYVMRI EYCLFCGLCVESCPKDA
 I RFSNVFDMNQYRRDWRLTLVDRPAPEAI EEPSEAPMAAARVPGAEEK
 AKAEAAAAAAKPEAKDKPKPNKDKSGNGKAKGTEG

>2617921755 Ga0073689_13915 NADH-quinone oxidoreductase subunit J [pelotomaculum Ga0073689 : Ga0073689_139]
 MDSI FSI AI FYVLA AVI LGSAT LVVTLKNLVHCVLWLVASF I AI AGLYMM
 LNADFLAMVQI LVYAGAVCI MVVFAI MLTQRDMGHNSLNTQFKAAGLV
 ALLTALVSGFMGVRTAWTVSGASAPPKTVEAI AELLTKYVI PFEVAALL
 LLVALI GAI I LAKEVQSDESA

>2617921754 Ga0073689_13914 NADH dehydrogenase subunit K (EC 1.6.5.3)
 [pelotomaculum Ga0073689 : Ga0073689_139]
 MNLP SLAI GI PHFVVLSSLLFGI GLFGALAKRNAVMVLI CI ELMLNAVNI
 NLI AFSKFVTPLAFI GQVWAVFI TVAAAEVGVGLAI I I TI YRNKLSVEL
 DDFDWLKW

>2617921753 Ga0073689_13913 NADH-quinone oxidoreductase subunit L [pelotomaculum Ga0073689 : Ga0073689_139]
 MVEFAMHNAWLVP LLPALSFVI I VFLTRQFKLLSGLVCVAGMVSAFVI AA
 FATYGVFTNHEFI EKPLEYGVWRFTLGNGLSI DVGVR LDPVSAMMMFMVS
 LVSSLI FI YALGYMEGEFGFSAFFAYLSLFGASMLLLVI SSNLLFMFVAV
 ELVGLCSYLLI GFYNH KI SAREAAKAFVTCRI ADFGLLLGLLSLMI VFG
 TLNI GELSEKI HHFEQYTNMAVLTVI AVLVLGPVGKSGQFPLHVLPDA
 MEGPTPVSAI HAATMVVAGVYLVGRTLFLFEAVPAAAYLVAI TGAFTAI
 FAASI ALTQRNLKRI LAYSTVSQ LGYMM LALGVMSLTASMFHLWTHAFFK
 ALMFLCAGSVMHGI ASHDDPDAFECGGLRKKMPI TATTFAI GGLAI AGI P
 PFAGFWSKDEI LAATFSSGHYVLFAMATI TAFMTAFYMWRI FLVFWRDE
 NPKI HAHESPWMTVPLMI LAVLATVGGVGTWPANFWGEWI VFGHPHGG
 EPNYTMGVSVVLAVAGI SLAYNNYVRNI DNARKLAERFRGI HTLLYNKY
 YVDEI YLWFNHTFI DGAAKLI YLFDI YI V DGI I VNGI GALTRESGSGRL

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FQTGRLQNYALI FFLGLVLAVAVI LALTGGPSSASLLGGGVK

>2617921752 Ga0073689_13912 NADH-quinone oxidoreductase subunit M [pelotomaculum Ga0073689 : Ga0073689_139]

MDFPI LMTI LLSPVVGCI FLLFI PKDEHKLI KSVGAVFLGI PFLLTLYAY
FSYDQSI GGLQFVERYPI QDLGVTFLGVDGI SLPMLLLVTVI GFTAVF
ASWNI GDRPREFMI LFMLLDGVI GTFVAQDLFI FLLFYEVVVI PI YI LV
I I WGSSKRVTKEYAGMKLTI YLLI GSAFLLVGVI AVFVRSVAI TGVPDFS
FTGLARVPFPADFQI VMFALMLFGFGSLLSMWPFHSWSPDGYAGAPTAVS
MI HAGVLKKI GGYGLI KI AVYTLPI GAKFWAPVI AVLGVAGVAYAAI AAL
AQKDLKYVVGYSVSHMGYVLLGI ASLNVI GI NGAVANMFHGHVMAALFF
STI GFI YEKSHTRWI PDFGGLI QQVPRLGVAFMLAGLASLGLPGLVSFI P
EFTI FVGAFKVYGLLAI LAI AGI I I TALYI LRAAANTLFGPRKPEWDHLT
DI KGAEMVPLVVLGTLVLFGLPSLLMDMI NSGVAPMMAEI GDALQI GG
KF

>2617921751 Ga0073689_13911 NADH dehydrogenase subunit N (EC 1.6.5.3) [pelotomaculum Ga0073689 : Ga0073689_139]

MGI DLSLI SLEMATAAVGLGLLI LGLI VPHKGRTGFAYLTVFCLMGLLGL
SFSLWNNQGTLYDGI YI VDRFSI FFKQI FLVAAI LVALGSVRYVDEMGAQ
AEYYGMMVFATLGMMVMASAGDFLTLYLGLLEMTI SFI I LVCYKKTDSKS
VEAGI KYVLLAGLSSAVLLFGLSLVYGLTGTATI LEVTEALLAPGAFTPA
LALGLVMLVAGLGFKI SAVPFHMSWDI YEGAPTPVTAFLAVGSKAASFA
I VLRLFAASFAGI WEHWTMLI AI LAAVTI I VGNLVAI PQTNLKRMLAYSS
VAQAGYI LVGLVTASPAI KGVMFYAFLYVFATVGAFTVASHFYTVTGSD
EI KDYAGLSQRSPLMAAVLVVAMLSMAGI PPLAGFAGKFLYFMTI VEDYL
WLAFI GLI MSMVSYYYLRVALVMYRDMPADPAPI NVPGSAVATLI LAMV
FTLLI GI YPGPVAKI TNAQAQSFMLH

>2617921750 Ga0073689_13910 putative endonuclease [pelotomaculum Ga0073689 : Ga0073689_139]

MTI QRKMLGRLGEEAAARYLEKSGYRLLDRNYTCRLGEI DMVALDRDVLV
FVEVRSRSGDAYGLAQESVTGRKQYKLKQLAWHYLKAAGKTGRSCRFDVI
AVLFDREGGVKRLHI ENAF

>2617921749 Ga0073689_1399 Peptidase S24-like [pelotomaculum Ga0073689 : Ga0073689_139]

MAFDKKI FSQLLARAKGDRSI NSFGNLAKVDPGYI SRLLRQKI ETPPGPG
VI RKLAEHALI GVTYEDLMAAGYI HEPLGKDI YCVKSALEQKVAEALQK
PLAEFLPLKSI PVVNPSI LDFDGLKTVDVDYI NVPRELEADFAI TVKDN
AMI DAGI FPGDVAVCRKKVRALPGDMVI ARLESGNAGI RYLLGGNGSFRL
KAANDLI PEQKI KSTDI I GTVLM I QKKALRYEQFEALREKDRRDEVI AED
FLLEKLAESSGLPLDRLRKWLYSLKRK

>2617921748 Ga0073689_1398 Helix-turn-helix domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_139]

LEVNI EALKSLANGKWSTPELARRLGVDYSYLSRI I NGKKKGSKLFAI
I YKLCNEEGLDFEELI FLTAPLSVCNEGRKY

>2617921747 Ga0073689_1397 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_139]

MSMVGKSRCTGSYFCPPKSVPPGMEDLYLFFRGVI SWFI LRLPLGKLRK
AEEERI ERATNWGRW

>2617921746 Ga0073689_1396 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_139]

LKGRQTGVGGKSLRELRAAKLNLT I TGSVKLLLRKI EYQPGSLSSPDS
TDTRTVQSRSESSSFPVKNRHGTAGI PACFNSQNPWSLFI Y

>2617921745 Ga0073689_1395 carboxylesterase [pelotomaculum Ga0073689 : Ga0073689_139]

MKEVKPFYFSGGKTGCLLI HGFTGTAPAEMLPLGRYLAGRGMTVMGVRLAG
HGARPGLRGVSHRDWVGSATAGLAELKKKCSSVYVI GLSMGGTI AFHLA
ANYRVDGAVSI CAPVYLDLKLCLARPLRYLFGFKGEVERNI KDPEARKNH
LAYPAVPPGALLQLFALLRAARGELGRI TVPVLLFQARDDCI VTTGNAPF
I YNHLVNSPGKELI WLERSGHMATI DYDREI VFAETYRFVDGGD

>2617921744 Ga0073689_1394 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_139]

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VFVDI RDLKKGVLGGI RQKALRVAGGSGEEGAERLTRI LMYAALTGGI I
AI NYLAARYGDLEALGRALLSF

>2617921743 Ga0073689_1393 Nucleotide-binding universal stress protein, UspA family [pelotomaculum Ga0073689 : Ga0073689_139]

MFKKVLVAVDGSENSLRRAKYAAALAEANSLQI TI I HVGPNCA DI FKTP
GVCAMPEQELEKYVQI YMDEI KGKI LPVFEEAGLKPEFAGLTGDPAGTI
CQYAREGGYDHVI I GSRGFGTI KGLALGSVSHKVI QLCPVNLI VI K

>2617921742 Ga0073689_1392 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_139]

MSRSRDKETAPEVVETGLDLETGLDLLEVLHCSYAAVAVGALVI MLGVL

>2617921741 Ga0073689_1391 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_139]

MASWKKI HEWFVRAL EEPFYRAEI HRVDMYLPEGDNPLQLI DRGVKTRP
DKSPVKI KRARGSTART

>2617921740 Ga0073689_13831 Transposase [pelotomaculum Ga0073689 : Ga0073689_138]

MKRKRYPKNFKEQLI VEAQEVGNTLSVARRHGVSPKTL YR

>2617921739 Ga0073689_13830 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_138]

LLGLI RGHWSI ENSHYVRDVAFGEDRSQI KTGSAPRVFATMRNLAI AI L
RLNGVKNI AKELRNLI RKSGQVAELI GI

>2617921738 Ga0073689_13829 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_138]

MLWGKYYYSDASLDKFFDNI I TAPTVTSKSF SKKI KVSNRWN

>2617921737 Ga0073689_13828 C0 dehydrogenase maturation factor [pelotomaculum Ga0073689 : Ga0073689_138]

MFKRRVI AVCGKGGSGKTTLV ALMAKI LI EDKNKKI LLI DADPTAGLLYA
LDVKPKKT VGEVREELI RTARQVRNOAEKFR LADSVDYLLMDAI I EYNSF
DLLAI GRQDGP GCFCSVNELLKQVMESI AENYDLI I I DGEAGI EQI NRQV
I QNVDTCI I VTDPTLRGFETAKLI EEI I ESMMRSTKPYLLI NKLPKGDQN
SVNRAKKMNI ELLGCLEEDDKI SEYDSLGRPLVELPSSSI VFSVRDI LEK
I FEGNNNVMG

>2617921736 Ga0073689_13827 C0 dehydrogenase/acetyl-CoA synthase complex beta subunit [pelotomaculum Ga0073689 : Ga0073689_138]

MECC EELLGCLRQYVD TMEI QGQLRKI QCLPNGKTGSSETSSGPDNQVD
SGVV LLENMAVELGNPKCGSSSFLLWSTNSDLI NDDQI TFI GPDI I EVVG
QSLPFGQVLLI GSTGLEKDHVI EVARVQRLSHNLKGYMVRSTPRYLWSRI
SKHAVEKGFSFKTLGQALI LASKMKVSMNLCTEVI FI TSSKEDI I QLDVI
GSKAREKLMKLKSMI TNFDECI GKDCNDCTEKPTCDNI REI KNLRRERI
FNRLA

>2617921735 Ga0073689_13826 CoA-substrate-specific enzyme activase, putative [pelotomaculum Ga0073689 : Ga0073689_138]

LKTAGCDVGSTTGKAVI LQDGNL LSSVI I PCTPNPVKTATLVMNNAI QI A
GLSSMEEI DYI VGTGYGRLKI PFANENI SEI TCHGI GAHWLSPDI RTVI D
I GGQDCKVI GLNDEGRI I NFI MNDKCAAGTGRFLEAMCRVLQLTLEGLSA
TSLESEEP AQI TSQCSVFTESEVI TLLNDGREVS DVVAGI HQAI AGRLLS
LVRKVGQREKI TVSGGCAKNTGLI KI LEVKLGSRMQPLSYDPQFLGALGA
AVLASNKVNI EE

>2617921734 Ga0073689_13825 Benzoyl-CoA reductase/2-hydroxyglutaryl-CoA dehydratase subunit, BcrC/BadD/HgdB [pelotomaculum Ga0073689 : Ga0073689_138]

MLEI KPFNSKEMEGVI TALRSI PEVLAAI PTERPTI AATEAFADYFASI L
KAHEEGKPI CYNQFCFYPI MYAFDI QPLCPEAWTI VPLL VMPDLAQKHL
DAAMDAGVHAELCAADRAI VGELLTGNAPAPSF I VTSSQPCDNTRMGNSL
VNHI TKAPLFLADAQYWETEDCI TY YENQI RQLI TFFEQQTGKKLDWDF
REVI KESNRSI EYVLELNL RKMVPCPSDGKVPTYVFLGNMALLGHPSLT
TMYKVFRDDAQERASQNLGVVPKEKI RAI WFYTIM AWDLMWQNW LQOQELG
HI NVMDMFGYLT CRPI DI STPDKMI RDLAERNYLT I PMGRQGRGLTDI YI
DDL FYVYEEWKADCVVL AGHDGCKWLKNASGMVREMCREKEI PLLFFD VD
I MDPRPVSKETYRAQVEDYFATVVEPSLVNKKL

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>2617921733 Ga0073689_13824 Benzoyl-CoA reductase/2-hydroxyglutaryl-CoA dehydratase subunit, BcrC/BadD/HgdB [pelotomaculum Ga0073689 : Ga0073689_138]
 MSVLEKLLPESGTLI NSAI ENWLKKGKKVI GYCPYVPEEI FIAAGMLPF
 AMRATGSTSTELGDI YCHSGTCSYLRHI DLSMRGSYNFLDGFVAI SCCD
 HFRRSFDVWRYKFI PVPYKELFLQI LSI PYKI DSLALDRVKDELI KLRNN
 LEDYFKVKVSDDDLRAAI KLCNKTRRLRELYELRKRPDPVSGEETLSI
 VI AATAMPKEDFNRLSEFLKDVSGVEKKKPNTRLMVVSGI MDDPNYLK
 I I EELGGLVVADYLCNGTMYFWDVDES LPPLEALAKRSLEHI SCPRMVG
 DHPRRWEFMKDI CKDFQVDGI I SQRLMFCDI WGAESSMMRWAEDQDI PV
 LALEREYI LGGMGQLRTRVQAFLETI GRR

>2617921732 Ga0073689_13823 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_138]
 MLNELSAI LLAFSTCFSRNAAFYWF I VI VFGLI VRLDFHGVTSFVRWLEL
 EPNYYETLLHFFKASSWRLAEI QWRWGQYYSKVVPDYTKRASFNRRRN
 QSLQRSQENAGSKENSPGI GKLRQTFLYLRSLRGGGPLGRHCKKHVLHS
 GHGLNPRGSRKASRFSRQTGAGGKWRKKRDHRYPDFFSREPNAFQSQT
 YADPGCLLCRGTNFSNRQVRRLRATAAPRNHPRHKDNAVGYTGPPPV
 GKRKGKPPVWGKRVKLWKQFRQRAGDFQTLTLTYGKEVTLSYLCLDLL
 WKPI KEKVRFLVTDGT

>2617921731 Ga0073689_13822 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_138]
 MEKELI VRPI RGEERETWDQLMAVHHYLVLKHVVGESI RHVALLNGQWVA
 LLGWTSVACQPRSPG

>2617921730 Ga0073689_13821 Transcriptional regulator containing PAS, AAA-type ATPase, and DNA-binding Fis domains [pelotomaculum Ga0073689 : Ga0073689_138]
 MNKDI I LKDEI QLLI NLI SAAFVDVGI VGEGLNSI AGTKI YFQKI GLI A
 PEDSHAANVLNSGEGYI NELPCSNQCLI CNKRTI CPFLTGLYQPV I VGD
 LVKGVVFFLASNKKQREFFQYKHEQLKEYASLTASLMSKI I EEEQAKLHY
 AELGLI CNSI DEGI I I VNTDKI I TFLNSAAQEMLNMTKECI GQKLDLFF
 PEI FNGKQVVNYEPVKI ADKNRVRNLVVKPVI DGQDKDYVLI FKKQTNK
 I I KQI I DPQKNLRPI ETQPLDRLI GI SKAI TRLKAELLKI AQNNSTVLLL
 GETGTGKELCAQVI HELSPKRGPFAVAVNCGAI PNELLESELFGEYEEGAF
 TGARKTGKAGKFEQANEGTLFLDEI GDLPLI LQVKLLRVLEDKNVERLGT
 CKPRPVNVRVI CATNHDLEVQVNKGEFREDLYYRI NVVPI HI PPLREHPE
 DVPSLLDFFLRLCQCAI STSVQECSEPI GLLTAYSWPGNVRELKNLVEY
 I CNMENENTATI KSLPAKI RDKLLFKCGPLKSI KINPDEMEWLRI KEALR
 LFGDTTEGKKKAARHLGI SLATLYRRLKLVQQSM

>2617921729 Ga0073689_13820 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_138]
 MAEEEGTLTI WESVYHEKEDI WEARLTGFVREREKEMYRKFEVHREKAY
 RPAEVEAALKPANLKLASYDAFTFNHI HEKI FYVAKRIS

>2617921728 Ga0073689_13819 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_138]
 MSAI FYYEPARI GNI LLNTLKRLEAVQTCRCPELRKPTLLQEK

>2617921727 Ga0073689_13818 Pyridine nucleotide-di sulphide oxidoreductase [pelotomaculum Ga0073689 : Ga0073689_138]
 MEKRELVI I GGGPAGLAAGI YASRAAI GTI LLERGI PGGLVVSTESI ENY
 PGFADGI GGPELMI QMENQARRFGLI I SASVESI NPAENGFTLKTDSGE
 I FSSAVI I ATGAQPQLLGVGETEYTGGRVSYCATCDGAFFRGRVAVVG
 GMPRLKKPFF

>2617921726 Ga0073689_13817 Pyridine nucleotide-di sulphide oxidoreductase [pelotomaculum Ga0073689 : Ga0073689_138]
 LTRFAEKVFI I HRRGELRATKVVQKRAFENPAI EFVWYNVVDI HGTDTV
 ESLLVKDVRNGEKTRLSVNGVFI YVGYPSSGLVKDLVKMDERGYI I TDE
 NMQTSI PGVFAAGDVRRLKLRQVVTAVADGAI AAVAAEKYLEDKK

>2617921725 Ga0073689_13816 peptidyl-prolyl cis-trans isomerase B (cyclophilin B) [pelotomaculum Ga0073689 : Ga0073689_138]
 LKKAVI ETDKGN I VLELF EKDAPNTVENFVSLI DKGFYNGLTFFHRVI PGF
 VI QGGCPHGTGTGGPGYTI KCEI NPNKHLRGSLSMAHAGKDTGGSQFFIC
 HDAFPHLDGI HTI FGRVVEGMDVVDAI KQGEKMNKVYTLQ

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>2617921724 Ga0073689_13815 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_138]
 VEKTFNEYGELLLEQLKKI LENSDFRELTGGGLYRAFLHGQVMGLVLAL
 KIMFPGDGLGEQASQLAAVSLGEDECGCHHYDI DEASPG

>2617921723 Ga0073689_13814 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_138]
 MSI AAGYVELGCRVVFAPGLTIGI I SGRVAVDCSTEMNDPGEAGSELYN
 LLHHCQAI VYFELNSRWY

>2617921722 Ga0073689_13813 Uncharacterized integral membrane protein [pelotomaculum Ga0073689 : Ga0073689_138]
 MQAYI FMVLLLTVLVSFVAVQSSQVDLKFGLGWTFRQI SLVMVI VASFTA
 GGLAALLGLPRQI RAAVRI RELTGQNRYLGEI DKLQSKLKKQRKTGSG
 E

>2617921721 Ga0073689_13812 ATP-dependent DNA helicase DinG [pelotomaculum Ga0073689 : Ga0073689_138]
 MVKTFI VCDLETTGLDPSGDKI I EVGLVRLEEGRVI GTYHTLVNPRPLT
 LKI KRLTGLDDSDLLQAPPI AGMLSEI LDFIGDI PI TGHNVQFDLGFLAA
 ARGLPLOQAFDTLELRLVAPAAPGYRLDKLCSALDI DLKDGHRALNDA
 LATARLLTVLVQKLRETDPGLLI TLNGLLQEACSNWSGFLADLI KDI LKK
 FPNKKI AAAPYWKREDKQKNNAPRRERFNRRLPLVKKDVTALVGKEG
 RLAAI LPGYEYRPQOEKMGAVNRALGEEKFLLMEAGTGVGKSMAYLI PL
 VLWSLLNGERVLVATHTI NLQEQWLKDI PLLARVI EEPFRAALAKGRQN
 YI CLRRWFSAI ESRHQPEEAAFYARVLSWLTATSTGDKGELNI SPSEGDF
 WLAVCGEAEGLGSRCSYQKSCFVNKARRAAEEADLI I ANHSLLFADVRS
 ENRVLPSTYGLPI I DEAHHLEESATAHLGRLVSQSALNRWL VAGRTLAKL
 GEKAPPGEGAKWLKSI KSAQEI RLEAAEAARFLFQLLWEMAAGKSTGAEG
 ESGRLSLRLPCCADQYADFLTAGGRCADLLRSFAGEI ENCI EFLWSVS
 EEAWVGPDGLSNVRQSGVLVAGDLQFI LENRDEGYVYAELETYSGGAA
 RHCTLLAAPPI NVGSLLYECFFKEKSTVVLASATLSVNGNFSHF I ERTGLN
 RI PEERLLMAHFNSPFAYDRQALLCVNRDLPVQGTVKEEVYLEQLENTI F
 QLLQI TGGGTLVLTSHRTLRETYWRLKPRLEALDI CLLGHGI DGSRSRI
 MEEFKTTGRTVLFGSSSFWEQVDVPGDALTCVI MVKLPFQSPAVPVVEAR
 LEDLARQNRDGFQALS I PQAVI RFKQGFGRLI RSGSDRGCVVLDRLRLT
 KSYGRHFLNSLPLKSHI RGGTDLI GKKI TEWTGKGI I KNGHHVNTWKEVN
 FKKI AHSDMI

>2617921720 Ga0073689_13811 putative membrane protein, TIGR04086 family [pelotomaculum Ga0073689 : Ga0073689_138]
 MPLI KKEGFSSQI NI FAVLKGTLWTI VLSLLLSTGMGVFYHFTTVTEQSL
 TWFAAGI LVASAFGGSLAAGREAGNKGLYHGLAVGLLFFLAVWL VAGLFI
 PGQMTLGVFYKLLLAFAFAGALGGAVGVGLS

>2617921719 Ga0073689_13810 radical SAM protein, TatD family-associated [pelotomaculum Ga0073689 : Ga0073689_138]
 MNEQVFAYRLGGAI YLNI TNRCSDNCLFCI RRTREGLGSHDLWLKREPEL
 DELLAAAGNVPRPFREVVFVCGYGEPLI RAGFVAEAAARELKKQGRPI RVNTN
 GOANLLHGRNVLPVLAGFVDVSI SLNTADPGQYLEI CRPQHGEQAYESL
 LGFI SESKKHI PVVVLTAVTWPGVMDRCLVLARKLGVEFRVRLTGTFN
 FTS

>2617921718 Ga0073689_1389 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_138]
 LI KRSGDAFVREKTGSATMI NLDGRWEHNSVDDNNPAGNKPVENTRSTV
 KK

>2617921717 Ga0073689_1388 copper chaperone [pelotomaculum Ga0073689 : Ga0073689_138]
 LKVEGMSGCHCKAAVEKTLKGTAGVQDAEVDLSAKSVTVTYDPGKVGRED
 LTKAVVDAGYDVAR

>2617921716 Ga0073689_1387 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_138]
 MSRI TSTNNVARQSSCLSAVKRESLSVGRRTTKNI CSI PDI VGDSCRTSAQ
 NGEI FKKSFPNNR

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>2617921715 Ga0073689_1386 6-pyruvoyl tetrahydropterin/6-carboxytetrahydropterin synthase [pelotomaculum Ga0073689 : Ga0073689_138]
MYEILVRNRF AAAHALKEYDGPCARLHGHTWHVEVAVRGRKLD RRGMLVD
FKEIKAGVKKII EELDHQNLNELEPFKDGAENPTAENLARYI YLRLGEM
VKPELGLQLALVRVWESPDA SAAYLGVD

>2617921714 Ga0073689_1385 7-cyano-7-deazaguanine synthase [pelotomaculum Ga0073689 : Ga0073689_138]
LKSLVLLSGGLDSTVSLAQALKESEVVLALTFDYGQQA AAKEKTA A AALA
AHYNLQHRVMNLLFLREI TETALVSADRS LPEPDLNDLDDYKKATTTAAA
VWVPNRNGVFI NII AASI AEAHRCDLVVTGFNREEAVTFPDNSPGFVNAV N
GALGYSTLNRVRVI SYTQRLDKVEI I KLGLRLGVPFRYI WSCYRGGEDMC
GRCESCLRFRAAEEAGLYNI G

>2617921713 Ga0073689_1384 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_138]
VLQYFI DETTYNGAQLSSLWAFRNYGLQGDSI VSFRGPCRVELTEMVDQ
EDVRKKNP I YSTDMLHFLI EHFDLDLEKTI VRQRFLMAI I KDI I QEKTGV
I LCRQGD DLFLEGRKLSVSI ATLTPVSTVI HTGLNVSGKDT PVPVGLAE
LGFKEGGVSSLG VSI CAAYARECEEI RMARCKVRGVK

>2617921712 Ga0073689_1383 Organic radical activating enzyme [pelotomaculum Ga0073689 : Ga0073689_138]
MAGAVSEI FSSVQGEGLLAGRRQVFI RLPGCNLKCSFCDTVSSGNPAYCR
LEAI PGRGDFKLLPNPLRAEDVA AVAAAFGLPLHHSVSLTGGEPLLRTSF
I RELVPLLRGTRRGI YLETNGTLPERLSEVI DLVDI VAMDFKLPSTTGLP
PFWNEHEHFLKI AAAREI FVKI VVGEETTFREI EKAAGLI SSI AADI PLV
LQVPSPAGRI RGI TPAHALELQGRALEKLVDVRVI PQTHKMMGQL

>2617921711 Ga0073689_1382 GTP cyclohydrolase I [pelotomaculum Ga0073689 : Ga0073689_138]
MFDLPKI EKAVRMI LEAI GEDPDREGLRETPTRVARMYSEI FCGLMEDTE
MHLOKI FSEDHEEMVI VKDI PLYSMCEHHLLPFYGKAHVAYI PHRGNV TG
LSKLARVVEGFAKRPQLQERLTSQI ADSI MRRLNAKGVLVVVEAEHMCMT
FRGVRKPGSKTVTS AVRGLFQKSEATRAEAFSLI KD

>2617921710 Ga0073689_1381 Protein of unknown function (DUF4264) [pelotomaculum Ga0073689 : Ga0073689_138]
VENKEQPDQGKLELI AVKSFKTYDDMYKVVD FLNKNLKNKKVI FGLTKDH
QKGTMTI SI YEI

>2617921709 Ga0073689_13720 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_137]
LGLLVI EADI TNLASEQLLKHQI KAFDLTVFCVYSSYRI I LFTNLKDLPP
SVFRKLF

>2617921708 Ga0073689_13719 Predicted nuclease of the RNase H fold, HicB family [pelotomaculum Ga0073689 : Ga0073689_137]
MPRRFKVVLTWDKDNKYI ATVPAI PGCSTFGDTKEEALVMAGDAVKVTL
EGLAATGQVPESD VDSI AEVVTA

>2617921707 Ga0073689_13718 threonyl carbamoyl adenosine tRNA methylthiotransferase MtaB [pelotomaculum Ga0073689 : Ga0073689_137]
LPYTFQI RTLGCPVNOQEGRLAGAMTGAGFTETTD PADVYI I NSCVVTR
AAAAETRRLAARAKKENPEGLVVLAGCYPQVYREEVAEKLPGVDLI TGTT
GRAKLPALI SRRLAGEPVERLLVTPHGPGEVFEEPPAPGHYGRVRPVI KV
QEGCDEACAYCI VWAARGLPRSMAPERALTWVRRFVEQGSREVVLGAHL
GAYGKEI PGWNLARLI QEI GRLPGDFRLRLDYVEPMNVTLELLESMAASP
KVCPFLYLPLQSGSDRVLQGMGRRYTAGDYARLVLAARELI PGLSLWTDL
I AGFPGEREEDHRTLR LVEQLALSHLHVFPYSPRPGTAAATI PDQVAPE
LKKKRVD ELRTL DRELSLSFHKRLVGKQTQALVEKI TDEQGE GYSEHYVK
VRFPATGLERRGSLVTQVLAARQWGVGQVTRLNENHETSSKYFS DTKT
HDL

>2617921706 Ga0073689_13717 transcriptional regulator, TetR family [pelotomaculum Ga0073689 : Ga0073689_137]
LNNI PTGRYVI SKI QDMPDEQRPPAFVDTGGI QI STREKI LKVALDFFLN
NTYRDVSI NDI VRAVG I TKGGLYHYFKSKDDLFSEVVENFI DRYTQMYLA
FFI DETMEFKQKLD FVAARTVELYKSEEVKRVYSNLDKFFFELRKHNDR L

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FTKAI AMNKEI LNLVTDLFAREKQKGGLENLDCEGTAVQFLTSLKGVAQ
YSLYVEEERLEKNVNTFMENFWRGI QAGPVLQ

>2617921705 Ga0073689_13716 putative ABC transport system ATP-binding protein
[pelotomaculum Ga0073689 : Ga0073689_137]

LNAGAKRDEEAMDII LKARNLTYYQMGEVTVKALEGVNFDI SAGEFI VM
LGPSGSGKSTLLNI I GGMDTPSSGEI YFKDKPLHGASEKVLTELRRNAV
FVFQFYNLMPNLTAYENVMLSVEI AKNPLKAEDVLEQVGLAGRAGHFPAQ
LSGGEEQQRVAI ARAVAKNPEI LLCDEPTGALDSSTGKQVLQVLKDFNERY
HKTVVI I THNASI AQMADRVFYLDGGLESIEVENPVSLEEVSW

>2617921704 Ga0073689_13715 putative ABC transport system permease protein
[pelotomaculum Ga0073689 : Ga0073689_137]

MLTRKMWREI LGNKMAYVACAI VVI I GLAAYTSMQMAKDSLFI ARDKFYT
EFHLADGFAGVKNVPYSQVEKLKDI PGI DQI QGRMVEDVRVI SLDKDKN
I FLRLVSLKEHKPYALNGI KLLKGSFPEENSKALLLADKFFSAHGLSLGE
SLTVI I EGKKVDLKI AGTGQSPEYVYAI RNMQNI YPDPQTFEVAYMPYEV
MESLFARKGMVNDI SFTLPGFEFEDVEQPLETGLEKYGLESVARKDQL
SSAMLAEELKQLEKSSQTVPVFLSI AAI I LYI MLKRI VESQRGQI GTLK
AFGYRNNEI LLHYLSYGLI VGLTGGVLGGFSGTALANSMTKLYQQYYSLP
DLAGRFLLYFLSGVMSVSFSLFAAYQGTCSI LKLPVDAMRPPAPSFK
SKSRLEQI PGFWAAFTVQGRMAVRNMI RDKGRSFFTFI GI VFTFSMMASV
WSMYGLMDVLVDQFTKVQYDLKI SFARPLPLSEVVRELOSNKGVKRI E
PLVEVPVTLQKEYRKDDVALGLTPDSELYTPI DKQGNRI RLPQDGMLLS
EQI AGKLEAKVGDIRI RLESVWAGESPVYVHVAGI I PQYLGSNVYMNQKAL
LALLROGNI TTSALI SMDHQWLPELKERYNTSRYI GNMEERQOSI DLYEK
I MGTSKSMFWVMALLGVI TGFAI VYNSSI I TLAERERELASLRVLGMRPG
EVMVVSVVEQWFI GVSIGI LVGI PVAFAMNKG I ASGVSSDLYTLPAI TTPP
ALFLALLGTVLAI WFAQLWVFRKI EKLDLVGVLKERE

>2617921703 Ga0073689_13714 HlyD family secretion protein [pelotomaculum
Ga0073689 : Ga0073689_137]

MKRSVKLI SIVII I AGVAAYGVFNARKPLKAELI EVKPOAVAH I FKEEGI
VEAVAERPVSLSVNGEI I NLAVQEGRHVSAGDLLAQLDTGDLGHQLAQLT
ARRKSLAGEEQKSLQEMDQV I QQQI AVEETKROLEKSEKDYDRI KLLYD
SGAVAKTELETAESMVKQLQNDLARQESRLKYLREQAGAGTI AAAGNSAT
ROYQGLI EGVEAQI SQLEEQI EKSRI TAPI NGVVQELNVKRGMVVSPQT
PLMKLAGTGGFEI NAYVLAEDVLPVKVGMKVTLI QKRKDGDKFPGTVQA
I APAAVEKVSSSLGLVERRI KVTI QPGKNSPGLRPGYALDVEFQVLEQADK
LAVPKTCLFPYEGGDALWLVRDGRAQI QKVMKGLETDELVI EQGLKDG
KVI KNPQLEGLKEGKGI SGI

>2617921702 Ga0073689_13713 Sporulation protein YtfJ (Spore_YtfJ) [pelotomaculum
Ga0073689 : Ga0073689_137]

VATSPSAPGKI ALI SSNLVKLFHPLNKCGSGGGGGAGGRVAASAVI VI K
GEHI QVI QI KKSTSLSKLVEI I PEI ADKFKQGKEKGEENKEG

>2617921701 Ga0073689_13712 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_137]

MPDNNELVNMLRVVI QEELKPI NERLDRAEQGQOEFKRVNTRFATLEAG
QOEFKKEVNTRLATLEAGQELKEGQTTI ETTLNDLRAI NRRTHKEVFSQ
LNAI WDDI KLLSSQREKAI R

>2617921700 Ga0073689_13711 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_137]

MFNNRQPDWPDQTLKQSLAPLAALVRRRYRLETVRLTLTWGLAAAAGALV
FLKLTPFSAFLFLAGI PGATAAI FI FI FRRLSFGALEI VRI ADELGLNA
RAI TAYRLAEKNSRDPWNRAAI EEGI KACRELECKETYPVLPSSRSWQGI
LFLAGVLLTTI LLPAPLASHWQAGRAEKEALAAAFQAEAAAAPLRQMSP
EQKEFLPEKLQEDLNDLSRAVSRADKROEAARNLERAGQEMEDALASLEP
SERSLRQLTGVMQKSREPLLQKI AAALKEGNLEETVRLAGELHELAQSAG
PGKNELALSI FQAAEATGDPVLRDLRRLAGSLLSPGGDENAKEGSESPG
HESLSRALSSLGQKATAARRLAQASPAMFNLANTLASGGQAQDI ALAGSG
LNTKSSGNNGLPGEAAGSSPGAGATGSNPGAYPGAAGSNGAGSTGSASGS
PSGLGADGNFAGGAGNSGAGNGPGNGAGEGQGNGGSGNGDGGGGGNGS
GAGTGGGGSGAGGRGAGMSGGGPDRI YAPHLLGGSGQETHVSGRI GPGQG
GTETSLPESPTELGAVRPYREVLPYREEAI NSLSAAPLPDLESVWQY
FTSLD

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>2617921699 Ga0073689_13710 ABC-2 family transporter protein [pelotomaculum Ga0073689 : Ga0073689_137]

MTEETRRREQPAGTAEKENNTAMTAVKRRSWTGGI TGGVKNALLEGRLCGLA
PMLGKEMRGRTRGWRAVLLSVYLGVLTA CVLLFLWFLNLRMPFI NPQVG
LSLYTLFI F I L I M L I S F I A P A V A A G A I S G E R E R R T Y D L L L V T R A S I T G I V
LGKWLASVAYLI FLAVSALPVFAVVFVFGGVPPATFGLAFVVC LAAGLG
GALGLALSALTRRSQAATI I SLVLVVFVI FGI PVI SGI VLAGSQAGQVQM
POETPGAAGFAGSPWYLFPSPLTAFTSVLP GSGDYNPRGDI PI I SELMNML
LRGNGTGGI DKRAFAHGYSYPAYAGGEPEI KPPGMAAWAPWARFTLYQGF
LI LFSLTAVLAI TPRNPRAAWRVWKARRQAARG

>2617921698 Ga0073689_1379 ABC-2 type transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_137]

MI KVRGLOKNYGRVQALKGLDMDVPPG SVYGF I GQNGAGKTTAMRI LAGL
LI PAEGQAEVAGLDVLKHPRALREAVGYMPDFFGVYDDL RVGEYLLFYAA
ANGI RGPRAFQLRDDLLELVELRDKREAFVDTL SRGMOQRLCLARALI HD
POVLLLD EPASGLDPLARI EMREI LKELGKLGKTI LVSSHI LSEMADLCT
HVGMI TDGRLVROGTSELLSGTPVRTMVLRLCPVEEVGKVLADRPGE
VVNCLPGEI TFHLAGEPAQAAELLKELI YRSI PVTHFAREEQTLEDTFVQ
LAKEGELND

>2617921697 Ga0073689_1378 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_137]

VTLWLPLQGSADYLAVRFRSGEKVLGMEAKMPLVASFSSGLMPPVTGVL
GPVPPALEKVRI TMPDGVPRAPLAI ELTPELI PPTGEQLDAFGLI LVTGE
AAGSLTAEORRALFEWAETGGHLLLAGGVRI SDTLAI FPAGAGGI TSRET
TGNSDWRSAAAWLGTPEPSAAAPAAARLHGAGEPFGPPENPLGRQVEAGEG
KVTVLAFDPTCSPWDADNLGRAFWERLLQPEQPGRNKNKNTDPFHLYPLL
NMVHSLPAGAFPDWRLVGI FLGI FLI LAGPLTYRFLQKKQRPEYTWLAVP
LLALLFSGAAYLYMLQAGKTVI VNI I QTVDARENAPAKQALTAAGFFAPT
MPVFHVALAEPCPVNAQPFGGGPPPGWRKPEEEPPFTVVRGSDLEVTFR
ETSQWGMRSVLFRQDI GGTLDGLSASLRI EGNRLAGKVRNDTALLLEHVT
LFLGGDYRGLGNLAPGEEKEVDMEI PAAPVYNSQSPFSHPAGPGYFPNW
I FVYPEGKEAALQAAGLTGSPRPDPFGPPPRRLTI EEQRRQALLEQLLNP
SRRRGPGPEFQSGRPLTLAAFSRDSVKEVT LKNLRARPHYLSI I LKKPAL
VI PPGNFTI PAGLTPEI I NAQTGGTI NRNNVFGI QGGNI TYAFRPGLPQ
NAQI KEI AI EFQYFPGTAQPGMPKGAPGPPADAAADVEAGVLEI YNSSAG
QWQNL SGAKAFRLPGEYALPGGEVRLRVNGI DPTSGKFVYFLPPAVSCQG
VME

>2617921696 Ga0073689_1377 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_137]

MPFFKKRMLFWPVI I FVFLPVFLFSSPSLSAPGPESMDSPVQI SAEI GWE
GQGVPGRTAPAVI HLKNTTSGDLRGVVEAI NYFRFI PPPRPVRPRARRLP
GRPSI TLYLPLANR

>2617921695 Ga0073689_1376 Putative glutamine amidotransferase [pelotomaculum Ga0073689 : Ga0073689_137]

VGI SFSSPWWWLLPPLLLAAWYLRLPWL RMARRLGGSRRREFGRLAVR
LFI F I L L V A V L S G T H L V T T L K R Q A V I F A L D A S A S V G V E K S R G E Q W V R A A L
EKKPPDSVTGVI SFGEKALVEPPGPAPT FNRTGAEPGEGASRI GDALNL
AQALLPADTRKR VVLLSDGRDTQGEAVATARRLRAEGVRVDVAGLGKVG
PDLRLDSLSPPTQTRAGETFSLEVI I TAGGESTGTFLERDGTLLGSAPV
NLRAGQNRFSFPVTAGNAGLHSYRARLAAGDGQKDVFTANNEAAAAQETT
GPPRVLI VAPAPREAEALVWSI KAAGGI DVELVNPESVPQGLPAWARYQA
VFLVNPAYS LGKTM AEI EAYVRDGGGGLVMTGGPDSFGPGGFAGTPVE
RALPVKMDI SGRGELPSLGLALVVDKSGSMSGYAGSADKMSLAKEAAARS
VSI LNEQDQGV I AFDTL PWWVPFGPAKD KESI RAEI GRI YAGGGTEI Y
PPLAAAVQALKGASTRVKHI I LLTDGI SASGGSYQKLLLEEARGAGI TLTC
VAVGQEAADAGLLKALAE LGRGRFYATADAGSI PSI FTRETLMTTRSAVN
ESFLPGI ASSSVLLQGI REAPALEGYVATAPKDRAEAALVSHRGDPVLAA
WQYGLGRAVAWTPDAAGRWSAPWVAGQI FPRLWGNVLSWVLPAGNTGAVQ
I TTKVEESGDVWI TVDDPAHWQQVGSYLLKVTGPAGESGDVALTPAGPGR
YTARLASPGTGSHLLSVSSGDTGQTLI ARSALLVPYPAEYKETGVDLSR
LAEI AAAGGGEVLDAPGQAFSPNLSPVRAKKDLSSLLLI LAGLLWLLDVA
GRRLHF GAEEREALRKAWLQAYSRLTFQKARARRETVP SAPWTGRALAGV
ERLRRHKWGRETAGRHASDDRNGQEEEFPPESPSTAGQPI PASRQNRPP
GI PGSRAESTAATLLAAKRRRK

Table S2

>2617921694 Ga0073689_1375 Aerotolerance regulator N-terminal [pelotomaculum Ga0073689 : Ga0073689_137]

LHLSSPQALWLALTI PAI LALYI LRPRQMOKI VPSALLWRQI TVPQQAAR
PWQRLRPQLLLWLQLLAAAMFSLGAAAPVWYLNKPSPATI VLLDTSASMQ
AVDSGETRFSSRAI AEI EALALGLEKGARLTVI AFDROPRVI I KDSNNYNE
I KRALKNLKPSFCSADPEPALSLARALAREQNQPRLI CLTDGGLTGLKNE
QVAPELRLVGTREANLAI ASLSLRQAGTGQAALAVLVNYSARPASGKI Q
FRVGDQRQNEKTFQLEPGQASSFLWPDLPFGMPVAAHLQADDSRMDHFPL
DNQAWAVPGEKRRKI LLVTEGNI FLEKI FNTLPALAI YKATPGRYPSLL
AGNYAYDLTI LDGVAQPLPPGAVFLLNPPPGI AGGLDVREEFRPGGLAP
EODSPFLEYVELSQTHVAAARALELKS NWREDVAAGGKVI MAHGTAPEER
MAVLSFALSNSDLPLRPAFPVLMNLVSWLLPSELEVPARVTPGEEVKI N
ALPRAQKI TVEDPGGVVTGLAPPFPSPWI PEKPLFRLTQTVRADNQDV
SRVSRLLVAVNGYSEQSDI VLKDI SPGEAKI PPPSAPAQRSPLTGGTLT
LALLVALLEWGVAGRGH

>2617921693 Ga0073689_1374 Protein of unknown function DUF58 [pelotomaculum Ga0073689 : Ga0073689_137]

LSDI NLLDAGI LKRLLEGYRLFRQRPVFGHPGGI LRSLOKGGAVEFADYRE
YTPGDEPRRDWRAYARLRLRYVKEFLDERQQTTLFLI DASASMDWSGAN
GHDHKGRYALQI AAGLGTCLLAGNDRLLVI I CAGGEETGKGAGWKI SPEFK
SRTALPGLWSFLKTVAFGDSAGMAAGLRNALKLLRGI NSLYVFSPLYDLS
AEQEMFHLAAGHGMEATVFHI LSPEEREPAGDGEYLLLDATGARI EITL
SPAAYLAYSRRLI FQOEVDNCCRCWGVQRVSLDSGEEAADTLFKTLPR
A
GVLKPKG

>2617921692 Ga0073689_1373 MoxR-like ATPase [pelotomaculum Ga0073689 : Ga0073689_137]

MPDHNVPENKEVYRI AADGENAI PEATVPEI LERCKNRLKEMENAVAGV
I AGQEEVI HQVLTALLAGGHVLEGVPLGKTALVRTVAQVTGLI FRRI Q
FTPDLMPADI TGTQI FDEKGADGPFREFSPGPVFAGI VLADEI NRATPKTQ
SALLEAMQERTVTGGI TYPLSDPFFVLATQNPLEMEGTYPLPEAQLDRF
LFKI NVTYPSAGELMAI AGRTTGAREPKAPSLAPGELRGWLRRLVRRVVV
VDDVI AYAVRLVLATLPDNALAPARVRRFVRYGASPRGLQALI LGARAEA
LREGRPOAGYDDVRRVAPAAALRHRLI LSYEAAAEGI GADELVRDCLNSVQ

>2617921691 Ga0073689_1372 GGDEF domain-containing protein, diguanylate cyclase (c-di-GMP synthetase) or its enzymatically inactive variants [pelotomaculum Ga0073689 : Ga0073689_137]

MI QGFGKVLDAKNI MGFSNKVLI GYQNLKDTNLLKI I NSSLENLKPVI V
LYFDI TKFHEI EQI NGCQAAARVLTMFNGAI KQKI PELFWNAKLLAVENL
LGDDFVLLGMEQETDLLTMQDI AI ASRI GI KESLKQEMLKI TGEPI EVH
VGYAI I SFKSENLDSQLYNAVREARDI AKGTI DLQATARLQSEFRVLLNSL
QFNI CKSSYLEKVCSGLAAVRPGSKHTGFASPF

>2617921690 Ga0073689_1371 AAA domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_137]

LGEQPKHRKI DVFHQI QQAI SSLHYDKRI TPVLVLDEI HKASNKLLLEDLQ
LI FNFKMDSQNPVYLI LAGOPPI RNKLSLNMRI YKY

>2617921689 Ga0073689_13623 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_136]

MGRRLRSRYLSI I LGLSLLLTLLSAVPAGAADSGELRRMFDRDLTVNNGN
WSKDANNEESQLAWGESYVLDAYVTMYETTGDYTYLDKFVTHGKGVLVQR
DSVRGMKDYRGLSLPAWRNGKYTLNGEYAI FAGHTGMI VYPMKFAAI VA
GNPALNKYRDDAGMFLQAAKDAVAVHSDEWVDKGDGTGYKFRDGMYPYKQA
GLGLPFNQYLAMARAEMLI YRATVESRYLDRVEKMLKHFKNNLAVDQSV
GYTWRYSAFYNPSEYEDTGHAKTVDAAFGQYAAGLVFDAGDMARFANNAA
KKI I KSDGSI ADNVLGGGSTPYPWF I GFWSAYGQFAPVI TGAAYEKLAAM
SYGGPTGLLLAAAMLNKANSEPGYRGGVQPPVDPNPPPGDPPPPADNPPA
GEMVNVGDFSQGHGTWAGPDVVVKTDADGNKYGS AKYGNWFYQYVPVQSG
GKYVLSARSRKGSAAGEARVAYFFYNAAGKQLAGGDI LYRHRGAGWEQVP
ARTVTAPAGAAKI LI KLLVNGGSGAHDNDI SMRPADSPPPVNNPPANN
TPPVND

>2617921688 Ga0073689_13622 looped-hinge helix DNA binding domain-containing protein, AbrB family [pelotomaculum Ga0073689 : Ga0073689_136]

VYTVKI SSRGQI VI PAEARKNLSLKEGDI LSCYVEEGKI I FKTKSAKI KK
RDC

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>2617921687 Ga0073689_13621 Glycosyl transferase involved in cell wall biosynthesis [pelotomaculum Ga0073689 : Ga0073689_136]

VVGAGGRSLWI MNHHAGGPGRHESFARELAARGWRVTLFASSFI HNLFS
LREYPPGRGHLVEELRSVSRVWI KTPPYRGNGPARLLNHLAFWRLSVLG
RGLAPPDAI I GSSAHLTLGLAAFYLARKHRVPFI FEI RDI WPRSLVDI GA
I SGRGFLAAGMGALEKFLYRQARLI I SALPGGVEHVAGLVDRNKVAHI P
NGVDLAWHDCARENGLTREQADFFHRYGDCTVFTYAGAHGFANGLETVI
EAAGI LYRVGAGGI HI LLVGDGPGKAGLVRAARERGLTNVTFWEAMEKDR
I PAI LKNTAVCLFHLRNSGAYRYGLSSNKLFDYMAAARPVI AAVDVPPAP
GFSRFGHLHI PSDDPAALARAMLMAAGTPAFREMMGRAAREYVERYHNI P
ALAGRLADI LENL

>2617921686 Ga0073689_13620 putative peptidoglycan lipid II flippase [pelotomaculum Ga0073689 : Ga0073689_136]

MRKGRAARAVAI VI VFTALGKLLGFI REMAMAAHFGAGAATDAYLTAALA
I TLLFNI LGGRSPGTVFI PVYHRI SAAGGAERAAFTGTVLALACAVSTL
TALLGFALAPQLVGGGLAPGLPPHTREAAI HCARLLTAGI PLLTASGLLAS
LLNAHNFTVPAALGI PLNLMVTGFI FFTGAGDLDALVFGTLTGylaQVM
VTLI ALVGMRI KI FAGI DRREPGLARVGGLLLPVI AGGFI TQLNPLVNRV
LASGLPEGSI SALAYADRI I QLPLGLLVTAI TVSYPALSGAAALEGRGS
AVEAANRWAGALLFVTPTALVLAALSRPLARTVFERGAFDGDATAATAC
ALLFYSGLPFI AWSRFLTRFYI YHDSGTPVLI GAATALANI LLCLVLV
KPMGYRGLALASSI SAAAGI PLFLI CLRAKTGCVFNAMKI KLLSI TTAA
AAAFTMLAASAAAGGTEKNLWGNLLYLLL VGGVGMVSYSFVARFLKLE
EAEMI TVMLKRI KFFPGRRSTW

>2617921685 Ga0073689_13619 Glycosyl transferase involved in cell wall biosynthesis [pelotomaculum Ga0073689 : Ga0073689_136]

VI KLLLYLTVTAPLGQREAFI PEMNCLARRGVELTI I PVNPAGRVFHRD
GAGLLSRTI AAGLWGGEVLLSVLAWLI RAPLRVALLLLLLLKS GAPANRV
KNLLVFPKGLFI AGKVRLGI DHI HAHWASTPSTCALVASAMTGVAWSFT
AHRWDI ANNNLI REKVDRCSFVRVI SSRGREI TGI AGVDVKEKVFYCPM
GVDAPGEAPARRRAGGRRPVI AAVGSLTPVKGHCILLRACRLADWGGNF
RCLVI GDGPERKYLEVQALRELGLVTFGTALPHDRVLRI LGSGAFFVL
VHPSVETPDGQHEGVPVAVMEAMVRGVPVVVTATGGVTELVDGETGLI VP
PGDSMLARAVGRLLDDPAGARRLAEAARRRI DRDFSLEARNVAALMDRMN
MAP

>2617921684 Ga0073689_13618 Glycosyl transferase involved in cell wall biosynthesis [pelotomaculum Ga0073689 : Ga0073689_136]

VRVLM I SGVNAATGGDLI HTLEMAGGLAAAGARVTLVLRGKYRGPGRPG
VKVVGLPVAGWKYLDWLLRPVLMCAAALFLT LKGDPAVYVRDSVYETPL
VLLLGLLGRVVVLEVNVAEDLRAGGGAPWKI ALAGRAQRRACLSATLV
LPVTTVLAGWLAVQGAPSGRVVVVANGANPYLYHPGDRREALAGLGLDPA
RRYLCFAGNLAAWQGEVVLEAFARLARTRPDTVLLVVGDLERSKLEAR
ARRPGLRDRVI FTGRLPYQRPVAYMRASVAGI GGGWWGGDRRVERFRHS
GSSALKVFSYLACGLPVVI PDFPDLAGLVRRAGCGLVTQPDREVDLAAL
GAVLDHPRQWAEAGLKGRAFI OREAWEHRAALALALLEGPARRTGGGSG
D

>2617921683 Ga0073689_13617 O-Antigen ligase [pelotomaculum Ga0073689 : Ga0073689_136]

MASVKWPFPLAGGI MAVI TCLAAPEVLGFFI CGGLHLTGRTLSLGQEEFL
FLNTGSFI FPLYCLLLLLLLRRRAGALAAALGCWEFWAVLGLLMLVRL
PDSLFAEYGVKVKYYLANNTTGFFGPVLATAVWGSEGLRRFLRGAFLGG
LALTAYFWLSKSYDLTLNTYAVLNFNPI GLGRLI GLFALLAI FGRMLPL
PVQFRI PLAAAAAAAVVMLNARGPALALAAGLVAGGLLPAGGRSRRLLLL
AVPAFLLMAVLI NSNYWFSFGFFSVDDTGRLPLYRAALDAFLQNPALGAG
TGSYAWLAPAGVLYPHNLFLEAAVELGLPGLGLAMLLVFVPLARLALWK
KRAEDGALTGALLVFCLVNAMLSGDI PGNFPLWLSSGVAVSLAI VPGEER
R

>2617921682 Ga0073689_13616 Glycosyl transferase involved in cell wall biosynthesis [pelotomaculum Ga0073689 : Ga0073689_136]

LPRVI MVVNSDFRHDARVWKEALSLSRAGYGVTVFSLAMAGPREQYHEGI
RLVNPAAGPLARFPYRPSYLRVYLQVI TALLREKGDVWHGHDLTLPFVY
LAARLRGGKVYDAHELWQGYDWPGRGGGWNVRRRLVWKGWLHLEGALAR
RCDLVVTNESCALAMAGALGI KPPPVI RNCADPVGEGGRPAAGLREVLG

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LVRGEPLVVYSGLLKKGRGLENLLQAWAGLPVEAHLAFVGRGPSESELRD
LALAAAGFNVHFLPPVKAWELPGFI RGASLGVVLTGERNLNSRYSLPNKL
FEYLAAGI PALASDLPEI RRLVKEYDAGVLVDPDRDHNGI RLALTGLLDDR
EGRERLRKNAFRAGENLTWQGEVKRLI DEYSKI TGKVL

>2617921681 Ga0073689_13615 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_136]

MYFPI SGVEVSPLI PPLVAFVSSI TASAGVSGAFLLLPFQMSVLHFTSP
SVSPTNLI YNI VAI PGGLYRFI KEGRMAWPLTWVVVGTLPGVFLGSWVR
I FYLPDPKAFKLFVGCVLLYLGVRLATEFTGGSKKQKAANKALDQKFKER
VARI KAE TNKKI TSGLP AEAI VKTKTFS LKKI EYEFWGETYSFPTMTI FY
LALVVGLI GGVYGI GGGAI I APFCVSI LGLPVYTVAGAAAGTFLT SI AG
VVFYQI ASATSLGADTNVAPDWLLGALFGVGGLAGTYCGAYI QKYLKEKI
VRVMTALI LFLALRYI LQFLF

>2617921680 Ga0073689_13614 competence/damage-inducible protein cina [pelotomaculum Ga0073689 : Ga0073689_136]

LRGEI I FTGTELI LGQTLNTNAQYLQQLADLGI DI YYQVTVDNLNRLA
EAI QAASQRAELI I I GGGLGPTEDDLSREALSQSLGLPLI QDEQALKALR
RFFDERNI KMAANNLKQALI PKGGLVLDNPVGTAPGI I LEHLDHI YI LLP
GPPMEFKFMI DROMVPYMI KKFNGQRSI I KSRVLKLCGI GESAADERLGD
LLHSANPTLAPTSRFGEVFLRVTAADNPEQAEKMI DEMEARVRERVGEY
I FGKDEENLAGAI GNLLLRSLTLATAETCTGGLLAYQLTGSSKI GENFI
TGFI FGTGKVSFPFGDI PPLPSDDRELAEQLVSRVQEQTGAGI CMAVTG
QLQVNGLESGPGGLVYI STGTDGKVKSRKLSLWVGVEI RERAVQMALI
I LWRSLTR

>2617921679 Ga0073689_13613 4Fe-4S di cluster domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_136]

VSWE LRVLPERCTGCR I CMMI CSWANEKNFQLVHAHI QVKNRDSEEEACFE
I AFDQYCKSCGI CASYCPSGAI VKERRAPVVV

>2617921678 Ga0073689_13612 aldehyde: ferredoxin oxidoreductase [pelotomaculum Ga0073689 : Ga0073689_136]

LLFKLLNI NLTNRKVDVVDGEKLHQEFLGGLGVNTKLAVDLI PPGSDPLG
PANVLI FGAGSLVGTLLPTAARTELTAKSPLSGRFGTANSGGLWGAALKF
AGYSHI I LTGRSSVPVYI I I DDDQVKI EDAHLWGLDTWTTVKNI RQKLG
DQFQVASI GPSGEKLVRFASVQNNYHGAWGRTGMGAVMGSKNLKAVAVRG
TGEI RVADRP AFARI MREAFKKVLNNEHFGPTRRYGSMVADPYDKI GAL
PGHNFTCGSLPDWVSTRGRYFVETYKEKDLACFSCPVAHAHWARVREGP
HAGYEA KGLEVS YTFEFGAKLGFREI PEI LKCV EI CNRYGI DVI STTGVI
AFAI EANOHG LLLKEFSREVPLEWGDFTGI AGLLEKI GSRQGVGDLLAEGV
RTASTRI PNSTHYAMQVKGEI AARDPRGRWDVWTLGYLTNNRGGDHLRT
RSPVEI LLSPLVNLHLEELGVSEDVVKLDMPEDI KNEI FGSPPSKVN I P
RMAKYAEDLI TI I NSTGLCI RPPTHRTLGPDFYARALTAVCGCTFTAREV
LQAAAKI WDI QHHFNVRGEQI DEYVFP RRFYEEALPFQGGSRPPLSNHE
VAETVKQYLAARGRENI SL

>2617921677 Ga0073689_13611 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_136]

MSGLSHSYTGLEWTPSSSLAKRLKDCLVGFFKTREI SKVAEI YHGAFSYE
LVPDTAI RDTNMGVTSI QSGDLYVCVFEGPRYQGQYRI LGPGEKAGVG
I CGSVI VSAGTFSVDAVRENASPPAGFWELSGPMYLFHFFSGYRCA

>2617921676 Ga0073689_13610 molybdate/tungstate transport system substrate-binding protein [pelotomaculum Ga0073689 : Ga0073689_136]

MGGLRQFGVNI LGKLNTI KPGRPPLG SVRGVDGLLTFNTSLKSEVEVE
RLLDNRNMEGTTERTLKI I QAAALSHPFKKCI RRFWDKYPDI NVELDAAGS
RNCARRVMEGADVLI GLADPAVFAELLAPRFVDDYFVI ATDQI VVTYDD
FSRRRREI SADNWM D LLLSEGVS FARADHRVVP CGYRTL MVWQLAEKFYR
RPGLYQRLCEKSLPEDDYQSVTDLTAAI LEGRADYSFQYLSVAKQFGLNY
VKLPSRI NLSNPAHVDYFSEATVVI WEKRCSPQPI I KGAPI EFAVAVAK
HSPRKELAGAFVEFLTGREGGS I LEECGLI PC

>2617921675 Ga0073689_1369 Transcriptional regulator PadR-like family protein [pelotomaculum Ga0073689 : Ga0073689_136]

MSKEKYGGKNQLQDI PLLGLSTEKMFQPTMLTFI CRKPTHGYELI QEI SR
HGFAEGEI EPATVYRHLRRMEESGYVKS RWD TGN SGPARRLYEI TPDGI E
LLRAWGDLLKRRKEKLEEFSLFEQVMMSGVGLK

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>2617921674 Ga0073689_1368 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_136]
MGVLADKHKYVYPVANKSVAKEKHDFKERDSYMEQLTRSFLSNFRAFIET
ANQS

>2617921673 Ga0073689_1367 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_136]
MGVLVGRI PGNTGGCLGEERKKRLLNTMKGLFTFAENFGLAAGEREYQLR
KEATGKEVLTGLENYGLAVCEI GTNFWKSR

>2617921672 Ga0073689_1366 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_136]
MGVAVI KNYAKRECSLRHAVSRFI NGFMDFADKGFWYI GR

>2617921671 Ga0073689_1365 superoxide dismutase, Fe-Mn family [pelotomaculum Ga0073689 : Ga0073689_136]
MHYYPLQPGGHQLPPLPYNALEPVI SSVTLQI HHDRHHKSYVEGLNKA
EI KLAEARRDKDFALVKHWERELTFHSGSHI LHSI YWTVMAPAGSGGQPG
I KTQSQI AGYFGSFPAPQEQTAAI DVEASGWAVLVWQPAWGRLEI LNA
EKHQNLTQWGGI PVLVLDABEHAYYLDYQNRG DYVRQWWRLVNWREVER
RLVLAMQARVPLTERY

>2617921670 Ga0073689_1364 ATPase, P-type (transporting), HAD superfamily, subfamily 1C [pelotomaculum Ga0073689 : Ga0073689_136]
MLTVDI PGKGTFRNFRHI VLDENGAMACDGI LI PGVEERLNRLAEQLAVHI
LTADTFGLCRSSCRGI KGSIDI LTSETGAPEKEKFVEALGAESVI AVGN
TNDALMLKRAALGI VI VGPECASAAAI RSADVAGDI NAALDMLSNPKRL
IATLRE

>2617921669 Ga0073689_1363 monovalent cation: H⁺ antiporter-2, CPA2 family [pelotomaculum Ga0073689 : Ga0073689_136]
MASPAPDVI LNVGLAFLFI TAASWLAANKI NYSSI PFLI FTGMLVGPYAPE
YGAVSFKI I SETESI ELLSRFGVLLLLFYLGLEFSAGKLAIEVGKNLFKGG
VLYVVLNFAAGLFGFWI FFHWPVALVAVGTGVSSSAI I TKLLVDLKRT
ANPETELI LGI MVFEDVFI AI YLSALSGI LTAGFFDVRQTVGSAFLI LGF
I VALI AFGRII GAFFEKRLKPGKTEVFAVGI FTLLLLLAGI LVEKLHVAEA
I GALLLGLVMAETTHSHRVI QMI TMRDLFGAMFFFAFGMAI DYRVFGEV
AFI TAVAVLMTVVGNI AAGLLASWLSGHRKRRVAVNAFTI I ARGEFSI I L
ASFAAASGLSSDLPFAALYVLVAFI SPVLARNTRLFYEI FEKGKGLFK
KTPVQS

>2617921668 Ga0073689_1362 potassium/proton antiporter regulatory subunit, CPA2 family (TC 2.A.37.5.2) [pelotomaculum Ga0073689 : Ga0073689_136]
VTVI REAELPGLGKKYQLSLENGEQI AVVI YDDGRREI YFLEDADEPLA
SVTLSDQESRQLGSI I GGSFYQPRALERLDTAI SDLRI EWLKRVREGSEI T
GKSI GELGLRKNHGI I I I AVMEDKGRGRKETI HI NPGPGYFFEPGHLVI A
AGRHDRI KKFEMFGANG

>2617921667 Ga0073689_1361 possible tyrosine transporter P-protein (TC 2.A.45.2.1) [pelotomaculum Ga0073689 : Ga0073689_136]
MAGAAMVVI LGI I SPEKAVHAI DFNTVGLLVGMMI I VGTTRRTGVFEYLA
I RAAKGSKEPLKI LASLSLVTAVLSALLDNVTTVLLI VPVTI ALAKQLG
I SPAPFLI TEI I ASNI GGTSTLI GDPPNI MI GSATGLGFMDFVLNLTTPV
VVI YVLTLLFI I ELI YRQLAARPELKENI MKLHEEDEI KDAALLRKCLAV
LSLTI TGFI LHQYVHLESSVI ALAGAALLLLL TREDPEHALNVVEWPVI F
FFI GLFVVVGALEETGVI EVLAAWALGVTGGEMARTGLLI LWLSAI ASAF
VDNI PFVATMI PLLQDMGRLLGI TDLNFWWSLSLGACLGNGTI I GASA
NVVVI GMAEKRGLI NF I EFMKI GFPLMVMSI VI STGYLLFWYFLHTLTA
KLVTLGAGVLLVVI LKLFTKRRAEAGLPELP

>2617921666 Ga0073689_13525 LL-diaminopimelate aminotransferase apoenzyme [pelotomaculum Ga0073689 : Ga0073689_135]
VEKI I ENDFRPRGVDLAVDEVFVSDGAKCDTANFQELFGAGNI LAVSDPV
YPVYVDSNVMAGRTGPVNAKGQFEKI VYLPCTEENGMPPLPRTRVDMI Y
LCFPNNPTGMTVSREELKKWVGYAHENRSVI LFDAAYEAYVREDWAPHSI
FEI EGAREVAVEFRSFSKTAGFTGARCAITI VPREVRYDSGGKAHSLNS
LWLRQTTKFNQVSYVQAGAAVYSEEGKTQVREMI SYMENARI I REG
LEKAGYRVFGGVNAPYI WLKTPDRMGSWDDFDRLMKYANVVGTPGAGFGA

CGEYLRLTAFGARENTQRAVERI RTRM

>2617921665 Ga0073689_13524 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_135]

MKVLFIH NEAERWPRVI LNI SNFI CDVGPGRASVEVVANGAGVLGYGPDK
RDLEKMEELHGGQGVFAACRNALNMHDFGEELLPPFVRVVPAGI TEI VE
KODAGYAYI KP

>2617921664 Ga0073689_13523 aspartate aminotransferase [pelotomaculum Ga0073689 : Ga0073689_135]

MRLADRARNI SPSPTLAI DAKAKEMKAGGLKVI NFGAGEPDFDTPEHI KE
AAI TAI RSGKTKYTPVAGTYELKEAI CRKFKADNGLAYEPEQI VVSAGAK
HSLYNTI QVLLQAGDEVI LPSPYVWSYLEQI KLTGAAAGI VETREENGFK
LTPDDLAAAI TPRTRLLI LNSPGNPTGAVYTRAELAALGEVVLKHGLMVI
SDEIYEKLI YDGAGHVS IASLSPALRECVVVI NGLSKAYAMTGWRI GYAA
AARPVAKAI ADLQSHSTSNPTSI AODAGVAALDGDQGPVAMMVAEFVRRR
DYMLERLLAI PGVSCARPGGAFYLFPNVKRYFGKSYKGKLI GNATDLAAV
LLEEARVAVVPGVAFGNDDYFRLSYACSMESI KEGLDRI AGLMYKI K

>2617921663 Ga0073689_13522 TIGR00255 family protein [pelotomaculum Ga0073689 : Ga0073689_135]

MTGYGRGEAVAPGKFTVELKAVNHRFNEVVLRLPRALSPLEDRI RRLIQ
SRVSRGRVDGFLGVEECGEKTTVVKVDKALAAAYYKAMKELQEDLGMKGE
I KLKHLVALPGVLAVEEPAEDVDWWPAVREAVEGALES LVRMRTAEGGQ
LAADLSKRVEKVAQLNVKI RARSPVVVEDYRERLKI RLGDFLKEGCLDAD
RLAAEAALFAERSNI TEETVRLDSHLKQARSCLGAEEPVGKFDLQEM
NREI NTI ASKANDLEI SRWAVEVKSELEKI REQVQNI E

>2617921662 yIzA hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_135]

MEIKLI NI GFQNI VSANRI I AI VSPESAPI KRI I TEARDRGMLI DATYGR
RTRAVI I TDSDHVI LSAVQPETVAHRLVSREAPAQVEDPAD

>2617921661 Ga0073689_13520 guanylate kinase [pelotomaculum Ga0073689 : Ga0073689_135]

MKRKGI LLVFSGPSGAGKGTVCGLRRDNPGRFRLSVSATTPRPSGEVNG
VHYFFLNREDFMKMI DEGQLLEWAEVYGNYYGTPRRFVQETLDRGEDAI L
EIDI QGALQVKEKFPEAVLI FVAPPSMAELRLRLTARGADSREEI ERLG
CTVAEMKLAGRYDYI VINDEVTRALDKVKAI I TAEKSRPRYFTSFEEQFA
R

>2617921660 Ga0073689_13519 DNA-directed RNA polymerase subunit omega (EC 2.7.7.6) [pelotomaculum Ga0073689 : Ga0073689_135]

MDQPTLDELMEKVDSTRYTLVVVAAKRARVLTGGDAAADGAASKPVTAALK
EI AQNKVRYKRTKI GI K

>2617921659 Ga0073689_13518 phosphopantothenoyl cysteine decarboxylase / phosphopantothenate--cysteine ligase [pelotomaculum Ga0073689 : Ga0073689_135]

LFGGGNI TI GVTGGI AAYKAAQLVSSLASGGADVNI MTRSAREFVRPLT
FOVLSGNRVYTDLFDPAAGDGNVQHI ELAVRSDLLVVVPATANI LGKVAGG
I ADDLLSTVI MAATCPVLFCPAMNVNMYKNPVVQRNLADLRGLGYHFVEP
GSGRLACGAEGRGRLAELETI MEKI ELLLSAGDLOGLTVLVTAGPTVEP
LDPVRYLTNRSTGKMGYAVAGAAARRGA AVI LVSGPTALKPPAGVELI KV
ETALEMYNAVLD RFPGVDDVVVKSAAVADYRPRERAGQKI KKSGETMTI EL
EKNPDI LAELGRRKI TOI LVGFAAETEELEQNARQKVVGKNLDLLVANDV
TLSGAGFGADTNI VKLVYPDGS I VPLSRMEKKT LAHRI LDEVLT LRGT AH

>2617921658 Ga0073689_13517 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_135]

MNPMETFTSQHLI DGHVHI MTQRR I KGGI RWMQQLAPKHKMLDPETTAE
ELI GHLRRAGVEAFFNYFYPLSPGESREI NRWQDMADRH PGLLPFASLH
PDDQDKAGI I KEALEELDFPGFKFHPYI QQFGLLDREMELI YERLEEADR
PVVLHTGFAEFYGLPSLTADFRELLRRHPGMKI VTAHMLYPELPLEELAD
LAENYPNLYLDATNI FWLCRPDTPEEEEKMRDFI KRFSRRMLFGTDYPMSM
TI PVEKLYTQGYTI CPDRESLEDLFWRTAARLVGKKRLPFLKRSKTKLTT
CQSRWVCDRLKVD

>2617921657 Ga0073689_13516 CxxC-x17-CxxC domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_135]

MFEEKLLTCKDCGREFVFSAGEQEFFAGKGFEHAPSRCPECRSARKSRRN

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EAGSGGRGYNQFGGAQATKQSFETTCSECGNPTTVPFKPREDRPVYCGDC
YKQKKRRYY

>2617921656 Ga0073689_13515 replication restart DNA helicase PriA [pelotomaculum
Ga0073689 : Ga0073689_135]

MDKNGPYAEI I VDLRTRKADRVFHYAI PPEYKDQI VVGSRLVLPFGGRRL
AGYVVGFYPEDAVRI REI DGI LDREPVFTPELLKLARWMAENYLCSTAG
AFGRI LAPRLQVKASRVVNRVVPAGEELERVLGTMDRSPRQAAVLQKA
VGSPGLTRRELA AAAAETSPKTVDLLVEKGLLEVALEMPGLPEEPVKDVG
SGALRLNPDOAEALROI KGALAEKFGVFLLYGVGTGSGKTEVYLQAI AAA
LAAGROALALVPEI SLTPQMVDLFRERFGGRVAVLHSALSDGERYGWRR
VKEGKASVALGTRS AVFAPLPRPGMFVI DEEHESYKQDDHLRYHAREVA
LKRAQLTGAVVVLGSATPSLESHFKARTSGPYRLLTLPRRI DGRPLPPVR
VVDMLRELKKEGVRGI FSRTLAEAVGGRLAVGEQVLLFLNRRGYSTI VVCR
ECGLVVKCLRCDI SLTYHLDGRLRCHYCNYTTVLPCLPCRCGSRYI RHFG
TGTOQVEEEVMRLFPGARAVRMDSDSTARKGSHORI FDAFREGRADI LI G
TQMVAKGLDLPGVTLVGVI NADTTLHMPDFRAAERTFQLLTQVAGRARG
DLPGEVLVQTYCPEHYSI TAAAHDCAGFYRSEAPVRRSLGYPPFAHLAR
LLFTHKDEEEVKKGAGTAKAVLEGVVGCGDRI DI LGPAPAPLAKI KDRF
RWQLVLKGP RRNTLKEI I KEGLAGLERSGPFRPAVNI DINPQGMF

>2617921655 Ga0073689_13514 peptide deformylase (EC 3.5.1.88) [pelotomaculum
Ga0073689 : Ga0073689_135]

LAVYRI VELGDEVLKAKARAVPKI TPNI LKLLDNMADTMYSGRGVLAAP
QI GVS KRVI VVDVGEGLVELLNPEI LSYEGRETDSEACLSI PGI MGDVVR
AAVI EVKGLDRRGKECI FTAKGFLARALQHEI DHL DGVLF I DRATNI RKL
KQKEE

>2617921654 Ga0073689_13513 methionyl-tRNA formyl transferase [pelotomaculum
Ga0073689 : Ga0073689_135]

MRLVFMGTPDFAVPSLKALVEAGHDVA AVVTQPDPRPRGRGKKKAPQPVKE
AALALNI PVLPQSGVKEPGFI DLLKKLAPEAI VVVAFGRI LPPGI LELPW
YGC I NVHASLLPKYRGSAPI HRAVI DGAKETGI TI MYMDEGMDTGDMI LR
EAVPI GEDDTVGA VHDRLAVLGARLLVKTLDLVGRGOALRI POTGI PTYA
PMLRAGDELI RWD RPAREI YNQI RGMNPWPGARTSLSGRVLKI WRAAVPA
GNDTAFEPGEVLACGPEGI TVGTGGGKLI I TELQLQGARWLNAADFLRG
T QAPVGTKLGED

>2617921653 Ga0073689_13512 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_135]

VKVS NLI PVKR LFI GLLGVSI LVAGLLLAGI WRLALNPSRTVFDQALLL
TLAGLLVGGMVVAGFGVGGI VLT VLYARDI TALHGPMRVAVNI FFPFALA
LGGVFHI DKDRI KNSFI EVNNHLVRSKAFRLPAQI LLLAPHCVQKSDCP
HKI TVNVDNCHRCGCCVVKELLELRDKYGI KMGMATGGTLARKLVQEYRP
RAVVAI ACERDLTSGI QDSNPI PVLGVTKRPFGPCFNTWI EVPKVEEAV
RFFLNTATSI TGGEI RKG

>2617921652 Ga0073689_13511 16S rRNA (cytosine967-C5)-methyl transferase
[pelotomaculum Ga0073689 : Ga0073689_135]

LAKI SARELALKVLR AVEEEGAYANLALNQVLEKYRPGKLDRAFATELAY
GTLRSLNTLDWVLA FVKQPLKAQTA AVRN I LRLGVYQLMFMDRVPPSAA
CNEGTEMARKHGHAGAVKFVNGI LRNVSRRI KDI EFPRLEDHPAEHI SLH
YSHPAWLVERWLKEFGLEETI ALCRANNGPAPNTARTNTLKI TRVG LAER
LRGEGLAVRETAWAPEG LHI EGFFSPGSLVAFREGLLQAQDESSMLAGRA
LLPAPGSFVI DACSAPGGKTTHLAQLMENRGRI LAVDI HSHKMALI EKNC
ARLGI TI VEGLTKDARELPKEYHN RAGFVLVDAPCSGLGVLR RRPDARWR
KEPAQLLAI VKLQAEI LEGVSRCEVGGVLYSTCTI TSEENLEQVENFL
ARHPEFELESLVPYLPEGVDSAGTLARGYLQI LPHRHGMDGFFI ARM RKK
GI G

>2617921651 Ga0073689_13510 23S rRNA m(2)A-2503 methyl transferase [pelotomaculum
Ga0073689 : Ga0073689_135]

MMKNNCKVNLKDLNLP ELERLLKELGA EK YRAGQVARWI FQKGVASFQEM
TNLSREL RERLAATAWLSRPEVLARQVSRRGDTV KYLFSLPDGOAVESVL
MKHNYGNSACVSTQV GCRMGCRLCASGLEGLVRNL TAGEI YDQVLGI QD
SGERVSHVVI MGSGEPLDNYGAVLDFI KNLTAPYGLNI GCRHI TLSTCGL
VPGI RDLAGEKLPLT LAVSLHAPNDR LRDSLVI NKKYSLKELMAACRDY
ARETGKRI TFEYALLAEVND SREHAEELGRLLSGMLCHVNI PANP VPER
GVQPPPRERVELFKQI LEKYGI AATVRREL GADI DAACGQLRRVAGKWT

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>2617921650 Ga0073689_1359 FHA domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_135]

LGMFSGLEGSLEKYI EGFFKDRSSGRI QPVEI AKRLARAMRDSRRVSI SN
I YVPNQYTVHLHPSDWENLSAFVSLLSGELQEYVKQKAEKKYTLAGPPV
VNFAGNETMAVGSI LVEAAFSEAPPGGEQPVAEKELI EQTQRFI PVKECF
KVDMAPMVYGRLOVNAGPDSGKTFNLSAVSVVI GRRSGCDI VLHDTSI SR
RHARLELHRGRYTI SDLGSTNGTMVNGVKI NTKVLEPGDVI TLGATI CTF
KVE

>2617921649 Ga0073689_1358 FHA domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_135]

MRVFAI ALLVLRVI FLLFLFI F FRLVKWMVGDRENGDPQPARLRAAGP
RKEKGPQGEPGGRI I VVENSSPAPTPGDTFGI GGGI TVGRGDGSDI I I KD
SFASTRHARI YLREEQWLEDLDSTNGTFLNGVWVKQPI VLANGDRI RI G
GI TFQFVRWGYEVGSDN

>2617921648 Ga0073689_1357 protein phosphatase [pelotomaculum Ga0073689 : Ga0073689_135]

MRWARI TDTGLVRTL NEDSLLVLPGI GLFAVADGMGGHRAGEVASRMALQ
LMERDLI RRLASGENPENALVNSI KEANRSI YDQAGRNPWGAGMGTTVTA
CLMRDGOI LVAQVGDSRAYLLRDGGI ALLTEDHSLVWELLKNGGI TEEQA
LVHPQRNVLTALGTEPSLAVDLYRVKAGPGDMLLLCTDGLTEYLRPDDI
HLTVRNSPELDAAARNLLEKALRSGGADNI TI VLVEL

>2617921647 Ga0073689_1356 cell elongation-specific peptidoglycan biosynthesis regulator RodA [pelotomaculum Ga0073689 : Ga0073689_135]

MSPGSFNYKI PRALPGGRAVERGLLLLAGI YTI TGMLALCPGLSGACARQ
TLPAGLATI AAFFLVSLYWNRSRGYRGDRFLLPI TAVLSATGLI FLFRNP
VYGARQFTWLLI GLGALLLTSRVLI DVRFLSDYKYI YALAGLLALI LPI F
FGVEQGGAKSWLDFGLFQFQPFSEFVKI LVLFLAGYLSENRAVLTAGTRS
LGWLALPRLOEWAPLAAMWGVSLI LVFQORDLGTALI YFGAFLAMVYAAT
ARVFYVLI SMGLFVGGAVASFLLFDHVRSRVEI WLNPPWYI DTTGYQVTO
SFFAI GSGGVLGTGLGQGYPNFI PAVHTDFI FSAI CEEMGLAGGAGVI I L
FMI LI FRGMKI ALI AGGDFEALAASGLTALLGLQGFVI I AGVTGLPLTG
VTLPFMSYGGSSLVANFI LLGLLLNI SHEANESHEK

>2617921646 Ga0073689_1355 peptidoglycan glycosyl transferase [pelotomaculum Ga0073689 : Ga0073689_135]

MKNNI LKLSYLLGLFVVL TAYLSYLQVFRGPALANPNYNNRRFREI EAQV
RRGNI YDAKGVVLAGMDFSGGRVRRVYPRGTD AHLVGYI SEQGRTGLE
SAYDRYLLGMEGPDRVRNMVNNLLGREQAGGDLI LTVDAGLQRLAMDLLG
NRRGAVVLLNVKTGAVRVMASSPGYDPNHLDENWPSLVKDEASPLLNRV
QGAYPPGSTFKVVTAAAGALAADPGLAGKTFNCPGYLMVNGFKLTDLAHAG
NVDLKKALAVSCNVTFAQLGLSLGAEGFYRTVKAFLGLEQDPDPGI PARPG
TLAPPGRMTPSELASSAI QGEVLVSPLQMALVAAGLGNDGVSMRPYLVE
KI RDSLQGTVHQAVYHPWL TATTPEI AGI I GDGMVDAVRYGTARTAAVQG
LQVAGKTGSAQNPHGQTHAWFI GFAPADRPR LAVAVI LENAGAGGSVAAP
VASKI LAAAAAKGY

>2617921645 Ga0073689_1354 serine/threonine protein kinase [pelotomaculum Ga0073689 : Ga0073689_135]

LI GKLLGNRYEI LEQLGGGMAI I YKGRDTFLNRLVTI KI LRPEYTCDEE
FVKRFRREARAVASLSHPNI VSI YDVGWEDDVHYLVMEYVEGDNLKNLI R
GEGALPPGRAVEI ARQI SEALQHAHENNI VHRDVKPQNI LI TSVGRAKLT
DFGI AREASAATLTQTDAL VGSVHYLSPEQARGETAGPRSDI YSLGI VLY
EMVTGKLPFQGDTP I GVALKHI QEEPPRPSSLNP I FPGLEKVI TRAMAK
APVERYQAARDMAAE L GALSGASSGETTRVGPVDEFATRV I PTVRPPEES
I RPTDGERAVVRRRTGWFGVLI LLGLLAGGAVVFQLYVNVPEI TMPAV
EGKTL EEAREI LREKSI KNI QVTLNHYHPSVPQGV I SQDPPKDEKI KVTR
GVTLNVSQGP EYRDVPPVVG LNVNAARI ELSKHELNI ADTRYDFSNDYLP
ETVFSQDP RAGTKLPK GSGVLYVSKGPRPVTRQVPDLTGMTEDKVRTTEL
EKVKLKL DENI NKASSTDYFPQGV I AHNPAAGGA EVQEGSAVQVTI SNGPG
PSRRFAKVEAKVPDDGKDHELKI VVKDARGTGVA YTGPHRSGEKVVKDDV
PYYGKARVEVYI DGKLVGEKDFD

>2617921644 Ga0073689_1353 ribosome biogenesis GTPase [pelotomaculum Ga0073689 : Ga0073689_135]

LI NWE DN LVEGVVI RAYSGYYYYVDGRWEWECSLRGRFRHEKRQALVGDR

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VLLKPGHGQTGVI EKVLPRRSALVRPPVANVDQAVI I FAVREPDNPGLL
DRFLLTAAVNKI EPLI CFNKVDLTGDGRVELI SRYRGNRYRLVTSAKTDA
GLDNLREALMGKVSFAGPSGVGKSTI LNALLPELKLKTGEI SEKLKRG
HTTRRVELI FLPEGGLVADTPGFTSLDLPMEPGELAAYFTEMEDYQRKC
YFTGCLHHKEPGCAVKEAVEAGRI EKARYQQYLEFLEELI NRRRY

>2617921643 Ga0073689_1352 ribulose-5-phosphate 3-epimerase (EC 5.1.3.1)
[pelotomaculum Ga0073689 : Ga0073689_135]
LI PVVKLASSI LSANFGTLLLEDVLKAEAEAGVEYLHI DVMGDGHFVPNI TIG
PLVVRALRSRSCMCFDAHLMI ENPDLYI EQFI KAGADLVTVHVESARHLH
RTL SAI KER GALAGVALNPATPPSSI EYVLPLADLVLLMTVNPFGGQAF
I PGVLPKI RTVRNMLEQRGLNAEI QVDGGI NI DTAAAVVAAGATVLVAGS
AVFGRKDI AGAVRELKKAEEGGE

>2617921642 Ga0073689_1351 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_135]
FFDAYNKTSTI EWWEGASHEAPVRLTRACSRRRWEWPRQTSRDDRQAENKM
ROEMALGKYH

>2617921641 Ga0073689_13427 chromosome partitioning protein [pelotomaculum
Ga0073689 : Ga0073689_134]
VSKVI ALANQKGGTGKTTTTVN LGI GLAMQGKKVLLVDADAQGNLTDSL
G FHEPDNLPVSLATVLT KSMLEEPYEPDEGI LHHAEGI DLMPGNI ELSAI E
VSLVNTMSRET VLSYI NTVKDRYDYVLI DCMPSLGMMTI NALAAADSVI
I PVQAHYLPAGKMTQLQT I ARVRRQI NPKLTI DGVLVTMVDNRTNFAKD
I SFI LRRDYGDKLRI FQTEI PLSI RAAETSAKGKSI YAHDPHGLAAKAYE
AFTKEVRDI GEKRRAKQHKADLSR

>2617921640 Ga0073689_13426 chromosome partitioning protein, ParB family
[pelotomaculum Ga0073689 : Ga0073689_134]
LAKNDVRNSI KLTSVDDLFTTEESRAEQQREKVM DI PLSEI SDFPNHPFK
VKADEAMLEMADSVKQYGVLPGLVRPKADGGYEMI AGHRRKKASELAGM
NTMPC I VREMDDDAAI I I MVDSNLQRESI LPSEKAFAYKMKLEAMNRQGO
RTDLTCSQLGNKLDGKKSSEI LAEQMGESKNQI FRHI RL TALLPSI LEMV
DEKQI AFNPAVEI SYLAENEQQDLYSTMQSEDC TPSLAQAQRMKKLSQDG
RLNMDVI FSI L TEEKPNQKEKFNI QRERI DRFFPSSFTEKQKEDLI VQLL
ESWYKKRQREQER

>2617921639 Ga0073689_13425 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_134]
MYFTEGRLLWAYEHMMQEKPKHERDPAKNMQYRDCGHCPRFDKQLKKCGKE
KCDI SKE

>2617921638 Ga0073689_13424 L-amino acid N-acyl transferase YncA [pelotomaculum
Ga0073689 : Ga0073689_134]
LAMKI REASI NDAPSI AKVTVDTWKTAYRGI I SDEYLNLSYEEREKGWR
EFPFHNSFVYVAEDET KNI I GFVAAGPERTSNPVYTGEI YAI YVYESHQN
KGVGSSLLRSVMKRFEQLGVYSVLVWVLS DSPYRRFYEL YHGHQVESKTL
EI SGLKNEVTAYGWLDI KENF

>2617921637 Ga0073689_13423 pilus assembly protein CpaB [pelotomaculum Ga0073689
: Ga0073689_134]
LKLLKNRI FLSALCLI LAAGVSFFLLPRFYESKNATVTVLRAATDI PAGT
AI QDKHLVSAEVGSYGLPEDVMNDKSLI I GKVAQADI AKGDFLFPQKLGG
TI VNELLDRI AANNQRLVTI SVPSI AAGLSSHLSRSGDI VTVAVFTDKSPN
GQSASPQVI I YPELKELEVYSAENARAQDAAQVRKQQAESQSSTGDPI VK
AVTLI VSETQAERLI QAEYTGKLHLVFEKRSVSHEQ

>2617921636 Ga0073689_13422 AAA domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_134]
MSSKI I AVWGGSNSGKSTFATNLACALSAHERLVGLI SSNLVFGELQI FF
GQNVPPKEGLFRALSEDNPNI GEKFAASGESKNLFFLSAPTRYAGLLCDT
I TFEQVEQMI TAAAVVFDI LVI DGAAELTNPVSGVGLWLAETI CTLHRPS
I AAQMW HQGVSD FVRELHI AEKQTHI LQATNGEFDDQTYREMTGPSFPFE
LPYVKRASELQAGTPLYFYRDRACRYYSKVLEQI ADGI CGGGKP

>2617921635 Ga0073689_13421 pilus assembly protein CpaF [pelotomaculum Ga0073689
: Ga0073689_134]
MNSRFSI HDLI YRANKRRSATEESNLEARDYGEI LDRLQRI I AQNHSTEL

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AQVLYSQEAEAKLKDLI MRYLNSEQLVSKDLWNI SELVDAVYNDMAFVGL
LSPYLQDADTEEI NVNGCSGVWVOYKDKKVRLEPETFGSPEACANI VRKMS
RFGGVI LDGSKPVGDSYI SRGVRMSGAI EPCVDANAGGI ASI RKQKPSFI
TRQNLI RWGTATAEELDFLT I CVNNGVSI AI AGATGSGKTADMGYI LSTV
APEKRI VTI EDTRELSLAKYDENG I MTNDVI HLLTKEAPNPVTMLDLLKL
SLRLHPEI LVP AEMRGAEALTVQEAGRTGHTI VSTLHANSARSAYDRI LT
MCLEAGTSLSEERLLRNI VEAFFI MI FKRQLPDKSRKYMEVF EATGVQNG
EVTGTTLYRYTV DHYEHDKSGRI TKVAGNHQRLGNI SPALAEKLLVGGVP
QKEI RRFAEGAEGGSP

>2617921634 Ga0073689_13420 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_134]
MNSI HLSLMLVFLLI SLALFLLKLNP FVVERNPLKKRRLHLAGAKLKTA
ERI AI RLQTLFRQTRCTRKKFLTQLSI

>2617921633 Ga0073689_13419 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_134]
MMMLAAAAGFLAGMMLFDSPDLAAVAAGCLLPAPYI YLTVKSATVAREE
I EGLENTMSVI TNAYASCDDI VKAI ELYVEEKNRYLP PHLRTVTPFDEFV
SEI KYI NPNI EHGLYRLSAKI RNR YFAEWTKI LI LCHHDRRLKFALFPV
KAMNDAKSMQVESDGMVVRVWRDYLLTAGLMFSVI PLMRFSNAEWFSI LT
ATAVGKLLVVLMLLTALGTAFYVLRATK PANR

>2617921632 Ga0073689_13418 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_134]
LFYQTVVFI LLLAAGFFI CREFLKI PKASMKKNLRLNQTQKEKPGKRLLN
RLVMP LVKPVARLI RLDPVQEARMF SMLRRGGLALTPQEYQARALI CAAF
TLLLLI PLLLI GATSLTPI I VI FAVVVYFHFTSD LKDKLAKKKRI EMEM
PSFI RSI LYKLDDMRENNQKT VVQADLVQI FEDYLRVASEVFYDDI SI LV
LEMKSI SI EAALRNFNARLGLTDI SFLVNALI GLHRGERQGDALAYLARD
MDVKAREALKTKLNKLP SKVKI ASI PLVAVTLATLLYVI GSHMTRSMGGL
F

>2617921631 Ga0073689_13417 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_134]
MRKRMATALVKAGNV LAKRDGDMTGWLI VVLVVVVVGAI FMTLYQSSI T
DI WNSI VAKI TSLLN

>2617921630 Ga0073689_13416 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_134]
MMTALKNKI KMAGLKARNVLANPSGDQMTGWLI VVLI VVVVGAVFMTLYQ
GSI TTI WNSI VTKI TNLLN

>2617921629 Ga0073689_13415 protein of unknown function (DUF4320) [pelotomaculum
Ga0073689 : Ga0073689_134]
MNSQHRGMGERASLPRPFPKLLDKGSSYI DLI VKTLVVI TLMATVI SFL
GVFTTYLNLN HMCRRVVRVVELEGQVADTAYDV FYRLKQQTGLSPEMTI E
DVAYCDEQNQKI QLRDTFTI TMTYSHAFTLFRPSFTDPI QI HI PMRVSI T
GMSEKYWKLP E

>2617921628 Ga0073689_13414 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_134]
VDYFKRMMNNRKGDVFLFI LI LVFFI LTLAVI LSEYFRI ESLYQQA EYVI
QRGVNSSVEYAMRDDYRRDGYSRMDSALAEETLYAYFHENMGLDSELNKY
AGNQWVYQLEVERI DATDSPCLTLTGALKTRSVFNFLSGAI RLPFTI SS
VNI RI EEEVPHD

>2617921627 Ga0073689_13413 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_134]
MI KKLI FTI PLVLVCCLLSAKAFALSESDI TI NI ASPI DNLASESGVI A
VEQFPARI SI NTTAKTGSLTEVRLEYGGQSQAI TPNHTLTI EDKQACGPY
TVTAQTDEGAVLV TANVVFQVPATYDTRYRTI GMNVKEI YEGETLLRAF
PDPQRI DLVSANTVADHEQERI AAWI NRCDGGTYTLKGS LVVEI YGHASG
RLYGTYD TD DFEPLTTRYCWTKKALI AFETMRDTALSYQAPVKI DVEAT
WCDESKQEI FGRLTAQDKGVPELLYPYQTTSVTFHKDDI KLSRNFQYMGL
EWDYTPETA EYTDGESVTQTEI TQKI HYQI PAAQFYFKF KACEGNDLSVA
I RAPATVNRGDSYSFTVI YLNSGSSPAYDVPLKGTVDGATI EEI PVTQDF
PANTSKAYEVKRTADTADEI RLWAHI GVPEGFI DGNPDNNTATAI I KVV
DPAPEPTPNNNNTPD EPTDPEPTDNPNNPGNPPDEPPGLKEPCDLSA

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AI LAPPTVYEEKYAYTVSFTNHSGRELNAVPLAGKSDENTLVQI PQTAA
FQPGETKSFTI EGTAGKASEI YHLWANVQAPDGF I DGNLSNNTAVSSI TV
VEKPAGSPDNPPNDPNPNPEEPGNPDNDPNPNNDPNNDNLLCDVWVNLS
SPPI AYQEEYSFTVYFANSTGKALTDVGLNVAI DGHMVLAVPATANFRA
YEKKSYLVTGTAGEKGAAI QLAAQVSPPADYTDNTMGNNQAAAEI MVLEC
PYDLDVQRI TPDYKQNSVI TTVKVSNRGSLDFTPGQNVTVLFQI PELT
FSKRI NMVVMKEDTWNVSVRWDTSPVQTDKNI TLI ATI NPDEI LDNETS
TANNTYTQQAVI KNVTYEKPEESRALPDPPQRNEQPRVTWWEQRYENGQF
VWRQFYAELRVNATLDYDTKSRGYLKSGYGYAI RVTATVDTNYDRPELI T
APQTAEVYLP EHYETAI PLEKEGGQFVFRENPA SPFKYRKQYVPI WFPD
NRDYI AQLLVTD AHTPGGTL SKWLTGGALKI YVVD SMYDDDDTTVGN

>2617921626 Ga0073689_13412 leader peptidase (prepilin peptidase) /
N-methyl transferase [pelotomaculum Ga0073689 : Ga0073689_134]
MDWKKRI I PDWTWI SI LLI GGVSALFSEPALAQRI AGLLLLGVCLLFLA
VKYGGVGGDVKLTAALGFCFGLNALAAI LFFALLPAFVYGLATRQRSVP
LAVFLCI GFSI YAGVLF I YGLTC

>2617921625 Ga0073689_13411 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_134]
MTEEKRMVDTYEVI HAI HVG DREI LFAVDEGKTDCPYMVCDNWDNPLGI
DOFFDPAGSDDYLEMMTEFTDRVQAQLEAVKAERDKI I I PLSPFTPEHCT
PNNYGESI ENKVVI RTERLRPEYRTADNQLVLAVGGFGTYANARGRAVY
TI NLYSGKESRWNREDI LGVLKTEYMPD WAKEQLKQI LAGQQAKHKKQVQ
ER

>2617921624 Ga0073689_13410 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_134]
MEKEI NAGYVI TDR LAVGNAEFVI GHNEKASTQFVTWKCRKNEKD YFWGH
YLGDR LAAVEDLCKRALEEI EYLRSLQSQRDTEDEKERLREQTQGKSI HK
KKHEPER

>2617921623 Ga0073689_1349 Helix-turn-helix domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_134]
MNDLT KYRLCEGLHAPASAKLLYCYLLDMAGGRHNSVVI SI KNLA KSVGL
SRSATSRNLNRLGR LDMI GI VPRYSEDGGRLSNQYTLK

>2617921622 Ga0073689_1348 Adenine-specific DNA methylase, N12 class
[pelotomaculum Ga0073689 : Ga0073689_134]
LATKLQLI TELSERTARSLTRSHANWI SFLKTAAWSYKYPFQDQLLI YAQ
RPDATAACAPI EVWNGKLGRWVNKGAKGI ALI DDSGNRLRLRHVFDVSDTN
SHYSRPVPLWEMRDKYAEAVTESLENTFGELDDKTNLPAALI SAAQNAVD
DNFSDYLSELMDYREDSVLEDVDDLNI KVVFKDTLKI SVACMLLTRCGYT
ADKYLPLEDLQSVI SFNTLNAVSR LGAAATSDI AEMLLREI EATVKDMQKA
ERKQSR TFAKDQGP AHNKGVKQTDERSGKHGTDLHAAGRLSDTRPGPAGG
PNAHQI WDVAQNI PEKPPERDVQPNNAVGRPEQPPGGDRPDGEGARRAD
HGAAPGKEPRTQGQSDGLGRPHEQPQAPGRGKRTDGAYLQLSLLPSEE
QQI EAI EQAEDEKSSAFSI PQEAI DAI LQQGSGVQDGKYRI YLQFQQNAS
AKENADFLKKEYGI GGRAPVLI GTDI DEWHDGKGI TLTREKRTGPEAKI L
LPWMKVQKRI GELI AADRYLNEKEKEHLPAYRQQMEERHQQLAE EAYARE
I LNQEPAPAETKPPSRENAPYAFSLGSTVYI GADEYEI LAFDNSAVHLRD
MSFPLFSKKLARSDFERMLRENPLNDHLI APEQPAGEKMEKPLPHALYRE
YLPQVI DRVRTDEI PPYLRDRDTPD SAKQELDEALDRI ALSMRKEHPDF
YEAYATLPKFREWLAEDVFQRTYQDYLTEPRDLATI HGDDPDAP EWARQT
GDETVSRQGDTI TFDSDSSEDEKSSVELDPELDPDQAGETGKQPAEKEI A
AGLELSI DGRRF AI DMI DEETGTVSLRDI TFQNGVGFPI FRRESVGFVRR
ALEQKQAQDGEAAKARLHLAEPPEPKQPRVNFQI TDDNLGAGGQKTKYAWN
VAAI RLVSQLEENRLATPEEQEI LSKYVGWGGLPQVFDKDN PQWGKEYA
ELKELLDEDEYNSARASTLNAHYTSP I VI KAMYACLANMGFQTGNI LEPA
CGSGNFFGLVPESMKNSKLYGVELDSI TGRI AKQLYQQANI AVQGF EETN
LPDSFFDLAVGNVPFGSYGVADKKYDKYFYI HDYFFAKTLDKVRPGGI I
AFI TSKGTMDKQNP EVRKYI AQRAELI GAVRLPNNAFLANAGTEVTTDI L
FLQKRDRVMDVEPDWVHLSTTADSVPVNQYFADNPDMVLGTMVFDKSMYG
NESETACLPHEADLAELLREAL ENI HAEI NDYEI DDI SEDTDTPSI PAD
PSVRNFSYCLVDGEI YFRENSRMNRVETSVTAQGRI RGM I ALRDCVRELI
EYQTEDYSD ETI RMOQRKLNRLYDAFTAKYGLI NSRGN SMAFADDSAYCL
LCSLEVLDENGEMERKADMFSKRTI RQRTAVAHVDTA AEALAI SI AEKAC
VDLGF MHSLTGLSEEQLADDLOGVI FRNLGDQDPAQVPQAFFDI TRCPFV
TADEYLSGNVRNKLRLARGLAEMQPD LAAQI ASNI KALEAVQPKDLSASE

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LDVRLGATWLPSPDVVKDFMFELLETPPMYRQYI DVFYSSYTSNWNVKGKN
DDRSNDI KANVTYGTGRVNAVYKI I EDTLNLRDVRI FDTI FENNVEKRVLN
KKETAI VQKQKEAI KEAFRDWI WKDPRRRERLTRI YNDRFNSI RPREYDG
SHI KFTGMSPEI TLRQHQVDAVAHI LYGGNTLLAHCVGAGKTYEMAAAAAM
EGKHLGLCQKSLFVVPNHLTEQWAGEFLQLYPSANI LVATKKDFETKNRK
KFCARI ATGDYDAVI I GHSQFEKI PI SAERQKRQLQEQI WEI TDPLHQDE
ERGGPGPDRGPEVQRPVCMPLPGRTDGRPRHCFCHRHTLQLHDRDVHH
AAVSAI RSPAPTRASAF

>2617921621 Ga0073689_1347 Helicase conserved C-terminal domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_134]
MQRYLQYEALRQQLQHFDCWASTFGETVTAI ELAPEGTGYRAKTRFARF
YNLPPELMSMFKEVADI KMDMLDLPVPKANYHNNAVAVKPFSEFQKDMVAELG
ERAEEKVRNRKVEPYEDNMLKI TNDGRKLALDQRLANPMLPDHEDSKVNAC
VDNI FRFWDQHRDKKLTQLVFCDLSTPKNDGTENVYDDVRHKL TARGVPA
DGI AFI HDANTETRRKELFAKVRAGQVRI LVGSTFKMGAGTNVQDRLI AL
HDLDCPWRPRDLEQSRGRI VRQGNNDDEVHI FRYVTGNTFDAYLYQI LEN
KQRFI SQI MTSKSPVRSIEDI DETALSYAEVKALATGNPLI KEKMDLDI Q
VSKLKLKLANHLSQRYALEDRLLKQFPRQI KSTEERI AGYEKDI ARYERH
SEKEPAGWDVEESKFAGMTVKDI FYPEKAKAGAAI LEACNLMTLPEPQEM
GSYLGFPMLFSFDSFNKKYQI TLOGALSHTVALGADVHGN I TRLNALAE
MPKKLEYCREQLKTLRQOMETAKKEI DI PFEKEQELQSKSARLHELNI LL
NMDKAENEI MDDQPEDLDI PEKAVGYER

>2617921620 Ga0073689_1346 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_134]
MDEPFI FQTLPERI VALFPEI DSDTAI DLLHNNDYQQLHQRGELTERH
PFI SAVLEGE GPI ALSAEH KI LTDYLD TATRMEDMERMQLYFRGHTDGF
SYLKKI GAI

>2617921619 Ga0073689_1345 Protein of unknown function (DUF3991) [pelotomaculum Ga0073689 : Ga0073689_134]
MPYVAPEQI KRAKQMDLLTYLQHYEQELVHFSGNVYTTRSHDSLKI SNG
KWCWWSRGI GERSALDYLI KVRGMTLPEAVMRI DGOAVVQPVPSKARET
AEPRKLLLPEKNKSNDRI AYLRGRGI HGTLI DYCI QTGRLYESRHRRNA
VFVGFD PQRI PRYGAPRGTCSSRFMGDASGSEKHF SFSVPAREKSTKLHL
FESAI DLLSYGTLELLSGRDLAAGKLPLPGGYLQAEKEHWGKHPARRSDA
VPQGLPANNRNC PASGQ

>2617921618 Ga0073689_1344 prevent-host-death family protein [pelotomaculum Ga0073689 : Ga0073689_134]
MQI KPSASI RQNYNEI ADLCRSTGEPVYLTKNGEGDLVMDI EAFTRREK
MLKLREELLAVEEDRLAGHAGTTPDELD SYLDSI I DEVEHGKEASV

>2617921617 Ga0073689_1343 Plasmid stabilization system protein ParE [pelotomaculum Ga0073689 : Ga0073689_134]
MEKKPQYKVI I SDRARQMLAGHVRFLAQKSPTAARKI KNDLMDAI RSLHQ
MPERFPFLEAEFI PPNKYHKMFVEKWYLI LYQVKDQTVYVDYI MDCRQDY
GWLVR

>2617921616 Ga0073689_1342 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_134]
LKHTEI FNRLTGI SCPVFGVSWNPPEQRKI ARKI I I FLESKRVLYSPYE
YETVHPVI NSVVEI KHFLTSELPDI NENSDLQNYVRAMRNACNFKLSKCR
DDDDFRHHASRP GNI DNWI FTSAI GEMRGVFGI MI GQI SSSYGI DVEDDL
AQI I PVDKNNRSQYKG

>2617921615 Ga0073689_1341 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_134]
MKGGI RGEKPLI SEFGRPN SVLAAATQDCCLVLGVGYDCSQI QPAEKKNR
GLLPVALVI FVLGQKKGDTFLVPLKDI HFTI SI LSFLFNKSKFLLLSYQ
FTCI SFI KI

>2617921614 Ga0073689_13335 Uncharacterized conserved protein YacL, contains PIN and TRAM domains [pelotomaculum Ga0073689 : Ga0073689_133]
VVRKI VYVVLVFGFAGLGF TGLRLMESGLI TLPANLPHQLKFGLI GLAT
LI GLI AGI LLSPLL MRGALRLTVFI EQYLQKTPTQDLVMSVGLI TGLI I
ANLMGSI LSSMGLFGKLI WI LVTLL LAYLGLSVGVKKREDLLALFASFPK
FGKERGVKAEFRAGQYKI LDTSVI I DGRI ADLCESGFI EGI LLVPAFVLE

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ELRHVADSPDLLKRNRRGRGLDI LNKMRKDPEI KVQVYDNSRGLEDI AEV
DTKLVLKLAQKLSAKI MTNDFNLNKVAELHGVKVLNI NELANAVKPVVLP
EEMVVLQVKDGKEASQGVAYLDDGTMI VVDGGKRYMNQTI PVLVTSVLQT
AAGRMI FARPKYDRRGEGQYGEI VSMQ

>2617921613 Ga0073689_13334 2-C-methyl -D-erythritol 4-phosphate
cytidyl transferase [pelotomaculum Ga0073689 : Ga0073689_133]
LLVKVAAVPAAGSGSRMGTTETKKQYLSLAGI PVLGHVLKVMEASRVVQD
IVI VVGPGEEEEYCRSAVVEKLG I KKVRAI LPGGKERQDSVYCGLLALSPA
TGI VVVHHDGVRPLLSAGDLEKVAVAEKEHGAVTLAAPVKDTVKLAESDGF
VSGTLPRERLWLVTQPAFRYDLI LGAHRRAEDMFTGADDAGLVERLGL
PVKI VPGSYENI KI TTPEDLVVAAALLGSRRS

>2617921612 Ga0073689_13333 2-C-methyl -D-erythritol 2, 4-cyclodi phosphate
synthase [pelotomaculum Ga0073689 : Ga0073689_133]
VTHTRSKI I EYGVPI RVGFGYDVHRLVEGRPLVLGGLRVPFEKGLMGHS
DADVLAHAVMDAMLGAAGAGDI GRHFPDSDHRYKGI KSLI LLETVRKI LI
NKGLVVNI DAVI VAQAPRLSPYLEEMARKLAGTMEI EPARVNVKATTTE
GLGFTGTGGGI AAYAVALLI AAP

>2617921611 Ga0073689_13332 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_133]
MHVKLPYGEKMSRTFSAGVAGFGGKI SNVEAVI NAADKALYSKEAGRNR
VSVAGGGRVDLPVVMTEHGGKAPRI I AVWSPLPAGKTFVAANLAAVL

>2617921610 Ga0073689_13331 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_133]
VLVVTRPEI EWYNARPVPLERVAGNQAAWKMGGQCGEVPWVMLVSGNVG
SI ETLKQLPCDVVVDDGMLFFKQLENFEGRLKVLHDQDVHFI TCFVNR
RRI I YFQVMVNWQVKVGQTLDDHFMGPVPLCTYI DKYLNQTRPCRHCFL
SQRFTVTFHI SRSQFLHENALI AL

>2617921609 Ga0073689_13330 phosphonate metabolism protein PhnM [pelotomaculum
Ga0073689 : Ga0073689_133]
LPDRVI ENCR I LI SDGLI SKVTGCEEI GADRETTI I DAAGKYI FPGFVDL
HCDAI EKEI EPRPNTLFPTGI SFRELEKKLAGQGVTTFHFI SFAEGELG
LRSNAMAARI I KQI KKDTAQYSLI RNRI HVRFEI SNMSAGEMI AALI RRR
VFDLLSFMDHTPGRGQYQKVEDYRAYLANTYRMSSGSI DEI LARLGPDSG
RGSFCCVKGLSGRFHAGTETEI YEI LRSAGSSQNNGGTGGFDLSI YLYM
YTTGPAP

>2617921608 Ga0073689_13329 alpha-D-ribose 1-methyl phosphonate 5-tri phosphate
synthase subunit PhnL [pelotomaculum Ga0073689 : Ga0073689_133]
VADI LVVKNLSKI FI MHI LDGKAI QGCKDI SFALPEGCSLGI LGPSGVGK
SSI LKCI YRTYI PTGGQI I YHSRQFLSI DLSAAPEI KI LALRDREI GYVS
QFLKVMRVSALDI VAEGLLKGLMEHEARYLARDYLSRLRI SPELWET
PSTFSGGEQQRNI NI ARTAI VKPRPLLLDEPTASLDARTKEAVI DI LLELK
REGTSVVG I FHDLDTMRRADQTYNVPVNGSYAEVS

>2617921607 Ga0073689_13328 putative phosphonate transport system ATP-binding
protein [pelotomaculum Ga0073689 : Ga0073689_133]
LEHNSEI VLYCRNVSKI YGLSCPACI AETGPEAGSNI CPRCGSVVACGDI
FLDLYEGEI LGI VGESGSGKSTLI KCLYFDLEPTSGEAYLSCYQSGKKN
FAENSQKKRYI RNHLTGMVYQNPGLRLDFSCGGNMAEKLLTADCYNLG
KI RRRAAELLEKTEAPI ARMDDLKKNFSGGMQQRVQI AKALANNPPI LLL
DEVTTGLDVSQAKVLDLI KYLQRLGI SMLVVS HDLGI RLLTNRTAVM
KDGR I VELGLTDQI LEDPRHPYTQLLVNSLL

>2617921606 Ga0073689_13327 Phosphonate metabolism protein PhnJ [pelotomaculum
Ga0073689 : Ga0073689_133]
MVNKRYVMDPSPI PRWDI PKLHMAETLYLFGAGREKRI YAI PPYTEVLPL
EFEDHKFRVENFSGRLRCSRCSTDAYLDEI FDDTGKKI YLCSDTNYCDQR
LAALNKPERKA

>2617921605 Ga0073689_13326 Phosphonate metabolism protein PhnJ [pelotomaculum
Ga0073689 : Ga0073689_133]
VFREI AGLRKNKKYNFAFI DEQAKREI RRKTLKAVAI PGYQAPFGSRELP
I ARGWGTGGLQI TLALLGPDDVI KVI DQCGDGSVNAVNLRLVVKTTGI K
TTLNTKEATI I QTRHRI PEEKMTVEQI LVLQVPYPEALRI VEPSEVNTRV

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I HAEMDYSKLWVHL

>2617921604 Ga0073689_13325 phosphonate metabolism protein (PhnI) [pelotomaculum Ga0073689 : Ga0073689_133]

MRGYGDVHPALGELRVGYVPLRI PHPCGTGRLYPGRVLVTEAEVI ARFSD
RKG I PKFTVGYGLCFGHNELKAI AMAVLDRMTMAAAEVRTPAEDQEFVLSH
I DGVESGFSAHWKLPYI TFQSDLDRLRSARRRKVEQDRVQGNCRPKEK

>2617921603 Ga0073689_13324 phosphonate metabolism protein (PhnI) [pelotomaculum Ga0073689 : Ga0073689_133]

MSYVAVKGGTEAI ENAEELLKYFRLKHKSKPI EVRQI QDQLRLAVDQVMG
EGSLYAPYHAALAI KQAEGLI EASF I LRAYRSTLPRNHYSLPVDTTEMQ
I I RRI SAAFKDI PGGQLLGPTRDYTORLLDFELAGETEEQAVGFLAGFLA
DLEI NPGEESPTFPKVI DLLRAEGLI EESRANLLEEPVDI TRDAI TFPCP
RAGRLQAMARGEAGGLMAI RLQYAWVR

>2617921602 Ga0073689_13323 alpha-D-ribose 1-methyl phosphonate 5-tri phosphate synthase subunit PhnH [pelotomaculum Ga0073689 : Ga0073689_133]

MI LQVWEDYNQVFYNQKI FRLLDCMARPGKI NLLPQPQPPGDRDYSFLL
HI AGALLDNEVSFACLNGETGFAAEI VRSTGARPVKVEQADFI FCDGRE
KQAGLFLANPGTLQFPDGTATVI MTI NQLSDKEFAGCPEFTRVELTGPV
NGKROVWLAGI HQDNLKWLALQNREYPLGADAVLVDRGRI ACVPRSGKL
TGEVAANELCCG

>2617921601 Ga0073689_13322 alpha-D-ribose 1-methyl phosphonate 5-tri phosphate synthase subunit PhnG [pelotomaculum Ga0073689 : Ga0073689_133]

LESSDRGRI LAGETRAWERLAGEI LSCARVRI RPPAASLVMMRARDPV
EGI VFNPGEVLI TECEVEMDQARGWGC I MGDEPAKALAAAI DAALNNGH
HLKDKI LEELRLQEEKI NSLLQLEYKLAGRTRVDFETMEGPR

>2617921600 Ga0073689_13321 phosphonate transport system permease protein [pelotomaculum Ga0073689 : Ga0073689_133]

MLMPESTARESETGSHSLGSKKFI KRLSLWAVVI AVYVWSAYGTNLSVT
EFVRGYPFMKDFI I RMI PPDTGI LKNLI KPVI ETVQI ALWGTTLAI I LSI
PLGI FAAQNTSPHPVVYQFTRMI LNSLRAI SEFI FALI FVAAVGLGPFPG
VLALGI HSAAGMLGKYAEAI ENVDRGAVEALEAAAHLQI I I YAVAPQV
LPEFI TYNLYRFEHNLQATVLGMVGAGGLGFELI TSMRLFKYQETATIL
LVI LFTVTVDYFSSKI RARFI

>2617921599 Ga0073689_13320 phosphonate transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_133]

MI KI RNLSKSFARNI LALNNI SLNI AEGDFVLLGPSGAGKSTFLRCING
LVRPSGGSVEVYGRNVHRSWKNLREVRKYTGMI FQQFNLVKRLTVFENVL
CGR LGHONI LASSI KFFSREDREFAI YCLERVGLVEKAFQRADQLSGGQQ
QRVGI ARALAQRPRI I LADEPVASLDPKSTQNI MNI LKNI SLEDKI TVLV
SLHDLAVAKQFAQRVVG I KNGRLCVDKKI SLLAESDI NEI YQYERVDGCF
PGKVKYAHA

>2617921598 Ga0073689_13319 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_133]

MHKEAPEALGGYGKI I RYDEAEDSDYEI I RETAKI LNLDLNKMK

>2617921597 Ga0073689_13318 phosphate/phosphate/phosphonate ABC transporter binding protein [pelotomaculum Ga0073689 : Ga0073689_133]

VLSWKVKTAI TFGLVVSFLFGLMAGCSAGSKNSQEQPRKDAKQVVRIGL
I PAEDSQDMI KKFKPTI EYLEKKLGTKVEAFTATDYSQVI EAMRAKHI DI
AFFGPFSYVLAADKANGEAFVGVDRDNGKSTYQSI I I THKDSGI KNLGDI
KGKDFAFVDPAAAAAADNDI TFERMVKEGLI SPEENVII A

>2617921596 Ga0073689_13317 GntR family transcriptional regulator [pelotomaculum Ga0073689 : Ga0073689_133]

MLI DKENGI PYYRQLAAFLQKI EEEVYKEGDKI PSEAEISLI FNVNRHT
VRQAI SELTHLGI LYKI KGKGTFTREKADYVNYRI SKKTRFTQNI LEVG
LTPGAKLNKAVI I PAEEKVARNLNI NQGEKVFLLEI LRFANNDPFSLSST
YLPEYLTPLGLEKLNKFNSSLYQI LESHYGLQPARTRSTFHAAFPSI DDSL
QLSI PQSLPVLKVESVMVTDNGTAVEYSI TRFRGDRGKI TVDFI

>2617921595 Ga0073689_13316 nondiscriminating glutamyl-tRNA synthetase [pelotomaculum Ga0073689 : Ga0073689_133]

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LSTVRVRFAPSPTGPLHI GGARSALFNWLFARRYRGTFI VRI EDTDVDRS
FRRSEENI LEALRWLGWNWDEGVQGGPHGPYRQTERLELYRRYASLLLO
SGRAYRCYCTEEELAAEREALMARGELPRYLGSCRGLTPADCAGLEAEGR
KPVI RFRVPENRVI HI ADLVRGDVSFECAGI GDFI I VKSDGI PTYNYAVV
VDDHTMAVSHVI RAEHLNPNTPROI LLYEALGWEPPEFAHVSLI LGEDRS
KMSKRHGATAI EQYQARGYLPEALVNFLALLGWSPGEEEEVLSLDELKRO
FSLDRVSKSPAVFDLDKLNWLNHYI RQAPLERI TALALPYLVRAGYI TT
PLSPEELERVGMVNSVRKYLSFLEEI TEHVKI YFERVGVRRDEEARRVLA
GEQVPAVFGALKDKLAAGGELTTPGARAALKEVGKVLGVKGPQI YMPVRV
ALSGDTHGPELDKI MAI LGKDEVI RRLEQAGYGT

>2617921594 Ga0073689_13315 hypotheti cal protei n [pel otomacul um Ga0073689 :
Ga0073689_133]
MRRGKYDLGCGKGLLSLKKLPMRMFVLAI NHENRTSKLNLEFAQANSDFP
DV

>2617921593 Ga0073689_13314 serine 0-acetyl transferase [pel otomacul um Ga0073689
: Ga0073689_133]
MFGRLRKDI RVVMERDPAAKSAMEVI LCYPGFHAVLMHKVAHAFYRRGWF
VTARLI SQFSRFLTGI EI HPGAKI GEGLFI DHGSGVVI GETAEI GNSVTI
YQGVTLGGTGKEKGKRHPTI GNNVVVSAGAKLLGSFTVGDNSKI GAGSVV
LKAVPPNSTVVGVPKVVARDGRRVAPAGESEI DLRHDLPLDPVAETLI C
LOADI ERLGKRVRELEKQNPATTPPDEPVST

>2617921592 Ga0073689_13313 cystei nyl -tRNA synthetase [pel otomacul um Ga0073689 :
Ga0073689_133]
MEI YNTLTRRKEI FQPREPGKVRI YVCGPTTYNYI HLGARPLVFFDTRV
RYFAHKGYNVLYI QNFTDVEDKI I NRAREEGKDPLELSRKYI NEYFKDAD
ALNVRRADRYPKVSEHI PEI VGMVDALVQKGSAYVVEGNVYFEVRKFPY
GKLSGRITLEDMAAGARVEVDDRKRDPDLFALWKAAPGEPAPWDSWGSGR
PGWHI ECSAMSLKYLGI NFDI HGGGFDLVFPHHENEI AQSEVATGEPFVR
YWMHNGFVI VSEEMSKSLGNFFLVLDI LVKFTPELVRFLLSTHYRSPL
DFDDEKMVAAGRGLERI KTSI RLLEEAVNREGDTPNAGRHI FRYGNGG
MSPMECI QNKADGEAPAATGDLGAALDGLRASFEAMDDDFNTALAI SVT
FDLAREVNSAVQRLGLTVSPLDREVLQKAMALFGTFNETLGI FRVDESSG
KI LLDGGAGDSSGLVQGLI ELI I QVRQEARKKKDWDAAARI RDGLKELGI
I LEDTPQGVWRKKQR

>2617921591 Ga0073689_13312 ri bonucl ease-3 fami ly protei n [pel otomacul um
Ga0073689 : Ga0073689_133]
MSLLFKTESDKTGRPADLPALVLAIGDVVYELAVREYLI STGLVKVSRL
HCEVVKYVNAGAAQARI LRSLEGLSSEEEAAVARRGRNARSPTPRGVDVI
EYRHSTALESLVGYLYLKGAARLCEI MALALKTVGKDF

>2617921590 Ga0073689_13311 thymi dyl ate synthase (FAD) [pel otomacul um Ga0073689
: Ga0073689_133]
MVYNANTSKI LI LAHTPEPEKI CAAAARI STTLWPAI ENFENTTSESAGE
LVSKVLQYGHQSF I EHVSTI AFENVSAFVEQFMI EFRSSFTVKSRRYV
NFGGMGYVPDFRSEDVSKNKKQVLDLYHDQMNLYLFTSEYSLVDSGVP
KEDARFLLPYSYKSNFYCTANARELAHI I YSAVSGRGSRFPEI KI I GETL
LAQAKI I CPNI FDN I ENLEYGTEDKELKLRLFGNNKRSYSDNACELI S
HTKDPERVVVALATVI NHLLYPTKEAEELLGSNSMI SDCLKI ACEDKRKR
ELEQI CFTFRI NNI SLAGLTHLARHRMQSI NI PSFTVFGI SDRYI I PDTI
ASDSKLLFKYNSVWDRHKSVI QKFKSLGVACEDLVLYLFGNLLDVVTM
NARELFHFI QLRSCYRAQWEI RTI AI NMLKKLRVAPGI YSKLGPSCFTS
GVCPEGKLNCGKMREVQVLFGRKEI

>2617921589 Ga0073689_13310 23S rRNA (guanosi ne2251-2' -0)-methyl transferase
[pel otomacul um Ga0073689 : Ga0073689_133]
VREALKSNRP I NKI LMFAGPLSGPLQEI YALAREKNI PVQKVDRRLNKF
VSENAHQGVVAAAAREYVDVEDI LAGAGPGEEPFLI LLDEI HDPHNLGA
I LRTADAAGVHGVI PRRRSAPLTPAVARSSAGAI EYVPVARVANMAQTI
ESLKGGGLWI VGADAGGPEVFWDAGLDGPI ALVI GGEDKGLGRLVKEKCD
I LVRLPMAGRVNSLNASVAAALLAFEVVRQRRKALGNEGVSY

>2617921588 Ga0073689_1339 hypotheti cal protei n [pel otomacul um Ga0073689 :
Ga0073689_133]
MKEFLI VDGYN I YAWPEFEKFKETDLKHARARLVSI LANYAPLSGQNI V
VVFDAHQAKNADERTEVI DGLEVVYTRQGETADSFI ERLAGI LSDEGRVL

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VATSDWDEQRI I FGRGAYRLTPGELRAQVKRAGREI EELYTRDTPADSYL
ENRLLDRI RSELEKLRRERG

>2617921587 rpoE RNA polymerase, sigma 30 subunit, Sigma [pelotomaculum Ga0073689 : Ga0073689_133]

VI LQAQREVPNGYQVLVDEEVVKFAREGDDEALEYLI NKYKNFVRAKARS
YFLI GADREDI I QEGMI GLYKAI RDFRMDKLSSFRAFAELCI TRQI I TAI
KTATROKHI PLNSYVSLNKP I YDEDSDRTLDDVI SGSKI TDPEELI I SRE
EFDDI EEKMGEL LSSLEWKVLSYLDGKSYQEI AEDLKRHV KSI DNALQR
VKRKLERYLEKREA

>2617921581 Ga0073689_1332 glutamyl-tRNA synthetase [pelotomaculum Ga0073689 : Ga0073689_133]

MTTNSQI PSNFI QNI I DEDMRTNKYNGRAHTRFPPEPNGYLHI GHAKSI
CLNFGI AAEYGGRCNLRFDDTNPAKEEA EYVESI KEDVKWLGFWD DRLF
YASDYFEQLYEYAVQLI KAGKAYVCDLSAEEI KEFRGTLTEPGKESPYRN
RSVEENLDLFRMRAGEFPDGSRLRAKI DMTSPNLNLRDPVLYRI LRV
HHRTGDRWLI YPMYDYAHLSDSI EGI THSI CTLEFEDHRPLYDWVLDAL
GI YHPRQI EFARLNL SHTVMSKRKLRLQVLEDGYVSGWDDL RMP TI SGLRR
RGYTPEAI RKFC EI I GVAKSNSFVDI AMLEHCI REDLI LLAPRVM AVL RP
LKVI I DNYPEDRVEELDAEYNQENPALGSRKLPFARELYI ERDDFMEDPP
KKFFRLAPGREVRLKNAYI I KCERVI KDQRTGEVLELHCAYDPETRSGAP
DVRKVGT LHHVSAAHAI PVEARLYDHLFLKENPEEEEDFKTCLNPGSLE
RLTGCLVEPGLAGAAPGTRYQFLRHGYFI ADSVDSSGRAPVFNR I VPLKD
TWAKI QKAGQPGKR

>2617921580 Ga0073689_1331 Elongation factor Tu GTP binding domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_133]

MAKQKFERTKPHVNI GTI GHVDHGKTTLTAAI TMVLATVGKAAVKKYDEI
DNAPEERERGI TI NTAHVEYETEK

>2617921579 Ga0073689_13226 NfeD-like C-terminal, partner-binding [pelotomaculum Ga0073689 : Ga0073689_132]

MSPALI NWLAFLAFL LGI LALI LEVVFVPGFGVAGI TGI I LVGWGI LLMA
VDVTQATAALALALVATVI I FVLGLRLMSRYKMWYKLT LQNKQWKEEGYV
APPAGLALFTGKGGVALTTLRPAGAAEVDGRRLDVVTEGEFVRPGSRI KV
I KVEGTRVVVKEI ST

>2617921578 rpsU small subunit ribosomal protein S21 [pelotomaculum Ga0073689 : Ga0073689_132]

VAEVKVGKNETLDSALRRFKRSCQKAGVLA EARKHEHYEKPSVRRKKKSE
AARKRRFR

>2617921577 Ga0073689_13224 histidine triad (HIT) family protein [pelotomaculum Ga0073689 : Ga0073689_132]

MQDCI FCKI I NKEI PAEI VYENEHVLVFKDI KPAAPVHLLLI PKKHI PTF
FDVTEEDAGI I GGI QLAAGHVAREMGLTDRGFRLAGNCGRDAGQI VMHI H
YHLLAGRPFKWPPG

>2617921576 Ga0073689_13223 threonyl carbamoyl adenosine tRNA methyltransferase MtaB [pelotomaculum Ga0073689 : Ga0073689_132]

MREKRVTVYTLGCKVNQYESAVLAGLFRERGRVVDFTDEADI YI I NTCT
VTHLGDRKSRQLI RRAARTNPDALI AVTGCYAQTSPGEVLEI PGVDLVVG
TRDRTRLVDLVEAAVKGDLPNAVTEYQAGDEFEEI PTLPYQDRVRAFL
KI QEGCSNFCYCI VPHARGPLRSRRPEKVI EAARAMVAAGFKEI VLTGI
HSGAYGRDLVGGTLAGLVRDLGI PGLVRLRLSSI EPNDI TPELVEVI S
GSKI FCRHLHVPLOSGDDWVLERMGRRYTTWDYFRLVEVLRENI PGLGLT
TDVMVGFPGETEDNFTNTCRFAKKVSFSGLHVFKYSRRKGTPAAEFQDQV
DPRTKEERSCELI QLGGKLSARFASQYLGLELDVLVEQPFQDDKELYEGL
TGNYI KI VFPGNEQLRGEMVKVKAERLRGTVLEGEI V

>2617921575 Ga0073689_13222 16S rRNA (uracil 1498-N3)-methyltransferase [pelotomaculum Ga0073689 : Ga0073689_132]

MPQFFI SHEKI KGGVYI TGPDVNI TRVRLRGP GDCVTVLNRRGGAYEV
VI EKAGREEVI CAVTRELTVRVAPPLRVTLVQGI PRGDKMDLI VQKGT
ELGMSKI I PLI CQVVVKLEGDRAARRRERWQRI ALEAAKQCRRPDVPEVGE
PVDWDGVLAGLPPGAAAVI PWEEESI DSI KGYLLRSGPKKEI FVFI GPEG
GFSPVEVERAREAGVRPVTLPRI LRTETVGLAVLAMI LYQWGLGGSFD
ERKESDGLHPGV

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>2617921574 Ga0073689_13221 ribosomal protein L11 methyl transferase [pelotomaculum Ga0073689 : Ga0073689_132]

LKWLEI TVLTPPEGVEPI AGVFHEAGAGGVVI EDPAVI LRYASEI HPDEW
GVPESATAGLPRVKGYLPVAEGLTGRLEDLEAAFGRLPLNLALVVMTRTV
AEEDWANAWRAYKPFVRVGRRLVVKPTWENYI PAEGDLVI EMDPGMAFGC
GTHATTALCLGLLEKYLOAGGI VYDVGAGSGI LAI AAKLGAGRVVAVDT
DPVACRVAVDNVERNGLSGQVRVVRGSLDLLEGGAGLVVANI IADVI I N
LAPDAAAALVPSGI LI ASGVI AERADAVRVALEAAGLTI REQQANGRWVA
LVAEKAGEAKNN

>2617921573 Ga0073689_13220 molecular chaperone DnaJ [pelotomaculum Ga0073689 : Ga0073689_132]

MAKRDIYEVLGVSRLNASVDEI KKAYRKLARQYHPDANPDNPEAEARFKEI
SEAYVI LCDPEKRASYDRFGHAGVNGQDFGGFGGFGDMGGLGDI FEMFFG
GGARRRTGPERGPDJ RTDMEI ALKEAAFGLERDI KVPRTETCSTCGGTGA
AAGARSGKCTACDGAGQMQFAQSTPFGR I VQSRI CDRCRGTGRI EKPCP
TCHGAGQVRKRSI KVKVPPGVDSGARLRVAGEGEAGLRGGPPGDLYVI
HVKAHRI FKREGDDLI CDVPI SFAQAALGDVLEVP TLEGTASLRI PEGTQ
TGTVFRLKGKGI PHVSGYGRGDQHVRVKVVTDPKLTEKQKELLKEFARLG
GEQLQGPDYAGEKSF FEKMKDAFMG

>2617921572 DnaK molecular chaperone DnaK [pelotomaculum Ga0073689 : Ga0073689_132]

MSKII IGI DLGTTNSCVAVMEGGEAVVI PNAEGARTTPSVVGFSGTGERLV
GOVAKROAVSNPDRTVSSI KRYMGTDHKVNI DGKSYTPQEI SAMI LQKLK
ADAEAYLGKEVEKAVI TVPAYFSDSQROATKDAGRI AGLEVPRI I NEPTA
AALAYGLDKEEDQTI LYYDLGGGTDFVSI LELGDGVFEVKATSGNNRLGG
DDFDQRFV DYLAMEFKKDTGI DLRNDKMAMQRLKEAAEKAKI ELSGVATT
NI NLPFI SADAGGPKHLDI NLTRAKFEELTADLVEKTMGPTRQALSDAGL
SPKDI DK I LLVGGATRMPAVLEAI RKFLAKEPHKGI NPDECVAVGAAI QA
GVLGGEVKDVL LLDVTPLSLGI ETLGGVFTKLI DRNTTI PTSKGQI FSTA
ADGQTTVEI HVLQGEROMAADNKT LGRFTLTGI PPAPRGVPQI EVKFDI D
VNGI VNVSAKDMGTGKEQSMTI TASTNLSEQEI DKMVKEAEKHATEDSRR
KEEVEI RNQADSMVYQAEKTI KDFKDKADAAA I EKLOKAVDELKEAMKGG
DTGAI KAKLEAVTGPLYEMTAAMYRETGTQTEGQDAGAAGGAQAGPGQKDT
VVDADFEVKEDK

>2617921571 Ga0073689_13218 molecular chaperone GrpE [pelotomaculum Ga0073689 : Ga0073689_132]

MNAEEKMDNRDELKENGAFDDPTGQDGQSAALAEENDPAVL RQKLVEQTA
RAEDYYNRLARLQADFNRYRRRTQETENFYKYASEQLVCALLPVLDNFE
RALAAEGDSMESFKSGVEMI YRQFLDVLTTTEGLAQI PAVGEQFDPARHEA
VLKAESEEHPEPNTVI EELRRGYCLKDKVVRPAMVKVARLP

>2617921570 Ga0073689_13217 Chaperonin GroEL (HSP60 family) [pelotomaculum Ga0073689 : Ga0073689_132]

LSLKREATSGSEVDERLAALMTNSNAI RAI ASAVEGT LGPKGLDTMLVDK
FGGVVI TNDGVTI LTMMEANHPAARMLI NI AKAQEEI GDGTTTATVMAG
ALVGAGVEQVARGVPVARVI EGLRTGLKRALEAMRGQARPVRLDDPMLR
QVSLVAGRDHEDI ADLVVRAAVLI GEEKLKESSEFKFSDTI MAEEGAENQV
FMGVI VNKERMNRQMPGELEQVKVLVI DDALPEEI DDEALGTEAGFNRY
LQLQAEFKENVQKI I DLGVGLVLADRGVDDAAEEMLT DAGVMVVQRVANK
ELRKA AEHTGARM I KRTGLKKAVRELEKYLGTAEKVYNDEKLEQVWVLGG
GGKPMATV LVGAATSEVVGERERI AKDAASSVQA AVKGGVVPGGGSLELA
VAREVEKVREGI RGMAAYGDCVVEALKRPMAQI VTNAGFNPLEKLGDI
AAQAESGSNSLAI DCDSGQVAGMFERGVVDPADV KI YALKAAGEVAEAI L
RI DTI I KKREEKEQQSGDAG

>2617921569 Ga0073689_13216 heat-inducible transcription repressor HrcA [pelotomaculum Ga0073689 : Ga0073689_132]

MKMDDRKQKVL LSI I HDFI ATAEPVGSRTI AKKYRLGVSPATI RNEMADL
EEMGYI EQPHTSAGRI PSQQGYRYVVDYLMKRQELTREEEELI RREYEA
VKDVGQVI QKTGLLLSQLTHYTAMVLT PRMGTSSFRHI QLVSMQSTKAMV
I VI MDNGTVHHRMI EVPRSI SASDMETI SKVMNAKLOGLTMESI KLTLLK
EYYLELARHKHI LDLAMELI QDSLALRSEDKI YLGGVFNMLNQPEFHNVE
KVKTLLSI LEQEDLLHDL LAGGSGGPGVTVRI GGEI NNRDI RECSMVVAP
YSI CGRRI GSI GVLGPTRMEYAKVVSVDYMTENLSRALERMI RGI GK

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>2617921568 Ga0073689_13215 oxygen-independent coproporphyrinogen-3 oxidase [pelotomaculum Ga0073689_132]

MTIALYI HVPFCVVRKCLYCDFVSRPFSPGAEEAYLDGLFKESRLYGSSLP
DEEKEI SSLYVGGGTPTCLPAAFLKRLLLENVRSI FHFLPGA EVTVEANPG
TI EPGKLDVLR ETGANRLSLGI QSFRRDLLGALGRVHSAGEALEAVRLAR
EAGFTNLNLDIFI FGI PGQSLDHWRETLDI AVCLAPVHI ALYGLQLEEGTP
LEHAVSRGELKACPEEELTMYQLAI EFLKTHGYSHYEI SNFTRPGRESV
HNSNYWLNRPFLGLGPAHHSYLGRRFANHPSLEKYCEKLFGRGEYPLETA
ETI LPETEMSETMFLGLRLLKGVDLGRFQRRFGRRRAEDVYREQI ARLAEA
GLVEVALGYLRLTEKGLPLANRVFRAFV

>2617921567 Ga0073689_13214 hypothetical protein [pelotomaculum Ga0073689_132]

VSMLKEELHRMVDTLPEKKVMEAVKLLKALLDLNKSSEELWDEFLTNP LI
NDEPWTEEDEAGWCERI NDI NEGRI KPWEQVKKNPASESNYNRKGRKGFG
GVGQI QVKALPGRGLRGAIL

>2617921566 Ga0073689_13213 GTP-binding protein LepA [pelotomaculum Ga0073689_132]

MEWEKDRI RNFCI I AHI DHGKSTLADRLLEYTGALSRRREMTEQVLDQMDL
ERERGI TI KMQAVRLKYRAGDGREYQLNLI DTPGHVDFS YEVSRS LAACE
GALLVVDAAGI EAQTLANVYLAL EHDLEI I PVI NKI DLPSAEPERVKKE
I EDVI GLDTSEAMLASAKSGAGVEE I LERI VTRI PPPSGKAGAPLRALI F
DSHYDPYKGI AYI RVVDG SVKEGMQI KMMATGKEFEVNEVG I FRPSLTS
VGELRTGEVGI AASI KNVKDCRVGDTI TEAGLFATAPLPGYRKVTPMVY
CGLYPVENVDYDDLREALEKLKLNDA SLVYEPETSEALGFGFRCGFLGLL
HMEI VQERLEREYGLSMI TTAPNVVYRAI TTGEAMEI ENPSKLPPAGKVE
FI EEPYVKATVMPKDYVGAVMELCQERRGVFTNMEYI SVNRVI LNYHMP
LSEI I YDFFDQLKTRTRGYASLDYVL AGYKQSDLVKLDVMI AGEALDALS
VI VHRDKAYQGRQLVERLRSLI PRHLFEI PI QAAI GNRVI ARETVKAVR
KDV LAKCYGGDI TRKRK LLEKQKEGKKRMKQVGNVEI PQEAFMAVLSEGR
K

>2617921565 Ga0073689_13212 hypothetical protein [pelotomaculum Ga0073689_132]

MSWI KYKLVI I LFALVVAGGVSI VLSGFNHMI RPAGPVSAFRLEDGGSGV
YRLELLGEKI AAETPPDI VTDLI NRAEI KNGREYVKETLQKLERKGGPCL
NEI SAVI KDAMKRAVSDI ESRAGEI KERLSASYGLFQEK

>2617921564 Ga0073689_13211 stage II sporulation protein P [pelotomaculum Ga0073689_132]

MYLAPASRLRRI CPLKLRRFI AAAGLFFAFI LFLSRVLPLAAI YFPLVEI
VEHFSERSLALYRKDPLKI I RI AMPVLGWSSFEGDDSTLNVMLLKGAVR
TVTGMDLRGPAALLSSQMPLLADVEPPGAI I LEDPDYQTFENSTAQPASN
LPGDALVSI YNTHGTETYGLTDGTDRLDGR LGGVTVAAALQEALESKYG
I KVARSDRI NDAKYNDYI ESKKTAQELLAANPETRVLLDI HRDSGKTR E
QSVVKI NGREAAPI LLVVGSDTRRPFDPWRRNYAF AVELSNKI NEMYPGL
SLGVRVKDGVYNQSLHPRAVLVEVGTTKNSTEEAVRSARMLVDALAPLI M
EKVEFGTTDTQEEE

>2617921563 Ga0073689_13210 4 TMS phage holin, superfamily IV [pelotomaculum Ga0073689_132]

MQWLGP I RFVVSALVLI VVSWLSPGFVVRGGFVGALI AAVVI AVLGYVA
EALLGDRVSQSRGLVGFI TAAVVI YLAQFI I PGLLSVSLVGALI SAFI I
GLI DAFVPTVLR

>2617921562 Ga0073689_1329 small subunit ribosomal protein S20 [pelotomaculum Ga0073689_132]

MPNI KSAKRVEI I RKRTLNRARI KSALKTAI RKFE EI KTADKEEAGLK
LRNAV KVI DKA VTGVLHKN TASRKKSRLTKRFNKLTG

>2617921561 Ga0073689_1328 Xanthine/uracil permease [pelotomaculum Ga0073689_132]

MKEANAPEENGSLLYNLKDRPPLNRTLAYAAQWLFFTLANS AVVPI VVGS
ALGLDRAGI AALAQR TFFFQALASLLQVFFGHR LPI I EGPSGMWWGI FI T
LAAMAPGLGKPLDTLR TDLEMGVI VAGLI LVMMGV TGLI GRTLKLF TPAV
TGSVLVLLGLQLSGAFLRGM LGI SVHGSVDLKSSMVSFVVALV VLI NLK
ARGFVKS I AI LLGAAAGWI I AALTGVTOGVYWHQAPVALPRVFAWGPPT
FDPGI VLTSVLTGLLVLSNLVASI LAMERVLGVLSRRAYDRGVAFTGLA

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DI LAGLGATVGFVPYSAGAGMVS LTRVAARLPFAVFALALMI LGLLPAA
SFLASI PEPVGYSVLLASFQMI GFGLKDYARLKFSRDRYFVVG LPI LAG
TGI MFLPPGAFEGVPALARYVLGNGFI AGMLLCMLLDHVL LPKRYFEK

>2617921560 Ga0073689_1327 DNA polymerase III, delta subunit [pelotomaculum
Ga0073689 : Ga0073689_132]

VNYFI ELLNSLKRGLSPVYLFYGEESYLREQAVFHI KKFCAGEGDAGLN
YDLI DGETATPEEI TASAETLPLFAERRLVVVRNP AFFKPSGRAGEGVHV
AGENKKALGKEAPLLDYLKNPLSSTCLI FTTGEALDKRKH L FQVI KKTGR
VVEFKRLVRDELARWLTOKAQRDGRFAAGAGEALMDVAGSS LQRLVTEL
EKLFSYTAGCEVI TSEDVRELCPPGAEE NI FAI VDAVGNRRRCGEALAGI K
ELLAAKEPPARI LSMI ARQFRLL LQVHDLLERGC PAREV PARLN LHSYVA
RRVADQSKNFNRQALI KAI ESLAELDLAVKTGRREFYPAVEV FLLKLSTG
GERPAHPARGF

>2617921559 Ga0073689_1326 uncharacterized protein, MTH1187 family
[pelotomaculum Ga0073689 : Ga0073689_132]

MFQWVI RMVVVDVTVI PVGTPSTSLSEYVAGCVKVL EESEGI SYRLTPMT
TII EGELDLVLELVRRMHEQPF AKGAVRVVTI RI DDRRDKELTMAGKVA
VVEAKLGR

>2617921558 Ga0073689_1325 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_132]

MPERKI VTGQDI NFSI LKFFTRYPSNHLRRDTLSSNFYLLN

>2617921557 Ga0073689_1324 protein of unknown function (DUF1540) [pelotomaculum
Ga0073689 : Ga0073689_132]

MNQHI HCI VNDCHYWDSGNMCKANEI LVATDDFARKQPDRI DAHQAAQLT
PATAGSCPATACKTYVTKGSRDSNMDGVKRM

>2617921555 Ga0073689_1322 protein of unknown function (DUF4338) [pelotomaculum
Ga0073689 : Ga0073689_132]

LPWRHVEPVPPPEEQAVWNATVAQHPLGFRRAFGAHQRYWI RGNVAGRRV
VVGALLFAAAARNVAVRDALWGTRHQQQHFRQRVVANSRYLI LPGVDVP
HLASHALALALRRLPEDWRARYGYAPVVVETFTVPPWRGTCYRAANWVHL
GQTTGRGRQDRNYDQAGTI REV FVYPLVRNWRRALVAQAPT PESAGATAK
PRTGRRTKRSAA THGGDDGMI TAEQQLKAMTEERI KQRYESLAPFLDERQ
RRLLAGAEALAYGTGGQKRVAALLGMSESTVSRGVREL RNPETI ETERVR
QPGGGRKPTTGSDPELLSDLERLI SPETRGD PQSPLRWTCSTRKLA AKL
KAMKERSVSQYLVRDLLHKMGYS LQAVRKTREGSEHPDRDVQFQHI NAT
VAKYQKRQRPVI SVDTKKKELVGDFKNAGREWQPKGKPETARVHDFVI PE
LGKVNPHYGVYPTRNEGWNVNGI DHDTAAFAVASI RGWWQSMGQPAYPDA
TKLLI TADGGGSNSSRSLWKVELQKLADETG LNI AVCHFPPGASKWNKV
EH

>2617921554 Ga0073689_1321 Rhodopirellula transposase DDE domain-containing
protein [pelotomaculum Ga0073689 : Ga0073689_132]

LFSHI TQNWGRPLESHEVI VNLI ANTTTEAGLTVRAQLDENLYPTGVKV
SDEELKAVEI KRSDFHGDWNYVI CPRNRP

>2617921553 Ga0073689_13128 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_131]

MANRI FFSLAELKEAI RSGVHEMNSRPFQKLEGSRRTFLETDRPTLKPL
PLYCMDNKI

>2617921552 Ga0073689_13127 Putative DNA-binding domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_131]

MTARELLEI I ANGENSEAVEFKRETI RPEHLGEEI VSFANLEGGTI FI GVA
DDGFI EGVQREDMEEWLMNI CYHNV I PAI I LYYEKVQVEGKPVAVLKI PQ
GAHKPYQTAAGKYFI RVGSTRKRLATREDLARLFQLSGMVHYDI TPVPGTA
EKDLDMVKLRSYFLEFNFFFWLTLYLE

>2617921551 Ga0073689_13126 TIGR00266 family protein [pelotomaculum Ga0073689 :
Ga0073689_131]

MAADI I DFOI HGDDMQCVEI ELDSGEGVRAEAGAMMYMEDGI EMQTSTSG
GI FKGFKRMLTGESFFI TTFLNNSRGKSRI TFGAPYPGKI I PLDMDKLGG
EFI CQKDSFLCAARGI EI EI AFTRRI GAGLFGGEGFI LQRLSGEGLAFVH
AGGTI I QRELGPENLRVDTGCLVAFAPT VNYDI QFI GGFKNALFGGEG
FLARLTGPGLVYLQSLPFSRLADRI AAASRFQQRDEQKGI AGI GGGFLGG

ILSGDRD

>2617921550 Ga0073689_13125 GntR family transcriptional regulator [pelotomaculum Ga0073689 : Ga0073689_131]

MPDEVQI VDRLLVLI ASGKYNAHDQLPSENV I AEQYKVPRI TARKAYERL
EEMGYI YKKQGRGSYVRDRHKQI ELVLSGDVFSRKM I EKG YDFQSKNI F
CKEI KYNKKI YDFLETDQNDRVFKVGR LRFI DQQPI AI HI SCVARSVFNG
I ETEGMAI TSMFKYYNNKGYTEFSSKTRDI PSFLQNPAA

>2617921549 Ga0073689_13124 N-acetylglutamate synthase, GNAT family [pelotomaculum Ga0073689 : Ga0073689_131]

MLI REAVEAELPELLEI LTGMDGEDGLEPGEALPI WRR I NEYPYKI FVA
ECDRMI I GTCSLI I I DNLGHKGAKLAVAESMI I RPEFRGRGI GSQMMQFV
MKRAREENCYKMLSSNKKRAFAHRFYKQLGFQQHGI SYMI EVGKND

>2617921548 Ga0073689_13123 alpha-D-ribose 1-methylphosphonate 5-tri phosphate diphosphatase [pelotomaculum Ga0073689 : Ga0073689_131]

MRAKTTYI YNAQI I LPEKI I KGYI EI DGSRI SRVGESGSTRAGSHSGAAV
I DAGGCYVMPGMI DI HSDAI EKEI QPRPNTLFP I NMAFYELEKKLAVSGI
TTMYHSLYLSDEWGVDRDKDMVTGI I SSI DRFRKTRSMI NHKI HLR YELTF
LEGLSI LEKFI REKSI DFMSYMDHTPGQGQFRDAETLKSFTI QI YGREEK
EVEAFMDKTMELQAMI DWPR LVDLARLAKTRGI GLASHDDDTKENI DRLL
ECEGVVSEFPVNLETAVYAKAKGI HVCVGAPNI VRGKSHGNNMRAI DAI T
NNAADI LCSDYLPGAMLPA LFRLTGEGI ELTEAVKMATLNPALALGI EQE
AGTVEAGKYADLI I VELHQDYPVVRQTLVG GTTVYQADYQVFNRERVDHR
C

>2617921547 Ga0073689_13122 phosphonate transport system permease protein [pelotomaculum Ga0073689 : Ga0073689_131]

MOI EESFKGWQLSGDETKESMYPGAI KPMNRASPAMRI I LLVLLALTI Y
ALVTI DYRGVDI PKAVAGTLSNFKTMFLQPYSHRFSWWEAVYEVVVTMGL
AFLTTLFGAVI ALFLGLLAAQNLAPKQVTNMI KGFVAFI RAVPTI LWVLI
FAVVAGLGSEAAI I GMTFHSVSYLT KAYSESFEDLDADVI EALMASGANW
WQVVFQAVI PSSI TYLLSWTFLRFEI NFANAVAMGAAAGAAGI GFDLFMA
SGYYFDLREVGLI TYLI LAFAVVLETTSI NMKGKLRKRA

>2617921546 Ga0073689_13121 phosphonate transport system permease protein [pelotomaculum Ga0073689 : Ga0073689_131]

MQADI FAKRRNDSL I FFTLLAI LTVGSI I I TRYDVLKGFTSI AKALI WGI
SNFYPDAGALEKLADI SLKLWETVLSI ASTTVA AVFALLLALAGSQTTR
MNSLFSVVSRI ASFFRNI PLVAVAMVLM LAFSQSPLTG YLALFLGSI GF
LTRA FI ETI DEVGNNPVEALQATGAGYFHI I FQAVLPSSLPQMI SWLLYM
I ETNI R DATLVGI LTGTGI GFSFELYKRLDYHAASLVVI LI VI TVI I I E
LVS NKI RRV I L

>2617921545 Ga0073689_13120 phosphonate transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_131]

VALLELKNVTKYNGMTPALADVSFTVREGEFVSI I GPSGAGKSTLLRSI
NRMI EATGGEI FFDGVVSKLRK RDLRLRTKI GMI FQHYNLVDRLTVI E
NVLHGRLGYKSTLAGVLGHYSQEEKKQAHRI I RI LGLTDQI YKRC DQLSG
GQKQRVGI ARALI QNPKMI LCDEPI ASLDPNASKI I MDHLRNVSTRMGI T
VI VNLHQVNVALKYADRI I GVNGGRVVDGPPDALTAGQI SDI YGAESGD
LI I DLGERNAS

>2617921544 Ga0073689_13119 phosphonate transport system substrate-binding protein [pelotomaculum Ga0073689 : Ga0073689_131]

MKYRLSHRFI MKAWFYVLEI QWKSSI FEI ERGI YVRKI CLVALVI VLVAS
LLAGCSATSGSSSGKEPDTI TMAWLPNNAGEDFKDARAEI EKVI EKATGK
KVVEKLT TDYAI TI EALASGNAQLGWVGAQQYI VAHAKNDKVLPLVVNSG
PSGTLEDALYY SRLVVKKNEDQYKSGNGYSI DNI AGKKFSFVSTSSTSG
CKVPSAAI VSHFSKQDQWKNLQKEDLLQGGGGKFFSQVLFGGSHQLSLVN
VLTDKADVA AVDDI DVI SYVELTSGTTNRPGAVYTVKKDAAAPFDKLADA
QYVVI QATPV LNAPI VVNTGALSQKTI DAI AQALTSDEVAGNPKI FLPKD
SGGKGFFNQPQRF LKVEDAWFNPI RELSK

>2617921543 Ga0073689_13118 alpha-D-ribose 1-methylphosphonate 5-tri phosphate synthase subunit PhnL [pelotomaculum Ga0073689 : Ga0073689_131]

MEEI LVI EHLKSFTI HNLDKHI EALHDI DI AVKEGEFVGI TGKSGSGKS
TVFKCI YRTYLPQQGRI WYNSKKFGWI NLAEAPERRI I YLRKREI GYVSQ

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FLSVMPTTARELAKQAVLEMGRGEECAEREAEMLEHFDRELWDSYP
ATFSGGEKLRLLNI AGAMVKRPRLLLLDPTASLDYASKI KVRELI EQLI R
EGTTMMGI FHDLEFMGNLCGREYTMRDGKLFDRPEKI TLI

>2617921542 Ga0073689_13117 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_131]

MGKRLGKEPWI HENCQLI NAEFGYEYEVGMHNYLENNI LGDYSYTSRFCI
IQNAVI GKFTNI AAMVRI GPTAHPMARPSLHHFTYRRVMYGFAATDDEQF
FQWRAEQKTYTGHDWI GHGAI I MPGVTI GNGAVVGAGAVTGDVEPYTI
VAGVPAKPI RQRFPAI VQGLEGI KWWDPHEMI KEKLADFYLPI QQFVE
KYYFPAVCKAGD

>2617921541 Ga0073689_13116 putative phosphonate transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_131]

MDFEQPVLSVRRLNKKFGNGCAACRDARGERLLRNFCPVCCTVYACREIT
FEVYAGEVLGVVGESGSGKSTLMOCIFYDQDVSSGEAFI SSKGGRENI F
AGSSQKRYI RNHMMGVYQNPVMSLKMDFSSI GNI AGKLI AAGNRNARG
METRGKELLERNI PVYRVKEAPKNFSGGMOQRVQI AKALSNNPPLLLLD
EVTGLDLPVQASVLDLI KEI QRELRI SVVI I SHDLGVI RMLADRAMVML
DGRI I EQGI TDQI LEDPQHSYTOQLVQSLLI

>2617921540 Ga0073689_13115 alpha-D-ribose 1-methyl phosphonate 5-phosphate C-P lyase [pelotomaculum Ga0073689 : Ga0073689_131]

MPDSYNFAFFDEGSKREI RRATLKAI AI PGYQAPFASREMPI ARGWGTGG
LQLTSLVGGKEDVLKVI DQGSDESNAVNI KKLI TATTGVAVTDATAEAS
I I QSRHRI PEVPLREGQI LVLQVPLPEPLRYEPSELETKKLHAEQEYSG
AWLMLFEQI MNYGNMSTGADHPVMVHDYVMAPSPI PRFDNPKLNRLKAL
I LFGAGREKKVYAVPPYTGVSSLAFFDFPFVAVESFQKSCRLCGAKGVYL
DEI PDDATGKTFYQCNDTSFCMERVKGKGTHLPGYR

>2617921539 Ga0073689_13114 alpha-D-ribose 1-methyl phosphonate 5-tri phosphate synthase subunit PhnI [pelotomaculum Ga0073689 : Ga0073689_131]

MGYVAVKGGTAAI EESI KRLKYERLKKGRVLDLHSI EAGMRGLI DQVMSE
SSLYSETLAAI SI QAEGSPEEAVFLMAYRSTLPRKHYSRTVHPEQMLV
ERRI SASFKDI PGGOI LGAAHDYTQRLI DFDLI NETEKDAANWLHEFNIGD
NGI DSDNTDLASLPKVLHLRAEGLI AACVNNDGEPDDI TRECWHFPTSR
SARLQI LTRGRTGAVTSLGYAALRSYGALHPTVGELRVGYLPVYVDNPFN
EENEDGDAYYI GDI KVTEVETLFPVTAQKENGKEVEFGI GYGI CYGQNE
TKAI AMSI LDHCLTGHPEYFTHNEEFVLLHVDSVESTGFI SHLKLPHYV
TFRSELDVSRKSKKAGKNDAGQL

>2617921538 Ga0073689_13113 alpha-D-ribose 1-methyl phosphonate 5-tri phosphate synthase subunit PhnH [pelotomaculum Ga0073689 : Ga0073689_131]

MKLDLVHDI QRAYRKTVDMSRPLI SNI REQADKVDI ETGCFKATVI LA
LMLFDTEVTFKVFSGRAEI TKLI NQLTYARTTEARSANFI LVLQDTGPL
EMEEAFRAACPGDLTDPHRSATI I VEANTLSNEPDLTLTGPGI DGKTHVK
VQI ADRWVDLRAEKNSEYPLGVDLI FTDPDHHI LCI PRTTQI MKRVAG

>2617921537 Ga0073689_13112 alpha-D-ribose 1-methyl phosphonate 5-tri phosphate synthase subunit PhnG [pelotomaculum Ga0073689 : Ga0073689_131]

MNRKKRTEI LVKGSPEVAKRLAQEI LRKYDVRTI EQPNGLVMVKVRETA
GRSLFYLGCVFI TECKALI NGCVGI GI VRGQEPDLAHLAI I DAAYNADL
PETREWITI TMLLEEERI KQSYEAFRNKVLKTKVSFQTMVD

>2617921536 Ga0073689_13111 Ubi quinone biosynthesis protein C007 [pelotomaculum Ga0073689 : Ga0073689_131]

MALLGNPFVANAPROLSTEELI QALRVDMAGELEAI I GYEAHAMATSDER
VKKVLYHI ADEEKQHVGELOQLI FLLNPI EQQSI EKGKQVVVQQQSQGFQ
APMQ

>2617921535 Ga0073689_1319 Membrane-bound acyl transferase YfiQ, involved in biofilm formation [pelotomaculum Ga0073689 : Ga0073689_131]

MKNAHLGEVDYLRVFGLI AI VCI HAFGFFLSMPAASAYTRI FQEI NVNLL
RFGRYAFMFVSGLVLFYSYNGYKLSLTHFYKRRFKNLVI PYAVWTAVYLL
I KRWANMVSWPGLAGFSTLWLQNL NGNAYI HFYI LAAI QFYLFPLLI
PI FKPRQPRWLAKI I LVGGFLLYTFYFFLEI RGADVNTLVAGTSWEAVT
SLVLQYKDRLLFSYLPFYFLGGLAGLYLEEWKWLGRNNLI FGGLI LSA
GLVCGEYFYFYRHLGQEWELTI SVFKPSI YLYSLVVI VI LSWLSVLERR
GFMRSILI TI LAANSLGI YLI HPAVLFI FHSFLWGQLKFLGSFVFI LDPAA

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AI AVSCLVSLVLGGNQYTRFI VGEAGNLRDNRLFNLHFHRI SI RRLADI
VGFMLR

>2617921534 Ga0073689_1318 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_131]

MLKHKFFWKNLASGSKGVI KVELVSSYSYWKLYRDRALYEEEEKEKVAET
VMDLI EKRFPGI KNOQEVVDVPTLI TWERFMGGTHGFSNMPNKEI NI I GS
LFNRGLETTLPGLSNFHLVGAWVTTTGALFANALSGRKVI KAI CKSDGKR
FNAIP

>2617921533 Ga0073689_1317 PAP2 superfamily protein [pelotomaculum Ga0073689 :
Ga0073689_131]

MSEI GPTSAWKRRQEAFOI REEAALFQRDLPPLPGHPCNGDEDLYPNKI AN
FPKALPHNQLGEVDLFAYKGLI RALSTGDPDEFETI PLGGVVKLANPQAA
YAFDMVGPDSHLSMI PAPAFASSAEI ASEI AELYWQALTRDVPFTDYDTD
PLTLAAAASDL SGFSDFRGPKVNGMVTGTGTLFRGNTPGELVGPYI SQFLWK
EI PFGATTI VQRYRTTVAGDDHLTAYQEWLNI QNGFPSVAQNEFDPTPRY
I RNGRDLGEWVHRDFS YQGVLATCSI LLGFGQSALDPSNPYLRSLTQVCF
TTFGSAHI LDFVARAASASLKAAWFQKWL VHRRLRPEEFGGRVHNRLTGT
TDYPI NPELLNSQAVSAVFDKFGTYLLPQAFPEGSPHTHTAYPAGHATI TG
AGVTMLKAFFKESFVI PNPVVASADGLSPLPFGSPPLTLGGELNKLVTNI
SLGRCTAGI HYRSDGI GGLKLGEAVAI GI LDYRNTYNEDFSGFSLTKFD
GTVVHI

>2617921532 Ga0073689_1316 Putative peptidoglycan binding domain-containing
protein [pelotomaculum Ga0073689 : Ga0073689_131]

MLYASRYLRI MEPLMEGPDVQYVQKRLTEMGFYTGPIN DVYSPETRDAVI
RAQQSFI LATDGI VGPDTYNALGLSPEDEVTI APEYVI VVDARTLQLSLR
QFGRQI GVFPVAVGTPNTPTPLGDWKI I QKVKNPGGPFVGRWMKFSCPWG
GYGI HGTDNEASI GTAASHGCVRRADDI I RI YDLVSLGTRVKI TGNAFT
GRLLRI DMEPGSDVLRVQQI LRI LGYRGLDLDGFGYPATEAAVI QFQRDQ
GLDPDGI VGPQTYERLQLANDLI LGDRRP

>2617921531 Ga0073689_1315 MarR family protein [pelotomaculum Ga0073689 :
Ga0073689_131]

MDNLPSNSPQELLI QALGRQSAFWGLGKTTGEI YAALYLSRKPVSLLEDLA
LRLGVTKGNI SVLVRNLERLGMVRRAWHRGDRRVYFEAEADLWQVARRVL
EQRQKPEFDLSFQLVGQAVEEAELAEQPDALFTLERLRLSLQNFYRTL DG
LVKALLSLDPAQLAALARMIEVQAKIF

>2617921530 Ga0073689_1314 NADH dehydrogenase [pelotomaculum Ga0073689 :
Ga0073689_131]

MI LVTGATGLAGRHI VPALLEAGYRVRCLEARNTEKARSLLGEKPEYRPGD
VTDPASLSSACRDTETVVHLVAVI REKGTVTDFRVNAQGARNVVEAAERA
GCQRFVHLSALGAREDPAYRYAYSKWRGEEAVRRSGLAWTI FRPSVL YGS
GGFFFDMAQSLRAAPPFAPVPAARTRFQPLAAADLARCVALALKDPGS
VGHI YEI GGPEQLTYGQMLDAWLAAGGRRRI KLPVPLPLMLRLAVPVMERL
LADPPVTSVELKQMELDNLTDPNVVEKYFGFKPRPLGRGLRELLQTSR

>2617921529 Ga0073689_1313 Adenine deaminase [pelotomaculum Ga0073689 :
Ga0073689_131]

MEKNARAVSGNI VDMNSGI YPGTI RI SGGRI ADI I REDSEYETYI VPGF
VDSHI HVESSMLTPSEFARAVVAHGTAVVSDPHEI ANVLGVAGVKYMI E
DAGTAPLRFYFGAPSCVPASPSETGGAVVGPDQVEELFKLDAVKYLGEVM
DFPGVLNGDPVI MKKI DLAKKYSKMI DGHAPGLRGDL EYASAGI STDH
ECI TKEEAMKKAGLGI KILI REGSAARNFDELI PVI EEFHESCMFCSDDR
HPDDLAKGHI NDLVKRALRHGI DVMKVLRVACVNPVLHYKLD TALLRTGD
RADFLVI DNLNDFNVLETYI NGKVVAERGKPLI NRRTSKI I NNFTAGKKE
I ADFI I PCENGGI NVI EVMENQLI TNKLRAAAKVV DGCASDVSRDI LKV
AVI NRYGGAKTATGFVKNFGLKKGAVGSSVAHDSHNI VAVGVADEDI CRA
VNLI I ENKGGI SAVSEEKSMVLPVAGLMSDGDYRDVAERYTAI NNMAK
SLGSR LHAPFMTLSFLTLLVI PEI RLSDKGLFDVEKREFTGVCVS

>2617921528 Ga0073689_1312 aldehyde:ferredoxin oxidoreductase [pelotomaculum
Ga0073689 : Ga0073689_131]

MYGWMGAVLRVDLSNEKLEVKPLDGOVARKFI GGRGLNSMTL FDEI KPGI
DPLGPDNVLCFANGPFTGAPLTI SGRTEVSALSPQSNILGDGNGGGSFAV
FLKRAGFDQI VI TGRAGSLKYLWI DDGNVELRDA AHLKKGKSTWETTDLLK
ETHGKDI SVACAGQAGENLVRFASTI FDKYSSAARGSGAVLGSKNLKAI A

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FRGAGRVEI AAAAAEFGRLAREDRAYFRENKFYRESVSVCGTHLGVLDWYP
GYRHFQKYLSPAEI PEHLKPKAWKKYEVGRTACHSCVI GCKNVFRI PEGG
RAGEVGAALEYEGI HCLGI NCGVLDPVAI MEMENLADAYGMCVI GLGNAL
SLAKELYNLGI LSPEDTGGSLDWEDAASQI ELI HQI ALREGFGNSVAEG
I YGLARI TGKGAMDYCYHVKGLSRGPHPVGVFTLAHAI STRGADHLRGRS
WAFGENDPVEVPDLVRNGFVPGDPVGALTVSERATTFADATGRCKGAVNS
WCAVPLVFKYPLWDGAAKLLSAATGCDYDAAGLEEALDRI YI LEMAFNA
RQGI TRKHDRLPQKPELKGTPAGEEELKEHEEMLTEYYLAHGCDPVSGI P
ARERLERLGLGDVAGELEAGCPYPDWGPPPLWPPEQYPHGGKRT

>2617921527 Ga0073689_1311 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_131]
I KSVLRDSKNI RQYLQMVVLMP I AFTPVELMWVI WVGRLCRFAYLLCAL
I LARI YKFR I Y

>2617921526 Ga0073689_13032 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_130]
MKRKRYPKNFKEQLI VEAQEVGNTLSCSCPRYLASNKSMPI LLSNYMVVT
VNGND

>2617921525 Ga0073689_13031 GTP-binding protein [pelotomaculum Ga0073689 :
Ga0073689_130]
LYVVKFRNI AI I AHVDHGKTTLVDAMLRQSGI FRENQQAERVMDSNELE
RERGI TI LSKNTSVRYGDVKI NI VDTPGHSDFGGEVERVLKMGVGLLLV
DAFEGTMPQTRFVLRKALQLNLKPI VVI NKI DRADARGAEVVDEVLELFI
DLEASDEQLDFPVLYTSAKVGATADPGVPGRNMRPLFEAI LEHI PASSG
SPDGPLQLLVNSTEYDNFVGRMGLGRVKRGTVSPGRPVNI I AYDGSFRQG
RI GNLYTFEGLERVAVQEAGCGEI VAFSGLEEI RI GETVACI DHPEQLEP
I TVDEPTLKMSFMVNDSPFAGQEGRYLTSRHLRRLFKEMERNVSLRVEE
TGSPDVFOVQSGRGLHLSI LI ETMRREGFELQVSKPEVI YRREGDRLMEP
VELLMVDI PEDKMGVI MEI I GARKGEMLNMTSLGQNQLRLEFRI PARGLL
GLRSQLLTETRHHGVMHSLFLGYEPYKGEI KGRYQGVLI AFETGEATMYG
LHSI QDRGVLF I TPGTKVYEGMVVGEHSREQDLEVNVCCKKKHLTNI RSST
AEAALRLEEPRRFSLEDALEYLGADELLEI TPQSLRLRKRI LNKHDRGRS
QKCPRTA

>2617921524 Ga0073689_13030 HTH-like domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_130]
MCRI FGVSRTGYCVWLKRPKSRRKI WNRELLKKI RKI HKI SRGTYSPPRI
ARALKKEGI TYSRNWWVRLMRENGI VARTKRKYKGSKRTVPMLPMLPLMG
DSLWESAEI DQI LFDLVEHVGYQFPGYMFEI TRLVGFWLCPEDLFNFGI

>2617921523 Ga0073689_13029 restriction system protein [pelotomaculum Ga0073689
: Ga0073689_130]
LVVTI HEKTVSNEYLGVTETI KGAYPAEVGVKAEQALAMWAGLEKRRKER
DAI QSLSTLAEYDSGQAREFLEERENI LRANLNACGKLNWVSLYNDEPYP
PFVFKPPPPRYDQI AREMGVPQKSFFTELFFPSARKRRLKLEQEAKEVFD
DOMRQYEARKEAARTAEHERRDDYVRKQSEYNQSVQDQLQDFEKGLEAV
ESCLRI ALAGLTHPDI FNLEFDTQYNREEKLAVVNCLMPVPEEAPRTVKY
I YNEEEYDI I PVEMEQUEFNLYESI LLQLTLGI RVAFDAAPARLVQRV
AFNGLVKGTVPETGGDANI CI LTCKVSRDRFDSQDLTRCPPAEI FTDLP
VMTPPMTELNPPVQPVVDI DRTPPLYSEVEQI LGAKPETYQPGDFKHI ARE
LVSDMFDQI EKDLI DLGRLPKRVAH

>2617921521 Ga0073689_13027 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_130]
LNKPGPAKKLTI YMGEAMQWKGKSLYHALVLKLKEAGI AGATVI RGLEGY
GEANRLRTARLLDLSADLPVI VTAVDQADKI DQVLDPDI RTMVTRGLI TLT
DVQVVK

>2617921520 Ga0073689_13026 camphor resistance protein CrcB [pelotomaculum
Ga0073689 : Ga0073689_130]
VFYI YVGI GGVLGAI SRYAI SKAI NERI GFVFPVGTLLVNI TGAFLLSLL
LGLGI AHQGPAGKLELALTTGFLGAYTTTFSTFSYEALQLI QDGEHFRAL
GYVTLSVI FGLLAAWLGI LASASLVQ

>2617921519 Ga0073689_13025 CrcB protein [pelotomaculum Ga0073689 :
Ga0073689_130]
MI YLYI GAGGFLGAI ARYAVESLAGI KFSASFPAGTFI VNVAGCFLI GLI

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MTLALERMAI GTNTRMGI VTGFLGGLTTFSTYTCQTI TFLEKGAWGLAMW
YTAASVMACMLAVWLGVVAARLI PRFLSGGAVRREA AVNNRN

>2617921518 Ga0073689_13024 Predicted arabinose efflux permease, MFS family
[pelotomaculum Ga0073689 : Ga0073689_130]

LGNVKGGGNPRLWLI VLVNFLNFAI QGSMI FI PLLGAQLGASDFQI GLV
GAVYGASFLASSLFSGWKSDHVGRVLFVRWGLWAGSLAFAAQLLANNVI V
LMVVRGAVGFTLGI ATAAAI AYAFESGVDMGKYSSYGSGLWI FGALGAAL
I GEI QLLFRLSFLI CLAAFLLSLAFKEAPAYDFAAPPNLWRVMKRNRYRI Y
SAVFLRHLGAVAVWI I FPLYLVSLGLDKFWI GI LWGI NFAVQFI VMRYLE
RFSEYKTFAGQLLSI LVFAAYAFVTNLVPLI VVQVLLGVAWSCLYVGAL
LI VLRSGEERG TAGGI FQSTLNL CNAVGPLTGGLI AQGWGYRGMFFAVA
VG VAGMLVAVPAGPKERLAEDSHR

>2617921517 Ga0073689_13023 putative redox protein [pelotomaculum Ga0073689 :
Ga0073689_130]

LLNSLKWKKLRYPNQKGLKLAGLLYSGPDFGTVVI VCHGFTGSKEGGGRA
VTMAEELGRI GYAALLMDFSGCGESEDFTAVSLSGHI NDI NSTVDFCFE
TGFNRVI TVGRSFGGSAVLCQGGSDWRVAGVCSWAAPMDLTGVFSI FRQR
AAEI EGNLVPLSGEAGTVYI NKGFLTDLHLHDVTGQVAMLAPRPLLVI HG
SSDAVVPVENVHVI YKAAGEPKEI KI I PGADHQFTGRHREVWKALFQWLK
ENFPV

>2617921516 Ga0073689_13022 bacterioferri tin [pelotomaculum Ga0073689 :
Ga0073689_130]

MAGHLQLEQVI NGLNLDLSWEYAATI QYI QHASMLTGPEYAAVI DELLEH
AREEHEHAVI LADLI QYLGVPPTVEVAERLTSLSNVEMLRQDLQGEYDAI
RRYLQRI EQLEALRLYDSAQKI RNI VVVEQEHAI DLEKALGI QKVRPGAA
YPFTLKP

>2617921515 Ga0073689_13021 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_130]

MGVLTGRFPGKAREGYGERMLHGLMELVKRLI RFAEGYGVAVAEREVDVR
LNKTEKNFYL

>2617921514 Ga0073689_13019 hydroxymethyl pyrimidine synthase [pelotomaculum
Ga0073689 : Ga0073689_130]

MLTQLDRAVKGEI TPEMVRVAAAECVSPESVREGVAGGTI VI PRNI RREN
I VPVGI GAGLRTKVSASVGLYGEADVSTELAKI RAAVEAGTDAI MDLSV
SGDI DAMRREALGSPKPVGTLPYQACAEAGEKYSSSARMKVEELFEVI
ERHAADGVDLFLALHCGTTMDVVERAKKDGR I DPLVSCGGSHLI GWMLYNQ
AENPLYTHYDRVLEI ARKYDVTVSLADGMRPGCLADSLDGAQVQELVLLG
ELVRRAREAGVQI MVKGP GHVPLNQLRATVT LQKSLCKGAPYFVFGPVVT
DVAAGYDHI SAAI GGAVSAWAGAEFLCYVTASEHI GLPDVHQVREGVVAA
RI AAHAADLARGLPGA AEWDLKI SQARKVLDWRGQI ELAI DPERARRLRA
ERDESSESGCAMCGKYCAMKVVAEYLG NVRDGAQYC

>2617921513 Ga0073689_13018 hydroxymethyl pyrimidine synthase [pelotomaculum
Ga0073689 : Ga0073689_130]

VTQVLQARAGKVTPMEMVAASEYLDVGAVQAGVAAGKI VI PKNKRRRQI
KACGI GEGLRI KVNALI GTSSDRDLI EMEERKLAVAEAGCDVMDLSTG
GDI DGMRRQTLAKANVPVGSVPI YQAAI EAI EKRLAI VGMTADDMFEAVE
KQAAAGVD FMAI HCALNFDVI KRLQAAGRVTDVVS RGGAF LTGWMLHNRR
ENPLYEQYDRLLAI LKEYDVTLSLGD I RP GSTADSLDGAQLQGLI VAGE
LVARARAAGVQVMVEGPGHVP MHHVEATMLLQKRLCHGAPYFI LGTLATD
VAPGYDHI TSAI GGA I AGAAGADFI CYVTPAEHLGLPTEEDVKEGVVAAR
I AAHAADLARGHKRAWERDLEMARARVALDP HRQAGLAI SPDKFATALKE
NGSKDYHCAVCGNECAARI AARYFGLV

>2617921512 Ga0073689_13017 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_130]

VFSAPQRRMDLPRSEYNKYMSKHRCHVDRKRNEYGNAMAKMRLDRMEKLN
KSAPLVEYNLESFTGRFEVYDPNKKKGRGNNDLTLA

>2617921511 Ga0073689_13016 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_130]

VAGKFANI KGGPLLT I DDKFKFACHGGLACFKKCCRD I SI FLTPFDVLRL
KNRLKMTSGEFLEKYTI PFKAGYLGFSLVLI RMVAEEDLRCPFI TGQGGC
VYEERPWSCRMAPVEI RGEGWYGFCDPSHCRGLKESKEQTVREWMEEQG

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MGVYEEVEELFKELPSRMKPSGFKELDKQMMKAFHMCYDLDRFRKFVFE
TPFPDVYGVPEETAKEI KKDDPALLQFGFWLGSFAFKDLEGMKKAERLLG
DFR

>2617921510 Ga0073689_13015 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_130]
MAEEKNYEELSEETARRLEQYARKTGRTEEEVCEFI FFEFLQKQAGIIE
KKARDTGVPVNELFNMQFARLLEYLTDREDTGNPS

>2617921509 Ga0073689_13014 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_130]
MQWAEVDLEKLKERLTWDFDVNNEFRDKGFRKQAGFTFVI DVWCGEPRVT
LYRVAVNGSESI EIDROPPAEMI I KAI EEQGCSPKKGDLINI NREI RNWI
EANI LDKKVC

>2617921508 Ga0073689_13013 TIGR04076 family protein [pelotomaculum Ga0073689 :
Ga0073689_130]
VEI RGDGKCSYGHKVGDSFEFSRFTPGGLCQFAHDSLSAVAALLYGGEF
PWAENKEVSTWACPDPRPVI FELRRAPLEKEWA

>2617921507 Ga0073689_13012 Uncharacterized protein, UPF0297 family
[pelotomaculum Ga0073689 : Ga0073689_130]
VSQDVSEKTMFMFKVQAEVDNLARDI LLQVYAALKEKGYNPI NQMVGYLLS
GDPAYI TSHGNARSLI RRLERDELLEELI KNYLEKK

>2617921506 Ga0073689_13011 Predicted oxidoreductase [pelotomaculum Ga0073689 :
Ga0073689_130]
LQYRVLGKTGI EVSRLCFGALTI GPLQANLSVAEGARVI RKALERGVNFI
DTAELYRAYPYI REALRGFDRDVI VSKCYAHTYRGMRSVEKALTELHR
DYI DVFMLHEQESI LTI RGHWEAVEYLLLEAKKRG I VRAVGI STHHVEGVL
GAAVNSEI DVI HPLI NMAGI GI RGGGVKDM LAI ETAAAAGKGLYAMKAL
GGGNLLDRAEKAFABI LSVPLASVAVGMSAEDEVEYNTRLFGGHLVPPG
LQSSVKRRPRRLHI EDWCRGCGNCVAKCSL GALSLSGGKI MVDSSLCALC
GYCGAACPEFSI KVI

>2617921505 Ga0073689_13010 putative holliday junction resolvase [pelotomaculum
Ga0073689 : Ga0073689_130]
MRI MGLDLGDKKI GVAMSDPLGWTAGLEVI ASKGS AEDDLKKI QEVARQ
YGVKVVVGLPRNMDGSPGRRRAKKAREFAGRLARVLDI PVDLWDERLTTV
AAEKLLI EADLSRARRRQVI DKMAAVLI LQNYLDSRSPERLI RETQD

>2617921504 Ga0073689_1309 Protein of unknown function (DUF1292) [pelotomaculum
Ga0073689 : Ga0073689_130]
MVTEAEEVI TLVDEEGAETHFTVI DI I EVDGSQYAI LLPSEEEEEDEAI I L
KFTRDDDDGNELLVDI EDDEEWEKVADAWEEEMMVEEEVE

>2617921503 Ga0073689_1308 Vancomycin resistance protein YoaR, contains
peptidoglycan-binding and VanW domains [pelotomaculum Ga0073689 : Ga0073689_130]
VLI VFAKI NRLVLSLLI AAAVI SPLALLSSGFFAFANEKVLPGI RVMGI G
LDGLNRTGGGLERLAGLEKDLRATRV I LRHQDRNWPLLLNNAGFDLNEGAI
MDAALQAGRRGSLLRQWQERKQI EKNGLSLPPVI NFDKRLARRVGE LAG
EI I VEPRDAAFKI NSDVTI VPGKDGVDVDYDRLEKDI TNVLAEGKKPEV
TSLAPVPPTALLES MGVNGLLAAYTTRFDPAKTSRTYNI SVAARAL
DELLVRPGHEVSFNDVVGPRSS EAGYKNAPVI I NNEFVDDLGGGVQCVST
SLYNSI LLANLEVVERS NHSLPVGYVPI GRDATVVYGA I DFKFRNNTDSY
LYI KTSVSGGQLTFKI YGNTAYKRDAVNTRVTEEI EPKVI YENDPNLPK
GEQLVKQEGAKGFKVSGERVRLNGVVEKREQLSTSDYSPVNI VAVGSM
EKVLPQI VPVTPSPA E I GQNKQPSGSGELPHNPGQVHQAPAGDTTGGFGGQ
ARQSPDAAAENGGQVSETAGCGGI I NPAI PGAGLAGNTGGGGKPPDA
GGPAPDRANRP

>2617921502 Ga0073689_1307 UPF0755 protein [pelotomaculum Ga0073689 :
Ga0073689_130]
MVVRI NKGGGKTASAGFTRRYRNVALAVAGLLCFAALYLF I TLSPVAPAG
RASDVVVAVPPRATAGQVGKI LEQGLVRSPFVFSLYARWKGMDGLI KAG
EYRLNNGLS TPEI LRELVDGRLAMQAF TVPEGFTTTQVADLLVSRGLVDR
EKFFVAVMGEDFPYSFTRNLPKDERRLDGYLFPD TYQVI RSGESSI I NL
MLKRFDEEMKELDYP AQAVRMGVTLHEAVTI ASMVEREARVDGERPLI AG
VI YNRI NRSMPLOI DATVQYALGGGKPKI YYRDLEI DSPYNTYKVPGLPP

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GPI AMPGRASLLAAVNPVRTNYLYI ARPDGTHAFAATLVEHRANKERYQ
Q

>2617921501 Ga0073689_1306 putative protease [pelotomaculum Ga0073689 : Ga0073689_130]

MRPELLAPAGDLEKLKVAVLYGADAVYLGGRHFGLRAGAGNFGAGEMAEG
VRFAHGKGARVYVTVNI FAHNRDLEELPDYLOSVAAGVDRVI VSDPGVV
EMVRRLLHPDLPVHLSTQANTTNWAATRFWEERGVSRI VLARELSLEEI KE
I RKRVGAELEI FVHGAMCI AYSGRCLLSNYFTGRDANRGDCAQSCRWRYA
LVEEKRPGEYLAVEEDGRGTI LGSRDLCLEI EYI PELVQAGI NSFKI EGR
MKSVMYVAGVVKAYRMVLDAYLADPGNYRFDPAWLEEI GKVSHRRYTTGF
LFGNPGPSGQHYEGEVYRRSHVFGVLRVSYDERTGMALVEQRNRFVAGDE
VEVMVPGGNDFKQKVTAI YDEEGNSI DVAPHPRQI VRLPMVRPAPKYSI V
RG

>2617921500 Ga0073689_1305 Helix-turn-helix domain [pelotomaculum Ga0073689 : Ga0073689_130]

MI SVVDKEI I RKLYHVQKSI HWI AREMGCARQTVRKAI QDAEPPKYNLA
KARPKPI GOI KAI VEQWVEEDKDRPLKQHRTGRI YERLVEEYGYQGSE
SGI RRLGQLRRKEKETFPLETPGSNAQCDWCKATVI I AGVKI LVQVF
LI RLGNRMPFVMAFPQYAGLNLSPKR

>2617921499 Ga0073689_1304 protein of unknown function (DUF4258) [pelotomaculum Ga0073689 : Ga0073689_130]

LTSWPEAWLELLKKTGRTRNYI FSNHAFTRMGERRI SDDDVQRCSELEGQY
I EHQGHGQDLKVLQGECDGSTFYMVALAFPRPI VTVCRFMDGI WDD
LGAMKKRKK

>2617921498 Ga0073689_1303 DNA binding domain-containing protein, excisionase family/YgiT-type zinc finger domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_130]

MQCYVCDANMTKVQKDVETTGWGKTVVFKGI NVYVCESCGEEAYEPDDVK
AMQYFI EGAARNNEYPI MNVEEVADFFRVSNQTI YNMLRAGKLPAVKVG
REWRFPDRKI KAMVFKDQEEQPVELVARSSSAGLSKKDTDI I SRHLESEM

>2617921497 Ga0073689_1302 protein of unknown function (DUF955) [pelotomaculum Ga0073689 : Ga0073689_130]

VALRKELKLTGGI DPFEI AKOMGVLVYYEDLDEI DGCLLKKAENKRI LI N
KNI PHLNRQRFTHAELGHLQI KSHNEEMYRCWASDI QRYKGVK

>2617921496 Ga0073689_1301 AAA domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_130]

LGEQPKHRKI DVFHQI QQAI SSLHYDKRI TPVLVLDEI HKASNKLLLEDLQ
LI FNFKMDSQNPYYLI LAGQPPI RNKLSLNVNPLRQRI TVRYFFRGLNH
GEVKPYCETRLKLAGVNEEI FTAPALEAMYSVTNGLPRLVN

>2617921495 Ga0073689_12925 Helicase conserved C-terminal domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_129]

MRCLYEYRSI KTHVI VRGPI FPEPVQVI VVTLMGDSVKLTGKGLNPGHVH
EPVLSPEQLSTLEATPEKESFDGDAGKFRGLI EAMRLGLAYEYDPYFTLS
I ARVDPLPHQLEAVDYFI KLPRI RFLADDPGAGKTI MAGLLI KELKI R
GLI KRTLI I TPANLSFQWQREMKDKFRENFEVI RSDI LRANYGSNPWQEK
NQVVTSSVWSRI EDARESLLRSHWMI I VDEAHKMSAYSSDKKTLAYQL
GEALSDMTDHYLLMTATPHKGDPQNFCLFLALLDKDI YGDVKSLEEAMRR
QEAPFYLRVKEALVTFPDSVTGEVKTFTKRQVETVEFQI DEDEWDFYD
ALTRYVEDQSI KAASDDSARGRALGFTMAMLQRRFASSI YAVRRSLERMK
DKREKI LADPEGYRREQMOKKLPPDFDELPEEERQEI I AHLEGVVASVDP
AALKEEI MOLGRLI DRALI LEEREVESKLVKLKKELMHGI FKDPKMKLL
I FTEHKDTLDYLVKKLAEWKLTVTKI HGGMKI GDRDTQGTTRI NAEREFRE
ECQVMVATEAAGEGI NLQFCWFMI NYDI PWNVPRLEQRMGRI HRYGQEKD
CLI FNFBATNTREGRVLQKLFDR I KKI EEDLDPKRTGKVLNVLDGVFPAN
QLERMLRDMYAHNLT I DVI TSRI VEQVDTFRKLT DSTLEGLLAKS

>2617921494 Ga0073689_12924 Right handed beta helix region [pelotomaculum Ga0073689 : Ga0073689_129]

LEI YVLLGVLLLLAWLFI YFKYFREKDAVI TRKKPGGTGAGGMVYAVAPW
GDDNNAGFLESPWKTLOHSVEQLAPGASLLI REGTYKEDVFFKSGTGDN
PI VLKAPRGETALLDGSAGGKYGFNFAFGVSFVTLISGLQI KGFQSGSVV
LWGENRFI QKDLDPVPGCGAGLRI I SAADLLVEGCNHFHNSGPGLVVSPG

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PLTRARI I RTR SAYNGSPDL PDGFSLD SGEDTVMEKCTAEDNAGSGFNVCV
 TSGTVI SAGI ARDNTRYGI QCRGEGCKLVNCI VDGNGMAGI SLPGGGI YE
 LSNNLVVNC GQKGDYGLS AAPGEC PSTARLALVNNI FAYNCGGVYI GSSA
 ALEKEDHNI YWSREDAEI SLGSRYSREEI NGSI WFOETGRGEHSFCRDP
 LFVDPAGRDFRLARNSPA I DRGAGEGAPGADI NGSVRPQGWGFDI GPYES
 PEGSLI PPVAAI THSPVYSSDSSNSLEFVLKWE GVAEGREVAGFNVQFKD
 GREGAWQNWLAGTTANEAVFOGAGGRTYHFRVRARDDLGNWGNWSGDRCT
 VVPVDDQSPLI KYEGAWDFTNSEEAYLNTLHHAASPGAAASLRFTGTEVA
 WI STRGPDRGQALVYI DEALRCTVDLYCEDHQFRRPVFSTPLDGRPHI R
 I EVAENRNLF SKGRRVDI DGFVVK S

>2617921493 Ga0073689_12923 UDP-glucose 4-epimerase [pelotomaculum Ga0073689 : Ga0073689_129]

MRLRGYKVLVTGGAGFLGSHLCEKLLAEGAGVRALDI LTSGRREN LGAVL
 NKI ALLNCDI ACEDAVVGAAGDVDSI VHLAFPMALRQRSI ETRVVTEI LT
 GLLNLI KAALERNALFVYI SSI AVYGNDKYI PMDENHPLEPVL I HGA VKL
 AGENFCRTLAASHGLRVVI LRVADI YGPRNSRI SVPI KFL LQAMRNESI T
 VFGDGS DSRTYTFVSD FTEAVVLSI RPGAVGGI FNI GGDECVTMRRLAL
 EI KKI TGGDSPVLHQDRPPAGRRLCVSSLR AKEVLGFKPAFDI TGGLELT
 HRWLKDNPDYYQS QEEQK

>2617921492 Ga0073689_12922 exopolysaccharide biosynthesis polyprenyl glycosylphosphotransferase [pelotomaculum Ga0073689 : Ga0073689_129]

MAVI RSKQAFKRVDLI GALLLLVLLSPLLI AVALAI KI TSPGEVLFKQQ
 RLGOHRKVFWMYKFRSMI PNAQNTGSGMFVEKDDPRI TPVGKI I RKASI D
 ELPQLFNVLRGEMSLVGPRPAPLHHLDKYDERQLKRF AVRPGLTGWAQVN
 GRVALYWPERI ELDLWYVENYSFRLDLKI LLKTI AVVLFORGGTAREDRK
 DVDPFMKV

>2617921491 Ga0073689_12921 Acetyltransferase (GNAT) domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_129]

MGQYYI LGQRQREQLRELENI KEARPD I HYRPEYCGLFSEQGEPRLFVY
 REGSASVVPYFLLRKVNLI PALAGRVERELYDI TSPYGYGGPLAPADGAS
 LRDSFYRCFEDYCHNGI I AEFI RFHPLLGNHRFLEKHI RVERVASVVCV
 DLEKSEEEI WSGYERNNRKNI KKAYREGLVVLEETPTRFPEYI SI YHHT
 LARNRAGQFYFFSDDFYDRLHGE LQGCFLYAHTLKGG RVI STELLLYNGT
 YI HSFLGGTLD EFFFQCRPNNI LKHEVI KWAKGKI KYFLLGGGRREGDGI
 FRYKRSFAGEGVLD FYVGKKVHDHAAVRMLEEMLAGKKPEEDEGYFPGYR
 RY

>2617921490 Ga0073689_12920 Uncharacterized SAM-binding protein YcdF, DUF218 family [pelotomaculum Ga0073689 : Ga0073689_129]

LFGFSLVLF GALYRPPWPLLARLLVDDRP GKVDVLI VPGGDAERELHAA
 ELYRRGLASKI I MSGCGSSARQMARRAGGAGVDERDI I I EEKAESTYQNA
 LYSRDI VLKQGFKSAI VI SSPYHMR RVKLA FERVFRKTGVKLLYSSTKNS
 GFNTDGRCESEI DRR I VRREYLKLVYYWLR YW

>2617921489 Ga0073689_12919 Glycosyltransferase involved in cell wall biosynthesis [pelotomaculum Ga0073689 : Ga0073689_129]

MKKVLI I I SNFNGVGG AETATHRFLAGI NNRNFNVDCFFGFEDEFARSV
 KKA VRNI YCI DVRKHGHI HTFAKI LRLI KSEKYEI I HTHLALADLYGLFL
 GWFTPAKLI STEHNLSDRRKMTAPGRI YYRLAKLRVDYFVGVS GKI I DWL
 KSAGI PGRKLVLI PNPI EI QQGP GDTGI KRNFLKSCGWPE DSAI I GTVAN
 LRPVKGLPYLI DGI KI LVDEGFNVRLVI AGEGERGNLENRI KARRLDGH
 VKLLGFRKDT RDLYALFDI YASPSI MEGFGI AI VEAMSHRLPVVATEVGG
 VTDFLEHMKNSYL VGPQDPRALASGI RHFI NDPGEAARTGERAFNDI KKY
 RTDNLVRYVESLYEGAPRDFGP EETTF

>2617921488 Ga0073689_12918 Glycosyltransferase involved in cell wall biosynthesis [pelotomaculum Ga0073689 : Ga0073689_129]

MSESFSPRKP GAPRVVHVTTI GI TAYRALLAQCRYFRERGLAVGFVFS
 PSEI LRRLEFPVKEI YI DRKI NPWADCRAI LKLFNYFRQI RPGI VHTHT
 SKAGVGR I AAKMAGAPHVI HTVHGFPFPQPGTPGVKHQLYLQI EKRMAGI
 TDLMLSQSGEDVASAAELGI RPRRGGLLHI GNGVDLGEFDPGRYSASGRL
 RVRANLAI GETEPVI TMI GRVNREKGYHDLVEALGGVGDLSWRTLFVGP
 D EFLAAVKQOI DSHGLGERI RI LGKRDDI ADLLAATDI YVLP SYREGLPR
 SLI EAQAMALPCVATGI RGCREVVENGVGTGFLVAPGDSEALGGALRRLLL
 DPDLRCRMGREGRLRMRRFFDEAEVARKVMAI YEEVLKDEKSSYYHQQL

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>2617921487 Ga0073689_12917 UDP-glucose 4-epimerase [pelotomaculum Ga0073689 : Ga0073689_129]

MSTFLVTGGAGFI GSNLAI ALVEMGHRVKVLDNLTTGNPDNLKPVMGDI D
FHQGLRNLDDVRRVAVGGVEVVFHQGALPSVPRSVADPVTANEVNI TGTL
NVFLAARDAGVRRVYASSSSVYGNSDI LPKVESMPRPLSPYAATKLAG
EVYGRIFELYGLETVGLRYFNVFGPRQDPHAEYA AAVI PRFI NALLKGI P
PEI YDGGQSRDFTYI GDVARANI LASGAVEAAGEVFNI AAGTRTTVNEL
LNHLMDI TGSKAAASYAPVRPGDVKHSLAGI EKASRVLGYPRTGLREGL
RMTVAWFARKNGQ

>2617921486 Ga0073689_12916 receptor protein-tyrosine kinase [pelotomaculum Ga0073689 : Ga0073689_129]

LNSHELVTYSQPRSYMTEFRVLRANLHFFFEAGNTMKAI MVAGGGFGEET
SFVTANLGI VFAQTGQRV I VDCDLRKPPQHLLI FNVDNQFGLSSI LAGFK
EPGEVLKLLPAAGLKLLTAGPLPENPAELLGSPGMNQLI AALKEKAEVI L
LDTPLTVVADAAVLSKWVDGVL MVVRSRVASYKSVVKTKEFLVNARANL
LGVALNCVRADDI SENYSSYYGEGSRVKQI KKKESKPEKAK

>2617921485 Ga0073689_12915 Capsular polysaccharide biosynthesis protein [pelotomaculum Ga0073689 : Ga0073689_129]

MKFKDFGRVLGELKLVLLI PVVAMLTSAVI SLFVLPVVKSTTTVI VLR
DOMTPFSEI NINTI VLNQNLARTYSQLTKSRAI AEEVI KNNNLNMTPEEL
SSKI EVELAGNTEMFKI SASDSNPAMAALLANGVAQALSGKVYKVLNI KN
IQVLDPVAPPAGPVSPNAVLI LLAGI I GLI LTVTI I FVREYLD DDI RNP
EEVESYLKLPVLGVI PAADFQTGRGRTEFE

>2617921484 Ga0073689_12914 SH3 domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_129]

MWLGALI AGTVLSALFLI I TLAKI EAGTKGKSGWLALTFCSLAAVAGLI I
FKPETKMEQVQYMPAPPVLEEKERKGEVVKKSAPRPAEPAGGPAAVEKKS
PGNALSEKSFPM DGI ERDPLLEE I LSLKROAMENRQKSASGEPAAADSS
QEEQSGEQSGASGSVDNNSGQTDHSGEQKPEERQDTS LSPDGR TDQQNN
AESSDKEDRQODREGGAVRAKVLVSSLNVRDKSGLDGAVI STLKAGDVVE
I VHKAAGEWVEI KLNSGQTGWLMMKYI EILP

>2617921483 Ga0073689_12913 thiosulfate/3-mercaptopyruvate sulfurtransferase [pelotomaculum Ga0073689 : Ga0073689_129]

MVTKRTLAAACLLTVLI VLGAGVLLGGCARKETVAVPVAVEEKKEDPGL
HQAEEKI AGYTRPEALI SVYELNRRLED SGTFI I DTRGRSFKVLQASYP
FGHI PGAVPVLHSNYCHPAYPGRI AAPLQLQDFLGKCGAGAESNI VLYGN
DGLQARLYWALKMYGFDNVKI LDGGLDKWKEAGYDVATASSRRPPDTFEF
DLADSKAEQTMVAFNDVAAAVGDSGCVI VDARRNDEYLYKHMPGSVNLSS
EELFNQDKTFKTAPELKVLA EAKKI TPDKKVI VYSNAGVRSSLVWFALSE
LLGYPEVKNYDGSLQEWI KLERETESLQTKPVTLO

>2617921482 Ga0073689_12912 thiosulfate/3-mercaptopyruvate sulfurtransferase [pelotomaculum Ga0073689 : Ga0073689_129]

MNKRSLTLI YI LATI FVFVAVAGAI ATYSRYKSWKAVHPAVKSPADLAV
EKI SRYSNPHTLI SVHELHDI LNDPNVLVVDTRGRSFQVFRTTYQVEHI P
GAVPVLHSEYTHPVYFGRI GI PLLTQNNLGKKGF DNRKRI LLYGNDGLQG
RLYWM LKMYGSDNQVQI LDGGI EKWKEAGYPVTAQVAPLAPSRFEFNGLK
AYPNVYTTMEEVI DAI LNYTPDRI I VDARSRNEFLVGH I PYSVNVSFDDL
LNADKTFKPAQELTAI FNSKGVTPDKTVFVYSKAGVRSSLLWFLHELLA
YPNVKNYDGGFSEWHFRERMKEFGEERPVAKSVK

>2617921481 Ga0073689_12911 alginate O-acetyl transferase complex protein Alg [pelotomaculum Ga0073689 : Ga0073689_129]

MLFNSFEFI FI FLPLALFI FYFLVNKKLHRQAI FSLVLLSLVFYGYWNHK
YVLLI I ASI AVNYGTGCLLRKTGSKKVL I AAI AFNLLLLGYKYCNFFI D
NI NHI FDLNI ASLSI FLPLAI SFFTFTQI AYI VDVYRNREI RYDPVSYSL
FVLFFPHLI AGPI VYHREI I PQFLDEKTFKVNYLNLSTGI LLFFI GLFKK
VI I ADYFSPHAAAVFDLAENPTFFEAWAGT LSYTMQI YDFDSGYTDMALG
LAYLFNI KMPHNFDSPYKSNSI I EFWRRWHI T LSRFLRDFLYI PLGGNRL
GKARKYLNLLI TMLLGG LWHGAGWTFVI WGGLHGI YLCVNHQGRAMGI KI
HWLAALKALTFTAVVVAWI FFRARDLDSALQVLSGCFGLNGFDLHPRYATK
EEI FFI LLALAAVNLLPNLQLAGNLRPTVKWLAFTVLLALVSLTMI DNP
SEFLYFQF

>2617921480 Ga0073689_12910 SGNH hydrolase-like domain-containing protein,

Table S2

acetyl transferase Al gX [pel otomacul um Ga0073689 : Ga0073689_129]

LTPKKFVRI FCL I I CLFLTCHLVLYCFTRESLALPEKLLKSAVTGRHEP
EKQVEVDTI GDLARLSYLRLGTHRRVRDTSDEMGLNKKYGENAAFPVV
VAGDSFMLFNGDGRFRNNLLEDLLGVNCYNMAANGVEDPFTYLQSGSKKE
ARVLVWESAERNI SAGVFDPGKVDY YATAAKKLACAEDWESKGAFQKQF
RVI NLANFKFLI NNI AHSI GKGPLLGDGTGI VRLDNGKELLFYKNDLYSFQ
RPDLAEDLRQSTAFI THVDRELKRGVTLVFLAVDPKYNAYYDRI AGKEK
LTGDARFI DQLTEELKKNV I AVNLLNMFRAELAKGNELYHFD DTHWNT E
GAALAAGLVAEEI KKRGLLD

>2617921479 Ga0073689_1299 Protein of unknown function (DUF2837) [pel otomacul um Ga0073689 : Ga0073689_129]

LVI VI LTLVVHLI STLAYSVRVAGVRRRLTAFSLYNI I YLLASVSNTI
QAPLLTSVMEHGI KAVLMDAGI TGSAEQLI YHEAYREQLSLLAGQI RLVI
VASTFGTLLGAALI PVFI RI FI RAI RLFEKGSVAGAFKLAA SFLQRGE
RPVRRHSLLSFTSI RKLAKGKLSI PI NFLLANI VVTGLYTTGVLSALYAG
AMFPDFRSTAAMLAAMVNGI ATVLGAVVVEPAAASI TDEALRGDRDET DV
KQMAFYMALTRLAGTI LAQALFLPGAYFI KFLAQLLA

>2617921478 Ga0073689_1298 Ubi qui none/menaqui none biosynthesis C-methylase Ubi E [pel otomacul um Ga0073689 : Ga0073689_129]

MKFNSLLRLCLLPDI TLRYI FERRFNFFPTDRWQRYSAVTNKI RECDNNN
SSNSI LDVGGSEGI NNFLKPENFKLI VADLDEKAI FRAGKKQNLOAI LA
DGCYLPFKDNDFDI VVSASLEHVPDELKPAYCTELKRVT KD T VI VYCPA
DSRDGI FQGSVFDQKYFDWYRQRFATEERNTREHLEAGLPTI DELSALFP
GARLEGI QNGHI WLDI MKMKEAPYI GLLTSWRYSLFLKKKDVSPPYACL
LVWKKSRDFSVHEGPI VQPGQL

>2617921477 Ga0073689_1297 hypothetical protein [pel otomacul um Ga0073689 : Ga0073689_129]

VI I PNWNGRKLL ETCLVSLGRQTFRD FEI I VVDNGSTDDSAEMVRTCYPD
VKLVPLLENEGFSRAVNHGI NAAAGKYI ALLNNDTEAHPEWL GELVKTMD
QNPEI GFCASKMLNFFORDRI DNAGDKLAFYGN I TGKGELDAGQYDRPRL
LFSACAGAAAYRGEMLRDTGLFDEDF FAYYEDI DLGLRAQLMGYRCLFVP
TAVVYHI HQATSDRMPAKRFLFLQRNI VFVHLKNMPLRLLLKI LPAFLT V
HLLVSVTYLI KNDPKTVLAI YLHLLKKLPSTLRKRRLI QKKMRVTNPYI
ESI TGPFP T LSSMLLKWLKKLPGLGKRKKNEI V

>2617921476 Ga0073689_1296 Protein of unknown function (DUF2837) [pel otomacul um Ga0073689 : Ga0073689_129]

MVEGSRGEGMERLI LVI LLTGLI HLVI TLNYAVRLAGLRTGRLLTAVSI F
NVI NLLASAANTVQAPLLTSLVEHTI KTGAALAGAAVPGDLLVHQEAYNG
QLTLLAGRI RLVI LAASAGTAVGALLTPVFVKI FTKAI RLYEETGSVPRM
FVKLVFSYLPGR I KGDKPLSPPLPGELFYWAGRKI LI PRTFLVVNI FVSG
LFTTGVL SALYAGALYPDFRSTA A VLSAI VNGI AI AI VALVVEPTASLI T
DEAMQGRRGEE DVKQMAFYMI I TRFLGTLLAHALFLPCAYLI KYVVQQLA
R

>2617921475 Ga0073689_1295 Ubi qui none/menaqui none biosynthesis C-methylase Ubi E [pel otomacul um Ga0073689 : Ga0073689_129]

LNRLDKPKDYTYNYLRDDFMELAPRSYRRVLDVGC GEGNSAFYLKERGAG
FVAGI EI NPGAAAAARKKMD FVWEGSV EEE LPFTRGQFDLI I CGDVLEHT
VDPWKALERLKP LLAADGYLLASI PNLRYAKVLYELI VKGLFQYTVSGVL
DYTHLRFFTRTTMKNLI KESGFTI VRWGLPVKTRKCAWLNKI TLGI FNDF
LTTQYYI LARPTT

>2617921474 Ga0073689_1294 Glycosyl transferase involved in cell wall biosynthesis [pel otomacul um Ga0073689 : Ga0073689_129]

LRVLFLPTASWNDPPSRYRVHQYLEGLRERGI TAHCKAGVSDYI YGRFTP
YKGWWAKAVFFGFGALSRFLACLI I WRYDVI FI QRLI LPHI YLPPEMFI C
LVAGMLGKRI VDFDDAI FATSPHRKKT LVEKSTDLNRVARI I ARCAVI
AGNSYLATYARAFNGNVVVI PTTI DLTRYPVKEAADKKPGEP CVI GWI GM
PGSLPYL NMLKPVFQEI AGEHNI LI RI I GGWNYHCPGVRVEHLPWSLQSE
VSRI I TFDI GVMPLAENEEARGKCG LKLLQYMAAGI PAVASPV SANKEI V
TDGLNGYLAVSPEEWAEKI RSLI RSPRLRLLMGRRGRETVERRFSLOANI
SKLI GVI EGPCVEADAC

>2617921473 Ga0073689_1293 dTDP-glucose 4,6-dehydratase [pel otomacul um Ga0073689 : Ga0073689_129]

Table S2

MKLLVTGGAGFI GSNFI HYI YREHPDWRI I NLDKLSYAGNLRNLEGLNGG
RHRFVRGDVTPDGPVDELVGPERDVI I NFAAESHVDHSI DDSAPFI ENNI
RGVQVLLLEAARRRGVEKFI QVSTDEVYGSGLPGDGSFSEDSPLAPNSPYSA
SKASADLLCRAYFKTYHLPVI VTRCSNNFGPROYPEKFI PVVI TNALENM
PAPVYGDGLNVRDWLYVI DHCRALAVI RGGRAGEVYNI GGGRELTNLEL
AGAI LRQLGKPASLI RQVRDRPGHRRYAVNSGKI QRELGWRPVYDFPRA
LRETI RWYVDNRNWWGNH

>2617921472 Ga0073689_1292 dTDP-4-dehydrorhamnose reductase [pel otomacul um
Ga0073689 : Ga0073689_129]
VRVMVTGAAGMLGRAVAEEFTRRQAEVI PLTRADLDI TDLGRVRKVI ESS
KPEI I I NCAAYTNVDGAETEPHAYLVNGLGPRNLAVACREAGAALAH I S
TDYVFDGDKPDAYTI HDHPRPLNI YGSSKLWGERALSI I AGSCYLVRTSW
LFGPGNNFI TTMLRLGEERGSVQVVNDQKGCPTYTVDLARAI ADLSVSG
CFGVYHI TNRGNTTWYGFKEI FTRKGLHI DLTPCDTPAMKRPARRPRNS
VLDPFPLEETTGYLLSAWEDALARYI I ELTEK

>2617921471 Ga0073689_1291 dTDP-4-dehydrorhamnose 3,5-epimerase [pel otomacul um
Ga0073689 : Ga0073689_129]
CLKTGVGNI KLI EGVEI RHLKMI PDERGFLMEMLRSDWPEFMNFAQAYVT
ACYPGVVKAWHYHKLOWDHFVCVAGMARTVLYDPREGSPTRGEI NVFHLG
YLNPLVLLKI PPMVYHGFTAEGNKTSLVVNFPTRLYNYARPDEYRLPYDDP
SI PYRWEVVNG

>2617921470 Ga0073689_12831 Peptidase S24-like [pel otomacul um Ga0073689 :
Ga0073689_128]
VALLEEEATVKRFFKENGQVRLPENRLMEPI YTNDLRVLGKVI GLI RKI
H

>2617921469 Ga0073689_12830 DNA-binding transcriptional regulator, LysR family
[pel otomacul um Ga0073689 : Ga0073689_128]
MNFQKLEAFLWVAELQSFTKAARQLYMSQPAVSFQI KALEEDLQVSLFQR
GDKRVI LTEAGRLLYPEAKQMLRHYHKI KAGLDDLKGLKTGHLVVGAGTI
PGEYLLPLLI GGFKEKYPGI QI SLKVAGSGQVGRWVQEREI DMGI TGASV
EDEGI ECI PWLQDQLVLI VPPAHPWSNVNAVKVSDLKNESMI MREQSGT
RRTI EQKLGEHNI PLEKI PQSMELGSTRAVI TAVEAGLGI SI VSRCVRE
ALELGRVREVQVGLDLSRYLYHVRHGQGMGGFAI EAFTEFI NDRDI CKR
FLFW

>2617921468 Ga0073689_12829 Cystathionine beta-lyase family protein involved in
aluminum resistance [pel otomacul um Ga0073689 : Ga0073689_128]
MVKNI NLERLAAEEVVKEVQAVYHI I DKKALSNHAKVLEAFCRARI SDFHL
KGSTGYGYGDRGREALEEVYAVVFRAEAALVRSQI VSGTHAI ALCLYGVL
RPGDELLAVQGEPYDTLGEMI GLRGNTPGSLKELGVVYKQVEPLEGGGI N
YAAI GOAI SDRI KMVMLQRSRGYHWRSTPGI AGLREVI SYI KMKPDVVV
FVDNCGYGEFVEDEEPVEAGADLVAGSLI KNPGGGLAPTGGYVVGKSEYVE
MASHRWSAPGI GAEVGPSADYQRLLFQGLFLAPHI VAEALKGAVFAARFF
ERLGFVDLPGYAEERSDLVQAI RLGAPEKMI AFCRGI QQYSPVDSHVLPE
ANAMPGYGEPI MAAGTFVQASLELSADGPLRPPYAVYLOGGLSKEYVR
LAALSAAREVLKI G

>2617921467 Ga0073689_12828 stage V sporulation protein K [pel otomacul um
Ga0073689 : Ga0073689_128]
MPVKKI KI WNSQETGGGSGQKVEFRARKI HPAQSTGKGARTGEDPDQQKN
VREI MLELNSLVGLHSVKLI EEI YAFVEI QKRRQKEKLI AEPLVLHMI F
RGNPGTGKTTVARI LGKLFKEVGVLPKGHLVEAERADLVGEFI GHQAQKT
REQLKKALGGI LFI DEAYSLARGGEKDFGKEAI DALVKGMEDHRDNLVLI
LAGYQDEMDWFI ETNPGLRSRFP I HI SFPDYTVRELLAI ADLMLKQORQYC
LSNGAREELRFNI EKGHKRHEHSGNARLVRNLI EQAVRRQAVRLLRKGGE
LNRDDLMAI TREDLEGALGEV

>2617921466 hfq RNA-binding protein Hfq [pel otomacul um Ga0073689 :
Ga0073689_128]
MTKPQI NLQDAFLNQVRKENI PVTI FLVNGFQLKGMVRGFDNFTVI LESD
GKQLMVYKHAI STVSPLKPVNTSFSEAKPPERV

>2617921465 Ga0073689_12826 tRNA dimethylalyl transferase [pel otomacul um
Ga0073689 : Ga0073689_128]
MRNKGHELPPLVVI TGPTATGKSEVGVLVAERTDGEI VSADSMLVYRGMV

Table S2

I GTAKPTRGEMRGI PHHMI DI VEPDQEYSVALFQEQARSVI NDI YGRNKL
PVLVGGTGGLYI RAVVDDYDFSGARGDNSLRERLAVEAKELGPESLYRRLC
EMDPRVAAKLHPKDTRRVI RALEVYHLTGKPI SSYQRLEESDHPLYHLFM
FGLTMDRERLYQRI EQRVDRMI AVGLI DEVRGLLRRGYGVELNSMRGLGY
KEI AAHLTGTLSEQTVELLKRNTRRFAKRQLTWFRDQRI RWAYNMDECG
SCEAVAKEI AGRVAGVLSDL

>2617921464 Ga0073689_12825 Putative SAM-dependent methyl transferase
[pelotomaculum Ga0073689 : Ga0073689_128]
VTACTEPATPKPRFAI TTSHRPASDQLEWAKRLAAELEAPYADRNDLSLD
TLAKRLRVDGLVVVSANKVAYVSGTGKFFFHPGLAGLRI MEVKNGKTDQM
I KAVSFHKGESLLDCTLGLGTDAL VASFVAGPEGWVTGLESSLII ATLVC
HGLSVYSAAEEDTI RAMRGI EVVNADYKKYLAGLPPSSYDVI YFDPMFRA
PRFHSPAMNALRALANPAPVDREAI ELALRAAVKKVVLKERRGSAEFERL
GFKKI YGGRYSPVYGVMDLQASNEK

>2617921463 Ga0073689_12824 DNA mismatch repair protein MutL [pelotomaculum
Ga0073689 : Ga0073689_128]
LANI I I LDEFTANQI AAGEVVERPVSVKELVENS LDAGAGRI MVDLEDG
GLGTI TVTDNGCGMVEEDLLAFHRHATSKI RYASDLGRVTTLGFRGEAL
PSI AAVARVSVI TRTPEALSGVGADLEAGSPVSPAPVGCPPGTI TVRDL
FYNT PARKKAMKSPSTEGALCGDMI SRLALARPGVSFELRTKGKRVFYSP
GTGRLLDSI TAVYGVQQGREMVAVNTTDGDLQI NGFAGKPSLSRSTRGHI
TVI I NGRYVRCPVVAGAVEEAYHTLLPRGRRPVAI I SLTVPPCLLDVNVH
PAKFEVRLLDDEERVAGLVTKTLRAALRVRTVI PATLADGRKWNAPARSHA
QVALGLTPESPEAVTGEFLHKLPEI GSATNDVEQKTGGNREKSCGLQPE
KNRGVGTACESSVDYHAAKRSLPALNALAQLPPTYI LAVGGNGLYI I DQH
AAHERI LYEEFLAVDEKRPSQYLLVPATLELDHREAAI LTDHVLWFTDAG
FVI EHFGGNTFLLRGI PHQFPVGREKEI FLDI LDYFRERGPANRVEFFD
RLASSMACRSVAKGERLSPSAMDALLQRLARTENPHTCPHGRPTVI HLS
YRDLETRFKR

>2617921462 Ga0073689_12823 Acetoin utilization deacetylase AcuC [pelotomaculum
Ga0073689 : Ga0073689_128]
MKRFRCKQTGLI FFPADFDAI SPTHPEREERLLYTRDQI FEEGI I DLPQI
AEYTP I LASTHI ARAHFCVPRVEDQTTEAHLI AAGAAI LLADQVVAGHI
ENG FALVRPPGHAMRVVHGNRGFCNI NNEAVMVEYLRRRHGI KRVAI VD
TDVHHGDTQDI FWHDPDVLFI SFHODGRTLFPGTGFTNELGGPRAFART
I NI PLPPGI TDESLLYVADSLI LPVPKDFKPDFVVSAGQDNHYTDPLGS
MRI TAQGYALLTEKLRLPD LAVLEGGYAI ETALPYVNMAI I LAMAGLDYTG
VREPDYRPGRFKESPERAGQVRRMVERLLQYWEMRDQMTDPQHI KGKFI
ERKKS I FYD TDYFEENQLERLRLCDNCPGYLAI DSRASHGYAGAGKI LCL
SVPFTACAGCQGEAAGLYEQAKNTGEYSYI YLQDKSTDTFWSYDSGCRWE
WRSEG

>2617921461 Ga0073689_12822 N-methyl hydantoinase A/oxoprolinase/acetone
carboxylase, beta subunit [pelotomaculum Ga0073689 : Ga0073689_128]
MYVGVDVGTFDAVLLENLVRATAKVPTREDLLSSI LEAI DTVLKNVD
AGLKRIVVFSTTMI TNLI AERKYDQVAMLLI PGPGLSHEYNSNSNVHI L
SGAI DYRGREI VPLNEREI EAALANMALKGFKKVGVGKFSRNTSHEKY
VAEI I ADYRDPWOVELGSQI GGQNFPRRVETTYLT CATRESYRYFMNSV
RQALARRQI TADVFI LKADGGTLPLEQSEELPVETI FSGPAASTLGVQAL
TPPGESSVVVDI GGT TTDLALI LSGQPLLSAKGARVGDRLTQVRTLAVKS
VPVGGDSVLERVGSEI I I YSERLGPAYCMGGPMPTPTDALRVLGMTMLGD
GEKAREAMAI LGNALGLGAGDVAGKVL SLVVD SI AAEI RKM FLEWEQEPA
YRVWEVLQKKKVRPTNVAGVGGGAAGFVSQI AAKLGICYPI I PPYAPVANA
I GTAVAKPTLQVNL RADTEQGYI I QEEGFQGI ESELFNEQKALDLARE
WLI KRAAKYGLEVAPEEI EI TRREVFNMI RDWTTTGRLFDI TVQTPRGI V
GRI GMGGKV

>2617921460 Ga0073689_12821 DNA mismatch repair protein MutS [pelotomaculum
Ga0073689 : Ga0073689_128]
VSFTPMI RQYLDI KEQYPDAI LFFRLGDFYEMFFDDARLASRELEI TLTG
RDGGGDDRVP MCGVPYHAADGYI ARLVAKGYRVAI CEQVEDPTTARGI VR
REVTRVI TPGTVM EGQLLEEKNNYLACI TPGADGYGLAVTDI TTGLFMT
GSFFGEKATAALLDEL SRLAPAEVI MPLSEMDRFTDDLKLRGI QTVCGYR
DESFDLEEAVRMLEKQFGRGVGGESTGDSGFTVPAAGALLRFLKETQKRE
LTHI NRI RFYRPGRFMLLDAATTRNLELTRSI ADGSRKHTLLSVLDHTVT
AMGGRLI RNWI EQPLLEKDEI DARLAAVEELVGQVFLRQDLKDI LKKI YD

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LERLAGKI SFGTANARDFI ALRKSLACLPLGLKRLLGQAEAPLLKEI ALGV
DPMEEI VELLDAAI VDDPPLSLRDGGI I KEGFNPEVDRLRQAGREGSLL
AGLEERERARTGI KSLKVGYNKVFYGYI EVTRANLDAVPEDYRRRQTLAN
AERFI TPELKEYEDMI TDAEDRLAQLEYHLFDEI RERLAGEVHRI QGSAL
AVAKTDALYSLAKAAVEGRYSKPLVGGGGRLYI KEGRHPVLEQAMGPGRF
VPNDTLLDDEKNRLI LLTGPNMAGKSTYMRQVALI VLMAQAGSFVPALEA
EVPLVDRI FTRVGASDDL AGGQSTFMVEMNECRTI VAGATEKSLVI MDEV
GRGTSTYDGI SI ARALAEYI QMRI KTKTLFSTHYHELTGLDAI PGI VNHN
VAVKEDGEDI I FLRKVVPGRADRSYGI HVARLAGLPREI I SRAAEI LKGL
ETAGAAPPQVAAAKDENESFLKETELSVLKELRDLSVLEMTPLEAI NKLY
QLQKRLNDCI L

>2617921459 Ga0073689_12820 Cell fate regulator YlbF, YheA/YmcA/DUF963 family
(controls sporulation, competence, biofilm development) [pelotomaculum Ga0073689
: Ga0073689_128]

LSVLDKARELGVEI SRCNELI NMREAEVMMLQNSEAQEI I KEFNEKQRAF
QMI QSQGGQLTEGQKQEAEELEKKMLDNPYI YNFFKAQQTFEKVLEGI NK
I I GEAI GAGSGCSCESDCADGACSCNDCH

>2617921458 Ga0073689_12819 tRNA-i (6)A37 thiotransferase enzyme MiaB
[pelotomaculum Ga0073689 : Ga0073689_128]

LKSYMI KTFGCMNEHDSEVL AGMLEGMGYQPADDAGDADI I I LNTCCVR
ETAENKVFSLLGLRRRRKVENPGLI I GVCGCMPOQEDMTARI RQLFPHVD
LVFGTHNMQRFPPEI I EKVLESREPVI I WTGSGGI TEDLPVKRMAGVRAW
VTI MYGCNNFCTYCI VPHYVRGRERSRRPEDVVAEVARLGEGYKEVLLG
QNVNSYKDLAGAMDFAGLLEMLEGI NGI KRI RYMTSHPRDFTEKLI KTI
TASKKVCHEFHLPVQAGSNRI LKLMNRYGTMEEYLAVVERI KTLI PAATV
TTDI MVGFPGEGEEDFNDTLDLVRARFDSAYTFI YNTRPGTPAAEMAEQ
VSGAVKKERI QALI RLQNEI SLARNREEEGKTQEI LVEGESKEKPDLLWG
RNRGNKMVVFPGDKDI GEI VPMTI TGSRLAQLKGTMAKN

>2617921457 Ga0073689_12818 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_128]

MLEKLTGLAVLAGLVSVAGAVMNHENLKL TGNLALLVI ATI AGYRFI KF
HALNPTREFTGACVEQKRLPTHYLLTFRITGGAGLYSGRAGLDLGEKI KMG
ETARVKVKQVI LEI NRLKK

>2617921456 Ga0073689_12817 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_128]

MRKKLI KYCPKCGYDQLDVEQEPAYTVLCRHCNFYCEI I VFDEGDFEGI
F

>2617921455 Ga0073689_12816 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_128]

LPQI NDYEAQQLI EMQLRDI ENI RSKAPYGLETYFWEDFTAKI I DRIYS
NESSQRHGFQAGRGCFVSFESYSESQRREDFNEI LNCKKEYLEDLI KD
MEKHFPNQEFRHPSQEENPEKPAI FDGNLEEI LKSQAASPLDRAMAEI LA
GI KDPRI LKEARANLLELRDELLKPAPSWTKLKRSMI WLI EFGKDEFFSI
LPFI VLYI RKI VE

>2617921454 Ga0073689_12815 Nucleotide-binding universal stress protein, UspA
family [pelotomaculum Ga0073689 : Ga0073689_128]

MMMTRVLLPSDGSDTAMKAAVYAARLMKTNPKMKLTVLVVI PRSNEFLGK
NNNNRKEI MEKI DRVI EAKAAEI LEKTMNVFKEEGI GVEGLI EKGDPAGV
I LDYSGKGKYDHI I MGSRGVSELRGVAVGSVSHKVI QLADSRVTLVK

>2617921453 Ga0073689_12814 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_128]

MRVNI TOTGLI LSDLLVAVYERGNQRTGGGSFLQVDGKMI EYSI ANHASR
I LALVEQVANTNTPRGVN

>2617921452 Ga0073689_12813 HpcH/HpaI aldolase/citrate lyase family protein
[pelotomaculum Ga0073689 : Ga0073689_128]

LLYHTMLFTPANDLRKAGKVLMSDADAI VLDLRDALALSEKNQHQSPPQR
GI EFAAQKGCLHASQHHPNRI NLERFAGCCV

>2617921451 Ga0073689_12812 Uncharacterized conserved protein YliO, alkaline
shock protein (Asp23) family [pelotomaculum Ga0073689 : Ga0073689_128]

LENKDDQLI I EGDGGGAI KI SEDVVKI I AGLAATEI TGvagmsggi AGGI

Table S2

VEKLGRKNLSKGVKAEVGEKEAAI DI SI I VEYGVNI QEVASRI QSAVKNT
VENMTGLNVLEVN NVQGVSVFGPDRDEGRTK

>2617921450 Ga0073689_12811 enoyl -CoA hydratase [pel otomacul um Ga0073689 : Ga0073689_128]

LSYNNI LVEVEGFTSLVTI NRPKVLNSLDLETKELEEV MAGLELNPEVR
VVI I TGAGDKAFVAGADI SFI QSLTPMQARSFSRTGQWVLSRI ENLSKPV
I AAVNGFALGGGCELAMACDI RI VSEKAKFGQPEVNLGVMAGFGGTQRLT
RLVNPGMAKEMFTADI YDAQAALKMGLVNHVVPAAELLDYCKDMAGRI T
SKGPVAVRLTKEAVNOGLEMDMEKALALEADLLGLTFTTADKVEGLSAFL
NKAKPNFKGE

>2617921449 Ga0073689_12810 glycogen synthase (ADP-glucose) [pel otomacul um Ga0073689 : Ga0073689_128]

MFDRLPKI LLVSSEVVPFAKTGGLADVAGSLPKALAVVGNNDNLGNDVRVA
MPRYRLSEGGSYKMDFPVPFKSRFETAVI RESSI ESHYHVQHRSI PVYMI
DNHHFYFYRDRMYMYDDEAERFAFFCRSVLEMLPRLDWQPD I HCNDWQSG
PI PLFLKTHYRQDPFYNRI ATVFTI HNLQYQGNFPREALRVGLGLGDEFFH
PERLEFYGMVSFMKAGI LYADVI STVSRTYAVEI QRPEMGERMDGLLRNR
SADLYGI VNGI NYHEFNPGADPRI HRNYDQFSI YNKKENKFALQKEI GLP
VKDVP I ALI SRLVDQKGLDLI AEVI NEI MSGDLQFI VLGSGDRYYENMF
ESI KSRFPDKMGLYI GFNAI LAQRI YAGADMFLMPSRFEPCLGQLI SLR
YGTI PI VRFTGGLADTVYDYNPATGTGNGFGFSEYSGKMLLOTSERALRL
YREEPQEWQRLVKNAMEQDFSWARSAVEYI QLFQEAMSRRLVASKI A

>2617921448 Ga0073689_1289 UDPglucose--hexose-1-phosphate uridylyl transferase [pel otomacul um Ga0073689 : Ga0073689_128]

MSEWRKDPI VGRWVI I ATERRKRPFDYKEI TEEKKAQVCPLCEGNERQTP
PEI MAYREKDTGKMPGWWVRVVPNKFPAAVAVDGDFLKQKGLYNFMEGV
GAHEVI I EAAVHEPGLDSQTVKQVEEVI WAWRERSMDLRRDKRFKYI QI F
KNTGSTAGASLEHTHSQI AMPMVPQEVKQEI EGMKEYFTRRGSCVLCDI
I RQEVVERDRVI VDGVIYFLAFTPFASRFPFETWI VPKEHQHDFGQI REEQ
VRDLAALLRTVFLKMSVLI RNI PYNVVLHTSPVNLEELQYHWHLEI LPR
LTI I AGFELGAGYFI NPTPEMAAQALRETGEVYPLQERHLETVQSYV

>2617921447 Ga0073689_1288 septum site-determining protein MinC [pel otomacul um Ga0073689 : Ga0073689_128]

MI RDLVSI KGTRNGLVI VLDSNREFEEI KNTLLNTMESARGFFKGAKFSL
FQGHRI PQQKNELENI CQYGLVPSTEEQEA VRNSFRAGPGRQA AVLQ
HSGAGESALMVRRLRCQRI SYPGHVVLGDVHPGAEVVSGGSVLVMGS
CRGVVHAGAEGDH MARVI ALRLAPTI LSI AGRRHALI PASPPPAECRLAR
LVDQEI I FEKYDV

>2617921446 Ga0073689_1287 ADP-ribose pyrophosphatase [pel otomacul um Ga0073689 : Ga0073689_128]

LSDFTEKVLSSKRVEGRI I NLRVDTVAFPDGRTGTREVVEYAGAVAVVP
VNERGELLLVROQYRHAVGNLLEI PAGKLEPGEDPATCAERELLEETGYE
AEQI TRLI SFYSTPGFTTEELHLFLATGLKLKEQDLDEDEFI DVVPVPFA
RALEMI WSEI CDAKSVAGI LAVHSLKSKPAEVF

>2617921445 Ga0073689_1286 protein of unknown function (DUF3786) [pel otomacul um Ga0073689 : Ga0073689_128]

MPLMNLNPAVEKAREDFKCGGPEQMAAARVEYDERVNLFKVPFLGSEYR
VSYPDGGVTGPRETCVTLAVQVLI LHYLTGASGI PVNGRLI SFKELPGGP
I YI GPFTQRAVNPLVKFFGDNDPKLVEVALHLGGSRYELGDVAVRVPFFP
LVPLI YVLWLGDDEF LPVGNVLF DSTAPTHLATEDFAVMAGMGVFELKKL
AGI

>2617921444 Ga0073689_1285 3-deoxy-D-arabinoheptulose-7-phosphate synthase [pel otomacul um Ga0073689 : Ga0073689_128]

MI I VMRSGADSRQI NMVEERLKEFGFNAHPI YGEERTVI GAVGDKRELNA
EVI I NLPGVEKI VPI LKPYKLVGRELKQENTVI NI GGVAI GGGELVI I AG
PCAVESREQLLEAARAVKRAGGQI LRGGAFKPRSSPYSFQGLEKEGLEML
AEAREETGLPVVTEALDTRDVELVARYADI I QVGARNMQNFRLLSEVGRA
GLPVLLKRGLSATI EEWLMAAEYI MAAGNQSI I LCERGI RTYETATRNTL
DLSAI PMVKELSHLPVI VDP SHATGAWKLVAPMAKGAVAVGADGLMI EVH
PDPQRALCDGPQSLTPENFKTLVADLVPVARAVGREVLLQQI PA

>2617921443 Ga0073689_1283 HSP20 family protein [pel otomacul um Ga0073689 :

Table S2

Ga0073689_128]

MSI MRWDPFGELTYLRSQMNRFDFHTFRSFLTGAEPFGPRI DLYQTDQE
 VVATAELPGVESKNDVEI TLTSDSLRLGELKRSHDVGDENFI HVERYYG
 SFSRTLPLPAEVPKDEARASYQNGI LEI RMPKTEKGRKMAHNVPI Q

>2617921442 Ga0073689_1282 Predicted nucleotide-binding protein, sugar
 kinase/HSP70/actin superfamily [pelotomaculum Ga0073689 : Ga0073689_128]
 LAVKVGI PGTLLYYLYYPMWRAFFNEI GVQVVTSGKTTKGI LDKGVREAL
 TDACMPVKLFFGHVMEI KDGVDYLF I PRVVCLNHKTVYCPKFLGLPDMIR
 HSDVDDLPLI DVRMDTROGRFALLKAYFEI GRQFGADKSALYRAYWKACR
 VSQRYTGLLRRGWNPFAMAMLNSSGPRKLKPPESLKFVAVLGYPYTI Y
 DSFI SVNLFDKLRRLGVSULTADNI HPALLALQKNCGLPKRFLWTFSDI A
 LKAAHFLFKQGRVDGVLHLTAFGCGPDSLLNKFI ELEAKQQRNI PFMTLM
 LDEHTGEAGVATRLAEFVDMVRRRKEALLCRK

>2617921441 Ga0073689_1281 CoA enzyme activase uncharacterised domain (DUF2229)
 [pelotomaculum Ga0073689 : Ga0073689_128]
 MPKVTFPRMGESWRTFKMLLEDLGNEVVPPRPSKRTLDLGVRHSPEFAC
 FPLKI LLGTYLETVAAGADTI VTTGGVGPCRAGEYALLHHRI LKD

>2617921440 Ga0073689_12733 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_127]
 MKI GFDYYVEDALVAYI VKQWKSQKI KI GRTVVQKI CYFLKAQGVPMLYD
 FEMHHYGPYSQDLYYRMDELVADNI LADTSETSKWSHYLPGDRADEI I TI
 YHEEFELFKDKI DNLLGLFSRFGPTDLA

>2617921439 Ga0073689_12732 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_127]
 VVYETSAFAGVKNRMTAERI YETLLKEFQDHSFI I DKNVRGTI HKFVI PE
 EDEMGDFFYYVRTKQGNWKLI TEVSKI I RDMPKVFHVI RI YAKNEDG

>2617921438 Ga0073689_12731 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_127]
 LLDGSYRGGKTVVKKI SVAI SVLTLI AAFI FASAI NEKKS I STPGPAPP
 AGETKPETPPDRTSTQNTAGATPAESGSGSGSAI PPGLKPD I PPDKI DGQ
 SARGAYDKATSLAAKTPELNDI KMLI PVMLKFSPSELSTLTRLANRTMSK
 DEI EQAKSI LLSKLNQDEVSLLLQLGPEYGLDFRAVLGVTDKKK

>2617921437 Ga0073689_12730 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_127]
 MSENQI DHDRLFKELPETYLVWPTLLI RPCSKSRFKI LETEAKAQLGDE
 FTDHLVLKTPDVKLSPR

>2617921436 Ga0073689_12729 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_127]
 VDI LVETRLKDEPGLI LVHVEPOSYAQTDFNGRMFVYFSRLYEKYRRRI L
 LMAVFSYDRVRDEPDSFELGPFLEVLNFRFYKLELKKLNWREYI QSDNP
 VAAALLSKMGFRRMEKVRVKLEFMRMLVRMNLDPARMELLAGFFETYKLK
 NCEEEEQYNREL GKLD RKEVDVI MQI TTSWHEEGRERGRVEGRVERTREI
 I CKYLVRKFGKKSAGLQQKVGRMTDLEKLDYI LEELFAADTLDEACTI I S
 DGVAEQS

>2617921435 Ga0073689_12728 looped-hinge helix DNA binding domain-containing
 protein, AbrB family [pelotomaculum Ga0073689 : Ga0073689_127]
 METRI SSKGQI TLP AEARKKLG I KTGDVLKVRI TEEGVVI LSGKAGLKND
 PVSASEVLRETSGI WKDMEKSGEDFVRRLRAEDNERWKVLGLE

>2617921434 Ga0073689_12727 Protein of unknown function (DUF2283) [pelotomaculum
 Ga0073689 : Ga0073689_127]
 MEEKLI FRYDRESDI LYI DKVTPYPEQETTELGDVVARLNPFTEEVENL
 EI LFFSTRLLRDTLDFALPI SADLRLAFQNA

>2617921433 Ga0073689_12726 Nucleotidyl transferase [pelotomaculum Ga0073689 :
 Ga0073689_127]
 VLPVDHYI RDVPRFREVLOS AVADAGRWEEI VTPGI THHRPETGYGYTCR
 VECFCEKPGYERRLEFLAGGNYLSNSGMFVLRI ER

>2617921432 Ga0073689_12725 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_127]

Table S2

VLKI LELLNKSRI DSYEI QDFRQGSDFYI KVRASLHNKTFLYI RQYVS
NDEYSYSFHWQDESGLLI I RWDNAPHHKQI QTYPHHKHLGEKI LASDEMT
LEGVLEYI NTFLEKR

>2617921431 Ga0073689_12724 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_127]

MGI LEVSKSEI KEYQKLKI I SEMVLLKEHI KLFEQKYGCI FKEFEERI KQ
AAEDFESWDDYLEWKAYQRNFEEVKKKI GEI DRAKDI RI AE

>2617921430 Ga0073689_12723 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_127]

MSENI DHDRLFKELLETFEAEFI ELFFPEAARTI DLEHLKFLQQECAAD
GKAPWVVS GDKHLLRLGSYKDI TI VTAEQYDKI QPSQVI GRR I PV

>2617921429 Ga0073689_12722 DNA processing protein [pelotomaculum Ga0073689 : Ga0073689_127]

MDLYWI WLSTVKG I GPVTQKKLLAVFQTPEHVYKADREELI KRTGLPVSF
I DSLMASRSLEKAKKI QNSLNRHDI RLLTI DDRLYPTEASAFPTSPALLY
YRGNLKEDSMGVTI I GSRRCTEYKQVTSETATYLAEQGI PI I SGMAKGI
DGYAHTACLKAGGYTI AFLANGLDI CYPPEHQI LMEQI I ENGALI SPYPP
QTRPLKSNFYKRNALMSAWSLKVLVVEAGI KSGALMTAQFAGEQKRTI LA
APNSI YSPESI GTNQLI SOGAKI YLGPAQLLPEGFEKRMKTSLETKTHAK
SSNRQVAAEQLSHFEEQI LERLKI PKDI EQMVDI FDGNMAALLDMLCTME
LEGI I KI GHGKI VSAKI

>2617921428 Ga0073689_12721 magnesium chelatase family protein [pelotomaculum Ga0073689 : Ga0073689_127]

MATVI NSF AI AGI DGYQVEVETVTMYGQPSI TI VGLGDAAI KESRQRLEA
SI NYAGYEFPMKI AI NLAPGDVKKSGSHFDLSMAVGLLI ETGQLMVSPE
MLNSYGI GELSFNAFLRPCSGVLPMAI TARDAGI KEVI VPAENI REASL
VHGI RVLGFSTLKSVDYLEGKECYVSPVVKVSGQGSTNEI VDFRDVQGO
DALI QYI VVAAAGGHI LMSGSPGCGKSMI AKRMATI LPDMTEEEALEVT
KI YSVAGLLKDRSOLI TKRPFRAPHHNASMSLVGGGNPAVPGEI SLAHN
GVLFLDEI AEFNKKTLNALRQPMEDKVVTI SRVKS I VTFPCNFMLVAAMN
PCPCGNYGHVQCKSDYEVLYKRYQKI SGPI LDRI DLQKYVHAVNYLELSV
OSKETSSSELRRERVQNKI QQKRFahi PAVNCNAKMTEALVKEFCRLDE
GGNKLLQLAYDKFHYSARTFHKFLKLARTFADLDGAVQI RKQDVAGALLS
RDLKDQSRLLVVRG

>2617921427 Ga0073689_12720 Transposase IS200 like [pelotomaculum Ga0073689 : Ga0073689_127]

MPYLLHSYCLMTNHVHLQI ETI DI NI SQVMKRI NMLYAI YFNKKYNFI GH
LFQDRYSELI DATPYYLEI SRYI HLNVPVRGNI VALPESYEWSSYRTYI G
ERQDRLTTTEKI LGCFSPPRI QHYREFVEEALKFI KVKPKGDETGDNSN

>2617921426 Ga0073689_12719 conserved hypothetical protein (putative transposase or invertase) [pelotomaculum Ga0073689 : Ga0073689_127]

LPENDKKDPKPPHNPHDKGYRQLLTNSKTFLELLQTFVGEDWVREI SEDD
LTLVDKSYVLQDFSDKEADVYRLRLKRTEI I FYVLELQSTVDHTMPFR
LLQYMVEVWRDAYNNVPDKERRRKGFRLPAI VPAVLYNGEKGWAARRSFR
EYQAGHDRFPGRLLDFS I LFDVVRYSEEDLYRAANVSSVFYLNQTVDP
RDLVARLRKLVGVLGMTPEQFRQVTWLRNVI KRKLPGPLQDEADRVLE
ENDPREVEKVI TNI ERALDEMQRQALMEGVLRGKAEGKAEGKAEGKAEGK
I EGKVEVAKAALRKGFSDVDAEI TGLSRETVLGLKNEMEN

>2617921425 Ga0073689_12718 conserved hypothetical protein (putative transposase or invertase) [pelotomaculum Ga0073689 : Ga0073689_127]

MSENI DHDRLFKELLETFEAEFI ELFFPEAARSI DMTHLKFLQQEI FTD
VTAGEKHEVDI LVETRLKDEPGLI LVHVEPQSYAQTFNGRMFI YFSRLY
EKYRRKI LPVAVFSYDRVRDEPDSFELGFPFLEVLFNFRFYKLELKKLNWR
EYTHSDNPVAAALLSKMGFKRTEKVRVKLEFMRMLVRMNLDPARMELLAG
FFETYLKLNREEKEQYKRELGLDRKEVDVI MQI TTSWHEEGRAEGRAEG
RAEGRVGRMERTREI I CKYLTRKFGDKSAALQKI QVNDLEALDYVLE
ELFTANTLEEAAAI NDGVDVPQ

>2617921424 Ga0073689_12717 UDP-Gl cNAc3NAcA epimerase [pelotomaculum Ga0073689 : Ga0073689_127]

MKVVTVVGARPOFI KAAAVSRAI AEHNLENPDNI NEI I VHTGQHYDHNM
SEVFFEELDI PRPGHNLGVSGPHGRQTGRMLEAMEEVLEKENPGWVLVY

Table S2

GDTNSTLAGALAAVKI HI PVAHVEAGLRSFNRRMPPEI NRVLT DHAATLL
 FCPTEAAVENLRHEGI TGSVHRVGDVMDCLLHYRSKI SDNPPTLAALGL
 KPGGFALATVHRAENTDSPEALKEI FEAFFNEI SGQLTVLVALHPRTRKYL
 DSYGI KTAPGVKLLPEVSYLQMI ELECNA RVI LTDSGGVQKEAFFVGAPC
 LTLREETEWVETVQCGANVLCGASSDRI VGAYVSLERNHFKRI NCI SGI Y
 GDGEASKSI VNMLRDDSI G

>2617921423 Ga0073689_12716 DegT/DnrJ/EryC1/StrS aminotransferase family protein [pelotomaculum Ga0073689 : Ga0073689_127]

METANRYNLKVI EDTAQAMGATYQGQKACSYGHAGCLSFFPTKNLGAFGD
 GGMVSSDPEI AEKLRMLRVHGSRRKKYYHEI VGI NSRLDELQAAVLVVKM
 KYLDQWI AARNKVAEDYVQLFKQYKLEEVVTVPYASENTLHTNQYTI RV
 PHRDELQTYLKERGI GTAI YYPLPLHLQPSFANLGYPKPGDFPEAEKACRE
 VI SLPVYPELATEQQEYVAETI RQFFKEKGLIR

>2617921422 Ga0073689_12715 conserved hypothetical protein (putative transposase or invertase) [pelotomaculum Ga0073689 : Ga0073689_127]

MSENQI DHDRFLKELLETFVFEFMELFFPEAARSI DLEHLKFLQEQVFTD
 VTAGEKHEVDI LVETRLKDEPGLI LVHI EPQSYAQTDfNGRMFI YFSRLY
 EKYYRRI LPVAVFSYDRVRDEPDSFELGFPFLDVLNFRFYKLELKKLNWR
 EYI HSDNPVAAALLSKMGFKRMEKVRVKLEFI RMLVRMNLDPAARMELLAG
 FFETYLKLNREEKEQYNREL GKLD RKEVDVI MQI TTSWHEEGREKGRVEG
 RAEGRAEGRAEGRAEGRAEGKVEAKQEI I CKYLVRKFGKKSTGLQQKVGR
 MTDLEKLDYI LEELFAADTLDEACAI I NGSVGEQS

>2617921421 Ga0073689_12714 Predicted RNA binding protein YcfA, dsRBD-like fold, HicA-like mRNA interferase family [pelotomaculum Ga0073689 : Ga0073689_127]

MTVREI LKI LYQDGWREVASRKKGPHI QLKHPAKTGKVTVPNHKGDI APG
 TLNSI LKQAGLK

>2617921420 Ga0073689_12713 Predicted nuclease of the RNase H fold, HicB family [pelotomaculum Ga0073689 : Ga0073689_127]

MRKI TYLAVFEPTETGYSVYFPDLP GCVSYGEDFEEAQRQAAEALGLHI Y
 GMEKDGEI PVPSKVPQVDPETAAGYMSVPTVFPDLVRNELDNRAVKTN
 LTI PAWLKELAEAQGVNYSKVFOVALMDYLG I SQTPRQKP

>2617921419 Ga0073689_12712 Phosphoglucosyltransferase/phosphomannomutase, alpha/beta/alpha domain III [pelotomaculum Ga0073689 : Ga0073689_127]

VAFDGDADRI GVVDETGGI I RGDMLMCLYWREI MPKHGAPAI I EVKCSQ
 TPVDEVI RLGGRP SFYKTGHSLI KARMKEI GAVFTGEMSGHMFAD EYYG
 FDAAFYAAGRHLRI LSNADGSLSEMLAGI PKYYSTA

>2617921418 Ga0073689_12711 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_127]

LI LLGLRARKGQKWAESFKLEFDFTGTGPACRVERFCEKPDNERALELGL
 CGTEELVPCPGKKQGTGRMEKVRVKLEFMRMLVRMNLDPALMELLAGFFE
 TYLKLNRREEKEQYNREL GKLD RKEVDVI MQI TTSWHEEGRAEGRVEGKVE
 AKQEI I CKYLI RKFGKNSTVLQQKVGRMTDLEKLDYI LEELFAADTLDEA
 CAI I NGSVGEQS

>2617921417 Ga0073689_12710 Transposase [pelotomaculum Ga0073689 : Ga0073689_127]

MYARTKTFTNKDGSKRITYI QI VEAVRENGKVRQKVLLNMGRI EDMQDGI
 DRLI ASLAKFSRKKWVMAEAEKFLVHNAREWGLELI FRHLWDQLHLSI L
 NDSFSRAYTCNQLAEAVYAMVLNRI SDPLSKRGVNRWI EEVYRPAFSELE
 LHHFYRALDLLTEHKERI ETGLFKRTQSLFNMQVDI VFWDTTSTYFEGKG
 PDELGCYGYSKDHRPDR I QVMI GVVMTQMG I PI AHEVFPGNTSDAATFRQ
 I I ADLRKRFLNLRVI FVGDRGMVSKDI LDEL DENHI EYI VGMRRMRKVRDV
 GEVLKTGGRYKVVRDNLKVKEVWYDADRYI VCYNPAQAEHDKKAREEI I Q
 KLKKOLEKSGVKS LVGNSGYRRYLLKKDVTAGI NQDLLKEEARYDGKYV
 LRTNCQLDTGEVALAYKDLWRVERAFREI KSSLDLRPVYHWKDSRVRGHI
 MVCFLALVLESALRRKLHEKKSEVEYLYLLRDLOQLRAVELTI GGDRYLC
 RTELAGNSYEAFKALGI RPPLQI EKL TNNRKTGGNKKEPEYFNLTLPDA

>2617921416 Ga0073689_1279 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_127]

MFI RWKAVRNEFYAQLEQRI WDKGKVKTKVFVYLGKNPF EKLLQMLREGK
 I TVDEVAQI RYREKPI AFQDI MVDALAMECRGTPWARVSFLEQI FGADKA
 SDMVEKP

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>2617921415 Ga0073689_1278 pseudouridine kinase [pelotomaculum Ga0073689 : Ga0073689_127]

MEPNI AVI GTVFI DCKGFADKRYNPFGRNLGNVVFVHGGVGRNVAENLAH
LNLPVSVFSTVDNSALGKEVVNRLRKANVNLGFLSFAESKGI GMLAVLD
QKGDVLVSGI SQMPDLGLMERLI DEKGRQI VETASHVLEI DLNERI SRTV
I DYAGKFDKKVYGI PGNLEVI LNNRDFLCYTDCFI CNDVEAGRLI GTDLG
GMEI KGLLNVLERYVMEADI PSMVI TLGERGSVYYDSRTREKGYQPALKT
EVDSSGAGDAFFSGTVMGLVRGRPLSEAVVYGTRVASWTLQAEENNCLE
MAVKLREEEFFSGMLMSVG

>2617921414 Ga0073689_1277 methionine adenosyl transferase [pelotomaculum Ga0073689 : Ga0073689_127]

MSKYLFTSESVTEGHPDKI CDQI SDAVLDAI I AKDPYARVACETATATGL
VLVAGEI TTSTYVDI PHLVRETI RGI GYTRAKYGFDCDTCABI TSI DEQS
PDI AMGVDRAFEAKEGSMASIII EALGAGDOGMMFGFACDETPELMPLPI
SLAHLRARRLASVRKSNELDYLRPDGKTQVTVYADGRPVVRVDTVVVSTQ
HHPNMDLDI KNDLVEHVI TRVI PTKYLDNRTRYFI NPTGRFVVGPGQD
TGLTGRKI I VDTYGGYACHGGGAFSGKDPTKVDRSAAYAARYVAKNI VAA
GLAGKCEI QLAYAI GVANPVSVLVDFTGTASVPDELI VELVRKYFDLRPG
AI I RDLNLRPI YKQVAAVGHFGRGDLDPWEKADKAKALYEEALNFVPA
LAEEAAGREPR

>2617921413 Ga0073689_1276 GDPmannose 4,6-dehydratase [pelotomaculum Ga0073689 : Ga0073689_127]

LOYLDI FDKVDLI PADLVDAISLI EAI KVSQPDEI YHLAAQSFVGTSEFQ
PVGTEI TGLGVTRI LEAI REI NSGI KFYQASTSELYGNGNTEPQRENT
FRPASPYAAAKLYGYWI TKI YREGYGI FACNGI LFNHESPLRGLEFVTRK
I SNMVAKI ALGLEKELI LGNLESKRWDGYAPEYVESMWLI LQSEPDYV
I STNETHSVREFVEKAFTFAGLDWQKYTKTNDKFLRPLDVNYLQGDYSKA
KEKLGWEPTTKFDQLVKI MVNEDLNRWKRWI KGERFPWDAPSYSENRI L
SRTLRLER

>2617921412 Ga0073689_1275 Methyl transferase domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_127]

MNI FGSYSFYNNLLYQDKDYAGEATYI QSLI QKYRPETKTI LDLGCGTGR
HAVLLSQKGFKVHGI DI SDEMLSAAMD I ADGETLTFSREDI RTVRLGKTF
DAVI SLFHVMSYQVNNEDLOSSFRTAYEHLEAGGVFI FDCWYGPAVLTD
PVPRI KKI EENAI KI I RI AEPVI HVNENI VDVHYLYFI HDKNGGNI KELQ
ETHCMRYLFKPEVELMLKQTGFI LEDCFEYMTGNDPGCETWNVCFI AKKT
L

>2617921411 Ga0073689_1274 perosamine synthetase [pelotomaculum Ga0073689 : Ga0073689_127]

MNLFI PVNEPI LDGNEKKYLNECI DTGWI SSEGPFVRQFEGKMAAFVGRK
YGI AVCNGSAALEVAALQLPGDEVI LPAFTI I SCAAAVRCKCVPVL
VDSEPFSWNMDVSI EAKI TAKTKAI MVVHI YGLPVNMDPVLKLAKEYEL
KI I EDAAEMHGQTYKNQLCGGFDLSI FSFYPNKHVTTGEGGMI LTDNER
LAERCRLRNLCFKPEKRFVHDELGYNFRMTNLQAALGLAQLERLEEFVI
RKRVMGKLYTELLSELTCLELPLPRDYAENI YWVYGVVLKESI PFDADE
MMNHLKKQKI GTRPFFWPMHQQPVFQKMGFFQDEQYPVAERI ARRGFYLP
SGLALTAEQI ERVAKTVI TI LREAI

>2617921410 Ga0073689_1273 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_127]

MI EKI I YDDQLLSI I I RRNYSQPGI NFFTPNHFSQQLAYMQHPAGKVI EP
HLHNI VPREVI FTQEVLI LKRGRLRVDFYDENKRYLESRLVAGDVI LLA
FGHGFEALDEI EMI EI KQGPYAGDI DKRHFKGVEKSQI KMEV

>2617921409 Ga0073689_1272 Membrane protein involved in the export of O-antigen and teichoic acid [pelotomaculum Ga0073689 : Ga0073689_127]

MTNNYMKFTKDI LLVGI AQVANTLKGF I I LPI LSKTLGTSSYGI WSLI MT
TVLLFLPI CLLELQYAMTRFLTGEVDKSSVNKGVS I FVAI LLNTLLI SL
LI TI FAKPVAVLVFGGADAI YFAKI TACLI FI TTMDQLI FQYFI SFRQMM
RYSI FMLLOAI GEVLLLTFVFFGYGLSGAI ASLLI I RI I I FI I GGYVLA
TKNEVKI TSPNFSI LKYYLRFSLPLI PFTI SFWI I NSSDRYVI GYLI NAD
AVGI YSACYAMGSLGLFYSPLAQI I LPAI TDLYKNNRI PELKNHLKYSF
KI FMLFAI PSLFGLTVLSKPLLI TFFTPEFAQGYMI I PI VALGI LMYHSG
NLFSEVLVLFKRTKLMSLVYGLSALI NLVMNI FLVPLMGI MGA VATLI T

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FI I QLI FLYFVSFKLLPFNLDLKFI I KSVLSSAAMSLI VVWLSPSGPI KI
AI SI GI GAVVYFGFLLLLKGFTKVEYAFVNMAI RSVKKTAVDRQVQKF

>2617921408 Ga0073689_1271 Uncharacterized membrane protein [pelotomaculum
Ga0073689 : Ga0073689_127]

II I LRVLKLDNI SVI ENI LFSI GLSLAFLMSI GAI I NGLFPNLGFSKPI S
I LPLI I AI VAGLFMLCLI GNKTNKYFNHGVNI DPSKI KI KPI PSLFLFLL
PCLGVWGAYI FNI NKNI LLLLI LFVI I AI I I AFNKYI SEALYPLCI VAVA
LSLLLSI SLI GVYLPGFSDTHLEYFQKLVATNFYWNSSI YNNYNAMLAV
TI LPTI YSFI MNVDAEWI FRI VYQI I FSLLPLGLYQVYQQLTSKYI AFLS
VLFFI SANAYYKQLPYLMRQEI AEFFVVL LLLLI I DKRI NPQKRSLLSI I
FAFGLI VSHYSTSYLFMFCI I FTTI SI YLRKYI QSKNI FFENQI NSLSTV
FVVLVI VFTLTWYMSATGSSSFNTI I NI GYHI YSSLYTDFNPAARESNI
LVAI GI GSGAKSLVDLI NRFI FYI TEFFI LVGFI GLI RGKFKKLI LYKEY
TLI ATAGMVLVLSI I LPYFSGKLNMARLYQI I LI FLSPFFVLGGHYFI S
SFYNLI RNLSLKVWGGGNTI FTRYFTLDTKYI NMTI TI I LVI YFI SGTEV
FNLFNKQSASFPLCI NNVEQYGNDEKAKYYSVLTLEQDVFSI WLSNI
NYKNREVYADDI SRNHSLLGYGMVPPVNTLSI DSKKKI NQESI YLRYNI
I RHNI I LNYKNSCI YEEI LPFI SKCNKI YSNEGSEI YYYR

>2617921407 Ga0073689_12632 Methyl purine-DNA glycosylase (MPG) [pelotomaculum
Ga0073689 : Ga0073689_126]

AGPLYVCRGEPAREKI VTTTRTGI REGAGLPLRFYLEGSSYVSRK

>2617921406 Ga0073689_12631 Putative GTP cycl ohydrolase 1 type 2, NIF3 family
[pelotomaculum Ga0073689 : Ga0073689_126]

MVKI GEI YRLAI ERGMERDPRSKEKVLELLERERKAFDELKDDEKKEFDQ
DRLFNPHYGDTRVLFGDPEREVSRI LAGI DMETGEVLLAERLSSRGNRI DL
I LAHHPEGKAMAALYQVMKLQEDVLAKFGVPI NVAEGI MTSRI NEVKRGL
MPLNHNRAVDAAKLFDI PI MCVHTPADNHNVDNFLQRLFDEKQPETLGDVV
KLLKEI PEYAEAVKYNAGPNI MVGGKEKRAGKI MVDMTGGASGSEDAYAK
LAVAGVGTLLVMHI GEKHKRAEAKNHVNVVI AGHMASDSLGMNLFDELA
RRGVEI VPCAGLLRYERKE

>2617921405 Ga0073689_12630 putative protease [pelotomaculum Ga0073689 :
Ga0073689_126]

MSGKPELLAPAGNWESLVA AVENGADAVYLGKMFNARQSAGNFDNDELA
RAVDFAHVRGVKVVYTVNI LLDERELPEAAEFLHFLQRCGTDAAI VODLG
LARLARRVI PELPLHASTQMTVHNLPAAALLKEAGVSRVVPARELSLAAL
KEI AQRGGVEVEVFI HGALCVCYSGQCLMSSLI GGRSGNRGRCAQPCRLR
YVLVDRRGHPLADPGEVGDYLLSPRDLNMSGRLPDLI SAGI ASFKI EGRM
KRPEYVATVVRI YRALLDRAAAGGEFAVRPEEAGELAKI FNRDFTAGYFY
GRPGRELMSYKRPNNRGVRLGRVKGFDPAARRLAEI LLEEPLRVGDGI EVW
VTRGGRAAGEAGRI LLEGRPVDRAVPGALVRLDVPARVFGDRVFKTHDA
DLVERARASFTSPREQKKI PI LFTVSARPGEPLRI GVADPDGFTGEAETV
SPVRAALKRPLTREYLEKQLDRLGNTPTFMAGLRCELAGEVMAPVSEI NE
ARRAALDRLAERRAAAFRRAPAPEDVFSRRLEEALRPLPGATRALGSARP
VLSVAVTDPA SLRAAVRAGAGEVYFGGEYYRSRGPVALDDI YAAGEI CGE
SGARFI LSAPRI QODGELEGYCRLLLEKAAARRLDGVOAGNLGLI KKAREI
TGKPVYADFSLNVFNHQTALFLQEA EVSRVTL SQELTLEQI KGLAPRLPV
PAEVVVHGALPLMVSEYCAVGSLLGGGGARGCTGPCKDRACGLGDRTGAV
FPLELDQNCRMHI FNSRDLCVI EDI AELAAAGVAALRI EARREGPGYVRD
VARAYRSVLEALPDKLPDGKLRALKESLAGYSPAGFTKGHYRGVL

>2617921404 Ga0073689_12629 Uncharacterized membrane protein YkvA, DUF1232
family [pelotomaculum Ga0073689 : Ga0073689_126]

MDRERAKSFVLEFI KQI PAFLKLMYNLVKDPRVSTTDKAI LGASI AYI FS
PLDI VPDAI PFLGQVDDVYI VAI ALQRLI NSAGAEI VREYWEGDMEVFGS
LQRAVDAALFFLPRGVVDKMTKKI P

>2617921403 Ga0073689_12628 prevent-host-death family protein [pelotomaculum
Ga0073689 : Ga0073689_126]

MPFI NFVSTRELKNKTNKI VHI AEKGGVI I VTRYGKPVAVI KSFQENDLK
EKKHGALYQNI RQOI GEKCELLTMTKEELRNLNDEL SGMVKGFSWQEM
DRVAKGDHYGLSGQ

>2617921402 Ga0073689_12627 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_126]

MVFLDSNI FI I DRFFTRDKNYPVNKQLLEQLKKMRI NTALPYYTLLEI CG

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I TSFNLSGEEQGRWLYSFQEVYPVDI LDPYNSGOAGQSNI ADYLLSLTPY
I LKMTVG DANFLREAELYSKEI VTWNKKHFLGRD I QI LSPDEYLAI L
MM

>2617921401 Ga0073689_12626 DNA mismatch repair protein, MutS family
[pelotomaculum Ga0073689 : Ga0073689_126]

LTWFTWEI L VVKFKVREGKRM DKKTLRRLEYHKVLEQLAAAFAGSPLGRER
VLAMAPADDLDLI LRWQAETSEGRELLRLDPTAELGGWKDI RTQLRRAAR
GAVLEPEDLI AVADTLTAGRMI KGFFNERGERYP L LADLALSLVSLPEME
RKI KKA VLPGGGI TDGASPELAQI R R K I VNAQARI KEHLEHVI RSPNYQK
YLQDPI VTVRDGRYVVPVKI EYRAQVPGI VHDQSASGATLFI EPM AVVEK
NNELRRLAVA E KQEV L K I LTEL TAGVAENAGAI E I SLDALGELDFI MARA
EHSRKLDAWPALEGEAF LDI RRG RHP L L KGEVVPVDLRLGGDFDTLVI T
GPNTGGKTVTLKTAGLLV LMAQSG LHI PAGEGSRLGVFRRVFADI GDEQS
I EQSLSTFSSHMTNI VEI VRRAGRDSL VLLDELGAGTDP AEGAALAQAI L
ERLHAACVKT VATT H YSELKNYAFTRE RVENASVEFDAI TLRPTYRLLI G
KPGRSNAFEI AARLGLPGELVEKARGFLTVEQAQVEELVRNLERTQQEAE
VERQRAAI LAEEAGVLKEKYEKMEVDLAARRESI LARAAEAAAALVRSAG
REAEAAVKELREKLAE EAAARAREGAI REAREKLQKLQHRVSRVPEK RPA
GDAPEDLRSS EEFVLPKFNQRGYVLT PPGPGGEVQVQVGI I KMNVP LKEL
RRLEKPA PAEGRTGVAGVLLGKAREI SPELDLRGQYAE EALLOVEKYLDD
ACLAGLSRVFLI HGKGTGSLRTAI HKQLKGHRVKS FRLGEHGEGGFGVT
VVDLA

>2617921400 Ga0073689_12625 hydroxylamine reductase [pelotomaculum Ga0073689 :
Ga0073689_126]

MFCYQCEQTAGGTGCTKVGVC GKNEDI ASLQDTLI LGLKGI AAYAFHARE
LGARDEQVDAFMHEGLFTTL TNVNF DLNSMI EKALKCGEMNL RAMELLDK
AHVERFDSPAPVKVSTGFKPGPAVLI TGHDL L DLYELLKQAEPEGVNVYT
HGEMLP AHAYPEL NKF PNL AGHYGSAWQ NQKKEFDEFPGAI LGTTNCVLI
PKDSYKDRMFTCGI ADLPGVTHI KGRDFKAVI EKAKECGPLPAKEGGVLT
TGFHHNAVLGI ADKVI EAVKAGKI RHFFLVGGCEGSKASRSYYTEFVQKA
PKDCVVLT LGCGKYRFNYL DLGEI DGI PRLLDMGQCNNAYS AI QVAVALA
NAFKCGVNDLPLSLVLSWF EQKAVAI LLTLLHLGVKNI RI GPTAPAFI TP
NV LKV LQDNYNL KLI TTVDQDLKEI LG

>2617921399 Ga0073689_12624 Starch/carbohydrate-binding module (family 53)
[pelotomaculum Ga0073689 : Ga0073689_126]

LYHHGWSDEQRGVHVRSLSPDGSDFSVI YNGLLDKGGANQI FLHAGFGDP
MOWKI VDDYRMQRTPEGWKTLNME DKQLI FCFRDTVGNWDNNSGYNWAY
KI

>2617921398 Ga0073689_12623 penicillin-binding protein 1A [pelotomaculum
Ga0073689 : Ga0073689_126]

LAQRRRKRLNLHRLFFI L LCL AALGAGSAGAGLVFASVKDMPALSPATL
ESGASTMI YDKDGNLVT K I G I RNSVPVDLKNVPENVKNSFLAI EDPRFYQ
HHGI SLRGI VRAAWNDLTSRSAREGGSTI TQQLVRI SFLNPEKTVKRKI Q
EAI LAI KVERRYTKDEI LEMYLNNI YLGEGAYGI QAAAQTYFGENVDKLN
LEE AALLGGLPQAPSAYSPYRNPOAAVARRNMVLD SMARNNFI SQGOAEK
AKAAELKLDTKEVAQKQYPYFLDYVTDRLI EKYGEAEVFKGGLQVYTS
LDQKVQKI AEAAMANKANFPSPKVDANGLSQPQGA VVI LDPHTGQI MALV
GGREHTQKRQWNRATQTTRQPGSAFKPI AAYGPAI EYKGLGPASVDDI P
VRYGSYEPKNFDGRYRGLI TLRMALTHSVNI AAVKLLMDTVGI REAI NFA
SGLGI KLDPOVHGASTALGGLHSGVTPLQMAAA YGAFDNQGVYI EPTAI L
RVEKLDGVI LDQVPVKQRQAMKATTAFLI TDMLKSAVEGGTGAGA QI GRP
AAGKTGTTDDGKDI W FVG YTPELVGAVWI GYDKPTAMPQAFGGTYPARI W
REI MSKTLGGAPVKEFPRPAGLV TATVDGKSGLLPGPNTPGDSLVTDLFT
EGTVPTETDNVHI FVEI CAVSGQLPNEYCPDRVI VQRI KLPYNVPSFVED
YNQRVPTESCALHGP GTSQSRPELKKQVNP AI PGI SRTPPDKQI TNSI RD
FGKTKKEP

>2617921397 Ga0073689_12622 signal peptidase I Serine peptidase. MEROPS family
S26A [pelotomaculum Ga0073689 : Ga0073689_126]

MLSETRKI LDWALTALAVLLSLVI RSYVAEARWI PSTSMLPTLKI GDRL
I I DKVSFKFNGI SRGDI VVFHAPPASRLDEVMI KRVI GLPGETVSI KKG I
VYI NGKPLTEPYELEKPREDFRPFTVPAGSI FVMGDNRNNSFDSRFW GVA
PVDLVI GKALARFYPLGDAAI LE

>2617921396 Ga0073689_12621 transcriptional regulator, TetR family

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[pelotomaculum Ga0073689 : Ga0073689_126]

MDHRQRI I SALKELSATRGFYRVTVDELAARAGMSKRTI YRYFSSKEEI I
 NAALEEFI STVAKKVRQALDSSSDPVEKI LGVI RTLMENI KFVQPLALYD
 LQKHYPHLWEKI EQFRAGKI QQI FDEVLTGDDQGRFRQVNPKEI FTTALLS
 SVRAVVNPAFI VENNITPEEAI KSLFTI FLHGVVRDGEDF

>2617921395 Ga0073689_12620 ABC-2 type transport system permease protein

[pelotomaculum Ga0073689 : Ga0073689_126]

MGRIMAILKKEILQMRDRRLTGMVFMPLMVQLLI FGFAIQTEVKHIPTA
 VFDQSLSAESRDLEAFSASGYFDI AYNAGYAEI TKMIDSGKARVGI IF
 PPDAERLKRGDTPVQVLVDASDSMSSASAI ATANSIGLLKSQKI LLQK
 APAQNI PYDI RVRPWYNPDGI TAYYMPAI LGI I VTMTMVMMTSMI VRE
 RERGTLQLLVTPI RSYELMI GKI I PYI ALGYVQI TVALLVGVAVFRVPI
 RGS LAELYLLTLFFI TASLGI GLI SNI ARTQM QAFQMSFFVLLPSI LLS
 GFMFPREAMPVI I QYI GNLI PLTFYLT I RGI I LKGI GPFYLI SQVAALL
 VFMSVLTALSI LKFKKKI A

>2617921394 Ga0073689_12619 ABC-2 type transport system ATP-binding protein

[pelotomaculum Ga0073689 : Ga0073689_126]

VDYVSTSELTRVFGSFTAVDRLTINI RRGEI YGFLGPNNGSGKSTTI RML
 CGI LEPTSGTGTVLGHDLVREAEKI KREI GYMSQKFSLYEDLTVYENLDF
 YAGLYGI PVREKRRI AEMLDMAVLTGRERELAANL SGGFRQRLALGCAI
 I SRPSLLFLDEPTSGI SPI SRRDFFKVI QGLAGRGTTVMVTTHFMDEAER
 CYHI AFI SEGRLI ANDTPDNLKNNI I RGCLVELDLPSAMDRVEEELKLPY
 VKEVSI HGPLLHVLLSEDRVAELNRHTGARAKKI KPSLEDVFI TLARQK
 KRRVV

>2617921393 Ga0073689_12618 ABC-2 type transport system ATP-binding protein

[pelotomaculum Ga0073689 : Ga0073689_126]

MLEAQALTKVFGRLTAVDNVTLKI EKGDI FGLVGPDGAGKTTLI RMLCGI
 I APTGGRVALTGGRDENPGSGPVFGYMPQRFSLYGDLTQENVTFYGS LY
 RLDKRTLSQRAEELLQMTGLAGFKSRLADNL SGGMKQKLALTCALVARPA
 LLLLDEPTFGVDPEYRKEFWKI LYQLNKEGI TII VSTPYMDEAELCONVA
 FMDGGRI I SMDTPGGLKSKYPYRVLELKAGARELDFVGS LPEVVEAGFYG
 DKYHVAVKEI APARAAI AALLAEREI EI MEMEEI PPSMEDVFVHLAGKEV
 V

>2617921392 Ga0073689_12617 HlyD family secretion protein [pelotomaculum

Ga0073689 : Ga0073689_126]

MRKKVAVI LMLAI LGSGAWWGYDRYVKEKQPSALQATGTI EATQVELRAK
 LPGTLRNFEVAAGDQVMKGRQI AVI VRNDLI AKRERDALGVLKARAQLDD
 LTSGAREQEI REAEI AVNTAQTNYDKAVSDHNRASTLYREKVI SESEMER
 AQTALKQAQNOLES AKARLDLLKSGNRPDQI EAARAELESAAVLKSSEA
 LLEDTKI I CPI DGTVLNKNFEEGEYVQAGASVATVADLNDMMI KVI PT
 DLPRI KLGQRVKFTVSGSATEYTGTVEEI ASKGEFTPKTI QTKKERTNI V
 YAVKI RVGGENGVLKPGMPADVTFR

>2617921391 Ga0073689_12616 prevent-host-death family protein [pelotomaculum

Ga0073689 : Ga0073689_126]

MPQI RPI DELRDTSKI SEI CHSQSEPVI TKNYGDLVI MSI ETYERLLA
 LTDVYKNWAKLKNRLQTEFPYWRGSRYSNI

>2617921390 Ga0073689_12615 23S rRNA m(5)U-1939 methyltransferase (EC 2.1.1.190)

[pelotomaculum Ga0073689 : Ga0073689_126]

LRKNEKI ELKI TGLTHAGEGVGRWQGLAVFVPGTAPGETVLAGVVVELKK
 HARARLLEVTGSPARRRPECGHFSTCGGCRLOHVDYGEQLRLKTALVRD
 SLARI AGLEGTVTRDTVGMHPWHYRNKVHFQVAEHGGGYKLGFYEEGSH
 I MTAFFGEGEAPAPGCLLVERELNETAPVI ERLLNKYGGAVSGRKRGRF
 FRHVLLRKAFYTGEVMAVLVTGSGHWSGEGAFVRELMALRPGLASLVNI
 NDGPPGAVLGRENLLAGREYI TDRLGHLTFRI SPSSFYQVNPAQTLVLY
 OKALEYAALTGSETVLDAYSGI GTI ALFLARRAQKVYGLEVAPEAVADAR
 ENAVLNEI KNVEFYEGEVEGLLPALAARGLRPDVVALDPPRRGCGREALE
 AVAEMRAPRVVYVYVCHPGALARDLGCLAEMGYRI MEAQPVDMFPWTHHVE
 CVIRIER

>2617921389 Ga0073689_12614 transcriptional regulator, ArsR family

[pelotomaculum Ga0073689 : Ga0073689_126]

MDNFVKI FKALGEPTLRRI LRI LSVRPMYVCELEAVLGI SQPRI SQHLKI
 LKEATI LQESKEAQKTFYMLNGDI MGKTMQGFMDFLNADI GELPEFQEE

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RRI RQLDKDSYI LKCKSDSKGNCG

>2617921388 Ga0073689_12613 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_126]
MAGCCGPRVPRPKMVRI GNNTI GI LGLEGAMEEVASLGRLTDDQLAAELL
SRI

>2617921387 Ga0073689_12612 small redox-active disulfide protein 2 [pelotomaculum Ga0073689 : Ga0073689_126]
MDI KVLGSGCANCNKLEKMMVI DVLAQLNEKADVSHI RDYKEI ASFGVMRI
PALVI NGQVKI TGMVPAKDKLKEI I ASEI AKRG

>2617921386 Ga0073689_12611 Predicted permease [pelotomaculum Ga0073689 : Ga0073689_126]
VWQQI VNYI VYVLI GLPPESRPGSAVNFFI YDTVKI LFMLTII I FII AVI
RSFFPPEKTKKVLGHKREFI GNI VAAFMGI LTPF

>2617921385 Ga0073689_12610 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_126]
VPVFI GFVEAGVPLGVTFSLI SSPMVNEVALGMLWMMFGWKI ALI YI AS
GVI I AI VAGTVLGRMKLEHLVMEYVYQVSSPKCACATDGPPAVETGEAAG
ACACNTEEYEEETWGDRI GYAKSYTI QI LKKVWI WVLFGI AVGAVMHGYAP
AGFLSKYAGPGNPLAVPLAVI I GI PLYSNAAGMI PVVKELVRTGMAMGTA
LALMMSVTALSLPEAI I LKQVLKPKLLAI YFGI VGLSI I CI GYLFNVI L

>2617921384 Ga0073689_1269 arsenite transporter, ACR3 family [pelotomaculum Ga0073689 : Ga0073689_126]
MAETATRKLSFLDRFLTLLWI FLAMFLGVGLGYAVPQTAAMLNKFQVGTTS
I PI AI GLI VMMYPPLARVRYEEI GKVFRNGRVLGLSLVQNWVI GPVLMFF
LAVI FLQNYPEYMAGLI I I GLARCI AMVI VWNSLARGDAEYAAAALVALNS
I FOVLFFYVYAYI FVT LAPRWLGMSSTVI HI SI AEVAKSVAVYLG I PFAA
GVI TRFTMI PVKGREWYEKKFVPAI SPLALVALLFTI VVMFSLKGNYI VS
LPLDVVRI AI PLLFYFFI MFYLSFFLSKRAGVNYEQSTTLAFTAASNNFE
LAI AVAVAVFGI NSGQAAFAVI GPLI EVPVMI GLVNVALYFKRRYFDLKW
RMDH

>2617921383 Ga0073689_1268 prevent-host-death family protein [pelotomaculum Ga0073689 : Ga0073689_126]
MQMI SVTDI RKN I RGI LSEVVKSKKPVI LQRSKPVAYLI DAESFDKMQR
CGESESEMLTRSRMESLDRI SOLRTKI AKRGI WSDSTQI I QELREGQGRY
E

>2617921382 Ga0073689_1267 Predicted nucleic acid-binding protein, contains PIN domain [pelotomaculum Ga0073689 : Ga0073689_126]
MSRYI CLDTSVLVKTLL EEEDTEKALALMEKVAI LGQLI VLPFAFAWAEVG
SVLRKMRRRNELTVQEADDLWLEFKNFQGI EYLSDDVI MERVWKI SRYFD
MPTLYDASFLAVAEVVAERTGEMCEYWTWDEKLI NQLNGRREYVRWLKDF
AL

>2617921381 Ga0073689_1266 C0 dehydrogenase maturation factor [pelotomaculum Ga0073689 : Ga0073689_126]
MKLAI SGKGGVGKTTI AAALVKLFSKTHRVVYAI DADPDVCLAAALGI PD
NI TSELKPLVEMKELI SSKTGGQGAFFTLNPKVDDDLNYCI EHGN I RYL
RMGGVKKGSSCYCRENSFLHAVVSALLLDKEDVVVMDMGAGI EHLSRGT
ARGVDLMLVVVPSLNSVNTAGLVKKLAADLGI KKVRI VGNKI RNEREKG
FI VKSFQDGEVLGFVGFDDVWESAMDGSSVVGSGGALI SSLEQVHQKI S
SEVGE

>2617921380 Ga0073689_1265 Ni -dependent carbon monoxide dehydrogenase precursor [pelotomaculum Ga0073689 : Ga0073689_126]
MPRFRDPNHTCQPSNAPQVVEPKSI KRSVDPVAVLQMI DLAKEKGI I STFD
RVVAQQPQCQFGVKGI CCRFCMAGPCRI KAEEGPGSKGI CGASAWTI AAR
STGLMLLTGAASHSEHAQVI LETVHKTAHGKTRDYNLKD TDKLRRCARV
GI ETGGKDDMALARELCDLAL KDYSRLKGEGYSTWVQTTVTPGRKEKFFS
HDI MP SGVF NVI SELVTQAH I GMDNDPVNI I FSALRVALADYVGMHVGTD
FSDI LFGTPOPI VSEANFGI I DPDNVNI VLYGHNPVLSELI CDAVDEM QD
EAKAAGAKGI QLMGI CCTGNEVI MRRGVPI VTSYAAAEMPI LTGAMDAYV
VDVQCI MPSI RTVAECYHTRI I TTSP I AKI PGSYHI DFQAEENAI KDAKSA
VRMAI EAFKL RDQSKYAPI PKDRYKVVAGWSLEALYDLFAGVNPDPNPVSV

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LTDAL LAGEI KGVAMLAGCNLKRFDQDLSHLTI AREMI KNDVFVI GTGCV
 MQGCARAGLLAPEAMEFAGEGLKRLKRLKEETDLKVGLPPI FHMGCSCVD
 NTRCNDLLMDMAKQMGVDTPKVPWVASAPEAMSGKAVSI GCWCVAMGMPV
 HVGAMPPLQGSMDI YSI VTQVASDVYGGYFI FELDPAAEAKKMLSALEYR
 TWKMGVHRAAAENFETALCONY

>2617921379 Ga0073689_1264 acetyl -CoA decarboxylase/synthase beta subunit
 [pelotomaculum Ga0073689 : Ga0073689_126]

MSEQI NFDQI YEGCI EPGKEPKLFRQMYHGAVAATSYAEI LLNQAI RTY
 GPDHPVSYPDYAYLPVI RCMSGEEI KKLSDCVPVLNRMRAQVREEKTFE
 NMI LWGEATWYAADI I EAVRYLKHTPENPLHVTPTWTFI GDPVVRQYGTK
 MVDWTI PGEAVI VGRAKTSKDAKKLVDSLMAKGLMLFLCDEI I EQLLEEN
 VKI GI DYI AYPLGNFTQVVHAANYALRAGMMFGGI PAGDREAQRDYQRRR
 VLAFI LYLGERDMVKDAACAGAI WTGFPVI TDQPLGEDEQI KDWFI SEPD
 YDKI VQTALEVRGI KI TAI DI DAPI TI GPAFEGESI RKKDMFCEFGGQKT
 PGFELVRMVSADKI EDGKVEVI GPDI DTLKPGGRLPI GI VVDVYGRKFQE
 DFEPVLERRI HYFI NYGEGI WHVAQRDI NWLRVSNDAFGKGFRLLKHFGNI
 LYAKFKSEFSAI VDRVQVTI I TDEAKVLEMREVAREYYKRRDDRLKQLSD
 EAVDTFYSCSTLCQSFAPTHI CVI AAQRVGLCGAVSWLDAKASYEI NPHGS
 NLPI PKEGLI DEKKGQWSAI NEFCYKNSQRNVETVNFYTI MEYPMTCGCG
 FECI LAMVPECNGFMVVNREHGGMTPSGMTFSTLAGTI GGGAQMPGFMGI
 GKSYLASPKFVPADGGLARVWMPKALKDQLRPMLEEAEEAAGLGRDFVD
 KI ADESI GVSSDEI MPFLEEKGHPALTMDSLI

>2617921378 Ga0073689_1263 CO-methylating acetyl -CoA synthase corrinoid
 iron-sulfur protein large subunit precursor [pelotomaculum Ga0073689 :
 Ga0073689_126]

MGLTGLEI FKQLPKTNCKECGQATCLAFAMALASGKASLEQCPHVSDAAR
 EALDSASAPPVALVKI GVGEKQVELGNETVLFHRDKRFEHPTAI AVSVC
 SQSNDEI AAKI AKI NGLVFRVQTHNVNLVAVGNCSGSPDRFVEAVKVA
 ADNTQFPLVLMTEQDAAMEKALEAVAACKPLVCGANASNYEAMTALAKKF
 DVPLVVKGVLDNELAAVVEKVVAMGHKQLI LDSGAREVGKVLADQTQI RR
 QALKKKFRLFGYPSI AFVTNEDSI QAVVDAGVYI AKYAGVI VMNSADPADI
 LPLI TLRLNVYTDPOKPI AVESKI YEFLNPGPDSPVYVTTNFSLSYFSA
 GDVEASRVPGYVLPVDTGSI SVLTGWAAGKFTPEKI TDMLNKSGI ADKVS
 HRKVI I PGGVAVLSGKLNELSGWEVLVGPRESAGI PSFVKQRWGA

>2617921377 Ga0073689_1262 CO dehydrogenase maturation factor [pelotomaculum
 Ga0073689 : Ga0073689_126]

MALNI AI AGKGGTGKTTFASLAI SQLI KAGKKPVLAVDADANANLNEALG
 I EVEETI AEI LDR I KNDLRPLPAGMTKDQFVEYKVHQSLEAGDDVDLLSM
 GGPEPGGCYCYANNI LKGFMDLSKNYPVVVADNEAGLEHLSRRTTQNV
 DFLFVI SDASARSI RAKRVKELVETLKLEI KRMVLTQVTKVQEGSI EALQG
 EI DNTGLELI GTI PLDGHVVEYDLHSKPLVDLPDDAPAVVAVKEI LKKAG
 IL

>2617921376 Ga0073689_1261 CO dehydrogenase/acetyl -CoA synthase delta subunit
 [pelotomaculum Ga0073689 : Ga0073689_126]

MAVTI VKEKWTISKVEMVI GAEPNVVKVGEGTLPFLHFEGEMPKNKPVVA
 LEVWDMPEADWAEVLSSAFAGAMGDPVAWAKKCEYGAADLVCLRLASHP
 DNKDTTPAEAAATAKAVAEAVNVPLI VI GCGVEEKDAEMMTAVGEALAGK
 NALLGCATI NNYKTI TAACMVNGHNI I ASSPLDI NLAKQLNI LMNEMGLS
 FSRI AI

>2617921375 Ga0073689_12535 Chromosome partitioning ATPase, Mrp family, contains
 Fe-S cluster [pelotomaculum Ga0073689 : Ga0073689_125]

LASGFNKKGYAVGVI DADI TGPSLPKMFGVKDMAESMGFALLPASTPSGI
 RLMSLNLLI PNEDDPVI WRGPLLAVGKQFWTDVWGDLDYLFVDLPPGT
 GDI PLTVMQSLPLSGLI VVTSPQDLAVMI VSKTI KMAMQVNVPI LGLI EN
 MTS AI CPHCGEEFPLFGTGKGGEVAEKFGI PFLGSLPVDPHLAKLCDEGK
 VEEYNNNLFNNLI PERLI H

>2617921374 Ga0073689_12534 Predicted Fe-Mo cluster-binding protein, NiFX family
 [pelotomaculum Ga0073689 : Ga0073689_125]

MKVVI TAQGQDLESVDPRFGRCGWFI VADTETGEYRVVSNEQNNAARG
 AGI QAAENAGROGVEAVI TGHCGPKAFRTLKAAGI KI FTGAGGTVAESLE
 SFGSGRLKESDAADVEGHWL

>2617921373 Ga0073689_12533 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_125]

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Ga0073689_125]

MPGFDGTGPVGAGPLTGYGRGYCLGYAGAGMNFVPRFGI GGGRGRRWRY
AAGLTRWARWSREAAWGVAYVPPAGKEAELDMLKEQVANLENAMERARNR
IQELEQKE

>2617921372 Ga0073689_12532 MinD superfamily P-loop ATPase, contains an inserted ferredoxin domain [pelotomaculum Ga0073689 : Ga0073689_125]

VRPARGNMMTMNLT AVASGKGGTGKTTVSANLALAAVEAGYETCYLDCD
VEEPNGHLFLKPRRLRRSHRVTA PVPEVEPEKCTSCGACGEI CQFSAI VCI
NKTVLTFDKMCHGCGGCLMVCPATAI RERGREI GI VEEGSAGGLSFVHGK
LNVGEAMSPPLI KAVRSAGKRAALNI I DAPPGTSCPVI TAI KGVDYVLLV
TEPTPFGLNDLGLALDVVRELGI PYGVVVNRSGPDSMDARLFCRERNAGI
LAEPEDRVVAETYSRGEMI YNALPEYREQFNGLLLAVEKEVGR

>2617921371 Ga0073689_12531 MinD superfamily P-loop ATPase, contains an inserted ferredoxin domain [pelotomaculum Ga0073689 : Ga0073689_125]

LKEI VVLSGKGGTGKTSLVASLATLAERPVLADCDVDAADLRLVLEPEI I
RSGNFTGGKKAQVI PEKCTGCGKCFDLCRFGAVI ESGDREPVTI DPI SC
EGCGVCSYFCPAQAI RFEPVNGRWFI SRTRYGPMVHARLGVAEENSGKL
VSLVRKEARAI AGEKANYLI VDGPPGI GCPVI ASI TGADAVLI VTEPTV
SGAHDLERVAELTGHFKI PAYLCI NKFDLNPAMSKRI EKRASARGI KMGV
GI HYDRVFTAAQI KRMPVALYTEAAVAGEI RNVWRELARAVD

>2617921370 Ga0073689_12530 Predicted Fe-Mo cluster-binding protein, NiFX family [pelotomaculum Ga0073689 : Ga0073689_125]

MKI ALPI AGGALCAHFGHCERFGFYEVDPGTGEI LRKETMEAPPHEPGLL
PRLLSEKGANVVI AGGMGMRAQDLFTQGI KVVVGADPSAGSPEDI VRAY
LSGSLTTGANPCDH

>2617921369 Ga0073689_12529 Cysteine-rich domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_125]

LNRYMEI RRLSKNEPADFLFLWDPREI KYYPNNVQSI AKI MWYVGANWTC
SSRWWDATNYALFNGNDEESRI I TRRYADEVKRLKVKELVVTECGHATHA
NKWGPVKWLKDNDYPVKS I EKYVEWF EAGLLKVDKTKNPEPI TLHDP
NTVRKQGLGDAI RYVLNRI VMEFREMHPHGKYNCCGGGGGGLLAMGADI Y
PNI NR

>2617921368 Ga0073689_12528 Helix-turn-helix domain of transposase family ISL3 [pelotomaculum Ga0073689 : Ga0073689_125]

MLFNNHLLFAAALGLTPPWEVKDLRFSAEHRDI WVGYPTEFTTFPCPVC
GKNASI YDTREQTWRHLNFFQRETYLHARVSRVNCPOGCGVKTI EVPWAR
ARSGFTLLFEAYVMLLVKEMPVNAVAALVGEHDTKLWRVLKHHVQRFMLG

>2617921367 Ga0073689_12527 undecaprenyl diphosphate synthase [pelotomaculum Ga0073689 : Ga0073689_125]

MI QPKFQRLPKHI GVI PDGNRRWAVKNGLSKEAGYEKGLEPGLKLYEMCV
ELGI KELTFYGFQTQNTKRPSVQRKAFQKACI DAVKI LANRDASLLVI GD
SSSLLFPRELI PYTRRYTFGKDLI RVNFLVNYGWKWDLNQAQNRVPSGKG
GAAENLVESI ASAEI SRI DLI I RWGGRTLSGFLPVQSI YADFFVDELW
PDFAPEHFYRALSWEYETQDVTLGG

>2617921366 Ga0073689_12526 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_125]

MDRFTKGLLAGI SGGI VMNI WDFI SYYGRLRLSTDYLDWAAI I LLGDI PA
SLFGTI FSLVVQI LFAGFVGI FI YLYSLVNSSNYLLKGGAGGFAAAFI L
YAI PVVYKMPYLSKTPVATAFSHMI GAI I WGLVLAQMLHWDRTNKTSI

>2617921365 Ga0073689_12525 sporulation protein YqfC [pelotomaculum Ga0073689 : Ga0073689_125]

MSWREVKRKVKRQFSDFFEI PGDVMLDLPKI I LI GNI QLFI ENHRGI I EY
TPGGVRVGVEGEVAVTGENLI LRNI LPDELCVEGKI RSVNFR

>2617921364 Ga0073689_12524 similar to stage IV sporulation protein [pelotomaculum Ga0073689 : Ga0073689_125]

VFLFKLSYLLGYVVI LVTGEAPEKFVNMAASRG I YLWDI ARTGDGAI I L
KVRLDGVKPLRHI ARRTHNFRVRGRVGLPFYLA RLRRRKALALGAVFFI
AALYFLSSLVWFI EVRGNEQLSAAEI LGVADEAGLRGVPKWQVDTGLVE
AKVQEKPLVSWAGVYI KGTKVTI EVAERVVPGEEDRRPAHI VAGKAGLI
KEVLVLSGHPAVKEGDTVAPGQVLI SGVI PPQEEQLKPGEDKKPGETPQV

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AKPLRYVHARGI VRARVWYEGRGEAAVETGRRPTGRSVSRFSI KFNGKE
I I LSGNQNI PFERYEEETFI KRPEWRNLNI PVELSVKYLELADYREDR
GRGGALRLAREQALAAAAEHL PKDALVLDRRVEEI NAVHPENMVRVKAVL
EAVEEI GVERAFHPREDKSI RNNNLESGKRNPASGARRPE

>2617921363 Ga0073689_12523 phosphate starvation-inducible protein PhoH
[pelotomaculum Ga0073689 : Ga0073689_125]
LA EKFEARVELDDI GSAAEI FGKHDEHLVQMEKALDVR FVARGQELVI TG
EREKVGQAVEVLSQLQKFYRAGNRLTLHEVAYAI KAAQGGI KNALESLAR
DVAMVTPRGKQI KPKTI GQOKYVEAI KNHDVVFAI GPAGTGKTYLAVVMA
I KALRNKDVGRVLVLRPAVEAGEKLGFLPGDLQEKI DPYLRPLYDSLYDV
LGVENTQKYLEKHI I EI APLAYMRGRTLEDSEFI I LDEAQNTPPEQMKMFL
TRLGFGSKAVI TGDITQI DLPRGQVSGLTNALKVLKNI EGLAI HTLTGED
I VRHPLVEEI I RAYEAGQ

>2617921362 Ga0073689_12522 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_125]
VKPVLAI GRAKDKI KAVLSLLARQRKVRRGSAAVLFLLLI TLI I AI EFPF
EKTNLVVGQVSPKNFFAPKSI VFEDKYKTDEQRRLAAEKVEKVYRKDPKV
SI AVQKDI SLAGKVREVQGDADLDLPGKI AGLRATLPFAMNEDGLKNLA
QASPEDAQDTENKLNGLVAAAMESGDGI TQDRLEAAKKHLNDQI AGMRLS
RHFEDFSRGAVERYLRPNFI DYEETRQKQEDI MVAVPPVMVSVKENEKI
I GEGEI I TEDHLAKLQALGLTRPRLPI TSI AGI FLLVAMLMVVVLFYLYQ
QNREI YDHAGHLYLLGI I VVMVLAVGKAI VAI NVNQWPEFGAQFGYMPVL
AAGMLI AI LLDSRLAVLI VAVMSLLLGVMTGNQLRFGLVGLI GGI TGVY
SVSKLSQRGDLVRAGI HTSGANVVAI FI VGLVGGAPLGLLI SSSLALGI T
NGI LSSI LTNGSLPFLEHTFRI TSPVRLELSNPNNVLLKRLLTEAPGT
HHSI I VGNLAEAAATDAVGESLLVRVGAYYHDI GKVKRPYFFI ENQMACD
NPHDKI APSLSTLI LSHVKDGVEMAREHKLPQGI I DI I EQHHGAGLVSY
FYHKALESDRAETVSEDEYRYEGPKPQTREAAVMVLADSVEAAVRSLQNR
TPGRVEGLVRKI I KDKLNDGQLDECDLTFKDLNVI ATSFVRVLSGI FHSR
VEYPDMAQEI ERRSKHAGSRKQLTGKSGGG

>2617921361 Ga0073689_12521 probable rRNA maturation factor [pelotomaculum
Ga0073689 : Ga0073689_125]
MPVLVNNLQEKVAVDESLSFTLGTVRTVLANEGYGNEAEVSLVFVDDAY
I QGLNQYRGVNSPTDVL SFAMREGEAI AGEEEEMI LGDVVI SLQTAERQ
AEEYSHTFRREVAYLTVHGVLLHLLGYDHQDEEERRAMRRKEEEVLSRLSP
PRK

>2617921360 Ga0073689_12520 diacylglycerol kinase (ATP) [pelotomaculum Ga0073689
: Ga0073689_125]
MGLRKL LDFSFNAAAAGVVYTLRTQRNMSI HFTAALMVMGLGLYLRI SSRD
LLFLVFVAI TLVI MAEMFNTAVEAAVDLYVQNFHPLARI AKNVAAGAVLVA
ALNSLVVAYI I I YPHLEGLSFHMSPR LK DAPLSATLTSLLLVSLVAAGK
ARSGKGI FAKGGMPSGHTAVAFAGGTVALLTGGALVATVALI MALLVAH
SRVDSEI HTLPEVI AGALLGI LSTLVVFRLAGW

>2617921359 Ga0073689_12519 cytidine deaminase [pelotomaculum Ga0073689 :
Ga0073689_125]
MDYPVEKLI SAAAAARERAYAPYSKFLVGAALLTRGGRCYTGCNVENASY
GLTCCAERVALFKAVSDGEREF EAI AI TAGTEDYCPPGACRQALAEFGP
EI NVFMANSRGAYRMLTVAELLPASFHI PTKGDSPLL

>2617921358 Ga0073689_12518 GTP-binding protein Era [pelotomaculum Ga0073689 :
Ga0073689_125]
LAKEKSDFRSGFVSI VGRTNVGKSTLMNKL VGRKVAI MSDKPQTTNRNKL
CVLTRDDVQI VFLDTPGFHKPRHRLGEHLVQVALKTMREVDVFLVLEAD
RPPGPGDSFI I RQFAGLTTPVLLVI NKI DLVKRDELLPVI EQYSRLYEFS
EI I PMSAFTGENLPRLDVLVGYPAGPKYYPEEMVTD RPESFI MAELI R
EKVLHLTSQEVPHSVAVVI EELEERPNDVVAVRAVI YTERESQKGI LI GK
GGQMLKKI GOLAREEMGSLGSRVYLELWVKVRPDWRNKEAQLRNLYGRE
EE

>2617921357 Ga0073689_12517 4-hydroxy-3-polyprenyl benzoate decarboxylase
[pelotomaculum Ga0073689 : Ga0073689_125]
LRVVVGI SGASGAVYGI TIL KYLRECDI ETHLI I SRWAHRTI ELET DHTP
EQVATLAHRHYRADDMGAAVASGSFAHSGMVI APCSMKT LAAI ACGYSDN
LI ARAADV TI KEGRRLLVLLPRETPLSSI HLENMLKLARI GVVI MPPVPAL

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YHRPGTVKEVI GHSAGRALELLGVKNLDFRRWESES

>2617921356 Ga0073689_12516 DNA replication and repair protein RecO

[pelotomaculum Ga0073689 : Ga0073689_125]

MRLYKAEAVLRARDCEGDKLLI LFSREYGI KVMHGVAKPSSRKRG
VQPFTRTRFLI HRGRELDVSQCEVEMFPYLRNDLGRI SYASYLAELVD
TLAPEGEPNEPLYLLLETL SLMAGNDAEI LARAFEI RAAGLMGYRPVLE
ACADCPGPVEGDLFFSPERGGVLCGACSAVRDALPCSRGTVEI LKI LLN
WPPAKLRQLKVERRDRNRI KSI LHEYLYHLERDLKSA AFLNRFYSAPGG
ADV

>2617921355 Ga0073689_12515 protein of unknown function (DUF4342) [pelotomaculum
Ga0073689 : Ga0073689_125]

VNSELEKI DI LRRLGVGYKEAKEVLEAAGDGVQALVNLEEKGRNFG
ER LOATGOEMLGQVKELLQKGREYRI KI KQGDKTVEI PASMALGI I GALA
SSEI ALLGALGTMAAMAKKYTLEFERLEESLGKKAAGEVFSNPGAGDNI

>2617921354 glyQ glycyl -tRNA synthetase alpha chain [pelotomaculum Ga0073689 :
Ga0073689_125]

MNFQELI LTLGHFWSRQNCI I QQPYDVEKGAGTMNPATFLRALGPEPWRV
AYVEPSRRPTDGRYGENPNRLQHYQYQVI LKPSDDVLEVYLNLSRAIG
I DPDEHDI RFVEDNWESPTLGAWGLGWEVWLDGMEVTQFTYFQCCGGI DC
RPVCAEI TYGLERLAMFI QGVDSVFDI TWVDGI AYGDVHHRGEVEHSHYN
FELADTGMLFKLFDMYEQEALRVVEKGFVLPAYDYVLKCSHTFNLLDARG
AI SVTERTGFI ARVRNLARI CARAYVEQREAMGYPLLLKKKGA

>2617921353 Ga0073689_12513 glycyl -tRNA synthetase beta chain [pelotomaculum
Ga0073689 : Ga0073689_125]

VEERKDFLLEI GVEEMPARFLDPALAEKELASGALQESRLPFSRVSA
YGTPRRLLALYVEGLACYQEPLMEVKGPAAKVAFKPGGAPTRAAEGFAKSQ
G VAVSELVI KPVGHVDYVFAI KREAGRPAREVLSGMAPGLI AGLHFPKPMR
WGELEVR FARPI RWI LCLFGSDVDFEFAGLKSGRTTLGHRFLSKEPLVM
ASPREYFEKMRHSYVMVDPLERKQTI RROVTELAAGVGGSV EEDLLNE
VTNLVEYPTALLGEFSRDYLELPKEVLVTPMREHORYFPVVGPGGGLLVK
FI AVKNGAADHLDI VRAGNEKVLQARLADASFFYREDLKTPLEGKVPALK
KI VFOESLGTI YDKMERVSALAAYL AGAMGAGEEEKKQAI RAAYLAKADL
VTNMVYEFPELOGVMGREYAERSGEERAVATAI FEHYLPRFAGDRLPETL
AGKI LSI ADKMDNI AGCFAI GI QPSGSQDPYALRRQALGI CHI I LGGRI A
LSLAKLI EAA YRGYEGKFQ LKFDLEKVKEEVAEFFRQRLKGI FSDEGLSY
DVVEAVLAAGYDDFSDALLRARALAEFRDP AFAGLLTAFVRANNLAANA
VTHRVPALLEDPGKEKLHQLLSTVREKARRYLELDYRSLLASI ATLOE
PVDKFFNSVMVMEDEKARENRLALLANLAGLV RQVADLSKI MADTK

>2617921352 Ga0073689_12512 CBS domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_125]

LELTRRQETI LEI VKNFGPI TGEHI AEKLSLTRATLRPD LAI LTMAGLLE
ARPRVGYFYSGKSPNRVVAEKL AGVLVGDVKSVPVVS DKSVDVAVVTM
FI EDVGT L FVI KEGGLLEGVI SRKDLLKTTLG GHD I HKLPVGVVMTRMPS
VYVYTPGETVWLAARKLI TREVDALPVVRKI TPPEGGEGLVVGRLSKTN
VTRLFVELGEGN

>2617921351 Ga0073689_12511 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_125]

MSPGFLWNWGKEI KGEFI I STKNDVKPVI YI VSDSI GETAELVARAAASQ
FNHGGVDI RRVYPYNDPGEI PEI VEEASAFNSLI AYTLVLPELKEVLVRE
AARYGI PTVDI MTPMMDAMI DVI HRQPKLEPGLVRKMD E DYFRKVEAI EF
AVKYDDGKDPRGI TRADLVVI GVSRTSKTPLCMYLAHKRI KANVPLVPE
VAPPEEI FRLPSHKLI GLVI RPQQLNEI RRERLKTGLT SNADYASMDRI
LKELEYAEGVMKRAGCSVI DVTNKAVEETASKVLEI YFRGERI GK

>2617921350 Ga0073689_12510 pyruvate phosphate dikinase [pelotomaculum Ga0073689
: Ga0073689_125]

LASKKYVYLFEEGGAGMKNL LGGKGANLAEMTNI GLPVPPGLI I TTEACK
DFTAMGQKFPEGMEEQVKEKI KI LEEKLGKKFGDETNP LLVSVRSGAPVS
MPGMMDTV LNLGLNDR TVEALAAATGNERFALDCYRRFI NMFGDVVMSVE
HHKFENI LEHRKERAGARFDNLAAEDWREVVAEYKKLI QKETGRSFPQE
PI EQLFMAVYAVFNSWNNDR AI VYRRI NKI PDDLGTAVNI QTMVFGNMGD
DSGTGVAFTRNPSNGEKKLYGEYLI NAQGEDVVAGI RTPQPI AALEQDMP
DVYRQFAGVCQLLDKHYRNMQDI EFTI ERGKLWI LQTRNGKRTAQAAI KI

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AVEMVGEGLI SKEEAVLRVEPGQLDQLLHRQI DPNAELDI VAKGLPASPG
AASGI VVFDADAEAEKLGQEGKKLI LVRTETTPDDI HGI VAAQGVLT SRGG
MTSHAAVVARGMGKPCVCGCEAVRI DYENNEFHI GDI VVKHGETI SI DGS
TGNVI LGTVPMI DPESPEFQKLLKWADQI RTLGVRANADTPQDAKARE
FGAAGI GLTRTEHMFMAODRLPI VOEMI LAAGLKDRQAALGKLLPMQOQD
FYGI LKAMDGLPVTI RLDPPLHEFLPNAEELLVEI TRLRLTGGDKKEI R
QKEELLRKVRALSEFNPMLGHRGCRGI TYPEVYAMQARAI FOATAQLVK
EGLNPI PEVEI PLVI EVKELAFLRDMVI NVAEEVMKNYNVDFHYTVGTMI
EVPRAALLADEVATQAEFFSFGTNDLTQTTLGFSRDDAEGKFMFAYMEKK
I LDDNPFVVLDRKGVGKLMRMARELGRRTNPDLI GI CGEHGGEPSI EF
CHI I GLNFVSCSPFRVPI ARLAAAQAKVKNPEGEKEDYGAL

>2617921349 Ga0073689_1259 2' -5' RNA ligase [pelotomaculum Ga0073689 : Ga0073689_125]

MRQMRLFVAI NFPDQVKQVLGSLI KELRRFPAGARWVEERNLHLLTVQFLG
NAPEGQVPDI VASLERSAAGVPPFKLELGGVGVFPSI ERPRVFWAGVTGE
TAVLSRLHHRVREEEAGLGFVPEKRRFSPHLTLARLRSPQGF AEVMERAE
GLARQHGKFGSTAI NSVELMLSELPGGAKYSI LARI PLSGR

>2617921348 Ga0073689_1258 dGTPase [pelotomaculum Ga0073689 : Ga0073689_125]

VDI RLRAEELERRI LSPCACLSSKGRARPEEECSVRTVFQDRDRDI IH
SKGFRRLLKHKTQVFTI PEGDHYRTRLTHTLEVAQI ARTVARALRLNEDLT
EAI ALGHDLGHTPFHGAGEEALNEVFQPGFKHNEQSLRVVDELEGGKGLN
LTWEVRDGI LNHTGPVRPATCEGOI VKI ADRVAYI NHDI DDAI RGGVLT
EQLPEECCLDVLGKEHNRRI NAMVLDLI HTNWDEPAMI KMSPAVQAATDRL
RSFLFSHVYI GSDAKREEAKARHVVRRLRYRFQETPSALSVEYLKRASTG
EVDRAVCDYI AGMTDRFAI RVYQKYFLPLPWVD

>2617921347 Ga0073689_1257 DNA primase [pelotomaculum Ga0073689 : Ga0073689_125]

VGAI PGEI I ETVRLRSDI VEVVSRYVQLKKKGKYFTGSCPFHHDQAPSFT
VTPDKQI FYCFGCSAGGDVFKFLMLKENLTFYEAVRMLAQAGVVI PATE
SPARRERDKROAELQI NSLAKDYFHQTLQHHHTAAAAREYLTGRGLTPE
ALDRFQVGFAPPQWDSLLGFLGKKGFRPGDVTEAGLAVRSDSGKYYDRFR
NRVI FPI WDATGRVTGFGGRVLDNAVPKYLNTPETPFFSKGRTLYGLHLA
RPAI REKGI VVVEGYMDVVT AHLHGATNAVASLGTALTAEQGRLLMNYS
RDVVI AYDADAAGVAAAI RGLDLLQELGCQVRVASVPDGKDPDDFFRRHG
YQAWERLI DEAPSLI EYKLQAVAGGPVGTAAKLEVLRRVFPNLI LKDG
VEKEEGLKAVARTLNL SWETVAGEFKRFKASOGKKWSNPDNI VKI KHNI S
SKDEGRDARGKAEAGLLRLI LEEPSLGKTVLAEAPFKNQCYQRI FRHCMK
TAERPVRPAEI FSYLDEEDQTM LSLLLTQEI PENPVQI MKGYLECI SR
SNRRERREI LLREI GEAEKAGDHLLYGELWSEYI I LRGI DQAEKVG DQSR
I EKLLQEYRQFLQSSSELV

>2617921346 sigA RNA polymerase primary sigma factor [pelotomaculum Ga0073689 : Ga0073689_125]

VRDGI KTEGVRELI EKGKKRGVLT YNEI MDSLQGT ELTPEQI DDI YEKLA
GLGI EVVPEVPEI EPLDGAALEENPPEEVEVDLT I PEGI GI DDPVRMYLK
EI GRVPLLTPDKEVELAKRMENGDEEAKRR LAEANLRLVSI AKRYVGRG
MLFLDLI QEGNLGLI KAVEKFDYRKGYKFSTYATWWI RQAI TRAI ADQAR
TI RI PVH MVETI NKLI RVSQQLLQELGREPNPEE I AKEMNI SEDKVREI M
KI AQEPVSLETPI GEEEDSHLGDFI EDQEARAPAEASFTLLREQLDEV
KTLTDREQRVLRRLRFLDDGRARTLEEVGQKFGVTRERI RQI EAKTLRKL
RHPSRSKKLKDYLD

>2617921345 Ga0073689_1255 CBS domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_125]

MHLSEKRVKDI MI PI GEYSSVSANCTVGEAI GVLKKSFCPELEPCNSHR
TVLVYDGNTPVGLI TFRGLLTAI EPRFMKVDQWAVPVFWEGLFTERCREE
AVKKVRDI MTPI TLVALDADDTI I KAVHAMI KYKLGSLPVI RDGVFAGMV
RI TEI FHEI SSLVTEQTEMGETPATTKRALSYHI

>2617921344 Ga0073689_1254 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_125]

MSDLKATALKSSARPDKVREI TPAKVEVAPEQLKYANLLLYGSWTGI AV
LAATFFLYMTGMTSSFI PPSQMPQYWGKASEYLTATGAPHGWGWI SMI G
HGDYLNLMGI AFLGSLTLVGFLI LLPAYLAKKDSI YTAI VAVEI LVLTLA
ASGI LKVGGH

>2617921343 Ga0073689_1253 hypothetical protein [pelotomaculum Ga0073689 :

Table S2

Ga0073689_125]

MLELLAAKYSM LTTTSAGPI LASATTTI GATVNTAAGTPGTPWWWPLLLF
AVTFVMGVVAVLAGVGGVLFVPI I GSFFPFNLNFVSGAGLI VALSGALA
AGPGLLLKANLANLRLALPVALI ASAFSI VGAFI GLALPTNI TQTALGI TI
TLI AFLFI VSKNSEYPNVGAPDGLSKKLGLVGAYFEATSGKTI NWSI WRT
PQGFLLFTVI GAVAGMFGLGAGWANVPVLNLLMGAPLKI AVGTSKFLLSI
TDTSAAWI YLNOGAVLPI I AVPSVLGI MLGSLI GVRLLAGAKPKAVRYLV
I TMLFFAGLRSLLKGLGI WN

>2617921342 Ga0073689_1252 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_125]

MTEI KGTSPDKTTGCPKNI I QRKRGKPEKVYPLYWLAPSRDLGARLVRTA
FLCQSVGI PVKHVQDSNI CHYPGGTRI VKYVLNLLGMGFGGSKEPVI RVV
KI NGEFFVERGQRLLLLAQALKLDYI PI RI VEYSYEFLLKRKMQI FKYPDL
EI VGI AAGQKGGYDQGVSAENANVLLKHHLVPLVDHTAPPLEESPGAPP
SRRNRRRGAPVPSGKHPGLTVI KKKRK

>2617921341 Ga0073689_1251 CBS domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_125]

VSKI NEKKVKDLLTPI EEYSTVRADSTVKEAI TVLKKSLRPGDPAAGGVH
RSI LVL DNGEI AGLLTLRALLQAI EPRFI KVDQWAVPLFWEGFLTDRCR
EESAKEVGELMI PVKLI SL DADDTI I KAVHAMLKHKLDLSPVFRNSKI VG
I VRATEI FQEFVSLVADQPSTGEALPDLRGAVPLQG

>2617921340 Ga0073689_12436 L-aspartate oxidase [pelotomaculum Ga0073689 : Ga0073689_124]

MPEARADAGQFLGGNDI RL VVSKLDTVYQLLNGGFPLPEKYMLNFDTRVL
PQDEDEYI I LGSGI AGLYTALAAASQAGGSVTVLTKYTMMDTGTDMAQGGI
AAALGDTDSPALHQEDTLVAGAGLCDAEAVTALVSEGPSRVRELI ELGAI
FDTDSEGLVFTREGAHSRRRI LHASGDATGAEI QRVLTQRVQENNKVRVL
ENHYVVDLLVRDNTCYGVLA FDRGVRALNVFRGKVVVLATGGLGRLFEHN
TNPEVATGDGI AI AFRAGAEVMDMEFI QFHPTVLSLPGVPRFLI SEAVRG
EGAYLRNSKGRFMPRYHDLAELAPRDI VVRAI LKEMALTGSNLVYLDMT
HLDPEVI KLRFPNI TRTCATYDLDI TVDRI PVAPAAHYMMGGVKTDLVGG
TSI RRLYACGEVACPGVHGANRLASNSLLDGLVFGGRI VEETGKFLKNLH
LRHQEFAC

>2617921339 Ga0073689_12435 quinolinate synthetase [pelotomaculum Ga0073689 : Ga0073689_124]

MOELANEI I RLKKERNAI I LAHVYQRPEVQEVADYVGDLSGLSQQAAKTN
ASVI VFCGVHFMASASI LSPDKI VVLPDEHAGCPMADMVNAVELVRKKQ
EI PGAI VVCYVNTSAEVKAESDI ACTSANAVKVVESLPRDRPI LFI PDKN
LGQYVMSKTGREMI MWEGYCHTHDRLTPEDI LKAKAGHPEALI LVHPECR
PEVVTLADSVASTTGM I RFARESDAREFI VGTEMG I LHPLRKQCPDKQFY
MASEQLVCPNMKKTTL DKVHRALVNLESKVAVPKEI RERANRCLKRMLEI

>2617921338 Ga0073689_12434 L-aspartate 1-decarboxylase [pelotomaculum Ga0073689 : Ga0073689_124]

MYLNMFKSKI HRAVVTGADLNYMGSI TI DEALMKAADI LPNEKVQI VNNN
NGARFETYVI KGPRDSGI CLNGAAARLVQPGDTVI I I SYAMMDRGDALA
FKPTVMVDENNKI SKI KKGEI HGEI G

>2617921337 Ga0073689_12433 pantoate--beta-alanine ligase [pelotomaculum Ga0073689 : Ga0073689_124]

MFI YHTI AEI RQFVRRTRAEGRSVGFVPTMGYLHEGHLELMRRAKERCDT
VI TSI FI NPAQFGGEDFARYPRDLERDARMAEGAGVDAI FNPSVEEMYP
RGYCTYVDVERI TGKLCGLSRPGHFRGVATVVTKLFI VKPDLALFGQKD
AQQALVI KRMAADLNMKLEVV TAPT VREADGLAMSSRN VYLTPEQRRAT
VLFRSLSRARDAFRTGERDAKI CQLVVDLI KAEPLVEI DYVEI YSHP
DPVERI EGPVLLAI AVKI GKTRLI DNI I LGDL

>2617921336 Ga0073689_12432 ketopantoate hydroxymethyl transferase (EC 2.1.2.11) [pelotomaculum Ga0073689 : Ga0073689_124]

MSKDRVTTATI RQMKAEKPI TMLTAYDYS LAKMVDDAGI DI I LVGDSL
NVVLGYNSTLPVTMEDMI HHI KAVCRGAGRAMVVADMPFMSYQI SVEEAV
RNAGRFLKETGVQAVKLEGGREVAEAVRRI VGAGI PVVGHGLTPOS I HQ
LGGFKVQGDAPAAQKLI DDAKALEEAGVFCI VLECVPTPLAKMVTETVR
VATI GI GAGPHCDGQVLVI HDMLGLYPRTS PRFVKKYVNLHENI AAALKQ
YKEEVAARVFPGEHSFGMSEEVLRKLY

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>2617921335 Ga0073689_12431 Predicted oxidoreductase, contains short-chain dehydrogenase (SDR) and DUF2520 domains [pelotomaculum Ga0073689 : Ga0073689_124]

LSKPGI AVVGAGKVGSAALALLSRRGYPVAGVASRSI SSAGRVAEELKVP
ATTRPEEI TNGADVFI TTPDREI ARVAGEI TERGGFRPDQI VFHTSGAH
PADEVGAVRRAGALAASLHPLOSFADVKMAMESLPGSYFALEGDAGALPL
AEQI VKDLGGKSFFI DGRDKPLYHAAACI ASNYLVSLI HFATGLYGRFGL
SREEAFGALFPLI RGTI KNI SRVGPAPALTGPVARGDSPTLEGHLEALKE
VGDOLELELYRKLGLYTVKVALEKGS SPARGEAMEEI FKERGASR

>2617921333 Ga0073689_12429 Imidazole propionase [pelotomaculum Ga0073689 : Ga0073689_124]

MEI I KMGRFPAAVI RTALLI DGTGTPPREKVDLYVENGVI RRI VPCRDGD
SGAGNEDCQAGGAGNGSPGKGPFTPRADGRTGAPSRVVQRADGSGEI H
CGDLTVLPGLVDCHVHLALNGVDFDSSLQRWENGEEI TRRLAGSLENTLR
AGI LAVRDGGDRRLI GLMAACLAGGKATPPFI I ATGRALRKKGKYGSFLG
KGVTAPEI RAAVRETAASGAAQI KVLVSGI VSFREYGVKVPLOFSREELS
LLVSEAHALGLKVMHASSDEGTALAVACGVDSLEHGYFI SRDTLARMAG
RGI AWWPTI I PVAAQACEPLHRNHSPGQLALI EKYRROQVMVDTARRLG
VI I GVGTDAGASGVRHGLSYAGELTLLAEAGLSPA EVTCAATAGGARI LG
LEKQI GMVAPDMAACLI GVRGNPLENPDLKKPVLALI P

>2617921332 Ga0073689_12428 poly(A) polymerase [pelotomaculum Ga0073689 : Ga0073689_124]

LFI KKVLAET AGFAAGNKKI YLVGGFLRDLYLGNPGRDLDFAVSGNALG
FAEEAAEI LDGSYI PLDRI NGVARVLLLEHRGEKWQI DFASLKGWNLEEDL
SNRDFTI NATALELSTYLGFTEENDSGLAAARPDRRRWHE TVI DPCGGLAD
MENKI I RAVNNYI FETDPLRI LRAVRLAGQLKFFI QPETMSLMEQGRWLL
HEVAGERI WDELLGI LALPDSYPWMAMMDAI GI LSEI FPFVEKMKLTGQN
NHHVDNVVHSLKTYQLLEDLCRDLDGDI TLTTSRGKELRETI LNNLNSK
LAAGHGRSOLI KLAALFHDAGKVD TANVLEDGRI TFPAYEAGLVYVAEF
ARRLKI SRPEEAYLRNL VGNHMYPLYLFVNQPVGPAI HRRFNKMSRDTT
DVLLLSLADLTATYVAGEKAHDLARYRTFI GDLLHKYHFETEI YVNPPEL
VKGADLMEALGLPPSRKLGELLKKI SEARVRGEI TSRDEAI AYASRLNT
NTE

>2617921331 Ga0073689_12427 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_124]

MKRI FCKYMNEYTKDKCLENDEKYQMTDQEVKLYFSWGLVDIMN

>2617921330 Ga0073689_12426 2-amino-4-hydroxy-6-hydroxymethyl dihydropteridine diphosphokinase [pelotomaculum Ga0073689 : Ga0073689_124]

MNGVI VMPEI AYI GLGSNLGDKEANI KRALELLNASSGVRVKRVASLYRT
APVGFTGQDWFI NTVAEETGLGPHDLLALLLAVEKKLGRVTRVWGPRT
VDLDLLLFGEEI TTPDLTVPHPHMSERAFVMAPLAELAPELTI PGPGKA
AVLARTLAGEQLVQRDSWDRSKAPG

>2617921328 Ga0073689_12424 dihydroneopterin aldolase [pelotomaculum Ga0073689 : Ga0073689_124]

MGI RVGDLVWKAAGWGKGNVGMGSEPTSSFAFTPWVRKAWEGDFPAGEL
KGVVPMDKI I LEGMEFYGYHGVNLNEEQSLGQRFI VDVELYLDLRPAGESD
DPDRAVNYARVFELVESI VGGRRRLI EAVAEAI AAAMLERFPVREALVR
VKKPQAPLPGRFTWMAVEI RRAGTRDRGTG

>2617921327 Ga0073689_12423 dihydropteroate synthase [pelotomaculum Ga0073689 : Ga0073689_124]

LAI RI YI I SVENREEALKAI ASVGADRAGCRWMAKAVHRLVMLDGVQPR
QANI I KOEMLGKGGEAAVARGVI DCSADESRVLLMGTLKQYDAFLDKLKS
QPFGLAALAGRI KEALTGREGFYDYDLDCRGKTI RLGERTLVMGI LNVTP
DSFSDGGKFYDPGLAVERAARMVEEGADI I DLGGESTRPGHTPI GVEEEL
VRI MPVLKRLLDEI PAPVSI DTTKSAVARRALEAGAH I NDQWAFRADRA
MAGVAAEYRAPVVLHMHNRQGT EYRDLI GDI VEYFRESVDTAVEAGLAREK
LI VDPGFGFGKTPQNLKALRRLKDLRCLGLPI LLGASRKSTI GKVLDLP
VDQRMETGAATVAVGI VNGADI VRVHVDKEMVRVTRMTDAI MGRGR

>2617921326 Ga0073689_12422 HD domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_124]

LKRVEYI LNDRFYRECLEKNALHEVERRFCRHDFQHMLEVARI TYI LLLLE

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EGLTDRLAELPDLSDQAVVKEVI YAAGLVHDI ARWROYETGEDHAQAGAE
LAAPLLDRAGFDREETLVI AAVREHRTGGRKSTLLGKRLSRADDLSRPC
FRCAAREDCYKFTDNGEQRTLLTV

>2617921325 Ga0073689_12421 Nucleotide-binding universal stress protein, UspA family [pelotomaculum Ga0073689 : Ga0073689_124]
MYRKI LVPFENSSQALSAVEHALKLALVSGAAVTI FHVVDALIFSDERI
VKRTGI DRDAVI NQAKAGAKAMLNKLKEGLSEHEVKI DTAVAVGSPAREI
CKKAQI EGYDLI I MGSRLGKI PGLLMGSVSNRVCNNAFCPVI VIHAN

>2617921324 Ga0073689_12420 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_124]
LVNLPQKQHPDPEDKTPPAAGFGRPRLEGGVRAPVVPDYLGTI LKGHI L
SEGAPLPSSCGTVRI LLVEEGEEWKI DNI TAPTSCSMQTVKSPGTSPGRQ
DSNRYFLEQAHNFAGFCVYVDSPEGRVGAGAGHQADGTGHRAKELGSRKD
QDVANR

>2617921323 fhs Formate-tetrahydrofolate ligase [pelotomaculum Ga0073689 : Ga0073689_124]
MAYDATKLKDYQI AELAEQNMPPTPEEWREKLNQKDELI TYGRI AKLDFM
KII ERLKDRPDGKYI NVTAVTPTPLGEGKTTTTMGLVEGLGKRGNCGAA
I ROPSGGPTMNVKGTAAAGGGNALAI PMTEFSLGLTGDLNDI MNAHNLGMV
ALTARMOHERNYDDAELAKRNLRLDI DPTRVEMGWI I DFCAQALRNI I I
GI GGRMDGYMMQSRFGI AVSSEI MAI LAVAKDLKDMRERI GKI I VAYDKK
GNPVTTSDLEVAGAMTAFMRNAI NPTLMSTAERYQPVLVHAGPFANI AI GQ
SSI I ADRI ALKMFYDYNVTESGFAADI GFKEFWNVKCRFSGLVPNVSVI TA
TI RALKMHGGGPKVVAGRPLPEEYVKENVGLVEKGCENLVHHI NNVRKAG
I NPVVC I NAFYTDTKDEI AAVRRAAEAAGARCALSEHWLKGGDGALELAD
AVI DACNDKVNFKFLYPLDMPLRQRVDVI AREVYGADGVAWTPEAEAKAR
MFEENPEYKDFATMMVKTHLSLSHMPEAKGVKPGWI LPVRDVL I FAGAKF
LCPMTGTI SLMPGTSSDPAFRRI DVTETGKVMGLF

>2617921322 Ga0073689_12418 nucleoside diphosphate kinase [pelotomaculum Ga0073689 : Ga0073689_124]
LERTYLMVKPDGVRNLVGEI I TRFEKRGFKI VGLKMLRI SRELAEKHYG
EHVGKPFEPVQYI TSGPVVAMVI EGKDAVSAAREMMGATNPLKAAPGT
IRGGYGI DI GRNVI HGSDSPASAAREI ALFFKEDELI EYSRGVDRWI YE

>2617921321 HflB cell division protease FtsH [pelotomaculum Ga0073689 : Ga0073689_124]
LNKVVKNLSI YLLI VLVI I ALI RYTAPTKTVTPVTYNKFLEDLDAGQI K
KVTI QSENLTNI I TGEKKDGVRFETKGPATDAALYDVLKEKKVWSSSELP
PQPGWWTGLLTSLLP I LLFVI LFFFLLMQQTQGGGNRVM SFGKSRARLQTD
EKKKVTFAADVAGADEVKEELEI VEFLKNPKKFQELGAKI PKGVLLFGPP
GTGKTLLARAVAGEAGVPFFSI SGSDFVEMFVGVGASRVRLDFDQAKKNA
PCI VFVDEI DAVGRQAGAGLGGGHDEREQTLNQLLVEMDGFSPNEGI I I L
AATNRPD I LDPALLRPGRFDRQVVVDAPDVNGRKEI LKVHVRGKPLDEGV
NLEI LARRTPGFTGADLANMTNEAALLAARQNRKKI SMADLENSI ERVI A
GPEKKSKVI SEKEKWLVCYHEAGHAVVGFLLPNTDPVHKVSI I PRGRAGG
YTLLLPKEDRYATKSQLLDQVTMLLGGRVAAEAVVLKEI STGAQNDLERA
TDI VRKMVMEFGMSDLGPMTYGRKTDTPFLGRDLARDRNYSEEVANAI DN
QVRETI DRSYNNAKELLEHLDTLKL VARTLFEKETI EAEFEALMKKAG
EGERKDRI E

>2617921320 Ga0073689_12416 tRNA(Ile)-lysinine synthase [pelotomaculum Ga0073689 : Ga0073689_124]
MDLLHRVCDYI HRHRMVERGSLVLVAVSGGPDSVALLHI LYNLKDELGI S
LHVVLNHNMFARGAESEADALFVAGMAERLGLPATVESRDVPAYRQRRRLS
AQVAAREERYRFFAETAGRVGASKVALAHQADDQAETI LI NFLRGTGVTG
LKGI LPVREGFYI RPLL VVRRSDVERYCTEADI SFRRDFS NLKPVIYARNR
VRLQLMPLLEKEYNPGLVSTLLRLGEI CRGEDSYLEEQAEEAFRGVLREK
APGRVVLGLAGLKEMPVAVKRRVRLTWHLTGATKDLAFQHTAVLDLI
EGGATGSR I VLPNGI SAFRSYDLLELTREREKPGAPYYI HLLQVPGATGI
PELEMTI HAGLCFRTPAHDPKSLPDSEALLDYDKLPPQLFVRMRREGDVF
YPFGGVSEI KLKDFLI KQKI PREERDRI PLVSTPGEI VWVGGVRTGEKWK
VDQNTRRVLHLKI AQWELSSL

>2617921319 Ga0073689_12415 stage II sporulation protein E [pelotomaculum Ga0073689 : Ga0073689_124]

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LFENIGIYPYRRVGKDKKKQSPPPGKNNVKKRRPLFRSKI GEVVPWTVI
LCVTAFFLGRVTLLGELAPFGASFAAAVI RVFGRSGLPAPPAVLGLATV
SKGVPLAASI LTVFCWLLTVSVPSGVKRPWI LPALVLAI TVI VKASFT
AFTTPSSYNYFTVLFEAVFAGMLTPVLI YGLDSLKKRAGGLRPFSGEEIS
CVLLI LGGVI AGAGDLRFEMI SVKGVLSRLAI LLAALAGGAGSGAAAGAV
VGI PGLAYTVVPMVVGAYSFAGFLAGVCGNFGKAGVVTGFI LGNI LSV
YVADYGNI VAVLAETGLAALFFLLI PAPLVEDLKI SLGLETKKAGEPGEE
KTALREI FKERI KGWARVFNELSRTFEQVSSAAGQSREEQGLQRLLNQVG
EKVCSDCTFHRTCWEREFYKTYQGM DLLALLDI YGKVTPDNLPGEI KRR
CSRTKELAVTI SCLYETYSLNRYWSRRLQESKEI VSEQLRGI AEVI AGLP
GELEFETEAGEVGPALRKKLKEAGAKVDSLAVYRRDNGGI EVSLTHAPCG
GRLECRNLI APLLSSLMEQPLYLAAPVCTTVDGEPACHRLRYPGLNYRLV
PGVAAAGKNGSI VSGDSHAFHKLKGGFRGLVLSDMGAGPRAALES GTTI
SLLRHLLESGFGKDLAI KTVNSI LVLSPGESFATVDLVVNLVNGQTD
VKI GAAPTFLI RGGQVGR I KASSLPVGI VEDI EVTSLSRMELGDVLMV
TDGVLDAYRGTDGDEEWLTEI LLDMDMPPRETAGLI LKLAQTAAGGP
APDDMTVI VAKLEKQKDASKRFNKL

>2617921318 Ga0073689_12414 exopol yphosphatase /
guanosine-5' -triphosphate, 3' -diphosphate pyrophosphatase [pelotomaculum
Ga0073689 : Ga0073689_124]

MKRVAADI GTNSTRLVAEI TGARLETVEAGLDTTRLGEGI DSGVLLPG
AMERTVEAI SRFHRTALGLGAERVAVATS AVRDAANRDEFLALVGRRTG
LAVRVLSGAEAAASYRGVLSGLAVEPRSTVMDVGGGSTEFVWTI EGYL
RLVSVNVGAVRMTGAGAGKDEI AAI LRPALAEVCQGQVETLVGVGGTVTT
LAAI DQGLALYDRERVHG YRLTAGRVSDI LEYLKKI SLEERRVPGLQPE
RADI VAGI VI VKSVLEGLGRDRLVSECDI HGLVLEEVEI KKG I FFLN

>2617921317 Ga0073689_12413 S1 RNA binding domain protein [pelotomaculum
Ga0073689 : Ga0073689_124]

MPI EVGI VLEGVVTGI TNFGAFI ELPGETGLAHI SEI AEVYVKDVHDFL
KTNDKVI VKVI SVDPKGKI GLSI KQANPSSHNRKKFQPSFEELAKFLK
ESEERQOI LKRSADSKRGGRTTRKLE

>2617921316 Ga0073689_12412 cell division protein DivIC [pelotomaculum Ga0073689
: Ga0073689_124]

VSHALRREQKVYSSPVESLAPEGRPEQRRSFKLSKSRLPALVALLLLTYV
VVSFCSQFGKLSVLQNDI NSI QQQVQELKEKNASLREELHMQSDAYVEK
NAREKGLI KPGETRMPVPPGTQLKRLEPPSTDGAVNH

>2617921315 Ga0073689_12411 Sigma-70, region 4 [pelotomaculum Ga0073689 :
Ga0073689_124]

VKI EIRGAERLSFRERQVVALKEMGYSTERI AKQLALSPSTVSTLYSRAR
SKGYEVVI VIGHNLALFGVEEEEEI KE

>2617921314 Ga0073689_12410 S-layer homology domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_124]

LFKKGAFTLLLTVALVLGI AASSYADPGKKGKNWKA KHANWKVI QLTDI
SSHWAEEPI RAMTLQGVVLGYTDFSRPNAPVTKFEAVMMI AKASGYEGS
VGAEDSWDI SVPLWMRGCLDYAVEAGI LSKSEASSLKGWEPAKRYEAVW
ASRAMKLNVD SGLSFQDLDEI PVFARPYVGGMFRYRYMVGYPGNFFQPNK
PVTRAELAAVLYRI MLEHPPGNAVYRVVKGEVDEVNEDSI EIGNKTYGI T
GDTEI FVNSKKAAL EDVKEDARVTA FVDYNNNEVI LLYARDNDKEDDDDD
GDTGEEVKLSSLTPADGSDVDPATGELVAKFDAEI EAVDGLEEVKEGI K
VRNVTDSLEI DRVSI DGMELTI KLTD FLEGGKTYRVTI GENVI EAGES
GRGFPGI SGGDWEFS AAGSLKI VGLDPRDGANNVDGSRTKVLKARFDDDL
AVVSGKGLLGAVAVYNRSDDKNVDVKVEI DDDTLVI TLEDYLEDGDTFE
VTI KPGYLEDEDTGTD FAGI DSGDWRWFSTKN

>2617921313 Ga0073689_1249 stage II sporulation protein R [pelotomaculum
Ga0073689 : Ga0073689_124]

LNKKMAI TLAALLLPGI LLLSHNFRQPDREKTYPPGDLI RLHVVANSDSA
FDQELKRVREI RNVAPFLEAGNI DSARRTARAGLGRI KEI AAREVK
AAGKDYPVRVELDRFAFPTKHYGPFVLPAGDYEAVRVVI GAGGGANWWCV
LFPPLCFVDMKSVAVSEPEKAPPPVAAI PPRDFTAAEEQAAEEQRPV
AAVPLQTGDMAGANGATPPEDGCVKVEFRFRI LDFLQKFI G

>2617921312 Ga0073689_1248 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_124]

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LNVTATVPCRKNGKQKNRPYASSSGGWELGFPVPVPGKPGTGTRRLSPCP
KSGSGRGVKSRSNENFLEKSENFLEKKENRRRFQNYKPSVFLVSR

>2617921311 Ga0073689_1247 Spore coat associated protein JA (CotJA)
[pelotomaculum Ga0073689 : Ga0073689_124]
MFRRYQHPLFRGRTPAAAGEKEKNGQPAGEVKAETVPPDFQAAGLYPPPR
LAQTYVIWQKYGPTFTPAEAELEKGTIFPDLYSPYPY

>2617921310 Ga0073689_1246 CotJB protein [pelotomaculum Ga0073689 :
Ga0073689_124]
LTAPGTCPLSQPQLSGSLQALSLLMEDQTASNHYRAFQIRDFNGVNKKMD
ERLSILKEIQELEFVAVELNLFLDTHPEDQSAHRDFYTVRDKLMALRKRY
EEIYGPLTVTGATPPHRRWLWSESPWPWEI EYV

>2617921309 Ga0073689_1245 spore coat protein JC [pelotomaculum Ga0073689 :
Ga0073689_124]
MWIYEKKLEYPVRVYKNDIGMAKYLMAQYGGPDSELSASVRYLTQRYTMP
TDMAGLLTDIGTEELAHWEIVATMIYKLVKGIPAKQLREAGLGAHFAEH
DHAVYPGDAAGVPWTAAYIQATGDPLADLHEDLAAEQKARATYERLILLT
DDPGIKDTLRFLREREVVFHFQRFGEALNDVQVVLGSKKYY

>2617921308 Ga0073689_1244 protein of unknown function (DUF4338) [pelotomaculum
Ga0073689 : Ga0073689_124]
MGYWQKPMTKTRYCGRNFTAAELDLIRSIARPEEYPTRAARAVCQSL
AWVKPDGGLKLMSARVALLRMYRDGLFELPPPRGGNGNGRWNPQPTPATD
PDPPLTGTRRDGPGLILHRVAFPI DSRLWNELIARYHYLGYTLPGAQIR
YLI RNETHLLGAI GMGAAWKVAPRDLFI GWTSEQREQLHLII NQARFL
VLPWWQVKNLASSVLSLLVNQLASDWEELYAYRPLVMETFEQERFQGTG
YRAANWI HVGQTQGRGKLDITYKLKDKPI KDI FLPLDKNFRKALTTP

>2617921307 Ga0073689_1243 Transposase IS66 family protein [pelotomaculum
Ga0073689 : Ga0073689_124]
VERKVHRRLSYHKTCQCPGVPVITTAAPPPKVI PKGLFTAVFIARLIIEK
YVLGRPLYRIGASMRMEGLDLAQGTLVGVFQQVSSLLIPLYDAIRAHCVS
AGLWQADETGWKVFEEVAGKASNRWWLWAFASSDTVVFVMDPSRSAAVPK
RFFGLTEDDPNPAQGILLGSDFYRVYQALGERILSFFCWAHMRRYFLEAAR
GYSKLSQSWTDEWRERIALYRLYEVRQALPPGAQSCLEADNELRRFVKDE
IEATWRAQVADRTIPAGRDVLGTMQRHWEGLTRFLDNPLPLDNNFMER
ILRGPVVGKRFYFGSGSQWSGKFAAI AWTITATASRANLNPLLYLIDFLT
ACANNGGKPLVGQDLDRFLLWMMSEADKKSWAIGRSP

>2617921306 Ga0073689_1242 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_124]
MHFPLGGPVPEEDI VGRDDFI TSLETRLAEGQSIMLAGPRRI GKTSLAFE
VLRRLLKKKGFYVASVDFFRTSSRRSIAESI NSCLENRTGIRKTLNAVWD
RAKLLAGSAKIAVKI EDLELNI GFPPKEMDDETLLEFAFNLPELLAERDG
KRMVIVFDEFQDAGQIGGLDIYKVMRSHFQHQKKVSYLFLGSKESMMQSL
FAGKKHAFYRFATVLPPIQILEEDWMSYITRKFNERGIEVSSDYVLKEIV
QLAGGHPQDTMLICTEAYYTLLIEIDKKLSSEIVRIAYERALI TLTPVFD
EILDEVGKKPLVREVLRLAI GEVVYKEKNNPNDIKRAIDALSI SAIIEK
EGRGKYRFVEPMLKEYILRNY

>2617921305 Ga0073689_1241 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_124]
LLYRKNI VGFLIFNYKPGIFHLASISTPYILMADLAVSVTRCP

>2617921304 Ga0073689_12340 Peptidase A24 N-terminal domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_123]
VEFLWWALVFTTGAAVGSFLNVCICRLPAGGSVARPPSHCPACGQNLRAL
DLVPVLSYFFLRGKCRYCSYRISWQYPAVE

>2617921302 Ga0073689_12338 Predicted nucleotidyl transferase [pelotomaculum
Ga0073689 : Ga0073689_123]
LTVGQCFLSFSRRCPNPVIRKVSIGMSLTLOQLLWLEERKITAKRQKDALA
RAKKVAAHLKERYGVKKVFLYGLARGNFSHISDILDYIEGFDQEKMYWR
MQVEAEI ALPYPLSIVPAEDAFPSLRREVYREGVEL

>2617921301 Ga0073689_12337 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_123]

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MTMRDLLI VEARAKKELENTGQLKSALAGRGLYPLTRKGRQNLNDEFMLR
AVSVVLDYYTALANI FKEVAKNI DGRLPAGPDWHKDLLTQVGLNLPGLR
PPLLSGETFAEVDLRRFRHLARNI YGFNLKPERVI SLLEKLPELDKKI E
SELSCFLEKYRQEMI SSI I SDNP

>2617921300 Ga0073689_12336 3-dehydroquinase synthase [pelotomaculum Ga0073689 : Ga0073689_123]

MEI VEVDLGARSYPYI YI GAGI LPDLGVFLQKLPVEKKALLI TNPAVNRLY
GHVAADSLRRAGFQVATAGMDDGEEYKNLATAEKLYDLAFEAGLDRRSPV
I ALGGGVVGDAAAGFVAATYMRGVPPFVQAPTTLLAQVDSSVGGKVAVNHPR
GKNI I GAFYQPLMVLADVSALATLPAREVRSGLAEVI KYGVI WSADFFAW
LEKNI EALLNGD TDALVHAVRESCRI KARVVAEDETEQGLRAI LNFIGHTV
GHAVEALTEYKVYTHGEAVGI GI AAAARLAESLGMFEPADRERVI NLI RR
SGLPVDI PGGVSPKAMI DSFYHDKKVTGGRLTFVLPERI GKVI MKRDI DE
SLLLALLHNDI KGCPI

>2617921299 Ga0073689_12335 shikimate kinase [pelotomaculum Ga0073689 : Ga0073689_123]

VKNI VLI GFMGTGKTALGRRLAQRLGREFI DTDAEI ERVTGKTVAQI FAQ
DGMTRFRSEETLLVRKLAGRKGLVI STGGGLVLNPENVLTLKENGVL I AL
TAAPEVI YQRVKSKI DRPLLLKGELKERI VNLLKEREGVYDVAEYTMDTG
VLGQEEAVERI I GFLKERGCV

>2617921298 Ga0073689_12334 chorismate synthase [pelotomaculum Ga0073689 : Ga0073689_123]

LLRYLTAGESHGPVLTAI VEGMPISGLPLTEEYI NRQLVRRQGGYGRGARM
KI ESDAVRFLSGVRGGLTLGSP I TLOVENKDWANWAEI MSPGSGARVDER
TVTRPRPGHADLAGAI KYRHRDI RNVLERSSARETAARVVVGSAAARRLLE
ELGI KI I GQVVL I GSLAADVENLSPEELARLAGSOLLCADPGAEQMI A
KI DRARETGDSLGGI FEI RVFGVPAGLGSYVQWDRKLDGRLAAALMSI QA
VKGVEVGLGFAAAGQMGS HVQDEI FHDRRRGFYRQTNRAGGI EGGVTNGE
TLVLRAMKPI PTLYRPLRSVDLI TKEPF EASVERSDVCAVPAACVI GEA
VVAWELARACLEKCGDSLAE LKDNWDQYLSYLRQV

>2617921297 Ga0073689_12333 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_123]

MMRRFTLTVKVKRGKNNQAVGNTLFRAERTAI RLKTGFRKKDHLVHKRK
LMAEQLNSMRLPPVSRERNLNKSGLLRFOKPG

>2617921296 Ga0073689_12332 shikimate dehydrogenase (EC 1.1.1.25) [pelotomaculum Ga0073689 : Ga0073689_123]

MVNGI SGRTKVCIGI FGHPVEHTFSPAMHNAAFAALKMDYVYVFPVPPTG
LAVAVAAVRALGLAGVNTI PHKESVLPLLDELSEEARLI GAVNTI VNRS
GRLYGDN TDGRGFLRALEGKAGFTPAGKTALI LGAGGAARAVAAQLALAG
VSKLLLANRSRNRAGELAGFI TDKTGVR AEI VPWPEGGGGTLP AEALLEA
ALVVQATPLGMHPNYSETAPLPDFRQGLACDLVYNPLETLFLKKARQ
SGAVAVDGLGMLLYQ GALAFELWTGATAPVEVMRQALAGTVLKKE

>2617921295 Ga0073689_12331 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_123]

MRQFI I TTAEGKLLI GKAMAAHHEI RRALDCGTI LEKHPDGYVAYPLGLK
GVVVEKWDTHYRTTEI TNQFYCLQI CQD

>2617921293 Ga0073689_12329 Group II intron, maturase-specific domain [pelotomaculum Ga0073689 : Ga0073689_123]

VLEV KFPGVTHLLI LCKTREEAEAAALQVADLLNRMKMCLSPEKTVI SSF
QEGFDVLGFHFGKRHVGMGKESLKS VYTKVLEVTRRSQGN I PVEKVI AEL
NPKI EGWANYHRYGNNI VLFKLD R WVRNRI RAYI RRRWRDRGRWKLHLA
EELDRMGLARMERKI SRDRQLKLFESLGS RDSI GAAGCGKTARPVTTGAG
IP

>2617921291 Ga0073689_12327 Reverse transcriptase (RNA-dependent DNA polymerase) [pelotomaculum Ga0073689 : Ga0073689_123]

MRQI LELPFADVI RTVQENLKDYRPTPI RRVHI PKPGKAETRPLGI PNI L
NAFDWSI AKAWEEKPTRFPYTA KSNKI QALRKQGLKPAYLI RYCDDWVL
I TDTKANAEKWKRLQNYLQTRLNLTLSEEKTKI TCVKKSPI EFLGFTYK
VMQSGTARKGHVSRTRPNLDR LKNKI SEVRKQVKRI GKCANL DLAVCQI H
RVNSI I RGLI NYQAATLVNSDLAKYAWDI SRLAYREI EKLGGKWVPAHQ
TNNLMAVHSQYLSMI PAVEYYNRTI GVTSLRFCKWTKTKLKNQDENPYTP

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EGRERYQKRTGKRQALPRNDELLGNHLI EKI ARNRGSPRYNFEFFMNRGY
ALNRDQKGCRI CNI ELNTANI ELHHLQEHPLPLKTLNRPVNLASVCKACHM
LI HSNWDNLKLT KAI QNKLSMRKKVELRLR

>2617921289 Ga0073689_12325 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_123]
MYRQCMEQAVTFI SRAKKMHDEMEKYVVSFMDFEAI NARRGKTLQRI I GL
AAESG

>2617921288 Ga0073689_12324 pyruvate-ferredoxin/flavodoxin oxidoreductase [pelotomaculum Ga0073689 : Ga0073689_123]
MSKDMKTMDGCKAAAYVSYAFTDCAAI FPI TPSSPMAEYVDEWSAQGKKN
I FGQTVKVAEMQSEAGAAGAVHGSLSAGALTTTYTASQGLLLMI PNMYKI
AGELLPGVMHVTARALASHALSI FGDHNDVMACRQTGWAMLASGSVQEV
DLAGVAHLAAVNSRI PFI HFFDGFRTSHEMQKI EVI GYEDLAGLVDYEA
KAFRDRA LNPEHPVSKGSAQNPD I FFOAREACNSYDAVPDI VMDYMKKI
SKI TGREYLPFNYYGSKNAEYVI VAMGSVCDTI EETI DYLMKDEKVGVI
KVHLYRPFSAEYFFDVLPTVKKI AVLDRSKESGALGEPLYEDI RTI FYD
AELKPVI VGGRYGLGSKEVLPSDI MVVLANLKADQPKNGFTI GI VDDVTN
LSLPRGENI DTTPEGTI QCKFFGLGSDGTGANKQAVEI I GNTI DMYAQA
YFSYDSKKSGGI TI SHLRFQKKPI KSPYLI TSADFI SCSNQSYVYMYDLL
AGLKKGGAFLLNCVWTPPEELDEKLPAQMKRCLAQNNI NFYI I NAVQI ARE
I GLGNRTNMI MQSAFFKLANVI PVQDAVSHLKDSI KMAYGKKGENTVNMN
YASVDKGVTEL VKI EI PAVWADAVDEPAAEKEVPTFI KNLVQPMNRLEGD
KLPVSTFKEAADGVFTGTSTRYEKRGVASF I PEWNKENC I QCNQCSYVCP
HATI RPVLLNEEEAQKAPAGFETKPAVGKQLAGLAFRVQI SPLDCMCGCV
CVNTCPAKQKALEMKPLESQKEVQAAANWNYAMTVPVKDNLWNLYSVKGSQ
FAQPLLEFGSACAGCAETPYAKLVTQLVGDRMI I SNATGCSSI WGASAPS
I PYCANREGKGPWANSLFEDNAEHGFI LMGVKQI RDKI AALMKEAMSL
DI SPALKEAFQEWLDGRDDAGTSKAAADKI VPLLEGQTHSVLQEI AGRKD
LLVKKSI WVFGGDWAYDI GFGGLDHVLASGEDI NVLVFDTEVYSNTGGQ
SSKSTPTAAI AKFAASGKTKKKDLGMMAMSYGYVYVAQI AMGADQNQTL
QAFREAEAYKGPSLI I AYAPCI NHGLKVGMGHSQSEMDKAVKAGYWHLYR
FNPDLKKEGKNPFR LDSKEPSGSFKDFLMGEVRYAALKQMFPAEAEQMF
KTEQDARERHET YKRLAQGC

>2617921287 Ga0073689_12323 oxaloacetate decarboxylase, alpha subunit [pelotomaculum Ga0073689 : Ga0073689_123]
MAKVL I TDTTMRDAHQSLLATRMRTGHMI PI AEKHDKVG FYSMCEWGGAT
FDTCMRFCD DDPWERLKVLRRLKKTQTQMLLRGQNVVGYRNYADDVLI E
FI KKAVANGMDI FRVFDALNDYRNI EVAVKTVI DEGAHAQGTI CYAI SPV
HTVEYYVKLARDLES MGCQSI CI KDMAGMI APYVTYNI VKGVRDAGVKLP
I QI HCHYTSGMAAMAYMKGI EAGADI I DCAI SSMSCQTSQPAI ETMVATF
RGAEYDTGLNLKLLTEI AEYWKGV RPNYTEFDLAQKYPDANI LI SQVPGG
MMSNFLSQLSQANALHRLPEVLEE I PRVQEDFGWPPLVTPSSQI VGSQAV
LNI LMGRYKMC TNEVKQYMRGYGRPPAPI NEGI RKMI I GDEKPI DCRPA
DMLPELPKAREVCGAI MEKEEDI I SCAI YPQVAPKFLEERMAKKLKVDI
ELAKQSSEFY PV

>2617921286 Ga0073689_12322 malate dehydrogenase (NAD) [pelotomaculum Ga0073689 : Ga0073689_123]
MKRNKI TI I GAGNVGATAAHWAASKELGDI VLVDVLEGVPQ GKALDLMEA
SPVEGYDCNI TGTNNYEDTTGSNVVI I TAGI ARKPGMSRDDLNTNFKI V
SSVAENI AGYSPNATI I VVSNPLDVMTYAAF KAGGFPPNRVFGMAGVLDS
ARFRTFLAMELGI SVEDVSAFVLGGHGD SMVPVLSYSYAGGI PVSKLI SE
ERLKAI VERTRSGGAEI VNYLKTGSAYYAPSASVI QMAEAVLKDKKRI LP
VTAYLNGEYGAKDI YSGVPCI I GAGGVEKI I EI DLLPGEKAALDKSI EAV
RNLMKI I GF

>2617921285 Ga0073689_12321 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_123]
LLLKTTVRDI I LQLTAVQKVFLNRPPGTI LCRNEMAVKKA FGGLLENLWTC
DCQYRVSLVSRQANDYNRI TAPVYMACKPSPKTALVNGRNYRQMFLDDLK
TGRVYLVENI RENGRIYYVHI TI EEELSVPRTTHNGVVGI DTNPDGLGMSH
ADYLGQLI NQLEAADAI KKTVI FTVKKQTERKLQA

>2617921284 Ga0073689_12320 DNA binding domain-containing protein, excisionase family [pelotomaculum Ga0073689 : Ga0073689_123]
MEKLLTSRQVAKLLNVWPHTLRRWEREGKLKPLRTPGGHRRYKESQVMAL

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I GEEI TESGTHKCAVYARVSTLEQAEAGNLQRQKERLI AYAVEKGYQVKA
VYTEI ASGLNENRRELAKLAKTATKREI DI I VI EYKDRLTCFGYKYLEQY
YQSCGVEI DI VELDEEKSPQEELVEDMI AI VTSFSARI YGKRGRCAVAKKL
TELI EQEAI AAENHG

>2617921283 Ga0073689_12319 Biotin carboxyl carrier protein [pelotomaculum
Ga0073689 : Ga0073689_123]
LRKFKI KVNGEI YEVEVEEI GGNPGCYAAPAPTPAPAAAALPPTPVDATPA
PAPAAASPGFVAPAHKPAVPAAGGGAGAI CAPMPGI I LDI KVNVDGVVNVG
DFLLI LEAMKMENELTADRVGTVEI KVTKGQSVNGGDPLVVI G

>2617921282 Ga0073689_12318 hypotheti cal protei n [pel otomacul um Ga0073689 :
Ga0073689_123]
MSVYRKI TTGI KAEVMVAI TAALVQYGYSLENGYQI NNVI RI GNPWRKAG
I VELMMSRELNREFL

>2617921281 Ga0073689_12317 propi onyl -CoA carboxyl ase beta chain [pel otomacul um
Ga0073689 : Ga0073689_123]
MSMQEKLEQLSKLRDTVQAGGGQERI EKQHASGKKTARERI NMLFDLGTF
KEI DVFAASGGDFQKLKNPGEVVTGYGYVDGRKVYI FAQDFTVVGSLG
RI HAAKI CKVLDMALKVGPVI GFNDSGGARI QEGVDALNGYGEI FFRNT
I ASGVI PQI SVI MGPCAGGAVYSPALTDI I MMVSGTSQMFVTGPQVI KTV
TGEEVSM DALGGASTHNQVSGVAHFMANNEEECI ATLRALLSYLPSNNLE
DPPVFTPVPAI DREI LVDVCPADPNKGYDI RDVI RAVVDGSQFLEVHSH
YAMNGVVGFARI NGQSVGI VANQPKVLAGCLDI NVSDKI ARFI RFCDCFN
I SI I TFMDVPGLPGVQQEYGGI I RHGAKMLYAYSEATVPKI TI I TRKAY
GGAYLAMCSSSLRADAVYAWPTAEI AVMGPGGAVNI I NRKEI SEADNPVE
MREKLVDYQARFANPYI ACARGFVLDVI DPRDTRATI I ETLKNFSTKRE
SRPRKKHGNI PC

>2617921280 Ga0073689_12316 CobN/Magnesi um Chel atase [pel otomacul um Ga0073689 :
Ga0073689_123]
MKI QDTKRQRTCPRNTREVACSHSEPTKI YCPTVCRREKGRRI RPOSPA
ELNDNCRRVAVAFEKFDSEI DLLDCCHI YGVYGGFTVAEQVASGK

>2617921279 Ga0073689_12315 Pyri di ne nucl eoti de-di sul phi de oxi doreductase
[pel otomacul um Ga0073689 : Ga0073689_123]
MKRI FI DPELYAGCKSCQVACMANPANQPRNFVEPERAGRPLPLTCROCD
EPQCAAVCI TGALAI KRAAGGAVRAVVPGGGLVGI EAVESLARNGLRI TV
I EI AEHI LPLQLDWKAARVTRNFKRSK

>2617921278 Ga0073689_12314 transcripti onal regul ator, BadM/Rrf2 fami ly
[pel otomacul um Ga0073689 : Ga0073689_123]
MRLNQATDYAFRAVLYLSRLPRGQVVEARLI AGEENI PMRFLKI FRLLT
RAGI VESFRGVNGGYALARPPADI TMLDVI EAI EGPI KI NRCLI SPEECS
KKFSRKCPVHQALFMVQALAREFSRHNF DALNKKVEENLNLKMK

>2617921277 Ga0073689_12313 ferrous iron transport protei n B [pel otomacul um
Ga0073689 : Ga0073689_123]
LKYLNKEVI VVAHCHGPVGLKNI PKGAKKI VLAGNPNTGKSVFFNYFTGL
YVDVSNYPGTTLEI SHGRFGANVI I DTPGVYGI SSFNDEERI ARDI I LSA
DMVI NVVDVHLELDLFTQQVI DTGVPVI VALNMVDEAERQGLKVDVEL
LSDLLGVPVPTVAVRKKGLDELKGQLSQAQTGHMTPGLEPLI NRQLNRV
GSRGEALLVLEGPVVAERHGLEPESMREEI YLKRREVRNDLVKHVLKES
SKGASI GTLLGRWMI KPVI GI PI LALALYAMYQVI GVFI AGTVVGVTEET
I MLGMYEPAVRALVGQFI PEQSALGAI LI GEFGLLTMTVTYI LGLLMLPV
I GFYFFLSLFEDSGYLPRI ATLVDRLNLGLNGRGVI PLI LGFGCVTMA
TI TTRLLASDRERRI AVL LGLTI PCSAQMGVI AGMLAAVGGWYVALYAL
VI FAVLVI I GTLLNAVLAKSTDLLI DLPLRLPRLDNVLKKTGTSYNF
LKEAFPLFALGALI I SVFQVTGI LEFLQDLLAPLTMGWLKLPKEAATAFI
MGI VRRDFGAAGLADMVLTPLQTVAALI TI TLFVPCI ASI LI LFKERSKK
EAAMI WGASWVAFVLGGVVSQLSAFGGDGSAGI LLI I LAFI GI MLVT
VAACTLAKRGKTRGLAG

>2617921276 Ga0073689_12312 putati ve ABC transport system ATP-bi ndi ng protei n
[pel otomacul um Ga0073689 : Ga0073689_123]
MSLLELQGVSKVYGAVALRDI DLSVEQGEWMAI MGPSGSGKTTLMNI I G
CMDRPTGGSVI LDGKEI STSGSRELTAI RRDKI GLVFQGFHLI PYLTALE
NVMVAQYYHSLPDEKEAMAALERVGLKERARHLPSQLSGGEQQRVCI ARA

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LI NFPMLI LADEPTGNLDETNERI VLGLFQELHREGHTI I TVTHDPEVAE
LAGRCLVLEHGRKTALNKAVG

>2617921275 Ga0073689_12311 putative ABC transport system permease protein
[pelotomaculum Ga0073689 : Ga0073689_123]

VKREKFSLYTRMI FNFLVRRRSRVLAALLAVTI GAAVLSGLVTI YYDVPL
QMSREFRSYGANLALI PASGSRFLPAKDI AAAAALLPPDKVVGMAPFLYE
GVKVNEQPLMAAGTRWVEAKKVSSYWQVKGLWPEESSKDALI GAEVAERL
KLEPGQEI TLLAEETGAQTQI VVKGI VKTGGTEEMVFDLSLLQKLTGK
AGQVSAAYLSI MDNEEELNNOARNLEEKI SGLAAHPVKHI AQSEGTVLGK
LRALVYLVTI VVLLLLTLLCVATTMMTLVAERRKEI GLKKALGAENRGI I L
EFFGESLALGGLGGLGTALGSLFAQVVGLSVFGRVSVFQPALAPVALFV
SVAVSGLACLVPVKI AAEI EPAVVLRGE

>2617921274 Ga0073689_12310 putative ABC transport system permease protein
[pelotomaculum Ga0073689 : Ga0073689_123]

MFWRILQGAI TKQWRGKLLVI ATI ALGASLVTAMLNVALDVGDKMRELK
AYGANI LVTPRTVSLNDLYELKAGSGTSDQYLDEADLGKI KTI FWANNI
I GFTPYI QAKATLDRGGPAVTLI GTWFNHRLDLPTGELLETVGRQLKLWW
EI DGAWVEDADERGALVGSLLARKLGI RPDGGLDLVLAEEERRERLTVRGL
LNSGGPEDEQI FAPLVFVQAGNLEGKVNQVEVSALTTPENELARRAAQD
PESLTRKEWDTWYCTSYVSSVAYQI EEVI PGARAKPI LQVAESEGP I LQK
TQLMLLI AVLSLI SAALGI SNLMTAGVMERSREVGLLKALGATDGAI LA
LFLAETMI VGI I GGLAGYI LGLGFAQI I GRTVFGAAI AMKGMVI PVMVL
AVGVTLAGSLPALRMLRLRPAEVLHGR

>2617921273 Ga0073689_1239 Uncharacterized membrane protein [pelotomaculum
Ga0073689 : Ga0073689_123]

MVI MLQSLI PVI QAATAI SLPPAMLMFLHRQDQGLPAWVWRGVI LGAV
TAFVVVYGLKSGVREREI YEGWVSLAFLGETVLLTLLWRAFKKAFKVP
GCI PGGVLVFLVASVFVLRATGI LFLFNKI FGMSSDFLNTDFMTKFAGI L
LGVLGLFVALAVFRAAAGLTAGVLLTI TTLMLFLVLMGQQAQVVLQVLLA
TGI LPMFRWLLAI MI PLI NNQEWFFYSLLAVVPLPVLNI RWREKI KEG
LNPAEQRKI KASARGRQWGAVALGLSLTLLSTAGKI YANSEAELSKA
NPVTASEGRI QLPLEAVEDGKLHRFVYTASDGTDFRVI I I KKSAYSAYGV
LDACEI CGPAGYYQRKDQVI CENCGVAI NI STI GFKGGCNPVPLEHKI AA
GKI I VQASLMEKEKKRFR

>2617921272 Ga0073689_1238 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_123]

MKRRKNYRTLFFVLLAVI ALLLAGCGNRLSNQPGNEQGGQAVQNADKSSG
SKAETDKKTETNPQKGFQEIPI GDEKEMEGLKI AAVYFQPVEMEPAMGLP
PEKADI HLEADI SATPDNKTGFGI GEWVPYLTVKYKLNLTGQATEGNF
MPMNASDGPYHGDNVKMLGAGKYELTFI I ESPEKQHYMLHTDKETGVEGR
FWQKPLEVKWEFDFVPRKW

>2617921271 Ga0073689_1237 high-affinity iron transporter [pelotomaculum
Ga0073689 : Ga0073689_123]

LRKVTLI LFI LLALI LTWOGTALADSSWGGVVNDI DTVMQOQSLNTYRQGD
VEKAKGLVNDAYFGFFEKEGEMERAI LSNLSGRRAAELEYKFSNI KKMMSN
GEPAPEVERAMAEVLGMLREDAAKMDGPESPVENFLSSFLI LVREGFEA
I LI I GAI AAYLI KSGNNRKVGTVYHSAALAVLASI LTAI LFQMVFRI SGA
SQEI LEGLTMLLATLVLFVSHWMVGKAQAGAWQRYI EDKVQGSLSGSGT
LALGAAVFLAVYREGAETVLFYQALLGNSDSTGMVWLGFALGCLTLGI
FVVI LYGSMKI PLKPFFLGTSI LLYYLAFFVFAGGGVKELQEAGLVGVTPV
PALPTI GFLGVYPTLETLLQLSI LLGAAI GGI YQRLKAPSVKVLPGVAG
RVSPRK

>2617921270 Ga0073689_1236 Predicted heme/steroid binding protein [pelotomaculum
Ga0073689 : Ga0073689_123]

MKKQI LFLTSLSLTMTLLAGCTGQRSQPPSNQSI QGLSQNESSAQAKTD
NGRDASNLMFEFTRELAQYDGTGKPAYVAVNGLVYDVTNNKGWRDGVHS
PWSYKGVAGCDLTYLSKAPASHRQKDSFANI PVVGRYTPSGGPCPKYEE
NK

>2617921269 Ga0073689_1235 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_123]

MSI LVVGADHLGDI ATNLKSMGCHSLTHLKGRKNI HRRNLQI PI GTDLVL
VMTDYVDHNI ARSVRDI AGSLSI PVVFSKRSWAYLSQKLKMKVGLS

Table S2

>2617921268 Ga0073689_1234 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_123]

MNRLLDVGCERQMKVGKKGCGWLTDRDELKALLSRVLTTELRTAI VSSVAM
RSHSKTDARDI ALI WEGFLGAFI GYI MKKGRETGQNLLDGI SFRNI WRR

>2617921267 Ga0073689_1232 Uncharacterized conserved protein, DUF39 family [pelotomaculum Ga0073689 : Ga0073689_123]

MAI EKTYAEI NEKI KSGKAVVLTAEVI SLVEEKGVGAARQVDVTTGT
FSPMCSSGVFLNFGHPKPRI KMQKVLNGI PAYTGI AAVDAYLGVTPELPE
DDPGNSNYPGEFRYGGGHI I QDLVARKPI KLEAVSYGTDCYPRRELETYI
TLDDI NEATLFNPRNAYQNYNCVNLGNRTVYTYMGMLKPNLGNHAHYCSA
QQLSPLLNDPYFLTI GI GTRI FLGGGVGYVAWHGTQHFPGI QKDAAGNSY
GPAGGTLAVVGDLLKQMSPKWLVGTSYLGYGATLTVGI GI PI PI LNEEVMR
CVSVSDKDLFAPVVDYGEAYGRRRI PGNLGYVSYTQLKTGKVTVNGKEVPT
APLSSYPKAREI AGSLKDWI RKGEFLLTEPVKLLPSHKDGI AAKSLEI KE
Q

>2617921266 Ga0073689_1231 4Fe-4S dicluster domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_123]

VAPKKI VLRFSKDI SDKPI I YRLVKDYDLVNI I KANVNPKNKEGTMVMEI
TGEKYDQGLKYLEROGVRVQPLAEVFRNEDKCTSCGACTDI CPTGALHM
ERPSMEVKFDESCEVVCQI CLKVCPVKAMEVR

>2617921265 Ga0073689_12231 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_122]

MSCSSVKHRFEEERKKGLTFORAMELYQDVEGSVAHRTEDELTRANAD
LHEI GHLRQHI AEGEKLI NELKSMKLH

>2617921264 Ga0073689_12230 protein of unknown function (DUF3842) [pelotomaculum Ga0073689 : Ga0073689_122]

VRI AVVDGQGGGI GRVI I EKLLKLYRYPYKEVEI I ALGTNALATSAMLK
TGANEASGENAVI YNAGRVDVI MGSVAI LFAHSMLGEMTPGMAEAI AGS
PARKVVLPLNRCNVDI AGLKGEPLPHLVDEMVS I VRNMLLVEI RKKYGP
LLEKKTESK

>2617921263 Ga0073689_12228 Prenyl transferase and squalene oxidase repeat-containing protein [pelotomaculum Ga0073689 : Ga0073689_122]

LLSRLLAATWLSRRGLKMKSGKAALALLVLVSFLYVTI FSFGVPLRPCF
AGGTLAVAEMAGKAVEFI NGKYCAGEKI DGYTAYVLKLAGEDLAAAKWAG
NPEWTSDSNTLKSKI EKLADLLGDNNSLVTFI TGTQADGSFGPYANEYG
AKAPLOALAAVKADTVGTAVYDQVKSSI DRAVSFYKSGYQSGSTAYDVNG
WNFDYRCVEALAAAGGDLVSVDWVYNGI SLKDAVI ASATAAAKDPTVKDA
VYLAKELTALHAVSPASGHI DTLAGAI I AKQNTVDGQVYFGSSI YDDVLV
LTALGKAGKLDRI DQAKALAYLNSFKHPHTNSWGSPPAGAAWGGYYQEEP
LTAQALTALSFYTGAGDQSDVYQSI RDGLTYLADI QDADTAAPPAQWDS
TFATSETLI ALKSLGKTYNDYAGAASTWMKKSCTKI AQCLLALSQWEDG
TDRDLRLANLLAGRQRAADPGKGSFENSVMWAYI ALGEAGKMSCI DT
AAKAYI LSKQAGDSWGETWGTGYYPDFMSTTQAI RALTYLPDAAGDKQV
QTAI NNGLAYLKGLOQADGGVYSTAMDDPVVDNAELI VTLKKLGKDPAGA
DWKNSAGLTPVDYLLNNTMNEDGSFGASKNVFGAAESLAAYLLVGGGGP
GGGPAPGQDEYSVDI AVVGMNGELLYGPGSAVSKTGRWGLTAMGALDA
TGLNYTDDNGFVKSI DGQANS GMNGW MYKVNGAVPMVSAKDKQVNGKDRI
I WWYSRDMNSPGPEWDSLLKGSAPAGVAGI KTEPEFPALRPSKEASEAL
AQI DRLLGVKQNTTELGPLVETAKTVAVVGGDKLPSRAGI VALKKELAQN
AVDLSRKI EAAKGGTI ADKLGEVGLAI PANTLKSDVSI TVKKASVSDTG
I TAGTGAPPVPADYRLASAVYNFGPDGTSFKEPATLTLRVAWPPLAKPEN
LALAWYDKAGGKI ALPAVVDAGKGLI LARI SHFSDFAVLVKDERKSFND
VNSTTTGWARDAVEI LAGAGVI AGVDGKHYPEPERAVTRAELTRI MVKALD
LPAVDGGATFKDVPDNRWYSGCVAEAVRAGLVKGYEDGTGFPDRI I TREE
LAAI LARALELEEPSGAEI TFTDAGEVSAWAKDSVAAAASAGLI KGYPDG
AFKPOGAVTRAEI AAMVYRALFNF

>2617921262 Ga0073689_12227 protein of unknown function (DUF4430) [pelotomaculum Ga0073689 : Ga0073689_122]

LLLLGLLGPAI YAKKVS KGNAPPVLAGDVAAPSSPENI LPGGEGGSAAAE
AGVSSRSPDEASQSGTVREDEGLTGPSTPTSGKSSPSLAPI DPNNGE
I TVSI AVVGKNEI LFGPAAVQLTKNNRWGDTALGALDATGLPYDI SGGW
SGFVESVAGQRNKGQAGW MYKVNEETPMLAADKKSVRAGDRI I WWYSKSM

NI PPPSWDGLI KK

>2617921261 Ga0073689_12226 Squalene-hopene cyclase C-terminal domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_122]
 MMEI KRLFYALLFVVVTAVLLVSPAAARALPAAGVKPAMDRAAAAYLLMHE
 NNQGRQLTPWSYLALAGCGRDLAGTRVLESCRQQFAGLSSGELNNYSLLV
 LTLLAAGSNPYDYQGQNLVEKI RSAQLPGGKFADNVDGSGLDGKGEQI LV
 NAHI WAVLALHAAGAEI PDAQKAGQWLI DQQHEDGSFNWNLADNEPDVDT
 TGMALMALGALGEKKDNPVVQKASAYLKSVEEDGGFSSWGAANPESCRM
 VI SGLTAVGI DPAGADWTRSGGNPVTALQSYQLPDGSFEHVRGTGSEMA
 TEQALQALTDVYYGKTFFERLREKKI ADATNSGKAQPORI I RFKLGETRY
 EVSTEGQKHVREADTAPI LENGRTLVPVRYLALALGVPEGGI NWFPSSQT
 VTLAHKGVTTLAVGGNI LYVNDRPGTMDVTPI LLPPGRI YLPARYVAEA
 FGYSVLWDEKEQSI LISR

>2617921260 Ga0073689_12225 energy-coupling factor transport system permease protein [pelotomaculum Ga0073689 : Ga0073689_122]
 MLQRFYQEKGLFLOSI HSAVALFYI VVLLALALI FSHPVYLI GIFI VVA
 LTI WAADGLAAWEGYLLKI ALGMVLLI MVI NPLVVRAGQTVLWHGPYLPVL
 GRLTI TLEAI CYGAAMGVRLLDMVSI FCLYNLI VHPDRLLNLSRFAHKS
 ALVVSLAARLFPVMAASMSNI KEVQQLRGVDFQTGTLKERAGKYSALFNI
 LLVSSLEGLSLOMAEAMQARAFGSGPRSCYRREFFRPRDALCLAGSI FSLA
 VSI CGAVHGFNGNYTYPQLGYLFDGSATVTVLVAVLGGLSLPAVLSWGWO
 RCQYLKLLKI

>2617921259 Ga0073689_12224 energy-coupling factor transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_122]
 LTYYYPESTQQALREVNLAFAEGEFLVTGGSGSGKSSLARALTGLI PDF
 YGGKI GGGVFFRGNKI RTLDRRKLAGEVGI VFQDPEKQLVMTGVEAEI AF
 GLENLGLSHPEMFRFVAEVMGFLGLTPLKKEFTANLSGGQKQKLALASVL
 AMQPRALI LDEPTSQLDPMAAEELLNLVKRLNEEMNI TI I LI EQRLECF
 HLADRVAVMEGGRI VREGPPGEVAWQVKNFPPFVPPVAALFAHLGFPA
 PLTVKEGRKI LKKYFLSRGAGEAALPSDRREESGRAVGEGPVVEVKNLWF
 TYPGREALRGI NLVFNAGEFVAVLGENAAGKTTLLKHLAGLLRPGRGKV
 MLMGNDTGH I APOQLARLVGYLSQNPNDYLFQDTVENELRFTLANLGLPD
 GGVVERLLERLGRVHRQTNPRLSSGERQQRVALASVLVAGPQLLVLDPE
 TRGI DYRLKAGLGKLLREI ALEGVAVVLVTHDVEFAAEYAGRVVMLFDGQ
 VACDDPKHI ALAGSMFYAPQVSRLFRDI DGGVLTFREAVEKLRFLPAQAA
 SCGDKC

>2617921258 Ga0073689_12223 energy-coupling factor transport system substrate-specific component [pelotomaculum Ga0073689 : Ga0073689_122]
 LPEYLSKWRFPFLFLLVAGLLVLSTGVESPLTRQNWGLLSAEI VFI AI VL
 LYRGFEKSRVSSREI AI I AVLGTVAAVGRVLFAALPHI QPATFLVI VSGS
 VFGARAGFMVGSTVAVVSNNFFLGQGPWTPWQMFTWGLAGSSGALFRI AFP
 RAGRWSTAI FLFAWGYVYGI MNLWFWTAFVAPLNLQSFLI TYAASFWD
 TCHAVGNVI FYLLCGPGTEKI LKRTKNKLEVSYPARELGEPY

>2617921257 Ga0073689_12222 Adenosyl cobinamide dihydrolyase [pelotomaculum Ga0073689 : Ga0073689_122]
 LFEELTAFNANVPI KGI KFYLVKENTFLI VSLRRLKVLSSAVLGGERRA
 RFI MNHTVENNYSSDPAEDLRLVEKMNLGKDVLLMTAVDVRRTVMSF
 GTRQVLAVATVCTAGVSNACSAGSI VAAHKSMAMPGTI NI VVLI DGNLTE
 AAMVNAVI TATEAKTMALFQAGI RMPDGAMATGTTTDAI VI ACTGRGEPL
 PYAGAATDLGSLVGRTVYRAVAQGI RDYLAANGHEKFERPPGGVLLN

>2617921256 Ga0073689_12221 peptide/nickel transport system permease protein [pelotomaculum Ga0073689 : Ga0073689_122]
 MQI YMLKRLFYLLPVLLGVSLI TFGLI NLAPGDPAELI LRAGGVEPTREA
 VEALREELGLNDPVYI QYGRWLWNAARLDLGKSFRTGQPVSVET LCRFPA
 TLELTCAAMALVVLFPFGI LAALYRHALVDHLTRFGALAGASMPGFWL
 ALVLI YLFAVRLHLLPVMGRGGI DHLI LPAI TLAFGMAATYARLLRASML
 EVLGQDFI RVARAKGLAEKWVI GRHALKNALLPVVMTMLGLSFGHLLGGTV
 I VESI FAWPGVGKFCDAI FNRDYPVVQGYALFMAVVFVVVNLAVDLSYR
 LLDPRVRLGDKA

>2617921255 Ga0073689_12220 peptide/nickel transport system permease protein [pelotomaculum Ga0073689 : Ga0073689_122]
 LHHMSRKVVRRNAFI MPSPARLRLRFADRLAVLGVLLLAGFI LVGI FA

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PYLAPNDPVAVDLGRFLPSSTVYPLGTDHLGRCVLSRLI WGRVSLSTS
FLVLLTI I G I S I PYGMLAGWCGGRI DNLLMRLVDTLAFPRLI FALVI AG
MLGPSLI NI MLALGAVSWVRFARLI RGLVLQVKEREFI LAARACGTSARR
I LFTHI LPNI I GPVVVLTALDMGWL I LGI SGLSFLGLGAQPPTPEWGTML
NDSRPYFQVAPNMLYPLGI MLAVLAFNLLGDGLRDVLDPRGFTRRR

>2617921254 Ga0073689_12219 peptide/nickel transport system ATP-binding protein
[pelotomaculum Ga0073689 : Ga0073689_122]
VLQVNNLTVRYQVTDGSPAVAGVSFTLVRGEI LGLVGESGCGKSTVALA
LLGLLDGNAAVDQVSLSGRQLPLGRATGGFSWREVRGKMLAYVPQDPLT
GLNPVLRVGFQVGEAI QTHRKLARGGVRAEAELELLKKVNI PVPGRAYLSY
PHQLSGGQRQRVLLAMALAQRPOVLVADEPTTALDVTTOAQI LGEI KRLA
SATGSAVLFI THDLGVVAGLADRVAVMYAGRLVETGPVI DVFTDPAHPYT
RGLLASLPRLERNGLAPVPGQPPSLFELPPGCAFYPRCPVAEERCRQVP
PPLLSFDQGWGVACHRYAAALRDNKPAEADDVARLI NQQLATA

>2617921253 Ga0073689_12218 peptide/nickel transport system ATP-binding protein
[pelotomaculum Ga0073689 : Ga0073689_122]
VNLLQI AGLVKHYAPAGLTGGRRQAVRAVDGVSLDVAAGEVLGLVGESGC
GKSTLGRILAVGLEEPTAGSVRFLGREI SNCSGNELRAARRSLQI I FQDPT
TSLDPRWSVGLI AEPLLNYRVGKADRARRVRELLELVGLEPLHAGI YP
HELSSGGQRQVSI ARALALNPGLI VCDEPVSSLDVSNRAQI LNLLRELKE
SMGLAYLFI SHDLAAVSYLADRVAVMYLGKI VEVI QTEQLKSARHPYTH
ALLAAVPEALPGRGI PEAPLI GEPPDPRNPPAGCRFHPRCPGAVETCRSE
EPPLAAVGEEHQVACHLAR

>2617921252 Ga0073689_12217 peptide/nickel transport system substrate-binding
protein [pelotomaculum Ga0073689 : Ga0073689_122]
MHHLKKMLAGLI FLVFLAPI LAGCGNTGGAAGKPKQELVI GYVGFGENGDL
KVMDEKYPDLLI RRTVQEPPLLYLKNGKPAPALAESWEVADGGKDI TFHLK
KGVTFHDGAPFNADAVKFTLERI KFQKGTHPLSFDEKATI EI KDPYTVVF
HMSRPSYETLI GLAEYHLDI I PPTSVEPAGEPAGKMKQCLGTGPWKVKEY
KKGEYVELVPYEEKYWGEKPKLSKLVFKAVPDPNTRVMALKSSELGMVLDN
I HGGI GYVPRSLNLQLEESGYGI VGVDI PSTRAVFSYQKEPFNNPEVRK
ALAYAVDKEALAKAVMGKWWDPALNGVLSPVLPFTKPNQTKWFPYDPERA
KTI LAQQGWKPGPDGI LEKGGKKLSLDI I VSAKELDDKQVVEI VQSQFKK
AGVQVNI KGLESAFDDARKKGDFDLAYFYAGGPECRI FMRYGWQFCSKG
SATAPPI YTDQQLDAI VEKALTTFDDREREDAFVRLGNVYVNAVAI PVF
YDKVFAVTGKNVQGFKNQSDPDFSGVTVGQKR

>2617921251 Ga0073689_12216 Ubi quinone/menaquinone biosynthesis C-methylase Ubi E
[pelotomaculum Ga0073689 : Ga0073689_122]
MSI VLQDKI TRCWDERAAVDNQYGHGLKSEEEKTAWQETLKESVGAGTL
RI LDVGTGTGFLALLLAE LGHRCCTGVDSLQSEMLRQAQKKARQARLKI DFY
GGDAENLPFKECSFDVVI NRHLLWTLPRPETALRDWVRVLKPGGKLI I I D
GRWVAPNI FTKVKRLVGNCL I ALAERRNPCKWKGRYKEI QKQLPFMGGA
GPDKI APLLKAAGLTDVSI QSLTRVVEAQKTTMPLRYRLVYAHQRYLVAG
RKPE

>2617921250 Ga0073689_12215 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_122]
VQLI SDVLPDVLKLVKNVLPSSMLLGCFLGNLFHNTVLLQRLGRGMLPLAR
LGHLPPGCATSLTCLVNRI AAYTMLAELKNTGVVGSREVVSFLVSALP
TGLYFTI FFFSPAVI ASLGCRGTGAI YLAI YLGI NLMVSAVGLLLGRLLLP
RPGRGQEGSEQMRVAVHTSWRDKLVAATRRTI PAFCLAVVFMPVTFVLVS
I LLYTELVGQI LRQVDPVLSYGLPGPVLFVI TTGVMSMI AAI GTLGPVL
OAGLVTPAEAVTALLVTSVLHYLYEFWSGGPLPTNVS I FGPKLGGKVSALAA
LVVRECTTCLALGLVLLLL

>2617921249 Ga0073689_12214 protein of unknown function (DUF4198) [pelotomaculum
Ga0073689 : Ga0073689_122]
MKEKKNVTLCDDTDLVMYGHEPWLEMAAGSHGHAGGSVDVYI KWGHNMQTD
GLARKEGMAVLVAVPGGEKEELPLADGGPDYI I LRFPTVPDGFYHVVAKN
TGSYVLDREGKYHQGTREHPDAVQAVFYNQYAQTFVPVGHDLGGVPQRA
GMPLEI MPAVWKQWRVGEI GLQVQFRGEPLDGAALDVACNGPGGYRQRO
EMTGGDGCFLNQAAGEPGRYL VVARYRVPEGEEGVYDALSLTATLFFFVTK

>2617921248 Ga0073689_12213 extracellular solute-binding protein, family 5
Middie [pelotomaculum Ga0073689 : Ga0073689_122]

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MI I HKSMAI MVI LLLI AGLAAGCSTGRGTGSGSDI NGKSKNVLVKVGWDWDV
 TPTDVPKSAFYQYRAGI LETLVDVDFEGNLKPGLATAWECLSPATAWKFTL
 RGVRFHDTGSMNSKAVKVFVDRLAANSKLI PI SSVETPADNEVVVNTTR
 PFI AMPAYCATSTTAI YAPGSLQDGKFAKPVGTGPFKFI EYTPDKGVYCO
 AFHSYWKAEAPKFSEVI NRYI PEGOTRLMALQSGEVDLI RMVPPAGAKVLA
 GNPDFVVSAPVARTRQI I FNTGKAPLDDLNVQAI NYAI DRKAI VDSVL
 EGYGEAAVGLFPPNLPWGSPNLKGYSYDLNKAGDLLEKAGWKDI DGDGVK
 GKQR

>2617921247 Ga0073689_12212 extracellular solute-binding protein, family 5
 Middle [pelotomaculum Ga0073689 : Ga0073689_122]
 MELI LETYNDRPELPFI AQVVSQSLGAVGI RVKI ETKEYGAVEKSLTAKG
 YDMVLMARGLAFTPDPSVPLDDFKSDSKSTWRPI YANPRVDNLLEQALGT
 TDEKNRKELYKQVEI I EQDAPVTFLSYMQI DAHKKSLQNYQVHPTEAN
 VLTEKLCFKN

>2617921246 Ga0073689_12211 Acetyltransferase (GNAT) domain-containing protein
 [pelotomaculum Ga0073689 : Ga0073689_122]
 MSTDTGVFI KKAGDGDQI QPAMEFAFKMI KEVYGRGI NPVWDHDLNLFEDV
 YI KTHGNAFWAAFTENDKVVGSLAVRRYDGRVRVLEGFYDLI ATAELAKC
 FVDKRYRRTGI GSLLLKEAEQFCKMSGYKLI YLHTHMYLPGALEFWQSRG
 FKVGLDEGGPQQTVMHEKIL

>2617921245 Ga0073689_12210 Copper amine oxidase N-terminal domain-containing
 protein [pelotomaculum Ga0073689 : Ga0073689_122]
 MLSI LI SCLVLAI I FTGGPPASAVTSKQVSVPTVNADSTTSLGTVI VKE
 EYGGSI KEGDCKSFSLPSYVELQTLRI FFPGVDSKSYHPKTPEVTVNYTV
 YSPGDSVSLGI SGI YLQVEDKNRFTLKVANTEGWEI TNTRFCYVYFDLVK
 I KAGAPESEEEVRATMDGTGGFSSSTQTVAKI AAGSGSATASADAPQI TD
 LGGEI ATI VI SENVSRLKRNDTDCKNKNTVKLVLPAGFTWDTVNLLPGW
 GFKAGDI DYTGVGDTSGYSVLFLKVNNETTDI TGRGRI TI KGNVTVDDSI
 ARAGKVEVSYEGTNSGVSPAMLAADYSLPGCGLKEKTTTEVI AGHI NNP
 LGFEI I SEGMAAGDLARGRTI TLTLPEGVKWHTYPTAKSEGNGCGLGAPEP
 VGDDGRVI RYSVDSANTGNDKTVCFSATVDLAVGAPEQI EI SVSGSAG
 VKGKVMVANVPKAPVKLSAVKTNVSAGVVOGQPVGEVTLSEEMPGALRADA
 TGAEAVLELTLPDGVTFEKMPPQVEVAEGDLI LDESGI SLARGDRALVI PV
 EKSGRAASTI KVSEI SLNVNRVI PEGDVTLEVGGTALSETGNLFSDSL NK
 LEVTLATCVTPVPDVTVKTSAVFI I GI TSYETGGI KOEMDVAPYI KNNRTY
 GPVRYI AYALGLGEQDVLWDEATQTVTLRLRGKRVVQLKVGRASVSMQGI E
 VPI DVAPEI I DPGRVMLPYRWVAYALGASVSWNEEKQQVTI QIM

>2617921244 Ga0073689_1229 protoporphyrin IX magnesium-chelatase (EC 6.6.1.1)
 [pelotomaculum Ga0073689 : Ga0073689_122]
 MGSYRCFTFPFPAI TGQEKMKKGLLLNAVNPRLGGVLARGEKGTAKSTAV
 RALAALLPEI EVVVGCPFNCDPNDPARLCHLCRARLSAARKLEKTRRRVQ
 VI DLPVSATEDRVVGSDFEHD I KYGRPRFEPGLLARANGI I YVDEVNL
 LDDHI VDVLLDAAAAMGVNVVERE G I SYSHPAEFI LVGTMNPEEGDLRPQL
 LDRFGLCVQVEGVTDPGERVEI ARRREAFDADPLGFI ARWSEKEQHLKER
 I TAACROLPAVTI APELLDLVAGLSL GALVAGHRADI I MAAAARTI AAWN
 GRTEVI EGDVYEAELVLFHRRAREAPPPPEQPEPPREEQEEPEQEEED
 DGREQEPPEQPEETPPPPEQQDMEPEDQEQEEQEEQEEQEQNTPPPAEP
 QEI VFAVGQTFQVKRI SHDRDRI LRKSGRRSRKTASKAGRYVRSTMQR
 KNNDLAFDATMRAAAPHQAHRRRDGVAI AI EPGDI REKVREKRI GNFLLF
 VVDASGSMGAQORMVETKGA I LSLLLDAYQKRDR I GMVAFKGNTAETLLP
 PTSSVEMAHKLLLEELPTGGKTPLSAGLI KAYEVAKAHLYKDPNI SPLLI I
 I SDGKGNVSVGAGKPLAEARRAAEI I RAEERI KTLVI DVEKNGFLTFGQA
 RELAVAI GAEYYKI DDLKADTLVQAVKGLSDV

>2617921243 Ga0073689_1228 protoporphyrin IX magnesium-chelatase (EC 6.6.1.1)
 [pelotomaculum Ga0073689 : Ga0073689_122]
 MGD FNKVYPFAAI VGQEEMKRGLLLNAVNPKLSGVLI RGEKGTAKSTAVR
 ALAALLPEI EVVADCYVGCDDVTMCAQCRRERLAVGEELPRARRKMRV
 VDLPVSATEDRVVGTLDI EKAI KKGEKRFEPGVLAQANRGI LYVDEVNLL
 DDHI VDVLLDAAAAMGVNTVEREGVSFTHPANFI LVGTMNPEEGELRPQLL
 DRFGLCVNI TGI LDPRLRVEVVKRRAAFEEDPEEFARQWEVEEEDLRRQI
 VAAKALLPAVRI SDEMLFLI ARI AVEMGVDGHRADLVMMKAAKTTAALRG
 REEVTEDDVRGSDLALLHRMRKPFQDLTI DREKLOGVI GGOQHSHPHS
 HQHSHPHTHTHAHAMPGRGDHHHHGH

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>2617921242 Ga0073689_1227 ABC-2 type transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_122]

MI ELRQLAKQYGS I QAVAGLDLKI NRGEI FGLLGPNAGAKTTTI RMLTML
TRPSGGSALI NGYEI TRDLSKVKEI GVVPOHMLNDLELTARENLELHGR
LHKI PRAKROQRI QELLAYVELADRANDLTVKFSGGMKRRLMI ARALMH
PGVLFDEPTVGLDPQTRRKI WDLI RRMNSEGMTVLLTTHYI EEAEMLCH
RVGI MDGGRLI ALGTPAELKKRVGETVVEALNHGDTEYRFFAGREQALEY
AGSLAENVVI REANLEDVFVELTGRKVG

>2617921241 Ga0073689_1226 ABC-2 type transporter, NodJ family [pelotomaculum Ga0073689 : Ga0073689_122]

LKVDYFYTWFWEI I VLRRTFNKFFASRLVGPLLYLVAFGWGLGRSI QMNG
GNYLEFI VPGI I ALSAMNTSFSAVGTNLNMSRLYHKTLDLEYLI API SAGA
FVLGKVLGTVRGLI ASLI I LVLAFLLFGAHLAVNGWFFLVVVLTCFLFST
LGAVAAMVVNSHEDMANFSTFVI LPMSFLCGTFFSPDRLPKVFGYI I DVL
PLTHASYLLRALASGQGLLPVSLTALTVYAGVFFTAAVAARVKVR

>2617921240 Ga0073689_1225 CobN/Magnesium Chelate [pelotomaculum Ga0073689 : Ga0073689_122]

VKKI AAI LWSHTTTMRRAKELLKDVLLKVKVYSARFLDEGKEDLSAALAD
MEQADLVFLYRSAAELI WDELEVAVRNLSKPVVCAHDPALWTLSTVGPE
MI SRCONYYVVGGEENFARMLRCLAAEVLGEQLEYAEPVI LPWEGI YHPA
APEYFTSRESYLEWYDSYRHSFKNSPQTDGLSPASQTALFFTPNVPTVG
LLFARNNWVNGNLAVEDLLI RLLEEKGYNVI PAFCYSLKDAELGTGSGSE
VVRQYFFDRDGRPRI NALVKLLSFFLEARTRTDDFFKRECGLFRRNPFFK
AQRPRLPARNLLLPHGGGMGRRSPGPEPGHRLVRVPARV

>2617921239 Ga0073689_1224 cobaltochelatase CobN subunit [pelotomaculum Ga0073689 : Ga0073689_122]

VSLPEFEGVI EPI FI AGAKREGEMEVVRPVEERCRLAERNKWI EMAQK
PADERKVAFFLHNNPCASVEATVGGGANLDTLESVARVLQRMQEAGYQVE
PPSSGKELI DTI MDRKAI SEFRWTTTDEI VGKGGALKLMPVEEYREWFD
LSPQVKERL TEAWGAPPGEKNGVPAAMVHDGKI I I TGVOYGNVAVCVQ
KRGCAGARCDGQVCKI LHDPDI PPPHQYLATYRYLERDFGVDVAVHVGTH
GNLEFLPGKGVGLSGDCCPD LAI GAVPHLYI YNADNPPEGTI AKRRSYAA
LVDHMQTVMTGGGLYDELAELDRCL EEEYKAKVADTGRAHMLEHLI I EEI
QKTNLDKQI NVEDGHESFAAI AEKAHAVLSVI RNTQI QDQHI FADLPKG
ERRVEFI NSI LRF DAGOEI SLRRVAVGLMDLDPAGLLADQARVSTRHGKS
YGALLEDI DAAAKAFVARFLKGQEV DAGLAQEV LGDTFLCAGALPALNAV
LPRVLDLDARI EASREI EALLSGFAGEYI PAGPSGLI TRGRDDVLP TGRN
FYSLDPHRVPTRAAWEVVGKRLAEKVLDKHLI DTGRYPENVALYWMNCNDI M
WADGEGLGQM FYLLGVRPKWLPNGRVAGI EAI PLEELGRPRI DLTVRVSG
I TRDNFPNCVELLDEAVQTVAAALDEPVEQNYVRKHTLAQLDGQSDSKSWR
DATLRI FASKPGTYQAGVNLAVYASAWKEEKDLADI FVYWNGYAYGKGVF
GKEAFRQLQAGLKTVDI TYNKVVTDEYDLFGCCCYFGTHGGMTAAARVAS
GKEVKTYYGDTREPEHVEVRTLAEVRRVVRTKLLNPKWI EGQKRHYGK
AGDI SKRI GRVYGWEANTQEVDDWI FDDI TRTFI MDEENRRFFEEHNPWA
LEEI ARRLLEAHQRLWNADPEMLEGLKEHYLEI EGWLEEKMGVEVKGEFQ
GGAI DI LTAGEVADWGARMQEI KAKLGS

>2617921238 Ga0073689_1223 iron complex transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_122]

MRLLI QNI CFSYSGSHSVLKGVSMEVAPGQVLSI VGPNGSGKSTLLRCLAR
VLKPQGGAVFLDGREAARI SSRELARLLGYVPQAMGEVFPFTVLETVLMG
RKPHLNNWGVAKKDL DVVAQVVKFMGLDEMARRQMDQLSGGQKQKVF I ARA
LAQEPQVFLFDEPTSSDI RHQLEVL ELVREL AGQKQKQVVMVLHDLNLA
ARFSDRMVMLKDGLI YAAGQPGDVLTPENVGAVYGV EASI KDSALGPYVL
PLRPVAAGPAPLRAAVS

>2617921237 Ga0073689_1222 iron complex transport system substrate-binding protein [pelotomaculum Ga0073689 : Ga0073689_122]

MGLRKI I WSGFI AVFI PSLI LLAGCGQKERPRAGEATI TDSLGNVTVP
RPLNRVVVLNSDAAEAI HI LKAQDAVI GVGD TVQKNPYLGLRDKPVVGKW
NEPGYEKI VELKPQAVI TYSKTPGEELTQKLEPAGI KVVRLDLFKPETYD
SDLRSLAVMFGREKRAEDFI KWKVGNTTAVANSLOGLQPEQKLKVFSI WS
SNFLRGWNKTFARGTSVHQGI ELAGGI NVAGALKDYPQVNPWEI LQONPD
AI VLGTYSDLEDLGYGANDYSNAGKLREKAI KSEVLSRTEAVKKGRVYVI N
TKLLGGDKTYI GALYLGKWFY PDRFKDI NPDQVLKDYFEQWVGVPFKGKW
AYPGE

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>2617921236 Ga0073689_1221 iron complex transport system permease protein
[pelotomaculum Ga0073689 : Ga0073689_1221]

MGLSGI EVDVCGNGGSPGEI QEI YARHAARKVSLAALVFLAAMALLAT
VVGAAAVSI GDVFRVI AARVVPAYOGSVNTLAETVVLQRLRPRI LLALI T
GI SLAGAGAVMQGI LRNPVSPYTLGMSGGASFGAALAI VLGSSFLGPYF
KVAGTYLI ALNAFVFGFLT I LLVYGI ARLKGTAPEVLI LAGVALGYLFSA
GVSALKYFSNNEALKELVVWLMGGMWGAAWQHVEI LI PLVLACMI I LMRY
AWDMNALSAGEEAVNLGVNVNRLRLI CLTVSALAASATVAFTGVI GF I G
LVSPHI CRMLI GSDNRFLI PCSCLMGAALLLVSDLARTI I APTEI PVGI
I TSLI GVPFFLYLLLKKRKCWWS

>2617921235 Ga0073689_12146 MoeA C-terminal region (domain IV) [pelotomaculum
Ga0073689 : Ga0073689_121]

AREGGQAVI VETGGQSPAGVKERLKKLLKQADLVLT I GGTAAGAGDRAL
PLLREI GARVLFWGVAMKPGSHSGAAVL DNKI VI SLSGNPAACAVGYHI L
AAPVLCALQGLDPPHPI SARCADPFPRGGRRFI RGFATCRRDGWRVN
LLPGQKSSMLRSLI ECNVLVDLPVGHPPLEPDTEVSLLPLVPLPTGPCRT
GFSPEGRSCR

>2617921234 Ga0073689_12145 MoeA C-terminal region (domain IV) [pelotomaculum
Ga0073689 : Ga0073689_121]

MTEGVGASRFI RGFATCRRDGWRVSLPGQKSSMLRSLI ECNVLVDLPAG
HPPLEPGTEVSLLPLVPLPYGKGNNDEGNE

>2617921233 Ga0073689_12144 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_121]

MKETNDRI DVI EQCLNLSLLDDRHRQGI I NKVTVKLLLEGYPEGKALSMF
FWELADLEPPVTNEEQMFRTLHRMFHTCGEI KI NCREAAFEALKI PKER
LDLPPEELVKEAKI AYWEQFNNLARDPKSLFLNAREI ALKKKAFSFLQQN
I PPAGV

>2617921232 Ga0073689_12143 molybdenum-pterin binding domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_121]

MDLSTRNRLKARVKEVKTNDI SAEVLLDVGGQEMCSTI TTGSVKRLGLKP
GDEV I ALI KASSVM I GK

>2617921231 Ga0073689_12142 molybdenum transport protein [pelotomaculum
Ga0073689 : Ga0073689_121]

LYI LDECI ERFI KEDVPFI DLTTLVLMGGTEGRI QFHSREKAVLCGTEE
VLR I FKKLNI KAVSYLPSTLLEAGETFI EAGGKAADLHMAWKVSANI LE
YCSGI ATRTRRMVDRAKGI NPGI TI VSTRKI FPGTKELATKAVVAGGGFP
HRLGLSETVLI FKQHLNFLGSLDGLFKI VDEVKSKAREKKI I VEVENLGE
ALKAYKGGVDGI QFDKVPSEKLGYYVEEVRSI NQDVVLLAAGGI NENNVE
DYAETGVDAI VTTSVYFGKPVDI GAVI TRLESGK

>2617921230 Ga0073689_12141 molybdate transport system ATP-binding protein
[pelotomaculum Ga0073689 : Ga0073689_121]

VNVALLEVEGLRVDVGRFSLQDI GFSMARGEYVI I LGPTGCGKTVLLES
AGLRPLEKGRI FLNGGEI THLPPEHRRLGFAVQDSLLYPFLNVEENI LFG
ARARGI AGDPEVLGRMNRLVESMDI AHLLGRYPRFLSGGEKQRVSLARAI
LTHPPLLLLDPLSALDPRTI AMQDLLREHRSEGLI I HVTHDFSEAL
QLGTRLI VLNNGRI EQDGEPLDI FFHPATI FVAEFLQGENVI RGTTI I RD
GRFWFKHPESP LLLGLPI SSTAGGEI KPVLF I RAGNLI VDRSPESLVKA
SVAVNKWTASI YHVTFNRTDVDVYCNGNGQWQASLSLARWRELRLSVGDR
VTLSVGPEDLHVI PQP

>2617921229 Ga0073689_12140 molybdate transport system permease protein
[pelotomaculum Ga0073689 : Ga0073689_121]

MI NFRFGI FQGLFWLVFI LMTI FMLALLGGLFLYGKWDDFLT VLRHPEFH
FAVGFTLWTTLLATFFAALAAPCGFVLSRYEFPKGKVFVDTLLEVPI VLP
PLVSGVALLI LFGPVLGDTLARVGMDI VFSTSGVI VAQWFI ATPFAVKTF
KHA FDSI DPRMERVARTLGYSPGKVFRLRTVPLAKSGI I GGLTMTWARAL
GEFGATAMLAGVTRLKTETLSVAI FLNMSI GDI RFAMATAVI MLLVATVL
LVI FKCPSGSEVRL

>2617921228 Ga0073689_12139 molybdate transport system substrate-binding protein
[pelotomaculum Ga0073689 : Ga0073689_121]

MNGFAKGAKI LSSMLVMLVFLGGCGGAPPKEAKTAAPQGQEPKAPLFAYI

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GAGLKEPVTELAQMYEQKTGVRI EMTFNNSGALLNQLETA KR GDI YMPGG
MPYVEMAENKNGHI AEMAGPI AYHVPVI ATPKGNPAKI SKI QDLARPGI KL
I MPEKEATALGKTAFKI FDKI GI DKEVEKNI I AYVETAPKVPAMLLLGQG
NAGI AEYSNI SKNLDKDLVEI DPALNMVEEI PCALLNYSSRKEQAGDFL
EFVKKEGPAVFKKHGFKTVI

>2617921227 Ga0073689_12138 molybdate transport system ATP-binding protein
[pelotomaculum Ga0073689 : Ga0073689_121]
MFEAVFTKKLWHFTLDLNLQVDNWI MVLWGPGSGAGKTTVLNCLAGLVKPS
TGFIKI NNRI LFSSGDRI NI PVRFRNI GYLFQDYALFPHMTVKQNVLYGL
KCGKHARGKSI PDPLGLLDSFGVGHVLDYPRQLSGGEKQRVALARALVV
RPELLLLDEPFSA LDKATKQNLRRRELKKLHRQWQI PFVLVTHDEEDASFL
GDRI LFLEKGQSRESVPQAL

>2617921226 Ga0073689_12137 molybdate transport system permease protein
[pelotomaculum Ga0073689 : Ga0073689_121]
MFLQLNDWRPVFLSLRVA AI ALAAVTCLGLPLARLLARREFPGKDVLEAA
LTLPLVLPPSVI GYGLLLLI KGNLLGKTLAGMGLSLI FTWWAAVLASTV
VAFPLMYQSAKA AFKSVDI NYEKAARTLGAGEI RTFFTI TLPLAWPGI MA
GLVLSFARALGEFGATLMVAGNI PGQTQTVPLAI YFAVETGDNVTARTLV
I I I TLFSFAVI FWWNRRARRQNY

>2617921225 Ga0073689_12136 molybdate transport system substrate-binding protein
[pelotomaculum Ga0073689 : Ga0073689_121]
VKKPLFLAGLI LI MAAVI AGCGGGKQPGATAEPVKLTVSAAASLTDALGE
LKTIEYEQRDNI I TYNFGASGPLQKQI EEGAPVDLFI SAGKSQMDTLAG
KGLI HEESRKDLLGNELVLI AGKDSSLSGFDGLAGADVSKI AVGVPE SAP
AGMYARETLTAMKLWDKVQPKLVLA KDVRQVRLRYVETGNVDAGLVYRSDA
MTSDKVKVVAAPDDSHKPI VYPM AVI KSTKHQKEAGDFTSFLQGGEASR
VFGKYGFKTMGTR

>2617921224 Ga0073689_12135 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_121]
MEGFYPALPAALLLVAVLTALSLGLHFFLEKLLPLRRGDGPDRPREEEAR
SVFEEALL

>2617921223 Ga0073689_12134 putative molybdopterin biosynthesis protein
[pelotomaculum Ga0073689 : Ga0073689_121]
MQEEI SLTPEEVARI LKI ARNTVYELI KRGELPAYRVGRKFRVDLKD VET
YKKQGGKTEFAPEPAPSPCRTLPLQAKVPLMEELHPSQGLVI CGQDVLLD
I LTRHLEKHPDGVRAFRHHVGSFTGLLSI YQERAHMAAVHLWDGDSGI YN
I PYVRRLLPGVPAVI VHLACRMQGFYVAGGNPKEI KDWRDLTRPDVRFI N
REKGCGRVLLDEKLRL LGI DRRLI NGYDKEEF SHLAVASAVARGEADAG
LGSEKASMQVRGI DFI PLHKERYELVI KKEDFEKPRFQTVI EI I RSGEFK
AELRGLGDYDLTETGKI VAEV

>2617921222 Ga0073689_12133 pyruvate formate lyase activating enzyme
[pelotomaculum Ga0073689 : Ga0073689_121]
VHEALYYEKKEONLATCRLCPKMCTI REGKTGFCRVRQNHGGTLYTANYG
KVTSYGLDPI EKKPLYHFYPGSFI LSF GTTG CNLR CGFCQNW TI AHGDPP
ASDLTPEQAVDLARRQI DRGYPNI GI AYTYSEPFMWYEFVLD TARLAQKE
GLKNVLVTNGYVNETPLREI LPHI DAMNI DVKGFSDKYYRENCAGRLEPV
LRTVEI AYRECHVELTLLVTGLNDSEEEI TRLVDWVASLDREI PLHFSR
YFPNFEVDLPPTPPETLV RARKI ARKLSYVYI GNAPQLDAGGTVCPECG
GELI DRAGYSAWAI GLAGGKCRNCGRKI RI AGEVRG

>2617921221 Ga0073689_12132 Uncharacterized membrane protein YsdA, DUF1294
family [pelotomaculum Ga0073689 : Ga0073689_121]
LFTYLLI VNLAGLLL MWFDKARARAGTGRAPENKLLLLALAGGATGVFLG
MWLFRHKTRHLKFTLGVPLI I VAQTVLI GLFREVG I LRQHFA G

>2617921220 Ga0073689_12131 uncharacterized protein, PH0010
family/AmmeMemoRadiSam system protein A/AmmeMemoRadiSam system protein B
[pelotomaculum Ga0073689 : Ga0073689_121]
VTVI YCGI CPHPP I VVPEVGGA EAKKVATQRALLELGGRVKKSGAETVV
I I SPHAPVFRDAVG I NMTPALKGDLGNFRAEQVRFELANDLALAKTI REQ
AAGLGLTVVELDREVESEYGI RLRLDHGVA VPLYFLRKAGVELPLVHVAM
AVAPVEKLYLFG LAVRRAAEALGRGTVLLASGDL SHGLTPDAPAGYAPRG
EEFDREMARLLAGPDAAGLLNMDRSLVREAGECGYRSI I MMLGALDGYDV

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KAEVLSYEGPFGVGYLVASYEPLGVNPERSI LAEMQAGRRERMQRHRAGE
SFLVKVARETLERRLKGPPPEVAGI PEEFKGRAGVFVSI KKQGELRGCI
GTVEPTRTNI VEEVI DKAWSAGLHDPFRYPVGVNELDDLEYSVDVLMPE
PVAGLDGLEPKKYGVI VQAGRRRGLLLPNLDGI DTAGEQVAI ARQKAGI G
PDETVRLERFEVVRYK

>2617921219 Ga0073689_12130 Malic enzyme, N-terminal domain [pelotomaculum Ga0073689 : Ga0073689_121]

VCLAAQEPRQI I ETVVACAPAFGGI NLEDI AAPKCFEI EEELSRLLDVPV
FHDDQHGTAI VALAGLI NALRVVGREMTGVRVVI SGAGAAGVAI TKI LNS
AGVRDI VVCDRKGAI TRDNLDPQPAKRWI AENTNGRRLHGSCLKDVLGTAD
VFI GVSQPGLLGREDI MRMTDRPVVFALANPDPEVDFGEI HDVAGVI ATG
RSDYPNQI NNALAFPQVFRGALDCHARTI NEEMCLAAAYALAGI I GEAE
TVENI I PSVFNDQVAPAVARAVYETAERTGVVRKI LDDDRGDSGI

>2617921218 Ga0073689_12129 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_121]

VAI PNENLVAI NI FPAATRREEENFRFYGI KYRPDFSDKEHDLVAVVGQI
PPAAYRVHKLLVHSNVLKTPGLI RELTGRRWAAVPVGGEAAELPKI ERL
WHLPTDI YI AACRPKTGPI PLEKQLKYLASDDI LVFYTLKEWWKNNRLGF
HQALKEYRNYLAGYYGRI RALRETDKNI DVRVGLVDEMCRYMAENNLSPD
EPLSWQEAARRMEKPQRPLCEEFPFPGPVGAI GEEFSAYI TFHSYDVSTG
NLTYI SALI ENNGNVI NQFLLWNTGVNDLLEDI DMI GSI LREYGVTRRQY
DYNLI PMLGVD

>2617921217 Ga0073689_12128 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_121]

MADREFLKTFFKEKKADREFLKTFFKEKKEEFEKHLRQGD LKI KPGRGRSVR
SSERLLDWFEEKWLESED LAEERRKAAPAMPFDVFLNQVMELAI KYLGEKD
PVLGAALAEARNKVGGKSWKLYSKSWKI LNI FEDPEVFYRI GKTPRKGT
Y QGRELLVI ELVLDGRKKQTFPLMERKREI EEKLGATLERELPRVEATGK
YRFKLFLPFELAYSGEAGAVAEKMAAMVLCTRAVLNELGI V

>2617921216 Ga0073689_12127 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_121]

LYRFI RFLNRRFYKWWGFLFFYFGWCKNLAWLSSRQDTAPFTFEFGI RDLF
PCPI CPNEFTFFPSGTSPSI DFTRLCDNI HRLI EYKQVYNI

>2617921215 Ga0073689_12126 possible tyrosine transporter P-protein (TC 2.A.45.2.1) [pelotomaculum Ga0073689 : Ga0073689_121]

VHDQTOQVVI ATAVFLI TYAVI VSEKI HRTVAAFVGAGLVVMLGI I DAEKA
VHAI DFNTI GLLVGMMI I VGI TRQTVGFYELAVKAAKGSMGEPLKI I AAL
SLVTAVTSAFLDNVTTVLLI VPVTFAI AKQLELTPI PFLI AEI I SSNI GG
TATLI GDPPNI MI GSATGLGFMDVFN LAPVI I I YVLT I FCI QVI YRKK
LVTRPELQAKI MELDAKGEI KDAVLLRKCLMVFLTVTG FVLHQYVHLES
SVI ALAGASLLLLI TRDDPEHSLQAVEWPVI FFFI GLFVVVGAL EEEVGI
EAVAKWLSLAVTGGNMVPTGMLI LWLSAI ASAFVDNI PFVATMI PLI QDMG
RLGGI ADLNLFWWALS LGACLGNGTAI GASANVVVI GMAEKRGHQI SFV
GYMKVAFPLMLMSI VVSTVYLF FWYLFHTRI VMAVTLGVGLVLALLLKPV
TRLLI RDESTGSRVKHF

>2617921214 Ga0073689_12125 solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2/3/5 [pelotomaculum Ga0073689 : Ga0073689_121]

MTTEWKRI VFLLLGMGLLLMFNFMPQLSPA VDPAGKVFELPKAGQSALGL
FLLAGVWWVFEVI PI GVTSLAI GLLQPI FDI RPAKDAFRDFMDPTVMFI F
GSLLVGLTFSKCGLTRKI AYKMLAI VGEDTRKI ALGVFI I TALLTHLMAH
TAVAATMFPI LLAI TSLYGEGERPTKFGKLLFI GMAYVAGAGSI CTMLGG
ARNPAAVGFFKEFTGQDI SFMEFSLHMAPLGWVS VFALFFMLI LI YRPEK
TRI PGLRETARDLSRQLGPMTRQEI FVMI VVALALLALVLQAAVPALKNL
DRSI PMLVAGLLFFI TRI LTVEDLEKMI PWNI VLLFSGAMSI GFALWKTG
AAQWMAI KWLALLQDAH WLFV LGI AVLVI VMTNFI MNVAI AI TLPVAL
VI AQYLG VNP ELI LYI ATAAAGMPMLLLI GAAPNAMAYESKQFSTGEFFM
SGI PGTI LVLVI MTVFI FTVYPLLGLNPLI K

>2617921213 Ga0073689_12124 Signal transduction histidine kinase [pelotomaculum Ga0073689 : Ga0073689_121]

VSLRLRLTFLYSGVLALTMLFFGALVYFFMLHNFTAEADWAVAETAEDLV
RSTKI VGGGVPLRHHVLPD VDF AAPNTYI QVVDRTGAVAAQSDNLGGQ

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AMPLSEETLRQVVRGRGFYETVMSGEQSI RVYNRPLVLNGQVFGVLQVGR
NMGLAEAAALNRLRLLLAAGGGLTLLLAGTLGWLLAGAALRPMERI TETAL
TI QKGHDLDRI DYSGPGDEVGRLAETLNQMLERFQKAYRSLEEAGAVQR
RFVSDASHELRTPLTI I RGNVELLKKMGDAEPEI REEALADI AGEAERMS
RLVSDLLALARADAGFRPDMSTVEAGPLLADI FRRAAVLTGEANFEVEGV
ESLGGVYI KANDDYKQLFLI LLDNAFRYTVPGGTQVCCGLREDRLEI G
VSDNGAGI SAKDLPYI FDRFYRADSSRQDGGTGLGLAI AGWI VERHGGAI
EVASKEGVGSTFTVRLPVSAAP

>2617921212 Ga0073689_12123 two-component system, OmpR family, response
regulator MprA [pel otomacul um Ga0073689 : Ga0073689_121]
LPCSRGCGTVPLDTAALPGVYPGGHGFPI CRLRQGGFFETRI YKI LKY
RREGVI FMRKI LVVDDDKKI TALLRRSLVFEGYDVRAAAGGEEGLRI AA
SWNPGLVVLVDVLMPLDGMVEVCRRLRAGGNI PI LMLTARDEVADRVKGLD
LGADDYLMKPFAL EELLARI RALLRRKKPGEATLQPLNYAGLVLDHTTRE
VRRDGRPVHLTAREFDLLALFMEHPGOVLTRDLI MERVWGLDFEGESNVL
EVYI GMLRQKLEDGGGKRV I QTVRGVGYVLKE

>2617921211 Ga0073689_12122 Do/DeqQ family serine protease [pel otomacul um
Ga0073689 : Ga0073689_121]
MGRFFKFPAEKI VVVFLVGVLVAAGVFAGSI HGFPHL SWADELNPGAAQS
APLPGLGPD TI PD I VSRVSPAVVRI NTVTERSGGGQI DPFFNDPFFRHFF
GDQFRVPAQPEVSRGLGSGFI VSADGYI LTNEHVI TGADKI EVEVAGRD
PYQAAKVGADHDLDAVLKI DAGGDLPTVPLGNSDSI RVGDWAVAI GNPY
GLDHTVTVGVI SAKERPI TI GDRRYKNLLQTDASI NPGNSGGP LNLKGE
VVG I NTAI NAQAQGI GFAI PSNTVQAVFDDLAHKGGVTHPWLGVYLOQVT
GDVAGYFGLQE QK GALI ASVI KGSPAGKAGLQRGDVVRYNGVEVTNPND
LTGQVEGATVGSQVEI QFI RQGQTQTVTATI EAKN

>2617921209 Ga0073689_12120 magnesium transporter [pel otomacul um Ga0073689 :
Ga0073689_121]
MI KTYYYSFTEKRMHYHVDI EKKDDI LKHEEDLLWVDLYKFTEQEI KSV
KVFDFHPLAVEDCLTYSRAKLDNYENYFYVMHALRYEEEESEEEI VLVQ
LSMFLGQNF I VTVHNQTLPLVGR I AKCSI KDPRYLEKGMEFFLYSI I DGN
TDEI FPI LDRI GVRI DELEDEMYEQPSKEVSEEFMSLKRTVLT I RRAI I P
QKRI FTSI NSGGHPYFDI REEI KPYFLDLVDHMERI TDSI DGYRDLVDAS
LATYYSLVSARTSETMRVLT VI STI FMPLTFLTGF FGMNVPLPYQSLI VS
TI SI TAGLFVSSMLAVFKKRKI

>2617921208 Ga0073689_12119 NAD(P)H-dependent flavin oxidoreductase YrpB,
nitropropane dioxygenase family [pel otomacul um Ga0073689 : Ga0073689_121]
MKFPK LKI GDLTPRYPI I QGGMALRVSTAPLAAAVANAGGI GVI GATGMS
LEELKNEI RSARRLTGGTI GVNVMFAVRQFASLVHTAI EEKI DMI FTGAG
FSRDI FKWGREAGI PVVSI VSSAKLARI AENQASAVVAEGVEAGGHLGT
DRSI EEI LPEI ASSI KI PVI AAGGI VDGRSI AKMI RMGASGVQMATRFVM
SVECAVADAFKKMYLKANVEDI VI I SSPVGLPGRALLNTFAARI LGGDAP
KPEECTGCLKDCSREYCI I RALENSRI GRVDEGVVFCGKNVYKI KDI LPV
QEI FNNLI REFES TV

>2617921207 Ga0073689_12118 hypothetical protein [pel otomacul um Ga0073689 :
Ga0073689_121]
LETLAAYLKDNLLGLTGTLGI I NLCLMFRGELAKKHLQI EI ADLEWCTL
REI EQGEFFSCKGPDNGAQDGEFHLDI YFYNP GAKVMLI SEVTMEVRVKD
VNFI I LKLHDATI NPPDLI ELMPGARAHKRYTVKMSNKLFI CREVGRFEN
YRVQI KARTSDGKLYKKRI R

>2617921206 Ga0073689_12117 Nucleotide-binding universal stress protein, UspA
family [pel otomacul um Ga0073689 : Ga0073689_121]
MFNKTLMATDGSENALRAARYAAALMKNNPNMSI TVLTVRSPSDNLTRFY
PWTS PQEI EAGI QKMAENAVKRTKEVFDEAGLQVDTDI I GGDPGKTI ASY
AKEKGFGQI I MGRGLSDLSGI I MGSVSHQVLHFAECPVLLVK

>2617921205 Ga0073689_12116 Predicted nicotine N-methylase [pel otomacul um
Ga0073689 : Ga0073689_121]
MEKFQKI LHLRGVNWLVEAKEVVI PLPGRELRLALVRDVEALI TDPGDED
KVP C WAEI WPAAWGLAAYI CDRLSFAGENLLELGAGLGLPGVVYGLK GAR
VTFSEFNPLALEFSARNALLNGLEHFCCLSGDWRRFPAAEKYEWI VGSDI
FYDPKLNPHLAGVI KACLAPGGRLLLAHPGRPVRF EFVRGLVEDGFGMEE
EALLSVYI EDPYFPYIEI RI NVLRR

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>2617921204 Ga0073689_12115 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_121]
MRKFVLI VVI LFSSLLTCPGEGSGEGQQGGWDPMTLEERRQALADQASLA
ERERELAAELLAWDVKI EAARREOERLROEI PAVERSLAGAEAGLAESGA
RLDGGMERLGRWVNFYRYGAVSYLEVLLGAVDFNQFVERAEMVGM I AG
QVRMLDEVREAVALKREQALALERARAELAAKSSLLAENLKEMEEAKAGR
GAFLAEI GQOSAVLAAKVARTETLWYRSLDSLHYLLTHLDVLPWRKLPD
KVAFTGKGLRLEVSEGI NRTFFEEGDAKLAGLSVRCAPGLFTI SGEAPE
GAGFRLDGNFVPAREGKVRFPQPNMYLAGTPVSREVGVSSERGMAMDF
GGYLHGYSI AGVRAEERKLVVTLGN

>2617921203 Ga0073689_12114 ABC transporter [pelotomaculum Ga0073689 : Ga0073689_121]
LKQDVLI EAENLTKVYGKGESMVKALDI GKLEI RRGEFI ALTGPSGCGKT
TLLNLLGRLDRPTGGKI YFEGKNI TGLGETALCRFRNRKVGFI FOAYHLH
PALRALENVMAFAFLGGGYRRRALELLGLVGLTGKEGRRPGTSLSGGEQQ
RGHRPGAVAGPGTDPGGRAHGQPGHGQRVGN

>2617921202 Ga0073689_12113 putative ABC transport system permease protein [pelotomaculum Ga0073689 : Ga0073689_121]
LSEVRLRNLSLFI FSVQNAFRKKAVAALAI MGVAFGTALMTLLFSLAAGM
EHRAERTLSELSNRI MVTSRDAI FGGLFLGMGTPI PASYVEAVKNI PHV
ERVNSQI SAI LRPEKVNYYMPLYGYAAGEAYAPAGSPYKNI I EGRVPEND
DEVI MGKSLQEYLAFNLTPFEI GNRYPFI VMEKGQAQETLLKVVGVYQTG
NEVLDGAFSGSEKLARAMGKVPEGRVSAI NVMVDELANVEPVARAI QQEL
AGEKPEVQVAVPREVLNPVKVLDVFGKFLLAI SLVAVVAGGLSI MVVML
LSVVNRMREFSI LKALGWTPANI I FMVLVESLVLSMCGAALGAAMGYGGL
AAARALI AADI AYLSWRVTAGVCLAGI LI GVAGGLYPAWRANSAAPAKVL
REV

>2617921201 Ga0073689_12112 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_121]
MRGLFCLQI VTAHKDGI TLGEFKKLFGDPAVLNVNLKDNSSGNTYNVSLT
ITLP

>2617921200 Ga0073689_12111 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_121]
LKLVMTGVSFYSI RYPYKSQNI GPMESDAKMNLDFENHI NDTI LARGWEY
YRGDCI KSI KKKDKNYTAI VAGTYDYNVI I GLGDEGVI LSSDCDCP

>2617921199 Ga0073689_12110 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_121]
MEQEHLCGRKQVVEKKTANI QLVKKMVDRSNI MSI LLYEI KAGI PLGKT
VNI LSNLCRYEGKASASGTI NLADI SLKKLAGLARI SEAELODSLDFLHR
NGI I I YKPVAGPES

>2617921198 Ga0073689_1219 CRP/FNR family transcriptional regulator, anaerobic regulatory protein [pelotomaculum Ga0073689 : Ga0073689_121]
MNKI LCMKDLAI FSTLEFLEREQI GRLAGKKVYRKNEFI FQEGEPADSI Y
LI KYGRVRLFKVSGGKEI TLDI LKEDGI FGENTFFEDSEHTMSAQTMED
TFVCSCKEHSLLLKNPRTALKI I QLLGKKLNDYTEKVASI AFRDVKGR
I SATLMRLAKEYKPSPOGTTI DI DLTHQDLANLVNASRVMVTNVLGSLR
REGAI ETRGHRI TLLSWDKLSKAVEAV

>2617921197 Ga0073689_1218 Protein of unknown function (DUF1638) [pelotomaculum Ga0073689 : Ga0073689_121]
LPQPCGI PYFTYLKAALHVDKLAGSLNNALDDLGEKGI I MVI GDQCLP
NMEKVAAERGGI LLKGKNCI EMLLGDMAELDEAKTFYLTGGWLENWRQ
I FI EGLKWDEVDARQNFQYYDRI LLLDNGLAPI DEEKI LEFYDYAQPVE
I MPVNLDNLRNLLEQALKRHWTEV

>2617921196 Ga0073689_1217 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_121]
MGCAGCGTDCAAVLTQEI KDVSQSFAFVPI TTVSREGQPHLI VVGKVKEI
RGNNTLVFGVYKMKTRQNLAEANGI I QAAVAEKKGYRFSGKGQAEDEV
ILTVDKVELL

>2617921195 Ga0073689_1216 Ribbon-helix-helix protein, copG family

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[pelotomaculum Ga0073689 : Ga0073689_121]

MLPHSPLKKI TFALPOPLLERLKTLAGENKI PSVNAAVREAL EEEYVARLE
KKDWGRSAAQ

>2617921194 Ga0073689_1215 processive 1,2-diacylglycerol
beta-glucosyl transferase [pelotomaculum Ga0073689 : Ga0073689_121]

LSKGLKLI FSASYGEGHAQVARALQCFHNRCVSSVKI VELYGEAHPVI
NTVLRYYAYLKSFYI APSVYGLWLYSSRRRTGSDSVFSKLLNSFGSKKLA EI
I MAEQPDAVI NTFPPPAI SEFRKKTGI TIPTYTVI TDFTLHHRWI HSEID
KYYVATGDLKNEMANTGI PPERI KVSIGI PLRETFTEFKDI TGLHQKYGLN
PAQRI VLVMGAYGGLHKI DQI CQSI LAASDCEI AVVCGKDKHTERKVKI
NFHDCKSVHVFGEFVEDI HELMKI SCCI VTKAGGI TLSEAVAAQLPI I I FN
PVPQGERDNALYFTKKKAAVVI DQARKFPGQI SKI LLSEDYLSRI KPAVN
SLOKYRATETVDDI LNELVKKRGI SNVI KNPCLI AGSI NAR

>2617921193 Ga0073689_1214 O-methyl transferase [pelotomaculum Ga0073689 :
Ga0073689_121]

MTKAESLMNVPFELLI LGAAVKAGI IESLRKQELTREELAAELKADARAV
RI I AEALVETGYLARKGSTLALAEETKKMLYDPAAPEYTGFAFMHRYNMI
KSWLNLDPDI I SRGRPRPRDFAPEDTAYFMAAMRQALKSAPDMAEFLLGG
SGGARVLDVGGGGLI YAKAFAGLGAKVTVDLQRVVDLMGEDAKASGI E
MVPEDFNVALPAGPFDLVFLGNI CHI FGERENRELYRKS YGVLD SGGRI A
I VDFVRGANPFAAVFVGNMLASTVNGDAHTLDQYTEWLEAVGFDGVK LDA
AGGRQI I TAYKRQLF

>2617921192 Ga0073689_1213 glutamate-5-semialdehyde dehydrogenase [pelotomaculum
Ga0073689 : Ga0073689_121]

MDMNELARRVKKASI KLAGAGTELKKNKALAEI AASLEKNKEEI I RANRED
LRRSEKENLPAPLLKRLKFDEAKI RDVVDGI HSLI DLEDVPGKTLSTEL
DDGLELYKVTCPI GVI GVI FESRPDALVQI STLCLKSGNGVLLKGGSEAR
ETNRVLADLI I RATEEACPLNLWLALLETRSDVSEMLKMDRYI DLI I PRG
SNDFVRYI MDNSRI PVMGHADGI CHLYVDEAADI DMAVRI AVDSKTQYVA
VCNAAETLLVHERI APDFLPALWKALESKGVELI GCPKTCABI PATPAAE
EDWKTEYLDYKLSVKVVSGLVEAI DHI NTYGS GHTDSI VTGDGEKAARFM
DYVDSGNVFWNCSTRFSDGFRYFGAEVGI STSKI HARGPVGLDGLVI YK
YKLI GNNGHI VADYANRSRSFKHRKMNREFSPGGSKNK

>2617921191 Ga0073689_1212 Methyl transferase domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_121]

MAHRLTANKWDSGLYDDKFSFVSEFGKSVI ELLDPRCGERI LDLGCGTGD
LTREI AKAGAVPLGI DLSTSMLEKARRKYPEI SFALGNAENFRAAEQFDA
VFSNAALHWI KNAGAVAETVWLALRPGRFVAEFGGKGNVETI I RGI SVI
LAGCGVSAAGKNPWYPSVGEYSTLLEKQGFVRMYAAHFDRPTPLEGGEN
GLFNFLDMFFGSGFSPGQKNDLYEKI AGYLPALYQDGTWTVDYKRL
RI KAVKE

>2617921190 Ga0073689_1211 Endonuclease, Uma2 family (restriction endonuclease
fold) [pelotomaculum Ga0073689 : Ga0073689_121]

VTVVNPHLKFNHYHDYCLLPDDKRVELI RGDFYVVPSPSVI HQRI AANI ED
I LRDYVKENRLGEVFYAPLDVVLTPYDVVQPDVMFI SGERGHI VTDANI Q
GPPDLVVEVLSPSTGERDRTI KKKLYARSGVRELWLVAATQVVEVFDLE
TVGETPPVVYRRSGKEPLI SKVLPGLTVDLNEVF

>2617921189 Ga0073689_12039 P-47 protein [pelotomaculum Ga0073689 :
Ga0073689_120]

MLTYGYDYSFGLKI EKINDI LKNNLAGTDI TLEYQDKDKETGSEI TI KAK
MAPWQI I KGSNTLLRLSLPI LGTMTVEGAAI SGHYDLAGVSATVEVSL
AWVGP GSMRQLKSGGDKTEL VSPENTSSPDNPGYI SVVSI NDPAGKLDI
VGKGLFRVYLLDTLVKNKTKI SYI FAKI FPDNSNMAGWLKPFKWTYFYSS
SKTQDALCFLCMLSDKEWPSEPAFESA AFSSNSANAVI LVSQQVFFNKVI F
PAI KKSFPDGEFQVDVAN ECKTLKNSGKFSVKTSKSGSI AASSFVLTESDS
GNGLVTHASGSGPLKFLFGLADLP GATFSWSCQTRNPLNFSNNKVTFLLD
KNPAI DHNQTI NWYDWVLLAVVGI TTLPGLI SVI VDSI NNFSDQVSKI GM
GNI NDEFEKSVGGSVNLASVVRWHTGNQEFSPDNAMLEGAFYVTGNVS

>2617921188 Ga0073689_12038 P-47 protein [pelotomaculum Ga0073689 :
Ga0073689_120]

MTTLKTTNLPVPDVVAEI VNHNDADTYGWDTVFSI RFNDANTAI ADNW
SSVGDKVKNFSQAASDAPSYNAKGI LGPWQLTVGGDGKNI RMVCPFI EGT

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YEAGGTTYNLKDYKVVV EVGMEWVPDPDQFAFTVTGNDKI NQI VSALDKS
AI SQI LKDEFAAQHNPLSDSASVTVI KNSLEWMI TDGKSNNYYI FFNI DKY
QDOFLHI YMFEDAWRNLLKI LQDEVSEEQPAVVI VTI ENNKTSGI AAVL
PELMSEWFNANI SDFNYVFSVLDLSPRLSKSDKYHWI KPTSTSYAVTDNG
TLDNSVFGVLTMTQNRPAASNHOVSNNAI PTGTGSNSANAGFLI NGTVFL
QNMMLSGARAI FSNAVEDNFTVTNDGLTI QNNAKLTWGRFKKEDSPVRSV
SSKFI GDLDAGNLTPDLKYAFGHWESVGEQSVFVGI DVSGYSI EVTEK GK
NWFLSKGEGSPGYLLEKDGDN I NAYTALVVTI EKNQFKMSLI HSYLEI EF
I DLKPESWEYDVHI NFTEQVQLSLKEI DGRQI FWYDQI ARNMTVNVTKT
KAAI TVAI I ENAI MTAI GLVAAPVVDGI RGAVAVGEI TEDAGSAMVTA
KGFQEA YEI VEDDWVLI DEV DAGTSAARQVRGGWTGFKNAFTATRWKVLG
GI AGAVTAI VGGEQLI YEI I ESCAKGDWEKVP AFDEFANAI I VPYSWPGV
SGYDLKCSWLASSLOI GLKTR

>2617921187 Ga0073689_12037 MerR HTH family regulatory protein [pelotomaculum
Ga0073689 : Ga0073689_120]
LELLTI SKEAKKLGVHPNSLRNWEKQGLI KPVRLPGGQRRYSVDELNRL
OSGQLTDGQAVVLYARVSMQSI HSVNHI KTFVPPGKNSI KTGI I NYLW
LSNGNLFI I EILIN

>2617921186 Ga0073689_12036 Resolvase, N terminal domain [pelotomaculum
Ga0073689 : Ga0073689_120]
MI TMQKQADAGNLERQMDRLRQYARGRNFTVKAEFMDTAGGLNQKRRGLT
NVLKLAERGEYKKLI I EYPDLARFGYSYI ERLRYCGVEI VAI SEKEPE
DAESELVRDLLAI VASF SARLYGARGGKKVRQGFRELI AGVGS

>2617921185 Ga0073689_12035 transposase, putative, N-terminal domain-containing
protein [pelotomaculum Ga0073689 : Ga0073689_120]
MKKRKKKKKKPI KPDGI NYTVCGEFFPEVYPAFRSGKWGRGMEDPLATE
MRI FCSCTRWAFNRLQKDNSRQELKKQGGTGLNSRYCDDAI LKAKAVI
ESQKELLTL

>2617921184 Ga0073689_12034 transposase, IS605 OrfB family, central region
[pelotomaculum Ga0073689 : Ga0073689_120]
VIFGGRSLWKRLCKGRVSKEEWRQARQDRLYARGDET KGGNPNPKVNW
GKFTLSI TI SHLSVQKGTDSKGRPVMTRAPKVTGKLWLPEKHRI KVLELL
LSGSPYTVGLLKGDGRYRAHI TFTVTAPVLVTNPNRGYLGMDTNPDGVA
LANVGYTGLHEPWPKGFDVLHPKALHKFAGEFQVTVHPNGFLYI KVPELQ
YSRGFRRTYLI GVMKVVVDI AGALGKPI AVENLDFSKDRLD TNKFRNM
AANFPYKKI VEAVI RKAKEGI GVKQVPAHTSTI GYWKYMARYGI TVHH
AAAYMI ARRAI GFKERI TKELKQKVQAVREKLSQKVDSLPGE GEGMTRKV
KQLFKRLGGKVS MHNGLTRFKQESFYSVWRDLKQLALLSR

>2617921183 Ga0073689_12033 P-47 protein [pelotomaculum Ga0073689 :
Ga0073689_120]
MATPGKENDAAALYTYGWDATFGI PI PLVNVKI VDKKSSPPGFSYAEDAFN
VTGGFGDWQI TRGGDGKNVRFRI PLKNI TLTYTNTGKKI QCPDGTAI I EV
NLHYI PHTTAMGDYKGMPHALVVKHTSDSPDQPAFVLI SLELGTDVGTIS
NALI QEGLKNWGNELHNEFNHI FNVVDLNRMI DKDQWGFVTPNYI SYAYL
DGETPETSTLGVLCTGDRGTGTLAEQI SENI I PKGSI AGFAI SQERTMM
DLVRPAI CHAYKGLNVNLMNNEGDELYLKDGVS I DLGPVEHNGSTYYP
KLARLNLKSNGLFTLTSFTETEVSPGI TATCQATNWTYI ELGNSKNGQT
LVFKEAQKGD I EHTI HHSVGI I I TEI I VSI VAAI ALI I LTVVTEGAALI V
GGLVI GLI I GAVI LTPDI I DLLNTDDAPAI DLLTVNAVDP I KWTGSSSFN
LNYACQNVSMQLGGTPLFV

>2617921182 Ga0073689_12032 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_120]
MNNKNYRTVKLKHALLVLRDCI AETHVFTMSFKSYDQGPLPKAENFGI TD
SDKI EKFNQI AKMLI SYDEPFFQWLEADAENTI LFTDDPVSAKSAFPEL
SANLFAI V

>2617921181 Ga0073689_12031 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_120]
LAKGKLI KVFPGGNTAYGFYSFYDHI I EPDANRI FVI KGGPGVGKSTFMR
RI GETMLEMGYDVEFHCCSSDNGSLDGVVI PAI RMALLDGTAPHVVDPKN
PGAVDLI I HLGDHWNKGLRGNKKEI I AI NKEVGRLFKHAYAYLAGAKLF
LDEVESHYTESGAFNTGAFDKLVLELTHEI FEGKPRRTDNPKARCLFATA
I TPDGPVSHLETVDGLKKRYI I NGDDGTGKTTLVRRLEAALARGYDVT

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AFHCALNPHLVDHLVI PDLGLAVI NNVEPHYYPQNGDVTI DTMTCVDPV
LNEAYLAEKGAARGMYROCMQAVSFI NRAKKMHDEMEKYYPFMDFEAI
NARREKTLRLI LEMAGEI FTE

>2617921180 Ga0073689_12030 response regulator receiver and ANTAR domain protein
[pelotomaculum Ga0073689 : Ga0073689_120]

MFGARI VI ADTDADFRKKLKDITLVRAGYLVTEVGDGRSALKVI FQTEPD
LVI MDPKLPAGAEGLI VRI FEEHRAAPVI LMTASHEQALLEEAKDSWI FA
YLVKPVNEAQLFPAI EI AI ANFRKFMKLEENRELKKNLEERKLVEKAKG
LVMEAKRLSERDAYKYLOKLSMDNCI PI ARVARQI I TYFNKKD

>2617921179 Ga0073689_12029 glutamine synthetase [pelotomaculum Ga0073689 :
Ga0073689_120]

MKAFNKEEVLEKAKEYNVKFI RLQFTDI FGSFKNI AVTVEELERALDGOV
MFDSAVI EGFVRNKESDI YLYPDPATFEI FPWRPRDGAVARLI CDI YAPG
GEYFPGCSRSVLKRVVKKASEMGYQLRVGAEI EFFLFHTDGGQKPTTI TH
DOAGYCDLSPVDLGENARRDMVLTLLEEMGFEI SSSHHEI APGQHEI FI KE
DSAPAI ADKI ATFKFVVRTVAQRHGLHASFMPKPVGGLNGSGMRLHQSLW
RQGRNVFDDPAGQAGLSETVYRYMGGI LRHAGALTALANPLVNSYKRLLP
SDLCPVLVAWSERNRSTI I RVPAQRGDGARI I LRSPDPTCNPYLVLAATL
EAGLHGI TAGI TPPPPMPENQLDPGGLRELKVKQGLPRNLGTALALAGD
GAMREALGEYI AGRFLAVKELEWERFQSEVHQWEI DEYLTIFY

>2617921178 Ga0073689_12028 Glutamate synthase domain-containing protein 2
[pelotomaculum Ga0073689 : Ga0073689_120]

MSFSKGI NASAATLTKLRTGDSKCEFSGMCVTCLDGCPLCEI GKSSVRS
KEVLYPQPFQGI TAASQKDYVPDYSHFNI MGTAVGAQGI DPDPDKAI FPA
VSLETEI GAENKI KMDLPVVVAGMGSTNVAANNWEHLAAGAAI CGI GI VI
GENVCAMDGPSEI KNGRVAHSPNLAGRVDKDFQRWYNGKGI AVQANVEDT
GLGVQEYAI EKLGVVEVI KWGQGAQDI GGEVKLNTLERALQKGRGYI V
LPNPEDPKVQETYKAGAFAEFERHSRI GMVSQESFNARVEELRKAGAKHV
MLKTGAYRPADLARAVKFASDAKLDLLTVDGAGGGTGMSPWRMMNEWGVP
TLYI QALLVKYLDRLAARGAYI PPVAI AGGFTLEDHMFKGLAMGAPYI KA
I GMARSALTAAMVGKTVGEAVKSGKVPAYEYKKYGETVEQVFVAACELKER
LGGEFDLSPVGVGVYSYFERLAQGLRQLMCGARKFALRYI TRDDLATLT
REAAEI TGI RYI MEVDAEEVEQI LG

>2617921177 Ga0073689_12027 response regulator receiver and ANTAR domain protein
[pelotomaculum Ga0073689 : Ga0073689_120]

VGEQRVI VI DSDATWRKNI KAMLAKMGYWI GEADGLTGLKLVRARQPD
LVI I EAFPLPGMDGHEVARI I HEDKLAPVLI ASSTRQNVLEKAKI AKVFA
FLVKPELEYNLI PAVELALTNYQEI VRLNQVKELKDTLETRKVI ERAKG
I LMETMGLSETEAFKRI QRQSMNKRI SMRAVAEAI I LAHNL

>2617921176 Ga0073689_12026 glutamine synthetase [pelotomaculum Ga0073689 :
Ga0073689_120]

MEATEKGQLI EKARNLGVKFI RLQFTDI FGVLKNVAI TI EQLDKALDGEI
MFDGSSI HGFTRI EESDMYLRDPGSGFVFPWRPREGGVARLI CDVYNPD
GTPFEGDPRHALKKVLAEEAEMGYTMQVGPELEFFLFHVDQDGNPTVDTH
DRAGYFDLAPVDMGENARRAMVLTLLEEMGFEI EASHHEVAPGQHEI DFKY
SDALDVADKI MTFKVVVRTTAQRHGLHATFMPKPI FGI NGSGMHMNQSLF
KDGNNAFYDPSTPDQLSETAKHYI GGLVKHSRAFAAVTNPTVNSYKRLVP
GYEAPVYI AWSGRNRSPLI RI PAKRGSSTRVELRNPDPSCNPYLAI AVAL
KAGLDGI KNKI QPPPTDQNI YHMTAAERDGLI GSLPANLREALDELAI
DEVI KSVLEPHI FEKFVEAKMHEWDSFRVQVHPWEVDEYLSKF

>2617921175 GluA glutamine synthetase [pelotomaculum Ga0073689 : Ga0073689_120]

VNSVAKLTNDDVRNLARELGVKFVRLQFTDI FGI LKNVAI TVEQLDKALE
GELMFDGSSI EGFVRI EESDMYLRDPSTFVFPWKPRDGAVARLI CDI Y
NPEGTPFQGDPRHVLRRVQAEAGEMGYTMNVGPEAEFFLFHVDNDGRPTT
VTHDRAGYFDLTPVDLGENARRDMVLTLLEEMGFEI EASHHEVAPGQHEI D
FKYSDALDI ADKI VTFKVVVRTI AQRHGLHATFMPKPI FGI AGSGMHLNQ
SLMKGGENAFYDPAAGDGLSGDCLHYVGGLMEHI KAI TAVI NPTVNSYKR
LVSGYEAPVYI AWSARNRSPLI RI PAKRSLSTRI ELRSPDPSGNPYLALA
VCLKAGMDGI KNRI KPPVPCNRNI YEMTPGEREQGLI GSLPESLQEI NE
LSKDKVI REVLGEHVLHRFI EAKQI EWDYRVRVQVHPWEI EEYLTKE

>2617921174 Ga0073689_12024 glutamate synthase (ferredoxin) [pelotomaculum
Ga0073689 : Ga0073689_120]

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MOGRKTCGLPPKQGLYDPRFEHDACGI GFVAHI KGKKSNEI LRQALTVLV
 NLDHRGARGSEPNTGDGAGVLMQI PHAFLEKECSKAGVQLPPAGKYGVGV
 LFLPHDHGLREQCEKI LEEVAAEEGQVRVLGWRTVPTNDYTLGETAKLVQP
 FI RQVFI AAGPEI ADQMAFERKLYVI RKRKKEVRCRCLDNGEPFYFTSL
 SSRTI VYKGMLTPQQLNEYYPDLDDPDMETALALVHSRSTNTFPSWERA
 HPYRYLI HNGEI NTLRGN I NWMHARQAMCESELFGDDMKKVLPI DQDGS
 DSAI FDNVLEFLYL TGRSLPHAMMMI PEPWSNHESMSDEKKAFYEYHSC
 LMEPWDGPAAI AFTDGI I GAVLDRNGLRPSRYVTRDDLI VLASEVGV
 DI PPENVLVKERLRPGRMLLVDTTEGRI VADEELKHRMAVEHPYRRWLDQ
 YLVGLEDLPPAPAVPEPDLEAVRQRQAFGYTFEDLTKI LEPMARNGVEP
 VGAMGNDAPLAVLSEKPOLSYNYFKQLFAQVTNPPVDAI REEI I TAWETT
 TGPEKNLI KPEPDSCRQLRLKTI LSNEELAKI RHI EREGFKAVTSLI LF
 KAADGGRLAEAMDNLCRAADRAI AEGANLLI LSDRGVDRENAAMPALLA
 LSGLHHHLI REGTRTRVGLLLESGEPRETHHFVLI GYGASAVNPYLAFE
 TLEDMVRQGLLAGVI YQEALKNYI KAATKGVVKVMSKI GI SAI QSYHGAQ
 I FEAVGI HQSVI DKYFTWTASRVGGVDLEAI AREAVLRHKKSFDRGCGA
 AVLECGSTYQWRYDGEELYNPRTI TTLQQACRNNDYNLFKEYSAMI NSQ
 GVNLRSLFGFKSNRPPVPLEEVEPVEI CRRFKTGAMSGSI SKEAHETL
 AI AMNRI GGKSTGEGGEDPARFI PDPNDDSRSAI KQVASGRFGVTI EY
 LVNSDEI QI KMAQGAKEGGQLPGRKVYPWI AKVRGTTAGVGLI SPPPH
 HDI YSI EDLAQLI HDLKNANPGARI NVKLVSEVGVGTI AAGVAKGKADV
 LI SGYEGGTGASPRTSI SHAGLPWELGVAETHQTLVLNDRDRI VVETDG
 KLMTGRDVVI ATLLGAEYGFATAPLVALGCVMMRVCNLDTCPCGVATQN
 PELRKNFKGDPQHVVNFMRIL AREMREI MAELGFRTI NEMVGHTEALEAS
 RAVDHWKAKGLDLTPLLWQPDVSASI GRYCRVAQDHGLDRSLDI QTLLEI
 CRPALERGEPEARLPVKNI NRVVGTMLGSEVTRRYGGVGLPEDTI RLHF
 TGSAGQSFAGFI PRGI TMTLEGDANDYYGKGLSGGKLI VFPPAGATFVPE
 ENI I I GNVAFYGATGGEAYVRGVAGERFCVRNSGARAVDGVGDHGCYEM
 TGGRVVVLGPTGRNFAAGMSGGI AYVLDENGSFVRCNKEMVLMENLSDP
 EEI AEVKEMVEKHVQYTGSRRGQWVLKHWEELTPRFVRVI PRDYKRLMLAA
 I QCARQSGLCGEEAI MAAFEENLKDVSR I SGN

>2617921173 Ga0073689_12023 glutamate synthase (NADPH/NADH) small chain
 [pelotomaculum Ga0073689 : Ga0073689_120]

MGKPTGFMEYQRELPA DRPPLERI KDWNEFHHPMPEEKLLQAARCECG
 TPFCHSGVMI NGMASGCPNHNLPPECNDLVYRGLWQEALNRLLKTNFPE
 FTGRVCPAPCEGACCAGLAAEPVTI KNI ECAI I ERAFEEGWMAPRPPQNR
 TGKKVSVVSGPSGLSCADQLNRAGHQVTVFERADRI GGLLMYGI PNMKL
 DKRCVQRRVDLMAAGVKFVTNTEVGGDYPAQKLLLEEFDAAVLCGGATKP
 RDLRI EGRELGI HFAVEFLKVNKSLNSNHADGNFI SAAGKDI VI GG
 GDGTDCVGTALRHGCRSVNQLI MPKPPGERGPGNPWPQFPRI YKVDYG
 QEEAAALYGADPRHYCI TAKRFVGDANGHVKEAHTVNVVWVKDDQGHFTP
 REI PGTERVWPAQLVLLAMGFLGPEDTLLEQLGVERDGRSNVKAIEYGFKA
 TSVKGVFAAGDMRRGQSLVI WAI NEGRGAALACDRYLMGSNGF

>2617921172 Ga0073689_12022 acetolactate synthase, small subunit [pelotomaculum
 Ga0073689 : Ga0073689_120]

LRGVELAVNRNTLSVLVNKPGVLARI SGLLSRRVFNI ESI AAGYTEEPD
 VTRI TLVVNGDTHI LDQVMKQLSKLVDVI KI VELKAEESVDRELALVKVK
 AEPNRRSDI VNLVSVFRANI I DVNKETMI I EI LGDEKKI NAFRAVLEDYG
 I I EMVRTGKVALSRPGAVKF

>2617921171 Ga0073689_12021 transcriptional regulator, CopG family
 [pelotomaculum Ga0073689 : Ga0073689_120]

MPRI KRI MI SLPDSLLAEVDGI AAAEQLNRSEFI REAMKLYI ADRKRRVL
 REQMKKGYLEMATI NLELAI EQYRLEAEVSQI FEI PAAEVK

>2617921170 MazF mRNA interferase MazF [pelotomaculum Ga0073689 : Ga0073689_120]

MI I RRGEI YYADLSPVVGSEQGTRPVL I QNDI GNQYSPTTI VAAI TSQ
 I DKAKLPTHI AMAASPGGLEKNSVI LLEQI RTI DKSRLMEKV TALDSEMM
 VKVNQAI EI SLSLVDL

>2617921169 Ga0073689_12019 HPP family protein [pelotomaculum Ga0073689 :
 Ga0073689_120]

MKDTI GENYASRPGTGEKI TNYLCKMKGGKCPTTGTVPLAQLLVTFLGSI
 AGI GLVGFLAEHYGLPLLLPSFGASALLYAACHVPMAQPRNVI GGHTLS
 ALVGTVVYQI SGNAAWAI TLGVTLAI LVMALHTLHPPGGATAFVAVYTE
 QGFGFI LSPVALGVVCLVI I AMLVNNLSPQRKYPEYWI

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>2617921168 Ga0073689_12018 Cupin domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_120]
VDVVKMANVAQFRSPKGI SARKLLENQSFVI MNLLKPKGEVLEKHKTPID
VFFYVVKGKGFVQI GDQESPVEATDI VFSPKGFPTASGPCMRNSRRWS

>2617921167 Ga0073689_12017 Imidazolepropionase [pelotomaculum Ga0073689 : Ga0073689_120]
MLAI AGGKI LSMAGRTLMEGTVLI DGGKI LGVEEGVEVPPGAGMVDAAGK
VVMPLGI DAHSHLGI VEEI YREEGDDCNEI TDPVTPHLRAI DAVNPVDLG
FRDALAGGVTTVVTPGPGSANI I GGEMVAMKTHGI VVDEMVRFPAGLKAS
LGENPKRSYGRDCKSPATRMASAAI LREALVKAQNYLHKDSPERDLKMEA
LGRVLKGEAPLRVHAHRADDI MTAVRI AEEFGVKLVI EHCTEGHVVASQL
AAKDI PVVI GPVI TNRSKVEMRGLTLETARVLAEGVRFVFI MTDHPVVPV
QYLAASAALTVKGLAVEHALRAI TI DAARVLGLEERLGS I EPGKDADI I
ILDRHPLDI TSRI EQVYI GGNRVL

>2617921166 Ga0073689_12016 two-component system, response regulator, stage 0 sporulation protein F [pelotomaculum Ga0073689 : Ga0073689_120]
LDVLI VDDQAGVRYLLDI VVREAGHSARTAQNGLEAVELARAARPDVFM
DVRMPLMGGLEALGKI KAMAPETVVI I MTAYSSEETVTQAMQMGAALCCIA
KPFVDVEI KDI LVEYGWKRANRGI AAAGCYGF

>2617921165 Ga0073689_12015 thiamine-phosphate pyrophosphorylase [pelotomaculum Ga0073689 : Ga0073689_120]
MREYVRVVDANLNRAGEGLRVLEEI ARFI LDDAALSARLKEMRHSALAT
NQLPGGVYELVRARDAAGDVGASSWTPGEKTRDDLFTLAVANFKRVQEA
RVLEEFGLKLLGPSLARTFKGLRFOAYVLEQEMLLKLLKAGYDLRAEAAVE
PGVPPEE

>2617921164 Ga0073689_12014 thiamine-phosphate kinase [pelotomaculum Ga0073689 : Ga0073689_120]
MKLFELGEFGLI DLLTGDMI HNPAGVI KGVGDDTAVLAVGGGPWLLFTTD
MMVEGI HFSLDWSTFRQVGWALAVNLSDI AAMGGRPHTHAVVSLAVPPRL
EPSALVELYEGLEAARTYGVNI VGGDTVGNPERLVLNVALLEGEVAGKA
VYRSGARPGDGYYVTGTGAAAAAGLHLFQNPDLSCPPDAADYCRRAHCAP
RPRVEAGLLARCGVSAMDDI SDGLASEMHEI CGAGGVGCLI RREDVPVD
SRVRAVAEGAGVDPVEWALFGGEDLELVFTAGPEAEEGI EREAAGEGI KI
YRVGEI TARAGVHLVPGGGEI LPLPRGGYDHFKE

>2617921163 Ga0073689_12013 tRNA threonyl carbamoyl adenosine biosynthesis protein TsA [pelotomaculum Ga0073689 : Ga0073689_120]
LSLI KTASQAETARVGEKLAFLCAGDVI CLNGELGAGKTRLVQGMARGL
GI DGPVTSPTFTLI NEYHGRPLPLYHMDVYRLGGSLEMDLGYEEYFYGEG
VTVVEWAEKVEGLLPAERLDI YI NRRPEGEDSREI VLTPRGERYRRLAEE
LI TVVCAGH

>2617921162 Ga0073689_12012 tRNA threonyl carbamoyl adenosine biosynthesis protein TsB [pelotomaculum Ga0073689 : Ga0073689_120]
LYVLGI ESATPVAAAAGVAGEGGI LVERMVFNORTHSVNLLPMI KAVLEEA
EVDPRNLGI AVSGGPGSFTGLRI GMSTAKALARVWGI PVAGVSTLEALA
FPLAGHGGVLCPLNARKNEVYTAHYDCAGPAPACLNPMALSPEKLVEL
LLQFQRLVTFVGDGVPVYGGHFKSGLGALARCAPRSASFPRGAAVAEMGL
GI FREGRGI DPAALRPEYI RLSEAEAVWLKKHSGGQNNCHL

>2617921161 Ga0073689_12011 ribosomal -protein-alanine N-acetyltransferase [pelotomaculum Ga0073689 : Ga0073689_120]
MNVTFEEMRLEHLDRVVEI EQVSFPSPWVRGVFAYELVQNSFAHYI VAAM
GGKVVGYYAGMWLVLEAHI TNVAVHPGYRRKKI GRSLMVEI I RRAALMGI
NRMTLEVRPSNAPARCLYAALGFEEGRRRKRYTDTNEDAI I MWRESPAG
GRRHTFTGCGV

>2617921160 Ga0073689_12010 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_120]
MTGRGRAI LRI SGFAFI AGGVLAGLPWPWPWLVVLGLGQI VAAGGFG

>2617921159 Ga0073689_1209 cell division protein FtsA [pelotomaculum Ga0073689 : Ga0073689_120]
MAKTLPSKENS I FALDI GTRTVI GI VALVESGMLRVVAQHI VEHESRSMF
DGQI HDI PRVADTVLKVKRSLEKKVGFKLATAAI AAAGRSLI TNRRRVEM

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ETNGDVEI DHALVNSLELAGI RNAYDELGREEAGEVERYHCVGWSVVKYY
LNNYPI TSLVGHGRNLI GADI LATFLPESVNGLYAVLRRVGLPEVNLTL
EPIAAI EVVI PENLRLNLALVDVGAGTSDI AI TRKGAVVAYGMAPVAGD
EITEAI AEAFLTDFNEAEKI KRALEKGED I AYRDI LGTENSVAEEVA
I EPVLDRLAAEVAGTI TGLNGGEPPTVFCVGGGARLPGLTARLAEKLG
EARKVAVRGREAVTNLVVDEAGLEGPEGVTVVGI GTVAI KKLQNFVTVK
VDGKEFSLSFNSRDLNVAGALGLVEFNPGDLI GRNGGDLKFTLNGAPWV
VY GGLARPAEI YVNGNRANLRTPI KEGDEI RVLKAVNGEDAGARVRD
FLEGL ACISI TVNGGHKTLELLCFLNGETAAYDDEI KNDDHLEI RVI
KTAGELFA GTDLKEYTI VVNGAAVGPYELKDGDNVQLVKNNPAGAG
GESAPAGKKEA EPAGGRAGLTVRVNGKPEVLEAGRQHLFVDI FNHI
DFDRSAPKGVLVRL NGAVARYTDVLKENDNI EI YWDDK

>2617921158 Ga0073689_1208 RNA polymerase sigma factor, sigma-70 family
[pelotomaculum Ga0073689 : Ga0073689_120]
LPSTTTEHTI NQTNFREYFERHYPVCRQLI RLLGSRAAAEDVAQETFIK
LYQSPPREPSNLGGWLARVATNLAYNHLRSENSRRRREAGAGLFTTVEAG
PEEALVRSEEALTRRVLELLPERDRACLLLFSGMSYAAI ARVTGVKES
SVGTVLARARARFKAELYKGKGSDDGVL

>2617921157 Ga0073689_1207 Putative zinc-finger [pelotomaculum Ga0073689 :
Ga0073689_120]
MVCYDTGAWQAFLDGEVTGDPKAGMEKHLLSCGACRERLEQLRENQIFTD
AGLAGYI RALNRSGVDTGAARFSARQPAVQSGARPRKGVLAMLLRYRM
AATAAVMVLALAVTFSGSVRTAASELLTI FRVENVKTVNI SPEDMSRI
N KALGDGAGAVDMENFGRI EFKGNGAPGEI TLEEARSAVDFRLKLPDQ
LPD GYHLOEI RRNAGGTMMNFTLDTVNTNRI LQSLGSEKLLPEELNGRT
FTMEL PAQI TARYAGPDSRPVFGQGRSPELKAPI EDAGVI RDALLGLP
FLPDDL RSQLA AI NDWQHTFVVPNVGGTSREVEVAGARGVFI TSPAGEE
AKGKQAP NCLI WQKAGVVYI I GGPLTLEQALAMAASMK

>2617921156 Ga0073689_1206 ABC-2 type transport system ATP-binding protein
[pelotomaculum Ga0073689 : Ga0073689_120]
MII EI DNLTMYGKKTGCSEI CLSVDGGQI FGFLGPNAGAGKSTLVKMLVG
LLLPTSGTARLLGWPLGDLAARRKTGFLPENFRYQDWLTGEELLSFHASL
YGMGSAKKRRVPVLEQVGLAGKEKQKVGSYSGMQQRVGLACALLPDP
ELI FLDEPTSALDPLGRREVREI MLELRDRGKTI FLNSHLLSEI EMI
CDR VAI I NKGRI VAEGALDLLAKTVEVEMRVEGLTPSALAELSARSRSVAVD
GRLLRLSLGGPGGYTGPRNGGQKRRPVVQPGGQAQFPGRSI YRHDSGGR

>2617921155 Ga0073689_1205 ABC-type transport system involved in multi-copper
enzyme maturation, permease component [pelotomaculum Ga0073689 : Ga0073689_120]
MQTI AGLTLREAVRRRI LLVTVVLAVTFLVLYGAGVHYGYKDI AAHAGPR
SGPLOALAAPMFLSVGLYFGGFI I AFLAVMGAVGTI SGEI ENGVMYAI VP
RPVRRTEI VLKGFVGHGLMLVI FAI FYVAVLLI VRSNTGLSAPVKAEAI
GLFCLQPMI LLAVTMYGATFLSTLANGVAVFMLYAVGVVGGMLEQI GNLA
GSQTLVNI GI I SSLI MPADAI YRKI VYTLLTVPGVPMSSLMVGPFGSNSE
PSAWMLAYTGLYI LVFLFLAVRTFSRRDI

>2617921154 Ga0073689_1204 Uncharacterized conserved protein YecE, DUF72 family
[pelotomaculum Ga0073689 : Ga0073689_120]
LFYI GTAGYSYRDWVGAVYPAGTKPGEMLELYAREFPFAEI NSTYYHLPG
RKMI AGLAAKTTPGFRFAI KAFQQMTHTRDGGAGVFLQFAGALNPLVEAG
KLACI LAQFPYSFGNTPENRDYLRFRRELLPGLPVAVEFRNQRI CQDTF
ALLREEGLAYVCVDEPDLKGLVRPVAVVTVPAYVRFHGRNAARWYHHRE
AYERYDYLYAEDELREWMPHLTLLREKAGEVYVSFNNHYRGQAVANVRMI
RELI GSAGI RPAPP

>2617921153 Ga0073689_1203 L-lactate dehydrogenase [pelotomaculum Ga0073689 :
Ga0073689_120]
LKNDSSRKI AVVGVGVGATVANALAMSGLATDLVLVDI NRRAEAGEAMD
IAHAAFI KPVTI YAGAYEDCRDAGI I VFAAGAGQKPGETRLDLLQRNYD
I LKESLAKLPSPGNDRI I LMVSNPVDVLTYYAALKI TGLPPEKVFSGSTVL
DSSRFRHSLSEHCGVAPRNI HAYVVGEGHGDSEVLLWSLAYI AGI DI DHYC
RLAGLPPVDRREVDQVRNAGYEI I SRKGATYYAI SLAVKRI CESI I RNE
NTLLTVSGLLDGAYGI KDCCLSLPAVVNSGGGRPLELPLAGEEEAALRR
SAEVLKGAAEKLGL

>2617921152 Ga0073689_1202 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_120]

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Ga0073689_120]

MFKTLAALAALSAI LTAGSGFALLMGSSATKGHVVLGLVTAVI TLVFAYA
AYRKT>2617921150 Ga0073689_11939 PIN domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_119]MKRLFLDANVLFSI AYGPSLEI FWNMSREGRCKLLVTAYVI EEARRNLS
RPGQI KRLLENLVMEVEVVPESDPEMPCPVVLPVKDRPVLLAAVQARATHL
ITGDLQHFSAIRGKNI QGVLVCTPRDYLQNVQSLPK>2617921149 Ga0073689_11938 looped-hinge helix DNA binding domain-containing
protein, AbrB family [pelotomaculum Ga0073689 : Ga0073689_119]MSVETVKVGRRGTVVPAALRKEYGLEEGALLI AEPRPEGI LLRPAI ALS
VEI YTPERKAQFLLNNALTAEDYAWAALEVKKLGLDPEDI PHERPGSI>2617921148 Ga0073689_11937 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_119]MVI MCHSTWNYFFKTPWRI SGI AGI LFVI LSF I ASGI NI LPSAYDQNKMI
LVAWFAVLLSVI AGI RYFI VI LAGN>2617921147 Ga0073689_11936 Helicase conserved C-terminal domain-containing
protein [pelotomaculum Ga0073689 : Ga0073689_119]MCNAGKKFLVFCHSRQDVENYYLRSLGSESLREKI MPYRSGYEASDRTR
I ENALRNGALSGVFCTSALELGI DLPDLDTCLMLGLPGTKI SFI QRAGR
GRSKKGSVI I LKTGGAQDEYYFSRPRELVEKGI EPLNI HLQNRQI I LSHY
ACARLECADFENPRLDEQI FGSYFKEI EKRVRDFDFPDEI LYHQSLDSLL
KKDTRQFG>2617921146 Ga0073689_11935 DEAD/DEAH box helicase [pelotomaculum Ga0073689 :
Ga0073689_119]MQI PQMLARTGARVI HAWPEPGRKTVYAGI PTGLAPQLRLLLLKLLHPEGL
YSHQAKSLEASLCGKHAGI CTSTASGKSLCFTLPAANELLRDRNSRAI FL
YPNKALSNDQTKLTGFLSFLRLGVLVKKLDGDVVGEERKKAVAAGRVLL
STPDVLHTSMLRLNREPGYEDI FKNLKFVVLDECHVYNGVFGSNMAYVLR
RLQVCENLGANPFVHHGERNLRSFRSPEDVDRTGRYHDHYRSGQRQSL
PR>2617921145 Ga0073689_11934 alcohol dehydrogenase, propanol -preferri ng
[pelotomaculum Ga0073689 : Ga0073689_119]LGKVLALPVLGEGVDKI MRAMVLEAPGRPLRLFDVPVPEPGQVLI RVL
ACGI CRTDLHI VDGLKEPRLPLI PGHQT I GTVVAAGAGADRFAGGTRVG
VPWLGFCTNRCRYCLSGRENLCGEARFTGYQI DGGFAEFAVADQRFCEPI
PEGYPDLQAAPLLCAGLI GYRSLTMAGDAERLGI YGFGAAHI I TQVARY
QGRQVYAFVRHGDLEARQFALDLGAVWAGESGMAPPEELDAI I FAPAGE
LVPAALRAVAKGGVVCCGI HMSDI PSFPYEI LWGERI LRSVANLTRRDG
EEFLALAPMVPVRTEVQSYPLDEANEALNALRLGKI RGA AVLTVSSVSL>2617921144 Ga0073689_11933 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_119]LHAYI KLGMDPSSPAVPI HYNLI QSAI YATLPEETAACLDHDEGFRSGGR
SSRMFAFSRLLGRFI LDCAAGTI TFPEELTLVVASPDTKFFLSLI NNLLT
QNHRLRGQAMFRADI FYADI I LTV>2617921143 Ga0073689_11932 Predicted arabinose efflux permease, MFS family
[pelotomaculum Ga0073689 : Ga0073689_119]VSEDI SSDKRKSGSAWLLRSFKYRNYRLFFGGQGI SLTGTWLQNI AVSW
LVYRLTNSALLLGVVGFAGQI PAFLVTPLAGVLVDRWNRHRI LVVTQTLA
MLQAFFLAFLVLTGHI TVWQVI TLAVFLGLVNAFDMPARQSFMEI VERR
EDLGNAI ALNSSMFNGARLLGPSVAGMLI AAVGEGGCFLNGVSYLAVI A
ALLAMKVAPKELVVKQSRMLQGLREGFVYAYGYAPI RLVLMLLALI SLAG
MPYAVLMPVFAREI LHGAHTLGLVGFSGVGALVGAVFLASRRSSGGLA
KNI PVAAGVFGAGLI AFSQSRTLWLSLLLMLFTGFGMMVQMASSNTFI QT
I VEDDKRGRVMSFYTMSFMGMI PFGSLLGGALASRI GAPATLLWGGI TTI
LGA AVFTGKLPLLEEALRLKLTEKQRPAKGGQEGMV>2617921142 Ga0073689_11931 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_119]MPCLKLLWEI QTLDGORKAETKLKEGQMSGELRALKNEI EEGRATFNRL
KEEYGALKKELKKKELDVTGGQLADLGQKLYGGAI TNVKELNTTSKKI

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DSLKEMVSRLEDGMLAI MEMRDALRARLEEMSAKLNEKAESYRQLHGSYL
AGQQRVROLAQI PLTRQKLLDRVDVTLWQKYLEMKKKFSDPLARVEKGT
CMGCRMGI PFNDLRLKQGEGLVFCCNCGRMLYWEK

>2617921141 Ga0073689_11930 dinuclear metal center protein, Ybgl /SA1388 family
[pelotomaculum Ga0073689 : Ga0073689_119]

MPVKCGEI FKMI EELAPRRLAEGWDNTGLQVGPRAEVYRVLLALDVGLD
VAMEAKEKGAGLI VSHHPLFLKPFGLI GLHRPEGELI TFLI RNNI TVYAA
HTNLDSAVGGVNDVLAELGLSETSVLQQAGRERYI KLTVFVPPGHVEQV
REAI VAAGAGWI GNYSHTFMTPGMGTFKPLEGTSPFI GKTGEVERVEEF
RLETI VSASRLDVVI RAMLEAHPYEEVAYELYSKKNQGPAYGPGRVGVLP
ESVSFPEFALRVKAFGLPAVRLGGSYGDAVRKVAVCGSGADLWPAVQ
AGADTFI TGDLDKHHHTARDMLSAGLKFVDAGHYGTEAVI LPAMQSYLAGHC
RRLDI DVEI LLSQTNTDPFVYL

>2617921140 Ga0073689_11929 tRNA (adenine22-N1)-methyl transferase [pelotomaculum
Ga0073689 : Ga0073689_119]

MELAKRLAALATYVPVGSVAADI GTDHAHLPI FLVEKGI CPRVI ATDLNP
GPFRSAERKVEEHCLRGKI DLRPDGLKPLRPGEAGVLVLAMGNGNTI RG
I LEESPDVLKNVKRLVLQPMADPGDLRTWLAANGWKI SDEYLVEEYGRY
VI VVAEPGREETADPLRMELGPRLLEKKEPLLASYI GEI I TMYERI LAGL
AAKNGVAHEKVRELEAKLTRI REVAGCR

>2617921139 Ga0073689_11928 Rubrerythrin [pelotomaculum Ga0073689 :
Ga0073689_119]

VSLKGTERTERNLLTAFAGESQARNRYTFFASRAKREGYEQI AAI FLETAN
NEKEHAERLFKFLEDREVEI TGSFPAGVI GDTATNLKSAASGENYEHTTM
YPEFARI AQEEGFPEI AAVLNAI ARAERAHEDRYLKLLSNVQQGRVFRD
EKVAWKCGNCGYI HEGTEPPGVCPACAHPRSYELWCQSY

>2617921138 Ga0073689_11927 GTP-binding protein [pelotomaculum Ga0073689 :
Ga0073689_119]

MKVTGAEFTTSVAKAANYPAGGLPEVALAGRSNVGKSSLLNKL VNRKNLA
RTSNTPGRTRLI NFFLI NGAFRLVDLPGYGYAKVSTGERESWRKMI EDYL
KNREELRGVLLVDSRHPPTAQDTQMYGWLKHYGI PTAVAATKADKLSRN
KLLOSLNVI RTALPLAEGDPLAPFSAETGQGREEMLEI I GRWVDVSG

>2617921137 Ga0073689_11926 ATP-dependent Lon protease [pelotomaculum Ga0073689
: Ga0073689_119]

LKSEVKVLPPLLRLGI LVFPYTVI HLDVGREKSVQAI EEAMI QDRI I FLS
TQKEAQDDPVEDDI FRI GTVAEVKQLLKLPGGTI RVLVEGI ARAKVRFF
I SNGPYFQVEVEQYSEDFQKNSELEALMRSLVYQFEQYVKLSKRI PPETV
VSVVNLEEPGRADII ASHLSLRI EEKQQVLEAVNI VQRLERLCAI VAKE
LEI VELERKI NI RVRKQMEKTQKEYYLREQMKAI QRELGEKDERMAEGEE
LRGKI AEAKLPKEVEEKALKEVERLEKMPMAAEATVVRNYLDWLLSLPW
NKGTRDRDLKAAEAI LEEDHYGLKTVKERI LEYLAI RKLAKKMKGPI I C
FVGPPGVGKTSLGRSI ARALERKFI RMSLGGRDEAEI RGHRRTYVGAMP
GRI I QGMROAGSKNPVFLLEI DKMSMDFRGDPSAALLEVLDPEQNSFS
DHYI EAPFDLSNVMFI TTANVQHN I PRPLDRMEVI YLSGYTEEEKLQI A
MRYLLPKQVKEHGLKDKMLKI SENTI RKI I REYTRESGVRNLERQI AAI C
RKTARQVVTGSGSVKKVHVTTQNLNQFLGTFRFRYGVAEQDDQVGVTGL
AWTEVGGDTLAI EVTI YKGNRGLTLTGKLGEVMKESAQASYSYI RGKSGE
FGLDETFFDKHDI HVHVPEGAI PKDGPSAGI TMACALASAVTGRKVRHDV
AMTGEI TLRGRVLPVGGI KEKVLAHRAGI KTLI LPKDNKKDMDEI PKKV
KDKI HFI LVDHMDQVLEAALTEKEYEPVNLAASPPVVPQPPAYQPSVVNE
GGASIPS

>2617921136 Ga0073689_11925 Lon-like ATP-dependent protease [pelotomaculum
Ga0073689 : Ga0073689_119]

VVEFPGVGSFLTFI QVFFAVI I GLYFWNLLKAQQGNKTAVERESKKELE
RLQRLRSI SLTEPLSEKTRPARFDEI I GQAEGLKSLRAALCGPNPQHVI I
YGPPGVGKTAARLALAEAAQKTPCSPFKEDARFI EI DATTARFDERGI AD
PLI GSVHDP I YQGAGPMGMAGI PQPKPGAVTKAHGGMLFI DEI GELHPI Q
MNKLLKVMEDRKVLLDSAYYNSDANI PSHI HDI FQNGLPADFRLVGATT
RGAHI VPALRSRCLEI FFRQLLPDEI ERI ASNAAGKEGMPLQAGALEVI
KKYATNGREAVNI I QI AGGI AI TEGRGEI RI ADVWVHSGQYAPRPEGK
I PTRPQVGLANGLAVYGNMGI LLEVEANAI PVARGQGRVTVTGMVEEEE
MGGGGKTVRRKSMAKSSVENVLTVLRRRTMEVDPRDYDI HVNFPGGTPTDG
PSAGVTI ATAVYSALMGLPVDNKAAMTGEVSI RGLVKPVGGI VAKVEAAR

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OAGAQLI PAENYQELFKEFTGVEI I PVERLEEV RTALI VPPPVEKRM
ELTNPAALDVLASGFAAGHSLSK

>2617921135 clpX ATP-dependent Clp protease ATP-binding subunit ClpX
[pelotomaculum Ga0073689 : Ga0073689_119]

MFSDKGQLKCSFCGKLQDQVKKLVAGPGVYI CDECI ELCNEI I EEELSED
LGLELGD I PKPKEI KEI LDQYVI GQEEAKKSLAVAVYNHYKRI NLGGKI D
DVELQKSN I VMLGPTGSGKTLLAQTLLARLLNVPFAI ADATSLTEAGYVGE
DVENI LLLKI QAADYDVEKAEKGI VYI DEI DK I ARKSENPSI TRDVSSEG
VQALLKI LEGTVASVPPQGRKHPHQEFI QLDTTNVLF I CGGAFDGI EK
I I MNRTGKKS MGFGAEI KAKKEQKI GEI LSKI LPEDLLKYGLI PEFVGR
PI I VTLDALDEEAL I RI LTEPKNALVKQYEKLFELDGVTLTQDALKAV
VEEALKRNTGARGLSI LEEVMLEVMYDI PSRSDI AKCI VTRETI LRKEP
PRI I AMDRKKKKEETA

>2617921134 Ga0073689_11923 ATP-dependent Clp protease, protease subunit
[pelotomaculum Ga0073689 : Ga0073689_119]

LNLVPI VVEQTNRGERAYDI YSRLLKDRI I FI GGPI DDHVANLVI AQLLF
LEAEDPEKDVHI YI NSPGGVVTAGMAI YDTMQYVRPAVSTI CLGQAASMG
SLLLAAGAKGKRYTLPYARI MI HQPMGGVQGGASDI DI HAKEI LRTKEI L
NGI LSKHTGQPLERVTDTERDFFMSAQQAEYGI I DEVFDVRKQR

>2617921133 Ga0073689_11922 trigger factor [pelotomaculum Ga0073689 :
Ga0073689_119]

MKANAERI EKNTVLL E I EVDAEQFSQAVDKAYRKI VKNVNI PGFRKGKTP
RSI LERYVKGALYEEAMESLVYEAYFQAVADTGI VPVDQPKVEI VQVEE
GKPVVFKATVQVKPEVNLGQYKELEVVKPSTEVKNKDVDKELERMQRHA
KLLTLEEGNVQKGD I TI I DFLGKI DGEPPFAGGEGKDYSLEI GSGSFI QGL
EEQVMGMSI GETRDI QVTFPENYQAEELAGREAI FI VTVKEI KRKELALL
DDEFAKDVSEFDTLEELRNDI SNTLKQAAENHANYQVRREVI TKAVDNAE
VDI PAAMADSQLGEMI GSFERQLLNQGFSMEDYLKYTNSTPEEMKAKI HK
DAERTVKTNLVLEAI AKAENI EVSNEEMDEE I KKMASHYREEVEKFHKML
ENEGQLGFI TRGI I REKTLQFLVDNANI VEDTNGQTTE

>2617921132 Ga0073689_11921 glyceraldehyde 3-phosphate dehydrogenase
[pelotomaculum Ga0073689 : Ga0073689_119]

MTI KVG I NGFGRI GRNVFRAAMDRADI EI VAVNDLTNACTLAHLLQYDSV
HGTLNAE I YANEEREFRVNGKEI NAFAI PDPCSI PWEDYGVQVVVESSGR
FTDRESASKHFNGGAKKVI TAPAKNEDI TI VMGVNEEKYEQEKHHVI SN
ASCTTNCLAPFAKI I HREFGI VRGLMTTVHSYTNDQOI LDLPHKDPRRAR
AAAMSI I PTTTGAAKAVALVLP ELEGKLNGLAMRVPTPNVSVVDLVVELA
KPATVEEI NGALKAAAEGELKGI LAYSDDLPLVSRDYNGNPHSSI VDGLST
MVI EGNLAKMVSWDNEWGYSNRVVDLVAYI GERG

>2617921131 Ga0073689_11920 Predicted metal-binding protein [pelotomaculum
Ga0073689 : Ga0073689_119]

VKVL I VSCGNYASQGYGCPGEWKCLKAAHDKEGEFAGYEGPVQVAGYLEC
ECNGRQLI PNI GMVKKNNFDVI HLSTCMVKA WPPCPNRDVDELI QKI EE
KFGVKVKGTHNYG

>2617921130 Ga0073689_11919 heterodisulfide reductase subunit C [pelotomaculum
Ga0073689 : Ga0073689_119]

LI I LFI I LKERRCI NLDLFLFDGDHSFYERVREKSNQPMELCYQCQKCSG
CKMAEQAEYTPSOI I KMQVLMKELVLNTSSI WLCSSCEI CGARCPNGI K
I AEI I DALKEI AI ESNI I KEKKI NLFNKVFLDTVRSMGRI HETRMVVYK
LKSGDLFSDLGMLGMQMFARGKLPLFMKSTKSKAKVKRI FDRCKKA

>2617921129 Ga0073689_11918 heterodisulfide reductase subunit B [pelotomaculum
Ga0073689 : Ga0073689_119]

VELSYYPGCSLEASAREYNLSSLAI CKALGI ELRELKDWVCCGATSAHNT
NQLLALALPSQNLALAQDAGLDLAI PCAACYSRLKRADHVLHRHNETKRKQ
I EEI VEFKYTGQVRVMSLLEAI I TGPGI DNVAKKVTNPLNGLQLACYGCG
LLLRPPEI TCFDNPENPVLFDRMLKSLGAEPVKWSYKTECCGANLSLTAS
KTVEGMVSRI LEMAE EAGGRAI VTACPLCQANLEMRRKDRGKGMPVFYFT
ELI GMALGLPESKNWLKHLI DPVPLLRSTSI AC

>2617921128 Ga0073689_11917 heterodisulfide reductase subunit A [pelotomaculum
Ga0073689 : Ga0073689_119]

LTSKNTESNKI GAVLVVGAGI SGI QSALDLAEMGYKVYLVEKSPA I GCKM

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PMLDKTFPTNDSCSMCI LSPKLVECGRHRNI EITLTMSEIVDLKGEPGNFQV
TVKKQPRYVDTQKCLGCGSCAEACPOEVPDEFNLGLSMRKAI YKPYQAF
PNAYVI DKENC LGCGSCCEACPVSAI NYEMEEEFVQVGAI I LCPGFEL
FDAGLKGEYGYGVYDNVLTISI QFERMLSASGPFQGH I KRPSDGKEPQKI A
FI QCVGSRDVCNLGYCSAVCCMYATKEAI I AREHVPGLESTI FAI DVRVF
GKNFERYYNRAKDDYSVRYI KCM I SSVKELQQNKDLRLRYRTPEGKMMEE
DFDMVLSVGMKPSTEAQQLADVMGLELNQYNFCKLKELSGTETTRPGI Y
VAGTFSGPKDI PETVTQAI SSAGDAATFLAPVRSTLVSEKTFPPEKDI AT
EEPRI GVFVCHCGI NI GSVVDVPSVVEYAKTLPHI VHAQEGLYVCSQDSQ
ASMKQLI ESLKLNRI VVASCSPRTHKPLFQETMREAGLNKQLFEMANI RD
QCSWVHMNEPQKATEKAKDLVKMAVNKTATLKPVTPVI VDLTPASLVI GG
GVTGMNSAI CLADQGYKVYLVEKSDRLGGI ANRI YQGFNGEDI NAYVSEL
VDRVKNHHHI TAYTGEVSEVAGYLGNFTRRLSNGQVI RHGATI I ATGGE
EAKPAEYMYGENPGVLTQLELDESI ARQDPGLLNAKTI VMI QCVGSRDEK
RPYCSRI CCTKAI SQAVKLKEI NPRVNVVLYRDI RTHGFHEDRYREARS
KGVLF I RYKLNKPLVTPLELDGKNI I QVSVVDRVLNEQI KI NADMLVLA
TAVLPAETNPKLSQI FRVPMDDPGFFLEAHMKLRPVDFTSEGVFLAGLAH
SPKSI GGS I AQSKAAAGRASI I LGRSKLESKGLTAVVDKDKCQACI TCI R
LCPFNAPKI KEDHKA EI EAVLCQGCCTCAGECPNKAI TLQSSSQYQDM
LDGLFNS

>2617921127 Ga0073689_11916 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_119]

MSCI DPAI KPMLCDI I DEYQNI LECI GTDFFQOKTLCLNAAKKKSAAVAE
AAKKI ALQI VMSSGASGASQAQAI LEKNDI LRNLEHI RQGLEKI MLLI SKK
I NRR I LFSKWAVEI STLI SCTQECLKQLAEFFNTNDEEVKDFLI DQADK
CLTLCQEYCDNHKNRFYKGQCLESSEAI YEPLI AEYRNI FKRI KCSI STY
EILT

>2617921126 Ga0073689_11915 5,10-methylenetetrahydrofolate reductase (ferredoxin) (EC 1.5.7.1) [pelotomaculum Ga0073689 : Ga0073689_119]

MKSGGSKLEQI LESGQLAVTAEI GPPKHASPEGI I HHTHMLKDYVDASNI
TDCQTAVVRMSSI ASGAHI LHNGI EPI VQMTCDRNRNI AI QADLLGAYSL
GMRNVLCISGDHQSFNGHPTAKNVYDVDSMQLI QLVRRMRDEKLFFSGEA
I KEHEPMFFVGAVANPFADPFYRVDRLLEKKI EAGAEFI QTQCI YDMERF
ARFMEKCVVERGLHERAYI LAGVTPLKSWRGAKYLQTSVSGMI VP EEI VQR
LKN AE E PKSEGVNI CI EQI KYI KDN I KGVSGFHI MAI AWEEVVPDI VQRS
GLYPRPKI D

>2617921125 Ga0073689_11914 Methylenetetrahydrofolate reductase C terminal [pelotomaculum Ga0073689 : Ga0073689_119]

LI I AEQKPI DEI SGMVENCNKVLLLGACGCVTVCLSGGEKETE I LASALR
I KRRLEERAI KTVTYTATROCDPEYI DALENLVKDQDAVI SLACGVGPQY
LAERYSDKYI VPAMNTKFVGGSKQHGVWEERCGLCGECI LHLTGGI CPI I
RCSKSI LNGPCGGSQYKCEI SKDQVCAWQLI HDRLKALGKFDNLQTI I P
PKDWSKSRDGGPRKMTREDVMI G

>2617921124 Ga0073689_11913 F420-non-reducing hydrogenase subunit D [pelotomaculum Ga0073689 : Ga0073689_119]

VGEFEPKI VAFCCHYCAYSAADLAGSMRLQYAPNI RIVEMPCSGTI DHRV
I LQAFEDGADGVYVAGCLEGDCHFLKGNRYRAKRVNAVKKLLDEI GFDSN
RLEMYNLSAAMGPRFAEI ADEMTERI KNLGPSPLNRKAKEGGAA

>2617921123 Ga0073689_11912 heterodisulfide reductase subunit A [pelotomaculum Ga0073689 : Ga0073689_119]

MVVGAGI AGI QASDLAESGYLVYLVESPAI GGTMPMLDKTFPTNDSCSM
CI LSPKLVECGRHLNI KTLTMSDVVDLRGEPGNYNVTI RKRARYVDI EKC
KGCGEACADACPDVDDEFNQGLGSRKAI YKPYAQAYPNAYVI DKENCLEC
GACEDACQVGC I NHEMEDETVEI EVGSVI LSPGFETFDASALDYGYGRF
KNVVTSL EFERI LSASGPFHGH LVRPSDHQEPKKVAWI QCVGSRNI ROEK
GYCSAVCCMYAI KEAI I AKEHSPHGLDTSI FFMDMRTHGKGFEKYYERAK
DQGVNFVRSRI FEI I EKDDGSGALFI RYADEAGNI CNEEFDMVLSVGLQ
PSK SFI ETAGKLG LNLNNYSFCEPAGLTGVGASREGI FVAGAFSSPRDI P
ETVMOASAAAGESARLLAEARGTLVAEKEFP AERDVSGEEPRI GVFV CDC
GVNI ASVVKVPEVEMAKSLPNVYAGEYI YVCSQDSQNTMRQLI EEHKL
NRVVVASCSPRTHKPLFQETMKDAGLNRYLFEMANI RDQCSWVHQKESEK
ATAKAKDLVKMVAKAALLEPVRQSSSGVI KQALVI GGGVSGMTSALS LA
DLGYKVSLL E KSEN LGGVASRI KQGLKGEDI PVFI SNLVENI KNHTNVEL
FTGSEI KDVSGYVGNF TTTLENGKEI KHGVTI I ATGGEEYKPTEYLYGQD

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DRVMTQLELEGA I ASGDPKVAGAKTAVLI QCVGSREPGRMYCSRCCA K S
VKLALKMKAQNPEMNVFVLYRDI RTYGFFEDLYREARSKGVI FVRYAVDN
KPVVEAAEGGLKVTVTDHVLCQPLEI DVDI VSLAAAI VAPESNGKLSQLF
KVPLNEDSFFLEAHMKLRPVDFASEGI FMAGLAHGPKNI EENVAQAKAAA
GRAQTI LSKDHLESHGVVAVVOODKCAACLTVCRLCPYNAPKI RNYAAEI
EAVVCQCGSCCAGECPNKAI TLQHYKDSMQI AMCKGLFKEVQ

>2617921122 Ga0073689_11911 Fe-S oxidoreductase [pelotomaculum Ga0073689 : Ga0073689_119]

MAEAI KAVNFDLKFRAEVQDLI KAFDFGNCLACGMCTAGCPYSDLI PGHD
PRKFLRKVLLGMREEALSDPYVWYCNMCERCTVECPMQI NI ATLVRTVRG
NFYNREQYPGFLOKVVNEQLETGNQMSVDQTDYI ETLWEI EEELQAELED
PNYKI PLDKEDADYFFGFNAREI KYYPQDLQAI LRVFYAAGFNNTI STKK
WDATNLALFTGLEEDFWNI QRPLFEEVVRLRAKELI VTECGHAFRSCRYA
YRTFWKGQPFVRHVLQLLNEALQDGRLLKVDPEKKI DTPVTYHDPNCTAR
KEGVFEEGRNVLKAFCTDYREMQPNRKFNYYCCGGGGFI AMPEYSDLRI K
VKGQRKADQVRATGAKLVAVPCHNCMDQFNDI TKHFNLTGKNEHVCSI I A
ESVVLPRKE

>2617921121 Ga0073689_11910 NAD(P)H-flavin reductase [pelotomaculum Ga0073689 : Ga0073689_119]

VKNPYMPAPVKLVKHVVETEDNLI HSFTFQFLKEEDEKAFAYRPGQFAEV
CVFGKGESPFGI ASSPTEPGI LKFSVARVGVTTAMHEMAEGSVMGVRGP
LGNSYPI EEFKGNLVI I GGGFAFTTLRSTI AYI LDPKNRGDFGNLTVI Y
GARNPGLLLYKDELAWEKRSOI NLVATVDRGDENWKGVGFVPAVTKET
APTAENSYAVI CGPPI MI KFTQPVLEELGFKPEQI I MSLENRMKCGI GMC
GRCNVGNKFVCKDGPVFTLAQLKTMPGEY

>2617921120 Ga0073689_1199 4Fe-4S di cluster domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_119]

VLLLLKKDQVNNWLNKLMQTYQVFAPEKEDNSFYFRQI SSGDQANLDYTNS
LI SPKEVLFPREKLFYRNEAGDVQLMEQI DEEKKVVFGRPCDAKSFL
LLDKVFNNGDEYVDPYYLTRRNNTVLVGLGCNQPAACTCFCTALGGGPFSP
GLDI LLTDTGDQYLVEVL TERGELLSGMDLPAAGQEAQAAKAVKASAD
CSSQVDLGGGLYRLDVNFDDPI WSMI AEKCLGCACTYSCPTCHCFDI VD
EVAGKEGCRIRNWDACMFPLFTLHSGHNPRTGKERFRQVRVMHKFKYFV
DKYGATACVGCGRVNCVNLDI RQVI EQI SSAGGDQ

>2617921119 Ga0073689_1198 4Fe-4S di cluster domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_119]

VFVKMLTDAI RETAQRLLQDKEVELVVGADGSLPLRNTPCFI RRPEDAQ
SLVWGYGCENNLANFLRRRPEKLAVVAKGCDRAI VALI NENQI NREKLV
I I GVSCQGM I DRNKVNSLLAGRELLSAEVNDGQVQLKGRDFLETAPLEQL
LHDSCLTCTHPNPVLYDI LLGEPVPEKGTDLLELSNEADFEAKSPA EKRAY
LQDEL SRCVRCYACRQSCPMCFCECFADCSAPEWLSKSSLNVSDNVFFQ
AVRAYHLAGRCVDCGACDRACPVGI DLRTLTHRMVKDVQEYDYTAGVSL
EEKPPLAAPI SLT

>2617921118 Ga0073689_1197 Methyl-violagen-reducing hydrogenase, delta subunit [pelotomaculum Ga0073689 : Ga0073689_119]

VQRLLLETLGVEPGRFRLEWI SASEGDRFAKLATEFTNQLKALGPNPMGAE
KAGCL

>2617921117 Ga0073689_1196 Methyl-violagen-reducing hydrogenase, delta subunit [pelotomaculum Ga0073689 : Ga0073689_119]

MQFEPNI TAFLCNWCSYAGADLAGSMRFSYPPNLKI I RVPCTGRI NPMFI
I KAFFAGTDGVLVGG

>2617921116 Ga0073689_1195 heterodisulfide reductase subunit B [pelotomaculum Ga0073689 : Ga0073689_119]

MKI GFFVGCNTAFNRPDLEQAVRYALPALGVELDNLGQSCCPSWGTLP
SDPAAWCAVSARNHTLAEKGLDI LTVCGSCYGS LAEAKYKMDHDP ELKA
KANELLKEVGREYKGTCTNI RLSFYLYNEI GVDKI KEALKYKLDGLTI AL
QPGCHSLWPSEVYYDKKESTFKPRVLKEMVETLGATVGDYTRLLDCCGMG
AMRSTDMGKSLALFKKKLDCI KQEVNPDLI VTGCSSCM I QFDTAQKMLQ
DKKI RFEI PVMHYMQLLALCLGAEP AQVVGLAQT DVKSFI DKFRKEQ

>2617921115 Ga0073689_1194 CoB--CoM heterodisulfide reductase subunit C [pelotomaculum Ga0073689 : Ga0073689_119]

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VSETQATLGVVNLSASDSELAGEI RELGGEKLLCEI QCGKCAAGTCPMVLA
GFPFFNKKVI QAVLLGLRDELLEDSSI WACQSCNRCTEI CPRELNPFEEV
QAMRRVAFREFALPTLAI NGLKSLYDTGHAVYLAGAGNTRAKVGLPEKPP
STI ADEKALQEI RTI MQNSALADLDI I PMGD

>2617921114 Ga0073689_1193 heterodisulfide reductase subunit A [pelotomaculum
Ga0073689 : Ga0073689_119]

VPRI GVIYI CHCGENI AGAVNVEEVRQYAENLPDVAVARNYLFMCSDPGQE
LI RQDLKSGLI DRVVVAACPTPRTHEPI FREAVAEAGYNKYLFEMANI RDQ
DSWAHWHDKGATEKAKKLVASAVAKAAYLEPLEDKFVDVTKSAMVI GGG
VSGMFSALDLARMGYQVYLVKPNPSI GGNMAKLDKTFPTNDCSACI MTPI
MVQVGTHPNI KMTYSEVESVEGSFGNFVKVRRKQTYI DWDKCTGCGDC
VNAKLAKKI PNEFNEGMDNRTAVYI EFPQAVPKRAVVDMEHCLNCGKRTI
GTAPKI SPKTGEPI LAPCEKACKTGALDRSRAYDPEGGI LEFDVGAI I VT
PGYKVMKTPPFKEYSPQSPNVVTSMLERI LSATGPTQGHFERPSDKKKP
HTLAFVSCVGSRDTRSHTYCSKVCCMYMLKEARLI KEKYPDTEI YMFFI D
VRTVGKDFDEYYTYCRNLGI KI I RGRVAAVDELPGDNLRVRAVDVLDGTP
VELEADLVVLATAI EPPQGLADLGRKLG I NLGSEGLKEMHTKLYPVETA
VRGI YI AGCAQGPDI PDAVSQARAASSAAAI PLTFGKI VVEPLI SEVI Q
RKCSGCGTCEKLCPYSAI KLMDKGGRLRSQI DEALCAGCGVCAASCPSG
AI TLHGFTNVQI DAQI KTLACS

>2617921113 Ga0073689_1192 methyl tetrahydrofolate--corrinoid iron-sulfur protein
Co-methyl transferase [pelotomaculum Ga0073689 : Ga0073689_119]

MELI GERI NGMFKDI KEAI LNKDPAAVEYWAKRQTEKGAAWLDI NTGPTV
AKEDQPAVMEWLKTAQSVSPLGCC I DSTNPDAI EAGLKVHRGTALI NST
TADQWKMDI YFPMVKYGAkli GLAMNEAGVPKDASARAALAMELVVNAD
MNLGPMQDLYI DPLALPANVGQDHGPEVMEAI RQI KMLADPAPKTTMGLS
NVSQRCSEHLLNRTYMLCMAVGLDSCVADVDDDELVRAAAAARVLLNK
DI YCDAFVKTFI QSFQR

>2617921112 Ga0073689_1191 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_119]

PI VGAMGYGLEAYSI MERARLGALTGDKMLAMPVI CFVGQETWKTKEAR
TEDNDEWGAQARRAI LWEVVSATSFAQAGGSI LVLRHPESLKQFNTHI TS
MMKSNAI

>2617921111 Ga0073689_11846 polysaccharide deacetylase family sporulation
protein PdaB [pelotomaculum Ga0073689 : Ga0073689_118]

LRVFTLTI RKNRI KFTLLTASI I LI AAGYFFKSWSSPVTAATAPVYQGS
GEKKI ALTFNVVWGEYI PQLI ESLKDNSVPATFFI GGQWAEDEFELTKE
I VRGGHEVGSHGYSHPHPDRI SLSANI DEI EKTEEVLNRVAGVKPTLFAP
PYGERSEVVLRAAEEAGYTTI LWSI DTI DWQCPDAI I VRRVI DKSHNGA
I VLMHPTAPTVAHALPQI I KELKRQGYELVKVSTLLEGLKNEKERLKEKI G
ESL

>2617921110 Ga0073689_11845 polynucleotide nucleotidyl transferase
[pelotomaculum Ga0073689 : Ga0073689_118]

MSDYPVLKREI VI GGRLMFLETGRLARQAGGAVFVRYGDTTVLVTATMAN
HSRTGI DFFPLTVDYEEFYAVGKI PGGFI KRESRPSEKAI LSGRLI DRP
I RPLFPKEI RNEVQVI ATI MSVDQDHAEI AAMI GASAALHI SEI PLKYP
I GGV I MGRVDGEFI I NPVLAQAEKSDLHLVVAGTGNVMMVEAGAREVPE
DEMLEAI VFGHEVI KEI VDFI EKFRAEALQMGLAKDKFVPEFAKPDPAI
EAI TDMATGKI DQALRRCATERMSKLVRDACLDGVKAELVRQFLEECPGA
EEGVI KNI LDSVEKKLVRRMI AVEGLRI DGRALNEVRPI SVDVGVLP
RPH GSGLFTRGQTQI LSVVTLGTI SEEQI LDGLGVEESKRFMHYHNFPPYSTG
ETKPMRSPGRREI GHGALAERALSIVI PGEFFPYTI RI VSEALESNGST
SMGSVCGSCLALMDAGVPI SAPVAGVAMGLI KEEENFTVLTDI QGFEDHL
GDMDFKVAGTTTGI TALQMDI KI PGI TREVFEKALAQAYEGRMHI MGKML
EVI PNPRLLESPHAPRI I HTTI DPKI RDVI GPGGKI I KKI VEETGADI D
I EDDGRVFI AAVDQENGKKALEI I ETLTKEVQSDEI YI GKVTRVMDFGCF
VEI I PGVLGLPGKEGLVHI SQLEHYRVNKVEDVVEGDMI TVKVI GYDNO
GRLKLSRKDAI PAPEGTPAKEGRPHRSRRRDSARG

>2617921109 Ga0073689_11844 SSU ribosomal protein S15P [pelotomaculum Ga0073689
: Ga0073689_118]

MALTEQKQNV I SKYKLHENDTGSPEVQVAI LTERI NTLTGHLKLHKGDH
HSRRGLLKMVGORRALLNLRDRHFERYAI I EKLGLRK

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>2617921108 Ga0073689_11843 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_118]
VGVPKFDSTEEI RKWLNHI AMI CLSEEFQSLKKELEI I YLQSNVENFRL
IAFQDALYAFLSQEEEDRAYQTSVY

>2617921107 Ga0073689_11842 riboflavin kinase / FMN adenyl transferase [pelotomaculum Ga0073689 : Ga0073689_118]
LYVYNNWYGLKDKHREI VVGLGYFDGVHLGHQKLI AELVRMAKEKGGTPA
VFTFHPHMAVLNPENSPPLLLSQESKQKFI ARLGVEVLLLAPFDVI FAS
LSPEDFI KI VLYEELGVKGVVGYNYTFGHRGRGTPALLKEQSTI FGYQL
QVPPVKI TGQTVSSTLI RGLLMKGEVAEAPMFLGYYPFI EGWVVSGEKR
GRTLGYPTANLEI DQI LLVPANGVYI VKVYFDGDTYLGVANI GTKPTFQG
KARNVEVHLI DFFGDLYGKHI KVSFTRRLREEKRFKTPYDLVKQI EQDI L
KARAEWSKVRE

>2617921106 Ga0073689_11841 tRNA pseudouridine synthase B [pelotomaculum Ga0073689 : Ga0073689_118]
MTSHDVDFI RRTLKI KKAGHTGTLDPGASGVLVI CLGI ATRLAQFLLND
DKEYRAEI TFGQATSSGDSFGDI TTEGDAAHLTEDTVRSVLPAFTGEI RQ
VPPMTSALKRQKKLYELARSGLVFDRPARTVSI YSLDFI RGTGWGGPRP
RALLHLVCSKGTYYRSLCDDI GSRLGCGAHMSFLVRTMVGTFKI FDSLTL
EELRSATGDGSLNKI VTI DEALSHLPVVVKSSAAPAVASGSRLYPPGV
DRLQEGLVGRRLVRLI GPEGLLAVAKADFPDDCERLI FKPVCVLAK

>2617921105 Ga0073689_11840 phosphoesterase RecJ domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_118]
MNSLADI TAALGRARNVLI CGHI MPDGDCLGSVLALGSSMELI GKKVTLA
GPDPVPDLYNPLPGVDRFLTGEPPSEYDTI I VLDCSVPERLGNGYRDLL
TGGAVVI NI DHHSAPSAPFGTYI YI DPHAAVGEI I FDLLNLMQI KI TPEA
AI CLYTAI I TDTGSFYDNTTTPETHRRARLLELGVPAARVNNRVFQEK
GEALI LLGAALDTLSLSPCGKVCWMVTRSMNNTGARDEHTEDLVNYAR
SVRGVEVGLFFREI SNGKFKI SFRSKDAVDVNQLAALFGGGGHQRAAGCV
LQALSEI VEKVVAVAVAAAGEI KK

>2617921104 Ga0073689_11839 ribosome-binding factor A [pelotomaculum Ga0073689 : Ga0073689_118]
MSFRPERLAEAI KKEVSELLREELKDPRI GFVTI TSVEVSKDLRCANI YA
SVLGDSKDQKATI EALQKAQGFVRGELGRRI RLRYTPEI TFKLDQSI SRG
SKLI SLMKEVKEKGGGERDE

>2617921103 Ga0073689_11838 translation initiation factor IF-2 [pelotomaculum Ga0073689 : Ga0073689_118]
VVKRRI HELAKELNI ESREI I NRLNKMGI SVKSHMSTLEDSEVERLLQHY
KKDKSGVESPDVKPAPAQGSAGVPAPGAVFRERQEGGKGTLPDAEKTE
KKGNGRGDQRKGGQGSRLDHYRGPGLVGRVPSRPPDKRFQERPQKTEKVK
PRDQGDHGARAQAEALQDRPKERHQPDPHGRQSRPQQGQAQPERPHHGGI
PONRLRQERAQQRPFOQTPAQSGPSRQERQESGAGKPADRPHEGTQTAGV
GOERRARSQSRGDREHRPGGPQAARPKQADRPVHTGAGQAARPRPDQI VK
LPQARLDEKGRPVVEKQRPQDKQKQGGQKPAKGRVDKRGTI SEQAEQ
KLLMKAAASRKKAGSKTRENI QRPTQPVEKKPVVLGESTTVQELALKMHK
SPAELI KKLMLQGI MATI NQEI DNDTATI LAGEFGYEVEVRLPVDMDAVL
MQEPEDDPALLOFRPCVVAVMGHVDHGKTSLLDAI RETNVMATEAGGI TQ
HI GAYQVEHNGKKI TFLDTPGHEAFTAMRARGAQVTDI AI LVVAADDGVM
PQTVEAI NHAKEAGVPI I VAI NKI DKPGANPDRVKQELTEHGLVAEEWGG
DTI CVNVSALKKEGLEDLMEMI LLVAEMNEFKVNPDLARGTVI EAELDK
GRGPVATVLVQNGTSLVGDTI I AGTAFGRVRAMMDKGRRI KKAGPSTPV
EVLGFSEVPSAGDI FVVVEDEKLARTI VARRQTKRREEELKTI TRVSLED
LFFKHI QEGQI KELGI I VKADVQGSVEALSQALLRLNTGEVKVNI I HGGVG
AI TETDI MLASASNAI VI GFNVRPDVNARKAAGNEKVDVRLYRVI YDAI E
DVKAAMSGLLEPEYREVM LGRAEI RKI FKASRI GTI AGCYVLEGKI ERDA
GVRVVRDGI VVYEGKLESLKRFKDDVREVTQGYECGLALEKFNEI QEGDI
IEAFTMEAVKRELS

>2617921102 Ga0073689_11837 Ribosomal protein L7Ae [pelotomaculum Ga0073689 : Ga0073689_118]
LALSEMI GLGQAGKLVSGDI AVKNALAGGRVSLI AKDAAERTLKELT
RMAGSGNI PTI I YGSKEGLGRMI GKSHRSVAFTDEQMARGI LRTLERN
VDRT

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>2617921101 Ga0073689_11836 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_118]
 VPKVKKI PRRMCVGCQEMKPKKELI RVRTPDEKI EIDPTGKRSGRGAYI
 CPGLECLNKAMKGNRLDKALHRPI TPEI WGALKQELAK

>2617921100 Ga0073689_11835 NusA anti termination factor [pelotomaculum Ga0073689 : Ga0073689_118]
 MNTEFLEALKDLEKEKGI TVDI LLEAI EAALLSAYKRNFGLQARVHI D
 RDTGDFKVYTQRTVSEQVEDPRLEI TLEEALKI NPNEYI GDI VETEVTPR
 NFGRI AAQTAKQVVQRI REAERNI I FEEFANREGDI VTGVVQRI EQKNV
 FI ELGKTEAI LAPTEQI PGEEYRHGERI KTYI I EVRKTTKGPQI LVSRTI
 PGLLKRLFELEVPELHDGVVELKGI AREAGARSKI AVYSRDENVDPVGAC
 VGPKGMRVQNI VNELNGEKI DI I KWNPDPSKFVSSLSPAKVVAVEI WEE
 EKVARVI VPDYQLSLAI GKEGQNARLAAKLTGWKI DI KSESQMGEI YPEE
 YGEYEYNDHEYEQGEGRCPR

>2617921099 Ga0073689_11834 ribosome maturation factor RimP [pelotomaculum Ga0073689 : Ga0073689_118]
 VARQRI AEMVEKMVLPPVQEAAGLELMDVEYI KEGNRWYLRI FIDKPSGI D
 VEDCRYVSERI DKLLDEKDPI PQSYTLEVSSPGLDRHLKKRDDYSRFTGR
 LANI I TYMPI QGEKKFSGRLKGLRGNDVI LDI NGSELLI PLEHVASARLE
 VEF

>2617921098 Ga0073689_11833 putative Mg²⁺ transporter-C (MgtC) family protein [pelotomaculum Ga0073689 : Ga0073689_118]
 VLTEGEI I VRLVMALALGGLI GLERERLHVGYRTYSAGFRTHI LVCMGAA
 I CMVVSSEGI HYQFKGDAARI AAQVVSIGI GFLGAGAI MREGLLVRLTAA
 TLWVVASVGLACGAGYYLAATLGTMLVLFALVI LGTFEDFVRGKRKYDML
 SI VASDQPEQVSLI GSVLEQQLGNVKKI EVNKTGEPGRVLLEVYMKLPTD
 ANMI DI LHLRTALPGVYRVEHRV

>2617921097 Ga0073689_11832 processive 1,2-diacylglycerol
 beta-glucosyl transferase [pelotomaculum Ga0073689 : Ga0073689_118]
 MRTAEALKKAVEEMYPEAEVAI LDTFRYASPFLEKVVLTGYMEI I KFSPI
 I YGYLYRQSERGQPLSGRGKAEFSRI LNLLTAPKLEDYI KSFKPEI I VCT
 HPFPLGI LSRMKGKGTFRGPLFATI TDFTVHSFWI FPEVNCYFVGSETLV
 AECEEFGI EPERI CPTGI PI DPAFDAAYDKCRLKEQLGLVPTLPAALI VG
 GGLGMGPLATAVKI I GRGQHGCQLLVVTGTNKVLRDKLERMAPEFTCRI K
 I FGFVDNI HOLMAASDLMVGKAGGLTCAEAMAVGVPLFI VDPLPGQEERN
 TKFMTTVGAGVRVEEGELADVVRDYLNNSGRLEI MARKAASHGKPGAART
 AVKI MTEAVSKYFKLYGL

>2617921096 Ga0073689_11831 prolyl-tRNA synthetase [pelotomaculum Ga0073689 : Ga0073689_118]
 MRATELFAPTLREVPADAENVSHQLLLRAGFI RRAAGVYTYLPLAMRVI
 KKI EQI VREEMDRQGGQELLMPI I QPAELWQESGRWEVYGPFLRLKDRH
 NRDFALGPTHEEI I TALVRGEVNSHKQLPLLLYQI QNKYRDERRPRFGLI
 RGREFI MKDLYSFDRDEEGLEVSYKKMYEAYTRI FQRCGLCFRPVEADSG
 AI GGSDTHEFMVLADSGEAAVLFCGREECNYSNVEKAAVHFPTGTDEG
 MEPLTAKETLGCRTVEEVSKFI GAPPQKI I KTLFYETEKETVATLVRGDR
 EVNEI KLLNTLNALRL ELAGANVVRDATGVAVGFAGPVGLKDVRI VADPE
 VAAMI NAVAGANKDDVHYLNVNPGRDFQADI VADI RMVEAGEPCPGCGAP
 LOEGRGI EVGQVFKLGEKYSKALGATFQDENGESRPI I MG CYGI GI TRTM
 AAAI EQNHDQDGI I WPAAI APFHAVVI PVSARDGAQLAMAGEI YDHLASA
 GVEVVLDDRPERAGVKFKDADLI GYPLRI TVGSKAVAEKQVELRVRGTR
 VTVAPVEKLGDTVRELLQKL

>2617921095 Ga0073689_11830 4-hydroxy-3-methyl but-2-en-1-yl di phosphate synthase [pelotomaculum Ga0073689 : Ga0073689_118]
 MQRKTRPVYI GKVQVGGGAPVSVQSMNTNTDTREAAATVAQI NQLAEEGC
 EI VRMAVPDREAAAAALPDI LRGI GVPLVADI HFDYRLALEALKAGVDGLR
 I NPGNI GGRERVAAVVEAARERRVPI RI GVNAGSLEKDLLAKHGGVTAAA
 MVESALGHI RI LEDLNHTAI KI SLKASNI PLMLEAYRLLAGKVDYPFHI G
 VTEAGTLRSGAVKSAVGI GI LLNEGLGDTI RVSLTGHPLHEVRVGYDI LK
 ALGLRRRGVEFI SCPTCGRTQI DLI KI AEEVEEKLRRDLRSLKVAVMGCA
 VNGPGEAREADVGI AGGKGEGLI FRKGEI I RKAPEDRLVEELLKEI EKLK

>2617921094 Ga0073689_11829 regulator of sigma E protease [pelotomaculum Ga0073689 : Ga0073689_118]

Table S2

MLTFVASVFVFGMLI FFHELGHFAVAKLVGI KVHEFSLGFGPKLFGI PAG
ETSYNVRTLPLGGFVRMAGMDPNEEEEDLRDEERGFKKSVGQRMVAVI FAG
PLMNFLLAI LLVGAVFFFGAPVPSTGTGI GAVVPGSPA EKASI LPGDRI
VAVNDRPVEKWVELVDLI NQRPEQNI NLTVARDGVQRQVAVKTI RDEGGS
GKI GI YQASDFVKTGFLQAVGKGVETGRVTFMI MDFI SKMI FGOAPAEL
GGPVRVVEI GKAAQVGFFLLQLSAFLSI NLGLFNLFPI PALDGSRI LF
LVWEKVRGRVPDPVKENFI HLVGFGLLLLLLMVVI TYNDI LQI FVSDKAPG
PR

>2617921093 Ga0073689_11828 1-deoxy-D-xyl ul ose 5-phosphate reductoi somerase
[pel otomacul um Ga0073689 : Ga0073689_118]

MKRLVI LGSTGSI GRQTLEVVRSLPGRFAVVGLGAGKNRHLLAEQI REFR
PLAVTLAGERDLVCLSNELPPSI TPELFWGQRMENLAGMSEADLVVVAV
TGAAIGI FPTLAAI RAGKDVALLANKETLVAAGHLVMELAARNKTTI WPVDS
EHSVWQCLNGCTKDGVAKLI LTASGGPFRKLSREEMETI TVEMALRHPN
WDMGRKI TI DSATLMNKGLEVI EAKWLFQVDYSRI EVVVHPQSI I HSAVE
FLDGSVI AQMGLPDMRLPI QYALTYPERVAGSI PRLKLSGLRELTFEED
TERFPSRLRAFEAGRAGGAMPAVLNAANEVAVDSFLKGLLPFTGI PVVVA
GVMEKHRGVSRRPGLEEI VAADRWARETGRKLI KTFFK

>2617921092 Ga0073689_11827 sporulation integral membrane protein Ytvi
[pel otomacul um Ga0073689 : Ga0073689_118]

VPKLLYI FYAAVAI VVVI AAFKYVPI LVPFI I ALVFSI LMEPVI RI LQ
LKARMPRGPATLTA VLVFFGGI AI I LSAI I FOLVAELVLLSTSLPGI VAE
FRLYYNDLI DRI TAFYVTLPOGMVSSLEQNI SNLAANLQGLI SRAVNSLL
QFMSI LPGTLTVI VVSMLATYFLARDRKLLADFLVRLI PAPWGEKTVVI L
REVANAFTGYLKAQVVLVLI TTGLSI TGLYLI GAKYALTGLLI GFFDLI
PVLGPATI YI PWI I WSFTTGETGFGI KI TVLYALVFVVRQVFETKI VSSN
LGLHPLATLLAMYAGLKTGLTGLVLGPI LVI AMQAVFKAGVFKPKD

>2617921091 Ga0073689_11826 phosphatidate cytidyl transferase [pel otomacul um
Ga0073689 : Ga0073689_118]

VLRRVLSALAGI PLI VLAVWHGGI PLLLLTGLI I I LGLREMI EMLARLG
LKASLGLALAGGLI LLGGAYLYKDGYPGPTI TVI LFI HLI ATVALYPRYS
LLDCAGTLMGTLVYGLLSYFYLLRTLDPDWI WLI FMFAGTWVSDTTAYFI
GKYFGRRKMAPVLSPKKTLEGAGGGLLGSLLAGYSFALI YPFLPLPKMLL
LGLLLGVAAEVDLLESFAKQAGVKDSSTLI PGHGGI LDRFDSALFTAP
LVYYFVLLFI I S

>2617921090 Ga0073689_11825 undecaprenyl di phosphate synthase [pel otomacul um
Ga0073689 : Ga0073689_118]

MI DKLVAFWRWKESGEHSGTDAGKLLKMVDKNRLPAHI AI I MDGNGRWAQ
KRRRLPRSFGRHRTGVESLRDI VKI CAELKI RI LTVYAFSTENWKRPLEEVI
TLMNLLVEYLHKEI EELCRNGVRVNP I GRLGDLPPSAREALQMAMERSAG
NKGVLNVALNYGGRTI VDAVRAI ASRVEKGELQAEI DDRTI SNHLYT
AGQDPDLLI RPSGDYRVSNFLLWQLAYTEFWLTPVMWPEFRRI HLLRAL
VDFQRRDRRFGLKK

>2617921089 Ga0073689_11824 4Fe-4S binding domain-containing protein
[pel otomacul um Ga0073689 : Ga0073689_118]

LAYKI TDECLACGTCMESCSNEATI EGNVYKI DTEKCENCGACI ESCPTG
AI I EE

>2617921088 Ga0073689_11823 hypothetical protein [pel otomacul um Ga0073689 :
Ga0073689_118]

MDRLPDI TGFLPDEALARCKEQGYKI ELLI TRPLKEYPQGEAKAVRFKPV
SGNKGVLTVYTI

>2617921087 Ga0073689_11822 ribosome recycling factor [pel otomacul um Ga0073689 :
Ga0073689_118]

MTSEI I KEAENNMKTI NVVKTEFASLRAGRATPALLDKI MVNYYGTPTP
VNQLANI SVPEARLLVI QPWDKSSLPEI ERAI LKSDLGI TPASDGTVI RL
AI POLTRERRAELMKVVKKKAEEGRVAVRNI RREVNDQLKARQKDGKMSE
DELKRGQDEVQKLTDRYI KDI DGLLTKEQEIMQV

>2617921086 PyrH uridylate kinase [pel otomacul um Ga0073689 : Ga0073689_118]

MVAPKYRRVVLKLSGEALAGSQGYI DPDVVNAI ARQI KDVVECRVQLAV
VVGNGNI WRGVAGSAKMDRATADYMGMLATVMNSLALQDALQKHGVDTR
TQTAI EMREVAEPYI RRRRAI RHMEKGRVVI LAGGTGNPYFSTDTTAALRA

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AEI EAQVI LMAKRVDGVYDSPLKNPEAKKFELSHI EMLNRGLGVMDAT
AASLCMDNKI PLI VFDLNQEGNI KKA VFGKEI GTYI GGELNDK RNY

>2617921085 Ga0073689_11820 translation elongation factor Ts (EF-Ts)
[pelotomaculum Ga0073689 : Ga0073689_118]

MSI SANLVKELRERTGAGMMDCKKALTETRGDLEKAADYLRERGLAAAAK
KAGRVATEGLVESYI HGAGRI GVLVEVNCETDFVAKTEEFKAFARDI AMO
I AAKPEYVRREEVPAALVEKERAI LRVQALNEGKPEKI VDMMVEGRI EK
YFKEVCLLEQPF I KDPDTTVGQLLTEKI AKI GENI NI RRFARYELGEGE E
KKKSDLAAEVEEATRNI CK

>2617921084 rpsB small subunit ribosomal protein S2 [pelotomaculum Ga0073689 :
Ga0073689_118]

VAVI SMKQLLEAGVHFHGHQTRRWNP KMDPYI FTDRNGI YI I DLQKTVKKV
EEAYNFVKQLSLEGDNI LFGVTKKQAEAVREEAERCGMFYVNRWLGGM
LTNFQTI RRR I DR LHELEKMEANGTI EVLPKKEVAELMHEKERLQKFLGG
I KDMRRLPGALFVI DPRKERI AVAEARKLGI PI VAI VDTNCDPDEVYVI
PGNDDAI RAVRLLTGKMADAVLEGROEQ LAE

>2617921083 Ga0073689_11818 transcriptional pleiotropic repressor [pelotomaculum
Ga0073689 : Ga0073689_118]

MRALLDRTRAI NKLLQKSAGNTVDFNEVADVLS ENI ESSI YI LDRNGKVL
GYSYLGWTCDI MKDI VEGQGGFPEDYNENLLKI DETNANLCQI ANACVF
LPQRCRFNNKI TTI VPI VGAGSRLGT LI LAKFDKHFTYEDLV LAEYGATV
VGMEI I RSRAEKMEEEARKRAAVQI ALGTLSYSELDAVQHI FKQLEGEEG
LLVASKI ADRVGI TRSVI VNALRK FESAGVI ESKSLGMKGT YI RVLNDR L
LEELKRVKQH

>2617921082 Ga0073689_11817 ATP-dependent Hsl UV protease ATP-binding subunit
Hsl U [pelotomaculum Ga0073689 : Ga0073689_118]

MKELTPRK I VEELDKYI VGQKKAKKAVAVALRNRYRRKKLPEDFKDEVI P
KNI LMI GPTGVGKTEI ARRLARLVKAPFVKVEATKFTEVGYVGRDVEGMV
RDLVETSI RMVKOEKMAVVEDRARKMADERI I ELLAPYPVHDAPPRNPLE
MLFGAAKPLAEQADKSQEQRMKRVEFERDI LREKLEKGELENEVLEI EVE
DTKPPMLEVFTGSGMEEMGVNLQDMLGGLLPKKRRRKVTVKEARGI LTQ
QEAQKLI DMDEVSTAVRRAEEDGI VFLDEI DK I AGQEGYGPDVSRGGVQ
RDI LPI VEGSTVVTKYGPVKTDHI LFI AAGAFHI VKPSDLI PELQGRFPI
RVELEGLTKENFOQ I LTEPRNALI KOYTELLATEGVRVKFTQNSLVEI AK
I AYT VNEQTENI GARRLHTI LEKLLEDI SFEAPELTVKDI TI DCGDVI EK
LGELVKNQDLSRYI L

>2617921081 Ga0073689_11816 ATP dependent peptidase CodWX, CodW component.
Threonine peptidase. MEROPS family T01B [pelotomaculum Ga0073689 :
Ga0073689_118]

MFHATTI VAVKKDGVAMAGDQVTFGQNTI I KKGARKI RRLFKDKVVAG
FAGSVADAF TLFEKFEGKLEEYHGNLQRATVELAKDWRTDKVLRRL EALL
I VANKEDLFI VSGGGEVI EPDDGVAAI GSGGPYALAAARALARHTPLEAG
AI AREALAI AADI CVYTNENI TVEEV

>2617921080 Ga0073689_11815

methyl enetetrahydrofolate--tRNA-(uracil -5-)-methyl transferase [pelotomaculum
Ga0073689 : Ga0073689_118]

MTVNRI TSQKGI PGGFTTYDQHPTSQSVTVVGAGLAGAEAAWQAAGLGI K
VRLWEMRPEKLT PAHLTGDFAEI CSNSLRAVAPEKAVGLLKEEMRR LDS
LI MACADETRVPAGGALAVDRYLFARCVTEKLSRHPLVEI I RGEVPGI PT
DGVVI LATGPLTSGAMTDSI RRTGENHLYFYDAVAPI VTAESI DMNKVF
RSSRYGKGEAA YLNC PMNREEYEVFWEALVRAEKAPRKEFEKELHFEGCM
PVEAL AARGRETLLYGPLKPVG LTPRTGRRPYAVAQLRQENAEGTMYNL
VGFQTS LKWDEQRRVFS LI PGLAWAEFVRYGVMHRNTYI NSPALLKPTFQ
SKKRLTLFFAGQ I TGVEGYVESAA TGLMAGI NAARLLAGEEPLVFPRETA
HGSLAHYI TEADPANFQPMNI TFGLFPSLA EKI RDKKEQYRMVAGKALDS
I TKFKEKL RPGRFDNSCRSELV

>2617921079 Ga0073689_11814 Nitroreductase family protein [pelotomaculum
Ga0073689 : Ga0073689_118]

MI NEFLELCRGROS I RKFTAESVPDEALKQI LEAAQTAPSAGNLQAYKI V
LVKEPQTKQMLAAASLN LATTWVGA FRDKEVKA AVGTEAYHVPVALLPVG
HAGGKPRRTDRRH LQNI VKVI

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>2617921078 Ga0073689_11813 Molybdopter in or th iami ne biosynthesi s
adenyl yl transferase [pel otomacul um Ga0073689 : Ga0073689_118]

MLSVÉQLI RYKRNI LLAGCEEAGQERLLAGKVLLI GAGGLGLI DPDVVEL
SNLQRQI LHNI GDLGRPKVDSAREKLLALNPDMKI ETVTGAFTRNATAL
VVRVDFVI DCTDNFAVRVLLNEVCVRTGRSFVYGGVLAYAGQAMTI VPGR
GPCLRVCFQEQEAPGEGPTTGHVGVLRVPGVI GAI QAEEAAKYFLGAGDL
LAGRLLTFDALTMTFFEAKVGRAPNCPVCQEQSGGI T

>2617921077 Ga0073689_11812 Molybdopter in converting factor, small subuni t
[pel otomacul um Ga0073689 : Ga0073689_118]

LEVEVWAFSGLEKFVPEVGSSKDLLVQI PEGATVRELI AQLRI PPDQI FT
MFANSRHALPDQVLQPGDRVALFPPI SGG

>2617921076 Ga0073689_11811 Al dehyde ferredoxi n oxi doreductase [pel otomacul um
Ga0073689 : Ga0073689_118]

MCCSNVYPLPDGKVCAP I EYESDWALGPNLEI GDLDVVGRNLNI CNDVGL
DTI ETGVTLGVLMEAGVI PFGDGEAAI NALKEVGKETS LGRI I GSGAAVA
SKVFGVTRVPVVKGGQLPAYDPRACKGI GVTYATSPMGADHTSGYAVTAN
I LKVGGYVDP LKPGGQVELSRNLQI ATAALDSTGLCLFVAFTVLDDPEGM
PAI VETI NAQYGTQLTMDDVTEMGKQI LKTERGFNRRAGFAEEHNRLPEF
FAI EELPPHNTVFDLKKELDQI FNF

>2617921075 Ga0073689_11810 Al dehyde ferredoxi n oxi doreductase [pel otomacul um
Ga0073689 : Ga0073689_118]

LLDAGDLAGKGTYEVTAI CRERYGSKVGV I TI GPTGEMGLCAAGVTNNDP
DGNSSRYAGRSGLSVMGFKRLKAI VVDSPKTFDALVKDPEKFKA AAKKF
TDVLRKHPTGKGLPAYGTSSLVNI VNEAGALPTRNFSSGRFAKAQEVSG
KKLAETA VRGVGKPP TSAI RVA

>2617921074 Ga0073689_1189 Al dehyde ferredoxi n oxi doreductase, N-termi nal domai n
[pel otomacul um Ga0073689 : Ga0073689_118]

MLLRVDMTKKEVKFMDVPEKYTL LGGRALTSQI LADEVPTCNPLGGFNK
LI FAPGLLSGTNAPSSGRMSVGGKSPLTGGI KEANAGGI TSQKLANLGI K
AVI VEGKPDWAGI F

>2617921073 Ga0073689_1188 i ntegrase/recombi nase XerC [pel otomacul um Ga0073689 :
Ga0073689_118]

MYSFI DNFLI YLKVEKNASPLTVENYQKDLFHGLDYFASRLKKKDHEI VP
ADI EHRI FRHYLAFLQKQGLARTTI ARRLAAWRSFYRYLRREEI I SDNPL
AAVTGPKMEKRLPKFLYEDEAALLVEAPDLNHPLGI RDRALLETLYAGGL
RI NELVSLDLGDLGQGYI RVMGKRARERLVPLGSRRAVEALRVYLAKAR
LRLLANSSFKKDKGADGLAKSGMI PTPGGFNNAVFLNRWGDRLSARGI RK
I LDKYVERVSLERRI SPHTLRHSFATHLLNAGADLRVQELLGHARLSST
QI YTHVTGERLKKVYRKTHPRAEE

>2617921072 Ga0073689_1187 DNA topoi somerase-1 [pel otomacul um Ga0073689 :
Ga0073689_118]

LSKTLVI VESPAKAKTI GKFLGKKYMKASMGHVRDLPKSQFGVDVKNGF
KPKYI TI RGKGDTI KDLRAAVKKSNOVLI ASDPDREGEAI AWHLQNLDDI
CDDRPCRI EFNEI TKQAI QNAVHHPRI DYNRVNAQQARRI LDRLVGYNL
SPLLWRKVKKGLSAGRVQSVAVRLI CDREEEI QAFEPEEYWTMTGLFEKA
GHAPFEGKLFKYDKKI EI GNEGRVREVLDALKGAKYEVAKVI RKEKSRK
SAPPFI TSTLQQEAYRKLNI ARKTMVVAQQLYEGLDLGKEGTSGLVTYI
RTDSTRVSETAGLDAQNYI RERFGAQYSSRGTAARAAGAGKGKI QDAHEAI
RPTSVFREPDRI KGYLTNDQYKLYKLI WSRFLASQMSPAVFDTTSDVI GA
GDYLFRTATGSI I KFPGMKVYTESRDDGEKEEERLLPELKEREVEARS
LTPKQHFQPPRYTDATLVKALEEKI GRPSTYAPI VETI I KRGYVVREN
KQFCPTLGLI VVDLLKKHFKEI I DI EFTAGMEEKLDGVEEGELDWVQVL
DRFYDPFSRTLEKAEIII GHI QVADEVTEEI CDQCGRNMVI KI GRYGKFL
ACPGFPECRNTRPILLEPTGVKCPCKGELVI RRSKKGRKFFGCSRYPECD
FVTWDQPSKVSCPCGGLLVEKKGAGKNTVLRVNEKCGYKDAPGGKKAR
SRRAGSRETVRKEVVI GREM

>2617921071 Ga0073689_1186 DNA processi ng protei n [pel otomacul um Ga0073689 :
Ga0073689_118]

LEDRI YWLGWQFLMPGTGKRLWSLVDYFGSPGVAWEAGARELAGAPGVGD
EGPEGLARRRSRLDPAKEAAKLESRG I TFI CHTEPGYPENLLEVDPPP
V I FLRGRLKQADKLAVAMVGTRKPSPYGLVVAEKMAGDLAAVGVTLVSGMA
RGI DTAHKGALAGGGRTI AVLGCPCPDVVYPRENRLLMERI AASGAVI SE

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FPPGSPPEAWHFPI RNRI I SGI SRGTVVVEAAEKSGALI TADFALEQGRD
VMAVPGNI VNPLSRGPHRLI KOGARLVEGAGDI LDEMGLDKLFPVPETGG
QGAVKMSDEKSLYGLLSLEPVSMDELI EKSGMSPQKVMAALMYLELKGM
VRQMPGRFYVRTGRNII

>2617921070 Ga0073689_1185 bi functional non-homologous end joining protein LigD
[pelotomaculum Ga0073689 : Ga0073689_118]
MQERYVEI DGVTVKLTNLNKLI WPEEGLTKAHLI KYYSDMAPYVLPYLYN
QPVVMKRYPDGPAGEPFYQKESPDYAPAWI QRQPVHSEKVVNYI VCNNK
ATLVWLANQACI EMHAWLALVENLESPDLAVMDLPAEGATFADTLEI AR
LVERALEEFGLOSFPKTSGASGLHLFI PI KPLYPWROVTAAMKYI AELVA
EAHPDGATTERSVDRREGKVYLDYLSGRGKTMAFPYCLRPLPGAPVSTP
LCWREVEEGDNRPRDFNI ETI FERLKMHGDI YNGVLGPRQFLDRLLRAAT
KKFLPAGRKM

>2617921069 Ga0073689_1184 N-acetylglucosamine-6-phosphate deacetylase
[pelotomaculum Ga0073689 : Ga0073689_118]
MASLFI HGGEI I GEFSI YPNPGLLVKEGKLGFRGGPPGGVETFDAGGMY
I AAGLI DLHVHGGAGADALDDPAALEEI TSFHARYGTTGLLLTI AAAPL
DKMI TTVRAVAEAKSKI KGARI LGVHLEGPYLNPSFKGAQNEEFLLRPDL
SELRELI EAGAGLI RMVTLAPELPGGLEAVANLASRGVI PSLGHSGATFE
EAREAFRRGLRHVTHFFNAMSPLRHREPGPAGLALTEPDI SLEVI ADGLH
VHSTVLKI LWQLKGDLSLVLTDAVAASGMPDGEYPFAGQTVAVKNGRVT
PGKLAGSSLTMAGAVRNMARLAELEI PQALRLASLNPARI LGMPDNGRV
AEGCDADI VLF SRELEPRLVLVGGERFSAESLPSL

>2617921068 Ga0073689_1183 bi functional non-homologous end joining protein LigD
[pelotomaculum Ga0073689 : Ga0073689_118]
MRPLWKGAVSFDLVVSAEPFDSADHLYEVKWDGYRGLAYLDGGTALRSRN
LLDLTGFRFPELAGMHKKVTGLPAI LNGEI VVFENGROSFAGLQSRGRMND
RKRTGRAAI ERPAVFI AFDVLYTGKPKVMELPLLERKKLLEGMVETGGEM
AVSQYI LRDGRAFFDACVKNLEGAVAKKLDLSYRPGRRSPHWQKFRHTN
EADLVI CGYQSPVGDGLASLVLGGRDGLVYQGVGTGFGEREAGALL
DVHGGI EVPEANLAVPQEEGRWTRWVRPLLVCAYEYLAI TAEGLLRHPVY
KGLRRDKSPGECRSVNNSGE

>2617921067 Ga0073689_1182 sporulation protein YtfJ [pelotomaculum Ga0073689 :
Ga0073689_118]
LPEQHPI EGLMKTAMESI KEMVDVNTVVGDPVETPDGTVI I PI SRVACGF
AAGGGEFEVGGERHQGGEGESQMPAFGGGSGAGVSVKPI GFLVVGNGQVR
LLPVDGNALYERLI DI APQI LAQI QSMFRRGDYQPGTKI QMTAQAPAAPP
PPPL

>2617921066 Ga0073689_1181 Protein of unknown function (DUF2953) [pelotomaculum
Ga0073689 : Ga0073689_118]
VSRVYFLTVLAGLLLLFLSLTRLRLRLYRRRGRDDEFSLEFSI WRGLLC
YKLEVPVVKMKVKTGPKRKRTRPRPLSRLAPRPVFKI KTEVEGEGGRPI A
EEKKQVRVPGPLRLGI LTNSI RLVKRYSAI VFLLRRVHLRRLQWRTEF
GAGDPAQTGFLAGTVWGI KSFLLTVI HRLFASGGARPVSVAPDFEKARF
GATLDCI FEVRI GYI I LAGFKALLI KLKS

>2617921065 Ga0073689_11753 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_117]
LSVAGRYRI WIMAI FIPMAI YLFYFALGVRESGETGRI EQLSGTYLEAG
VPAEI DGGTYRAGAPGYEI AFYDTLQAGHNTI MSDPGLI FAVI PVLLPFP
GGGQPALQWALI DDSGRVYKPI STSAARLSNLRRLPEREI LPGTAPDYLV
FKARTGGQTFYKLSTNGTI LYWRLAVPGR

>2617921064 Ga0073689_11752 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_117]
LFVRDYMTONPI TINKTPVFEALESRLKVTRARRAALKP

>2617921063 Ga0073689_11751 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_117]
LTQLTEMELFHI GEQLRAEALAI TKCAACAQQTADPKLQQVYVRAADRHR
GHYETLLRQLQNFQAQRQF

>2617921062 Ga0073689_11750 Coat F domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_117]

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MLDEKDRLTDSLVTQKYI ASGYNLAAAEASNSQLMDTFVGI LRDEHQI HH
EI FNE MNKRGWYQPKAANMNDI SQHVNKWSQELQRVQNTALRQPGAQPAA
YQAGYQTGFQVGMPPQYGFQTGVGMPQMGAEAQQQSLYRPPQNPMI

>2617921061 Ga0073689_11749 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_117]

MVVNELLNLLQLDFPEGVVTVMACFALLKLRFDWKI I LI LSLLWALTNLV
RLLPI VYGTHTFI LLI TI SVYLRI FTRAKLPEI FKATTLCFI I TAVLEMI
YI APLLKI AHSLEDAVTVSAYRALFSLPYESALLMMALLNNRTKKI GC
FI QI PLKDTVKNF

>2617921060 Ga0073689_11748 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_117]

LQNRFTKYRI SGFLTMAFAAEI TMGGRGVEKELVSLLLQDLPESI SFI L
AAFALLRLRFDYKKI FMVAI LQFTTNLI RLLPI AFGMHTVI LLI ALSI YV
RI FTGAKLPKI LSASTI VFVI SAVI QVLYI QPLHNLTGFSYEQVAASPVL
RGAFCCLPYELVAVGLAVFLNRKSKRMAMFSNTTN

>2617921059 Ga0073689_11747 accessory gene regulator B [pelotomaculum Ga0073689 : Ga0073689_117]

MGINQRI ASYLKNKLNLSNDQEEI I AFSLEVLTTLANI I LVVLAAWLAG
SFRESLVTLAVI SLYRSFAGGAHCNAAARCTLLSVLLI PSI GRLAI FLGG
HANTGLLI WLTVLSI LFAVI AVSLLAPVDSPAKPI TSPHRKLNRI LSFL
FLTTVAI QFI LLKASPGGAASTVTAVNI SVFWQTFMLTKQGHGLI NRYD
QLLVHLFSRGGEKNEI HPTHSS

>2617921058 Ga0073689_11746 cyclic lactone autoinducer peptide [pelotomaculum Ga0073689 : Ga0073689_117]

MKYI QHTI LLSMFGFLTFFAKTI GI GPACALI YYQPKAPKSLVK

>2617921057 Ga0073689_11745 diguanylate cyclase (GGDEF) domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_117]

MEKWKVNRKEYI SDHI LVAHI I CFFI FLMAFSLFI KI NVNNALVI YRQI L
VAI SI TGLLVAI YTGKRLVTGI ALGDKPTLTDI ALLLFSFLTAAGI VFLT
GNAGSPVKVI LLI PVI I AATSYGKVAGLI TGGTASMLLFTLDFLAGFGTA
PNLRFOADI VNSTVMLTLGWLI GGLADI ERKVRESLTNLANTDGLTGLSN
HRHFHECLRERLDYAKEKNRPLSLI MFDI DYFKFYNDNFGHQKGGDDVLKQ
TGLI LGRLAQPPNVAARYGGDEFMVI I PDTEEKALTAEEI RAAI ESHTF
EGMEI QPKGKI TVSVGVAGFPGHGQTPKELI RSEDAI YKAKYGRNRVQL
YFSVMDDLREGI AESEKDLFSSI RTLI TI I NAKDRYTFGHSERVITYSLK
LAERLNLPREEMVLLRLGSFLHDI GKI EI DRDLLNKVGPLRPKELAI LQK
HPVWGS DI VRPI SSLKKA I PAI FHHHENFDGTGYPSGLAGEGI PLLARI L
RI ADSFDAMTTDRPYKKAKTTAEACAELKSCSGAMFDPALVDLFLVQLI LE
ENDTHPTFKYHRSF

>2617921056 Ga0073689_11744 Ni fU-like domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_117]

LKEKVQEVLNKVRPFLQRDGGDVELVDVDDASGLVKVRLKGACGG

>2617921055 Ga0073689_11743 (R)-citramalate synthase [pelotomaculum Ga0073689 : Ga0073689_117]

VPMVQI YDTTLRDGAQAEI SFSCEDKI KI ALQLDKMGFHYI EGGWPGSN
PKDLDFFRRI RDYNLCAGI AAFGSTRKAGLAAENDANVKLI LD SGARVA
TI FGKTWDFHVKKALGATLEENLAMI RDTVAYLKSCGLEVI YDAEHFFDG
YKANPAYALETVRAAEAGGASTVVLCDTNGGSLPAEVKEMVELI RQQLRV
PLGI HAHNDGEMAVANSLTAVQAGATHVQGTVNGYGERCGNANLCSVVPN
LTLKCGLETI PRYNLVHLTEMSRFVSEVANVI PSHQPYVGVSAFAHKGG
VHVNALLKDPKTYEHI EPELVGNHRRVLI SELSGMSNLLYKYKELNLKVD
QQSPEGRRVLEEI KNLENQGFQFEGAEGSFELLLRKAYNGHREPFLVLETL
RLI I EMRENDPTYAEAI I KI RVGDEVVHTAAEGNGPVNALDNALRKSLER
FYPVI RQMLTQDYKVRVLDEKDGTAFAVRVHI ETSDGRRSWGTVGVSONI
I EASWQALVDSI AYGLLQKD

>2617921054 Ga0073689_11742 3-isopropylmalate dehydrogenase [pelotomaculum Ga0073689 : Ga0073689_117]

MYKI AVLPGDGI GPEI TVQAVRVLEAVGRRFHREFKFTEGLVGGAAYDAV
GRPLPRESLDLCRNSDAVLLGAVGAPQYDNLPAHLRPEAGALLPLRKELG
LYANLRPVKVSALVNASTLKPEVVDGLDLLVVRELTTGLYFGKKYREAL
PGGARVVDLTLEYTTTEI ERI VRMAFNLAGKRRGKVTSDKANVLESSRL

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WREVVTA VARDY PDVELDHMYVDN CAMQLVKNPRQFDVLVTENMFGDILS
DQASMLSGSLGMLASASI GGGTGLYEP SHGSAPKYTGMRANPIATILSG
AMLLRFSLNLEEEAD CVERAVTGVL DLGYRSADLMEEGKTLVNTIQMGDR
VIEQIEAGV

>2617921053 Ga0073689_11741 3-i sopropyl mal ate/(R)-2-methyl mal ate dehydratase
small subunit [pel otomacul um Ga0073689 : Ga0073689_117]
MQLKGKAWKFGSDVDTDVIIPARYLNTSDPADLAKH CMEDADPAFPFRVK
PGDIIVAGKNFGCGSSREHAPIAIKAAGVSCVIAPTFARI FYRNAFNIGL
PIFESPEAAAGI RESDEVAVDADTGVI TNLATGKTYRATPVPPFMQQIIA
AGGLI NYVAERVKKK

>2617921052 Ga0073689_11740 3-i sopropyl mal ate dehydratase, large subunit
[pel otomacul um Ga0073689 : Ga0073689_117]
MPMTITEKI LAAHAGKDEVVPGELI NARVDLALGNDITAPVAI REFEEKI
VTGVFDRERVALVPDHFTPNKDI KSAEQARLLKEFSKI HGLTNYFEVGRM
GIEHCLLPEQGLVGPGLVI GADSHCTY GALGAFSTGVGSTD LAAMAL
GETWLKAPESVKFEFEGELQPWVGKDLI LHTIGDI GVDGALYQAMEFAG
PTIEGLSMDGRFTMCNMAIEAGGKNGIIAPDEI TRAYIEGRCKRPYQFYR
SDPDAKYKKVYHYDASRI EPQVAFPHLPEKSRPVSEAGHVEIQDAVIGSC
TNGRMEDLRAAAQVLGGRKVHKNVRLI VFPGTQEI YLQALREGLIEAFIE
AGAAVSTPTCGPCLGGHMGVLAKGERAITTTNRNFVGRMGHPSEVYLAN
PAVAAASAILGRI AAPGEVD

>2617921051 Ga0073689_11739 2-i sopropyl mal ate synthase [pel otomacul um Ga0073689
: Ga0073689_117]
MSQRVYLFDTTLRDGEQSPGVSLSVNEKVQIARQLTKLGVDII EAGFPI S
SPGDFEAVRAVAREVKGVAVAGLARANFQDI DRAWEAVRQAEQARI HTFI
ATSDIHLKHLRMSRDEVLAAMA AVKYAKSYTTDVEFSAEDASRSAPDF
LCRVLA AAIEAGATVVNI PDTVGYAVPGEWGKFIETI CQKTPGI EKVVS
VHCHDDLGLAVANS LAAVTSGARQVEGTINGI GERAGNAALEEVMTLYT
RKDQYNFFTGVRTREIYRTSRLVSTLTGMNVQPNKAVVGKNAFAHESGIH
QDGV LKERTTYEI MNPAMVGI AKSNLVLGKSSGRHAFRQRLEDMGYFLSG
EELNKA FERFKKLADKKKEITDDLEAIVVEEMRLVPDTYALEYLHISSG
TTVPTATVGLKRNGELLEEAACGNPVD AISKAVDKI TSMNCTMI NWGI
NAITSGKDALGDVTLKI TADGEKI YTGRGI STDI LEASAKAYVNAV NKL
VWENRRSANHQ

>2617921050 Ga0073689_11738 acetol actate synthase, large subunit [pel otomacul um
Ga0073689 : Ga0073689_117]
VEITVAEALFHCL EQENVEVFGYPGGRI LPVYDALYHSSIKHVLVRHEQ
GAAHAADGYARVTGRVGVCMSTSGPGATNLVTGI ANAYMDSVPMVIITGQ
VPTSEVGTDSFQEVDTGITIPI TKHNYLVKDPRQLPLI VKRAFHI ASTG
RPGPVLI DLPEDVARMKI DFKYPGSVDLQGYRPTYRGHPSMVAQAARIIA
ASERPVI LAGGGVNNAGASRELLQLAEIAAPVTNTLMGLGSFPGKHPLF
LGMLGLHGAKYANLAVTD CCLI AVGARFDNRVVARVSGFAPGAKIIHID
IDPAEIKGNVKAHVPI VGDVKQVLQALLPLVEKKDRTCWLEKVKVLKEKY
PLQYQHDGSLKPQFIIEKLDELTTGGDAIVVTDVGQHQMWA AQYYHFNRP
SFVSSGGLGTMGYGLPA AVGAQLGAPDKTVVLI TGDGSFQMTMQEMGTIA
EQKLPLKI FVFNNQRLGMVRQLQSFFCDSRFSQTLFRFELDF AALAGVYG
MGAYTVKSP EQLNEVLPEALAASGPVLVDCLI SGEENVLPMVPPGSGID
TRVNF

>2617921049 Ga0073689_11737 ketol -aci d reductoi somerase [pel otomacul um Ga0073689
: Ga0073689_117]
MVQVYYDQDADLGLLKGKKI AVMGYGSQGHQAQNL RDSGLDVI VGLRRD
SKNWSKVETDGLKVAVVPEAAEADI IQILLPDELQARVYKEEIEPYLGE
GKALMFSGHFNIFHGQI VPPANVDVFMVAPKSPGHMVRRMYREGKGVPC
IAVHQDYTGRAKDLGLAYAKGIGGARAGVFETSFREETETDLFG EQAVLC
GGVTELI KAGFDTLVEAGYAPEMAYFECLHEMKLI VDLI NEGGLGFMRY
ISNTAEYGDYMTGPRIINEDTRREMKKILAEIQNGEFAKKWILENQANRP
VFNAIARQEKELLIKVGARLRNMMPWLKK

>2617921048 Ga0073689_11736 acetol actate synthase, small subunit [pel otomacul um
Ga0073689 : Ga0073689_117]
MRHTLAVLVENNPGLARVAGLFSRRGYNI DSLAVGRAHNPAVSRMTI VV
EGDESVL EQVTKQLHKLVDVIKISDI TKDEYVDRELVI KVNAEGASVRA
EIMQLVDIFRARI VDVGQKTLTI EVTGNEGKI NAFENALRPFGIKELVRT
GKI AMLRGSRSSSINYSQKEEEAS

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>2617921047 Ga0073689_11735 acetolactate synthase, large subunit [pelotomaculum Ga0073689 : Ga0073689_117]

VSGVKLSGAEI LMKSLAEAGVDTI FGYPGGQALPI YDALYDSDI RHI LTR
HEQGAAHAADGYARATGRPGVCLATSGPGATNLVTGI ANAYMDSAPLVAI
TGQVPRAALGRDSFQEADI TGI TMPI TKHSYLVEDPAELARI VKEAFHI A
TTGRPGPVLI DLPRDVSASETEYVRPGLNLPGYRPVLDGDPQRVQEAAR
AI AGSERPVI CAGGGVVI SGAHGEIVRFAELLMAPVTTTLMGLGGFPGDH
PLSLGMLGMHGTKYANFAVSECDLLI AVGARFDDRVTGKLETFAPGARI I
HI DI DP AEI GKNVRVDI SI VGDVKRVLNQLLEVLQPRLGAEWRDKI QAWK
KEYPLNYCNGSLKPQSVI REI YKLTEGNARI TTEVGQHQMWTAQYYTFT
RPRSEI SSGGLGTMFGMPAAI GVQAGCPDDVVDI AGDGSQ MNQI QELC
TAVNYELPI NVAI MDNGFLGMVROWQELFYNNRYSTELRNPDFVKLAEA
YGAEGI RVTKGSEAAPAVRQAI KSSKPVVI DFLI EREENVMPMPVPPGGDL
NKMLG

>2617921046 Ga0073689_11734 dihydroxy-acid dehydratase [pelotomaculum Ga0073689 : Ga0073689_117]

LRSDVMKKGVEKAPHRSFLKALGYI DREMELPLI GVVNSHNEI VPGHI HL
NDI AEAVKAGVRMAGGTPI EFP AI AVCDGI AMNHTGMKYSLASRELI ADS
I EVMAEAHPFDGLALI PSCDKVAPGMLMAAARLDI PAI VVSGGPMLAGRH
KGKDI SLSNLF EAVGVYAGNMTEDELREVEEAACPGCGSCAGMFTANSM
NCLTEALGMALPGNGTVP AVSAARRRLAKMAGVQI MKLVQEGVRPSDI LT
REAFNNGLAVDMALGCSTNTVLHLP AI AAEAGVEI SLEMVNKVSEQTPNL
CKLSPAGPFFLODLDEAGGI PAVMAELSKKGLI HLAARTVAGTVGDTI AG
KTVFRDVI RSVEKPYSSSGGI AVLRGNLAPDGA VVKKSAVAP EMLKHTG
LARVFNSEDEAVQALKERKI NKG DVI VI RYEGPRGGPGMREMLTPTATVA
GLGLDKDVALLT DGRFSGATRGASI GHI SPEAAEGGPI AVLRD GDI I E I D
I PNNSLNVALSAAEI AARLKD WQSPGPGVKKGYLARYARQVTSASTGAVF
RRG

>2617921045 Ga0073689_11733 branched-chain amino acid aminotransferase [pelotomaculum Ga0073689 : Ga0073689_117]

MMSLI I YLNGEFVPQERAVSVFDHGLLYGDGVFEGI RAYHGRVFKLDEH
LDRLYDSAKTI AMEI PVSKGEMQEI VLETLRRNNLRDAYI RLVVTRGTGD
LGLDPRKCSKPTVFCI AASI QLYPEELYRKGLAVI TVSTRNI PTACSPR
VKSLNYLNNI YAKI EAGLAGVPEAI MLNAEGYVAEATGDNI FVVKNGVLI
TPPSYVGI LEGVTRNVMDLARQKI SVEEKV FSLHDVYI ADECFLTGT A
AEVI PAVKVDGRTI GDGTPGKI TWELI DAFRELTKVDGLLI FPEKVAACG
CCCSKE

>2617921044 Ga0073689_11731 branched-chain amino acid aminotransferase [pelotomaculum Ga0073689 : Ga0073689_117]

VEKI PVVCI NGDFMPGP EAFVPALDGGVLFGRGLFETVLVADGRTVLVKR
HLKRLFTSAAALSI PPPFSPDEVEALLHGTAVRNL DAVRVTLTAGAE
GGRPNLI I HSRPLPYTREHYERGSRCGFVSI PRNERSPLVGHKTTNYFEN
LLARREARQRELDGLFLNTRGEVAEGSVSNI FLVRGGRVTPDGE SGLL
PGI MREVI LEVCRELGI PAERKVLPEELPHSDEAFI TNSLLGVMPLAAV
DGHEI GRGGAGGI TGLLSREI RRTQPYR

>2617921043 Ga0073689_11730 para-aminobenzoate synthetase component 1 [pelotomaculum Ga0073689 : Ga0073689_117]

VLPVFKKI NMVPDDVAVYQRLKGLPYSFLLDSAMPAAGLARYSFAAGDPF
LVFRSTGR LI ELCRPAGGGKGAYNKEI FLGNPF EVLGRLLCEYALARGSK
PVPFVGGA VGYWAYDLGRQI EKI PERAANDQGLYDCWLG FYDTLAAVDHA
AKEVYL VSTGFPEKGRAPVRAAKRLAEFEALLAGGALPEAAGAGGKKAS
LGNLPAPPRTPGRTI QEPGPAMSQEDYYALMEGTS LPLLRTDFTRAGYC
AVVDRAREYI AAGDI FQVNL SQRFC LPA GPD PWT VYRRLREI NPAPMAAF
LNFGDLAVVSASPERFLKVTGR LVETRPI KGTRPRGGDPAENRRWRNELW
NSAKDRAELVMI VDLERN DLGRVCRVGSVNVPELFRI EEYATVFHLVSTV
TGELDRDKGVVDLLAATFP GGSIT GAPKVRAMEI I EELEPVRRGI YCGSI
GYLGF DGDADLNI VI RTL VFTGGKI YFQVGGGI TI DSDPD AEYLETLDKA
LALVRALGLAGDYPLAGAVEI TRAGHYP

>2617921042 Ga0073689_11729 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_117]

LYGVRTGLFKLVFFI WVLDNNGFI VPANFSPQATEGEFVNFRHGHVKVI F
SHNI YGYI PKHQYI EAKYGF DGS

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>2617921041 Ga0073689_11728 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_117]

MDVKKEGVMDMDMGMGSHTPQHI I RMLAESEKMEALYSQI AQAVPSE
ELRRI I MHRAKHELREAERI SMLSHHFGVMPYGPAGMPYALEENK

>2617921040 Ga0073689_11727 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_117]

MHTVRPLI HKAI QI ELTQI CRLATLASMADDELTRGI I LEMI QEETAETAI
FWNTVDAAAYQVMP I PGVGPCPTMAPYPTLEPYPTVPPYPYPTGAPCPDPS
I LPPLGPEATLPPTMPSPGAADGSI PGLPGFFSEPEKKEEK

>2617921039 Ga0073689_11726 biotin synthase [pelotomaculum Ga0073689 : Ga0073689_117]

MLGEFVTRI EAGGEI TFDEALALGGLAGEELPDLFMAALRVTRRFHGGRV
DLCSI I NARSGRCECAFAQSGRYRTGAAVYPLLTKEEI LPRAYEMET
KGARRFSLVTSGRGMAGADFKEI LDYKTLGKTNLSLCASLGI I DYHQA
LRLKESGVATYHHNLETARGHYPKI CTTHSFDERVEMVRAAREAGLGVCS
GGI I GLGEI LAQRVEMAFQKELGVWSVPLNI LTP I GGTPLQGSPPVPPPL
EVLKTAAI FRLVLPRAVI RLAGGREAAALRDLQSLALLAGI NGLMVGNYLT
TGGRLVEDDLQMLRDLELEY

>2617921038 Ga0073689_11725 adenosylmethionine-8-amino-7-oxononanoate aminotransferase [pelotomaculum Ga0073689 : Ga0073689_117]

MGEKHRGELLEQWDKEYI WHPFTQMGEYVKERPLVI ERGEYSYLI DI EGN
RYLDGVSSSLWVTVHGHNNKELNDAI KEQLGKI AHSTLLGLANI PSVLLAK
KLVEI TPPGLEKVFYSDSGSTAVEI ALKMAFQYWRQKDGSAFRKKTKYI S
LGEAYHGDIT GAVSVGGMDLFHEI FRPLLFERI PVPVPYCYRCLRLDRS
SCGMACAGAVEKVMAEKHGEI AAMI VEPLVQGAAGMI VAPEGYLSRVREL
CNRYNI LLI ADEVAVGFGRGKMFACHEHEGVAPDLMCLAKGI TGGYLPLA
ATLATNEI YGAFLGTCEECKTFFHGHYTYTGNPLACAAALVNLELFEDSRL
I EGLGKKI AFLEEGLKTFAGLAHVGD I RQKGMMAI ELVEDKETKKPPY
GENI GHRVI LEVRKNGLI I RPLGNVI VLMPVLSMTI PELGRVLDI TYRAI
ARVTGEAF

>2617921037 Ga0073689_11724 dethiobiotin synthetase [pelotomaculum Ga0073689 : Ga0073689_117]

VTRGLFVTGTDGTGVGKTVI TGGLAGVLGKNGI KAVAYKPVQTGGI ESEEG
LLSGDALFYRVAAGLPYTSRELNPCCLKAPLSPNVAWAEGKVHPPALV
EAYRRLAAENDFVLVEGAGGI CVPLVDYRFTMADLARLLELPLLVARPG
LGAVNHTVLTVEYARRAGLAVKGVVI SGYREDRAGMAERTNPGVI EGMTG
VPVLGI VPHLPEVNVEEGRAGGLVDVI EAKVDWRRLV

>2617921036 Ga0073689_11723 biotin transport system substrate-specific component [pelotomaculum Ga0073689 : Ga0073689_117]

MKLTVMREMLVSMFAALTAVGAFI KVPMPYVPFTLQFLFVLFAGMLLGRK
LGLLSQVVYLLVGLAGVPVFAANGGPAYVMQPTFGYLAGFAAGAYVVGLV
VEKI RGEFGTKFLLAALAGLTVVYALGVTYLYLI LNLVVHKTFTFVQAVW
I GAVVCLPGDLFLSVAAAVSVRVLRRYTAAGGVLRG

>2617921035 Ga0073689_11722 putative transcriptional regulator [pelotomaculum Ga0073689 : Ga0073689_117]

VFKWMKNRLRDLRNHFNLRQEDLADRAGVSRQTI I SI ENGRYNPSLQLAY
KLARVFGTLT EEFVI FEEGE

>2617921034 Ga0073689_11721 Cation transport ATPase (P-type) [pelotomaculum Ga0073689 : Ga0073689_117]

VAALKGGYSPESLQERLPRVDTPFSEHNYMATLHSAGRGRPLVYVKG
ALEVLLDRCAAALAGGGEETGLEKTRI LAMAEEMAGRGLRVLAFAAGANCP
PAGTPWVMRTWLP

>2617921033 Ga0073689_11720 ATPase, P-type (transporting), HAD superfamily, subfamily 1C [pelotomaculum Ga0073689 : Ga0073689_117]

MI DPPRPEAVTAVQI CRSAGI YVKMI TDDHAGTATAI AGQI GLAGSPGAE
QKVSALTGQQLAEI NEKELI DVI EQTTI FARVAPEQKLNI VRALQTMGHV
VAMTGDGVNDAPALKQADI GI AMGI TDDVAKDAADMILLTDDNFASI EAA
VEEGRGVFDNLTKFI TWTLPTNLGGLVI LTSARNDNNLLYSSTEKTSSV
I WSVSGI FHGRI PWPFRAPSKRWFWMPPSWRPNNLLI GRFSLYRGYTPTE
R

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>2617921032 Ga0073689_11719 phosphotransferase system, enzyme I, PtsI [pelotomaculum Ga0073689_117]

MIISTTDGHKI SLTAHVRNRRQLGEAATVGAGVGLLELAPPEDFPAPGSE
EEQIEI FLEARRVSAGRPVTVLLPGPAPGWPEGGRCAPVKTVAFREGIR
SFLVRPEFYRPWLRALLRAGAEGLYELALPMVSHVSEI I ELKKYLSEI RT
ELEKDGVP HQPPAVGI MVDAPSVLPADAI I FEAGFFI VGKRFLGCLMAD
SGLPRDENDFVSFYHQAFLLQVESLI DSLRRRKSRTFCGPLVKDPVAI P
LLVGFGFGEI I APSEYI PGI KKI VQSI NYLDARMVASKTTSYWEPGKARE
YARERFPKLTR

>2617921031 Ga0073689_11718 arginine succinate lyase [pelotomaculum Ga0073689_117]

MTKLWGGFRFKKETDRLVEDFHSSI SFDQRLKYDI VGSVAHARMLGRVGV
ITPGEAGAI VRGLEEV LADI EAGRVEFSVGAEDI HMNVEQLLTAKVGEVG
KKLHTARSRNDQVALDVRMYI RDEI DQLMELLRGLQAALMDLAEKHLDTI
MSGYTHLQRAQPVTFAHHLLAYCOMFHRDGERLADCRRRANVLP LGSGAL
AGTTFP LDR EYVAEQLSFAAVSENSLDAVSDRDFAVEFAAAASLI MVHLS
RFCEEI VLWSSAEFAFI ELDDAFSTGSSMMPQKKNPDVAELI RGKSGRVF
GDLQALLTMLKGLPLAYNKDMQEDKEALF DAVDTVKKCLLVFRPMLLET LR
VRQDNMSEAAARGGFTNATDLADYLARRGVPFREAHAVVGKAVI YCLEKGC
ALEQLTLEEYKNFCPLVAEDVYEA I SI ACCVAARRAPGGPAPEAVREAVA
KARQRLGDQGCQR

>2617921030 Ga0073689_11717 hypothetical protein [pelotomaculum Ga0073689_117]

LVYHSGKI I SKKSLFGDVRGLSKMVI TFVCENRHDTVTFDLTWRGEVS
EEEI RQMI TKNCRCRCKGSDKFI YRTRYKK

>2617921029 Ga0073689_11716 iron (metal) dependent repressor, DtxR family [pelotomaculum Ga0073689_117]

MTKDFHTFREYMRKDDDLLTASMEDYLEMI YRLSRDNGFTRI HDLASALN
VQPPSATKMAQKLADLGV I NYEKYGM I I LSKKGEELGGALLERHRI I EDF
LKLLGI TQEALEETEKI EHTI STETLNCLADFAFFKNRPDVI QEFEI YR
KAQGRPG

>2617921028 Ga0073689_11715 ferrous iron transport protein B [pelotomaculum Ga0073689_117]

MNRGAARAGLNDI LEEVEQLNPAGSLKLNDI VSAI YGRAENI AREVVTR
RGKPEI DWDKRLDDI LTRSLFGYPSMLLLLAVVFWI TLAGANYPSELLAS
VLFVRQEDLSGLLGLLYAPAWVNGLFVEGI YRCLAWVVSVM LPPMAI FFP
CFTLLEDAGYLP RVAFNL DNL FKKTGAHGKQSLTMSMGFGCNAAGVI ACR
I I ESPRERLI AMLTNNFVPCNGRFPTLI ALAGLLTMGA AVSPGATLI VVG
VVL TGI ATTLTVSYALSKTLLRGVPSSFTLELPYRRPRVGRVVVRSVFD
RTLFLVLRRAVWVSAPAGAVI WLLANI HTGGASLLAHGADWLDPLGRLLGL
DGYI LMAFLLGLPANEI VLPVLI MSYTATGSLLLELNSLEALHRLLVLEHG
WSWLTAVCMMLFSLHYPCGTTLWTI FKESGSAKWTALAALI PLGI ACCV
CLAVAGAAARLLGW

>2617921027 Ga0073689_11714 Ferrous iron transport protein B [pelotomaculum Ga0073689_117]

MGLTQQSCGSGVTRESFI KGHAADYVI ALAGNPNTGKSTVFNALTGLS
OHTGNWPGKTVLRAEGGYLHRGLVFKLV DLP GAYSLMANSVEEQVSRDYL
CFGKPDATVVVVDATCLERNLNLVLQVLEI TPKVVVCVNLVDEAERKKI Q
I DYQALADELGAPVVPTAAREGYGLNRLVETI SDI AEGHI TTTPCVVRYR
EVI ENAI RKL EPGI KQLVGDAFNARWVALRLLDKDQTVI AAI EQWLAGRR
SSAAGSGELI LS

>2617921026 Ga0073689_11713 ferrous iron transport protein A [pelotomaculum Ga0073689_117]

MPVKNGKNGEPTGKVM SLGDLPGSWATVNDI RAGGI TRRRMLDLGLVPG
TRVEALRVSPAGDPKAYRI RGAVI ALRKEEAHKI LI EAGE

>2617921025 Ga0073689_11712 arginine succinate synthase [pelotomaculum Ga0073689_117]

MPKVVLAYSGLDTSI I I PWLKENYDYEVI AMAADLGQGELEPLREKAV
KSGASKI YI EDVRRREFVTDYI FLALKAGAVYEGKYLLGTSMARPLI AKKL
VEI AELEGAEAVAHGATGKGNDQVRFELAVKALAPGLKI I APWREWDI RS
REDAI DYAAARGI PVPVTRERPYSMDRNLWHL SHEGADLEDPWNEPSPEV
LLLI RPPEKAPDKPTYVKI EFERGV PVKLDGAVLDPVALI EKL NVI AGEN

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GVGI VDMVENRLVGMKSRGVYETPAGTVLYLAHRELELLTDRPTLHFKE
MVAARYAELVYDGVWFAPLREALDAFVESTQRTVTGAVVMKFYKGNCTPA
GTKSPYSLYNQELSTFGRDEI YNQRDAEGFI NLFGLPLKVRALMEKKLGL
R

>2617921024 Ga0073689_11711 ornithine carbamoyl transferase [pelotomaculum
Ga0073689 : Ga0073689_117]

LGPEKVNLRDRLSLRDFTPPEEVAALDLAGDLKEKQRRGVPHPYLRGK
TLGMI FQKSSTRTRVSFEVAMCQLGGYPMFLSANDLQLGRGETI ADTARV
LSRYLDGIMI RTYAQADVEELARHAAI PVI NGLTDLLHPCQI LADLQTI R
EHKGKLAGLKLAYVGDGNNVCHSLLFGCAKTGLHI SVASPEVYKPEEIV
RMAQEDAALTGSRVEI GADPVEAVSDADVVTVDVWASMGQEAQDRRVKV
FAPYQVNEKLVAHAKPDFI FLHCLPAHRGEEVTEGI DGPRSVVWDEAEN
RLHAQKAVLTLL

>2617921023 Ga0073689_11710 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_117]

LDVRGCSLDEKGVRTENFQCTRSKVAVLI DASFPVRFQGTALSYVVGLL

>2617921022 Ga0073689_1179 carbamoyl-phosphate synthase large subunit
[pelotomaculum Ga0073689 : Ga0073689_117]

MPKRSDI KKVLLVIGSGPIIIGQAAEFDYAGTQACKALREEGVVVLVNSN
PATIMTDLDIADHVYIEPLSRESVAGIARERPDGLLPTLGGQTGLNI AV
ELAENDI LAEYGVELLGTPLESIKRAEDRELKFNLMLEI GEVPRSAI AG
SVEECLAFARENGCPVIVRPAYTLGGSGGGI AHRESLMEIARRGLKMSR
IGQVLLEQSVAGWKEIEYEVMRDGADNCITICNMENIDPVGITHGDSIVV
APSQTLSDKEYQLLRASLKIIRALEVEGGCNVQFALDLKSMDDYVIEVN
PRVSRSSALASKATGYPIAKMAAKI AIGLTLDEI VNPVTGKTCACFEPAL
DYVVVKIPRWPFDKFGGADRSLGTQMKATGEVMAIDRTFEGALMKALRSL
EYVGDGLRLRGSAGWPMELEEKLSYPNDLRLFAIAEAFSRFWGLREIAQ
LTMI DYFYLSKIKGIISLERNLRAAGPRLSAALLRRAKARGLPDTLIGRL
TGQTARDVRALRKEYGIPSYKIVDTCAAEFESATPYYYSTYEEDEVEV
SSRPKVLVLGSGPIRIGQGI EFDYCSVHVS VWGLQKEGVEAVI INNNPETV
STDFDADKLYFEPLTLEDVLNVI EKEKPLGVI VQFGGQTALNTAGLAT
MGVRI LGTPVEGIDAAEDRDKFEKLLTRLGIPQSEGGTAVNVVEAKAIAA
KLGYPVLVRPSYVLGGRAMEIVSNDAGLMKYMTEAVQVSPKHPVLVDKYI
LGKEVEVDAIGDGRELFIGIMEHIERAGVHSGDSI AVYPPQSLSREVVD
TIVDYTRRIGRALGICGLINIQYVVGNGGVYVLEVNPRASRTVPVLSKVT
SVPMVQVATWAMLGRSLADQGYRPGLPESGFI AVKAPVFSFEKLGLVET
SLGPEMKSTGEVMGVDCAFQALYKAMRSAGLRLNFSGDVI FSVADRKE
EAVAVAREYAAALGFI LRATPGTANALRKAGLDVLAVEEAPFLIRSGAVGL
VINTPTRGKAPGRPGFLLRRIAAEYRVPCLTSLDTAGALAMVLRHLGKGG
EPAPVSMAELDVSGSK

>2617921021 Ga0073689_1178 acetylornithine aminotransferase [pelotomaculum
Ga0073689 : Ga0073689_117]

MKTKEIIELGDKYLMRNYRRIPLALVRGEGARVWDADGREYLDVFVSGI AV
NNLGHCHPEVVDACRQAKKLIHCSNLYYIEPQVLLAKMLVENSAMDKAF
FCNSGAEANEAMKLARKYAKLNHGPEKVEIVTTLNSFHGRTLAAITATG
QPKYQKGFEPPLGGYKYIPFNDLDALERVVGPATCAVMLEPVQEGGVNV
ASRYYLEGARMLCREHGALLIFDEIQTGLGRTGRFLAYQHYGVEPDI LTL
AKALGGGFPI GAMLAGEEVAGAFQPGDHASTFGGNPLACAAALAAMEETL
LGGVVENAAVGAAYLYDRRLRGLAGKYSYVKEVRGLGLLLGMELIVEGKDI
VNGCLEKGLLVNVCVNGNVLRFPPLTITADVDQAVEIMDGMAGAWPNP
K

>2617921020 Ga0073689_1177 N-acetylglutamate kinase [pelotomaculum Ga0073689 :
Ga0073689_117]

LSTAMKKA AVLVEALPYIKKFYGKIVVI KYGGHAMLNRGLKEAVLTDTVL
MKYVGMHPVIVHGGGPEITGMLQRVGKESRFVGGLRVTDEEAMEIVEMVL
VGKIKNGIVSQINRIGGRAVGLSGKDADLFQAVRKYHRVRTPEGGEELAD
IGFVGEISRVNPEIVATVIAEGYIPVAVPAVGAQGESYNVNADNAAGRL
AALGADKLLILT DVEGIMADRNDPASLISVLRVKEVPSLIERGVIDGGM
IPKVECCLDALAGGVRTTHILDGRVPHSILLEVLTDKGITMVEK

>2617921019 Ga0073689_1176 glutamate N-acetyl transferase [pelotomaculum
Ga0073689 : Ga0073689_117]

VEKERSNPEFISGGVTAAAGFLAGTAFARIKRKLKRDLTVLYSTVPASAA
GVFTSNKVKAAPVLVTMDRI AAGGARALVVNSGNANACNGEQGMRDALAM

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AAEAAAAALGI PEEDVLVASTGVI GQRMPMERVLPGI RAAVAALAPDGGAP
 AAEAI MTTDTCPEAAVRLELGGKPVTVGGMAGKSGMI HPNMATMLCFVT
 TDAAI SSACLKQALKHAVDRSFNMVTVDGDSTNDMALVLANGLAGNKGI
 DGECPDYALFRDALTEVCVRLAVVVARDGEGATRLI EVEVRNAATERDAR
 LAARAVASSSLVKAAL FGRDANWGRVI CAAGYSGACFSPGKVDI FLGDEQ
 VAGDGGALAFSEERALEI LGRDTPVKI TLDFKDGPGYATAWGCDLTYDYVK
 I NADYRT

>2617921018 Ga0073689_1175 N-acetyl -gamma-gl utamyl -phosphate reductase
 [pel otomacul um Ga0073689 : Ga0073689_117]
 LPVKVSI VGATGYTGAELVRI LSRHPEVELVALSTQSYAGKPFWEVYPHL
 YKYNQLTCEEMNLPELLDASDVVFVALPHGHAMPVALETARRGKKI I DLG
 ADFRLADYRVYEEWKVTHGARELLSSAAYGLPEI NREKI RGAWLVANPG
 CYPTSAI LALAPLLKHRLI DPGSI I I DSKSGVSGAGRGLSQGAHFCEVNE
 NFKAYNVAVHRHTPEI EQELGKI AGEI TVSFTPHLLPI TRGI LSTVYAK
 LAVPLGQGEAGELYSDYYKGEFFVRVLPEGLLPQTKWVAGTNHCDLGLMV
 DPRTGRVWVSAI DNVVKGASGQAVQNMNI VCDFPEDTALAGPGLYP

>2617921017 Ga0073689_1174 Uncharacterized membrane protei n YadS [pel otomacul um
 Ga0073689 : Ga0073689_117]
 MSTENAI I FEKKPVLKSEDWWAVWLGLFI FVLGLGPI FGADWLGWVTKQN
 VWMDSLKSI APMSKAYKMGSGFNSALLMYLFLLA I TTI GALFMRLRLSRY
 I I GFTI I YWLTFI CMI I GNNAYI AATPNARSGFGI TWSLGLGEMGLVI AM
 VVGLI I GNFFQGFARFLEEAAKPEWFI KTGI VI LGATI GI KTV DAMGLAS
 TVI FRGLCAVVEAYLI YWPI VYFI ARKYFKFTPEWAAPLASGI SI CGVSA
 AI ATGSAI RSRPHVPAI LAAVI I VFVAVELLFLPWLAQAMLYQEPMVAGS
 WMGLAVKSDGGAVASGAI TDALI RAKALKELGI NWEKDWI LTTTTVTKVF
 I DI FI GVWAFI LAVVWSVYKI DRCGVTEAGCKVSAGEI WDRFPKFI I GFA
 LTMLI LLAAGLI NPAI VKAAKTGADHTNVLRTMFFALCFFSI GLVTNVRK
 LWGAGMGRI VGAYAVCLFAFI LWVGLFI SWI FYHGI TPPVI GG

>2617921016 Ga0073689_1173 hypotheti cal protei n [pel otomacul um Ga0073689 :
 Ga0073689_117]
 MAELQVGQAEQTRVNAQEMLEADEWHDLLPI EKCLI GYSLGLGVLLVI F
 I FSFDVFK

>2617921015 Ga0073689_1172 PAS domai n S-box-containi ng protei n [pel otomacul um
 Ga0073689 : Ga0073689_117]
 MANANEGYVKANLVDSTFTLNLNLLLI NTSGRI VLSKGYDLDDKKEVT
 VPDSLREHLSAGLLLRHPNPESSTGI VLLPEGPLLVASRPI LTSEYKG
 PERGTLI MGRYLNSAKI KHLAEI THLSLVLRLDDSRPADFQAALSVLS
 EEKPVFVRPLNQEYI AGHTLI KDI YGKPGLLLRVDLPREI YTQ GKASVRY
 FI FLLLAAGMI FGVADLLVLEKTVLI RLAKLSDFVKKI GGSGDFPTRLAL
 AGTDELARFAAGLNEMLAALQSRRELKESEEKYRQLFDNDI TGNYI STP
 EGKI I LCNPAFARVFGFSSVAEAMRASAFSLHPGREDREKFLQAVCKGKK
 LEAYELKLI RRDGQAHNYYP

>2617921014 Ga0073689_1171 PAS domai n S-box-containi ng protei n [pel otomacul um
 Ga0073689 : Ga0073689_117]
 LEFEKTMARI SSRFAGAVEI DEAI NSALADLGLLSGADRTYVFLGPDRV
 TI SNTHWCAPGVTPQI NNLOELPCAMFPWSLAKLYRREVI QI EDI SGMP
 AEAIAEKELLEMQDI KSLI MPLYAGGELAGFI GLDNVRETGKWSEDDL
 LLRI SAEI I GNVLERKRAEEALRESEERYRTL FENALNPI FVVEDEGKYL
 DANEACLKFLCSREVLLASHVWDDSPPGI LGGLTQLSI

>2617921009 Ga0073689_11646 agmatin ase [pel otomacul um Ga0073689 : Ga0073689_116]
 MLELVDRYTGFMGGTDNYEQAGI VLVGAPLDLTVSFRPGAREGPRI RRV
 SQGLEEYSVYLQORDLADYRYDAGDVALPLGAVQESLRRI GLVAAEI LAG
 GKFPFLFGGEHLI SYPI I REAVNVPELAVI QFDAHADLREEYLGARFSH
 ATMRRVVVELI GGGNLYQFGI RSGAGDEFDFACDNTNI YI NEVMDPLVEI
 I PKLEGRPVYI SLDI DVVDPAYAPGTGTAEPGGCTAKEI LQSVRLGRLL
 VVGFDLVEVSPVYDPSQRTALLAAKLVR EAI LSFGRPAGK

>2617921008 Ga0073689_11645 spermi di ne synthase (EC 2. 5. 1. 16) [pel otomacul um
 Ga0073689 : Ga0073689_116]
 LDOKLFLWFKETQTKDMSLSCRVRKTFHEEQTSFOHLAVI DTWQFGRMLV
 LDNVI QTTVKDEFVYHEMI THVALNTHAAPKKALVI GGGDGGAVREVVKH
 QSI EKVVHCEI DGAVI EAARKYLPEI SCALDHPKVEI VVDDGI KYVRGK
 NTYDI I MVDSTDPVGPAEGLFSVAFYRDI FEALSEDGI FVAQTESPPFNR

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DLI PRLFKDI SGI FPVTRLFLANVPTYPGGLWTFI MGSKRYDPLEVDI TK
I PQLDTKYYS AEMHRACFVLPPFI KELVD

>2617921007 Ga0073689_11644 arginine decarboxylase [pelotomaculum Ga0073689 : Ga0073689_116]

MLPTPKKFFVTAGSAEGKNHLNAFDNALLKGRI GNLNLI RVTSL LPPGVQ
YCPMEI PPGSLVPTAYGYI I SDVPGELI AAAGVGFSKDSFGVI MEFSG
I CTREEAEKAI EKMLTEAFETREMELAGKRI AVVEHRVVKI GCALAAVPL
WY

>2617921006 Ga0073689_11643 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_116]

LLKTVVGLFGSKDQAEKAVSDLRGSGFHIEI SFLAADKGKASDDTERYNQ
LNRPATGGGVSATGVSAGGVLGGLAGLAMGAGALAI PGI GPVI AAGPI AG
LI SGAATGGI AGGLI DWGVPAERGRFYEGKI REGKI LASVRTDDKKVLEA
ANI LRRNGAQDVETH

>2617921005 Ga0073689_11642 deoxyribonuclease-4 [pelotomaculum Ga0073689 : Ga0073689_116]

MTI RFGPAGAPDSFYAEGHKSSLDI PEWLEKRG LNAYEYQSSRGVRI GEA
MAI RLGLAAERDI ELSI HAPYYI NLCSTDP AI KVKTKGHI LKSLRAARA
MGSKKVV FHPGAGSGGDRREI LTRAKAFLKEI LLDVEGEGLSGI LLAPET
MGKRNLGSL EELVLELCELGGQLVPTVDFGHLHAVTGGSF TGKSFAAVL
DRI EDRLGKEYLQNLHI HFSP I EFTAAGEKKHWTTLTRFGPDFTPLAEL
LVERELTPTI I CESFGRQAEDAI I YRDI YRRI RGLP

>2617921004 Ga0073689_11641 peptide/nickel transport system substrate-binding protein [pelotomaculum Ga0073689 : Ga0073689_116]

LHKFKLI TVI LLLLLPVFLI GRSGI VPVAGRLVGRDGGNLI YARGQDSAT
LDPALATDEESYKVI CNI FEGLVRFKPGNTEI EPCLAEAWRVSPDGREWT
FYLRKNVKFHDGTPFTSGAVRFSI ERQTPPQRQDNTPYASF TFGMVDKI E
TPGPYI VKFLLKYPYAPFLRNLAMPAAPI VSPAAASALGDDFGDRPVGT
GPFRAFAGWKKGKSI SLKANMDYWDKPPGSASLVFTVI KNSRWRSLAKLKG
LADI ADGLAPT GARYLEEKGCPVLETPGLDLN YLGFFTNKKPFNNPAVRK
AVSMAI DRAQVTSGLLNGAAFEARGPLPPGVP GYNPDTRPLPYDPNGAKE
LLARNGHPPGGMKI TI I TYTNRPYPNPAGGEKLA AFLREDLAKVGI DAEI K
AYPWEQYKDALLKEEGNAFLFGWVSDNGDPDNFLY TLLSSAQI ENDLNI S
RYRSKELDVLLVKAQOETEPALREQLYSYAVKI I LDDAPWVFLNHSKRLV
ATSPEVEGFVPHFAGFTYLHSCRRDKLI I PQTSTNNLEWYVE

>2617921003 Ga0073689_11640 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_116]

MDQI YQLQRQI KDLRQEVNAI SQVANQLQRSEANNAQLQQLSQSESMAT
QQLQQI TQLCNRLSQDVNTI NNVAQOI TAQVTNRMTSGQFGPGMWTQPV
GQFGAYGGGVSTGMYGPAQFGAFGAQFGLNRDNEFORNQYI SQWAANRYG
AGFNNPDYVTNQYLGSLANQALGAQSSLAPAFSAGADGAGMGMSQTGFA
GTSAGNFR I EPAHPVQTGQYGTTSFAGSQNMPYASQWATANQPGSGLY
GAQASLGTGAMNI GRYSNF

>2617921002 Ga0073689_11639 Spo0E like sporulation regulatory protein [pelotomaculum Ga0073689 : Ga0073689_116]

VSARKELLDEI ERLRAEMNKLAAAGVECAEI LEI SRRLELVLFHKTA

>2617921001 Ga0073689_11638 penicillin-binding protein 2 [pelotomaculum Ga0073689 : Ga0073689_116]

MEKKTVEKKMQVFLVI VSTVFFLLVARLAYMQLLQNDKYSTLARENRI RL
VTI TAPRGEVFDNRNGVKLVGNQPVYTVSLVKLGQDQDQVARRLAVI LGM
DFOELQOKI KEQKRVYEPVKI ASGAPTEVVTRI EEQRLELPGVVI DI EPM
REYPNGNLLAHVMGYVRQI NEEQLAANREKGYKLGDPFGQTGLEYYEY
LRGQDGGROVEVDKARPVRDLGVKEPAPGNLVLTI DQRVQKAAEEALA
RSSEAAALRQGYAEATAGAAVALDVRTGAVLAMASYPTYDPVKLSGVLSKK
DFKDI FNSDLKPMNLRLMAYAPGSTFKMI VAMAGLESGKTTPKDAI SDP
GYFFWDRTFNDWKPGGHGAVDLVRAI KVSCDTYFYQLGLRVGI DDI ARVA
RDFGLGEKTGI DLPGESSGVVPGPVSKI QQLRI YLSQDSRKKVKEI EQKY
DQLLAGTTDKEORRALLKKRSDRLSVYWELDWHDYDTI I SSI GQGDNRY
TLLELANYI ATLANGGTRYKPYLVQRI VDPGGKVLKEFEPVSLGRAGVSP
QNMAVVREGMREVALPPDGTAYGFFAGLPPVAAKTGTAEVHGHDTHAVFV
AYAPYDNPEI AVAVVMEYAGHGGTAAGPVAEAMLAAYFGMQKSGVKPI SS
PE

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>2617921000 Ga0073689_11637 rod shape-determining protein MreD [pelotomaculum Ga0073689 : Ga0073689_116]
VQFPVFLLLQGAFLVLTQTLLDYI SMAGVKPDLVMLLVNLGFLGPREG
AFLGFAGGVLEDLFSGSYI GLNALSKFAAGYLAGAAGERLYRENSI VATG
VVFSAFTGQVI SYLLLLLYLNWVI APFYALLRVAVPTAVYTAVLTPFLFG
RVLRSAQMRRMDL

>2617920999 Ga0073689_11636 rod shape-determining protein MreC [pelotomaculum Ga0073689 : Ga0073689_116]
VRWVTVKRLFFLVLTVTTLAAMRVTTTPERARLTPEAKFRDVLAPVQIG
LTWLGGRRARHLVSFPVSMVGAAKRSRALEEEVARLESQVI QLNEYKMENQ
RLFGLLNYKQTMARQYDFLPASVVARDPGNWFGTGTVNRRSGDGVANMT
VLI PEGLVGRVVAASAATCEVLLFTDPRSGVGSLSVQDTRTPGI I EG TAGS
LGLARMI HI PNDAPVEAGQAVTSGLGSVFPKGI PVGEI AGLRNESSGLF
KSADI RPYADLNRLEEVL I VTRVHPESGSPGGGL

>2617920998 MreB rod shape-determining protein MreB [pelotomaculum Ga0073689 : Ga0073689_116]
MRVGLFSKDMGMDLGTANSLVYVKGKGI VI REPSVVAI QKDSGQVLAVGE
EAKRMI GRTPGNI VAI RPLKDGVI ADFDVTQSMI KYFI NKSLRGRTFLVR
PRVVVGVPSTAVEERAVREAALQAGAREAYLI EEPMAAAI GSGLPVHE
PTGNMI VDI GGGTTEVAVI SLGGI VTSRSI RI ASDEMDEAI I NHVKRTYN
LMI GERTAEQI KI QI GTAYPMEI KETEEVGRDLVTGLPKTVEI TSEEI Y
KALSEPSSI I EAI KATLEQTPPELAADI MDRGI VMAGGGSLLRGLDRLV
CEQTGMPVHLADEPLLA VAYGAGRVLENI DVL RKVLI QPKKLA

>2617920997 Ga0073689_11634 DNA replication and repair protein RadC [pelotomaculum Ga0073689 : Ga0073689_116]
LVSPNYRPTMKELPEDNRPRELLKEGAEALSEI ELLAI LLRTGSREATA
LELASLVMARFRSLRFLVDATVEELSEVKGVGPAKACQVKALELARRLA
QFSELPRPVI KSPNDAAGLVMEEMRHLDRHFRTLLLNTNRQVI GTDRVS
VGTLNSSTVHPRELFRNAI KRSAASVI LLHNHPSGDPTPSREDLDI TARL
CEAGKI I GI EVLDHI I I GDNKFTSFKAKGLI

>2617920996 Ga0073689_11633 septum formation protein [pelotomaculum Ga0073689 : Ga0073689_116]
MMKKLVLASASPRRRRELLKQI GLVFRTLVSVPDETPTGLSPFELVELLA
VRKAMAVARTLEEVI VI GADTVVWRGEVLGKPSGAVEAMEMLRRLQSDV
HEVYTGAVVDGTGRVLADHEKTRVFFRAVEEEEI RRYVATGEPLDKAG
AYAI QGLAAVFVKGLEGCYTNVVG LPLARLAGMLKQFGYNVL

>2617920995 Ga0073689_11632 protein of unknown function (DUF4321) [pelotomaculum Ga0073689 : Ga0073689_116]
LKVKYMAKTSYKDSGNI WVLVLLLLVGGLSGSAAGDALAPALPWLKSTS
TI GLKPSNMDLRFFNLTFGFTFSLGPLTALGLI LGYLVYRKV

>2617920994 Ga0073689_11631 dihydrofolate synthase / folylpolyglutamate synthase [pelotomaculum Ga0073689 : Ga0073689_116]
MSFHYKEAMEYLTNLTKFGFNFGLGRI EELLKRLGDPHRELQVI HI GGTN
GKGSVTAMLAAMLQAAGYRVGFTSPHLHSYTERYLI NGEEI KEERMAGL
I RELRPHLETMVAEGFEHPTEFEVCTALAFLYFNREKVDYLVLEVLGGT
I DSTNVVTPLI SVI TNVSM DHI DYLGSAVGEI ARVKAGI I KPGRPVVTA
EGEAL EVI QEKAREKNSPLVLVGRDVTWESLSLSTAGQCFTVRGRRGI YE
NLRPLLLGRHQQVNASCAVSAAE I LMDLGAALGVEAVQEGLA AVRWPGRL
EI MGI EPLVI I DVAHNYDGARSLRRALEDYFPGRSLI LVI GMLGDKERAK
VAAELAAVARAVVTKPNSPRAGNWRELAVEAGRYAPEVHVVEDI GEAVG
KALSLSGPPEEVCVTG SFY MVAEAREALLGR

>2617920993 Ga0073689_11630 valyl-tRNA synthetase [pelotomaculum Ga0073689 : Ga0073689_116]
LTGKDI PTTYDPRSVGKWKYKWEENGFFHTVNPQEPEFCI VMPPPNVT
GQLHMGHALDNTLQDI LTRWRRMQGYNALWVPGTDHAGI ATQAKVEEQLI
KEGLSRYELGREEFLKRVWAWKEQYGNRI TTQLRRLGASCDWRRERFTMD
EGCSEAVLEI FI NLFRRGLVYRDYYI TNWCPRCKTTI SDI EVEHLDRPGH
LYHLKYPLKEGDGYI VVATTRPETMLGDVAVAVHPEDERYREMVCR TLI L
PLVGREMPVI ADEYVDPAGFTGAVKI TPAHDPNDFEVGQRHNLLOQKVI D
KEGKMSDAGPRYQGLDRYECRKKI VRDLEAGGCLLKTEDHTHAVGH CYR
CNTVI EPMLS RQWFVRMKPLAEP AI QAAI DGRVRFI PERFI KI YLNWMEN

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IRDWCI SRQLWWGHRIPVWYCGDCDEMI VSKKPVSRCPKCSGSSLEQDPD
VLDTWFFSSALWPFSTLWPGKTI DLAYYYPTSVLVTGRDI I FFWVARMIF
SGLAFMNDVPFREVFI HGLVLDALGRKMSKSLGNGVDPI DVI ESHGADSL
RFMLVTGNTPGNDLRFHFERLEGARNFANKLWNASRFALMNLEDFDPEGR
PGPYTLADRWI LSRVRAAVADVTAFL EAYELGEAARVLYEFI WSEFCDWY
I ELAKPRLYGKTTPEDRYTAQHVLASVLKGALELLHPFMPFI TEEI WQHL
PARGVTI MRAPWPAARGDLADPGVESEMAVLMEVTKAVRHI RSEMNVP
CRAETLLVAPEEAVRAVLEKGADYI RGLANAEI KI LPVLGEAPEQAAHAV
TRGVEVFVPLKGLI DVEKETARLQKELAAVEKDLARVRGKLGNGPGLAKA
PADVVEKEKAKEAELSGKQAAI RERLSMLAGDK

>2617920991 Ga0073689_11628 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_116]

VII YLGRLLPAASSDLTRGQRRAAANI PLFGLAPGGVYLAGRSPGRWCAL
TAPFHPYPVLEVGSLLEFGKTEFQQRSNLQYGAVRI SVALSLGSPPLGIT
QHPALRSSDFPQTPLI PGARDHLI YSLPYFYTSLYHLVNNKCNNRRAYDA
VKLKWI YYRNFQYKHNTI CWGI FSI AHRVRAALRRLTRLTPSESYFV

>2617920990 Ga0073689_11627 NADPH-dependent FMN reductase [pelotomaculum Ga0073689 : Ga0073689_116]

LKVLAVNSSPRGKNSNTDRI LQPFLEGAREAGAGTETI YLENKKI NHCTA
CFTCWAKTPGVC I QKDDMSELLEKVI QAEVI VYATPVYAFTVSGLMKDFM
DRLI PLLNPQVI KRGHYTHPMRHEGAWPKKAVLI SNCGFPERHNFLGLV
ETFRLFTSSGYDSELVTI LCASGELLKMPKLRNWI DASRSAGRELI EQ
GHI SPETOQAVLDQLLDPEVYNRI ANDYWDKVI ANQPKP

>2617920989 Ga0073689_11626 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_116]

MSSGLRESSQLVMDNLHSGAVI LLCAVFRDNTALDDLKVS

>2617920988 Ga0073689_11625 acetyl-coenzyme A synthetase (EC 6.2.1.1) [pelotomaculum Ga0073689 : Ga0073689_116]

MSI KKTRGVQSLMTENRVFSPPEFVEKAGI KSREORDEMYRRSVEQPNE
FWAEVAEKHI EWFKKWEAVEEYDFKONI FI NYFRGAKLNASYNCLDRHLK
TWRRNKAAALI WOGEPADESRI YTYDQLHREVSKAANMLKSLGVKKGDRVT
I YLPMI PELAI CMLACARI GAI HSVVFGGFSAESLRDRI LDARAEI LI TT
NYGLRAGRLLNSKENADKAMAGAPHVKNCI VVRRVEKDCNMAPNRDYWWH
ELTNMASPVCEPEQMDAEDPLFFLYTSGSTGKPKGVI HTTGGYMYVTTFT
FKNI FDYRDEDVFWCTADI GWI TGHSYI VFGPLSAGATSLMFEGVPNYPK
PDRFWEVVEKFRVNI FYTAPTALRAMMRDGDKWPLGRDLSSLRLLGTVGE
PI NPEAWMMWYHKVI GKERRPI VDTWWQTETGGI LI TPLPGAI PTKPGSAT
VPFFGI NPKI I RQDGSEAGVNEGGYLVMTKPWPGI MRGVYGDPERFKTTY
FI QYPGYFTGDGARKDEDGYFWLMGRVDDVI NVSGHRLGTAEI ESALVA
HPKVAEAAVVGFPDHI KGEI YAYI TVKEGVEVSDDLKKELVI HVRKEI G
PI ASPDVI HFSNVLPKTRSGKI MRRVLRKI AAGETEQLGDTSTLADPTV
ENLLAVARQSI

>2617920987 Ga0073689_11624 Major Facilitator Superfamily protein [pelotomaculum Ga0073689 : Ga0073689_116]

LSTNQPSLAKAWSVI AGVGTNLCLGVLYTWSVFKASLLKLGWSNVETQF
PYTLACLI FAACMI PGRMVDR I GPRWVVTLGALFVGAGMI LSSATMSVA
GVTI GFGI LVGAAMGFGYAAPTAAI RWFKPHKKGLI AGLVVGFGGAS I
YTAPLTTYLANQYQLKGAFI EGI I FMVTMVI LAQFLSVPTGYVPYGGD
PPATKAATAAVSKDYTPGEMLKTPQFYLLWLMFLFGASAGLMI I GHLAT
I GVTQSTDPKTVASGYI LVATLAI ANAGGRVVFAGALSDKLGRNTMLMV
CLQAAANMFLFHHYKDGTTLLLSI LTGASYGACLSVFPSTTFDFYGMKNG
GLNYSLVFSAWGCAALI GPI YAGKVADTTKALFGRPDYTEAYI VSGI LMV
FAAVLALVTKPPKTVTNTSLRSEAKA

>2617920986 Ga0073689_11623 Glycosyl transferase, catalytic subunit of cellulose synthase and poly-beta-1,6-N-acetylglucosamine synthase [pelotomaculum Ga0073689 : Ga0073689_116]

MEAI FYGTQTVLTI FTFFYFVI SLFGFYRRQEDNLLSPGSRFAI VVAAHN
EEKVI GQLI RNLRLDLPYKELYDI YVVADNCSNTARI ARDWGAI VLRF
NKVEKGKPYALEFAFNKI FDTSI PYDAVVVFDADNLVSTNFLT I MNTHLL
RGEKI I QGYLDTKNAGDTWI TKS I YI SYI LTNRFLQLSKYNLGLTCALGG
TGMCLSDVLKKGWGMTSLTEDLEFQTKALLNNI RVSWAHDAKVYDEKP
LSLMASWRQRKRWMOGHCHVAGRYVSRMLMREGI RTKNFAMI DGAVYLVQP
FFLMFTGMGLI SNI LFGPDHLMNKPVWATVGFFAQFFYFGLGLALERVKL

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GVYWWLI FYPI FALTWI PVAYI GFVMRKNKEWTHTLHI RDI KHENLQNL
LPAKANGRRPG

>2617920985 Ga0073689_11622 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_116]

MKI I VDADAAPRNVLDI CHRAAAEFSLSLI TVASFNHN DSEQHI VVGDD
POATDMRVANLAARGDI VI TWDWGLAALVLGKGAAALSPVGRVFRDNID
FLLEERDMKAKFRRKGGRTGPKKRTAADDDRFKSLYRLLETKGGPGS

>2617920984 Ga0073689_11621 Putative DNA-binding domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_116]

LLMTARELLEI I ANGENSEAVEFKRETI RPEHLAEEI VAFANLEGGAI FTG
VADDGFI EGVQREDLEEWMNI CSHNI VPTEDMSRTRTPFCFQ

>2617920983 Ga0073689_11620 Response regulator receiver domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_116]

VI VTDNGASVLELTHREKPDLI LMDI LLPGLDGLCLCCLCRKTDVPVDF
HCVQDRYP

>2617920982 Ga0073689_11619 anti-sigma B factor antagonist [pelotomaculum Ga0073689 : Ga0073689_116]

MKI QESRKETATI LELNGRLDTSTSTI LEKKLLSLLNEGEKDFVLDFSNI
DYI SSAGLRVLLMAAKRSGSSGGMVSLCRLQEHVREVFDI AGFTTI FSIH
TSLEEALACFN

>2617920981 Ga0073689_11618 sigma-B regulation protein RsbU (phosphoserine phosphatase) [pelotomaculum Ga0073689 : Ga0073689_116]

MAEPVI NLLLTLI KNMAVVI VMAYVLTRTRFYTDI LNKKFTI KNQALLI L
I FGLFSI YGTLSGMNI LGAI ANI RDLGPAI AGLVGGPLAGLGAGLI GAAH
RYPGGI TAVPCALSTI I AGLAGGVI FKLKKDEFI GI YGAVI FAALMESL
HMLGLVLLVSRPYDQALAI VKQVSLPMI LANSLGMAVFVAFI VSNLI RERNT
EAVKEMI ESELKVAREI QMSI VPKVFPPFPDRPEFDI YALLEPAKEVGGD
LYDFFFI DDEQLCFVI GDVSGKGVPASLFMAVTKTLI KTKTGKEMTPGEI
LFSVNNELCRDNDSGMFVTVFLGI LNI RTGEVRYSNNGHNPPYLFRTGTG
VELLKKTTGGMALGVMEI PYEKNKI VLKAGDGLLLYTDGVTEAMDTGGNL
FTEORLEEVLRRI SGASPEEMI RGVLAIEI EKYAKGAEQSDDI TI MALKYM
FPGQEMSLEI KNDLAQLERVAQAVEEFKTHHLPLKTI FEVNLALAEVLT
NVI SYGYSDDNRHLI MVHFSLEKEKELEI EI I DDGRPFNPPELPPDLKKP
LAERPVGGLGI HLVRNLVDELQYQWQDKNI LVLKKNKQ

>2617920980 Ga0073689_11617 molybdenum cofactor cytidyl transferase [pelotomaculum Ga0073689 : Ga0073689_116]

MI SAVI LAAGQSVRMGCPKLLLVGGQTI LERVVDAALASTLEEI I VVLG
HOADEPARLLAGRQVKLVYNPCYHLGQSTSLAAGI KAVDKRTRGI MFI LA
DQPLLTADLI NRLVEFFNSAHYL VVKPVFNNGRYGHPVI VDSGLI PELLVL
KGDVGAREI I ARYWERTGLLPVEDELLQMDTPADLKRFLRL

>2617920979 Ga0073689_11616 probable selenum-dependent hydroxylase accessory protein YqeC [pelotomaculum Ga0073689 : Ga0073689_116]

LEKPVKELDLSLTGALELGSRELVALVGGGGKTSALLI LAEELAGAGRKV
LVTTTTTRI YRQFSGCESVMAGSYQLLKDLKQALKNSSLVAAGKI DLV
EEKVLGLPSEWLDLLWQAGI ADYLLVEADGSRGKSLKAPAGHEPAI PSAA
TLVVAVI GMDVLGKPLEHEFVHRPELVARAAGVI PGSLVDTEVVSRLAI Y
PEGPGKNVPPGARRVFI NKVDGSVDLPLAGQLVAVLSI AGGWQVVLGSC
RNRYFLRPAFS

>2617920978 Ga0073689_11615 xanthine dehydrogenase accessory factor [pelotomaculum Ga0073689 : Ga0073689_116]

MKNI LMVI KGAGDLASGI AHRLYI CGCVPVMTLPQPLAVRRTVAFQAQV
YARRAEI EGVKAMLAENVEAVNSLRKGI I PVI I DPRGKI I PALSPAVV
DAVMAKRNTGTESDAPVVI GVGPGFFAGRDVHAVVETROGHNLGRVI RS
GEAEPDTKEPAPVEGYTHQVLRSPGEGVFRACRDI GERVAEADI VGYVD
CQPVQAQI SGVLRGLLNDHVKVTGLKI GDVDPRAVVAYCYSI SEKARAV
AGGVLEAI LHFRNRSG

>2617920977 Ga0073689_11614 xanthine dehydrogenase accessory factor [pelotomaculum Ga0073689 : Ga0073689_116]

MSI YHLI LETI ERGQEAALVTI VRGPRSVGEKRFFITASRI AGSLGHEWLD
EQADLLAGQALQAGRI EMAGI SSPECRKEEFTLVAEPFFPPNQLLI LGGG

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NI ALPLAKAASLAGYQI TVVDDRPDFANRNRFPPEARVI CDTFDRALEKI
SFGWLVSIVI VTRGHQHDLAACLARVI REEPAYI GVI GSRRKVKMFKEHLR
SQGI AESRLNRI YMPI GLDI NARTPEEI AI SVVAELI KVRWGGTARSLSE
AADGGRRQLAEQKPDVLLAAPDKELLRAVVTAGEQETPAALATVI ATKG
STPRKAGARMLVFYDGRLLGTI GGGCI EGEVRREALNALDQGWPRI LCSV
LDSEVAASEGMVCGGRMEI LI EPLI KKVTV

>2617920976 Ga0073689_11613 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_116]

MNEKTVNQEQDEYFI EPGQSFEI DLFRPEDAEGVARLFRTVYGEYPI QK
FI RPELLI EENAAGRTI SSVARTPKGDI I GHNALFNSAPYTG I YESGAGL
VLPGYRGTAGI FTQMI AHGQNVAAKGFGVELI YGEPVCNHLI SQKG TARL
GWI TRAI EVDLMPAEAYQKDQASGRVTTLLNFI TLKPKPHTVYLPVAVY
ETMRFLYSDLDSDSDI TLSDQDLPAFKTTMVKTQVDFARVARMAI METG
ADFERAFDEHEKTALDKGTVVI QAWLKLSCPWSGRAAGALRKRGYFLGGV
LPRWFNEDGMLMQI I GOPNWEI QLYSERAKRI LELVKADWQQVKNGG

>2617920975 Ga0073689_11612 Predicted arabinose efflux permease, MFS family [pelotomaculum Ga0073689 : Ga0073689_116]

MSEPERLFTREFLALNGVAFLTFCNMAVFFQFYLYLHTLPI ASEWYGF LI
ALFSVTGLI LRPLVSPFLHSGNARKWMLASAAGVI VSLLGYNLATDFWNM
FLVRAVHGI TYVI LGAALNARLVSLI PPSKSGQAFGLI TVI TLLPFAVI P
PVLDMATYRLGGFVTVLNLAAALMFLVFPLSLAVKTSAGKERDLAQORPG
I GDLVKNLKDRRI SMLLLLMLLYSSYTPVFFFLEGYAKKTGI PNPGLFF
TLSTVSEI GVRLLAGPLFDRMNKVFLAVGSLAAI GLGYLALAHLSGPI MF
YCLGI FLGLGWGVMPVLNLMFDVSPPHLRGLNTNLGVQMFQGGFFLGP
LI GGLI LTCGDFSALYYFCAVLTFGSMALI PLLTVRDKSLRRLSGL

>2617920974 Ga0073689_11611 C0 or xanthine dehydrogenase, FAD-binding subunit [pelotomaculum Ga0073689 : Ga0073689_116]

MSRVFLPRNLNSLWEI I EEPGALVYAGGTDLLVKLRQMSRPPSLVCL
RI EELKGVREGKEDLI GACTTHTLLMADPLI RNYCPVLARALKVLGSP
VRNMGTI GGN I CTASPAGDTLPPLYVLDAE I E I RSKSASRRMLLREFI LG
PGKTRLWAGEI VFGI WLRKASEYNLHHFEKVGQRNALAI AVVSLAAMLRV
SNSGMI EKARLAWGSAGPTVVTSTMVEEALTGRPLSPETLRKAGQLAHNA
VSP I DDVRAGASYRRAVAGNLLRRLHPRHFYSDS

>2617920973 Ga0073689_11610 carbon-monoxide dehydrogenase small subunit [pelotomaculum Ga0073689 : Ga0073689_116]

LKI SFMLNGKEI QI DAPPDRRVLDI LREDLNLGTKEGCGTCEGCACAI L
VDGESRLSCLMLAAQEGRSVTI EGMAPEGGLHPLQDAFVEYGAVQCGF
CTPGMVI SAADLLRRNPNPTRLEI REGLSGNLCRCTGYQKI VDAVQKASR
KI KKGETS

>2617920972 Ga0073689_1169 xanthine dehydrogenase, molybdenum binding subunit apoprotein (EC 1.17.1.4) [pelotomaculum Ga0073689 : Ga0073689_116]

MVKSDI LKI GRATPRPDARNKVTGQEKYAADYYGRNLVWAGVRRAGVPHA
RI KNI NI EGARSFPGVI AVLTKDI RGSNRQGV I RKDQPV LADDRVRHCG
DAVALVLAEEKAALRKALDLI SI DLEPLPGI FDLEKAMEEGAALI HDDSP
RGNVLLKGELETSGSEAAFECDVAVQACFEVPHQEHAYLETEAGWALFK
EDGGLDLVASTQTPFRDRLEVAEALGLDAEQI RI I APYCGGAFGGKDG I T
VQSLLGLAALHCPGRPVKI WWDREESFLAGVKRHPARLHYRLGAKAGGAL
HALEVRI YYDTGPHYDLGGAVMALGLEHTGGPYRI PNVSLKGWSVYTNNP
VGGAFRGFGVPQVTAAMEQTLDLLAAGLGLSPLEI RLRNAVKRGRDRNPVG
VTLAGSTGLQECLETLAKHPLWQEREKWKSSAGLFKRRGTGI ACVMHGMG
YGPVVPDYANAKI ELTRRGKFRVFCGVVDMGQGNAGAYMQI AGDI LNQDS
EHI ELVLPDTPGRLPSCSASASRTTYTFGNALI GAAQSLKQHLLGRAADL
FMAGQTDGMTMPGRI MHLPTGREI SLSGMARLLDESERSVCRFRAPAA
TERPTEDQDLRLHGI PHLLFSYGVHLACVEVDELTKGVEVKRYLAVSDCG
RI I NPQVFEQQVQGGVAQGLGYALCEDFLVEKGRI RTPNLSTYI I PGSLD
VPDMSVPVELGEETGPFGMKGAGEI AI DGPLPAVANAVADACGI RI SRL
PLTAERV LKALADKSROGAKP

>2617920971 Ga0073689_1168 histidinol phosphate aminotransferase apoenzyme [pelotomaculum Ga0073689 : Ga0073689_116]

MFNVYLDKLVPEYVKKFESYI PSKPDPELMKLYGCDRLYRLNNNENPFGP
PPAAREI LQFRPAGAAVYPSGDSYLRQKLAAEHGLDPDQFLVNGANE
VI TFVI KAFCEQGDNI I TADKTFVYEWVAEFSGFEARLVPLKDFAFDDR
GMLAQI DERTKI LFLCNPNNPTGTWDEVTLRRLNAVASRQI VVVDEAY

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FEFVEKKDYPDGI KLLKEYPNLVVFRTFSKMYGLAGLRI GYLVDGLKVVD
I I RRTCVVYSVNTLAQDAALASLDDDDHI QRTDRLI RTEKAYLKQELDRL
SLETOI AEGCYVMI RLPMSDTLAYRKLMTQGVMI RSMTGFRYPNWI RVSI
GAREAMEAFVTALKKI LS

>2617920970 Ga0073689_1167 Histidine kinase-like ATPase domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_116]
MKNHPARVSLKTHLVPGFLRLVTSFAEESARAFGLNAAEALKLTLACEEI
FAYLCRAGRDTDEVTI EAANGGYVHVHVKFLFKARDFNPRAFNLTAAVSLE
DTASLEEMGLLI ASRSVDRFYI AEELPQGLGLVLI KEKSYAPAGLQAPE
I KPLNNFRI KTPDPDSLKLLARLVTAHYPVHLYPQDFRLPGKVADMVASG
EYGAQAAADEQGRI GGGI I WRRVGAGTVESFGPYLNFQPVAPGLSEELLA
ACI GEI AKTDAI GLLSRYSTPELPGYFESLGTI DFVQPDGI VKPWPI YY
ROLREDPGCRVWAHAGLEAFLRAEYGRLEFFAREI RLTRHEGEQRSPYSTF
APOFDRANRQI TLRAI WDGADAAENLAQHVKVLKAENLPNI FFEVDLAHA
WQAGLTGTLLEQGLPRLVLPYGGVADVVFQYRGGE

>2617920969 Ga0073689_1166 methyl-accepting chemotaxis protein [pelotomaculum Ga0073689 : Ga0073689_116]
MFKKLQTKLALLCSVI LVFVVVVGVI YEI GVLNRSYGYLI HKRAEMVR
EAKTLVGDFEYSALYLSYLLAGHPDYLLKKHEDALARADGDLERI KGLAD
DERSRAMAQSLQDLASFSTYCNEVI GLKHKGNLKGVDYTLNKKGAI AT
I VQTGNDLADHQAKLMHEQTLNDRRARQI QGTVAGTVGFSI I LGLVI AI
ALAGNI ARPLVI LEKEAAVMAGGNLKGEDVPCKSNDEVGRLTRAFNHMRA
SLRSI VEQVQNSSGQLSAAVQQLSATARETSSQAEESAATI QMARAVDQ
VSGSAYTVAQASREASDLAQGNNEI DQVI SQMNKLGNAATEEMVKVI SSL
NVSTNEI SKI VDI I TGI ADQTNLLSLNAAI EAARAGEQGRGFAVVAEEVR
KLAEQSSLSAKEI YRLI RDVQGEAERAVQVI DI SRREFEAGQKVVEVGA
YFRTI I ERVRELGTQMQDVAAAQEMSAGVQNMAGI GREQSTAVGRVSSL
ARELEAMGRELEV MAGKFTL

>2617920968 Ga0073689_1165 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_116]
MGMVRHFGI GLLI YDDI I DWDNYESKI DPVMKEEFEFEGVEKKVYEVI I V
PEDRPYVGI LPSLWKQI RSAGRGGHLDLDEI DPRSIGI SVYALDTAAK
I LNKI SKRRI TLKELQLKFYEYWW

>2617920967 Ga0073689_1164 maltodextrin phosphorylase [pelotomaculum Ga0073689 : Ga0073689_116]
MFPYRVSVTPKLPESMGRRLRELAYDFWFSWKPGGVEFFRSVNPALWREV
RHPNVKFLMSVREKNLAAASQDEYLLLYKRVFDLYDRYMAEETWFAKHY
PGHKDDLI AYFSAEFGHESHPI YSGGLGLLAGDHCKSASDLGLPFI GVG
LLYKHGYFTQRI NGQGSQAEYPHLNFYELPI TPVNAPDGSRI TI SVDLP
GRDVYAQVWKARVGRMNI YLLDTDI PKNLKEDRHI TGTLYGGDRQYRI AQ
EI LLGVGGVRALRAMGNPKAWHI NEGHAFLI I ERI RELMRYGI SFATA
REVVRASTI FTTHTPVLAGHDLFSEELI GNFFI PI I TEMGVNFKEFKELA
WDEERNFSNMTLALRHSCLANGVSRLHGRVARDMFRGYYPGLHPPEVPV
TSI TNGVHI ETWLAWELRELYTRYLGRRWVDQI TLPGTWERVENI PDEEL
WKI HLLLKEKMI TFVRTSLRQYI RNREPAHRI SEVDEYLDLDDVLI I GFA
RRFATYKRANLLFREREKLSRLVNDPERPVRVVFAGKAHPADLAGQEI I R
QI YQI SNEPEFRGKVLLENYDI HMARHLLQGMVWLNTPRRPMEASGTS
GQKAALNGVI NVSTLDGWPEAYNGENGFAVG TENQYQDDELQDRDDCYS
LCNI LEDKLAPMYRKEAGLPREWLMMKDSI KSI APVFNTHRMVAEYTD
RFYI PAI KRG I HFANDNNRAAARAGAFKKFI MENWDKVQFVSVESNSTPT
MHVGEKI EI SALVNLGPVYPRSVAVEVVYGEATDDGLKNI TI APMHPAGD
AGNNVHRFTGSLELPQGAFGYTVRVRPHSNDFFHPELPLATWAPNL

>2617920966 Ga0073689_1163 Methyl-accepting chemotaxis protein [pelotomaculum Ga0073689 : Ga0073689_116]
LKI SQKI LLGYFLVLAVFVVTGI MSI TNMHKMQRSYADLI DHHVYLVSET
KDFLAAFEYEALMMRTYFI TGQAEWEEYRAQYQKGQEI LGGI EKKI SSD
EEMAMFKNLSGTVRAYHENYHPMMDI RNRSDLTEQQKLEAI TRLTLEQR
GTVRGI I RTGQEFVAHQQLLDQAVQVNAMWVQVNTTTTTMMVI TALVLV
LGAALYI ARLI AGPVTLLQEAKRI AEGDLTTRALPATSGDEVGSLVRSF
GTMGKLRNLAEKMONSAGLVTTYTRELKSSTRNAAEAANATSGKVSQLA
ETMRNMLEDSQAVVAAMDRAAANLAGVEKTA EKFLQKMGDSAAVRTRASE
AVKDMEERLRNVGDVI QFI TLI ADQASLLAQKAVTEVAYATEGENTFLAL
ADEI QKRSKEASNAAKGI TGLI ENVYRHARLAVASLEEDHTVI LEGYSSA
KEASASVKEVLHELQGLTGRAQDVAAAATEQLSKHI YGVI SAADEQAALAQ

GFAAAAGALNHVAGELQSTVATLKL

>2617920965 Ga0073689_1162 uncharacterized protein [pelotomaculum Ga0073689 : Ga0073689_116]

MRRLTEHVKQLKRMYSI EDGRLKGEFWEKFPLFWFQFLSYKCTRRRCNY
CYAFNQVGEDNRMEMDENTFSRLLEWI PEVWEKNNVKVNTI VFLGGEPLL
RTDRI KKI MDSVYKNTDGMQGSlyTNGDI I DSVTWDDLEDI QWI SI NI TD
I SI EELSRRMKI I SERSNAI GQTI VATLDDYNLERVLDI TTFGI ENGyRL
RYQKDLyRGLNTEYKKRLLKKYHELCDLLENYI VKGYDVHTTFLDLTLI P
LWDLESSPYPCGKRI ATVPDGTI GPCI RDHSFKTGTI FDANPLSKI QCD
MFHYDVAKSDI PDECRECESKTI CHGGCPHDKLLLTSTRSGKSVVCDI HK
EI I PRLRYLDKLNLDLGMKRI

>2617920964 Ga0073689_1161 mol ybdoprotein mol ybdotransferase [pelotomaculum Ga0073689 : Ga0073689_116]

MRNKNLTVSVVEARKI I LNSVSPLNCENI SMGNAEKGF I NI NI SKDYHTT
I STHGWRMNLPLEQARNLLLOHAVI RPERLPLMEALGRVI REDLTVQED
I PGFDRSSVDGYALLGRDTEKAGENAPVRLRVLEEVAAGRNPHFQVSTRT
AVKVMGTGAPLPSGADAVVKYEEVRREGADVLVYRQVLAGTNI VKAGQEI T
AGEI VVFKGSPVTPSLLGLLAAAGFNEI PVYSTVKAII I STGSELAGLGQ
TLGAGRI YNSNQYFLTALLRTI GVDPVPLGI VPDEAAKI AALVQTALERA
DLVI TTGGVSTGDYDLVEHALAMAGVERLFSGI AI RPKGsfVAGKKDGKL
I LGLSGHPGAAFTAFELLVKPVLKMMGYKDI LPCEVEVFLSGDYQKTD
ARRI KAARLYI EGGI ARVKI LTGGVLRTLADCNLFVDI PPGRGLLAAGEK
VSAI VELFNEKI ATCDHFHYSLCPAGHGGLM

>2617920963 Ga0073689_11559 Glycosyl transferase involved in cell wall biosynthesis [pelotomaculum Ga0073689 : Ga0073689_115]

MKLLI I SHMLPVSFKLSALSYRVYEALRYLSENYEHSI TMVAFKKKGDP
DYI KKYCDEI VTVEI PASFKKRLQFI MNYAGGI LRGEI SLKKGNLYCYR
HSLKLHNKI NELLKREKFDVI FVETPEMLFYVSDI NLPKVLEI WTI PQI H
YEAYKKLEKNFI KKVYRLI SYFEAKKFESKYENFNI CI TPTEQDRDI I KS
YLKELDI SVI PFGI NCDFNLGDLKEDFPSLI FI GNMGSTFNQRSI LYLYK
EYVPLI KASFPGI KLYI I GKNPSEEVKRLSRDKSVI VTGYVEDI KPYLAR
ASVVTLPVHGYGI KTRI LEAMAMGKAVVTNAEGI HGLNVI PEVNI I I ADN
PGEFANRVI ELLMNEQLRKA I GSNARKLVYEEYSWEMMSDMLNSTLQKAV
NKFHEK

>2617920962 Ga0073689_11558 coenzyme F420 hydrogenase subunit beta [pelotomaculum Ga0073689 : Ga0073689_115]

MVI TNRRGFKTI ATVVEEGLCCGCGTCAGI CPRDAI EMEI DEI KGI YLPH
I DNKRCNCS I CLSSCPGHEVDLPRLSQSLFHDTDFEHLVGRYLNCYMGY
SI DQSI RYNSSSGGLVTTFLI YALEQGLI NGALI TKMSDKRPLEPQPI A
RTKDDI I SAACSKYCPVPANVALKEI LRDDGRYAVVGVPCHI HGI RKAES
VNKKLRERI I FHLGI FCAKSI SFHGTEFLLKRMNLNKDAVEKI SYRGAGW
PGNMI I QLRDKQKDI LTFYPSYDLRFNSFVMPRCTLCFDWI SELADI SF
GDAWLPELKANDKVGTSI VI ARSEQANNVMCMAGEKDYI QI KPVEI NEVK
RSQHFFAWKKRDI SARFALNKI MGRNLPDYHQGLVKPNPGSYLKAI I LAS
OMYLASKPYLWKLNLNYCTLLGI AGKAKARVI NKR

>2617920961 Ga0073689_11557 Polysaccharide pyruvyl transferase family protein WcaK [pelotomaculum Ga0073689 : Ga0073689_115]

MTNI LI AENI PSLNKGEMAI FGGMLESFKLLDEVKVTMFSTAVI ESQRY
KDKAKI I DI SKSLFI PRDI KNQYAKFI LSLWGVLOHFSFLLLYKI LGRTT
LVLFROPI WRAYVEADVVI VGHGDAFGI GSGLATPLYCMPLYI PVMVKFM
GKPAVI YGGS I GRPI RFKTI QNFMMRYVMNKLDLI TLREHRSYDNLTI G
VI TERVHVLTPAFLCKPLKLSKAAEI LAEQKI NLNGGPLI GFTFTRKI A
SCACPELYDVNEKYKYHTQMMAAI I DDLI DRLGASVVFLPHCI GQSEKLD
DRLVGQDI FNKCKNKERVKVI TDEYSAEELKALI GKCDLFI GERI HSVI G
AI SMGVPSI AI SYTI DQRLNI I SGVFGEELI CKVEEFNTDSLLAKI MDL
WERRMEI GQRLQHKI EPLKKGAMTNGELLRKVLAKYNI L

>2617920960 Ga0073689_11556 Glycosyl transferase involved in cell wall biosynthesis [pelotomaculum Ga0073689 : Ga0073689_115]

LNI CLVVAPFVNSKDAKTRI SSFLKWMsGLANNI NI VTGNFPYTI ELEKG
PLVKI FNVGYDFKKQNL I ARAI RHVI LQI KI SLAI SKVI KGSDVLVFWLC
GTFI LPMLVGKMLNRKI I FVVTGSWSECAKVDFQNSLFGVGTfVI YHFER
QI ERI I YI LSDKLVLSPNLKEQI KNKAGQRLKKCI VMPARPI DTTVFN
I SNKFNNRNNI LGYVGRLDKGGVNI NLI KAFKLI SNNI ENI QLLI I GDGP

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LFYELNNLVVNECLQDKI I F I GWVSPEDVAKYLNKMKLMI LPSYSEGLPV
SI LEAMACGTPVLATSVGGI PDI I KDGYTGFI LKNNTPEEI AKSI RNI LN
SNNLNKI ANRSRLLVKKEYTFKALES I YKDI FNELI

>2617920959 Ga0073689_11555 Glycosyl transferase involved in cell wall
biosynthesis [pelotomaculum Ga0073689 : Ga0073689_115]
MNI LVVSEYFYPRLTGGEI VLWTI FNGLAAEGHKVYVVTSSFDGSPDYET
VNGI EI FRPFTSVDLTRGGNCSAI KVMAARSI FAVKLYRYLQDFLKYYAI
DLLYNMAYI PTLSSCTCAHRNKI PCVTGI DSFGGLTNFQI YSPLLAANI NC
LMEI LVLRFKGKHKALRCGSAEVVGRVQKYTRSHI I NI PCPLNDQEI RFVR
ETTDVEGI RRRNMG I PEGWRFLFVGS LVPVKNV DGLI RAAAGLTVDYNLV
I AGDGPDRASLEKLAQMLGVAKRVKFLGLVPHLEALRLMRACDVLI LPSK
SETFSMVVI ESLALGTPVI STLGVVPELDSPNLYKI SKLEEI TDDLLSK
VNRFD DCDI LESYSLTYI TSKFEKFFSSLI N

>2617920958 Ga0073689_11554 Glycosyl transferase involved in cell wall
biosynthesis [pelotomaculum Ga0073689 : Ga0073689_115]
LRI AVVYDVI YPWVKGGEKRVWEI ARRLTLRHVDVHLYGMKFWEGDDVI E
KEGVRI HGVCPRKELYKDGRRSI TEAI YFTQKVLKPLLQEKYDI I DCQQF
PYFTCI SAKLHSLHRTKLVI TWHEI WDHYWYEYLGSKGVFGVFI ERAVA
RI TKNNVAVSHTTAYKLKKLGTESHVI PNGMNFNEVQCVPGEYCDI FV
GRLI KEKNVDKLI EAVSI LKRDKHNLCVI VGDGPEROTLERLAQKLDVQ
KNI VFKGFI QSYHDVI ALMKGAKVLVLPSTREGFGI VVI EANACGI PVVT
VDHPGNAARDLI I KGENGYLTSLTPGLLAKTMMQALNDTTKLCKKI CHA
KFYDWNNI ALELEEYI SVLNKQDKRI HYEHFGR I

>2617920957 Ga0073689_11553 Glycosyl transferase involved in cell wall
biosynthesis [pelotomaculum Ga0073689 : Ga0073689_115]
LKKKNLVS VVI PALNEAEAI QGVI NAI PLNELSKQGYDTQI LVVDNGST
DGTGDLARAAGADVI RENRRGYGRAYKTGF EKAKGDI I VTADADLTYPVE
I I PELVGLLKEKKI DFI TTNRFAMHKDAMSTRNKI GNTI LNLTTKLLFF
ADI KDSQSGMWC FRK DVI RHI NLVSDNMPFSQELKI KTVKSRKFKWVEVP
I EYRARVGEVKLNGWKDGLFNLLHLLKLRFGI E

>2617920956 Ga0073689_11552 Glycosyl transferase family 2 [pelotomaculum
Ga0073689 : Ga0073689_115]
VRDSVEWTEPPKNTI KCAVI PAHNEAETI DK I QETKKYAEKI TVVDDG
SNDDTAGI TCEI I

>2617920955 Ga0073689_11551 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_115]
MCGGLSKCVKI I ELI FSNGWI AGNFR LPI LSGFFVSLDSLMKK

>2617920954 Ga0073689_11550 UDP-sulfoquinovose synthase [pelotomaculum Ga0073689
: Ga0073689_115]
MRVLVLGVDGYLGWPTAMALSKEHEVFGVDNYLRSLCRDL DVEPLFPVP
NLHERVRFLEESGKRVFI QVGDLQDWSFI SRI FQDFQPEAI I HYAEQPA
APYSMLNREAA MLT LTNLTVTANVI YAVREYCPEAHI I KLGTMG EYGT
NI DI EEGWLEVEHNGRRDFTLYPRHAGSLYHTTKI MDTDLLWFYVRMWGI
RGTDLMQGPVYGLTTPEAAENDSLLTFFNYDEI FGTVLNRFI VQAVAGYP
LTVYKGKGQTRGYLNI I DTI NCVRLSI ENPSROGELRI FNQLTETFTVNE
LAEKV KRVGNEMGLNVI I QQVENPRKEAEEHYYPKHTGLLELGLQPHYM
TEEVI RGM LDKVYKYRDI I PGRI MRNVRWA

>2617920953 Ga0073689_11549 Polysaccharide biosynthesis protein [pelotomaculum
Ga0073689 : Ga0073689_115]
LDVFKNKRI LVTGGAGTVGKELI RHL CGFYEPKEVRVI DNNETALFFLSE
EHKDDTRVNCFLGDVRDRDKLNREMQNI DI VI HTAALKHVI LCERSPWDS
VQSN I GVHNLI QAAI ANDVERVVFTSSDKAVNPTNVMGTSKLMGERLI T
SANAKKFNGHGPI FSSI RFGNVLGSRGSVVPVFKEQI AGGGPVTI TDRRM
TRFFMSLSQAI TLVLKSVELARGGEVFI TKMPVARI EDLARVMI DI LAPS
YGFRPRDI QVI EI GAKPGEKLYEELMNEEI RRTLELKNHFVVLPAFRSV
YEDI QYDYPDI VSLEI NKPYNSSLEEPVSLDYLCDFLI THGLVDNQPKNT
GHGFI PAAGADSI FQKEQKLPCGF

>2617920952 Ga0073689_11548 UDP-glucose 4-epimerase [pelotomaculum Ga0073689 :
Ga0073689_115]
MGQLEKDANLKRWLI TGGCGFI GI NLI ERI LRDEPGA I RVLDNLSVGER
EDLAQVCQFQEVPLSAMDVHAGGVELVI GDVRDAVAMEDVCRGADI I VHL

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AANAGVAQSMENPRFDCEANVI GTFNMLEAARLNKVSNI FASSGAPLGE
QEPPI HEEKVPRPVSPYAGKLAGAYCSAYYHAYGI KTVI LRFGNVYGP
RSKHKSSVAKFI KNALNGELLEVDGDNQTRDFI YI KDLVEAI LAARS
NLGGEVFOI ATYRETTVKELTGQLVTLLKQAVPNLENNVYGEKRPDVI
RNYSDI SKARRLLGFEPYDLERGLKETI AWYLK

>2617920951 Ga0073689_11547 Predicted RNA binding protein YcfA, dsRBD-like fold, HicA-like mRNA interferase family [pelotomaculum Ga0073689 : Ga0073689_115]
MPKNI PSLKVSQI RLLEKAGCKFYRKGGDHRLYRYADDKKRVPI DM
GADELSPAYVI RI LRKFGFTDEEI ERVLK

>2617920950 Ga0073689_11546 Predicted nuclease of the RNase H fold, HicB family [pelotomaculum Ga0073689 : Ga0073689_115]
MSFYTLVLRKSAGYWWALCLENGI VGQGNKDEAVLKLKEAI ASFEDAWK
EDPKI YEAPI PI KELHEFLTVENTLPVQEAFLRAI NA

>2617920949 Ga0073689_11545 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]
LYPQTHVYFAEI VLGKQGDEVTLGSI PDMLI GRYFNHYEAHSGAEMLS
FLKRRDLLLLDFGKAVATHGFVPQGLDYYGDEKYLDFERGYCFEKARALVQ
ETVEACNI PPEMGWWKAHNI VEMGVESLVSSSDYYSERI KSALFNMCLIS
EI DEMLHGLWKNNDFKFERRI ERFKLVLEI ERATAGSLARI YQVQMRFKH
QVEI DI PRVARLI ERAAEVDEDLASFDDTTMTMTVKNI NRFFPGAPGNV

>2617920947 Ga0073689_11543 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]
MPVSPSVKVVVVGGAAGMMAI TAGRGGADVTI LEKNPRVGRKI LATGN
GRCNFTNVNLGI NNYHGQNPKFAYTALTRFDVI KTI EFFERLGI SHKVEE
GGKVFPASNQASSVLDVLRYLEACGVEVLCEAAVTGI RKAGRRFVLDLE
DGRGVKADRVII ATGGKAAPNLGSGSGHTLAKNLGHSI VEPFALAQLK
LAASFLKQI QGVKFEQDAEI MINGKPLRRASGEI LFTEYGI SGPI FCLS
RKAGEYLQRKERVCLKLTMTALTALSPLELDRLRRFRWGPKKGLAFSFG
FLNKKLAPVVLKEAGVGVNMPAGQVSAADRDRVRI LRDWRFEVTGTAS
WPAAQVTAGGVVDREI NGRTMESKLAPGI YFAGEVVDI DGDCGGYNLQWA
WSSGHVAGESAARPCW

>2617920946 Ga0073689_11542 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]
MLETGGI LRLGSGRFAGVPGEGRKKVWGEWEMI RVTGLKLPI DEDQANLK
DVLLKKI GVAEGDLLGCKI FKQSDARKSGMI YFI YTVVALRNEETLLQ
RPGGVDI TVTPEMGYKYVQSGPEKMGFRPVI VGTGPAGLFAGI LAEMGF
RPI LLERGADVADARTEAVRKFWKGEINPESNVQFGEAGAGAFSDGKLT
LI RDRRCRKVLGEMVGAGAPEE MYSHKPHVGTDI LRTVVKNI REKI KGL
GGEVRFNSKVTGI VI KENKVEGVMVNGRERLDARVLLLAPGHSARDTFAI
LHAEGVGMAPKAFAI GVRI EHPQKI DRAQYKKFARHEKLGAADYKLVHH
ASNGRSAYTFCMCPGGEVVAAAEESGVVTNGMSFYARGAPNANSALLVG
VNPADFGGGHLLAGVEFQRRWERLAFI LGGGDYKAPQLVGDFLADRPST
GPGGVAPSYQRGVRYTSLKECLPGYVI ETLREAI PAMDRKLRGFALPDAV
LTGVETRSSSPVRI VRDENFEAPVRGLYPAGEGSGYAGGI VSAAVDGI KV
AEAI ASKYMPEFEPGN

>2617920945 Ga0073689_11541 ATP-dependent RNA helicase HelY [pelotomaculum Ga0073689 : Ga0073689_115]
LANNKTKQARERLLALLKROGAMPLEVI YSRCGPFDALAGALSSLI EKE
EVM I GRLKTRSGWLI GAKTPGPPDGGATWHTRRGQMRSLPKVLKELKKY
APSREPPADGDGEGQLKAVSELLADGRPRSRAEI AATGMEDI HAAVWRR
FPQLPDGRYTLPDSSGAWDYLLGYI REKPRRLPDLLRLFSRHGEI VNRLA
VENDRAPFVRMPRALI TTTDSPEGKSELEHRRQVDRWKEALDSLPHPFPI
PETMGLDPGAFRDLADSYTAPVEFAGKKYRCLRREFPGEALVEQLGEI SG
RHFAPPHSAGGSFLLKEHVSVEKEAANI LGVDRDVLHLLAGGELDYFLL
DGKTRLWRSLEDLKRKGAGLRELAKKYEKLTLYEAAVFLGI STDQLRRL
ADEGI I RPLSGGETRPKTLFRRVDLEKLWENI PSSIPGGSAPGDPAAG
RRGAGKKKPRRRREKTPPPAQEELVLDDFQI KAAEALRMGRSVLVAAPTGN
GKTLVAEMLAGDLMAAGRMVYTSPLKALSNQKFRDFRVLFGEAVGLVT
GDVSI NPGAPI LI MTTEI FRNWCSEPEQLEKTSYVVFDEI HYLDDAERG
TTWEESI LFAPSHI RI LGLSATAPNVEEMAHWI GSARGEVVVI QENRRN
VPLEI HWI LPGGRI AGEEEARSEVEDLTEYI KALRGKRRWAEI

>2617920944 Ga0073689_11540 Helicase conserved C-terminal domain-containing

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protein [pelotomaculum Ga0073689 : Ga0073689_115]
VSCGEI I ESI QDKLPALFFVFSRGRTEI LAQDLGREWDFLNDKEKRVVGK
OI REAEAEHPGTGSGPGWRGLRRLLYQGI AYHHAGLLPPVKYLVEKLYSR
RLLWVVFCTETFAAGVNFPAAASAVFDSTRKWDGHDFRI LQNREFFQMAGR
AGRRGFDRVGHAFI RVDSRFPEQTGFFKEEDVEPVLGRLI I SPNTVLSLL
RYKTDEEI HRFNLNQNFQMQLKKRKDFLGQELKKYSGRI SGI EAGLCPES
GSYVCPVERI RARROLKRLRWKGRNREQEQLQKQLSAHTPKRCRDTEOCR
I AVEDLKKARDRLQALRQEYKSVSEQEKSVFI EFGEVRDLLEELGYI KGR
EFYPRGVFALELHVQEI LVTELAFSGLI EETEPAEAAVLAGVEFI PGKN
SQGI RLDLPALQEI FSLRHNLLRMGAPERFCVWSNLPGLAFAWYNGASF
GDLEMSLQPGDVFSI FRREI DLLRQI ERAAAGNHS LAERARAI RSKLD
RDEI ALSF

>2617920943 Ga0073689_11539 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]

MKNSI CVYRLFVDAEEI NLEOVEKI LAWARPTSRMRLSRI RPKSI QFKNP
PVAVELGECPTI GAQNFKALFTGKI YDLGVI GI I MRVPLRPDAGYNEI L
DLAVEFYNNDDI ERVFLQQLNI KTALGEALVKEAYSGFVEDFTI YYFQE
WDAGQDPVPLLLAEREPVSDQVRRETLRTSFSYGLDDLAVI TWDSALVYD
STGSTDI PDLLEFANAQLLELRYYDNLLSGEMEGMYDAI EQAEKVGSRFR
LGHYRRI MNQLMELI ADVTEI TERI DNSLKVTEDEVFYARI YSAALAI FRT
RAWAESI DRKI SI I NQSYTMSNRI I NQSELEI I I I LLI LLEVI LGVL
GFMQ

>2617920942 Ga0073689_11538 Dynamically protein [pelotomaculum Ga0073689 : Ga0073689_115]

LNNLLRFI KCSEELRETAGPSAKSRVVI VGSFNAGKSTLLNNLLGEEVSP
VGTTPTTPCLI HFEYGGTFGAGYTGFRKRVFHRREDLRSFLAQLRSGGR
VDI EI PAPLLKKCRLVDTPGI DSPGGDAGRPALAAAAGADKVI YLFHQRG
I EEQNRLFLHRLAALWKNKNLNDLSFWLNCNLGRSDGTSLETTGAALREI
FLSQVRLNTVNTSRRESVEGLRLFLELELARENLVNLSGYLKELDSELP
RMKKAAGI KDDGAFLSEFWGVRETARLI LESKRLLHSLPSVVRELEEHFS
LMNAANLGVTLPGPGGRPYSPGTI WGGEI RKNLLDLI YRLLNDKRLEGFV
EREKLGDLRRRI AGESFTVMAAGGFSTGKSTFFNALLKEEI LPVADGPAT
TCVTRLSHGHGKTATVHLPLQVTLQI YGNTGGRAGLRREEVAALERWLG
PI ADI ARLEACVDGRFMPVDRPELLNMLNRARELFAAGFFKKTGLNSVRH
AAFRLI SFRKRLRGNRMPEKVRVTFKNSGRI DFDFARPGGI KDFQRAVGPD
NAFRI ETVEVRHPAGFLKLADFVDTPLDGLWQKHHLAKTAGYI ROADI CL
VFLNARHI LNNLDGDYFQNLRLRTAGDPGRDGI AGI DKDKFFYLI NFAD
VLTAAQRETVHNFVRKSLAPPANPWSHTFTGPGI FMI SSLOGLAGSGGGL
DVFLKNLEESI LKRRGRNFHLAKVNELFSLDRASRKAGGETFLAGQSSV
QREMELRQAQEVLRARRKLKI RSATYNTGR

>2617920941 Ga0073689_11537 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]

VENARLLDERLRI I GEI GGHTGGEI KKNLLGGFEKSVRAALEEHATRET
ARFLALLKKAVDKI

>2617920940 Ga0073689_11536 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]

LKLEKGOAENNGDRLI QQMLTDI LVGLRVKMQVPVLEENKKI AGLLEELK
GQDRAGVAELLERLDTLEDQVRQAPLAI LAALRDAI NRAGGGNRDGD

>2617920939 Ga0073689_11535 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]

MAI ENLTI QSELVNSLASTI RERI VAPAEGRVDSLSEI NEI KGRLALLE
RESASLAAHSRTGRLTARAAVLGAAAALAAALI I PFI KG

>2617920938 Ga0073689_11534 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]

VAKKKPATDI KPGLGTVPFACI EQEFEDVRKGLAPKKPVGGL

>2617920937 Ga0073689_11533 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]

MMTRAGTPGGVFKQLKEFI GRLWGFGEAGPAGAGYPLYRLAPSRDLGVRR
VRLSFLI GMTRAEPGRSRGKKAGNTVLNFPKPGKPAALVLTWLGLEPGAA
GEPPVRVARVKGDYI VEKGWERLI LASVLGLDYI CARVTEYDYEVFLKKM
RVFRFPEGTMVGVLSGNGKRYVYHGVGDGDLSELLGRYRVTI I DRTVAPS
DTGSPVKAARAGGGAAPVKTKRQLRLVRDLDD

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>2617920936 Ga0073689_11532 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]

MNNPRVLLLLFALAFLAI QVVSFMSGI NSHEERVGKLEKQSAQFETKGT
Y I DLKLDPSVELKKEKTRFRAETVNF I VKVLVI SGATAFVFALMKI DRGHK
GG

>2617920935 Ga0073689_11531 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]

MDYNTGALKVI EALRANMAAQVNWLACQI TSPGSGADGAI KRYPDQGWV
TPYFSNFAALAMLAVPSHHPQVERYLDWYLRNLEPNGVI LDYHYDEKLNA
RTAKPDSEDAYAGALLSLAAAYHERAGQSRWAGKNLLGLKKVARS I KLM
DRDGLTFALAGYRVKYLMDNCEAYRGLADFAALLDYLGDADDAPYFKARAD
AMAAGI ERALWNPRLSLYHPSKTGWFRAGLNLKKFYPDAAACQVFPALYGL
I EPGSARGARLYKLFNDHQPDWVRVQPPHYPWM I LGYCACLQGDYRRAYE
KLRHVREAYI DTGSGNWFCAEAFFVLTCALKI EKREEWLG

>2617920934 Ga0073689_11530 Antitoxin of toxin-antitoxin, RelE / RelB, TA system [pelotomaculum Ga0073689 : Ga0073689_115]

MKGVLNATNVRKEWGKFI DAVVHEKPQI VKRNRDYFLSLSLNHVDNLLKD
I SFKVKLVDEDDGSI TASLENLDLVVNAENI TEAQNALAEELLDYAHEYF
GEFQLYYNSLNRRLHFPVHLKVLVQKDLEGVTGLLHA

>2617920933 Ga0073689_11529 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]

LYKKTSHYYFRKQMPDGLKTRVSMGSGQI KDNLWQEI LKKQLQVTQEI
FNSKT

>2617920932 Ga0073689_11528 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]

MTQEI VVVQSQGQWLALAGGELVAAGESFEEI WQVSCAI QKAS

>2617920931 Ga0073689_11527 prephenate dehydratase [pelotomaculum Ga0073689 : Ga0073689_115]

MAKNVGYLGPAGTFSEEAVLRYLEGGEVGPVPCRSLEI FDGVSAGELAE
GVVPLENSYEGAVNMTLDLLADCYPVKI RGEVLPVSHNLLARPGVTGSD
LAGLI SHPOALAQCREFI RKRFPGLPLAESSTAEARRVAEMKEPWGAI
GNRRAAASFGLALLEYDI NDOAGNTTRFI VLGGEERCPAKPAKTSI I VAV
TDRPGALYHI LKEFALRNI NLTRI ESRPAKRRLGDYLF I DFRGHSGEAA
VAAALEAVARQAADFKNLGSYPAGPVPWDEGQPGRESPVTLEEVRANI DI
VDFQI VELLAKRTGLVTI LAGLKKGEQVRDPAREREVLDKVRQI AVQKGC
QDQVLEKVYSI LQHFVSI QDKKKKGEVC

>2617920930 Ga0073689_11526 oligosaccharide amylase [pelotomaculum Ga0073689 : Ga0073689_115]

MVVKKI I DPQI QPEMPEAI I GNSRMLASLRNNGEI FRLFWPNI EFGQHLG
LFWPGVKLAMAEGQSYTKWFHLNVWESSQRYLENTNI LETNLSSRTHHLK
VTQKDFVFPHRDI LARYYELKNQGEKTEKI SFFLYCVFNMEESVLYDGAY
LDFSNNALVFFRRDYVLAVAGSGYPLAGYHCGRRGAPSDPLQEASRGFLW
GNRENI RHSAGALAWDLGEVAPGESKFTFLYLAAGHREEEARTLLAEATA
REGRYWLEETRFRFHDWLKPAQTGGPADHPAYKRSLLAMKLMTSGETGAS
I AAPEFDPYYLACGGYGYCWPRDSYI AAALDEAGYHDLAQFYQFAASI
QDKDGSWRQRYFTDGSPAPFWGKQI DQAGTVLWGYRHHYSLTGDRNFLEI
VWPSLAAGAGYLADNLDNGLPVSSYDPWEDEYAQGTYSAAAVYGGKAA
AELAAKGERDVAERWGRASETVREAI LKHQWSPARNRFMRGI NRRVGRE
TYECALGRGERAFTGSDPTGLYETHWVGEDGRI DAALLGLAFPPFAVLDP
DERMRATARAI EEGLWNHGVGGLRRYEGDGYREGNPWLI TTFWLAI YHCM
AGNGHRAEELYRWCLGQANRHL LPEQADKDHGGPAWVMPNWSHAMQAL
THLALHGKLG I KTSSG

>2617920929 Ga0073689_11525 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]

MDLEI RTEI DREQSLDPSYI VRYQI FDNGRFI GDGVAQYHRLAGHNDHRI
PAAI KRPDGGPPAPGDLEKI KSEI DRAAKEYI KARREKG

>2617920928 Ga0073689_11524 Uncharacterized membrane-anchored protein YitT, contains DUF161 and DUF2179 domains [pelotomaculum Ga0073689 : Ga0073689_115]

MSSRLKARLPPAEAGTVALNLLTVTAGALLVAVSLNTLLI TYGLLAGGV
SGLALI LFYLFKI PVFLSI LI LNI PI FWWGAREI NRQFFLYSLWGTALA

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ALLPATHGLI PFPRVDMI LAAI FGGAI SGAGFGLVFRNGSTGGADI I AV
I LRKKKNMGI GEVGFYSNLMVI TLSLLFFPVNI VMYTVVSMFMAGKLTDV
VI AGLNTNKSIV I VSDKPHQI GDRI I NELHRGVITYLAGI GAFTREEKTVV
NCVANRFELSRLKNI VTETDPGAFMYI YDASEVLGKGFSI KK

>2617920927 Ga0073689_11523 DNA-binding transcriptional regulator, PadR family
[pelotomaculum Ga0073689 : Ga0073689_115]
MLREI FLGFI RVHI LHHASLNPVYGLELI KELESHGYNVSPGTMYPILGK
LEQNGLLSSTEMNVEGKI RKYRYI TPAGNDVLKKAREKVRELAGEI LREK
QDAF

>2617920926 Ga0073689_11522 putative ABC transport system ATP-binding protein
[pelotomaculum Ga0073689 : Ga0073689_115]
MLFNFRNI EFTPGLDGRRI PVSGSVAEGEVLVVRGPGAGKSTLLRI LA
RLQPCPGGEAHLKGKSWLQTPGI LWRI NVHYLAQKPVLFDGTVADNLAKP
FDI AVMTSKKFDLDAKGLLEKLLPPGLWEQDARTLSGGEASRVTFARA
LLI DPAVLLLDPTAALDEKSREAFYVALSNWLTGQERAALLI SHNEDYK
LLNKVSFLDLKSLPP

>2617920925 Ga0073689_11521 putative ABC transport system permease protein
[pelotomaculum Ga0073689 : Ga0073689_115]
VETSI I PI SNLQLAFTVLLVFI TGAI SSFLKLGLLKSLWGTVRTFLQLN
LVGYFLVYI FKI NNLWL VLLI VTL MCFVASKTAVARTPNVPTYPTI LAFI
SLLASTYLVGSI VTVLI I SPQPWYSARI I I PI FGMI LGNSMNGI AI SLDR
LYSESRSAGAAEI ETMLTFGATPWEAI RSRVREAVRAGMTPTI NSLMVVGL
VSLPGMMTGQI LGGADPREAVKYQI VVMLMI AAVAI GCLI LVSLSYKKL
FTPDGALQFPI LQSKKGA

>2617920924 Ga0073689_11520 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_115]
MSTVTI HLEPVVDDSAI ARVRSALPQI GKHDQLMI VMEAADAHQADRVME
VLEAHGFDYQPRGSHNGRDYHI I ATRLK

>2617920923 Ga0073689_11519 small acid-soluble spore protein F (minor
alpha/beta-type SASP) [pelotomaculum Ga0073689 : Ga0073689_115]
MSRRRGVMSERLKYELADELGVDVVRDGGYFGNVSSKNCGNLVR LAI
ERAERSMTGER

>2617920922 Ga0073689_11518 putative Mg²⁺ transporter-C (MgtC) family protein
[pelotomaculum Ga0073689 : Ga0073689_115]
VI I DEKEI ALRLFLAFLAGAVI GAERKVRHKPAGLRTHALVGLGAALFTI
VSVYGFLEFSGPPYFRTNMDPARI AAQI VVGVGFI GGGLI FREDNKVSGL
TTAASI WLTAGLGTGI GAGMYFTVLVA AVLGI ALRLNRI LERMGFNDQG
E

>2617920921 Ga0073689_11517 serine protease, ClpP class [pelotomaculum Ga0073689
: Ga0073689_115]
VNFLDYFWI LFI LMAFMPMLRQQRLEVMMRLI RRI EI KRNSRLI TLI HR
QESLSI LGI PI SRYI NI EDSEAVLRAI RLTPDEMPI DLVLHTPGGLVLAS
EQI ARALQKHPAKVTVFVPHYAMSGGTMI ALAADEI VMDENAVLGPVDPQ
LGEFPAVSI LEVVRQKGRDKVDDRTLMLAEI ASKALSQVREFVYLLSDK
I EEPGARELAEI LSCGTWTHDYPI DCEQLVKMGLPVTVGLMNDI YALMDL
YPQPPQRRPSVQFI PLPYGRREGQPGGK

>2617920920 Ga0073689_11516 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_115]
VFKKKTDFVFFFYFLLVAKNI HLAAQVFREI NNLNDAAEYALQI KTVESM
GDQYTHEI I LALNKTFI TPLDREDI LGLTLKLDDVLDI MEACAWGFELYN
I TEADDYMRLFTKNI EMCVQEI VHAI NCLVDKKMQEMKKHHTKI NDLENV
GDDLRLDSI KTLFSTCTDPI EI I KRKEI YGMMEAVSDACEDVANI LEGAI
MRNS

>2617920919 Ga0073689_11515 inorganic phosphate transporter, PiT family
[pelotomaculum Ga0073689 : Ga0073689_115]
MFDPTLLLI GMVVI LALSDFDI NGFHDANSI ATSI STKAMLPRVAI ALA
AVMNLGALAF TGVAKT I GGKI ADPLKLENGMYVVAVALI AAI AWNLI TW
YYGI PSSSSHALI GSLTGAVI AAAGLRAVNFHGFLAI LEALI FSPLAAGF
VGYI I MTLI KI FFRKGHPARLNRRFRTLQVFTA AWQSFSHGNTDAQKSMG
I I TFALVAGGFQTTLDVPLWVKVSCALAMALGTSVGGWRI I KTVGSKI I K

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LEPSNGFAADVGSAMVI I LATLI KMPVSTTHVI SSSI MGVTAKRVSSVK
WI TAEKMTAWMI TLPVTALI AGVTFLVVSFI

>2617920918 Ga0073689_11514 CBS domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_115]
MVEGRKTAGEI MVLDDYNTI SEKATVYEAI RVLRESFHRDGRAWYGHRS
VI VLDGDGEPTGI LDLRGI LRAAGLRELENDPDLKAESWGWNVI KKLREE
SRLRVRDVMQPLGLAVVRDDLTDFVARALLKHNVNSLPVLDKGRVAGI V
RAMDVFMAMDAYS

>2617920917 Ga0073689_11513 CBS domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_115]
VPI TRLVRSI MAPI EEYPVYEDAMVI EAI ETLRESFHQKDGTWYGFQTL
MVLNRKDELVG I LTLRGLLVALRLRDI VEHI LKGDPTGLFFTPHLQSDLR
I NVRKI MRPLNLI TVQEDAGI MEALLI I VKNNI NSLPVLSGARPVGVVRT
I DLFWFVGELLD

>2617920916 Ga0073689_11512 two-component system, NtrC family, response
regulator AtoC [pelotomaculum Ga0073689 : Ga0073689_115]
LDKLI LLVDDEASVREALTDI LNDSGYRVECAASGGEGLEKI ETLNPDVV
LLDI RMPDI DGI KVLELVRRRGERTPI I LI TAYGSTQTTI EAMKLGAFDY
LMKPLKI SDLLDAVKKAI EVKELLDRTSRGESLPEVDPDTMI GLSPVMQN
VYKI I GRVANTNATVLI RGESGTGKELVAQAI HYNVSRDRPFVKI NCAS
I PENLLESELFGEHKGAFGAVASKPGKFELAHRTI FLDEI GEMSMNTQ
TKLLRVLQEREFERI GGTETI KVDVRI VAATNKDLEKSI ESGEFREDLYY
RLNVVEI VLPPLRERKADI PALVNI I KGCSAEHKKAI RGFSEAATDI LM
GYDWPONI RELKNVCERAVLMSNGPVLGVEELPLTLKKKSRRYNWLNEI P
GSSLKEI VSEVEREI VLRALLEHNWNRSAQAALKMNRSSFYAKLKEGLI
LD

>2617920915 Ga0073689_11511 two-component system, NtrC family, sensor histidine
kinase AtoS [pelotomaculum Ga0073689 : Ga0073689_115]
MFKRLVTFI KGARKSFGNRI LGLVSLLLAVTI LLSLYMMHTI KYSELSLL
EHQKARLNQAAAFDQSFDTSLTQYLVEWNAAGKSRAEKI QI LAGYVNGV
I KDFNDKYPDVHI GLYVADLDVFYDGTQRFNENFSLRRKKAFFETI ENKS
SLVQNVGYEEGGI VEVYKPMVRGGNVEGVVRSAYLSEVGFYKKRREVEY
TI YTLVGVI AI GTVGALLI FRQLVTQVQAI KEGVRLLEYDYNRLLPEAP
GELGEI TGAVNRFWKI STLNLNETMLAAI DDAI LVVDTGGQI I I ANNM
AHRMFNLDDCLEKNYWEALPEGSPFQALLDRTLNEQRDLRDLKVSARG
QGSNVHEYFLSAFI LKERNYSVI GAVLCCDI TERVREEKLRRQERLA
SLGKLVTVGAHEI RNPLTSI SCYI QHWQGHKNGDQALATVHREI SRLDS
LVDQLLYFAKPAEAKFRPGNVNSVVENVLSFFGEVFGYKYN I KDLSSQI
PLAWI DI AQVERVLNI I FNAVQAMPEGGS TVATAPAEEGEFVRI TI GD
TGCGI PPENLPHLDFPFYSTRPKGTGLGLAI AHEI I QAHGGRI EVESAVG
QGTTFHI YLRTKGD

>2617920914 Ga0073689_11510 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_115]
MI SWKRI HHWMSKALEEPFFRAEMRRVEMTLPEHKAPCLHLVEGGGKRRG
GKDSTGI KGI EEFAARN

>2617920913 Ga0073689_1159 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_115]
MLTGLVKKRGLI VLAALLLSI PGVGEAAGEQLSEHDMVKTFI DLNSFSV
I FLFVLGFLGGLI SGFI GSGGAFVLTGMMSLGVPGAI AVATNMCHKFPK
SLVGAYKRFKYQVDI KLGLI MGI SATVGVI QI QI QKWI LAQWGPAGSN
LYVSLI FVGI LTVLGAFI FI DAI NTMRGRNQSGTSLAEKI KKI KI PPVI
NFKVANTRVSVMTVPVGLATGMLAASI AVGGFVGVPAMI YVLGAPAI VA
TASELVI AFVMGLSGSI NWALGGFI DI RLVL I LAGSLI GVQLGAVGTTY
VKEYVI KLVMSVMLVVSVRGFAI PTYLHELGMELAQSTVTLLKNI SF
YTMCLAMAI AGVI VLGSMLKGRKALEEAEARAALQSGKKGVYAAKAVKS

>2617920912 Ga0073689_1158 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_115]
MKKTGKASAI KOAI FWGI I SLAAYFLVFTNQAVMDYTTVGGSYGI I VI V
VAFASF I HGTFANFLVEVMGFKAACHGEGGH

>2617920911 Ga0073689_1157 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_115]

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VGDNRI ANEKRF GAWKELPGGGRQYFYDKLKGHDGRWARYVKI VDAQEE
TI KFYQEI YDRHGKLVHQQYPEDKGHRKVRKGVGHNDYTPNGSI

>2617920910 Ga0073689_1156 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_115]

MI TRQTVAYKI FDYLRHRI TLAELVDWAEKAMMDGEFEEKDHDKI RDI VS
SLGLADV KDFEI TWEDWTEFLKRLGYQVDLT MREI NAV

>2617920909 Ga0073689_1155 Endonuclease, Uma2 family (restriction endonuclease fold) [pelotomaculum Ga0073689 : Ga0073689_115]

MQI EKAGKFYTYEDYLKI DDENQYELI GGR LI MVPAPRTI HQLI KGN I FW
VLKDYI RKNNLGEI LDAPTDVLLSETEKQPDI LFI SKERLNI VTEMNVQ
GAPDLVVEI LSPSTGKNDRVEKSKMYKHHGVKEYWI VDPGYKTVEVFMPA
EKNWNLFQSYGDEDTLTSPLLTGLEI KLRDI FS

>2617920908 Ga0073689_1154 CBS domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_115]

MPERKAKDI MTP I SEYAGVNENDSLKHAI MVLKDTSGCHGALAVKDDHKN
LVGFLTVRTI LKALEAI AFRETDWALSWGFFLTRNI EHI SRAKVKGVMR
PVVKVFI DENASLEETAKTI LKNQVNNI PVTGEDGKVVG I VRAADVMDVL
AGFLKG

>2617920907 Ga0073689_1153 CBS domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_115]

MQKKMDSVKDLMI PLSDYSTI NDNATLEETVNLMDRSI RERGHRTLMVLD
GGGGVVGFLTTRAVFEALGKLAPKAGGWLGI SFNRPELFFWDGLKLI KDT
RVKKVMRPVVDAYVREAYPAKAVEMI LKRGVTI LPVLDEQERI TGVI RA
LDLLPFVKRLFESKI S

>2617920906 Ga0073689_1152 two-component system, NtrC family, response regulator [pelotomaculum Ga0073689 : Ga0073689_115]

MVPKI LVI DDEEHMCWALERAMRQEGYQVFTTTTRGQQGLDLI REEAPSLV
I LDLKMPMDGMEVLRRAKEMQPKLPVI I LTAHGTI ETAI EAMKVGAA DF
I TKPFDLDELKI VI KALMI SQLVTEVSFLRSEI TSRYGRI I GRSKAI KE
VVQLI ERVSASNATVLI TGESGTGKEVA AVAI HQASPRRDAPFVAVNCAA
LPENLLESELFGHEKGAF TGAVI RKI GRFELADKGTI FLDEI AEMPLNMQ
VKLLRFLQEKAFERVGGTETI KVDVRVI AATNRNI AEAI EQGDFREDLYY
RLNVVPI HLPPLRERREDI PLLAEHFLNKFOPTYLVNKI SSEAMEMLCNY
NWP GNI RELQ NVI ERAAI I CQGSEI QPDHLPKELQLQQKQAPVANGPVI N
FPDEGI SLEEVEKQLI I NALEKSGRNQTRAAQLLRI TRSALLYRMQKHGI
S

>2617920905 Ga0073689_1151 Signal transduction histidine kinase [pelotomaculum Ga0073689 : Ga0073689_115]

LRHTHSI FSLFTSKSLRFQI LLI VAAMLLI PVLVMLYDI FFASKEDDEVLL
KTNQDRLAI VTQNLVREI DGS I GGSQAVLQEMDLAERTAFLQI I FEAAAG
PI AEANPGVRLGLYI PENEVEFVRGYLHNYRQLSQDEEREREKRI LNEAR
VGI VAVVASKAPLARLTSTFDDQVFENLAPVFSKDGLVAVVWADERLHPI
FTQSRNFRVLVRYVTI I GFSFGAVGALI I I HNLASGVGRVKNGLGELEKD
I HNLLPEMPGEMGQVAGAI NKMALALAEKEKLEAELHRSERLAALGRLVT
GVAHEL RNPI GVI KATVQVMEKEFEMI PGLADYSTVI KEQVDRQNRVI QE
LLDFGRPSKPVI QMVSNTLLQAVLTFTEPLL RQHKI KLI KELGDGLPPV
DVDGERI KQVFVNL I LNAVQAMPDGGALTLTTFTEGGKVAI RFTDTGEGI
MEEDLPSI FDPFYTTKDG GTGLGLSI SHQLVKVHGGSI DVSSI KSRGTSF
TI NLPAAGYAAEQGQVNH L

>2617920904 Ga0073689_11459 monovalent cation: H⁺ antiporter, CPA1 family [pelotomaculum Ga0073689 : Ga0073689_114]

MNI HSI ELI FI LLT LSVGTALAKKMNRPYPI ALVLT GAVI GVLPTLGLF
QEFKTFFTSEEI FRTAVLSI FLPALLGEASLKLSFQELKENRGLI LMLAF
TGTF LAFGLTGGLTLLWLGLPLQTALVFGALMSPTDPVSVI SVFKNLGVN
RRLAVI MEGESLI NDGVAVVLFKI SAFSLAAI AALGPWGPAMGLVMFLKV
VFGLLI GLSLGFI I SQAVRFFDDYPLENSLSVVLFYGSFI I AEQAGVSG
VI AVVAAGLV LGNYGTVI GMSPTTRL SVTVFWDTLTLVANSLVFI LVGLE
I SLNTI VLHI LPI LSGI LI VLLGRSAAVYLTATGFKLPWSWKHVLNWGGL
KGSLSI ALALSLPPDFPARETLI SLTFGVVFFSLVAOGLTI DPLI RI MGL
OKTVOGLREYESLSFELQQA I TAANELHRLREDGRVSPQVFKKLENNAA
RI ARI EKELSLLYRQHPKLLFEQEYAARKLLI AEHQAVEKLLGEGVLSA
ESGDGKKRSI LERLEALEESEHTDVPVSEEKARQ

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>2617920903 Ga0073689_11458 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
LKGWPWKANSVTGKCPAYI TRYHRHLLPAFRDEADHLFMHHI LSEAQRAA
SKTARKAEVST

>2617920902 Ga0073689_11457 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
LSALTNPI DRSLKALAQNYPAAFI RLALGI SENRFFHTVENPEI NI PEKR
ADI VYQI EQEDVKYLLHLEFQLHHEKDVPERMFKYSAFLTESYRLPVI PA
VI YLERRNYRQLPSEYRMELDGKI MSRFTYQAI KLWDYSEAI AKGALKEL
APLLI MLAEESADVLAETROLI LAENKKWRADALSAVTVTAERYLDRE
FLLKFFKEEVAI LKESSI VQDWI NEGMEKGMEKGMEKGKTETLREDI MEV
LEERFDLI TKEI DEKLRETDSPAVLRFLLKKS VKVNSLEEFQEI LKAV

>2617920901 Ga0073689_11456 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
VEKRGGLAGCESGRFPDDYFPYPYCYRANVVVTKYVI NLEAI EHLEAKG
TPFSVFKNAYETI FRHQWPALTGGMLLGLFSI LVVAWDRPWGI VGGI RNW
ADWLFYGLGLFPDRPENPLLFSSSVMDI GLLLGAFAALI AQEFAI RRPP
I LEI YKGI FGGALMGVGAFAARGCNI GGFYSPLI NLSANGFPMFI GLAMG
AFVGLKYLFWLEKFPAGPAI SPDVGERKCGNGKFI QPYLGVLVFI GLI M
AAFLYSGRAYTI SGGI LLFGAVFGI I LQHCRFCFARAFRDPFMTGDASMV
KALALSI VI GALVGVI LKWTGFRSESLWVTPVFWGSLAGGFVFGTGMVI
AGGCGSGALWRAAEGQLKWAALI TFALVNSLVTVLLKNTGWQQKLGKAV
FI PDVLGWGGSII LLI ALFAFVWYLVVTWNEKNRFTLGL

>2617920900 Ga0073689_11455 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
MQTVLKI LAKQYPOAFLKLALGSVENI I YETI ENPEI NLPEKRLDFI YCL
QDEENEYI LHLDFQLRHERDLPLRMHI YNALLTASNQRPVI SKVI YLERR
EYRNLPGEYVVSIRGKRENVFSYEA I KLWDHTEEI I TGELKELAPLLI LL
TREKSEAVLAKTS

>2617920899 Ga0073689_11454 effector-binding domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_114]
MQYLNEL SEQPSGAPFSAYYNMDMDNLDVEMGFPVAKPLAGKGEI KAGEI
PAGKQVSCVHKGPYNQMEPVYNALLOWI EENGQTSTGVSIEFYFYNPSPLEV
PESELLTKI VFPLK

>2617920898 Ga0073689_11453 Protein of unknown function (DUF3795) [pelotomaculum Ga0073689 : Ga0073689_114]
MERI VAYCGLLCTECPAYLATKAEDREALERLAAQWREEYNAPDLTVDNV
YCEGCPGEGERKCGHCAECEI RACGAARGVANCGACPEYACEKI RGFLAM
VPQARAVLGDHQNKSTNQRGQNI VDHQFELSEQPSQPVLSI RTRTPVSPT
FDLKP

>2617920897 Ga0073689_11452 looped-hinge helix DNA binding domain-containing protein, AbrB family [pelotomaculum Ga0073689 : Ga0073689_114]
VI RAKLTSGQI TI PVAVRYKLDLQPGDELLFEFDRDDEVKLRAFKRRL
TELYASLTN

>2617920896 Ga0073689_11451 Uncharacterized metal-binding protein [pelotomaculum Ga0073689 : Ga0073689_114]
VVNCAKCGVYACWKGEPAKLPKNCPVREQTDI YEEASTAYRGEAGNMACA
SARVEAAGYGGWPRLREI MEFSRLAGFGKLGLAFVGLRREALAVAKI FE
ENGFTVASVMCKTGSRPKEELGLRKEEKVRPGQFEAMCNPVAAQALLNRT
HPDLNVLLGLCVGHDSLFI KYSEAPVTVLAVKDRTTGHNPAAVYAAHYF
QSKLKLT

>2617920895 Ga0073689_11450 DUF218 domain [pelotomaculum Ga0073689 : Ga0073689_114]
MKERGLQSALLVSDGFHLPWAKLLFREQGVVYGGSPAASPTSTI VSLRF
FFTRESVAI VAHYFGGAFKLVA

>2617920894 Ga0073689_11449 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
MI DRATPLI PAFREVI AYKDAATPLTYERFTHNTDGATSSFSWNPKKKFY
KNI FGLDVKTPVKLLI GSCWANQI GGI PGAI AAAYQYAHRI K

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>2617920893 Ga0073689_11448 putative membrane protein [pelotomaculum Ga0073689 : Ga0073689_114]
MSRLVIRI GANTI AFHAAALVLPVAVLNSVWAGLLAGTVLTLLHLLI RPF
LLLLTLPVNLI TLGLFTLVI NAWMVMLTDKI I PGLTVPGFWPALAASLLV
TLVNLLLNRFTFETVFHKPLNWK

>2617920892 Ga0073689_11447 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
MWSKRQSQLLLI RVSRRGLRRLVI PVPLFVLDLTAAFSDLACLI DSFAP
EWMRGMRRFELGGSGAGRI SAEATLAVCLRLFREMRKHGRFRLAEVQSGK
IGIFIDFY

>2617920891 Ga0073689_11446 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
MGDEKTRLLEMVRDGI SVEEGVELLGALDDAGNRAPGPGKKLEDRLRV
RVDSAEAKVNVNI PLSLLKVASHLGNMI AGFVPGEARREMAERGLDLSKI
DFGELLNLI EQGLADGKLVDDI EDTEKGRI RVEVYVE

>2617920890 Ga0073689_11445 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
MRFKAPNCCPVCGHEMTI SSLACSHCQTRI EGNFTSCKFCKLPAEQQEFI
EVFLKCRGSI KDVEKELGI SYPTVRNRDLGVI QALGYRVQKQDDEEGKNH
KQEI LSALEKEI SAREAAGLLKRQRGNANLERGK

>2617920889 Ga0073689_11444 Pyridine nucleotide-di sulphide oxidoreductase [pelotomaculum Ga0073689 : Ga0073689_114]
LHVVI VGSSAAGVSAVETI RRLKGTEVKI TMVSEEPGVSRCCLLPDLLA
GRKTEEGI RFRPKDFFQKAGVDFLNGVSAVELHPREKHLVLENGHVLSYD
RLLLATGGSAALPGVPGANAPGI FTLRTMADVRLLRKVMPGAHHVAVLGG
GLI GLKAAHALKMAGI KKVTVI VASSHLLSRQLDEEAASMVEKEQSAGI
EFLYNEDVRSFLPGAGGKLAGVLLKSGRELSADMALAAKGVRPNSALVEK
AGGLAGRGI KVDNLLRTSLEDVYAAAGDCI EVTDRLTGERSVGSALWTLAAE
QGRYAAANI LNLSPYPLPLTRLNSARFGRVDLI SAGMLTGPEVQRHYDR
I NNTYRRLVFDGDRLVGFI LAGKVDGAGVYTALARSGRPLGSLKRSLLHG
NAGEATLAQMMKRSSTI

>2617920888 Ga0073689_11443 Ni-dependent carbon monoxide dehydrogenase precursor [pelotomaculum Ga0073689 : Ga0073689_114]
MENARSI DKASLYMLKI AASEGVETAWDRFSAQQPQCGFGLGCCRNEN
MGPCRI NPFGDGPERGVCGATADI I VARNLLRMI AAGAAHSDHGRDVVE
TLRGAATGEAKDYQI KDVDKLRKLAVEYGVNVEERPVEI AQELAEVLE
EFGTRKGHLQTI KRAPAGRHKVGWNLGI I PRGI DREVESMHRTNMGVDN
DAANLVLOGLRCSLSDGWGSSLLATEFSDVLFGTPKPVRGQSNLGVLRAD
MVNVI VHGEPI LSEMLLAAGREPDLAAAKAKGASGI NLAGI CCTGNEI
LMRHGI PAAGNFLOQELAI LTGAVEAMVVDVQCI MPALGRVASCYHTKFI
STSPKAKFPGALHI PFDEYKAMEVARQI I GEAVNNFPNRKADKVNI PDEK
MDYMAGFSGEAI VEALGGTPAPLLDAVKNKSI RGI AALVGCNNPKTTQDY
GHVNLAKALI AEDVLVETGCAALASAKAGMLLPEAAELAGPGLSAVCRA
LGI PPVLHMGSCVDI SRI LVLASALANALGVDLCDLPVAGAAPEWMSEKA
VSI GAYVVASGI FTVLGTAPPVLGSQAVTSLLTQQAASLVGGCFAVEADP
FKAAELMVAHI DAKRTALGI

>2617920887 Ga0073689_11442 carbon-monoxide dehydrogenase iron sulfur subunit [pelotomaculum Ga0073689 : Ga0073689_114]
MKEVLI NFDRCCLGCHSCELACAVSHSRAGGLFGAVLSGEKPRTRI FVHQT
GTKKAPLNCRHCSAPCI DACI AGAMYRKEDGPVTNVGGEQQCTACWMC
MVCPIGVVRSAGTAALKCDRCDLDRGI PACVRACPAGALVYAEVDDF
SRQRREGVLKHI VGNIARA

>2617920886 Ga0073689_11441 Predicted nucleic acid-binding protein, contains PIN domain [pelotomaculum Ga0073689 : Ga0073689_114]
MNADKGRQFVDNMFVYAYDRNGI KQSLARELI TGLWENRRGCVSI QVL
QELYVTVTKKASTPLPPGTALEI I SGLGEWTHHVPDGTDI I DAVYIQQKY
GIFWDAMI VNSACKTGCAVI WTEDLNSGQAYGNVTQNPFI GEKRG

>2617920885 Ga0073689_11440 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
VDYQNI TLSIPKEI LKKI KHLAVEKNTSVSGLLSQHLEDI VARNDAYKKA

KTSQMEI MKKGFDLI GEGKVS WTREDLYERG

>2617920884 Ga0073689_11439 Predicted ATPase, AAA+ superfamily [pelotomaculum Ga0073689 : Ga0073689_114]

LKPVLETCKPRPEI LAGTFNPEVFTLSLGPVI DYYRSGKSI DSI YTNAE
 NFFREATYPTQGLRLTLAEVFGRI AGDMTPPAI HRLETAFGGGKTHTLIA
 CTHI ACKGKELLNI PDVLEPKLLPDPGSVAVVGAGDEI PVHMPKGNDL
 APYTLWGEI AWQI GGEALYREVEDDANSHAAPGKTYFNKVFANRKALI ML
 DELAQYAARLEAARPDGASQLAAFLMALHGYARNNPGI AVALTLASATDA
 FARQTERLAVLI SKVRGEEVTEDDALGI GEKAVRGVTSVVARDAVQVTPV
 QAAEI SSVLAKRLFTFI DRDAAGAVAGEYMQMYRRNSNLLPEEASSENFR
 GRMTATYPFHPTLVSLNNKLSSAENFQGTGRGVLRLVSLVVRSLWQGRRE
 APMI HACHLDLRSDRVVNEI LGRTGSSDLRFI LNADI GSVDTGALEGGYS
 NAELADQRNPHPEGHPLYEYTWKTVFLHSLVGREEGI NSKVFGLTESEAL
 FCASFPGLTTPQARTALEEI NETAFYLRYEQGKYFAGEEPTI NSVLARI R
 KTLNTNQVNELLEATARKVI TGGSGLFHI EHDVSLPEHLDPGKGRPVGLI
 VSLTAEAVDI QAMVTTTRGVNKPREEQNLI FIVLPETVAVKDTGELEEFPP
 ARTQEVROHI DGTARQVKAMRVLADKPQNYGVNPRRLEDADFKKRAERE
 QALVTTI SSI YTGLYYSSI GGHI VRKEI KTAGGEGGAPFI ELI YDI LKKD
 GEI LTGRNTTQSDLLNLSKLF FEHGDSSVLEKLNNFCCLRSWPVLENPG
 VFDQI I RAGVQKGWCVYRMGAEEENVKPEEFYHQENEI PMAFDPGAGGYG
 LI TLOGAKQRLVQSSKVEPARVREGVLYTVAGNNTATVRLVSEGLTEKY
 GEVPTADLDEAVVTLVREGRLYAI RGDQGGQKEKPDLI HGKI AALYNPQPG
 DI LI TPAQAAERWGI TDRQOSYSLAGREGAEKVLPLLRRLGSI YNKGAKS
 AI ETLDLTDLLELPQGGTLRLQLNNVTPASMKLLSELFALDGVVEKSELS
 EVYLDI VNPDDNCLLI RELKKRTREA

>2617920883 Ga0073689_11438 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]

MTNKSIVDMNLEEEFRRRI RVQAERAPWVI RVTEHKDKPAPVFI I KKRFS
 PGGEAGANGKPAGGPYLKEQGLLYGQSLRRCLPVI RAI AGRVCDDGGI PL
 ELSRFFNNGRI TFRGNLPLDEEAGAKLSLI FKLQERI KMDRVELI ARR
 ERF SREEAAWYLRTRTQYGADGNRWALAGMRI LLGGQPDDKAVLRMLEKL
 RS

>2617920882 Ga0073689_11437 Adenine-specific DNA methylase, contains a Zn-ribbon domain [pelotomaculum Ga0073689 : Ga0073689_114]

MRDTKTETDARLI EAGFPCHOVGAETQERERGASSALPPLYLHVWVWARRP
 LTPSRAAI LGSLLPAGADPGWFLRQLGI EKAQALVNGEPWTLDDKLI GQI
 KKDVS GREI LAVDSI I MRALKEQSAKGNRKL I EEI VNKNPPLVDHPI V
 QKWKELSKPLAGPLPGEGEI LYI ERI AADPAWFKDLMEI AASVGFRVPNL
 YGYSRAYSCQPEWQSNDI TVLDPTAGGGS I PFEALRLGHKVI VNDI NPVA
 AI I LYATLDYPARYSQDLI EEI YKWGQKLI DVLKQLDPVFPRI FLLPQD
 ERQI LKAHLNKYPDLVSEYDREDTTLYLYVRQVTCPHCGGEAPLLNTCWL
 SKEGEKWGVRI VTDGRKSGGKAWFETYRVAGGRGPQGGDPGFATVENGVG
 ACI HCRQAI PAD I KAQARGESPHGRWRDRLYCVVAVRYQPKLDRNGRPQ
 RYKTGERAGEI KTEKVRFFRPPNDRDLEALDEAEKRLRQRWPEWERQGLI
 PMESI PKGHKTMEPLRVGVTRWCDMFTPRQLLGHLLVEELNQLKPEI LE
 ELGQERGRAVVTYLQFAI DKGLDYNSRQTRWEYTRAI VKGTFGRHDFSLK
 WTFGEMI FCGPNSGAAWGLSQVLDAYKGMAELTAPLHERLGGAGPPVKI Q
 YGTA AHLDMPPDRSVDLCI DPPYYNNVQYAE LSYFYVWQRRTLHDLYPG
 I FTRRVNTKTDEAVANPARDGSAAAGAGLEYKRLMGEI FAECRRVLKDEGI
 MTVMFTHKTREAWALTRSLI ENGWTI TSSMPVESEAGESI HQKNMASAA
 SSI FLTCRKREAVDNTPATWTGFSGAGVARRI REAVREGLREFEPLNLNA
 VDEM VAGYGRALRVLSNPVLDGDEPVSP I RAMNEASAVVAQSQI ARMT
 RGR LQVDDL NPEAAMALTYGI FGPDI PYDQALNLSALNI SLEERPAG
 YTVSGRMI GVNLESRGGRANRAGTEDTGYHAPLLRRGSKRLRLALPEERHR
 KPVESPTQTEWDI LHGLI LAYREGDMPVARAYLAQHAQTRDQVI LDLLSVW
 AAETSDEKL RKEAGALLFGLK

>2617920881 Ga0073689_11436 SNF2 family N-terminal domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_114]

MTELI GASDPENKGLRSHRWRLSYKTSSTVI DGRPVDI LKDFYI PALQLS
 VRYDRVAGYFRSSSLAAASRGFSSFAGRRGRMRLVVGADLEPDDVRAI LA
 GDRVRLAVLLNGELDRPETWPKNI QNGVTLLAWMVARGRLEVRVAFRI HG
 ETGDPLSI DAVDDGYVHEKWFVLHDEFGRDLYGTGLNESKTALVLNAEN
 I DVHCDWWGDTDRRRVDEAVEAFENLWAGRVSHMPVMSLPEAVRRRLI RF
 AEGVDRPAEI DGTI SAPGAVQOPSALERLQFAVL RDAPKMPGGRFVGMET
 APVEPWPHQAVVVRRLVETWPYSYLLCDEVGLGKTI EAGLAFRSLYLSGL

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VKRI LI AAPAGLTRQWRRQMASKMLLSFGLVTRVPETGHEYI FPLEENRP
AASI YDPDLVI VSTGLLARPERLPALMQANRFDI ALVDEAHAARRRNPSG
GPGANPDFGRLYVAI RDCLRKKAQALWLATATPMQI DPVEVSDLLALTNR
VGAFOFDPELTQQYYDLLGKI VYKEKLNEHEWDFLRRMLQALVAQDPLFW
RFI GESVVDGRI RI AVKQWLENGRI PRVRDRELMRLI FSAAPLSRVMLR
HTRRLLEI YRENGMLRQNLAKRHVLPRI PRI EFTPLERHI YDQLEDYCRDL
ARQI RTHGDSYYRQMI GFLLSFLRLRFASSLYAFRETQNLRLRKVEATLO
SQSVVEAGESEPGASSLEDLVYDGEDEDDLPAAQSLLKNRTPEDLKWERE
RLRKMI DGMAGLAGPSSKTQELFQTLDRRKLRTGTGRI RQTI I FTRFYDTL
TDI VSRLRRADQRI LI GAYSGRGAEYSDPGTGQMVNVDREEVKERFLRGE
I DVLVCTDAAAEGNLQADLLI NFDLGWNPMKVEQRI GRI DRI GQRHKD
I FVLNLCYTGSAEEMVYGRLLGRLAENMI VGAQVSLLPVTPEDFQOLA
EGKLTPEGLEARARERI DI QKQTESMEI SPGDLYDI YMRTARTSVPA
NLAAI WEA VGGSKYLKDLGCVVSKEPARPAI TLNNFENI TNGAI LTVSRD
LYEEGMAGGGSRAHFASYGDPFCDAVLEHFSGFNLPPCI HRI SVPVHGMN
GVEMVGYAVACHGPGGSSEVRLVRSWPDLDGLQPAEALVLSEAEI GPLRE
QLERTARDELEPCLAANRI ERGNVRAAYAQEMLNLYLVARGLLELRARFAG
EGALYLPVLREVESLYQDRDRVNLPDLPAVLKPVEGDLLFECHVPAVGD
KARLYVPHI LARTSLNAASRLVDSMKARKSELRVDTVLARLQREI EAKRR
QLG

>2617920880 Ga0073689_11435 Endonuclease, Uma2 family (restriction endonuclease fold) [pelotomaculum Ga0073689 : Ga0073689_114]
MNLPLREI ELFOKEVYTYEDYAAALPEGAPYQLI GGKLVVTPSPTAFHQYI
SVRI GKRLI DFVEDMGLGI VLHAPLDVYLEEKETYQPDII YI ARERLFI I
EERI KGAPDLVMEI LSPSTAYYDLRKKARVYARQGVKEYWI VDPEEKSI E
I YTNQGDTFKLEQRAEGEGKASSLLAGFEVELKDI FVSI FSGVAKDSI L
PE

>2617920879 Ga0073689_11434 PrcB C-terminal [pelotomaculum Ga0073689 : Ga0073689_114]
LPALLLLAGLLFTGTAPSAGVAAELPVRVLVNGRAVDFPDAQPI DEKGR
VOVPVRFVARELGARVAWDEVSAARI SGHGKSI ALSPGQNTATVNGTAV
SLDSGAVFI ENRTYVPLRFI AEGGENYEACFWGTGGGEVLI LEKSAGDPS
AGLTGFKKI TVNEEEKPDGDDI FVLVREODLTGEERTFVEGVRRTKGVH
HKGGLYVVALGERPNPGYGLLELVKTELSWEQAKVYVRLTKPEPGKFYAAV
I SCPGLVGRVSLPPYTTI SFI DVDGTGSL

>2617920878 Ga0073689_11433 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
MSKVEELLNKVQLFFERQHKKSGKCALLGYMTMKLLKDMDESNI RVCVL
FDQTYI LGLQTVKLLLEKQALSPTGAEV

>2617920877 Ga0073689_11432 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
LEKKEKFYGKEI GSKLGRAYVFLLLI VFLALGVALKFSPLTVWKKMGMTI
NCYCTRRYNFVNRELL

>2617920876 Ga0073689_11431 Uncharacterized conserved protein YlxW, UPF0749 family [pelotomaculum Ga0073689 : Ga0073689_114]
LNRSFYFSI TFVTLL LGMMLAFQFRRTSAGNI TPPQNREQELTLEKKQLV
QDLLQLQGEI ANLSSKLDEAKGRGKASEALKKELARI KRMSGVLPLSGP
GVEVLI ESSPGQDEKNSSVLKSI TDEHLLKVVNELNNAGAEAVAI NGQR
I LAVSEI RLAGNHI NVNATPVSPPYHI AAI GNGAELKSRKIKGGI VEFL
NEPGVSVEI QI KEKVEI PAYNGVDFEYARNVKK

>2617920875 Ga0073689_11430 Uncharacterized conserved protein YlxW, UPF0749 family [pelotomaculum Ga0073689 : Ga0073689_114]
MKLKRFWALVLVSI I LGVMLAMQFRVTRDI QQNDAL KRMQDLSNQVAQM
KKERDVLQAQVTRMRARLDLSLSTGSLTPQMKEELNRVEI LAGFTELTGPG
LEVTLKDSVDLSLKPQGNPNRYVHDEDI LKVVNELKAAGAEAI AVNGQRF
I SSTEI SCSGPI I RI NKKPLAPPFVI TAI GNPDTMESALRMKGGVKDYLO
YFGI QVSMKKTQVTPAYTGGVKYSYAVDSD

>2617920874 Ga0073689_11429 amino acid/polyamine/organocation transporter, APC superfamily [pelotomaculum Ga0073689 : Ga0073689_114]
MI QRRRI KSI EKLMAKETGAHRLPRTLGA LDLASLGVGAI I GTGI FVLTG
VAAANFAGPGVVLVSLVLAGI ASGLAALVYAEMASMI PVAGSAYTFSYVSL
GEI LAWLVGWNLI LEYI VSAGAVAI GWSSYFVDLLRSAGVALPAAFTSP

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LEGLLI NLPAAALI VLALTALI I TGTQHSATANKFVVVAKLAAI I LFI I LG
ARHVDPANWQPFPLPFGVTGVMHGA I VFFAYI GFDTVSTAAEEVKNPRRD
LPI SI VASLGI ATVFYI LVSLALTGMVSYTTLNTASPVTAALLRVGLPWA
AAVI SVGALAGLTSVLLLVLYGQSRI FFAMARDGLLPPI FDWI HPRLRTP
LWDSVI I GVLVAVI GALLPI SI VAELANI GTLSAFTAVSAGLLI LRAKRP
DLPRPFRVPWAPWI PVLSI AASVYLAANLPALTWI RFVWVI I I GLAVYLV
YGRRHSLLAGRDAPSPAPGKGLPEPAAKRLPRPRRNDKR

>2617920873 Ga0073689_11428 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]

MKFTPFKFQPLAAGGVALMAYNLLLLALPRGEGSFTI SSI VWSKLSLEQ
TVMYYPLI AI MLVLT I I NLLVI I VFVKQLI QWLFNKEEYAFMSGPPTQS
I GI FVPI ASLSMTACVI FGPVTFFI PELSSNMQSLMLPGLI FYGFLLLML
LTLELTLLKVVWFQPLDVTCLNFWLLDVFAFGLVNLGTGTI AAMSNDRI
I SSTAAFASFLALTI GVFLLI I KLAYLI YLQI KANDLYPKVPQPSYFI MV
PI TCLFGFSFYRI TLYLQTHFEFNVEVLSFLI NFSYVI TI GWI I FSLNL
LSDYFKNYFYRSEFSATQWSMV

>2617920872 Ga0073689_11427 Ubi qui none/menaqui none biosynthesis C-methylase Ubi E [pelotomaculum Ga0073689 : Ga0073689_114]

MKRVAFFDDI AEKYDRWEETPLGALSSRLEREMFLSLFDEAVCGGPVLDVG
CGTGGNALLLSGRGLDVTGVDI SDGMMLVARAKAAREGLKVNFLRADAKS
LPFQDETFTGTCLLALFTGSPEKVVREMRVLRPSGCLI LAFLNRYSP
WAVLRRAKGWRRPSVYNSARFLSRQVSGLLGKAGFMDLNWRKAI YFPV
EHPLFLKFYRAFEAAGRLFPPGMAAYVAVRGMGRGS

>2617920871 Ga0073689_11426 selenophosphate synthase [pelotomaculum Ga0073689 : Ga0073689_114]

VDYI TPVVDDPYHFGMI AAANALSDI YAMGGKPI ALNLI GFPNQSLPLS
I MEAI LKGGADKAAEAGATI VGGHSI TDSAPKYGLVATGFI DPRRI VTKR
GAKPGDALI LTKPLGVGVI TTGI DI KLVNGDLVSRVNI MTALNKRAAEI
MLEVGVNACTDVTGFGLLGHLREI LTASKAGARVVASRAPVMPETEELI R
AGAVAGGTHNNYRHLDVVDWAPDLSREMRI LCDPQTSGGLLMAVPPEN
KDRLLTALRNDKEVPAAVEI GEVI ERPGEI SVVA

>2617920870 Ga0073689_11425 DNA-binding transcriptional regulator, LysR family [pelotomaculum Ga0073689 : Ga0073689_114]

LSEI NLYQLKI FYSVARHLGYSKAAEELALSQPAVSQVAALERSLGLLEL
FVRRGRQVALTDAGRSFLDYADRI FDLAGRAGRAMSQFI DLERGQVLI GA
GASI AGHVLPPLLRAFRERFPKI DI SLRLGNAAI ERSVAERELDLGFVG
GDVKNPALYVEPYFRDELVMI I SPEHPLANEKGVPI KDLAGETLI WREKG
SATRTLTEGFLSEHGV I FKNMEI GDI EAI KRLVAANMGMAFVSKNSLRL
ELAAGI LKTADSGKLV I PVQYHVI SAKDQHNYPTVLAFLNFI RKCAAVNS
RNI

>2617920869 Ga0073689_11424 TIGR00159 family protein [pelotomaculum Ga0073689 : Ga0073689_114]

VI NRNSTYEEI RESI KSKLSRTSDSI KEFDELLERKANCEEVFLHFTKI K
DI LLETESLLLYYHLEECLVPKLPFLNEI I DALNRLARDRYGALI VI QRE
DDLDPYVTHSEGGAI LDAKI SVALLOSI FQPGNPLHDGAAI I SGDRI VGA
GCVLPLSKKMVSSEGKQLGTRHRAALGI SEVTDI VLVLSEEMNRI SLAV
GGKLLRLDKACDLRKKLLDLLG

>2617920868 Ga0073689_11423 S-layer homology domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_114]

VDLRRSAAGMVAVFFALGFFFFQPGAVRCEVPPADI QGKAVVQKTPAEKL
DPAKGGEQAAVSLEQAI KTAKEAFTVPEELNQFTTGFDQSDKKSFWDLRW
SSDSRPGGAMNVRVNAATGDI WGMCRWTPLAPGQEYRGLPKYSREQAGGI
AAALAEKI QPERFKETRLQPDGRDYLPPLFEKRGQVEYRFNYARMVDGV
PCLNGI EFAVSGDTGEVTSFNLRWDDTRDFPSAAGRI SQARAQOI FRDE
AGPELNYFRPPI PGGKEVPKLKLYRLPAPQEQVI I DALTGKLLSKDGAMH
KYIDMAGGGGGDEADMAYSKRGA AKLTLMEEVAVEEAKNLLPREKALDLA
ASAVKAPQGYTLNNSRLLEQDYFFKGGKTWQFNWQAGEGPERKWMDAAVDA
STGELVAFSMERYYGKSGQPKVKFSEEAARKI AEEYI KQAQPGKWEQVA
FKSSRPMEVPLVSPAEPKQPLSYSFDWARVFNDI QFPDNGFFI SVDSATG
NVI SYRMTWWDVDFPGA KNI GREAAADKYLREAPLTAAYLRLWSSDQWR
GPEEAKVYLVYHMPRSFAMLDALTGQTLERQGNVVSAPGEESKFSDLEGH
QAREAVEQLARAGI I AGEKGKFRPDDAVTRAELI VMLAKSGDRSLDMEPR
PVAAAGKEPWYQRYYYDAAVRMGI I QAGEQPDAPVPTRETLARLTI NAMG

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YSKVARLSDI YVLDFRDAADI TGHLRGHAALAAGLGLVGPVDGKFLPKEV
VTRGRAAVTLVKMLNSK

>2617920867 Ga0073689_11422 2,4-dienoyl -CoA reductase [pelotomaculum Ga0073689 : Ga0073689_114]

VKLLFSPFRLGGI TLKNRVVLAPTSTSFATPDSKVTDKLI GYYEKRARGG
AALVI VEPGVVSPRGKLFERSMGI YI DDAI KPLSALTGAVKRHGAAAVI Q
LCHAGPKARSKFVGGEVLTPSGI PVYRGEPARELSEEEI RGI EEDFFQAA
GRALKAGFDGVEVHAAHMYLLSSFLSPLTNCRTDGYGRTTAGRARI VTEI
I SGMKERFGDGLLVGVRFNGKELDSGI DTPEAVEMGRLEKAGADYLHVS
AYTVPVPEMENI ATPATSI AGDEWPAGCFLEYAGAVKRAVSI PVI GVGK
LDDPAVAEEALVTGKCNLVALARALI ADPEWPVKVRSGVAPEQCCLYCGTC
LASLPKGEMVCAVNDL

>2617920866 Ga0073689_11421 ZU5 domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_114]

MDKHII I RRFWRI KLVTSGGGTI TGQGATVVI PAGAVDRDI MVKI EKVI D
TSGI PVPANAVLVSSVLNI TRDKTGDFKPKVTI TMAFDKTKVDREKQEPG
I Y

>2617920865 Ga0073689_11420 pseudouridine kinase [pelotomaculum Ga0073689 : Ga0073689_114]

MEPNI AVVGTVFI DCKGFANRGYNPFGRNLGSVKFVHGGVGRNVAENLAL
LNQKVLFFSTVDNSALGNEVI KRLRKSKVI LDFLYSAESRGMGMWLAVMD
QRGDLVGS I SQMPDLGLMESLI DEKGREI MQAASHI ALEI DLNERI SRKV
I EYAGEYGKKVYGI PGNLEVI LNNRDFLCCTDCFI CNDVEAGRLMGMDLS
GMEI KELOQVLENYI VTAGI PSMVVTLGERSVYYDSRTREKGYQPAFKT
EVDVSSGAGDAFFSGAVRGLVMGSPLSEAVTYGTVASWTLQVEENNCLE
MAVKLRGEEFFPGMLMSAG

>2617920864 Ga0073689_11419 phosphomannomutase / phosphoglucosyl transferase [pelotomaculum Ga0073689 : Ga0073689_114]

VVEI NPOI FRQYDI RGVAARDLTDDTI ELLGKAFGAYVRGSGSNQVLVGR
DNRLSSGRRLDAI TRGLLAAGCDVVDI GLVVTPLVYYARVHFGI DGAVMI
TGSHPDENGFKLALGGGTI YGKEI QKLKSLMAAGDFSTGSGGLEERDA
VGPYLAMLKEKI QPGPRRLKVAVDGCGNGTAALFAEQVLGNWGCEVI PLYC
ESDGSFPHHQPDPVKTDNLADLRKAVLENGADLGVAFDGDADRI GVVDET
GGI I WGDMLMCLYWREI MPRYPGAPAI I EVKCSQALVDEVVRLGGRPFY
KTGHSLI KAKMKEVGAVFTGEMSGHMFAD EYGFDDAFYAAGRLLRLLS
KMDGPLSELLAGVPKYSTAETRVSCPQDKFRVVSGLVERFRREYEVI D
VDGARVLFGDGWLVRASNTQPVVARCEARTPEGLQRI CAKMKEALGSF
PEVEDFEWEY

>2617920863 Ga0073689_11418 mannose-1-phosphate guanylyl transferase [pelotomaculum Ga0073689 : Ga0073689_114]

VSFAVI MAGGRGERFWPRSRMAEPKQFLNLLGDKTMLQHTVERLSGLAEI
MDTYVVGADFKDI I LRQI POLPEENI I VEPFGRDTAAAI GLAALVLERK
DPRGVI VLPADHYI SDVPRFRDVLRSAAAAAGRGEI VTLGI TPRRPET
GYGYI HQGEI HDTFAGLPAYRVLRFLFKPDYARALELLASGNYLWNSGMF
I WRVDLVRQLI EKHTPVLAVGLEKI GQVLDTEKCDRVLEQVYADLPRVSV
DYGI LERADNVLVI PGDFGWDDI GCWTALERYAEKSDGNVLEGRGVLLD
TCGTYYFSPDKTVAVLVGDDLI VVNSPDSLLVCHKGRAQEI KKVVALRE
QGLDEV

>2617920862 Ga0073689_11417 Predicted nuclease of the RNase H fold, HicB family [pelotomaculum Ga0073689 : Ga0073689_114]

MRFAYPI VLTPTTEGYTVKVPDLDI YTOGSDI AEAI YMARDI GMWI CYE
QDEGRAI PGPSDI VDI KTGPGEI KTLVDI DADEYRRTHDNRTVRKNLTLP
SWLNARA EKAGI NFSQI LQDALKNHLGI I DYNQVKKQP

>2617920861 Ga0073689_11416 tRNA(fMet)-specific endonuclease VapC [pelotomaculum Ga0073689 : Ga0073689_114]

LLDTNI I I ALLANEKPIV EKL I MAEKVFLPCI VLGEYFGAYKSVHVDKN
LARLDEFVSVNSVLDCDAHTGKYYGRI KNGLRI KGRPI PENDI WI AAI AQ

>2617920860 Ga0073689_11415 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]

MNTSLREEVLKQLNALPYEQQORVLDI RALTLSSSGVPGRKLLRFAGT
I EESDLKI MQQAI ENGCEKVDYSEW

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>2617920859 Ga0073689_11414 S-adenosyl methionine synthetase [pelotomaculum Ga0073689 : Ga0073689_114]
MPLPI SLAHLARRLI SVRKSRELDYLRPDGKTQVSVEYAGGRPVRVDTM
VI STQRHPNVLDLTI RNDLVEHVI TRVI PAKYLDNKTRYFI NPTGRFVVG
GPRGDTGLTGRI I VDTYGGYARHGGGSFPGKDPTKVDRSVAYAAP

>2617920858 Ga0073689_11413 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
VKVYEI RDPI FGI TI NDWEREI I DHRAFQRLRRI RQLAWTDMVYPGATH
TRFEHSLGVMKI ATEMFNSMVYFQHSRRAYDCHVANAMKHLNEVQSCAC
SHRGKFPPPI AKENI EDYLEWDDWLVLGLLQTGGGGEHGKI LRERKHHRA
VFETTETPAVEELTRLEEVNCGEMVSFI DQAEKSWYKFGKEFI QEI KS
I KPHFSEAEI ECALTELENKGI

>2617920857 Ga0073689_11412 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
LI LDYRKSPLLNVLNALYDDSLAETGPSDQCMHFGGGCFVRPLI YFGGTI
AKPLCKHMFYYNWDEEI LQR

>2617920856 Ga0073689_11411 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
LGCLMKKI HTI KSPRNF I VAVFFFYPEHDNKNHRLTDSWGGLKTLEFTYR
VI RVWEQPRQPVLDQQLI GLYPLPLMKSKAEIEEPQVLRRESMEI I NEI E
DEALKQDLLAVMGI LAGGKYVAEMVYSMI RREMI MQSPI YQDWVKEERAE
AEAKGRI EGKI EAI CKFMVRRFNADAGEI RAKVHQLATPEI LDGI MEEVF
AADTLEEAQSVI TRAVGKSLQ

>2617920855 Ga0073689_11410 conserved hypothetical protein (putative transposase or invertase) [pelotomaculum Ga0073689 : Ga0073689_114]
MSENQI DHDRLFKELLETFFAEFI ELFFPEAARSI DLEHI KFLQOEI FTD
VTAGEKHEVDI LVETRLKDEPGLI LVHVEPQSYAQTFNGRMFVYFSRLY
EKYRRRI LLMAVFSYDRVRDEPDSFELGFPFLEVLNFRFYKLELKKLNWR
EYI QSDNPVAAALLSKMGFRMEKVRVKLEFMRMLVRMNLDPARMELLAG
FFETYLKLNCEEEEOYNRELKGLDRKEVDVI MQI TTSWHEEGREKGRAEG
RAEGRAEGRVGRVERTREI I CKYLI RKFGEKSTVLQKQVGRMTDLEKLD
YI LEELFTADTLNEACAI I NDGTGEQS

>2617920854 Ga0073689_1149 prevent-host-death family protein [pelotomaculum Ga0073689 : Ga0073689_114]
MPI VNATNARNNFFKLI EDVVVTHEPI YVTGKAGNVVVI SEEDYRSI QET
LYLI SI PGMREKI LCGLNTPLEDLVEDDDE

>2617920853 Ga0073689_1148 toxin-antitoxin system, toxin component, Txe/YoeB family [pelotomaculum Ga0073689 : Ga0073689_114]
MNEPYKI LYTKQALKDKRNAYEAGFSDKI KSI LETLKENPFAACPPHEKL
VGDLKGAYSRRRI NLQHRVVYQVYQKEHI VKI I SI WLHYE

>2617920852 Ga0073689_1147 looped-hinge helix DNA binding domain-containing protein, AbrB family [pelotomaculum Ga0073689 : Ga0073689_114]
METRI SSKGQI TLPAAEARKKLG I KTGDVLKVRI TEEGVVI LSGAGLKND
PVSASEVLRETSGI WKDMEESEDFVRRRLRAEDSERWKLLGLE

>2617920851 Ga0073689_1146 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]
VDLDTI RNDLVEHVI TRVI PAKYLDNKLI I KYFSACLMFLFWVGVI I WAR
VVTLYSRLASI LVLRVNLLLDQEVLAGSQPGLLVLLPFTRTGMTPARMLQ
AVI RRLEELQVSPEYSSKI VTMLAYYLEGKHSEAELAEFNDVLRWEEMS
I QLRYI GKEWREEGRAEGCAEGRAEGR RSLAAYLNI RFNFDEETMAQKL
AGLHDLKVLEELAKAVYASEDPVKAGLVI EQYTAGQNSN

>2617920850 Ga0073689_1145 Protein of unknown function DUF104 [pelotomaculum Ga0073689 : Ga0073689_114]
MI KVI YNDNVLKPLAPI EELKNNERAWVI LCPRPKREALRELVTGLTHEE
AEEMQKLI DGEFEKI EGEW

>2617920849 Ga0073689_1144 tRNA(fMet)-specific endonuclease VapC [pelotomaculum Ga0073689 : Ga0073689_114]
LKANGNLAVDTNAI I AYRQGI PEVCSLI EGADTI LLPVI VLGELLYGAAN

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STRPKENEQATRKFQAQSVLVAI DEI I ATRYADVRLKLLKKGRPI PENDI
WI AAI CLELGAPLLSRDSHFDHVPNLQVVNWECC

>2617920848 Ga0073689_1143 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]

MQI I NQI NKNVGTVNNADTI NFSEQHSAKYFALELRNLLLEALEGENI SDY
HKTKI I SI I KEVI LLTERDTPRKTP I ERLVLSTAETRMPPHGGGQVYQG
AVL

>2617920847 Ga0073689_1142 conserved hypothetical protein (putative transposase or invertase) [pelotomaculum Ga0073689 : Ga0073689_114]

MSENRI DHDRLFKELLETFFAEFMELFFPEAARSI DLAHLKFLQQEVFTD
VTAGEKHEVDI LVETRLKDEPGLI LVHVEPQSYAQTDNFRMFI YFSRLY
EKYRRRI LPVAVFSYDRVDEPDSFELGFPFMDVLQFRFYKLELKKLNWR
EYI HSDNPVAAALLSKMGFERMEKVRVKLES MRMLVRMNLD PARMELLAG
FFETY LKLNREEKEQYNREL GKLD RKEVDVI MQI TTSWREEGREGRAEG
RVEGRVERTREI I CKYLI RKFGKKSTVLQQKVG RMTDLEKLDYI LEE LFA
ADTLNEACAI I NDGTGEQS

>2617920846 Ga0073689_1141 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_114]

DLELLATI HYFYVTHERYYRKPPSKNWWI DRVI MAKEDKFSHQLI DDAYD
ALEVVGLFEWDRI

>2617920845 Ga0073689_11357 sel enophosphate synthase [pelotomaculum Ga0073689 : Ga0073689_113]

MGPEVLSKI LKDLPKKSDRNMLVGPETSDDAAVYKI SDGLAI I VTVDFFT
PVVDDPHLFGQI AAANALSDVYAMGGRPLLALNI ACFPSCLPVETI SAI L
RGGAEKVLEAGALI CGGHTVQDDEPKYGLAVVGLAHPDEVLSNATAKPGD
VLI LTKPLGTGI I NTAI KGLLAGEKAYRAAVEQMAALNRDAAVCI KETGA
SACTDI TGFGLGHAAEMARASKVSLI ESSKI PLLPEALDFAGMGLI PA
GAYDNRHFLNGEVVI GELVRREI QDVL YDPQTSGLLVSVNPAKAEDLLK
KMHGI GLSEACLVEVVPPEGRLI NVH

>2617920844 Ga0073689_11356 methyl -accepting chemotaxis protein [pelotomaculum Ga0073689 : Ga0073689_113]

MKTKI NLYLVAMYLGGLMMLAGVLI SGI LNPWQVSQALTSPWCLSWVAV
NFGVLVI YFNYYI GPKI DQROTSGI TKOFFYVQVLLYSTYATVGPI SGLF
NKEWASAGLI VAGFLSGLFSLFSFGLPFLI KAQLTLEASVAELYFAETGI
LSLPI RGKLGLSFSVLVASVAAMTGAI GI AQVTPETSVTI TKI VLV LALV
I MSSLVSVYYLI RSLI ETMEPLRKELNTAERQQVDLSI RLP I ATDETGE
I AYYFNHLMERLGQVFATVK TASVSTTEVADI LFQNI RQI SESASQVAAT
SVEMASTTENVSQNMRMSDGAQKI SGI ASEGATNI RVVDEKVKDI VNTV
EI I QKTVDSLGSATSQVSKVTEVI GQI AEQTNLLALNAAI EAARAGEHGR
GFAVVANEVRSLAEQSGTSVKEI GGLMENVQKELAAATNVAVQNNSSAI QA
GLQAI TETSTM FYGI I DQVQEMARGFQDVAASVAQMSVGI QNMAATAEEQ
NASTEEMRAQAESLSLVQKLQQA I GKFKI D

>2617920843 Ga0073689_11355 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_113]

MGHVAPAVVLPMDRMLALNPAPLPAVTGTVI RVS RPAAGYLVAKRTAAGG
KQPLCRQSFKSLP

>2617920842 Ga0073689_11354 spore cortex biosynthesis protein YabQ [pelotomaculum Ga0073689 : Ga0073689_113]

LFTKGGFFLEPLVSQVSAFTATI VI GVVAGFCYDYRVVREI YRLKKAGA
VLGDVI FWLVTTVVVFFLLLRGNWGE LRLYVFI GLGLGVLLYFRFLSRGV
SRLVRYKFFLVHKTWALLVKAALFLWMAVLFPFRLLI LI I SYPLNFLSGL
AQKSRRLGTI FHKLVGGRLEAGLRRVKSKLSRLAFWKKKH

>2617920841 Ga0073689_11353 sporulation protein YabP [pelotomaculum Ga0073689 : Ga0073689_113]

VNERVI HVS I NGRKELNMEGVKHVDSFDESEI TLETNMG NVI LKGEGLH
I TQLNLETGI LAAEGI FTSVQYVEGKGKARGKGLLNRI LK

>2617920840 Ga0073689_11352 stage II sporulation protein D [pelotomaculum Ga0073689 : Ga0073689_113]

MI RSSLAKI FLVLLLSFI MAPGCVRKQAPAPKPAPPAEEPTI SLYI NKT
GEKKNI KLEEYVQGVVAAEMDTRWPVNALAAQAI LARTFTMENI KAGRVK

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QLHGADASTSVEEFQAYDPSKI NDNVRQAVEQTRGEVLT YRDNFI RAWFS
ACDGGVSATAEEGLAYTREPTYVKGGAAODGCLSI TEPKNKAWEVRI PTD
QARAAVRNVGTNDPGPVI SASI VKKGPSGRAEQLKI GNAVVGPPALRLAL
GSEKVRSMLLSDVRVEGGQLVLAKGFGHGVGMQWGARLMAEQKSPED
IVRFYFKDI EIKROWK

>2617920839 Ga0073689_11351 Ribosomal 50S subunit-recycling heat shock protein,
contains S4 domain [pelotomaculum Ga0073689 : Ga0073689_113]
LRLDKFLKVSRLI KRRTLAKEVCDRGRVSVNGRAVKAGTEI KPGDI LVID
FGYRALTVEI VSI QENVPAKLAAGLYKI LKDKI IEEKMTEDEIT

>2617920838 Ga0073689_11350 DNA-binding protein HU-beta [pelotomaculum Ga0073689
: Ga0073689_113]
MNKAELI SNVAEKADLTKKDAEKAVGAVLDTI GEALAI GDKVQLVGFGT
EI RERAARRGRNPQTGEEI NIAARVPVFKAGTKLDAVI K

>2617920837 Ga0073689_11349 tetrapyrrole methylase family protein / MazG family
protein [pelotomaculum Ga0073689 : Ga0073689_113]
MPHQARI TII GLGAGAPGDI TLGAWEALKTAPRI LLRTGKHPVVEWLRRK
GI SFSTFDHFYVEVDDFQEVYRRI AEAVI CAARRGPVLYAVPGHPLVAEE
SVRLI AGMAVREGLEVRFPAVSFLGALFSALRLDPGTGLQVVDGLRLEE
GLPLPTRPAVVMQVYSRLVASDI KLSLLEI YPPGHPVTVVRGAGI PAGER
VETVPLCELDRLAWFDHLTSLYVPRI EEGKSEVGSWKEGEDGRGARDVR
GETLGTGSGKRKETVVEGVFGDGEDLDEPEDVEVI QVYEGKDSVCNDEY
NI GDGPGGYSCDGVCFPLDPLVDVLARLRGEDGCPWDREQDHRTLRLPYL
IEEAYEVLEALDEEDMHKI CEELGDLILLQI VFHAQI AAENLHFDMMNDI VA
GI TKKMI RRHPHFVFGSVTVKDSSEVLLNWEKI KSKERKGSSPESLLSGVS
CSLPALMRAVKLQEKAAAGVGFDWPDYRGALKEKTREELEEELEAVI SSEDQM
RVERELGDLIFSNNLRLGVEPETALSETSVKFI RRFYVEKMMVRLAG
RSFSQCTLAELDDWWEEAKKQEKI

>2617920836 AbrB AbrB family transcriptional regulator, stage V sporulation
protein T [pelotomaculum Ga0073689 : Ga0073689_113]
MKATGI VVRI DDLGRVVI PKEI RRTLRI REGDPLEI FVDREGEVI LKKYS
PI GELGDFAKEYADSLHEALGHI ACI ADRDTI I AVSGAPKKEFLNKPI GT
AVEKVMEEKKAVI I NNPGENPLCKECLI VEDSECKYSSEVI API VAEGDP
I GAVI LASKELDVKMGEMELKLAETAAGFLAKQMEQ

>2617920835 Ga0073689_11347 peptidyl -prolyl cis-trans isomerase C [pelotomaculum
Ga0073689 : Ga0073689_113]
VNKTLKVSII AVALVLALVSVI AAGCAGGVVATVNGEKI TSGELSQRVSEI
KANLEKQGYDFSGDKGKEYMDSLQKQTLEQLI NNKLLLQEAKKLGNLTPE
QVQEKVKPLKEQFPSEEEYKKFLATQVKMSEEEVAYI LNLQEQVTRDVTP
PAEAEELKKYYDENKDNFSRSEQLQVRHI LFFI DGGDKGYPNKHDTAEAKK
MAEEAI DQLI RGKDFAEALAGEKSEDDGGTKVNGGLYTFSGKEAVKEFSDAA
YALKPGEYTKTPVKTEYGYHI I KMEKTI PAGVEPFDQVKEELASDLLEQA
RQDKFSRFVQEAKNKAAI VNKLAEKEGSQSKS

>2617920834 Ga0073689_11346 transcription-repair coupling factor (superfamily II
helicase) [pelotomaculum Ga0073689 : Ga0073689_113]
MRGI I KPLQAAAEFGSLVRGLEKDFTRQMVFGLSGSQRSLLFAGLTGVVA
PLPALAVTPGEREAGQLVDELGTLLPGVAVKLFVWQI LRCHVLAHSKEV
AAQRLEALEGLTKGERLVI VAPAEALLRRLAPPGI FSSAVLHLGVGERVD
PADLLRRLTEMGYERADLVEGRGQFSLRGGI LDI FPMTAHRPVRLEFFDD
EVDSI RRFNAVTRQSEEKI DALTI YPARELVVEGPVWESGRKI LEGEYRA
QLRKLD RSGEAGAVRGLEEEFGETLENFRGYFNGI EHFLPYFYREAPTLL
DYLPPRAPVFVDDPVRVREVVEAVQREAEITYSLLGKGKVLPSQLLAYT
DWSRLQAEALFSRRGI YCSLLPRQPRFI APQNVVNFP GKAMRSFLGNLEAL
AEEI RHWRKSGYAVVLLVSSHRAQQLSSLRDHRVDAFYTGSLGHHVRS
GNVVI AAGNLGGGFELPGCRLVVVTEADVYGQRRKPRREWKQSERLAPFV
DLKVG DYVVHVNHI GRYLGVTP LNI GGI QKEYLLVKYAGEDKLYVPVDQ
VGLI QKYLGGEGEAPRLSRLGGGEWARVKGRVKEAVREMADDLLALYATR
ETMRGHAFGDDTVWQREFEEAFPYEETPDQLRAAGEVKADMERPRPMDRL
LCGDVGYGKTEVALRAVFKAVMDGKQVAVLVPTTI LAQQHFNTFRERLAG
YPVNVEMLSRFRTPREQRRVLRRELARGAVDVI I GTHRLLQDDVRFKDLGL
LVVD EEQRFVGAHKERLKLRLKDV DVLTL SATPI PRTLHMSLVGM RDTSI
LET PPEDRYPVQTYVLEEDPVI I REAI RRELNRGGQVFFVYNRI MDLDRV
ALWLQELVPEARLATAHGQLREDELEQVMLDFI KGDYDVLLCTTI VENGL
DI PNVN TLI VKEASMMGLAQLYQLRGRVGRSNRLAYAYFTFRKDRVI GEA

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AEKRLAAI REFTELGSQFKI AMRDMEI RGAGNI LGAKQHGHI AAVGFDLY
 CRLLEEAVREARGEKAVQVETI ELPVEAYI PEGYI PDTNQKVEI YKRI
 AALASDEELRELADELVDREFGDPVPVQNLAVAGVRI LAGRLKVKNI SL
 LPGQLRLLFAPGHPLTGEDLVAAGERYRNMI KFSNAEEFEI KLRLAGDG
 KGAPDGLPGVLKRFLLTLOGREEDVAHGERLNDPREI QSAQHAGI

>2617920833 Ga0073689_11345 Protein of unknown function (DUF2757) [pelotomaculum
 Ga0073689 : Ga0073689_113]
 MKLLYI CECCDDVDEVEFPARPAASPPGGLTGLGRGDI I KADDGEVVVL
 TTLCSDCRELLYGEPGHTI I GGPPLH

>2617920832 Ga0073689_11344 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_113]
 MSFAYVVHSLPLSLLAGLLAAAAWQWNRGFAHLSEVGQCTCPLVSLLAP
 LGEEAAKTLLAMLLGADI FLSHFFFGAVEGI WEVFSVRRGGFYAGLAALA
 GHSVFGYLTVFALEWYGALLPALAAGYLAHTVWNFTVLTCT APRGK

>2617920831 Ga0073689_11343 peptidyl-tRNA hydrolase, PTH1 family [pelotomaculum
 Ga0073689 : Ga0073689_113]
 MKI I AGLGNPGGEYAATRHNVGFMVVDMAPELGAADVKKMGKALVGQGR
 LGAEKVALAKPQTYMNLSEAVGALLSWYKLTADLVVYDDLDLPPGKV
 RVRPGGGSGGHKGMQSI I QVLGSEDFPRVRI GI GRPADPGFETARTARYV
 LSRFTPEEAVI I EEALKLAI AAVRCI VQNGVQQAMNLYNRDRGDRERVP
 SRKDCD

>2617920830 Ga0073689_11342 Uncharacterized protein YrrD, contains PRC-barrel
 domain [pelotomaculum Ga0073689 : Ga0073689_113]
 MRKSKRLVSTPVI SLEEGRI GAVKGLVI DPAGKRVAALVI EQKGWFKEQ
 RFI PYHKVHSGGDAI TI EKTSGVERASGLPEI VKLSKEKVGLI GARI VA
 ENG TALGYVDEYYI DLATGTI AGLEFSGNLVNSVLKGRFTLDI AHVRTLG
 KEVVI I ANDGLDNI FKLEGLQESVKNVRESTGHLWESTVQKTREL GASL
 NKSLEKVRKDKKPGASPGDKDNPAETAAGKKDPENPAPAEPVVEQRD
 GMGGQDQPAAGGGRREEAVPQVVPLPPGSNGEARKDI PPA

>2617920829 Ga0073689_11341 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_113]
 MRYLGFVVAVAVFYTLISYAKYSWGRGNKTAALGAALLAWLALVLPVLA
 I LLSRY

>2617920828 Ga0073689_11340 spore germination protein KC [pelotomaculum
 Ga0073689 : Ga0073689_113]
 VRKTALLLVLCLLFTAI PAGCYDQRELDI AYVVALGLDKGVTDRLRLTL
 QVI SFKEGGGAPRGAGSGGGEDKEEGKVGNTVVI TVEGASFFNCLGLAN
 SASSRKLNLMAKMLVFSEEVARS GELDKYVAPI MRYREI RETMNI VTR
 GRAEDLI KELKAVI GREI YKSLELI TEQPSYTGYPFVKFYNFYNSLKST
 VEQPVAVLAGVNSFKNLQDSERI GPPREAADGSFFAGDVPRQGGAKRELF
 GAAVFDGPRMVGELTGAEARVMRLI RGDFARGFFTI RDPEAPGYFVMLDA
 ROARKPRVRVDLAGDVPEI YVDLRLEGDLLSVQSKVNYESPELKPVLERA
 FEEI RRQADGLI AKCRDQFKADI FGFGRSVAVRQFPTI REWRDYEWLEKF
 POARVYI GVGFI VRRPGMI LKSSPI I ATEEGGQ

>2617920827 Ga0073689_11339 spore germination protein (amino acid permease)
 [pelotomaculum Ga0073689 : Ga0073689_113]
 MLKEGKI GVFEATCVVLFMSTVKVLFSGVRDI VEALGPAAWYGTLSAAT
 ALAGFYLLYRLMQRFPGRRELQGVFETALGWFAAGGLAALLTGFFFLFNAI
 LTREFVEAVKI YFYPASPPSFI MI FFI LSMGTVI YFGFDVI ARTVALFFW
 PLLVSFLTIF I LAVSLYKGYNLFPLLGNPGVTLATGVMRSSSVYGDVLAL
 AVVLGSLQGLEHFKKSGAAGVAFSGLLI SASI LFYTLSPYFVAAENTI P
 LLKLTRFI EHGRFFQFEAI FLFI WSI SAVLAAGLNLYVAI SLYCKTFRM
 DDHRVALPPLAVVLFSAI I LPDFSSAVFI YLHLI RQFGWI I YFGLPLLA
 LAAAVARGKKGGPAGA

>2617920826 Ga0073689_11338 spore germination protein KA [pelotomaculum
 Ga0073689 : Ga0073689_113]
 LPQNRROGLFKKI GSLLSYRPPRRNTFVLPELKEEESYRVTPEDRRDMDY
 NYSDSGGERSGEGQKGEKKGKENGKEKGGKKPVRAAHWSRI KGAGKDGGD
 KKAGDDQI SPDQVSTEV I KKEFNI PQNVGVVFREFKLARRVEAFI I FVD
 GMADRNTI NDFVLRQLMNPFI LENHGGGCLMEFVI DNVLPVDQAKKTKRY
 GEAVNQALTGVTFALFI DGCDSCLLI ETRGYEKRI EKPPI ENVVRGSQEA

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FTENLKTNI TLI RRI I RNKDLI HENVMVGRTHAVAAI LYLKGI ANPAVV
REVKKRRLESI KTDVFLGDGMLLEHFI EDNPWLI I PQVLSTERPDRAASHLM
EGKVVI LSEGAPFI LVVPVTFHSLMQSPEDYYLRWQFGTMTRLI RTI AFF
I AMLLPGI YVAMTNYHQEMLPTDLLI SI SRSREPVPFPTVVEVI LMEI SF
ELI REAGI RVPGI I GTTLGI I GALI LGQAAVAANI VSPI MI I I VAVTGLG
SFAI PNYSLAFGVRI LRFFFI FMGSVLGFLGVSLGMVMVGATVLSMKSFG
VPFLAPSWPPAGARDQI VRYPVFMGEERPDHLNPLNKRROPEI SRGWAAE
EPPAGKRE

>2617920825 Ga0073689_11337 ribose-phosphate pyrophosphokinase [pelotomaculum
Ga0073689 : Ga0073689_113]

MSSRNRLKI FTGNANAELAEI AQYLGVTVGAAKVTRFSDGEI HVKI NE
SVRGADVFVQPTCPPVDENLMELLVMI DAVRRASARRI TAVLPYYGYAR
QDRKTRARDPI TAKLVANI LTASGARRVI CMDLHAGQI QGFFDI PVDHLP
GVPI LAEYI LQSGLENNVVVSPDLGGVTRARDLAERI GAPI AI I DKRRPE
PNVAEVTSI I GGI QGKTVVMI DDI I DTAGTI TKGAVALKQWGAREI YVCC
THAVLSGPAVKRLDEAPI KEVVTNTI PVPGEKLI NKLVLSVAPLLGEA
I I RI HEDLSVSKLFD

>2617920824 Ga0073689_11336 bifunctional UDP-N-acetylglucosamine
pyrophosphorylase / Glucosamine-1-phosphate N-acetyltransferase [pelotomaculum
Ga0073689 : Ga0073689_113]

MSLATVI LAAGKGARMKSKLPKVLHRI CGRPMLAYVMEAVAAAGVEKTVV
VVGHGADLVARQVDAALVALQAEQLGTAHALQAAPLLKDFLGQLLVLC
GDTPLI EAGTLVRLVESHARGAGAVATVLTAGMEDPTGYGRVI RDGARRVA
KI VEQKASPEEKLVRENTGI YCFEAAGLFDALAGI TPANAQGEYYLTD
I I EMYVREGKNVGMMLLENPVEVTGI NDRLQLAGVERHI RGRVLEDLMGS
GTVVVDPASTFVDRPARVGRDVI HPFTFI EGDTVI GEDCVI GPGSRLVD
STVGEGSVVHNSI VI ESRI GDRCSI GPYAYLRPGTELGRGVKVGDFVEI K
KSRI GDGSKAPHSYI GDATVGAGVNI GAGAI TCNYDGENKWPTTI GDGA
FI GSNTNLVAPVEVGAGAVI GAGSTI TKDVPAGALGVERAKQSVVPNWIG
RKKGKNKTRD

>2617920823 Ga0073689_11335 stage V sporulation protein G [pelotomaculum
Ga0073689 : Ga0073689_113]

VI FVEVTDVRVRKVAEGRMKAI VSVTLDDSFVI HDI KVEGHNGLFVAM
PSKKTDPGEFRDI AHPI TTLARELI HSAVLQAYAEAI

>2617920822 Ga0073689_11334 threonine dehydratase [pelotomaculum Ga0073689 :
Ga0073689_113]

MAKNELTLGKI KKAAGRLAGVAHCTPLDYSTTFSGMTGNMVFLEKLENMQK
TGSFKI RGAYNKI MTLGDKDRRRGVI AASAGNHAQGVAYAAATRAGLPCTI
VMPGGAPI SKVMAARGYGAEVVLGGGYDEAYRLAVELQKKGATLI HGF
DDLEVI AGQGTI ALELLELPDVEAVLVPVGGGGGLI AGI AYAVKKI RPEA
RVVGVAAGAPAMYSYRENRLVESESTCTFADGI AVRRPGKTALALI QR
YVDEMVTVDDEE I ASAI LMLLERSKI MVEGAGAVGLAALLHPKTSCLKGAR
TAI VLSGGNI DVNI LSI I I ERGLAKTDRHI RLRVTVDTRPGSLRTLTLASV
VYVGANVI SVTHDRI KPGVPLKQAEVGLVLETRNKEHVDEVLAALLRNGY
CPEI I S

>2617920821 Ga0073689_11333 transcriptional attenuator, LytR family
[pelotomaculum Ga0073689 : Ga0073689_113]

MMFTGRI RYWLVLVLSLWLLFNRLATAFTRPDPGGNI LVFWTEGERLKA
VTLMCVQGPQPVGI VAI PVHI RI NPGEGGGCTVTEAYGRLGROGLTARL
EELFKMPI GGYLAVDQTTLDKASELI GPVVMAGRVTCVSNVFEGTYTEGE
KEPQAEI RSLAARLVEPQVLVKAPQLVYI FSSEVKTNLRCNKI WNI YRAL
VEEGPEI LRKKALTGRDYYVDNRKYREVPPDAWMSI LYEVTRA

>2617920820 Ga0073689_11332 Signal transduction histidine kinase, nitrogen
specific [pelotomaculum Ga0073689 : Ga0073689_113]

VGTEVLYKSLVGVSAAVMAVDENMVVKTVSPSAENFLNI KKEKI TGRHV
KECAFLGQAVLEDLEKNLREGI EHKVTCYLCGAGGEKTAVGLQI RRLDLP
DGGI LGAALI FEA I PRHSNI ERI VNNEKI ELI EQMSI GI AHHI RNSLTAV
KGF I QVVKERGGGEPGAGI TEFSAI ALKELDRVNDI I GKLLHLADSSGSK
RESVDLAGLLENI YLFI RSKAALSGI LVEKNLSPSLPNPRVDVRI I HAL
FNI TENAI HSPMDGGRLLLHTYVI PAERKI CI EI SDTGVGI PPENLKKI F
NPFFSTREDGMGFLALANKI I YDHGGEI RVTSEEGKGTTFSVYLPV

>2617920819 Ga0073689_11331 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_113]

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LAVEVVEVSSRRRTMEVFNNFPGVI YRGFYRAPVFPDLDRSSPYFDQI FTG
VEARPFLAVRNGRAVGRI AACLYRARPGGAPGYFGYFESLNDPAAAAALV
EAAAGWLAAGSAGGMTGPVELTPHERLGLLVEGFGGYHHPGMPYNPPYYA
VLLEQSRVLVKEMDLAYHYHLTAAVPEKLARVAARAGRLRGLSLREI NFS
DPAGEGEVFSLLHNGSMEDI WGFVPLTPAQASAI WRKLGKGYDPGLI LVA
EVRGEPAGI CLAMLPLTRYPLFSLSGRRHVRVLAVLAVLPRYRFKGLEAAL
IMECGRRARCKGASTI EFSLVAEDNAMMNKI IQGVVGKKSR I YRI YKSE
HPLLI RN

>2617920818 Ga0073689_11330 MobA-like NTP transferase domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_113]

LMVDALVLAGSSNNGPLKGYSPARYEALI PI GAKTMVEHVVDALLEVRQI
RRVLVI GPVAELSLLLAGERI VLVDASAGGLMENI EAGLNHLTGKRALLV
TSDI PMLTARAVDDFLELCGDMAADLYYPVI EKNVVERKFPSTRRTYVRL
KEGVFTGGNLF I NPVI FEKCVONGQKI VSLRKSPLGLCRLLGLGFVI KF
LLRVLTLAEAEKKVSRL LGVSGVVVVSEFPEVGVDDVKPGDLELALQVI G
TSLQ

>2617920817 Ga0073689_11329 DNA-binding transcriptional regulator, GntR family [pelotomaculum Ga0073689 : Ga0073689_113]

MDQPRMVPI KLDNYKPLREMFESLREAI ILGRLKPGERLMEI QLAEEMG
VSRTPVREAI RKLELEGFVVMVPRKGAYVAGI SVKDI VDVFEVRAALEGL
AAGLAAERI TSEMDLLERSLLKI NAMGGDI DAAVEGDI SFHDI I YRAS
RNQRLVQI I THLQEQLLRFRMTLSQPGRVKI ALDEHKKI VEA I SDRNVE
MAQTLATEHI ENAEQSFLNALRGEEG

>2617920816 Ga0073689_11328 4-diphosphocytidyl -2-C-methyl -D-erythritol kinase [pelotomaculum Ga0073689 : Ga0073689_113]

MVI TALARAKI NLTLDDLKRPDGYHEVEMVMQSI ELYDRLEFTPAHGEI
SLAVAGGELPVGRDNLVYRAAEI RHHGGVRAGVKI RLEKAI PVAAGLGG
GSADAAATLALNEMWGI GLSLPELMALGEQLGADVPFCLAGGTALARGK
GEKI EQLPPCPRMGLALI KPPFGVATAAVYRAFTPRLVAKRPDTGAMMEA
I RAGDI GAI ARNLANVLEPVTAAMRPEI MEI KQGLLEAGALGALMSGSGP
TVFGLTPDQASARMVAARCEKFGERALVTGTYNPEQWI

>2617920815 Ga0073689_11327 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_113]

MFLPDQNKLPARI RNVI QRRLEDLESAAMDRRGDCLSLADLKETALEAA
RLSGCAVLSADGRQSPAGQGMKKLI YFSVTADSVVRRHLGVGGTAVF
I REDQVLAATGGRAKLI ATI NSNDGFSPEQFQLEDALAAAAGFLALGI QP
WELWPENGPRDAMMTDNTTLGI

>2617920814 Ga0073689_11326 LysM domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_113]

LAETMTRAYGSRI LI NLAARRLAYFEGDRQLNTYPVGVGKHSTPTPTGNY
AVI EKI VNPGGALGSRWMGLSI SGGNYGI HGTNNPSSI GGYVSNCGI RMH
NHHVEELFPSVEI GAPVEI I SGAGSRPGTVPAGAKNGAGGHTVQPGESL
WEI ATKYGDLDLTI QVNNLTDPEMI YPGQI I MI PA

>2617920813 Ga0073689_11325 zinc transporter, ZIP family [pelotomaculum Ga0073689 : Ga0073689_113]

LGGI LLMGLI AGFGTCLGALLATSCSRLRPGLLSFFLGLAAGI MAAVI VF
DLLPSALRYGSAQAASVSGFLGGAGI MAALDSGLNLFPTTEVGKKNYLKTG
SFI ATGI ALHDLPEGLAI AAGFAAAKELGPLLVLA I GLHNI PEGMACAAP
LRYGGLSTGRVLAI NALI SLVTPLGALAGLI LVGLSI TFI GLLLAFAAGA
MGYI VLNELAPESCRNNRPLAYLGM LGGMLVI LFLRLI

>2617920812 Ga0073689_11324 transporter family-2 protein [pelotomaculum Ga0073689 : Ga0073689_113]

MTLKI LPLVI AALSGVAMALQGS I NSALGKVVGLWETTFI VHFTGLLLLVA
ALLFI CRLGDGCLSNVFQAPWYTYLGGMGLVLI I YAVVRSI PKVGVAPAT
TAI I LGQVFTASLVDFHGLFGMNKI PFSMYNVLTLLMAGGAWLI LKQ

>2617920811 Ga0073689_11323 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_113]

LYRLLPFLFALAVPPESEKNLEKI GSFI MATKESVANI KNGI DNFHSTMM
PFMLVMRGENPEQTSQPPSAGKGE

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>2617920810 Ga0073689_11322 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_113]
LKRFFSPLLFLMANAPNAEKNLDSL MYALQATLESVKNI KTGI DSFHASF
LQMAEAVKGPEPGYSPAGTKPSVQTEKTGVKPEPPAEPVTTSEPLPSIQM
PPSTGEPAS

>2617920809 Ga0073689_11321 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_113]
LTEESKTAVVADEPVAKLLELQARYGMDQETMLI YVNSVNLMSI LSLI SR
RHSGGI PASVPALPPLPAPGAAPGGGPTMEQMMGAVMKMLGGQGGGAPGG
AGI NPAMLTSLLSALGQNVDLGNLMSMLAGMMGAGGKPTPKTTPGVVPQV
ATAVESGPPGRDAGDGGGARKTGEGTAAKREAPKI MKWDQLDEHKKA

>2617920808 Ga0073689_11320 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_113]
MINMGAVI AEVQKLQEEMRKAI EVSEGDGAVRVVMNGYQEI LDVRI SP
SALKPEKANELQAMVAAAFSRALAESKQMI RDEI AKI TGGLSMPNI SGLF

>2617920807 Ga0073689_11319 protein of unknown function (DUF3794) [pelotomaculum Ga0073689 : Ga0073689_113]
MPVQYLYTEVQPVNCI EVKI PVVVAEADLEKEVDNVI TLPELAI KVDKI I
ASVRDLKATPVFFEEDDVVTGPI TVEQLGELEPRRLI VKKVVTGTLHKQ
I FYVKNNEVKHTSEDI TFSKMVEFKEPRRI LKKREVSVDFRHI DLDVNF
ELQRASRLHQTVVI SMLVKVVEDRQI FVQTCPRPRECPGNRLRDGGLDA
WADATHPI FWGASNVAQTVAHSGSFAAEI GRLNPLLPALFQMI NRGIV
SGRQYRLTFWVKEDVLGARVSAFTLNAEVI FFDENGI QIGI GAQSLASNA
IPDTAYSQVQFI TPRTDENVASAMVRFSFNPAAGNTNTAKI DDVSLECV
LT

>2617920806 Ga0073689_11318 LysM domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_113]
MAGTERLKVHLVQGENRVQTI VRGQI EVPDAKPDVDKVL SKEAKAKVRNV
SI VPDKVI VEGTLSMQVMYVAFKPDQSVHSMHGEI KFTTFVDVKGAEPGN
DAFVEI TVEDVSLSPSKDDPRKFNVAAVLSVFKVTEVDELDTSTPEG
NEALETQDI TVEHVVDDKAVKQVI VSDTFEVPEEKPEVEKI LDSKAEVEI
TDKRI LTGKVI LDGEVKI QVMYVAMEPDQSVHELSTRI KFSEFVEVPEAR
PGMNQVQVHFQVEAVDVQPV I DPALNADVVI KLI VFVTETRTLEDVPTKLK
NEEGYEKI KLKVDREI GTGETQVVLRETEEVPTKEPDI AKVI ESRVDKTD
VTETKI LNGKVLVRGYVDVEVI YVSDKPGQDVHALHQRLNFRFTFVPVSGA
EPDMQVVKVKAEPFVSVEQVADVHKEVVLKVKATVTEMSQPTVYVPTGV
APTVCPTTTPCPTTYEVKSGDTLFTI AQAMGVDLQSLI KANPQLADPN
IKPGDI INI PCVPCPPMG

>2617920805 Ga0073689_11317 uncharacterized protein, YkwD family [pelotomaculum Ga0073689 : Ga0073689_113]
MQASSRSPWLSFAVTL SLLAI LLTFGALAPAPAAAEGVPLSADEQQMVNL
VNOARNSAGLPPLAVDPVLSGLARI KAQDMASNGYFSHTSPTYGSSFDMM
KKVGKRYRYAGENLAKAPSVSSAYKTLMYSSGHRSNMLNRNYDRVGVGVI
TSGKYKI I VQI FTGGQKVVPAPVPOPTPQPQPQESQPRPNPEQPQVAG
LSADEQKMLDLVNRERAGAGLKPLQI DPALVKLARL KARDMI DKGYSHT
SPTYGLPFEMMKSYGVEYRYAGENLAGAPTVD SAHINLMNSPGRHANI LK
GDFTKFGI GVPVGGPYGKMFVQMF I G

>2617920804 Ga0073689_11315 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_113]
MVYRPI VSGDCALTF LGENI PAI GPRFKSKEEAMKVRRYLEGI GKLAEG
TRETPOVI TLKKQVDGRYSLLEDVSRQVVGRLDNLDELLLRFSKGLKKK
LFI LTCFVEGADDL ECLVLTEGLGAVFYTPDAI KRWYP

>2617920803 Ga0073689_11314 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_113]
MERYLRAFKKNRGKLLSLQNVGVGVGYKHAGDESTGEPAFI VYVEKKLP
VANLVRSHVVPKKI DGLATDVVEI GVVKMLGVRTNRERPCQPGVSI GHYQ
STAGTFGAVVKDKATGELMI LSNHVMANGSSFQEI KAKSGDPI LQPGPY
DGGTI KDRI GI LHRYI PLVKNYTKTDCPVASAVARGGTRLLNLVRQDYEI
RFYKRYRGENNVD CALAKLDSPDVTMATI LEI GDLAGVTEVKPGSVVQKS
GRTTGI TTGKVKSI GTTLQVEMKEEEKVWFI DQVVTETMASQPGDSGALVL
DMERRAAGLLFAGSDKLT I FNRI ANVVDRLGI EF

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>2617920802 Ga0073689_11313 spore coat assembly protein [pelotomaculum Ga0073689 : Ga0073689_113]

MEGI KKGDI VGRKSYNLDI I FKVNLDYEDGYGKRSASLKGI HMRLYANAP
VEDLI RI EPEELVAHLREHAKKSGEHMRRI FARRERDREFFLGRRAQRDE
KVKKNGNQI DGFDVPGTVLHI DGDSYLDLCLTTYKQLSI PANGYNI DEE
RQPEVVEDLLKKHSPDLLVLTGHDGFI KGKVDFTDI NNYSSKHFEAVK
AARRYEKSDDLVI FAGACQSHYEA ILSAGANFASSPQRVMI HAYDPVFV
VEKI AYTSI YDPI SI KDI I TGTI TGFDGI GGMETRKGKFLGI PKSPY

>2617920801 Ga0073689_11312 Glycosyl transferase family 2 [pelotomaculum Ga0073689 : Ga0073689_113]

MLAAVVPARNEENRLKKA IETLLKVPFDLI I PVVNGSSDGSCDI VRQI KS
ARLAPLYFKEPLGI DVPRAI GARAALDRGATAVLFLDGDMDGDI AGSLKE
LI SAVATGGADMALNTCPGNNRAGLSALASCVLKVRRLNREI GLERI I
GDASPSHGPHAVSRRLLLSVPPRELAVPPVSLALATKNGLTVRVGATVPH
KALGSPEKDTRHSDLI AETI I GDCLEALRTYRGERRVRSLSAAYDGYHS
RRRWDLDDKFLGTDRGKPGGR

>2617920800 Ga0073689_11311 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_113]

MHFI SPTKGRMDFKEMMSDI TGYI RGLPTSSYKI I I GSDSQVKSDTCFI T
AVI VHLRGKGARYYYRKKTKRKI KSLRQKI FYETALSLEVGGLVHKYFAD
EGFDDLNVEI HI DVGRHGETKDLI REVVGMVTGSGFRAKI KPEAYGASSV
ADKHTK

>2617920799 Ga0073689_11310 16S rRNA

(adenine1518-N6/adenine1519-N6)-dimethyl transferase [pelotomaculum Ga0073689 : Ga0073689_113]

LLEI SSPAAARAI MORYGI AARKSLGQNFLI DRNI I KKI VAAAEMTPDDL
VVEI GPGLGALTVOAARGAGRVLAVELDRGLI PALAEI LAGVENVEVI QG
DALEVDVFDGLVAGRTGGAFGRGGKKYKLLANLPYYI TPI LMRLLLERFN
I ALMI I MVQOEVAARMAAAPGGKDYGALSVAVQYFAEPEALFRVPGTVFS
PPPGVDSAVI RLLARPVPAVAVRDEETFFKVVRAAFGRRRKTLNLSLAGS
GLGPGKETWRI LAGAGI DPGRRGETLTAEFASI TEGFI GAGI ETRNI F

>2617920798 Ga0073689_1139 2', 3'-cyclic-nucleotide 2'-phosphodiesterase/5' - or 3' -nucleotidase, 5'-nucleotidase family [pelotomaculum Ga0073689 : Ga0073689_113]

MRHLKMRRPVVFMVLPVFLLI CSAALAAGTLTDLDPENAAPGEEI KIS
GSFQGDTTNGVAVGI TVKDPSSGVVYVNETRTGNDGSFAFDFTLPGNAAG
GKWQARVAGGAVASENFVNGSSVSVDSDSVQQKAVTI EGKLGKGGVP
VGLTVRDPGSAVRGVDEKNAAADGSYSFDFAVPADAATGTWKAEVAGGGE
ATSVTFVTTTTGGGRQDGGNPGGDSPPGGNNGDSSPESGGGGTTGTRVTP
AAMPAAEGKEI DAATGGALSSADNMVSVTVPAGALTGNAL KAI AEI AGTS
NLPAGALRLGGKVEVTLAGGSI KPGNPVKLI FAYDLPGVDEEQI NAYYW
NGSRWVCLGRVNGKLEVDVTHFTKFVMAADPGLPALTDVKAHWAYKEI
KRLVGMNVVSGYPDNTFKPDNSVTRAEFAVI LARAMGWGAGATVAAQGI V
TTTTPGI YGGKAFAI QDATGGLYVYNTDYSLTVGDEVYVVGALKDYNGLL
EFDPVSSVVKSGGNSLPVQTI VI NQLGEDYESELVKLEGVKVDEI KKV
NNYGA AKI TVSRDNATVTVYVDNRGCVNYDDLVAEYKAGDI I DVTGI VSE
YKGAYEVKPRSATDI VKNQAPAAI NLTVP TGAAPGETVKI SGVLTGNEVS
GKPVGVTVKDPNGAVAYVDETVTGADGSFDFTFI PANAAYGDWQVQVAA
AGAAAEGKI SVRGAAGVTAAPDWMPGDNI TFSGKVSQRNVAVGI TVKN
PAGAVVLADETTAGADGSYQFTFNVPVDAPAGVWTVSAAGGGATGNATFK
VDSYWRLTVMHTNDTHAHLDDSKAGAI I ARRATAVKQVRAEAPNNLLLLDA
GDVFSGTLYFTQYQGGADLEFMNTLG YDAMGLGNHEFDKGRGLAKFLI G
GYAEGYKTPPAFPVNSNFDFSAEPALSGLAKTI VGEETAGSLGEAI YPA
VI LDVNGEKVGLI GLTTEDTDEI SSPGEQI KINDAI ASASA VDMLEGK
I DK I AI SHLGWDKDLALAQQVEGLDVVVGHTHTKPAEYPTVVDARNT
TLVVQAGEYGNLGLDVSFEDGLAKEWNGHLLDVKAKDEQGNVYVYAEQ
AVKDRLAVYSAPLEEFKNTTVVGSQVVL DGEKNNVRTKETNLGNLI ADAM
LEKASGLTGANLAI TNSGGI RASI DQGD I TLGEI LTVMPFGNTLTVLELT
GRQVVDALENGVSQVESKAGRFPPQVAGLKFTWNPAPQANSRVTQVEVKTA
NDYQPI DSDAKYL VATNNY MAGGGDGYVVFQASRVYDTGI VDYEYFKEY
LEKHSPVNPRVEGRI TEGAGGGGPVFTVGLAEKWGLGLDPDLLEPEYV
ALMPDGGSGALVSI QEGSAVA AI NLTGQAPQLVDI I TLPAGSEP DGVAI TG
DGLLAVMANEENQTVSLDL SGG LGNI SVAGAVYVLDLVKDEPNLKKTKK
GKVDPEGMMTFSRNGKRYAVVTLEKSASLLVLDI TDPQNVSKVALLPVG
SGDAAEPGDRMAEPEGVAVSPEGNLI AVGNEEEGTVTLI PI LDGQNGGVA

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FGQRTDFNPAGSECEI VAFTPDGKKLLVTNSAEKQVI LLDI SDTGNI REL
 RNMSVADGGEPTSAVTPDGKYALVSVANGANPTVNPGEVLAMSLQPGVE
 GOVLHRYTVGQVPDSI VVTSTGKWAVVAI EAENDGDI AEDDGI I GSVAVI
 DLASLPPVNGNNGGGGGSSAGKLVTAGGGTI TGQDATVVI PAGAVDRD
 VRVKI GKVTDTSGI PVPANAVLVSAVLNI TRDKTGDFKKPVTI I MAFDKT
 KVDREKQEPGI YWFNDNSKQWTRLENNKVDFTAGKVSQDGLHFTKFAVLA
 I GEETQKPVEPPVETPAGGI KDI AGHWAEGAI KOMVTAGI VKGYPGGTFK
 PDNGI TRAEFAVLLVKAFKLAPQGGVFTDTAAHWAKNDI ATAASHGI VS
 GYNDVAFGPDDPI TREQMAAMI VRVKI AATADVTSFTDSGDI SAWARAS
 VAAAVERGLMAGYSNTFKPGNNATRAEAVTVI SNALKEGFTI GTI AARA
 SGGATATGKTVKRSG

>2617920797 Ga0073689_1138 Alkaline phosphatase [pelotomaculum Ga0073689 : Ga0073689_113]

LKTCRNRQLYRI MAI VMI LSMI TCFI PVTPAAAAETPKNI I LLI GDGMGF
 EHVEAAREAVGGHYMDDVNDATGRVTTHSADAAI TDSAAAATALASGYK
 TLNRMGLMTPDDDDQWTPDEVPTLVELAEDKGLATGLVTTTQI AHATPAGF
 ASHVPHRNQFNNI AAQYFDNFAAKGKPMIEVLMGGGRNNFNDRANYTKGVK
 YGDKTDNQNL I DEFKNEGYAYAATASELASVNAAVYDRVLGLFHATNGLT
 QEQDRVDKGTGQDEPHLNEMTVKALEVLARDQDGGFFLMVEGGQI DWASHA
 NDFDNMI GETKAFDLVVKAAALDFQAANPDTLVI VTADHETGGLNYDNGNA
 TWNSTDHTAALVPVMAEGPGAELFKGDMNDTDI PRKI AQLMNLDPKPLVLH
 QTGATVGVPEFTVTSGLPLVAGAKVTVKQGVNNTLATLTGTANGKAGYT
 FKNTGDYSVSVSKDGLAGNSLALNVGAAI AGATI DDLFVLDGDFQPVAG
 DLQLGKQYYLNNWKARKNAEGSMGLAVVEALNGAQPVFLNAANNLEVKGD
 RDEKFSVLFQPTVKGSLTI KGFYWNGWTNNASWQSLATPLKKAVNVN

>2617920796 Ga0073689_1137 protein of unknown function (DUF348) [pelotomaculum Ga0073689 : Ga0073689_113]

MDWRAVAGWQREKRGKELRGPGRGFLFLWAVVALVAALLTCGYAWAKKS
 VVLVVDGKEVPVQTRAWTVEKLLKGQNI ALLEKDEVESSETPLKNGMVV
 TVSRAADVTI TVDGGEI QARTGRTRVRDVLDEYSI TTGPEDEVTPGPDAP
 VTPGMQARVVR I RRATVCEEAPLEFETEKQYTTKLPEGSTRVI QEGRAGT
 EFQTWQVTYRDNQEVARQLFSREVTVQPVNRVMEGSGKTI SRGGQNI RY
 SEVVNMLASAYSHTGYNTASGVYPYRGVAAVDTARI PMGARLYVEGYGFA
 TALDRGGAI KGNRI DLFFDTNREAMRWGLKRVKVYI LD

>2617920795 Ga0073689_1136 Uncharacterised protein family (UPF0158) [pelotomaculum Ga0073689 : Ga0073689_113]

MRHVPVTMAWI VNAFENSSEHSEYYLDMQTGDVQFFSPMDFPEHEETVKI
 LDQQPDRYVRLPKLERELSLKVKQDYI ATVTEPYLKGLLEKALDADPKFR
 SVLMEYEDARRQWYKFQNDRYTEYLI NWFGDKGI ELVDKPPI DTRRHKNK
 K

>2617920794 Ga0073689_1135 cob(I)alamin adenosyl transferase [pelotomaculum Ga0073689 : Ga0073689_113]

LGGI FI SEEKKGLI LVNTGEGKGKTTASLGMALRAWGQGMKVLVI QFI KG
 GWKYGELKAAEKLGNFEI RQMGEF I KKMDSKSLDEHQHAAREALESAR
 I EI SFGKYDLI I LDEVLYAI HYGLI ALDDVLALLNQKPEHLHLVLTGRNA
 PPEI I ERADTVTMQEI KHPYRQGMPAQKGI EF

>2617920793 Ga0073689_1134 TatD DNase family protein [pelotomaculum Ga0073689 : Ga0073689_113]

MI LFDTHAHLDSSEYDADRDEVI GRARAAGVVHI VNVGYDLDSRRSI AL
 AEEYDFI YAAVGI HPHGADEAGSGYLAELAKMAAHPKVVALGEMGLDYR
 NLSRPVQKKVFREQLVLARELDLPVI I HDRDAHRDLLEI LRGTTPGPAG
 GVLHCYSGSWEMAKECLAMGFYI SI AGPVTFPNAPKMKDI AVRAYLDRLL
 I ETDSPYLTPVPHRGKRNEPAHVAFTAEEI ARLRGMEAEDLSRMCTENAR
 NLFHIT

>2617920792 Ga0073689_1133 methionyl -tRNA synthetase [pelotomaculum Ga0073689 : Ga0073689_113]

MSKGTIFYI TTPI YYPNDLHI GHAYTTVAADAVARFKKLTGYDTRFLTGS
 DEHGQKI ERAARSGGETPQEYVDKI VAGFKHLWGRlaveYDDFI RTTEPR
 HKKVVS AI FORLYDQGD I YKAGYEGWYCTPCEAFWAESRLAEGNCPDCGR
 PVELLREESYFFRLSNYADRLLGHI EEHPFI QPVSRRNEMVSFI KSGLE
 DLCVSRTTFHWGI PVPFDPKHVI YVWDALTNYI SALGYGTEDDGLFRKY
 WPADVHLMGKDI VRFHSI I WPI LLMALGVELPROVVGHWLLLES GKMSK
 SKGNVVDPLALI DRYGVDAI RYLLRELPGMDGYSEEALVDRI NKDLA

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NDLGNLVSRSI AMVEKYYQGTQVQSPGVPEGPDLELMELAGQTPAVVEELM
DKMDLANALAAI WRLVGRANKYVDETPAWGLAKDPAQKDRLATVMYNLAE
SLRFI TI MASPFMPLLPARVWSQLGLEYPADLQWESLTWGGLPTGTVVK
RGPALFPRI DTAGLK

>2617920791 Ga0073689_1131 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_113]
LQRYSVGDVVKTRKTHPCGGDLWEVLRTGVDFRI KCLKCGRVLLLPRPKF
EKSVKAI I QQTGEASPPQ

>2617920790 Ga0073689_11274 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_112]
LQPWNDYNLI GETSFNQQGVVCPSCFYNFRI CYDDLTRYI KR

>2617920789 Ga0073689_11273 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_112]
MAANI DRLL NEI KALSRAEFELARRLDDEEAVFENQSWYWTPEWQAAEKE
ADEDI ATGRVHRFDNVEDAI KFLHQQAEEESNGE

>2617920788 Ga0073689_11272 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_112]
MFI LEFGNRFVRAYKKLDQETROQVDKTLRTMI KNTGHPSLRLKRVQGTK
DI WEASVNMSI RI TLRFSGDI I QLRNVGTHEQVFRPPY

>2617920787 Ga0073689_11271 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_112]
MVRGI SGRTNVCGI FVHPVGH I FWLRTKRSGI PLRRRCA

>2617920786 Ga0073689_11270 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_112]
LLKI FYPKMYVTSVTEI KPEI LKDLGI KGVLFDLNTI VRRDSRFTPDV
AEWLSLRLSLGFKLGI VSNNRKRVGAI AGSLAMPGVHRAVKPWVGPFR
ALRLLGTSSRETALI GDQI FTDI FGGNLTGLYTI LVVPMQGEFLGTRLL
SRPLEKVVLRARFKNPEVFHGKRD

>2617920785 Ga0073689_11269 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_112]
MTFI NSTLSRFMI QQAEGYDVTVPCHGI HLQPLFAVYSKTCVPAVKKSLS
ASRYKI VDFYPQVRVNYVNEEKLOALSDI DI VLFNVNTPVDLGKSRVI AQ
I EERSRESKI C

>2617920784 Ga0073689_11268 precorrin-6A/cobal t-precorrin-6A reductase
[pelotomaculum Ga0073689 : Ga0073689_112]
MARGFEVGEI LVLVYGTRESRELI YLLSAEGYQVAAVTATEYGGDLVGRN
GTAEVYTLPDDAVLEKLLRQKNI SLVI DATHSFPGPLSAAAGRVCQKND
LI NI RFI REETRLPENPLI HPVESVSEAAVKAAALGNTI FLTTGSNSLEL
FLREPAVRNKRVVVRVLPDQKI I RKCQDLGLSPRDI VGLQGPFSVKFNRA
I LQAYRADVI VTRDSGRESGTDKI TAALALKLPVLI RRAPAGEKYVVY
GVEQALALVRQLTVPEY

>2617920783 Ga0073689_11267 RNA polymerase, sigma 27/28 subunit, RpsK/SigK
[pelotomaculum Ga0073689 : Ga0073689_112]
MLPGLWALTVVSLVNGLLLLVSYI ANNTFPQPLSEEEAKYLRLLNRGDE
EARNVLTERNLRLVAHI VKKFDSTGEDSDDLI SI GTI GLI KAI NTFNPGK
GKLTATYAARCI ENEI LMHLRFMKKVRAEVSLYDPI GVDKEGNEI TLI DI
LGTHPEVVSEMVENRFEQKCLREKVCQLTRREKKVLELRFGLLEDGVRKTQ
REI AKSLGI SRSYVSRI EKKALNKL TREFTFESCR

>2617920782 Ga0073689_11266 GAF domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_112]
V I I F I VGSNRTDSLTELLLVCR I NSTLKLRSRTRFAI QKVLQSSVDFEF
SHAALVLLVNGKI LTCMQAADANESDNESDECKQKSLYYCRYLKDI HGNG
GKI DSLPSLYPSACTTI PVVLRADHPVGTMEI AVFNAPAAANVQNLDDKGI
PLGRHVANI I QESVFSRQKDRELRLKLSVWLETVSTI NSTLNI KQVLHI VA
QLTADLFNARCAI YLFSETDRDFI PTVAVGSYDQKLKKFKAQKGMAQFP
AFLTMLKDHPVI LTPENI ENGMPREVI DAFSYAWVVMLPLVFKSEMMGV
MQVDKPLESNGFTQEDI AI I SALARETSI AMENTRLI EDLAKKEKI LQQL
LKKS I STQEDERKRI ASE I HDGVI QAMLGI WYRLQNFTNRTCGLQEI ATE
MEKI KNQLEQOI KDI RNI VYNLRPI LLDNYGLGPAI RI LLTTLQEQSKI N

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LELVI DGPSQRLPPDFELTYRI VQELLANVI KHSQATKAQVI I I NSQDK
TVLVVKDNGVGFNTSRI I QNMQYGNLGLASI QERI LLLGGTCKVESRI GW
GTTVTI SVNTPSLD

>2617920781 Ga0073689_11265 two component transcriptional regulator, LuxR family
[pelotomaculum Ga0073689 : Ga0073689_112]

VYGI KVFI VDDHPMI REGLATMLSPYQDI HI AGSYSSATEVLEAI NTNVP
DVI LMDI RMGMNGI EATROI I AMMPGI KII I LTI YDDAESVRLSLQAGA
TGYI LKQATQEKLVESI RRANSGEI VI DPSLLSQLVTDYTRLAQNVSVQP
NNADVNESKYLTPREDEVLYLARGLTNKEI SAQTHMAVDTVKTHLRSI Y
RKLGMNRSQAI SKI AEKNKSLLFFHVDTVRTQNI LDFTNKDRKTF

>2617920780 Ga0073689_11264 de-hypoxanthine futilosine cyclase [pelotomaculum
Ga0073689 : Ga0073689_112]

MNKI DGI LDQAVRGGRLSPEEGVALMASPDLLI GRAADLVRRRI HPGGA
VTFI I DRNI NYTNVCRCRCFAFYREESDPEAYVI SKEELFKKI EETIS
AGGTAVMI QGGLHPRGLDYLDI LRSI KERYDI HI HSFSPPEVAYMAQT
SGLSLREVLLKLREAGLDSLPGGAEI LDNRVRRRI SPEKI TWEEMTVM
DEAHKI GMKTTATMMFGHVETLEERVQHMRVREQQDRTGGFTAFI PWSF
QPKNTMLGGDTATGVDYKTLAVARLMLDNVPNI QASWVTQGAQMAQLSL
SFGANDFGSAMLEENVRAAGVNHVRPMEEI VRCI KDAGFTPAQRNTRYG
I VREF

>2617920779 Ga0073689_11263 futilosine synthase [pelotomaculum Ga0073689 :
Ga0073689_112]

VSRLRLGQVEYLNCLPVYHAI EEGLVPLEADLVKGSPTRLNRLFLDGELV
STPVSSI EYARHYGCCYI LPGLSI SADGRVASI LFFSKI PVTELEGKKVC
LTNSSATSVLLKVLFDHYHVDVQFETTAPDMEAMNRRADGALLI GDDA
MLAHQVRI ESGLPYHVTDLGEAWKQFTGKEMVYAVMMVRQDYAEANPEKV
DLLSKTLLTSREI GMDRLPELI ARAREKTGLPLPVLEDYFQI I RHDFDQD
YRRALLTFYDYAYKSGLI DERVKLRVWDEANE

>2617920778 Ga0073689_11262 de-hypoxanthine futilosine cyclase [pelotomaculum
Ga0073689 : Ga0073689_112]

MHRLFQESDI ADI GGI LRGERLSREDGVRLYNTKDI LALGYLADAVRHR
KNGDKVYFI VNRHI NHTNVCENLCKLCAFGREAGRPGAFTLSLDEI EARA
MATRGERI SEI HI VGGLNPELKLNYVEMLRVRRALPGVVI QSFTAVEV
DYLARVHNMAVEDI LAALQEAGLDSLPGGAEI FSPRVRELI CPKKI RGE
RWLEVHEAAHRLGMRTNATMLYGHVETVEERVDMHI ALREAQDRTGGFLT
FI PLAFHPKNTGLEPMGLTGATGYDDLKALAVARLMLDNFDHI KAFWI MI
GPKLAQVSLSFQVDDLDTGVVEEKI AHDAGAATGQFMSKSEI I KMI KAAG
RI PVERDTLYNVI EEGF

>2617920777 Ga0073689_11261 4-hydroxybenzoate polyprenyl transferase
[pelotomaculum Ga0073689 : Ga0073689_112]

MVFKKLKI FLEMI KFEHTI FALPFAYVGALLTEKKLPAHDLLWI TLAMV
GARTAAAMSLNRI I DRHI DARNPRTAGRALPRGLLSAAEVWVYFI SFLLL
MYSSYQLNPLAFRLFPVAVLVLLI YSYTKRFSWACHLFLGAALGLAPLGS
WI AI AGRFDLAPALLALGVLFVWAGFDI I YACDDYDFDRREGLYSI PARF
GI RKALYI STAFHLVAPLLFLTAGLI LNLGI FYLAGLAVAVAI LI YQHTL
VRPDDL SRAGVAFFNLNGALSMI MFAFTFLDVLYPLYLF

>2617920776 Ga0073689_11260 4-hydroxy-3-polyprenyl benzoate decarboxylase
[pelotomaculum Ga0073689 : Ga0073689_112]

VAYLDLRAFMALENRGLLKRI TVEVDAELEI TEVSDRVVKSGGPALLFE
NI KGRMPVVTNLFGLTERMELALGVDDLRI GEELLAI I QPPELPTTFI
DKLKALPKLAQLSSFI PKTI RSGPCKEVI RKDNPSLAELPVLCWPEDEGG
PFI TLPLVFTKDPETGRRNVGMVYRMQVFDRTTGMMWHI HKDGAEHYRKG
RRGGGRMPVAVALGADPAVI FSATAPLPAGI DEI LFAGFLRKETVELVKC
ETVDLEVPARAEI I LEGYVDPEETRLEGPFGDHTGYYSLADHYVPVHFLT
I THRRDPVYPATI VGRPPMEDAFI GKATERI FLPLMRLQLPEVVDVNMPP
EGVFHNCVI VSI KKSYPGQAKKVMASALWGLGLMMLAKLI I VVDGDVDVQN
LSEVMWRVFNNI DAGRDVMMVEGPLDALDHSSPLPHLGTGMGI DATRKWP
SEGHPREWPADI VMSEEI KKLVDGKWEEYGI

>2617920775 Ga0073689_11259 demethylmenaquinone methyltransferase /
2-methoxy-6-polyprenyl-1,4-benzoquinol methylase [pelotomaculum Ga0073689 :
Ga0073689_112]

MQFRQHREKKEEYHVSFSSI AHRYDLLNTTSLFNDRKYWRKFTVEHSGLK

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PGGRGLDVCCGTGMLALEQARVVGLRGQVVGLDFCENMLARAVENI KRTP
YREVI ELVKGNAMDLFPDNSFNCAI GLALRNVPDI RKT I DEMRRVVKP
GGRVVSLELAKPGAPGFKQLYYLYFNHMPVLLGRLGVGLKGPYNWLPNSL
KTFPHQAEI RDI FTEVGLADAHYHELTGGI VAVHI GTKK

>2617920774 Ga0073689_11258 Polyprenyl synthetase [pelotomaculum Ga0073689 : Ga0073689_112]

MLSTI LQPI EKELQTVHNL I KKQFI I KAGHVGSFAHLELSFLNKMI RPAL
VI LTARI YGCDPKKTAALASVFQFI YLASKI HQEI SENDSDYI RGDS DPR
DGSQFPVLVGDYLYGKFFTFLCDAGI I NLLQPLAEI I CQI HEGGI LRKKI
SGTGVTSQVFREVVSKEI TAGLFAGCCSLTARLAGAAEDDEKLLRNFGHNL
GMACGFLENGAPVEYVSSYI DEAVVSLSLLPDKPERAVLEELALNLSGLG
LPARRMVI

>2617920773 Ga0073689_11257 S-adenosylmethionine decarboxylase [pelotomaculum Ga0073689 : Ga0073689_112]

MKHLGRHI LAEI CGCEFDI LNDI EKVEEI MVNAALEAGAEVRECVFHKFS
PQGVSGVVV I SESHAI HTWPELGYAAVDVFTCGEKNPWDACNYLTDHF
CAKHMTAKEMKRGFMFKEANLKEAVNL

>2617920772 Ga0073689_11256 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway) [pelotomaculum Ga0073689 : Ga0073689_112]

LQI GRFVYSNQVFI YGI I TGDEVAVI EGDYGGVVRTSGLVYPLWQKALAP
CRPTKAVCVGLNYRDHAGEFGLPLPEEPVLFMKPSTAVI GSGENI VYPPS
SRQVDYEAELAVVMGRTRKI KAGEAGAYI LGYTCGNDVTARDLQRKEGQ
WTRSKAFDTFLPLGPYI VSDLDPGDLTVI LRLNGEVROYSSTROMI FSVI
ELVSFI SGI MTLNPGDVI LTGTPSGVGPVAVGDRI EVEI EGI GVLI NGVK
S

>2617920771 Ga0073689_11255 ferredoxin [pelotomaculum Ga0073689 : Ga0073689_112]
LRVEVDQELCI SCGACI DTCPEVFVWNDDEKAHSI MEEVPSELEEQAHEA
VENCPTSAI SED

>2617920770 Ga0073689_11254 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_112]

MTLEAFI TFLVSQMEGI RKSQI KTLAAI GRAMKNLVKPKHNI KRVD RFLG
NARI DLLGMAGALFAMLI NRLPTASRLI AMDWI DLHDGRHOTLVLADI A
GGRAI AVLWRTTDKNTLKDNTKI EMDLLKDFRTI VPDGTEI VI LADRGF
GKI PLFDQAKRLKFGYVI RLKRNAHI FNKFYNGSLEKLV I KTGT LKDMA
TLYTAKNRYPLRLKCEI QEMDFYSRI I NI

>2617920769 Ga0073689_11253 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_112]

MREKI KAYLNKPFVLGELAVYFTSPQTAQVI ETDCRVEVI TTPNHCTCCT
FRFNSWKNPGAWCKHI KAVRHVLSLEE

>2617920768 Ga0073689_11252 circadian clock protein KaiC [pelotomaculum Ga0073689 : Ga0073689_112]

LNKVATGI KGFDELVYGGFVRGHSVLVEGVPAGKTTFGI EFI YNGI KEF
GEPGVI VTCEELPESI YRDAFNFGWDLQALEKAGKLRI LCTSPELLADPE
I NLI EEVVREV GARRI LVDSI SHFRNI LNDPLSLRRVVYGF CNGLRRLGL
TSFLVKEREI EGKREYAFEEYVVDVI RLENKDRPGLHRHRVLEI SKTRG
QDHI PGKHTFRI TDDRI KVFALTRGADRYGEAREENGLLHTGVPGLDDLL
QGGLPQGVSVAVAGSGTGKTVLGLQYLAKGALDYGEKGI FLSLEPPPO
LLANAHRFNWDLSALQEKS I KI MYMPLFEME I DETI I GLGEQAKSFGAR
RLVI DSI YGFLSRI DNAAVLHEKFYCLVLYNLRLKCATLLLS PAWETADG
GKVEVI HSVVQGTI LLKSI LQONRRVRQLEI YKMRGVNHVTGNHLLI NS
SGAQVFPRLG

>2617920767 Ga0073689_11251 RecA-superfamily ATPase, KaiC/GvpD/RAD55 family [pelotomaculum Ga0073689 : Ga0073689_112]

MDRAYFGVEGLDHSLEKGLSYSSQI MVEGDSGVGKTVLAGEFI KEGLRCG
DTCVYVACDEPPAVMRERLLSFKVGI PAYEETGRLVFVDAYEEGSAEKY
ALSDLRNLEKYFALEDEVLRGCAGRRVRLVDSLSTLFTNLDTAEI LDFH
RTRI KHLRKKCECLAMD I FVSGVLEPRLMNI TAHLYNFI LKMNFRGSRYNP
VRLMQI GKVKSQFVSSCNI YTI SPI YGI LVADDMGVVE

>2617920766 Ga0073689_11250 Predicted hydrocarbon binding protein, contains 4VR

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domain [pelotomaculum Ga0073689 : Ga0073689_112]

MKENDI SRKI I NYLYMGACKTMSQVPFSGRHWLEQFVFGVAQYFI DEYWD
ELQLTSSKKPVDI CRAYLNI LDREGFLNTDDHRLEESGEYLLMYVKRNNCP
YREYCLRAQAEYCVRLGTLOAI LRHVLGENYSASVEI DKEGVCRGKLLPA
ARSKEEI VTREGHI LKVAGRRVLLPLDLYASLLMSFREHAPHALKHVLY
DAGYLSGLSFARKTKALYPDTQKCLQVLLEEMKNVGI GNI ELVSFNLTRA
RI KFRCYGSFOVAATDEYGQLYRTPQVI CDLLRGI FAAYFSVLFEKEI I C
EEMSCQSMGGNYCEFLALPFPKPKPVGRREHHERKNG

>2617920765 Ga0073689_11249 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_112]

MNGKMDEGLNSVLQSVVRI ELLAFFQANPHTRDVTVDGLALRLHRPRRQVE
MALHALGALGI VEI GGNKKVTI YRLRNGNLI NNYFQEQRGEDSS

>2617920764 Ga0073689_11248 two-component system, NtrC family, sensor histidine kinase AtoS [pelotomaculum Ga0073689 : Ga0073689_112]

MVVYI EDWSHLAI NHLPGVLLVI NREGRVQVFNRTLSRLTGI RDGEVLGR
PLPEVLDSDEPGSNKLLLETLTGREFQDLKPRAVPAI GSI DYTASTYVF
TDQNGVTMGAMAAFI PAERRQELNAVFKAEKLAVLGQLAAGMVHEI RNP
LTVI GGFLOQLQKDLQGTPEEYLSI I FAELKRVNSLI ADFLQLAKPGYS
RRSRCI KKI I SDI MLLVESEAFRLKLEI NLDMTEDI QPI LADSEQLKQV
FLNI I KNAFDALTYGGKFLKTSWDRDNGYVRVAI RDTGAGMEEQTVASM
FNPFFTTKESGTGLGMFVCNKI I ENHAGRI EVKSKPGKGTTVI VLLPSG

>2617920763 Ga0073689_11247 bacterioferri tin [pelotomaculum Ga0073689 : Ga0073689_112]

LKQENYRRRMGLLHI I CKI KGKDEFKRRGSAGAAVTKKNTTGGVETVRGE
ALI AKLWNFYSLELEQVDLYTAQARAMEDI YLAKTLARI AAI EQQHVDNI
AAAI KRLGGEPTRLGDVAPLLGRAAGAVTGALGPQVVLKADI TLEEKAM
KDYKDLI LRVEDHSLFDLLWNNLI DEDLHTAWFANKLKELEQAVSI EERV

>2617920762 Ga0073689_11246 Glutamate synthase domain-containing protein 2 [pelotomaculum Ga0073689 : Ga0073689_112]

MAKI AHGRMLKNLGLLGLGLFGAAGAAKLGRWLLGRAARRALNDFMTEPY
HQNLEWVFSAGAKATPOVI I ETNLRSQQGDKI LRPLGGPKKFPDFSSLMF
NPAQLATLPTSEDVPVDTSVI LGKRAARPLKLEI PI I I SGMAYGFVLSEK
AKI ALAKGAALAGTATNTGQGPFLHSERKAAKYLI LOYNRGTSKEPEI L
RQADMI EI QLGHAGRTGTGOI VKPKEI DREVRKRLGVMPGRDVVTHARQP
GMSNPEQLGEI VAKLREI TGGVPI GVKI AAGNSLEEDLAYI LEADTDVI V
I DGAPGGTGCCSPI LQDDFCLPTLFALCRTVRFLLEDHGAKDRVDLI I SGG
LKTPGDYLLKALAVGADAVAI GSI ALFAVTHTQVLEALPFEPI QVI YQKG
RYRDKFDVEKGAGHLANYLLSCAAEMQEATRALGKTSLSQVSGKDLFALD
AQTAKI AGVPYGGTHSLYHRLKEL

>2617920760 Ga0073689_11244 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_112]

MRKNAETYLLKKPFLAGELAVYFTSPETARVI ETDCRVELTTTTDHCTCCT
FRFHSRLRTRGRCKHI KAVRQVLCLEPK

>2617920759 Ga0073689_11243 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_112]

VREQFRI KTG FYLDAGLTYSQQGVALSRRWLLDYFNRQPPGWSSVGRVV
FSVEKYPLPAGTFYVHDVKPPESGLTHGTPERRI I LMAVHWPYLLVATG
LPG

>2617920758 Ga0073689_11242 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_112]

MKSLEYI MGTPGSGKTVTVLGLAQKFRQEGYRVGYFKPVANVRSLADGNMD
MDAVLMKEVLNLEAPLKKI APFNVNPSYLSARANLEEALDNI LEAYREVS
DGAEI MLI DGALSYDI LGSYGMDCVSLAKKFGSAALLVLKVENDYSLDNA
I FLNRCLTCEDI PVI GTI FSNVPRPLYAKTDGI YRPLLDKAGFRTLGVSP
TRPEI ASPTVAEYHEALGGEI LAGHDRMDLLVEDVI I GAMTMEGALTHLR
RTANKAVI LGGDRADLALAALETSSASVLI LTGGLYPDVKVI ARAEEKRVP
VI LVHYDTYATVEKMGQVSRHI QPSDKVSI RVALDNI EQYCNWQFI QANL

>2617920757 Ga0073689_11241 acetyl transferase [pelotomaculum Ga0073689 : Ga0073689_112]

VADLTGLFKPRSVAVVGASKTPGKI GNAI LRNVI RSGYRGTI YPVNPKDS
EI ESLACYNVSKTI PGEVEMAVLAVPAARVLAAARECGDAGVKALI VI TA

Table S2

GFKEI GKEGLDLEKKLLETCTCQCGMRMLGPNVGLADTHTSI NASFAAVS
PSLGEI AFLSQSGAMLVAI LDWSKSAGLGFSGVSLGNKADLSEI DFI ED
ASNDPYTKVI LCYI EDI LDGARFLEVADRAARKKPI I VLKSGVSQAGARA
ASSHTGALAGSDLAYDTAFAQCGI I RAHSMTLFDLAVAFAKTAVPRGDR
VAI VTNSGGPGI I ATDNVELKGLHMARFEKKT I KELRANLPGEAGI YNPV
DVLGDAGADRYEFALQKVLDDPNVDSVVALMCPAAVTQPEETSRVI I KAR
DAYPDKPVFAAYMGGDSLAAGAGMLSATGI PCFNFPEPAI DCI RGLKDYG
RYRDTPEERETGGLPEVDKRAVKAVFNDVVKDNRLVLMGSEAAEVAKAYG
I PAAPI VMTTTPGEAVEEAGRMGYPVVLKVASPKI LHKTDVGGVKI GLNS
AEEVKRAFVEI MESVHRYLPKVI VYGI EVQKMMSRGTETI I GMTKDQVQFG
PLI AFGLGGI YVNLFKDVSFRLANGLTEKEI EDMLAETKAYTLLRGYRGE
APRDVVAVVDMI KRTALLVSDFPEI TEMDI NPVFAYEKGLSALDI KITI S

>2617920756 Ga0073689_11240 Endonuclease, Uma2 family (restriction endonuclease fold) [pelotomaculum Ga0073689 : Ga0073689_112]

MSVI PEHLKFTYKDYLLLPEDRRYEI I GGDLFMAPSPKRSHQKI SLNMAT
TI WSVFKTHNLGEVYEAPFDVLF SRHDVVQPDLLFVNDRDLAI VGENNI Q
GAPDLI I EI LSPSTAERDLDLKKLYARHAVKEYWI VDPDARKVTVYLWK
NNDYVETGVYGEEDNWRPHLLPDLVI EGKELFK

>2617920754 Ga0073689_11238 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_112]

LVEASPSTLVLAANYFLLVLFGGSAVWVFI DTRRRGRPLSESI AWFLFMA
VMFPLAI VVYI YFRRKKLL

>2617920753 Ga0073689_11237 protein of unknown function (DUF3786) [pelotomaculum Ga0073689 : Ga0073689_112]

LGGI DAFQEAQGLATLEPAAVAMASGAFYDSGRNI FRLDYCGSSYEI ER
STGLVAGVGI KDDI PYNDRTI I LQYLVESGLPPRGRWLSFLELPEGI HH
YAPFQVDALFPLAEKFGRPDPDGLRAAAGLNGEQI KMGDVAAVI PALPKI
PLAVVLWLADDEEFPACNI LFDDVSPHTLSTATLWALGVEVAKLLSL

>2617920752 Ga0073689_11236 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_112]

LSREI TKI LNKEFTLEPEELSLLGKTKRSLNREERRLYFQSLKPRERKFR
VYLTGEYGLLNEEGRQNWKLTVENMLAHGGEPDLADALVMDVI GRLTVF
HHLRKI SEEKGVRLNAMTNFGGLSMVLYLAVI I TAVI LYFTYR

>2617920751 Ga0073689_11235 penicillin-binding protein, 1A family [pelotomaculum Ga0073689 : Ga0073689_112]

MAGKKCFLLI VLFSLFAGCSVKSHLLSAEVPVPSKI LDVNGELI TTV
SEENRI PAPLES I SVYLREAVVAI EDSRFYQHHGI DPVGLVRALYRNVRA
GRVVEGGSTI TQQLAKNLYLDPRTI GRKLEELI LTVQLERKYTKKEI LE
MYLNQI YFGQGAYGVEAAARTYFNKPARELGLAESAMLAGI PRAPSI YNP
VSNFQKAKERQAAVLRMTLGM I SGEQARRAGEEYLOPAGVAVAFKKAP
YFTNEI LKHFEQNPNGLETLYSGGLTI YTTLDLKMQKAAEKALGQGLKS
SDPOLDGALVAVDPKTGGI KAMVGGKDYGRSQFNRAKASQPGSTFKPFL
YAAAI DHGYTAGSTI TCEPVSFQADGASYQPRDFQGGYHYRPFTLKEAL
FTSDNVVAVRLNQOVGPAMAAAYARRMGI ESEI RPVLSLPLGTSEVTLL
MARAYGVLANRGVKAEPYFI QKVTDASGRI MEERRPKLEQALDEKTAYI V
TDMLTGVLKPGGTAANI AGAVSRPAAGKTGTTFENFRDAWFI GYI PDLVAA
VYI GYDQKDRGVGRTGGQVAAPI WAGFMENALHGTTPPSDFPMPEGVVKVN
I CADDGLLAGEFNRRVI EAAFI RGTEPTAVCYGTGPEGLFNLPLPPERED
EKRGFFGRERI LFDLDRLI PPGFRRFAQ

>2617920750 Ga0073689_11234 Uncharacterized conserved protein YlO_U, alkaline shock protein (Asp23) family [pelotomaculum Ga0073689 : Ga0073689_112]

LEVFAVGPSTGKSHRATI VAHQFEAQAI I DDGLLI QGNRI LAGASAKR
QPTRI GAI KSALFMDDKHAQEI KEALATVAPEKI LI LGTSREMVYRI ASR
LDLPAPAKI I KI EDVASEKEI RKAKFLRTRFSKHVI PAPI LEVKRSFPGA
LVDPLKI FLRKDVDPGKKDWLEQSVVRPTFTFHGKLT I ANSALEAI AGHA
ATSVSGI SQAGKI NI HVEHEGI VTI DI API FTFGHQLHEVAAEVQRR I KQ
AVEDMTGLQVREVNI HVRGLSFSRAKTEATS

>2617920749 Ga0073689_11233 N-acetyl muramoyl -L-alanine amidase [pelotomaculum Ga0073689 : Ga0073689_112]

MSKFVPI I VFRLAALFTA AVI VASALVPAGECSHNSNAQFGRSDSTTVNY
KVEEGDTLYGI AGEHRVAVRELMRVNNLEGLI RPDGVLLVPDKKSYGGA
MSRGVI SREELMLLARLI HAEARGESFEGQVAVGAVI LNRLASPNFPKSI

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PEI VYQRSHKVYQFSPVGDGSI NLKPDES AVQAQALSGRDP TGGALFF
YNPDI SKDQWI RTLPVVTRI GNHVFATSL

>2617920748 Ga0073689_11232 precorrin-8X methylmutase [pelotomaculum Ga0073689 : Ga0073689_112]

MQVLTEPLAI EKKSMTI I EENLPGI LSRPVGERE I I KRVVHTTGDL SI AG
QVLI HPRAVESGLGAI RAGRTVVTDI NMLKAGI NAARLKSFGMGVRCYI S
DPDVI AEAKRENLTRAMVAMRKAAREAPGGI I AVGNAPTALFALCSLI EN
GEAAPALVVGTPVGFVGAKESKEALMQLSTPYI TVPGTRGGS AI ATAVVN
ALLYLV

>2617920747 Ga0073689_11231 CbiX protein [pelotomaculum Ga0073689 : Ga0073689_112]

MKTAVVLLSHGSR LPEAKATLEAYRGMVKSTGLFNI VEAASLQFNQPDLP
ASLAADVAGGAERI I VMPLFLYQGMHMQRDI PELLAERKKYPGVEI I LA
GNI GADERMGQI I LDRI REVRLCRC

>2617920746 Ga0073689_11230 precorrin-6A/cobal t-precorrin-6A reductase [pelotomaculum Ga0073689 : Ga0073689_112]

MI MVLGTADGREI VKALASRGLRVLACAATPYGASLLEGSGALRI SGG
LNGAGMEQMI EENKVAVLVDATHPYAEVSAVAAGACRKKEI RYI RYQRL
ESPVRKHPLLYYARSYGEAATKAAELGEVVFLT TGSKTLEI FLEVAQRKG
RRVVARVLPHPVELQKCFDLGLAPADI VAMQGPFGYEI NLALLRSYNASV
LVTKDGGAPGGAAEKI AAAL ELGI PVVLVKRPESVPGAVGSI DELLEMI E
RM

>2617920745 Ga0073689_11229 cobal t-precorrin 3 C17-methyl transferase (EC 2.1.1.-) [pelotomaculum Ga0073689 : Ga0073689_112]

VVGTPGELKQLSRCALERSEVVVG YKTYI ELI SGLLASKEVSTGM
TREVERCHLAI DRAL EGKKVALVSSGDPGVYGMAGLAI ELLEQRGALGT
ELEV I PGI TSATAAAACLGAPLMHDFVVI SLSDLLTPWEI I EKRL ELAAR
GDFVVVLYNPASKKRTEQI RTARRI MLEHKSGETPVG I VRNVAREKEEKT
I TDL DHMLEHNI DMFTI I I I GNSHTRLAGKYMVTPRGYQV

>2617920744 Ga0073689_11228 cobal t-precorrin 5A acetaldehyde-I yase [pelotomaculum Ga0073689 : Ga0073689_112]

VKTAVVAVTGRGA AVAVRVSAA LAEI PGAEVDLI LPAKFAGAYPGAQPIN
RPLGELCGEWFGRYRALVMVMALGI VFRLLAPLVKDKRTDPAVVVMDEGG
QFAVSALSGHLGGANDLARHLQRR LG CRAVI TTATDVHGLPAVDLLARDF
NLAMEPFEMVRANAAI VNGEPVHFYAEAGPAGWP GKI KPLPLECYHPG
RRAGGLHVF I TNKI I AEAPDGS LFLRPRNLVVG LGCRRGVGA AAVKAAVA
EALDRAGRSLSSVRL LATVDI RAGEDGLVRAAVEMKLSLVFFTREEI AGV
FRLRGEELTFSQYVFDKI GVGGVCEPVALLA APAAKLI LKKKSLNGVTVA
VAGEAWPWWEPDRGSSNS

>2617920743 Ga0073689_11227 cobal t-precorrin 4 C11-methyl transferase (EC 2.1.1.-) [pelotomaculum Ga0073689 : Ga0073689_112]

MMVYI I GAGPGPELI TVKGARFI AAAEVVI YTGSLVNPEI LNYCREGAE
I YNSAGMTLEEVLAVI KEAHAAGKLVARVHTGDPALYGA I QEOMDALGRE
GI PFEVI PGVSSFLAAAAAI PHELTLPGV TQTVI LTRVEGRTPVPAGEKL
AALAAHDSTMC I FLSVHMI EQVVAELASGGYTGDTPVI VVERASWPEQRV
I RGTMGDI AGKI REAGI TRTALI MVGRAFD FGYASSRLYDAGFSHGFRGS
AR

>2617920742 Ga0073689_11226 precorrin-2/cobal t-factor-2 C20-methyl transferase [pelotomaculum Ga0073689 : Ga0073689_112]

MPGKFYGI VGPGDPGLLTLKAYRALGRVDVLCVPRAAADRDSLALAVVR
KAI PRKYKLL ELDFPMSKDPGI LKNCWNEAGRAVAGLVLAGRTVAFVTI G
DPMFYSTYGYVLRYLGENHPELATETI PGVTAFSACASFTGTPLVEGDET
LAVVPAAYGLERLRESLETHDNVVMKVNR RFPEVLALLKELGLAGKAVY
VSRCGYPDQYFTRDLES LPSGLDYMSLLI VRKRGF

>2617920741 Ga0073689_11225 cobal t-precorrin 7 C15-methyl transferase (EC 2.1.1.196) [pelotomaculum Ga0073689 : Ga0073689_112]

MNKRWPYRTPGI ADEL FYRGKAPMTKEE I RVI TLAKARLAPGQAVWDVGA
GTGSLSV E AALQVPGGT VYAVERSPPGI DLI RRNSLAFQLDNLR LI EGEA
PEALAGLPAPDRVI I GSGGKLAEI LELTFKRLRPGGRVVLNAVTVETAA
LSLKLLEGLSSAVEAVWSAARAVPAGGSHLLKGMNPVMI I AA EK GEDI D
AG

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>2617920740 Ga0073689_11224 precorrin-6Y C5,15-methyl transferase (decarboxylating) [pelotomaculum Ga0073689 : Ga0073689_112]

MAKVAVVGVPGGREYLAPAAALRAVEEAAVLAGGERNLDLFEEHRGEKFI
I KNNLAELVDYI KTKKGTKNKVAVLASGDPGLFGI LSYLGKHFAPPELHVI
PGI SAVQYACARLALPWHDAAAMVSTHGRERDVFI KAVRRKGKVVVALAGPG
EAPAEALARALVDAGVGGKRVYVCSELSYPAAEI SSCAI EDLASRQEHWSE
KNYVMVI VDE

>2617920739 Ga0073689_11223 cobalt-precorrin 5B C1-methyl transferase [pelotomaculum Ga0073689 : Ga0073689_112]

LNELVKSRLRSGI STGASAAVAARAAALLFHGESRERVVI ENPLGQSI E
APVAGLVKNNGSARAVVI KDGDDPDVTHGLEI VVEASCAAEGI SI RGGP
GVGVVTRPGLQVAVGEPAI NPVPRKMI AGAVADLI PPGKGLVLVSVPRG
EEVASRTLNPRLGI VGGI SI LGTTGI VRPMSEEAFFKSLEPLVDMAVAAG
HRKVVLTPGRMGVRLAVEKHGFPADAVVEMS NFVGYMLDVCADRGLEAVL
LWGHGKLVKI AAGI FHTHSRVADGRLETI AAHAGAAGAPAGLI EKI LAS
PTAEALGLLLENGLGAVLETI AARASARAEYTRGRLLKAGTVLLGLNGS
I LGFDGTALAI GREMGWQR

>2617920738 Ga0073689_11221 replicative DNA helicase loader DnaI [pelotomaculum Ga0073689 : Ga0073689_112]

LTCKLCGERGI I LKGEAAVPCPCVQKSLERI FKDSCLPQKFLRCTLEGF
NFKYYAKNCYDPVREI SYHELAKLAHGAARFI VNFLKDPHTDGLLFTGQ
VGSCKTFLVCCI ANALLAKGKLVLFVAVPDLLDQI RATYDTGKNPDNI TE
FDLVDAKAKVPLLI LDDLGAHNYTEWTRNKVYSI I NYRLNHRLPVI ATTN
I I PEELEGYLGERTTSRLLMCRPYRLLVMDI RAVQRKEKDSRLVREFR

>2617920737 Ga0073689_11220 DNA replication protein [pelotomaculum Ga0073689 : Ga0073689_112]

MAEQRRGKI I KCDQKVN I TATFGSDLVLEGATAI PNI LLKVYSKI GI TDF
QMMI LI QMI RLNVEEGDFYPTPEI LGAYMESEPSRI EKELADLLEKEI I T
I SQYYDTGRNAVFTGYDFEPLFLI VSDI WAGI RAREI EECEKRLKAASQR
NELVGDRFDGKTTGLLLVFEKEFGRLSPI EAEQI EQWAAEI EEPLI VEA
LKRAVLRGKHNFKYI NSI LVEWQNNLYTLESI AEYDRDFQKRRVGRGKR
GREAGDAQVI PDDKNNAKKAFI RSLYV

>2617920736 Ga0073689_11219 histidinol-phosphatase (PHP family) [pelotomaculum Ga0073689 : Ga0073689_112]

MFDYHI HPGYSI DAEPSSI ADYCYRAVDSGLEEI CFTPHLEVPARRRLD
WFVRVNGRLHPMEDLSWLDYFVRDI EEARWEWAGRLTVKAGLEAGYEPGM
AKAI ERVVLGYPDFDFVLGSHCLDHLAI SSKRDSKLYFPGQLDRVLKKY
YRI LDEAVDTGLFDCVGH I DLYRRYGHLYFGDEI LHAHEGFAVSLFERMA
AKGI GLEI NTSSSLRRGHTFHPGTGAI LREAVNRGVKI FTVGSDAHLNLDL
GHGI DDAI ALLDDLGVEPATFDLRCPAFRKRVDKPPTLP

>2617920734 Ga0073689_11217 alanyl-tRNA synthetase [pelotomaculum Ga0073689 : Ga0073689_112]

LMTGSEI RESFLKFFESKGHKI LPGASLVPLNDPSI LWTAAAGMVPFKPFF
TGAAPPEFTRVTTQCKCI RTPDI ESGRTARHHTFFEMLGNSFGDYFKE
KAI PWAWEYVTGQLGPADRLWVTI YRDDDEAFEI WHRVLGVPAGRI VRM
DKDTNFWFI GVGPCGPCSEI YVDLGAVRGCGSPEGVGCDCDRYLEI WNL
VFI QFFRDEEGNYSPLAQKI DTGMGLERVASVLQGVPSNFDTDLLREIM
DYTAGLFNLKYGVDDKVDLALKVI ADHCRAI TFAVTDGALPSNEGRGYVI
RRLLRRAVRFGRLLGI QELFLHKVAEAVVRQMGGAYPELVERRNHVLRVI
HTEERFGETLAQGTLLNRLI EDARAAGNAVI SGEDAFKLYDTYGFPLE
LTREMAAEQGLAVDTDAFGRAMEEQRARSARQETEI SEQDALFKEVR
EEVGETNFI GYDTLEARAKVLRI FQDGGRVKSATAREEVEFI LDI TPCYA
ESGGQVSDHGRVTAPDLKVEI YGVTKPVENLFVHRGKVI SGVFKEHDPVL
VQVDRARRLATARNHSATHLLHKALKEVLGGHVNOAGSLVEPERLRFDF
HYTSLTPGEI HRVEEMVNNAVLANLPVEAFETSLDEARAMGAAALFGEKY
GKRVRI KMGDFSLELCGGTHLRSTAEVGLFKLLGESSVGAGLRRVEAVT
GEGALRYVNAKEEQLA EI ARLVKASPQEVVRRVESLLYQLKELEAGGEAL
QARLARYQVQDLI NRI KEVKGKVLAGRAAAPDMDSL RGMVDLLRDRI GT
GVI VLGSAGDRVNLVAAVTGDLLNKGLHAGKLVKELAAVVGSGGGGRPE
MAQAGGKDPSRLNEALERAYKVVEEQI K

>2617920733 Ga0073689_11216 Predicted PurR-regulated permease PerM [pelotomaculum Ga0073689 : Ga0073689_112]

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VGRKI LTFSLVVI DLTCWKEKRVGRGLFYLI LGLAFAYLI YLVRGLI FSF
I LAVLI TYLLNPLVNAI ERKGTSTRTGAI LLAYLALFFVAAGI FLYGVPRV
VEQLNRLVETI PLYTGQFNEMI RSLQTRYI ALDLPEGMRNVVDERI QWLE
ENI LQLLRQVV TALAGTVEYVFKI LLAPVLSFYI LKDLNLI KKKAI LAVS
EEWREEI I KLFKEMDQVFGSFI RGYLLVAAVVGGLTAI AMAMLGMEFALM
LGLFAGL TELI PYFGPVI GAI PAVGLALLKSKWLGVKVALAFLI I HQLEA
NI I SPKI LGDRVGLHPLLVI FSLLAGGELYGLAGMLLAVPAAAVI RVVFK
FI YFKV

>2617920732 Ga0073689_11215 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_112]
MRI NFWRGVI TGSII GAAI SMMAAGRRQERKGI LGYSPKQVRAQANRMFR
GVSKKVNDLIK

>2617920731 Ga0073689_11214 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_112]
LRCPVCGGKATGKVGVDQYYCWCCVEYRI NKEGVQI YEVAEDGTLVAFD
PQNEFLF

>2617920730 Ga0073689_11213 tRNA
(5-methyl aminomethyl -2-thiouridylate)-methyl transferase [pelotomaculum Ga0073689 :
Ga0073689_112]
LGKLYFFCKGDSVATKTRVI AAMSGGVDSSVTAAL LLEQGYEVI GVTMQI
WDPGRTEVGGEHVCCSLAAVEDACKVADRLGI PYYVLNFRDI FEEKVVN
YFTAELRGRTPNPCI ACNRYI KFGALLDKSMGLGARYVATGHYARLGFS
EKYGRHTVRRADRKKDQTYVLYGMTQNGI AHTLMPLGDYTKDQVRKMAA
DRGLPVANKAESQEI CFVLDDNYRGFLQEKTDI KPGPFLNMKGKVI GEH
RGI PFYTI GQRRGLGVAAGERLYVVKI DPENNTI TLGPPEAI WGAGLI AD
DVNLI LYDRLEGPLEVNAQVRYNGRPSQATMRPLHGGKVI VRFHTPQRSI
TPGQAVVFYCGDYLI GGATI ESTAGSATLIES

>2617920729 Ga0073689_11212 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_112]
LDII QTQVLKPLKESWPALSAGGVNMNI HANIRI GDGYFTNI

>2617920728 Ga0073689_11211 nitrogen fixation protein NifU [pelotomaculum
Ga0073689 : Ga0073689_112]
MYSEKVMDFHFNPRNVGEI SDANGVGEVGNPSCGDI MKI FLKVEDNVI KD
I KFKTFGCGAAI ATSSMVTEMAKGKTI DEALQI TNQKVAEMLDGLPPKKM
HCSNLAADALRKAI EDYKKNRGAS

>2617920727 Ga0073689_11210 cysteine desulfurase [pelotomaculum Ga0073689 :
Ga0073689_112]
MRRVYFDHSATTPLDPAVLEEMLPYLKEFFGNPSSFWYGRPARKAVEAA
RDRVAVAI GADPKEI TFTSGGTESVNMAI SGVALANQDKGNHI I TCTVEH
HCSLNTCKALAKKGFEVTFI PVDQYGMVDVDDVAAA I TDKTI LI NI MHAN
NEVGTI QPI AEI RRLAGERGI I FHTDACASFGR I PVNVDELGVNLLSLSA
HKTYGPKGSGALYI RKGTRWRP MFHGGQAERLRRSGTENVPGI VGFGKAA
EMAAANLEKDAVYLSGLRDKLI LEVMNKFDHVKLTGHPEKRLPNHASFCF
QFI EGESMLLHLD MQGVAASSGSACTSGSLEPSHVL TSMGI PHEVAHGSL
LLTLGKSNN EEDVDSYLEVLPPI I KKLREMSPLCAFDNCEI EEACMSCTA
RR

>2617920726 Ga0073689_1129 transcriptional regulator, BadM/Rrf2 family
[pelotomaculum Ga0073689 : Ga0073689_112]
VVSRLRLSTRGHYGLKAMFDLAQRFSS EPI PLKSVAERQNLSEHYLEQLI A
MLRKAGLVKSVRSGGYMLAREPACI TVGDVI RALEGPI APVYCVSEVD
PGECDEADYCI TRTVWVRVDCI AGVLDSI TLADMCREAEAEQQKRENAV
N

>2617920725 Ga0073689_1128 cysteine desulfurase [pelotomaculum Ga0073689 :
Ga0073689_112]
MRKI YFDHSATTPVHPAVAEEMI RYI TGNFGNPSSVHTFGREARKAVVEA
REKVARGI GAKPEE I VFTAGGTESDNMAVKGAA YADRVKGNHI I I SAVEH
HAVLNTCKALEKEGFS LTI LPVDGYGMI SPESVAAA I TDKTI LI SI MHAN
NEVGTI QPI PEI GRLARERGVLFHTDAVQSMGKAPVNVNELNVDFLAI SS
HKI YGPKGVGALYI RREARWQPI NQGGGQERRRRPGTENVPGI VALGRAV
ELVVADLAEE SARLLRLRDLI SGVMEKI PYVRLNGHPALRMPNHVNF SF
EFI EGESLLL SLDMQGVAASSGSACTSGSLQPSHVL LAMGMPHEVAHGSL

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RLTLGRDNTEEDVDYFLGI LPVI VERLRSMSPLYKKKLDKAVDKACQ

>2617920724 Ga0073689_1127 MerR family transcriptional regulator, heat shock protein HspR [pelotomaculum Ga0073689 : Ga0073689_112]
MSI WDDQPMFNI GVVAQLLOVHPETLRI WEKNKLI EPTRKNRQRLYSNN
DLKRLKFI HHLI NDKGLNI AGVQQVI TMYPCWKI KKCPGSQSRTKEQAVN
OSKPCWQELGLYCLVVDQADLCSTCKFFRNGCENTDCK

>2617920723 Ga0073689_1126 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_112]
MVFKFSKLDNRNDVI KQLLNAYQVTKEEYADLDKNI VGLVARLKRKAYRP
QPARRTYI RKTGTDKMMPLSI PAYEDKI I KMGSSKI LSAI YEADFQDCS

>2617920722 Ga0073689_1125 D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5/6) [pelotomaculum Ga0073689 : Ga0073689_112]
MSI I VLNRRKI FFLI LLI LFSLFSTQPSAAAPEI TGEAAVLLDGKNGHVL
FEKNPHQKI YPASTTKI LTAI VALENGRLDDLVTI QECECNI DGSALGLV
AGEKI YLGDLLYAMMLVSGNDAAVAI ARHI GGSVDGFVAMMNKAAELEA
VNSYFNNPNGLPDPKHYYTTAYDMALI ARYAMQNPEFRKI ADTKVKTI RRQ
VPEAQTFLLNHNKLLWRYGGAI GVKTYGTSARQCLI AAAERDGRELI SV
VMKSEGNDI WTDSEKLLGYGYKEFTSI SLTEAGRYVI DVPVRFGEKMPV
LQTGFPLTCNLPRDKQDGI KKEVMLRKDI TAPVRAGEKLGELVFFAGWE
LGRVDLLAQOEI ARRI SAQWWPWFFLAAGLFVI ASI I RYHRRR RRRRWEK
YYRRKYYSYRKK

>2617920721 Ga0073689_1124 carbon-nitrogen hydrolase family protein [pelotomaculum Ga0073689 : Ga0073689_112]
MTEVI KAACVQLDSRPGDVKGNI DKSFRLI EEAKERGAQLVVLPELFNVG
YDFCVLKDLDHYDYETRSLLSHSAKEFNI HI AAGLLEI EDGKWNSVLVF
DGGGVLLTRYRKI CLFPLSHEEEI FHPGNELATFFI GNLKFGI MI CFDI R
FPEI SRI YYKEGCSCVI VSSAFPFPRLDHWRI LLRSRAVENQMYI VAANR
VGKDGPPFFMGNSCI I DPWGTVNAI ANETEETVI LHELVDKVDEVRTI
PCTEGFNRLLELFT

>2617920720 Ga0073689_1123 protein of unknown function (DUF4338) [pelotomaculum Ga0073689 : Ga0073689_112]
LLFGSAAWSCAARNDFI GWDKSARVNNLHLLTNNTFLI LPWVSVPHLAS
HI LSI I ARRI QGDWQRKYGHGLI FLETFMEDVKFRGACYKAANWRYVGLT
KGRSRNDRIYI NMKVPI KAVYLYPLVKHLHGDLR

>2617920719 Ga0073689_1122 protein of unknown function (DUF4338) [pelotomaculum Ga0073689 : Ga0073689_112]
MI TETEFRTQI DEENI LAI KQI ADNPSWSRRRLSRELRCFWNWYSPVG
QMKDMACRDL LLLKLDQQRI I LPPRKSDAYVQCRGPI I HVPHTTTAI VSK
LKDLLPLQVEVVETRHPSWELFKCLLFQYHYLGFNGTVGENMKYLI FDNE
RRPVACSLALPPGVAPPGMI L

>2617920717 Ga0073689_11157 Nucleotidyl transferase of unknown function (DUF2204) [pelotomaculum Ga0073689 : Ga0073689_111]
MEREDDAGREAFSRLPTI EDI KKI SSELQRFVGYVLVGGGLAVNFQGLPR
MTHDI DLLI DPSPEK

>2617920716 Ga0073689_11156 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_111]
MDTKKYI VVRVADEI VI DLI GKI GDVDI SSAGSETYEVDGLKI FVADLDT
LI KTKQGLREKDKEDLSFLLLKRKKMRSGK

>2617920715 Ga0073689_11155 S-layer homology domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_111]
MSSFRKRWGRPLLLFPVLLALFLI TSCFSGLSASPGGDRPFPASLGF
LKQYI SVWFSGPAAGLPGSHPVSLNDRAADI TGAAVSAAGFVAPRGLT
GEGQI VAVADSGLDAGRTDDI HPDLRSQPGKMPKVALLKSWAGRDVDDP
DGHGTHMAATI AGTGTASGGKFRGVAPGASI YFQAI LNKDGNPEPPADLS
GLFQPAYASAGARVHVDGWGGGPDYLESAAQI DEFVRAHPDFLAVFGAGN
GGPSPTI STEANSKNALTMGASALPRPAFVPGAADTAGTAGFSSRGPA
DGR I KPELLAPASAVI SRSRLI ESDLPGYPDYTRMQGTSMAAAVAGGTA
TLLREYFKKYADI HTPSAALVKAALI NGARPAEKGPSNEGYGVI DLAGTV
I ALKDGAFAADEWAGVARGEI SYTFHVADSAAALFKATLAWTDPPADPG
GARVLVNDL DLVVVTPDGKVFYGNHFLGRNAPDRTNNVEQVYLPRPAPGD

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YTVRVLGAGI NRNVLSGSAAPVQDYALVWGOAPALDMVKGDDGKSI ALSG
 GR LI QPEEAPVNLVDGDVVPVDAGHI FPGAAVYVTPALGGGDGI PS LDK
 APPGGGGDEDRDRPPEKPPGLQRAYLVARLWRAPGVKAFKMGGETVFTEI
 NPAARLGGYTLAADAGEVVLNKSPPVPGSLPQGFVSAVI NPI DQEI HQV
 RAGCI EREGVVADVLDEKGEKKI RLAGGGGNYRVSP EAVYSYEDTYTGAD
 I EDMPFGTGALEEELEEI LPGMPVLLRLAPSSGEAQYLAVKRRVALGTVRE
 I SPADGEI KLENGASFRMFPGAPVKRDRKVASLGAVKHGDQAAAVLLPDT
 GEAI GLVAYSSVI YGKAVDFTGRDRTL YLLDDNNRYRSLRLPPDAVVYRW
 GVRVVADTI AAGSRVRLTADPDGEEVWRLDVVDTLDDKGI LAEYDGAAGI
 LATREGGRYRVAGSTRFYKNGHAVPPEAVRTGEQVELEYVTAPPPTGGVL
 VAVNTRTNADPPLLLASTVPLRDLAVTG TAGADADI FI REKDGSWRAVH
 VEEPGRFNYSPODEREGKYDLALVAVDRKTGGVAGMRVSRDAGGRRGRY
 DAAVLDAVSGAAARTGRDTLPDRAGAGYLPDGPLTRAAVAALARLFNWP
 GASRWPLLLFNADPDI PAALRPAAVEARARGI VRGYPDGSFRPAAVLSRAE
 AAVI LAAVLRDLGLVGNTTQAPTYRFAGDI PYWAAKAVAGTAAAGLI PI Q
 PDGAFTPDDPVTVKEMAVLLERLLAFYEGARAK

>2617920714 Ga0073689_11154 PIN domain-containing protein [pelotomaculum
 Ga0073689 : Ga0073689_111]
 MTNFLLAEAHALI LARMGGEI ARQWLLTFDWNLI VVSPGDEKCAI EI I KR
 YDDKDFSLTDATSFVQMQRHGI ELAFTFDRHFKQYGLAVTGWPD

>2617920713 Ga0073689_11153 transcriptional regulator, AbrB family
 [pelotomaculum Ga0073689 : Ga0073689_111]
 MDEQFEVI RI TSKGQMTLPASARKLLGI KKGDLAVYVNGEEVI LRVVVP
 FKKASPKDAI FSLI GKGEPPDLAENHRYLGTGKEGDLRK

>2617920712 Ga0073689_11152 Putative zinc-finger [pelotomaculum Ga0073689 :
 Ga0073689_111]
 MNCREAMFLI SLRMDGALSKDGETVLAHLEACADCARELALQERLSGAL
 REI GREDAQAPPELCGLVLGRLRTERRTALARLPATWRRSI AAAA AVLFL
 AGGSAWVNAGLVAGVGKMI GLGNPPKI DAHAGNGNPAGDGGGSPDRRVH
 GAPPGSPNTTGI ETKGNI PGSPPGNGTDTPAEPGNPSPDVKDGAKGGKTP
 PPAAVATTPEGERVLLSSGMKVTSTI LKVAVDLANARATATSLAAGASA
 GLQEFPEQSGGKQI VVLRMTVASDRAAEFTAKLAGLGARI DRQDES RDI T
 NLYNDTLVQYNDLRSRVSSAEDTAGRQQL EARAASYKRQLDAWQAEAGKR
 VI TLWL ESK

>2617920711 Ga0073689_11151 RNA polymerase, sigma-24 subunit, RpoE
 [pelotomaculum Ga0073689 : Ga0073689_111]
 VDHTRI LVKKAQNNDLSAFEELVRLYQNKVYALCANLTGNRDDAODLAQE
 AFI RAYRAMGSFRNEADFGTWLHRI AVNVCLNHRRKNGGRQTL SLDEPHR
 DDDGGEI QREVAEDGDPLQALEEKEFRGLVRAALNELSEHRTALVIRE
 I EGYSYEEVSRMLGCSLGT VKSRLSRAREAMKRRMTELARENGEYLPAGK
 GRR

>2617920710 Ga0073689_11150 Copper amine oxidase N-terminal domain-containing
 protein [pelotomaculum Ga0073689 : Ga0073689_111]
 VKFKRKALSI LLTSLLVAMLAPLASPALAAGGYSSLKAPTVDNDGVREL
 GTVFAHLTAGSLVQGDVTFTRLPSDFI WLQEGSSSTAVMTDPMWNTVTVAG
 SAYRYGTASNYI EVPEKYS GDKNGLYGAGMLQFSKI SDEEVKMTVTGVPS
 SGDDI YFYLYAKRVWVDSGFDGEI PVAFDAPSGSGFSPGKATI GTVSSTG
 LVLSASSVDSFSDSDPLKLRFTEDRAGALEDGND SI KLKLPTGFVFSSV
 DNASI I WGGNYRVNGI DQPKLTPADVLD CI HGAGTDELTLDFPNDFETTE
 AI SVEI DI TI AVDDETDAKTGDVVVRVSGNSDLNLSEAVI GRYGNYESKI
 ECKDAPTVYAGMLEQKI GAI VI SESVAESI I PGRTL TLELPTNAKWGDL D
 NDSNGLQTN I TSFPGTDGKTAKWTFSGSSDAATLELEDMEVVLEPGVT
 GDLKVKVGGTAGLTGELTVAKI VAPVKA EAAAAPEVKI GSVYEAGDVTI T
 EVAAGAI KDDKWL I LDLPQGVRFVSAPKVEVTEGDLKI EEDSVKTQKDGE
 EDDNQVAVYI DSESSTASKI KI SGMKYI VDRTPVEGDVVFVKVGDVAVEV
 NDKAEVDDYYDI NNNKVMVDNVVAFNLDS DHKVF SKTTTAAKTANAKVVT
 PAAGGFTGTATFVI GQTTYKVNDKEMTMDVAPYI KGDRTFLPVRYVANAL
 GVEDSNI MWNEADQSVI I I KGD RVVKMVI GSNEFMI NGVSFAMDVAPEI V
 DPGRTMLPLRFVAQSLGADVQWDAATQTATVVS K

>2617920709 Ga0073689_11149 Copper amine oxidase N-terminal domain-containing
 protein [pelotomaculum Ga0073689 : Ga0073689_111]
 MGPGAGAVVYFYGHRREI TVYVEI I GLNNRLEGADV KMRKRFI GSFLSLA
 LVCLLFLTATDADASYQSLRNPVVADNGVRELGVVFARFTADQLQKGDN

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VI FQLPADFI WTTAAPGSDGKAASA AVQTTADWNTTVDDAYNI RYGTAN
YVAVPATYSGNANGLSKGTGKVLTFMRI NDEEVKMEVTGAPTPGQECVFY
I YFKRI YVPGGYEGEI PI RFDAPAGSGFAGGTAVNGRVYGSSESKKDGVE
KPAPI DHEI QSI FVI GEKTFVLNGVEKAMDVAPYLKNDRTYLPVRYVARA
MGVAEPNI KWNEAEKSVTLTKGETVVKMLI GSKVMYVNNKPLTMDAAPEI
MEPGRTMLSLRWATEALGADVLWDADI QTVTLKLEQ

>2617920708 Ga0073689_11148 Outer membrane efflux protein [pelotomaculum
Ga0073689 : Ga0073689_111]
LRR LAVKVTTLFFLALTI FPVQAWAREPVMSEMTLQMAVERALANS DALR
NSNYDI KRAEEVRDFLGDKLDFVPSGPAPSSDEEKI FFSI TQSDI VYNMS
KR NHQVTEDTVMSVYQAYNGI I QTQEKVKVAELNVKNKDWLKRMAFVGK
MVGTVDSMGMI QAE TNYTAAKNSLEAAQKALDDAYQKFNH SVGLWPEDRP
VLS DMPAI APLKVGDL E EVSRV VNSNPTVWLAEQKVDLAKLTERLYDFT
EPGRTEPYKAKEI DVKKA E VTAGDI KDQTCKLVRTL Y YSAKQLEE QNAVA
LETVRQAEELRVAKVKYDVGI ATKADLLDAELALAQARQTVLDTAAQQE
I LAYAFYKPWAYANAS

>2617920707 Ga0073689_11147 REP element-mobilizing transposase RayT
[pelotomaculum Ga0073689 : Ga0073689_111]
MPRGAREKSQSGI YHI I LRGANRQVI FHDDCLRFLETLEKYKKQTGFK
I YGWCLMGNI HLLL GEGNEEI SVTMKRI GVSFVWYWNKYNTAGHLFQD
RFKSESVD CDAYLMTVI RYI HQNPAKAGLVKKLADWKWSSCI GYGGGETY
PPGLLDSELI LGMFSEKKTSSI ASFREFNEAENEDKCLNETASI KRLTD
DOARAKI KKI I SVTEMARI KSFPKHQRDEI LSKVKNI GGLTQRQAARI LG
I SPNLI FKA

>2617920706 Ga0073689_11146 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_111]
VREQNAGRI AFLI SLI FFFI VSNFLAEWYVYHRMGFDSRFRFEDGAQVKR
EVL DLYTEYVAKQKGYKI AMI GDSVVQAGVAGREQTVTARLEEEELRGSY
LPGARVFNFGFPGRPADLYMAVKQLHEAGAVQLFVI NI SYPFFSDEMAK
DPLLYFKVWRPQLTDROI KELKAPPEKPDERPAGADSGEAVAGSPAKEYL
QKKVAASWAVYRFRQEI NRYLFGPPPAVKGKEYFDLALKGELPAAEAGAA
TPEPGQAVEQAPESLPEKDRPENKYRVWHSFNWTERDREHLKKVFNVGTGM
DNVDYKYRRELLDYLAENDI PAVVFLSPLNHGLLRRYQLLDYGLYRKNTA
AI GEAARLRGVFLDYQEAVPPDFHDSLHLLDAGNAAVAGFLAGALRPI
IQVVRDR

>2617920705 Ga0073689_11145 alginate O-acetyl transferase complex protein AlgI
[pelotomaculum Ga0073689 : Ga0073689_111]
MI FNTWI YGVFLAAFFI LYWTVVPAKYRPVALLAAGLVFYTYYPVHTLL
I AGFI LVTYGC GTVI YNNKFHPPYFVLGGRPATGAVFVLSVTCLGLLAY
YKYFKLFAAI FNDLTGLLRGTS LQVPDLVI PLGLSFFVF EFI HYLSDTY
RGTAPRASL TEYAAFGLFFPTLVAGPI KRFQPFMEQLRNPAAFRLEFLGD
GLYRI LTGI GKVI VADSMVYFTDPLADPLNAPGDLWVAVYAYAVKI YF
DFAGYSDI AI GSARLLGFTVPENFNRPYL RQNI AAFWNNWHI SLSSWI RD
YI YYPLGGSRG TLLFTI RNLVI ALALSGLWHGAAWNFLVWGLYHGAGLSL
YRVYRKKGWFI KYVERLPVPLVKAGSVLLTFHFVCGWVFFATDLRDSF
RVLAVI FEPVRLIF

>2617920704 Ga0073689_11144 phosphoesterase, MJ0936 family [pelotomaculum
Ga0073689 : Ga0073689_111]
MKI AVI SDI HANMAALEAVWRDI RDRQVDAVI CGGDLVGYAPFPNEVTGF
I KEKQI PCVMGNYDDAI GNMRLI CGCDYKDDHARELGERSI AWTRQRVTE
ENKEFLRNLPQEI VLETGGYKVI I VHGSRRRLNEYLYEDTGDEYLKELLE
EAGADALI CGHTHI PYHKOPTAGKHVI NAGSAGKPKHGDPRAVYTLVEIG
DAVRVEFPKVPYDFESAARAI EAAGLPEEFARI I RTGRD

>2617920703 Ga0073689_11143 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_111]
VGRKEKDKKKRRYEVKKAVPAPENNAGQANRPEQPDQPDNLHLSADWRE
FYQLVTGRI GRRAV

>2617920702 Ga0073689_11142 Superfamily II DNA or RNA helicase, SNF2 family
[pelotomaculum Ga0073689 : Ga0073689_111]
MTGSSI SVHVEWI SGKGF I WSAGGDHTAAFHEL RHLLFARHRPSYYGTF
I DSGSHRGGQAVFSPSLTALDFFTTQTWSGKPDFQWDDGI ERLRETAPLL
KAALAGGHWRPAFRKWLEGRRGWRVWERDPSLSHLPKVPFI EEWADLI

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I NEVVEQDPEAGRAWKELLSSYPVLTTPGRDSRSFAGDEEAWLEAAGWRQD
RTPFKTCLELAPEEDGGAWRLNI I LQDKQDPGAVAAWDPVQSGRQSALP
PEWPAHRGRI ERDI KKWTDALPWLADNGGERPEEAAGLRREI DEAEAWEF
LTTGALQLARAGYTI LLPKWWEEVQKLVPAKI RTRSSVGSWTEGRLGLS
QLVQFDWNLA VGDELTEEEFRRVVAQRRRLFRVRGKWLRLDPPFI KKI Q
QFVRKKDGI SLGEI LHLRLLEETSSPPAARETGPEEAPRVEVELGGQLAR
MVEQLDNI SRI PLLEAPASFRGALRKYQQAGTSWLLFLRRFGLGGCLADD
MGLGKTI QWI AYLLRVKERENPERPSLLI CPTSVLGNWQKELARFAPELQ
ALLHYGPQRAKGPDLPSI RGAGLVI TSYNLAHLDEEELSAVEWDCVCLD
EAQNI KNAYTKQAAAVRKFKGRHRVALTGTPMENRTELWSI FDFI NPGY
LGSSGEFSRKFSVAI EKKGDPEDI GRVQRLI RPFLLRRVKSDPAI ELDLP
EKQEQKEYVPLTVEQASLYEGI LHDLFKLETSKDMARRGLI LATLARLK
QI CAHPALLLKDSPPGNI SGRSKKVARLLELVAELRRKGDRCI FTQFVR
MGLLLQEVLMKELGEQSFLLHGGTPRKVRDEMVARFQETARGNGDNCNI F
I LSLKAGGLGLNLTAANHVFHFDWWNPAVENQATDRSHRI GQNRHVMVH
KFI SLGTMEERI DEVLERKSGLNEQI VGGSEAWVTEI PTSELRELFSLRR
EWWGA

>2617920701 Ga0073689_11141 SWIM zinc finger [pel otomacul um Ga0073689 : Ga0073689_111]

LVMHKQNI PEEKLVNMAAAAAGLLPPEI YNKGKDHYHNGRVKFAKEFGPR
I YATVSDGKMYTVTI NI NDFSQSACTCLQRHACEHI AAVFLYYYDPWLRV
NEMLSGLNHSVDDQTKTARPPFQLENPDPPVAVSVTRLNHPGAGRAGQPK
NPGLAVPAPTPSVEGPVELWYEFHEHYVRLRKAQKDPWQPSI NYFFDKM
YFLAMSFELFTERVAVPGDDWPSPGKDLRYRLHSI LFFMTRMEKQMAGAI P
LPQDSYQDI I EKNFI KTLGQNLPRERAESGPFFLKAMEVVRRERLFQEI
NSI FDWLLFYRFMCVFFSENSAWREKETVFLEEOMRKFEKNQRGYYCAAL
GLASLKMAAREEEQALAVLRELQEI RLDDMLFYLEYLSGVENWEKLLALL
RWLAPGVKEARAALDDI CAYCVQAAENSGAGEAFI GLVRSWLPRSFDAY
ADYLLESPLYREWVELNMTYREYTWENMDRHLRLRHVESKDPALI PLYHQ
WTAGLI EGKNRKSYYQAVKLLKKLRTLYNRQKMNSEWRTFI SRLASHHQ
LRAFQEELRKGLI S

>2617920700 Ga0073689_11140 hypothetical protein [pel otomacul um Ga0073689 : Ga0073689_111]

LQNSLEKACQKQKFKKDPADI SSRRYNRARRI VDTI LKAFQELKAGFS
VERGNKDDI TIRI LSTEYPLNGRKCSFQ

>2617920699 Ga0073689_11139 Chitobiose/beta-hexosaminidase C-terminal domain-containing protein [pel otomacul um Ga0073689 : Ga0073689_111]

MNTI KQLCRPRESVFDQSRDVTLDLTDLI ENRI NPAEFFTENYLTTGGMR
HLLRESFRRFSGHSAAGVI KLTQAMGGGKTHNMI SLGLLAKQPDLRQVM
EGDYQTPHLGKVRVVAFTGRESAPLGWGA I AEQLGKKELFKNYYSPLA
APGQTAWI NLLKGPELLI LDELPPYLLNAKSRAI GNTDLAVVTTTALS
LLVAVNKDELSNVCVI SDRATYDEGTQI SNVLKNLENEVGRVALNLE
PVALNTDEI YHI LKRKLFVLPEDNAVMEVARAYAQALRDARQMDI TNVS
PDKFI QQI RESYPFHPAI RDLYARFRENPGYQQTRDLI RLMRKVAGLYT
GPDQKAERI QLI SAHDLDCNNQEI LTEI SNI NPALDNAI SHDI ASGGQAV
AEI I DANTGGRDAGDASTLLLMSSLANVQNAI I GLSLSEI VAYLCAPGRD
PVKLKEVLGALSTRAWYLHADRDGKLFFKNTQNLVAKLKTADTYNRESA
VKELRAI LNGI FTPTQRDCYQELHVLPADEI RVGPDKVSMVVYEPYPGG
LHPDLQSFYHNLDYKNRI VFLLSGQKDNMENLLEVAKEHRAI TSI I TEMDQ
EKLPPNDPQRI SAQEKLDKI LLSLLSAARETFVTLTYPYTESLVSADFRM
EYSNNQYKGEQQVRETLSRQKFTEDVASDTFRKKCEVRLFTQKAMLWTE
VKKRAAANTSWQWHRHDALDLLKDDL VYKDQWREQGGYVEKGPFPFPVTVG
VQI QERHRDENTGEVTLTTPVHGDQLFYEI NDPATTASLPVTGARAFKT
AELVVSFLCVDSSGKHQSGDPATWRNRI TIKSRAYQGAGGEKMMVELRAAP
EAPI RYTTDGSDPGLSGGGYNGPFAVPPGALLVLSVAEKNGI VSEQHRLE
I RWGAGGPGPGPDGDI DPVRPAI WRREHI TRTTRDTYGLLGRKKYQ
ATLPVAKI MVVEKNWAELELNLDEKLI LNAEQLEETI GQLRGLVGGGEVSLE
AMSI HFPTGRHLLDWVAEVKTEI KPGEVEQP

>2617920698 Ga0073689_11138 Protein of unknown function (DUF3780) [pel otomacul um Ga0073689 : Ga0073689_111]

MSGRRKSEGFGEI PGESGHHFLVTI PAARSEKI I I SEHFTWDESRERRSL
SFALGNEDDKMRVI LPRGKWQAI AGDAQAEFNRLKRNNLPAGRWKTGQT
PVSRLLGKELALLAWAVEDADPALI PVAI KNWGLAPEERWWLFTMTNAA
TGHAVYGRDKGWRKAI RYALTENPVSGDHQCESRQELFLI MEEALSWARQ
RETALTKARGEKGGDDKFI Y

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>2617920697 Ga0073689_11137 Adenine-specific DNA methylase, contains a Zn-ribbon domain [pelotomaculum Ga0073689 : Ga0073689_111]

MI NSFI ETQFPVSKVSKESYKERMANYSQTLTGLGKWWGRKPLI LVRAAL
I GLLMPASGDPVKDREI FLKI LTMDEGGLWRRKNKNI PLKEVYRRLTARE
RERWFDPESPEDRPRLKRGTTAEGREELQLSVFQRLSYDEKLAYCARPEQ
I DSPGERAWAEI NAHLGTKARSLPELVROLGERQFGRVPRVGDAFCGGGS
VPFEVARLGCEAYGSDLNPNVAALLTWASLNI VGGGPEVAEEVRRRAQQEVY
EAVI RQVREWG I EHNEEGWRADAYLYCNETI CPECGWRI PLAPSWVI GQK
TRCVARLKPNEELRCYDI LIEGVSTEEMRKAKEAGTI RNSSLVCPHCDP
HRERSI PVTMLRGDRRTGEGTRYGLRLWENEDI VPRPEDVFQERLYCI RW
VKTFYDEGGNPVTERHYREPDEFDRRREKRVLELLQERFDEWQEKGYI PS
RRI EPGEETGRLLRERGWHWHHLFNPROLLTLGLFMELSVRYFKKKVI I
I DNI LELGLRADRKGI GCKLLI WNSHSSKEMHANVFLNQALNTLFNYCHR
TLOVI ENTNLRATDI LSNFTI EPKDARAVKKKCDI WLTDPYADAVNYHE
LSEFFLSWYEKHI TCFFPDWYTD SKRALAI TGTDENFRSMVDSYRNLAH
HMPDNGAQI VMFTHQDAGVWADLALI LWAAGLRVTAAWCI ATETDSALRE
GNYVQGTVLLVLRKQTSDETAFADEI YHQVEVEVKKQLDAMLALEDQEDP
NFGDTDYQLAAYAAALRVLT SYRRI EDI DVVRELSRPRQRGERSPVVEI I
NQAVRI ACDHLAPKGLDAQLWKDLSPEERFYLKGLELESHGEYRAGAYQE
LARGFGLREYRPLL AGARANQTRLKTAGEFAARMLGDTGFDATLV RQVLF
AVRETVRTGETAAGRNFVKSELKEYWRRRQAI I KLLQYFAALGRNKNMP
RWEADADAARLLAGAVENDHV

>2617920696 Ga0073689_11136 SNF2 family N-terminal domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_111]

LI NRFSRRQMLGHSFLNSRLI GALSYDRI AGYFRSSMLEVAGEALETMA
GPVRVVCNSDLNLRDVETARAAQYAMRQEWCAAEPEKTGPVARPRFARLY
DFLTSGKLQVRVLPREKFGI HGKAGVI TLDGGGKTSFI GSANETGEAWQ
TNYELI WEDDSPEAVQWVQEEFDALWNSPFAVPLAEFVVEDI GRLARRTV
I SSVARWRREAEPAPVI EAPVYRREYGLWEHQKFVQAAFEAHRGGAR
I VLADMVGLGKTQVLA LSAQLMALYGSRPVLVLAPKPLLWQWQDEMNRLL
DMPSAVWTGROWVDENEI EYPPLGPGGI KKCPRRVGVVSQGLI TSRSEAV
EYLKQI SFECI I VDEAHRARRKNLGSKEDEKPEPNLLSFLYSI APRTK
SLLLATATPVQLNPVEAWDLDDI LSRDNEENVLGNTWSNWRAGEALQMVM
GKSRLPEDGRELWSWI RNPLPPAEHLD FHLI RRALKMPDEQTVAPPEAW
EELGDPGRSRVRRRLARTFAQGYNPF I RHI I RRTRDFLEESI DPETNEPYL
KKVEVALLGEKPEDSI RLPAYLREAYDLAGEFCELLGNRVKAAGFLKTLL
LRRVGSTI YAGKETA EKMLRDWQAVVENDNDNENNNNNNEDNVPATSEMK
KLTI EERRLLERFVAALI ANPERDPKYDVVLNLLKNGWLEMGC I VFSQYY
DSI DWLSQNL SRELPLEKI GI YAGGQRSGI MHGGEFARV SREELKGMVAG
GAVRLLL GTDAASEGLNLQRLGSLI NLDLPWNPTRL EQRKGR I QRI GQLR
DRVYI YNLRYQNSVEDRVHELLSGRMKEI HQLFGQI PDVLEDVWVHMALG
EI EQAKKTI DAVYKQHPFEI KYNQI KKAPWESCAKVLDADRRLYKQGW

>2617920695 Ga0073689_11135 uracil phosphoribosyl transferase [pelotomaculum Ga0073689 : Ga0073689_111]

LNSI TLLKHPLASDRLRLRDRETDTLFRKALRELGLMLAMESTRHLLT
RKTTVVTPLGVEAAVEEVDSARRLLVPVLRAGLGFVGSFLEFLPKARVAH
I GVV RDHDTLEARVYLSSVPGNPSKYDDI FVLDPMLATGNSI VKALDLLR
KTGYSDNKI I LVCGFAVEAGI KOVNQKFPDVRI VTATI DLKLNLDLGYI VP
GLGDAGDRLFLL

>2617920694 Ga0073689_11134 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_111]

LRLLNRRI I SRKI CALI QKWVYCRSGATPLYQARPVVI FQSTGGPAFGLV
FDNPAYSI CKFPADGRGMRYTVKDTLSYFI LWR

>2617920693 Ga0073689_11133 YKOF-related Family [pelotomaculum Ga0073689 : Ga0073689_111]

LLTAEVSLYPQKTTNASQI I NSSLNSLNRHKLQADVGS I STKLQGSDEEI
WAGLKTLFEEAKQSEVNMVVTI SNAAD

>2617920692 Ga0073689_11132 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_111]

MGGCSGDSGGPEMVRFCSEGGGQAQI EELVKATSMEEAGRSI REGHVLMA
VYWNCAARSAAEYVLGRLKKREAPTRKVGFSMD

>2617920691 Ga0073689_11131 Ni pC/P60 family protein [pelotomaculum Ga0073689 :

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Ga0073689_111]

MKKTFGGI MLVAALAAFFFLASYRLVVAPGAFGRFTI LRPALPGGTAPGN
 YVYGAVNPATVLWAAPGQLRDYDSLI LRTKNDPAAWAGGMDAEMRLGLV
 GKAETTVLYGEPVVI LERRGDWLKVAATAQKTTLNDLGYPGWVPAQI TG
 NETYLDELNRLTGAVVMKKI TRLYTDWEI TAPLGEVSYMTKLPLLEEKGO
 VAQVRLPDGDTGFLDRGDI KKDVELAFSRSGI VEEARQFLGLPYI WGGMT
 AYGFDCSGFTMRLFQSQGI TI PRDADEQAREGFAVTKGELLPGDLVFFAA
 QGGRGQI HHVGMYYI GDGMMI HAPNSSSTI CVETVDSGNYREEYWGARRYA
 R

>2617920690 Ga0073689_11130 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_111]
 MFSLLVLTKEGALEI I ANARAVYRATAEAKNPSAGEPVFPGAFSTAI

>2617920689 Ga0073689_11129 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_111]
 MAFEI YKPRGEKVPKLPLVTI SKNSI VLNKHAREKLNTDKVELAYDRETN
 TI RI KASEDGQNI KKTKVFSRGFFSFFKI DAKGKYKTVYDEKEKALFVNL
 DERLTDLQ

>2617920688 Ga0073689_11128 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_111]
 LVRKFSASWFLAI HMSMPLI I LLRVKMGLSAWFI PLTLGTAVAGQFLVGA
 SGENREQRDQI SQAG

>2617920687 Ga0073689_11127 threonine synthase [pelotomaculum Ga0073689 :
 Ga0073689_111]
 MLYESTRGQFKRVLSAEAI KLGLSPDGGLFVPRENARI TDEHI I NKMKG
 GYREKAVMI LKEYLTDFTETEEI RECVLAYASGKFDSPEI APVRKLDGGL
 YVLELWHGPTCAFKDMALQI LPHLLTRAAAKTGEESTI VI LVATSGDTGK
 AALEGFKNVPGTRI I VFYPEQGVSEVQKLQMI TQEGDNVSVVAVRGNFDD
 VQTGVKNI FGNAEFNRELAANNYKLSSANSI NWGRLVPQI VYYFSAYLDL
 SVKGELAPGEKVNFEVAPTGNFGNI LAFFFAREMGLPVHRLI CAANANNVL
 TDFI RTGLYDRNRQFKKTVSPSMDI LI SSNLERLLYLLSGRDHTKVRAM
 AELSNTGSYRADDLTRARI GRI FWSDFADDDTLATI SSVHRRYGYLVDT
 HTAVGLKVYKYHAATGDGAKTI VASTASPFKFNASVARAVLGEEAVRGR
 VEFRLLEDLAAI SGMEI PPGLKSLDKKPALHTRTAAGKEMLEAVKNI LI S
 QKGI LPTI TAWRLRPLGHVRDKLQ

>2617920686 Ga0073689_11126 trk system potassium uptake protein TrkH
 [pelotomaculum Ga0073689 : Ga0073689_111]
 LNRNLTFTKTLGLVLLCEAAAMVPSLLLSI YHGEEDFPAFVYSI VI TGVVG
 LALSLI PVPSKVVGREGFTI ATLSWLLTAGFGSLPFI FSGVLPGGVDAF
 FETI SGFTTTGASVI TDI EALPHGI LFWRSLTHWLGGMGTI VLI LALI PS
 LKI AGMQLYKAEAPGPTKSKVLPRI AQTTRQLYKLYLI I TAAEI VLLLLT
 GMPLFDSFI HTFGTVATGGFSSKNLSVGAYNSPAVELI I VFFMI I CGMNF
 ALHYSALRGDLRNYWRDPEI KLYLGVI AVSMILLI AADLVRTMDHPPGEAL
 RASLFTVSSI I TTTGFATADFDRWPEFSRMLLLI LMFFGGCAGSTGGAI K
 HVRLLI LFKSASRQVVRLLHPOAVVPVRLGREVVPEAVVDNVQTFFFLYL
 LI FATAAAYLSFLGLDLVSSI SAVAATLGNVGPGLGLVGPMTNYAALPGA
 GKVVLSLCMLLGRLELYTVLVVI SARFWR

>2617920685 Ga0073689_11125 trk system potassium uptake protein TrkA
 [pelotomaculum Ga0073689 : Ga0073689_111]
 MKI TVI GAGKVGMEI TNRLCEEHDI VVI EKDENKLDKI HEHLVDLCI RG
 NGSSAKI LKSPDVAGSDLLVAVTSSDEVNMI ACMTAKKLG I PKTI ARVRD
 PDYAQELVI SKEDLGVDLVI NPEYAAAMEI HRLLTVALPVHTEPFANGKV
 QMADI TI DESMTNI ASKKI KDI EFPPSSLI VAI SRRGEMVI PGGKDTVLP
 GDTLYI LGHAATI NKI CSKI KKKKQKMHSVLI LGGGRI GFYLADRRCRMG
 MKVKI I EQNKERCLELAERLPDALVLRGDGSDVDLLKREGI KETDGFVAV
 TGLDEENLLLALLARQMGAKQVAVKVSRSYAPLVERLGVDAAI SPRLI I
 VSEI LRFI RGRLLSLCLLLNGQAEVFELI VQPGTRVLGKPLSGAGLPKG
 VI VGAI LRGDKAI I PEGI DVI MEGDRLVI FALGQNVHTI ESLEFNVAGGT
 YLEQSYLQNSGTGAFM

>2617920684 Ga0073689_11124 Restriction endonuclease [pelotomaculum Ga0073689 :
 Ga0073689_111]
 LKFRI GGFFKFKERNLLRGFLSWRERRKRDEFRLFYLRQPGEDNRSFLGK
 KLDLAGWLLLAWLAGFLLAKLTGRPAAALALSLPLLAEEALLLRKLATR

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REQRRRRRRRLWLAGQKFMEI LKMDPRKEFI PYVRDI LAGLPFGQGVEL
TAGRKKKDTAGPGI DLTGSYRGVPVAVRCVRRAGDAGVTPEDVRAFAGVL
DPGGYKNGLFI TTGDFSPGVSAAVEEAARGGI KI KLI DRYRLMDLARQAG
TGAFTEDTSAGAAPGKRKVSALALRDAAFGSRKKAKSYFLYGLLLYGGY
LLLKGGSGLSLVYLFFAALNFTLGAGCLCFGKSPAETDPLEGLEPDK

>2617920683 Ga0073689_11123 Peptidoglycan/xylan/chitin deacetylase, PgdA/CDA1
family [pelotomaculum Ga0073689 : Ga0073689_111]
MPCKYVLI FAVVLTLLTGAGVPPTAAVTPVEPPAQNPKGAAVPSNP
VQAGPAKAEAAPAEPTVPATPGKKVYLTFFDGPNSRYTGLI LDI LKRY
GVKATFVVVGNI EKNPDVLRRI LAEGHSVVNHTYSHDYKRI YASPGALL
DDLQRCNQLLPPAAGSGVKI FRAPGGPSNLGKDFHALLDKNGYKSLGWNV
ASADTDPRGVSPEQI I NNVKDGVI RI EQMKKAPI I LMHDGTEI NFNADKP
CAAVHNYI RNRESVAALPVI I EFLQARGYTFAGVDENTPPAW

>2617920682 Ga0073689_11122 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_111]
MPLKNRI RYWRRLGAWNLOEFADLI GFSAWAVERWEGQNMQPTLEAVCR
I KERLLPHYPEI TLEDLDYI PEKQAAESAGC

>2617920681 Ga0073689_11121 tRNA(Ile)-lysinine synthase Tis/MesJ [pelotomaculum
Ga0073689 : Ga0073689_111]
MVKKYRKWFLGRVKRSI TDFGMI EDGDRVAVGMSGGKDSAFLLHALRLIN
RAAPVRFGLAEVFI DMGWPM DVPLLEEFCSRREVALHVVKTEI AEI VFEA
RRGENPCALCAHLRRGAFHGKALELGCNKVALGHHLLDDVI ETTFFMSLFYT
GOMRTFAPATFLDRSGLTMI RPLI YLPAAEI RKWVETEELPAI PNPCPAS
GHTKREEARELVAEASRYPD LKARFLTALQTFDRRNLWPEI RKKGRDRE

>2617920680 Ga0073689_11120 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_111]
LRGI RPGRGAGVFLEQYDTGVPLGLNCNRKPVLVRDVLEK

>2617920679 Ga0073689_11119 NAD-dependent deacetylase [pelotomaculum Ga0073689 :
Ga0073689_111]
VNYEEKI SHLTGLLKNSTRFTALTGAGI STESGI PDFRSPGTGLWTKLDP
MKTATVTVLRRDPAAFYERNLDRWGFAGAEPNAAHYALARLEREGLLTG
VI TQNI DGLHRKAGSQVWEAHGHLRTCHCLDCKKSHPFELVNQFMSGT
NPPRCSACGGVLRPDVVLFE DSGMEDFFHAVQAL TDCQLLVVVGSSLEVY
PVASLPGQARQLVI I NKTPTPWDDRADLVI NEMAGRVFTDTLAALGKQ

>2617920678 Ga0073689_11118 phosphosulfolactate synthase [pelotomaculum
Ga0073689 : Ga0073689_111]
VECDPGNYWRKI LKFPLSGRSKKPRRDGLTI VI DKGMGLSKMRDMLQTAS
EYI DMI KLGFGTPALYKPEI LREKI HLAVSHGVDI FPGGTFLEVAI MQGK
MEYFI HAARDTGFTAI EVSDGAI DLGDRLRARAVEMAVALGLKVFTVEVGK
KEPENVLCFKDLI RLAKRDLNNGAYRVI VEGRDPGKDVGLYDERGRLI EK
EAKELLSSLGDPFLLI WEAPRKEQQQDLI LHFGI NVNI GNVSPWEVI ALE
ALRVGLRSDTLRTVFEGDPG

>2617920677 Ga0073689_11117 Membrane associated serine protease, rhomboid family
[pelotomaculum Ga0073689 : Ga0073689_111]
LI I TNLI VFGYELSLGRALDYHLYAYGVI PAQLTAEGFTAQEI VRLTTAM
FLHGGWFHVLNMLYLWI FGDNVEDRMGHFKYLVFYLLTGYI ATI AHVLY
APLSKAPLI GASGAI AGVLGAYLI LFPRARVLTLI FIFI FIFI VPVPAVI
FLGI WFALQI LSGTAALSAQAAQGVAFWAHVGGFVAGMLLVKLFARREDH
YRH

>2617920676 Ga0073689_11116 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_111]
LPLSNFQVKA EVKTLI RFFCDCGNEDPAGFDI YVSQSDLC DVLT VVCRYC
GDVREEFVACSREAI TLQK

>2617920675 Ga0073689_11115 Alpha/beta hydrolase family [pelotomaculum Ga0073689
: Ga0073689_111]
MGMI L FVHGMGHSDDRNYWRKWDPVRSALAAQGLELDEGHFGGVYYYDL
VPCPQEKMAQKAESI KI QLLYLKERVTEELGSLRSPFPKGI GAI KKLADQ
I VDNFGDI FTYLYLEEI HQAVNQRLYDAFDGNGPFSLVGYSLSLVSYCA
LKENPAAARQVVHLI MLGSPLFWFRRGVAERVDLDSRPVAVGRFTNI AGI L
DI ACPQVVPRI LGGLEDSEI EFSI NPFDP I KGHQEYFYKEEGLEALASVLR

KGWVA

>2617920674 Ga0073689_11114 Protein of unknown function (DUF3243) [pelotomaculum Ga0073689 : Ga0073689_111]
MNTVNTNWD SWKKTLGQAVEFAGELGI SREQI GSMARQVGDFLAQNVQPA
NPEQKVVKELWDVAGPEERQALANLMTRLAAGRT

>2617920673 Ga0073689_11113 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_111]
MAFRKDDMFDDYNVKAGTI DWYTKNKRLLDKSI PEVI I ADKTVGGSRFQV
FRNENFELVFI HTVGGVSKKAAADLNKVDYHDGI RVQLTWGPGESYI KVG
DTTLEQNYFI VRCE

>2617920672 Ga0073689_11112 N6-L-threonyl carbamoyl adenine synthase [pelotomaculum Ga0073689 : Ga0073689_111]
MSII I LAVETSCDETSAAVVADGTEI LSNI I SSQVDVHRRFGGVVPEVAS
RKHLELI NQVVDEALAEAGLEFKDLDAVAVAYGPGLVGALLVGVSAKAI
AYGLDLPLVGVNHLEGI YANFLVEPGLDFLLCLVSGGHTGLVLLERH
GCFRVVGGTRDDAAGEAFDKVARAMGLGYPGGPLI DRLARQGDPEAVVLP
RVYLEERSFDFSFSGLKTAVI NYLRRAGQRDGEVNKADLAAGFQKAVTDV
LVDKTLEAARETGCTI LLAGGVAANRGLRADLAGRAAREGRRVI I SPPV
LCTDNAAMI ACAAYKYLRGAFAPLTLNAVDPDLKLGEERYEGNFKGRVFK
CD

>2617920671 Ga0073689_11111 Protein of unknown function (DUF512) [pelotomaculum Ga0073689 : Ga0073689_111]
VGEI QEKDEDYVRSI I MAEAAAGNI LPLTSACNVRCVFCSHRONPPGVEV
YRI APLSLVEVEQTL SFMDPEKPVVI GESVTRI I EGEPTHPALREI LQL
VRTAFPDITI QI TTNGSLI DEQVADLLSRLGNVVVYLSLNSAGVVGRALL
MGDESADKSI RSAALLNDYGVFPHGSSVAMPHMVGWSDLEETVRYLCAGG
AETVRVFLPGFTALAAPALRFKPSLWELNAFVTRLRGEVDVPLTCEPPL
I SDLAAEVAGVI RDTAAEAGI RTGDVI EAI NGLSVHSRVHAFQOVLKAA
SPEVAVRRGSGALALHI KKAPGRRSGLVMDYDLDPGLI GEMARTVRRRGA
AGVLALTSELAPVI NRGLEQFWQGGAEVAVVKNHFFGGSVRAAGLLT
VADFSTLENFLEKSAGKKPGLVLLPGAADFHRGRDLTGRSYLELEEKSG
VTCEVI

>2617920670 Ga0073689_11110 5-formyl tetrahydrofolate cycl o-ligase [pelotomaculum Ga0073689 : Ga0073689_111]
VLKSELRKDVLKDRGALSPAEAAEKSARI I ERLGMDYEYRRASTI MVI D
FRNEAQTGELVQRAMAAGKRVAVPVTDI ANRRLTPSLLADFPGLDQPGAW
GI LEPKPECLRPI APEELDLVVPGVAFDEKGNRLGYGGGFYDRFLPRAR
YDVTYVALAFELQVRPDVHPGPYDVPVHYLLTEDRLI KTKK

>2617920669 Ga0073689_1119 NADH-quinone oxidoreductase subunit E [pelotomaculum Ga0073689 : Ga0073689_111]
LAVCKCGEHAELPQEEALQKLFDLRYDQKGS LI PVLQEAQNI YGYLPKEV
LRQI AGELRI PFSKI FGVATFYAQFHLKPRGRNI I RVCLGTACHVRGGAK
VFDAI QEHLNVANGETTADLRYTLETACLGLACGLAPCVMVNDNTHGRLT
PNQAVALLDDYE

>2617920668 Ga0073689_1118 NADH-quinone oxidoreductase subunit F [pelotomaculum Ga0073689 : Ga0073689_111]
MDNLMKCCAKCTNSPETPCRDYI LCRTGGPFCHDDEACREKRRELLESI
HLSGDSGRROVLLCAGTGCI SSGSHKLVDLLAEEI EKAGLADKI SVKI TG
CHGFCEQGPI VI VEPQKTFYRRVEAADI PEI VSRDLVGGEVVERLLYVDP
ATGQAAATYETI PFYARQROVLHNCGHI NPEDI QEYVAQGGYRALTSVL
FKMNPQEI DEVKTSGLRGRGGAGFPTGTWKQGALNAKI KDKRYVI CNAD
EGDPGAFMDRSVLEGDPHAVLEGMI CGYATGSDEGYI YVRAEYPMI RR
LKI AI DOMEKYGLLDNI LSGSYNYHI KI KAGAGAFVCGEGTALMTSI EG
NRGMPRFKVGSRSTEKGLWDKPTTLNNVETFANVPLI I TRGGEWYASI GTE
KSSGTGI FSLTGKVNNTGLVEVPMGI TMRI I YDI GGGI LNNRKFKAVQI
GGPSGGCLPEEHLDP I EYDSLGPVGAMMGSGGLVVMDDTTCMVDVARYF
LNFTQSESCGKCTPCREGTKRMLEI LTRI CEGEGVI EDI DTLERLSRVI V
TTSCLGLGQSAPNPVLSTLRYFKDEYI AHI VDKRCPASSCTALLVYTI NT
EKCTGCGACARACPAGAI SGEKKQPHI DASRCI KCGSCI QKCKFDAI EK
M

>2617920667 Ga0073689_1117 4Fe-4S di cluster domain-containing protein

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[pelotomaculum Ga0073689 : Ga0073689_111]

MADINLSI NGQOQVTPAGATI LEAAEKLGYSI PTFCHDKNLPGVASCRI C
VVEVAKSKNLT PACMTVAR DGMVVQTESPAVVEARKTI LELI LANHPMDC
LTCEKNGDCRLQDYCFQYGVKESGFKGEKHSYPLEDSNPYI VRDMNKCI L
CGKCVRTCSQVEDRAVI DYAYRGFNTKI APAMD I PLGESDCVYCGRCVAV
CPVGALI YKSTI GKGR TWEI KKKPVT CMFCDSGCSFNLNI KDGKVI GVTA
GEPGVGRPLCLKGR LGMEL LHVSGSLPKPQI KKEDCFVEVPWAEALGLAG
I LDKLQEK E

>2617920666 Ga0073689_1116 NADH-quinone oxidoreductase subunit G [pelotomaculum Ga0073689 : Ga0073689_111]

LANVALTI DGRQVTMPQNTI LDAAKLGI FI PTFCHDPELSRPGSCRI C
VVEVQGSKNLTVSCAAMARDGMNVNTSSPVVI GARKMI LELI LANHPMDC
LTCGKNGDCRLQDYAYMYGVKGDFAFAGERHNYAI EEDNPFI VRDMNKCI L
CGKCI RMCDEVQGRNVI DFAYRGFNTKVAPAMDT PYSESNCVFCGNCVAV
CPVGALTEKGM LKSRRWELKKVTTTTCPYCGTGCTFDLNVKDGKVVGVTS
TDGEVNGRALCVKGRFGYGF I HHPDRLTKPLI KKDGGQFVEASWSEAI GLV
AEKLGTVKERYGSDAVGLSSARCTNEENYLMNKLARAVI GANNI DHCAR
L

>2617920664 Ga0073689_1114 formate dehydrogenase major subunit [pelotomaculum Ga0073689 : Ga0073689_111]

MTNTI REVAGADFI LACGTNTTESHP I GLQVKKAVRNGATLAVVDPRT
EVAELAHHLRI KSGSDI ALLNGLAHVI I AEELWNKEFVRERTEEF EALK
ATVEKYTP EYVVG I TGVPADTI KAVARGYAKARNATI LYTMGI TQHVCGT
HNV LAI ANLAML CGQI GKESG VNPLRGQNNVQACDMGALPNVFTGYQP
VTVEENRAKFAAAWGV PDLPAKLGLTVGEMMDSA AHGQI KGM YI MGENPV
LSDPDADHVHAEKLD FLVVQDI FLTETAQLADV LPAASFAEKDGTFS
NTERRVQRVRKAI EPVGGSKADWEI I CLVATAMGYPM SYNPAEI MEEI A
RVTSPSYGGI SYERLEQGS LQWPCPAADHPGAKFLHAGKFARGLGRFHPVE
HI PPDELPADEYPLVLSTGRRLYHYHTGTMTQRTGALEVAYPEEYLEI NC
ADAELKGVCDGDKVKLSSRRGSVEVTARLTGAVTPGLVFASFHYPDVAVN
KLTNPARDPI AKI PEYKVC AVKVEKI DAVKA EKVS

>2617920663 Ga0073689_1113 conserved hypothetical protein (putative transposase or invertase) [pelotomaculum Ga0073689 : Ga0073689_111]

VPDNGPPGQKQHHPYDKGYRQLLANRRTFLSLFKSFVREEWVNEI SEHDL
LLVDKSYI LPDFSEKEADLVYRLKSKEI I FYI LLELQSTVDYLM PFRLLL
YMI EI WREI YRNTPEKERERKDFRLPAI I PAVLYNGADNWTASLNFKAMQ
ANYQRYEKHLDFS YLLFDVNRYREEELYRTANLI AGI FI LDQKMNYPEL
VKRLHKLVDVFKLTPDFEQQVKA WLKNVI KPKMPARLQKEVDRI LNEAN
PWEVEKMI TNLEVTLEEMQEQSEARGI KKGKLEGKLEGKLEVAKNLLLMN
MDLESI VKATGLPK EELEKLRKQLQVH

>2617920662 Ga0073689_1112 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_111]

MAKRNFVWDGKTVEKEPEPEGTKTI GERSQVLAQLVFAD

>2617920661 Ga0073689_1111 Integrase core domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_111]

MYRWQOI KTLRFHFFGGTALELI I DNPQMVI I YTKDVVVHYNEEFLKFC
GLYNI RPEACRNYRARTKGKVERPFCYI QEHLRLGLEVENLQEFEEKLKI
FQDEYNLRSHSKLKEFSEQRFEREKRLPTASSPY

>2617920660 Ga0073689_11075 two-component system, OmpR family, response regulator [pelotomaculum Ga0073689 : Ga0073689_110]

MPKRI LI VDDEVKI REMVKSYLENEGFEVVQATDGP GSLESI SKDKPSLI
VLDWMLPGMSGLEI CRRVREKSNI PI I MLTAKTEEVD TLLGLELGADDYI
TKPFSLRELAARI KAVLRRSEP DENKNSDVI KI GELEI NLD RHEVRSEGK
SI SLTPTEFKI LSI LSGNPGRVYSRLQLLDAAMGFTYEGYERSI DTHI SN
LRKKI EPDPANPRIYI LTVYGTGYRFGS

>2617920659 Ga0073689_11074 two-component system, OmpR family, sensor histidine kinase BaeS [pelotomaculum Ga0073689 : Ga0073689_110]

LKLGAKI SI SMVFLALLATLI AAFLAGKAI RTSFDYYVGRNLSYRLERVQ
AVLTQYYLERGGWEGVQYLFNDLQPRGMGMSGYGRFGQGAPWSGHGMMG
QGLGLMMGPGAGDVLLVDLSGKVI AASYKEYLGKLP PGVSI KQGVVPQI N
GETVGTLI PVNTHHGEWESEFI NSVTRATLWAAAAASI LALLLGI I I SRH
LAGPLSVLSSAARRLAGRDLGYRVPVVTSD E I GELAEAFNQMA DSLERNE

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KLRRNLI ADTAHELRTPLAI LRGNLESLOQEV TASPEVI I SLHDEVVRI
SKLVNELQDI SLAEAGELRLNRREVPVEELVEKVAMPFGGEAKYKNVDF
VDI PAGLPPAHVDPDRI VQVLLNI LGNALRYTPSGGKVTL SAGLAGDKI V
FSI KDTGSGI APADLNNVFERFYRSDKSRTTGGGTGLGLAI TKGLVEAH
GGKI WVESKLOEGSVFSFTVPVYR

>2617920658 Ga0073689_11073 phosphate: Na⁺ symporter [pel otomacul um Ga0073689 : Ga0073689_110]

LLMI LSFSLGLTLMKGLQI MRDGLESA AHFKMRRTLAALTGSPAAALLT
GTVI TALVQSSTAI TI LTI GFVNAGMLGLVQAI GI I LGANI GTCVTAQML
SFNLTALAVPAVVTGLAFFI PGKKRPAYRYTGQSLI GLGI VFTGLEVI SY
SFVPLRQSAWFATLLSSLD CRPFQAVLAGAVFTGLI HSSATTTGVVMSLA
RQDLLDLPSAI ALVLGANI GTCI TAVLAGI GGTVTGRRVAMAHVLLNLGG
VLAFLPLLHPFAALAQLTDPSPPRQI ANAQTI FNVASSLAVLPFTHSFAR
LLTVLAKK

>2617920657 Ga0073689_11072 Fur family transcriptional regulator, ferric uptake regulator [pel otomacul um Ga0073689 : Ga0073689_110]

MI LAI NFVDKI KSI NYTI KKG I AGGVVMNKVI SNI GEKLRTKDCKLTTRR
ELI LKVLLENS DKHLSAEVYNLVKQAPEMGLATVYRTLELFKEFDI I H
AMDFGDGRMRYEFGVEEGSHHHHHLI CTRCGAI I EVNEDLLEELESRSV
KQHNFTI TNHQLKI FGI CDECYGMKQKK

>2617920656 Ga0073689_11071 1,4- α -glucan branching enzyme [pel otomacul um Ga0073689 : Ga0073689_110]

MPEGYLALVLHAHPYI HHPEEPGI MEERWLFEAVTECYI PLFRVFERLV
KDGVNFRVTLSPPLVCMLDDKLLQERYMRYLNNLI RLAEAEI ERNENA
PAFRDLAGMYKHLSDLRRCFEDDYGGNLLLPAQSLQALGVLEVI TTCAT
HGYPPLMTWEARRAQVQLAVEQYGR I FGRPPVGLWLPECAYVPGVDEI L
KEFGLRYFFVETHGMI LANPAPRHGVYAPVYCRSGVAAFGRDPESSRQVW
DRHSGYPGNPYREFYRDI GYDLEMDYLAPCLPGGGI RCDTGLKYYRI TG
SNAKEPYQPDQAALKAEDALDFVRNRVAQI ERLAAGMDRKPVI VAPYD
AELFGHWWYEGPLWLENLCRVI DTGQDTI KMTTPATYLG DYVENQVVDLA
ASSWEGGGYNQVWLNPSNDWI YRHLHRAEKSMVDLADLYPEAFGSVRRAL
NQAARELLLAQSSDWAFI I KTGTTVQYAMQRI SDHI GRFNRLAKGEVDEK
ELAEFEKKDSI FPELDYTI YSRHYRVS RAGRPGGKRGGEALKI I MLSWEF
PPRTVGGRLARHVYDLRSLARLGEVVHVI TCPVEETDDYQLVEGVHVHRV
NQSGLTSGDFI EWVROLNTAMTGLAAGLMRRETFDLI HAHDWLVEDAALE
LCGQFRLPLVATI HATEYGRNRGI HNELQORI HDLEARLSNLATTI I CCS
EYMAGEI TRLFKI PRNKVHVI PNGVDPANLGI PKRLVPGERPPRSGEKI V
LFI GRLLVPEKGVQVLLKAFSLLSGLLPDLNLLVGGRGYPYGFYLKEMAEKL
GLDGKVEFLGLFDEADRNLKHLKQADVAVFPSLYEPFGI VALEAMAAQVPV
I VSDTGGLREVVDHGI DG YKVPVGRPELLAYYI RGVLENPGLARDLTMQA
WKKVLT VYDWQNI ALETLDVYREARRI HRGPCPENTI G

>2617920655 Ga0073689_11070 hypothetical protein [pel otomacul um Ga0073689 : Ga0073689_110]

MVFEPEGLATGI G SMPFTDPAEALPLI KKYLP EI PHWPQLPLRGRQEHFV
NQFLQPLVKTGLLI DDGDKI YFDLSKPNWTKNLTEFYI YLACEEGNTRV
LNEFAFPVDSAEGFYAF LDELENGTG DATVLKGHVVGPLTVAFQVKDEQG
RFAYYNDQLRDLI VKTI AMHSAWQVRELGRFGLPVL I FVDDPAVG VYGNS
SYI TVTREM I KNDLGAVFEAVHSAGGMAGLHSCDAVDWSI LFESDMEVVS
FDAYNHFSSI I PFVSSLKDFFERGGSLAWGLVPTLH DRALEEDED SLLKI
LEGEWI ELI AREI PRETLFHRCLI TPACGAGLLESALAERI YRLTAAVSE
KLRFREGYFKP

>2617920654 Ga0073689_11069 histidinol-phosphate phosphatase (EC 3.1.3.15) [pel otomacul um Ga0073689 : Ga0073689_110]

MI PADYHLHTMLCGHATGEMAEYLVEAARLGI REVGFADHLPLYFLSPEK
TVPNYAMVDNELPRYVEMVKKCAEAPVGKLG I EADYAPDHEEKLASLL
AAHPFDYVVGSVHFI EGWAFDSPDEI EEEYGQREI DQVFEQYFTLLQQAAL
TGFFDVMAHPDLI KKFNF RPARDLGPLYEDTARAFKRAGVCVEVNTAGLR
YPAGEI YPSPALLGVFFKYGLPVTLGSDAHRPEQVGAGLGEALKLLLLNI G
YKEI ALFNRRRRNFAKI Y

>2617920653 Ga0073689_11068 hypothetical protein [pel otomacul um Ga0073689 : Ga0073689_110]

MDLASVGLVSASI VMFAATLSLATRPVQSTGTKKI KMSCKRKDDTI QRAI
VI KLPRGKDI PEDYVLDLRVSLSRGKKQGVGEKGNETNQQVKKFYRGLDE

YL

>2617920652 Ga0073689_11067 MraZ protein [pelotomaculum Ga0073689 : Ga0073689_110]

MFMG EYQHSVDAKGR LFI PARFREGLGDRFVVT KGLDGC LFFVYPRPEWEA
LEQKLKSLPI TRGDARAFVRRFFS GATECEVDKQGR I LIPGNLREYARLE
KDGVI I GVSSRVEI WAREQWERYNNLAASSYEEI AEKI VDLDPGI

>2617920651 Ga0073689_11066 16S rRNA (cytosine1402-N4)-methyl transferase [pelotomaculum Ga0073689 : Ga0073689_110]

MEFAHKPVLL EEVMEGLGLKPDGVYVDCTLG GAGHSEAVLRRTALGGRLV
ALDQDPEALAAAGGRLASFRGRVDLVRANFANLDEVLSRLGI PEVDGI LF
DLGVSSYQLDNPARGFSYQHDPVPLDMRMDPGRET DARELVNKL PVEELAR
VI REYGEERWASRI ARFI GEARGHRPVETT GQLVEI I KRAI PAGARREGP
HPAKRTFOALRMV NREMEI LPEAI R S A VRHLRPGGRI CVI TFHSLEDRI
VKETFRR L ASPCSCPKEFPVCVCGGKRELRI I TARPVI PGAAELAENPRA
RS AKLRI AEKV

>2617920650 Ga0073689_11065 cell division protein FtsL [pelotomaculum Ga0073689 : Ga0073689_110]

LI VAREKTGYRFSI AAPGPKKI RKI KSVSGGARLALTS LI LACFMVGVL
I TYYYSQVFALGYOI NRLQRELAVLRVENHNLEEEVRR L TS LERVEYLAI
NKLGMVKPDSNNI LVVTVAGETPPVPAPNP DGGPAVDSSPAGEEKSRLI R
AFTELVNRL ENKI WLGRGPGAGSGEETNANNKYSDPEENNRTI SYYSTGA
PRADLP SGLASAC

>2617920649 Ga0073689_11064 stage V sporulation protein D (sporulation-specific penicillin-binding protein) [pelotomaculum Ga0073689 : Ga0073689_110]

MRDVPVEARRGTI YDRNGQELVSSVSVD SAYAFPPQI EDK KAAA EKI AGA
LGM DKEEVYGR L NQNVGFVWLKRRLDYESARRL KELKLAGVELVEENKRF
YRQESLAAHVLGFAGDDNQGLTGLEGVYNKDLRGVPGRI VI EKDAVGRNI
PEALHRFI PPVPGNNLVLT I DQNI QFFVERELDKI VDVHHPKLAVI I VMD
I KTGEI LAMGNRPTFNPGDWRKY PQA VWDHNP AI WYNYEPGSTFKI I TAA
AALEEGAVKPGDTFYDPGYI KVADRTI RCWYDGGHGSQTFAEVAQN SCNP
GFI TVGLRLGKERFYKYI NAFGFGQKTGI ALPGEEVGI QI PQEATELNI
ATMSI GQSI AVTPI QLLTAAA AVANGGVMMKPSLVKAI TDTDGKTI KEFK
PEPVROVI SGNTARTLMGLLTDVVQKTGRNAFVDGYGAAGKTGT AQVVD
PGGGYADGKYVASFMGYAPADDPRI AALVMVAEPTGASHFGSQAAPAFK
AVARDTLLYLKI PERPEI EKP KSPFVFEEPKVKVTVPNVVHY PVEDAEGI
LKNAGLNVQI RGEKGI VSSQVPKGGAGVSSGATVI LELQSTGDRPADEV T
VPDLKGLTI KEAGSI LEKLGFN LNPVGSGLA VGGQVAPGSKVSRGT VVTV
EFQPQAVQGLRD

>2617920648 Ga0073689_11063

UDP-N-acetyl muramoyl alanyl -D-glutamate--2,6-di aminopimelate ligase [pelotomaculum Ga0073689 : Ga0073689_110]

LLFVELLQGV EVRDTGGDPGVEI MGI TCDSRQVEPGFLFVAI KGFKTDGH
EYVNOAREKGAAAVLERETALLSGAAWALVPDTRRALALLSARFFGNPS
AGI KVVGVGTGTNGKTTTTNLLATVMEVAGRKTGLI GTI HNRI GDRI LPVK
HTTPESTD LQSL LDMAAEGVDI CVMEVSSHALLHRVDGCEFDVAI FTN
MTRDHLDFHRDMDEYLKAKLKFSGLAAPGEKKDQKYAVI NADDPHADHF
VRAAGGRVYTYGI I APADARARDVRVNVGGVRF TVVGKWGTCPLEFRI TG
LFNVYNALAAFTAAAAMDVPVAVI KEALEKVRGVPGRFELVDAGQDFTVI
VDYAHTPDGLENVLKTARQI TERRLI TVFGCGGDRDRTKRPLMGEI AVRY
SDYAI I TSDNPRTE DPLKI I DDVEAGVRPVAGKNGYTV EPDRRRAI RLAV
EKACRGDVVVI AGKGHEDYQI I GGGKFPFDDHREAEAAI RDMRCGK

>2617920647 Ga0073689_11062 UDP-N-acetyl muramoyl -tri peptid e--D-alanyl -D-alanine ligase [pelotomaculum Ga0073689 : Ga0073689_110]

MKPFTLKEI AVVTGGEI I QGDSGVVLSSVSTD SRTI KKGDLFFALSGERY
DAHSFI RQATAAGAGGLVVSRRADWPPGVPVLLAGDTLAALQALAAANRR
RCGAKVI GI TGSTGKTTTKDLVAGVLSTR LRTFKTRGNFNNEI GLPLTLL
DMDGQCEVAVVEMAMRGPGEI DGLSRI ARPDGAVI TNI GETHLELLGSVS
NI AAAKGEI LEHI PPDGFALLHAESPFI RREAGRCRGRVVFGLSESAGI
RAENI RPEGGSRFDAVNGERYEYI PVPGRHN VVNALAAI GVGLEMGL
AAGEI AAGLATA TLTGMRLEI SEAGGLTVI NDAYNASPASVGAALQVLTG
TAGGRRRVAVLGNMLELGRSTGGHREVGETAAKLGV DYLVAVGDLAAGI
AGGALSAGLPAERI FHCEDNEGA AKVLGGLLLEGDVVLVKGSRGMKMEQI
VQRLLGSPVARAAGVNHPI

Table S2

>2617920646 Ga0073689_11061 Phospho-N-acetyl muramoyl -pentapeptide-transferase signature 1 [pelotomaculum Ga0073689 : Ga0073689_110]
MENLLAAFCI SLAVTLLLGPLAI PALRRI KFGQNI RSDGPARHLQKAGIP
TMGGI I FLAGTMAGGGYRPAG

>2617920645 Ga0073689_11060 Phospho-N-acetyl muramoyl -pentapeptide-transferase [pelotomaculum Ga0073689 : Ga0073689_110]
MTDGLVLLVALGYGFI GFLDDYI KVVLRSLGLRAREKLLGQVLLAGGL
AAWVLETDRGTGLALPFSGFI TPGGI HMELGWLFFMAFTVLLVVGI SNA
VNLTDGLDGLAAGVSLAALAMTVVALAVDKAGVAVSMAALAGGCLGFLF
YNRHPAKVFMGDTGSLALGGGLAAAVI TGSELVLLI I GGI FVLETLSVI
I QVI SFQTTGRRRI FRMSPLHHHFELGGWSENRRVI TFWAVTLVLAAGLA
GMYRLG

>2617920644 Ga0073689_11059 UDP-N-acetyl muramoyl alanine--D-glutamate ligase [pelotomaculum Ga0073689 : Ga0073689_110]
LRELGDKKVLVVGAGKSLAI SRFLAGKGA VVLTDA GNPVYPGGELEEL
AAAGVELSLGRYPVDKGSFDLVVMSPGVSLTVEPARSAAAEGI PVTGEL
ELAYHFTRAPMVAI TGTNGKTTTTTLVGEI FKDSGVNTLVGGNI GLPLVT
EVERYGP GDVVVAEVSSFOLETTTAFKPRVAVI LNI TPDHLDRHGTMENY
TAAKARI FANQEPGDFTVLNYDDPVT SALGGGSRGRNI FFSRRRVLAEGV
YVREGKI AANLDGKEELI CACNELGI PGAHNLENALA AAVAAKVMGVETA
SLARTLKGFKGVAHRLEFVAEI NGVRYVND SKGTNP DASI KALEAYEEPI
VLI AGGKNKGGDFREFAAKV KERV RAMVVLGQSAELI AEAARAAGFENI Q
FAGDLP GAVLLAHRAARLGEI VLLSPACASWDMFKSYEERGDLFKAVVAG
I KAGEY

>2617920643 Ga0073689_11058 cell division protein FtsW [pelotomaculum Ga0073689 : Ga0073689_110]
MPAKRSSPDFVFLFTVMSLLSLGVVMVFSASEYNTLVLYNDSFFFFKRL
VWALLGLTAMFVMNYDYRRLKNYFLPI LI I AFI TLVLVLI PGVGKEVNG
ARRWI AAGPLTFAPAEFVKLSI I I FTAYGLARQKDRVGQFSKGVLPYLAV
MTLAAGLI MLQPDLTGTTLSLAGI VFAMLFAAGARTAHGGI AAAGVAAVA
LAI ALEPYRMKRFLAFLDPWADPRGDGFHI I QGLYAI GSGGLFGLGLGQS
KOKFLYLPETHDTSI FAI I GEELGFI GASLVI MLFI LFWVRGLKI AVTSQ
DPYASLLATGVTAWGVQAI I NI GVMTGSLPFTGI PLPFI SSGGTSLLFT
MTGVGI LLNI SRYTRAR

>2617920642 Ga0073689_11057 UDP-N-acetyl glucosamine-N-acetyl muramyl pentapeptide N-acetyl glucosamine transferase [pelotomaculum Ga0073689 : Ga0073689_110]
LRFVVAGGGTGGHI YPALAI ARGLKERYPEAEI LYI GTARGMEADI VPKE
GI PFKGI TAAGLERKLSPKNLLALWQAGLGFWDQARDSI RRFRPDAVI GAG
GYVCGPVVLAALSGI PTLI HEQNALPGI TNRI LTRFVDRVAVTFADSI Q
YLSCREKVRLTGLPVRPEI LRVDRESRSENPDLSAGRFLLSFGGSQGAR
TVN RAMVAI KMFAGDPR LNI LHV TGOAGHREFLDGCKT MGI DLGEY GNI
TI THYI YNQDALGAADLVI SRAGAATLAELTALGI PAI LVPYPYAAENH
QEFNARALERE GAALVI PDRRLDGESLCRKVADLLDNRRERLAAMAAASKK
I GKRRALEDI MDI VEELLRGEKI KTN

>2617920641 Ga0073689_11056 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_110]
VKKLKQI NTRESGVRMREQVKTFQDI LVWRKEHLFVLGGLSSI LSQEV DK

>2617920640 Ga0073689_11055 UDP-N-acetyl muramate--L-alanine ligase [pelotomaculum Ga0073689 : Ga0073689_110]
MNGI AI I MRGLGYRVTGSDLKPSAVTERLEALGVTCYAGHAEKNLGDAEM
VVASTAI PLDNVELMEARRRGLPVVHRGEMLA WLMRRQKGI AVAGAHGKT
TTTSM TALVF EQNMDPTI I I GGELTDI GGN AKLGWGDY MVAE ADES DGS
FLKLD PFI EI I TN I EDDHLDYYKSVENI VAAFRRFMARVLEEGTAVVCLD
DPGI REI LKEYHGPRLTYALERPEADYTMQNLHLNGQVTAGEVYYKDEYL
GRLELNPGRHNL SNALAVVAAGRFSGI PFEGI AAALKKFRGAGRRFOLT
GEVGGI KVI DDYAHHPSEI KATLRAARQVKTRGVVSVFQPHRYTRTSI LG
ERFGEAFSDADVI I VSDI YSAGERPI EGVSARTI VSAI EKHEGRDVI YLP
TRQEI VDYLVRTASPGDI I LTMGAGDI WQTGVELVNKLKECRDVG

>2617920639 Ga0073689_11054 UDP-N-acetyl muramate dehydrogenase [pelotomaculum Ga0073689 : Ga0073689_110]
MLAESAWCELSRLLPGQVRAGEPMSSHTSWRI GGPADVFDVPADI EDLRL

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TVYYAYRQGI PLTVI GAGTNLLVSEEGI RGI VVKVGHGLGRI STVGNEI V
AGGGAKLAGVAVTARDTGLGGVEFSAGI PGTVGGA VI MNAGANGSSI STL
VREVTLLDFTGVFSRKSKEEMHFGYRTSI LQREPAI VVEVCF SCHPRNKK
AI REEMEKYI ARRLTQPLGLPSAGSVFKNPPGDSAGRLI EAAGLKGLRF
GDAQVSGVHANFI VNLGAASARDVLALI DRVREAVYGRFGVELQLEVKVV
GGG

>2617920638 Ga0073689_11053 UDP-N-acetylglucosamine 1-carboxyvinyl transferase
[pelotomaculum Ga0073689 : Ga0073689_110]

VKR FMI VGGNRLTGTI RASGSKNATLPVLAATI LNAGRSVI REAPNLRDV
TVMKDVLA YLGARI TCERNI I EVDTSRVRPLEI SEDLMRRMRASNLVLGS
LLGRFGKVRI SYPGGCQI GSRPMNLHLKGLQALGAGVQEKFGYI TAEAGK
LVGADI HLDLP SVGATENLMMAAVLAEGFTTI RNAAKEPEI VDLQNFLNS
MGARVKGAGTDTVKI EGVPPGSLKAAVHTVI PDRI EAGTHMVASAI TGGE
VTVTNVI PEHMEPLLAKLREAGVLI I VGDDWVKVRGPGR I RAVDI KTMPY
PGFPTDMQPMALLSLAEGTSVI SETI FENRFKHVGELRRMGADI KVEG
QSAI I KGVARLSGAHVEASDLRAGAALVLAALAAENGTVLENVEHI DRGY
ERLELKYNALGASI MRVHD

>2617920637 Ga0073689_11052 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_110]

MAFGAGGAAGGAAGGAVGGVGPFLGGFGSWAFI LFLI LI LLVFGI GFL
FV

>2617920636 Ga0073689_11051 cell division protein FtsQ [pelotomaculum Ga0073689
: Ga0073689_110]

MESI SFVLLI LI AGYI LLRSPVFEVHSLVRGNQFLSEDTI RSVADI SAG
ANI FKLDLAAPAVNLKMI PMI KEARI TRSLPATVVI TVKERRPLALLPDG
EGFVEVDAEGVYLQKAGVGPGLPVI TGVQGD I PGPGQVI RAERLGDALA
VI NGLPGEVVAAGLSEVHVGGDGRVWLYTLDRI QCRFGLPAEI REKGAVLS
QLLVELRRQEARVEYI DLSSAGQPVVRYKNR

>2617920635 Ga0073689_11050 Uncharacterized conserved protein YI xW, UPF0749
family [pelotomaculum Ga0073689 : Ga0073689_110]

LRGFQWAFVAVGLVLGVM LAVQFRVTRDI QSTEPVQRAQQLSI QVAQLKK
DRDSLQTVQDDLRSLDKVSTGPRAAGLKEELDLARVEAGVTELTGPGVE
VTLNDS DI SPKPSQDPNLYVLHDEDVLRVLNEVRAAGAEAI AINGQRLLA
TTEVRCTGPTI VLNKNKRLAPPYVI TAI GNPDTLENSLKMGGVAETLQF
WGI QVTVKKLPQI TVPAYSGGI KFEYGKAAA

>2617920634 Ga0073689_11049 Uncharacterized conserved protein YI xW, UPF0749
family [pelotomaculum Ga0073689 : Ga0073689_110]

VNKSI YI SI I LVAMVLGLMI AFQFRTTSSI DRGVPYDRVQELAI EKKQVE
RDI NHLQDEVADLTAKLEEAGKGHAEATGALESELAKI KLYAGLI TVEGP
GI EVSLDNPSGLAMGPGGASSLYLI KDDDLLKVI NDLRGAGAEAMAI NGO
RI MATSEI RLAGSHI NVNLTRLSPPYKVVAI GNPDAKSSLEI KGGLVEY
LNDLGI AVEVRTKDSVRAPAYNGALRF EYAKTVQK

>2617920633 Sbp Small basic protein [pelotomaculum Ga0073689 : Ga0073689_110]

LGLWLALFGLAAGVLI GLNI PLALPHAYAKYMSVAALAAALDSVFGGI RAA
MEEHFDDTI FI SGFFSNALLAAGLAFI GEKLG I DLYLA AVVAFGVRLFQNI
LAI I RRHLLKK

>2617920632 Ga0073689_11047 cell division protein FtsA [pelotomaculum Ga0073689
: Ga0073689_110]

VAKGRPFTLVGLDI GTSKTAVI I AEAGGGAPKPVGAGVSPGLGVQNGVVT
CPGATARS I RQALEQAGKTSEVEVAAYTYNGVGI AVRDCMSSRLGGV
SHRGGNGRGAGCTGAETAGI PENEKVLQLI PSRI I HERSGCCPGSGGRAI
TAPAGDLANI VESARLAGLAI QEI I YGPLACAQALLTPAERELGTLLVDI
GAGTSAVSFFYRGI RETAI LPVGGEHLAGDLAI GLRI SLALAVSVLKDY
SSMTEAGETGKLT I PAGQEGEEYNQVSLSLI REI VNARI TEI LDLI ALAV
KNFDYPVRPPGGVVFSGGSRLAGLVHLAGSRLQMPVRI AFPEI TGPDLN
PACVNALGLVKYGFTRLSDGWNGI SRGEQFASRFLNWLQDKMKSDSSHL
GC

>2617920631 FtsZ cell division protein FtsZ [pelotomaculum Ga0073689 :
Ga0073689_110]

MLDFELDLQDFANI KVI GVGGGGNNAVNRMI HAGLRGVEFI AVNTDAQAL
YLAQANHKI QI GVKLTKGLGSGGNPEI GQKAAEESRDEI I QALKGSDMVF

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VTAGMGGGTGTGATPI VAEVAKELGALT VGVVTKPFTFEGRKRASQADAG
I EDLKNKVDTLI TI PNDRLLQVI DKHTSI VEA FRI ADDVLRQGVQGI SDL
I AVPGLI NLDFAVDKTI MKETGSALMGI GSAGGDNRAADAARTAI SSPLL
ETSVEGARGVLLNI TGGASLGLFEVNEAAEI I AQAADPEANI I FGAVI DE
SMEEVVRVTI ATGFDQRSHKKERP KAELEI KPFSQHEDLDI PAFLRRR

>2617920630 Ga0073689_11045 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_110]

LDNWSKENLESLI DAVGKFDLI SQCPSGAGNVP GGTKMSDVPKEKADEFW
QQESVPFHSGSFVLEAVKGGHNPPI SI YETI KDATHKRRKLD

>2617920629 Ga0073689_11044 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_110]

MVRRKKDTRKAGTKGNRKEDLNRI RSARRVI DPERGPENK

>2617920628 Ga0073689_11043 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_110]

MFFSFFKTGREFFKKLKKQFAELAF TI QVLQSQLEQMRQESREYI NI KNVY
VEGI NVDRLEFSNNFGAMGVRELGGTLNI GVNYLDERI RSGQKKTTPPRE
GRVTGEPTI KQQPSPGGRTGGSRRQENQAKSFSNKI RAEKNHPDDL DNS
PDDGKEVSADKKHLKHKDSNKTI KSPKKGVLAVCNFFYGEHPSWQE

>2617920627 Ga0073689_11042 HSP20 family protein [pelotomaculum Ga0073689 : Ga0073689_110]

MFDPEKI LKWKMAQKNPAQDFWTKVFDSPQNTSLLEQI SNMI TPRKTFP
YTDI YQTGQEI VVLI DLPGI KKQDI QI QI ANDRLLI KGVAPESHYSSGLV
SSERFTGKFERTI NLP EMI AKTGYKASLRDGLLEI RLPRGYEATVRTI PI
DKDE

>2617920626 Ga0073689_11041 Spore germination protein gerPA/gerPF [pelotomaculum Ga0073689 : Ga0073689_110]

MYPVVI NI FLLKVNVI QSSSAMNI GQNYMADWNSFLKTNNGTGSQYGDQS
CMDAGDI LFDDSDLI DMP SLKETFP RKG PALCDEKI MR

>2617920625 Ga0073689_11040 Spore germination protein gerPA/gerPF [pelotomaculum Ga0073689 : Ga0073689_110]

MPVLFSPSFSSVLGFKVNTMDHNSSI NFGPTCLI DLTTFSKASTGSGSSF
GDFAFEPEGFSLVI DPDVI DTPESKAGTI L

>2617920624 Ga0073689_11039 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_110]

MFYPYTKI KGC I I RQLI ASVLLI LQWSTEQSNNNALALL

>2617920623 Ga0073689_11038 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_110]

LPSSFDLGSLMELI I AQLGHDKQKSDEDI SI NSSGRGDNKI NKVKKPALS
POKVLVI LGLLGGVLEVDSI LVDRDQI I QI RLNGSLRRKTRLDKMLDEI G
DMPFDDVLKSI LRRG

>2617920622 Ga0073689_11037 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_110]

MPAI SGAPTRDEI QHDL L LVI STALFI LLATGLAGPPRVEVPPTFP

>2617920621 Ga0073689_11036 stage II sporulation protein GA (sporulation sigma-E factor processing peptidase) [pelotomaculum Ga0073689 : Ga0073689_110]

MATYTVYLDQAFFGNMVMNYAI LWAAAKLSRTAACKWRLVAGAALGACYA
LTLFI PGDQFLFSI WFKTI ASVVI TAVAFVPLPSGKFLACLGC FYLTSFT
LGGLI FGM I FFI QSGRLAGYNGVG VVVAEYFWPGLFWGLAAFWAAGRGVA
ALLKKGSWENLFKMDLVVKWNGAQVRTGAI LDSGNHLKDPMTQNPVVVME
YPALKSLLPAQVQVHFERVGE PDVWGI LSSLAESGI APRFSAVPFQSLGR
ANGLLLGFRPDEAVVERTGRQTRLDKVVI AI YHKKLDPAGSYQALLGHGL
MERL

>2617920620 FliA RNA polymerase, sigma 29 subunit, SigE [pelotomaculum Ga0073689 : Ga0073689_110]

LALGI FRQTRWI VRLAALRLLI RLGYRPRVYYYGSSEALPPPLTTDEESF
LI NRLESGDGA VRSVLI ERNLR LVVYI ARKFENTGVGI EDL VSI GTI GLI
KAVNTFDPAKKI KLATYASRCI ENEI LMYLRRNNKTRAEVSFDEPLNI DW
DGNELLLSDVLGTENDI I YKYI EDEVDKLLHLALQKLSGRERKI MELRF

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GLNNGVEKTQKEVADLLGI SQSYI SRLEKRI I KRLKKEI HRME

>2617920619 FliA RNA polymerase, sigma subunit, RpsG/SigG [pelotomaculum Ga0073689 : Ga0073689_110]

MLVKNKVEI CGVNTSKLPVLTGSQMRTLFEAMHKGDASARTQLI NGNLRLLV
LSVI QRFTNRGEYVDDL FQVGC I GLMKAI DNFDLSQNVKFSTYAVPMI I G
EI RRYLRDNNPI RVSRLRDVAYKALQVRDALVNKHSREPSI NEI ASELK
VPREEI VFALDAI QEPI SLFEPI YHDGGDPI FVMDQI SDEKNQDQNWLEG
I TIRDALRKLSDREKLI LTLRFYEGKTQMEVAEEI GI SQAQVSRLEKAAL
NHMRKYV

>2617920618 Ga0073689_11033 sporulation protein, YlmC/YmxH family [pelotomaculum Ga0073689 : Ga0073689_110]

MVKI SDLRAREI I NMVDGRRLLGLI KDI EI DLEEGKI TAI I LPGAGGGRFL
GI LGKEEEI VVPWDKI RKI GTDVI LVEVNNFTDPRHEFKI KY

>2617920617 Ga0073689_11032 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_110]

MSSNGQARSRI NYTTAGAAFTI ATTDFFPNYSTAI TFWPRRRKYHSSR
GFREPTYFMSNSSI KALLPALVKI TTRTSLRRI

>2617920616 Ga0073689_11031 electron transfer flavoprotein beta subunit [pelotomaculum Ga0073689 : Ga0073689_110]

MKI VVC I KQTFDTEAKI TI NADGKI NDQGVSLI I NPYDEFVVEALRLQE
KHGGEVTVVSVGGDKAQDALRQALAMGADKAVLVTTELEAVDEYTTAAI L
AKAI AGMEYDLI LGGFRAVDDGSAQVAGRVAEI LGLPVVNMVTKLEVADG
KALATREI EGGSEVLEVS LPPVVI TAQKGLNEPRYPSMKGI MKAKKKPMDK
KDLTGLELDAAVA AAKVKALSYFLPAPRAAGKI I PGEPAAVAVALACALR
EEAKI I

>2617920615 Ga0073689_11030 electron transfer flavoprotein alpha subunit apoprotein [pelotomaculum Ga0073689 : Ga0073689_110]

MAI WI YAEHKNQQLKKVLTLELLSAGRKLADQLNDELA AVLI GKDVAVLAG
ALGEYDADKVYLAEDDALKNYTTDGYTNVLAALAEYQPAI LLGCTVQG
RDAAQVAQRLHTGLCTDCTGLELEDGQLVFI RPI YAGKAFVKAVI PEAR
PSMATVRPNALGVTEPQAGRSAAVI KVAAQPGDI RQVI KDI VSQI STRPE
LTEADI I VSGGRGMKEPENFKI LEGLADMLGA AVGASRAAVDAGWVPHSF
QVGQTGKTVSPVLYI ACGI SGA I QHLAGMGSSKCI VAVNKDPEANI FKVA
DYGI VGDLFVVPPLL TEEFFKKI LEK

>2617920614 Ga0073689_11029 putrescine aminotransferase [pelotomaculum Ga0073689 : Ga0073689_110]

LKDKKNSGNRGRKPDGFLSLTEALDQKREQI VENHKAYLNAGLAKMMGF
KFDKRYTRAEGVTVDWSEGNQYLDLFGAYGALNLGHNHPKVLAALDRKKG
LPNLLQASLGTLAGALAKNLA AVTPGGLRRSFFCNSGAEAVEGALKLARA
ATGRQRLVYCEDSFHGKTFGALSI TGREKYQKTFRPLLP GCVSI PYGNMD
ALESSLRGKTTAAFI VEPI QGEGGI I VPPADYLAGARQI CSRYDALLI VD
EI QTGLGRTGEMFACQHEGI TPD I MCLAKSLGGGVI PAGAYI ATEEVWEK
AYGSMRALLHTSTFGGNTLAAAAAI ATLEVI YEENLPERARESGNYLLA
GLNRLKEKYPLLKEVRGRGLMVG I ELNQPGGLAAKASFGLVSKLSEEYLG
SMI AGELLNKYRI I TAYTLNPNVI RLEPPLNVTRDQI DTLRLALGDI LA
TNKSFFSFATSGAKTMI TSLI KK

>2617920613 Ga0073689_11028 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_110]

LEKLFRI NNLYDFYGRLLTDHQKRFVELYYQDLSLGEI AENYNVSRQAV
YDTLKRAEQLLFGYEDKLGVLAKFDTEKSKLAAAVNLLDEYMAAPDGAKL
I EARKLLSDI LDMSG

>2617920612 Ga0073689_11027 signal recognition particle subunit FFH/SRP54 (srp54) [pelotomaculum Ga0073689 : Ga0073689_110]

MFASLAERLOETFKKLRGKGRLTESDVNEALREVRLALLEADVNFKVVKD
FI ARVRERAVGQELLGSLNPAQHVI KI VHEELTGMMGGSNSKI SLASKPP
TVVMMVGLNGAGKTTTS AKLANHLRKQGRRPLLVAADVYRPAI KQLQVL
GAQLDI PVFTMGNKQDPVSI GLAAVENAVKSGRDVVI I DTAGRQEVNEEL
MAELEAMNGAI KPHEI LLVVDAMTGQAAVNVAETFNSRLELDGVVLT KLD
GDTRGGAALS VRAVTGKPI KFAGVGEKMDALEPFHPERMADRI LMGMDML
TLI EKAQENFNAEQMAKMKKI RSMEFTLDDFLDQLSQVKKLGPI DHVVS
MI PGLGGAKKLKDLQVDEKELVYVEAI I HSMTPEERRDPERVLNGSRKKR

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I ARSGTSTVQEVNRLKQFEQTRKMMKQFMDMEKTMKKGGRMPKLPFFG

>2617920611 rpsP small subunit ribosomal protein S16 [pelotomaculum Ga0073689 : Ga0073689_110]

VAVKI RLRRMGAKKAPFYRI VVADSRSPRDGRFI EEI GYYDPLKNPAVI K
VNEEKALDWLKKGAQLSDTARALFNKAGVLKKTAGEGQVD

>2617920610 Ga0073689_11025 RNA-binding protein (KH domain) [pelotomaculum Ga0073689 : Ga0073689_110]

MKELVEI LAKALVDQPEKVLVDLVEKDKSLVI ELKVAPEDMGKVI GRQGR
IAKAI RTVVKAAATRQKKKVMVEI V

>2617920609 Ga0073689_11024 YlqD protein [pelotomaculum Ga0073689 : Ga0073689_110]

MESVTLI RPVLVKVKVTEEYKAAAAELQEAVRRI EELQLHLDQFQEKRLI
SELDKKNPQGI PAARQHLQEERKRAEGRRKLI DQLKEVGQLALGSEVVY
GKMESPVVELKVGDDWRKVLGVEI I LQDGI VKAI RQGGGTE

>2617920608 Ga0073689_11023 16S rRNA processing protein Rimm [pelotomaculum Ga0073689 : Ga0073689_110]

MTEEYI GI GKI LKAQGHGAVRVLP LTHDHPERFKMRRVRVSLKGTGRDF
SIEEACPHKNFYI VKFKEVADMNAAEELRGGVLEVARDELYPLPEGSYYI
FDI VGLKVFDTGGAFLEVTDLQGTANDVYVVDTEGKPLLI PALRRVVR
EIDLPGROMVVELPEGLVDL

>2617920607 Ga0073689_11022 tRNA (guanine37-N1)-methyl transferase [pelotomaculum Ga0073689 : Ga0073689_110]

MKFHI LTLFPEMFDGTFSSSI LKRAREHGLI EINLVNI RDFSTNKHHTVD
DAPYGGGAGMVMGPEALFGAVKHVARETGTAARRVI LMCPOGRPFSQLLA
GALAREKNLVLI CGHYEGVDERVRETLVTDEI SI GDYVLTGGELPAMVVV
DAVARLVPGLGEAASAEESFCGGLLEYPHYTRPREYRGHEVPEI LLSG
HHEEI RKWRRRQSLRLTLERRPELLKGAELTGEDKEI LKKVLADLEELD
TGDSIS

>2617920606 rplS LSU ribosomal protein L19P [pelotomaculum Ga0073689 : Ga0073689_110]

MNLI HSLEQEQVKKDI VDFKPGDTRVHVHVVEGSRERI QVFEGAVI RRR
GGGLSETFTVRRVSYGVGVERTFPLHSPKI DRI EVMRRGRVRRARLYLR
GLRGKAARI QDKR

>2617920605 Ga0073689_11020 signal peptidase I [pelotomaculum Ga0073689 : Ga0073689_110]

VEQEQQKGVSLKAGKRSI FSEVFESVAI AVLLAVLI RLFI LEPFYI PSGS
MEPTLKEHDR I VSKLNYRLQDPQRGDI VVFKYPRDPKRNFKRLI AVGG
ETVAI KNSRLYI NGQQVSENYLPRGLRFADYGPVQVPRGSYFMMGDNRNN
SDDSRVWGFLENLI VGKAI VI YWPPDRI GFAY

>2617920604 Ga0073689_11019 ribosome biogenesis GTPase A [pelotomaculum Ga0073689 : Ga0073689_110]

MDI QWYPGHMAKAKRLVMENLRVLDVMI EVLDARI PAASRNPDLDGLAAG
KPRLVVLNKSADLPVLRWRSYFAGTGCPAVAVDSVSGKI REI PSLV
QRLAAPKMASLVAAGRRPRAARCMVLGI PNVGKSFFI NRLVGRRVTRTED
RPGVTKGQQWI RVAGNLDLMDNPGI LWSKLDDPEVSFRLAVTGAI KEEVL
DLEAI AGRLLTWLRENHLLVI RERYRLTDLPEPERLLEAI GAKRGFVLP
GGTVDTLKAAQNVLKEFREGKLGRTFDEPGKD

>2617920603 Ga0073689_11018 septum site-determining protein MinC [pelotomaculum Ga0073689 : Ga0073689_110]

LAYSKGDI RGD LSGFGQGVSGQEDLVDEDTI LVQRTLRSQGSI RYDGN
VVVMGDI NPGAEEVATGNVI VMGALRGVVHAGAGGNENAVVMAFRLQPTQ
LRI ANHI TRPPDNEPPESDHPEMARI VNGVVTI EAI LTGGER

>2617920602 MinD septum site-determining protein MinD [pelotomaculum Ga0073689 : Ga0073689_110]

MGEVI VVTSGKGGVGKTTTTANI GTGLASMGYKVVLDADI GLRNLDVVL
GLENRI VYDI VDI TGGNCRRLQALI KDKRLEGLHLLPAAQTKDKTAVSPE
QMRELCAELKKEFDYTI DCPAGI EQGFRNAI AGAEKAI VTTTPEVSAVR
DADRI I GLLEAADLREPCLI I NRI RPRMVROGDMMSI EDI DI LAI DLLG
VI PEDEMI VI TTNRGEPVVLDQGSRSQAYRNI SRRI LGEDVPMNLEEE

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GGFFKKLRKI I GLK

>2617920601 Ga0073689_11016 cell division topological specificity factor
[pelotomaculum Ga0073689 : Ga0073689_110]
MLDFLTKLFGKDNQSKNLAKERLRLVLVHDRTSVSPQVMETLKNDLI QVI
SKYMDI DETALEVNLDSSGNTVALVANI PVKGMKRVAGTA

>2617920599 Ga0073689_11014 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_110]
VNKRDVFFI VSLACLGIFILLGAYLWKDNYVNAKTADSNQESYSGQVEGQ
RNEEKSAGAARTGQTEPAGSVPAAKNLGPAATAGKGQNQPANPDSVPNPS
SNPSLSAAAKI NSI LTSESKVGDI KLGDVEMI I TKSTS RHKI I DI TLKG
NTPQPPKLI MAKNNRI I YEI PANVDVNVNVTEKTVI DRSPLSYGGKEKPG
KS

>2617920598 Ga0073689_11013 N-acetylglucosamine-6-phosphate deacetylase
[pelotomaculum Ga0073689 : Ga0073689_110]
VVVYLASCGI I PSLGHSGATFEEAREAFRHGLRHVTHFFNAMLPLHHREP
GPAGLALTEQGMSLDVI ADGLHVHPALLKI LWQLKGCSLTLVTDAMAAVG
MPDGEYLFAGQTVVVKNGRVTLSGGKLVGSGLTI AGAVRNMVRLAGLEI P
QAI RLTSLNPARI LGLPDKGRVAECCNADLVLFNRELEPQLVLVGGEI FY
AEKE

>2617920597 Ga0073689_11012 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_110]
VNHEESVFCGI SSAKKQASQGGEAI KGSVNLAGRTVSYTVRRS GRAKKLR
LOVGLETGLEVI APEKFNLNALEDI LRNKQNW I DKLDHFARLVENRLFH
LRQDGWRVPYRGREFEVATAVI PGAARRVAVEEGRLVMMVPEGAEREAGA
VLEQWFRSMARLLI HQRLRVVNEKLNLSFNRFVI RDQKTRWGSCSQQGNL
NFWRLVMAPPSVI DYI VI HELLHLVEPNHSKRFWTLVEEI CPDYKAHRA
WLRKNGGRLKL

>2617920596 Ga0073689_11011 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_110]
MSI PASNLKKEVAYPAASKMETVTRVREKESYMI HLTKRLL ENYRALFEM
AEYTK

>2617920595 Ga0073689_11010 Transposase [pelotomaculum Ga0073689 :
Ga0073689_110]
MEI LYSHCCGLDVQKKTITACI I TPKGKELKTFGTMTNDFNLADWI KAN
GCTHVAMESTGVYWKPI YNI LEQYDLKEVLVGRHQRMLI STQLKRI DFLD
QEI ARLDQEI EEQMRPFQE I ALLDAI PGI GVRSAQVVLACI GTDI SRFP
SV

>2617920594 Ga0073689_1109 desulfoferrodoxin FeS4 iron-binding domain-containing
protein [pelotomaculum Ga0073689 : Ga0073689_110]
MATKVGEI YLCKI CGNKVLVKESGKGALVCCGQPMKSVG

>2617920593 Ga0073689_1108 Signal transduction histidine kinase [pelotomaculum
Ga0073689 : Ga0073689_110]
LRADLLSMGRLLI GNGVPAKFFI RLALLLLLFLLAGQLYLVI DEEVYPGV
HLVMEFASVVVAI CASLMSWYDYRYKRELRMLLFSLTFCTVGLLDFAHVM
SYLGMLDFI TPNSANKASTYWI I SRFLQGTGI LAAVI SGNLVKRI TRPAM
LLVFASLGI I ALI VAVAFFLPALPAMYNPAAQSQTALKI YLEYLI I ALMG
LSLAALLLSKKMERRDYLLGLALAVGI LSEAAFTLYSSAYDI YI FLGHVY
KLLSFAFI FKALLDEAVVALFETNRALERQREI LAETNRQLQEADRLKDD
FLANTNHELRTPLTAVI AFTELLDDSTGKLNELORDYLNEI NDSGKELL
GRI NGFLNLSKI AAGKTVLYREVFEVDG FVADMARPMCP LFDNKGVTLOI
SKRRDGRPMWADREKAGQVLTNLLSNALKFTPPGGRVAVECGVCKTGREV
YI AVKDTGI GIDPADREKI FQPFQQVDGTRVRRYGGTGI GLTLAKKLVEL
HGGDI KVDSEPGKGSVFSFTMPAEDKAEPGKLLGEPA

>2617920592 Ga0073689_1107 DNA-binding response regulator, OmpR family, contains
REC and winged-helix (wHTH) domain [pelotomaculum Ga0073689 : Ga0073689_110]
MERVGRTVPYRI LAVDDDPKILKI LQHALSREGFEVVTAAASGEEALEKAG
QYPPDLVVLDI MMPGMDGFETFQRLKARREMPVI I LSARTDEMDRVVGFR
MGVDDYQTKPFSPTELARVKAVLRRVGGQKAAEQMLSYGPLTLDYGKR
AVLLDNRKVELTPKEFELLWMASNPNRVFTKAHLLDKVWDSSSFYGGDNT
VTVHI RRLREKI ERDPSKPKYI KTVWGTGYKFEHEG

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>2617920591 Ga0073689_1106 superoxide dismutase, Fe-Mn family [pelotomaculum Ga0073689 : Ga0073689_110]
MRDSAGPGKSAGFSREHLEEHYRLYPAAHLAKI KEI EARLI RTDKAGADP
TYSPLRLSLKKEHAYALNSVRLHKYFFGNI GGDGSQSPSEMVSMLERDFGS
VEEWEQFSALAMCSRGVVWVLFGLKDGVLNFFTDHSEGVWSVLPMLV
LDVYEHAYCTVFPFRRAYVESFFRFI DWDSVNRRLKI AREVFKGLNAGF

>2617920590 Ga0073689_1105 Rubredoxin [pelotomaculum Ga0073689 : Ga0073689_110]
MDKWCAVCGYVYDPTTEGAEGAPPOTPFEELPEDWI CPVCGVGKDQFEKE

>2617920589 Ga0073689_1104 superoxide dismutase, Fe-Mn family [pelotomaculum Ga0073689 : Ga0073689_110]
MPKHELPELPHYAYNALEPHYDEQTVRLHHDAAHKAYVDGLNNAEAKLAE
REKGFALVKHWERELAFQSGHLLHTLFDWNI KPGGGPATGKVAEWI D
REFGGFEVFKQFSAAAVAVEGSGWALLCWNPAFKKLEI LTAEKHQNLTQ
WGVIPLLVVDI WEHAYYLKYQNKRAAFVEAWWNLVNWDDVNSRFASATT

>2617920588 Ga0073689_1103 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_110]
VTSI LPENMTAENKSANYVANFFKEHKI GRI HSVNHVKTFVPPGKNSI KT
GIINYYLWLSNGNLFII EILIN

>2617920587 Ga0073689_1102 DDE superfamiliy endonuclease [pelotomaculum Ga0073689 : Ga0073689_110]
MITIGQTLKQSNFFKQKGFPCDLLKFLVTLVFMGKNLWRYLDTDAGNAP
FOKDAVYRFLNNCYYNWRKLLLLSSQII QNRI VPLTDKKRVNVFI I DDS
LFSRSRSKAVELLARVHDHVEHKYVRGFRMLTLGWSGNTFLPLAFSLLS
SEKESNRLOGMAMDKRTNGYQRRKEAI RKSTEVLLDLLKQAKAYMPAS
YLLFDSWFSPGVI RKVSEQQQLHTI CMLKSVPTVKYEQYQ

>2617920586 Ga0073689_1101 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_110]
MPSGEPVQARI VFVRDRRAKKWLALLTADTELPDEEVI RI YGKRWN

>2617920585 Ga0073689_10986 Diadenosine tetraphosphate (Ap4A) hydrolase [pelotomaculum Ga0073689 : Ga0073689_109]
MRQI WAPWRTVYI GGDHDAKCI FCEKI ESDQDEANLVLLRGDKTFVLMN
LYPYNNGHLLI APKRHVGEI EELTEEEEMMELFKMTQRMVKKLRAFNPGEF
NVGVNI GRI AGAGVPGHFHI HVVPRWGGDTNFMVFGDVRI SESLEVTF
KS

>2617920584 Ga0073689_10985 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_109]
MLSCKTLVDLGGVTDVKKQCLVAETVNAFEDFANLDCVACGLQI LALNY
LMTTWRYKTRGRFRTKRTVPSSEEI VVWSSRKI IPI I STI SEI LRYFNYQG
ETATALTLVWQGCCEEGQKLLTLKVKKI F

>2617920579 Ga0073689_10980 Transposase DDE domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_109]
MMLFRNGQLFTAAREKVKDEAREKAASKRAAI EGTNSSLKRSQGAKKL
KVRSKVKATLVMGMKI I GHNFRQI VRFFNGKVVREEAAKF

>2617920578 Ga0073689_10979 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_109]
LRKSLI LDLDGTLLFAENHPGALVI KGRRRDSYLAGGTLERLRTLQKI YD
II LATGRSLQSAMS SSMLTDAGI HTGGMAVENGGVWVDREGKAQVLAGR
AWI KTTRRVLSTVTDI ARTEFVTCLALLSPSSAAAEYVLGAYTEAGLEFR
LLQDGNKLFVLGNI SKNSALTYGLGAERLRNAVAGAGNDTNDI DWLKTIA
CPACTGCSKGVEKKTVLERGGVVSRAEGHAGI QEI LDFSE

>2617920577 Ga0073689_10978 Phosphoribosyl transferase (PRTase) [pelotomaculum Ga0073689 : Ga0073689_109]
MLTAAGAERGAFFVRCMPGVRYLLSELAVVDPFAAPGLFRGEECFDGS
KGWRRWQRPSPPEKPDPLKTI VMQLMRERAGVLCALHDLLEKI LKTVP
ATOPV VFI SI LRAGVFVARGLSERMRHGYSEVPVTAALGLFHEAGFDRSA
FAAI LEDYPGYFPI FVDGWTGRGVVARELRKAYAEWKD SGKKGLPDSPL
LVSLVDPGRYGDLYGTDRTVPVCAHFTAPEVFGFSRAFI KNRI EMWSAY
TYSSKYYDQELVDTWLDVFATREPSI VPEADGRQELSALLEETARLTSTR

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PDQWKVNVNEVRSFVNRNPRELVLGVSEEESSRLLPDLVYLAGRTGTTV
RYLPDWGSRHNCLAAVRVK

>2617920576 Ga0073689_10977 Phosphoribosyl transferase [pelotomaculum Ga0073689 : Ga0073689_109]

LLVNDFOKSI VDEGFDGFDRI RHNNHLRKYAYVHRDLGKLGAVDPDDI I
RLAARMVNGALPFPKNPLVLGLSESSI LLGRVI CEFFGGGMFLFSTRYPHN
EVELVPFI EPHSHAPSQFLKLSGTGHC RDVCI VEDEVTTGNTI MNLVRL
AENMPVASI AVLALKVFCSGRRI AEMSLEADEMGI QLAHSMYHGMQDE
NAPAI HFVKSASARDGKVGPSVSPWEYGRGRI DPFSKEKAWFRYKRWSA
VLSRLSLPAAVTVI GASEAI DLAFEI TRVLAYRGHRTWLRHLTI SPWEVT
GWVFAPSTPGI RPLHL YQPPSKGGTYI VVYDHSFQEEQVKLSNCLKHVG
SKTHVLRGFEQC

>2617920575 Ga0073689_10976 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_109]

MSKARCVI ETLGLFVI SWVI EYLWL GAYGV LKGTTLSI MELSL SFDNAAL
NAI I LYTMSPKWRRRFI I WGI PI AVFGMRVFPALI VSVI SGINPI STIT
MAFSHSELYSFY LKQGEHMI KAFGGVFLMI I FVKWLYGNKENYWLTYI EK
PFTKI GNLSNPTGLTI LGIMFI I GAVQKDFVI VMASI AGFI VYEGI DSLK
ALLENNSVARKLOGDNNSNSLSDI GKFLYLEVL DSSLSFDGVI AAFAI SS
DI I LI VVGLGVGAFAI RTLTI FFVEQSTAELSYLENGAHWAI GFLGVYMM
ASLFVHI PDYI VSVVTMGVI VMAI LSSLNEAKKNKLGPPKTI S

>2617920574 Ga0073689_10975 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_109]

MCAI ALFENQNDETPGI RRLVQYFGGYRELDKEYGWNMRWAAGSK

>2617920573 Ga0073689_10974 tellurium resistance protein TerD [pelotomaculum Ga0073689 : Ga0073689_109]

MAVSLOKQGQKVDLT KGNPNI KKV MVGLGWD TNKYDGGKDFDL DAAAFLLG
ENGKVSNDADFI FYNNLKGAQGSVTHMGDNLTGEGEGDDEQVKVELDKVP
ASI HKI AFTVTI HD AEQRSONFGMVSNFI RVVNEETGQELLRYDLGEDF
SVETAVVVGEL YRHSGEWFNAI GSGFKGGLTALCRNFGVNV

>2617920572 Ga0073689_10973 TIGR00266 family protein [pelotomaculum Ga0073689 : Ga0073689_109]

MDYQI LYQDAFPVQARLAOGEVLKAEFDAMI SMSATVDVEGRLEGGLLG
GI GRI FAGEKFFFQTLTARRGPGEVLLAPATSGNI VDVELDGSYGLLVQK
DGFLTGTQGI EI SAKMQLMQGLFSGEGFFI LKVGKGTVFLNSYGA I HA
HNLNEGEEI I VDNHNLVAVPDYMKYSI EKSSGGWI SSFTSGEALVCRFSG
PGVVLI QTRNPKGFGHWLRQFLPQKS

>2617920571 Ga0073689_10972 tellurium resistance protein TerD [pelotomaculum Ga0073689 : Ga0073689_109]

MAI SLQKGQKVDLT KTNPGLTKVLVGLGWD TNKYDGGSDFDL DSAAFLLG
ENGKASGESDFVYNN TTGGDGSVVHLGDNRTGEGEGDDEQLTVDLGKVP
AGI FKVTFTVTI HDAESRKQNFQVSNFI RI VDESSGQELI RYDLGEDF
SI ETAVVI GEL YRHGSEWKFNAI GSGFQGGLAALC NNFGLSV

>2617920570 Ga0073689_10971 Stress response protein SCP2 [pelotomaculum Ga0073689 : Ga0073689_109]

LSVNLQKGQKVDLT KGNAGLGKI MVGLGWD PVKSGGGFLGGLGGGGGK
DI DCDASVI MLGADGKLSRKQNVVYFGNLSSPCHSVKHMGNLTGAGDGD
DEQVFVDL KMI PSDVHKL VVVNI YDCKARKQDFGQI QNAFI RVVDNAKN
QELLRFNL TENYAGRTALVVG EYRYNNEWKFAAI GEGTTDMSLSDLVRR
YQ

>2617920569 Ga0073689_10970 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_109]

MPENMGDARLDSI I RDALSNDYDKVTEEEI YRNLGVAI I SMGLEPETDAKS
SYFLKPLGNMNVKYAPFTSTSLI DTLSEI GADRAI KTAKVFWVFKEK
AAKRI CGDEGI KKLVEEAKLREALAVVATALLAAMGLPPVWI PVVAVI AV
GLLMLLLKAGI DVFCDWRGASD

>2617920568 Ga0073689_10969 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_109]

MKI KKWLA I SGAAALFGGM LLVGI PAAKALAAGGPPAGGQAGQAVRQGYG
MHMGRNFGSMAAPVAQFLGI DQTELVAARRSGKSMVQI ASEKGI SEQQLV

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DFVVGQRSAQI DQMVDAGKI TQAQADLHKQYMAEQVKTNLNRTDVGPKHT
NGMGKGFGGRGAGNGPGTGVCYPYGVAR

>2617920567 Ga0073689_10968 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_109]

MTDPKHKKVLFQKNNTPDKPWI KRTGI FLFVLSCTLYGGLLLVPFSPYTT
GVKAAI SSALI I SGEVSFWLGGLI LGKELLSKYRKHLNPFNWFEEKSD

>2617920566 Ga0073689_10967 Uncharacterized protein family (UPF0051) [pelotomaculum Ga0073689 : Ga0073689_109]

MLLDI ADSRLMETI CSI GGI PPGAHI RKNGLCI SRLSVPGEI RPKEQN
SGI DLI AAPGVKDRTVHI PVLVTATGMHDI VYNTFVI GEGADI VLVAGCG
VHNPGELDSCHDHGHEI QVKKNARLRYFEKHYEGSGPGARI LNPKTLL
LEEGAVAEMLLVQVKGVDSI RI TAATVHQNARLI MTERLLTHGAQSAES
TI TVRMAGRGASTKI SSRSVAQDESEI FRARLVAEPPSRGHVECDI IM
DRARI SSSPELSALHSGAELTHEAAI GKI AGDQLI KLMSLGLPEEEAREA
I LKGFLS

>2617920565 Ga0073689_10966 Iron-regulated ABC transporter ATPase subunit SufC [pelotomaculum Ga0073689 : Ga0073689_109]

LLVLKDVSLQFTDGAHVNVNLNKI NLVFRPGCFYAI TGPNASGKSSVAKV
I TGI YTPITSGAVTYKGLDI TNMTI SQRALGI AYAFQHPPRFKGI TVRDL
LRYSLDKDDEEAMLCALSSVGLCPELYLDRLVDSRLSGGEVKRI ELATVI
ARRADVTI YDEPEAGVDLWSDQLREVLHEFFLASRNI TI VI THSEKFLR
LANEVI VVAGGEVKSHGGYEDLKQYTFSGERCSNWKTCGGGADVAGYCR

>2617920564 Ga0073689_10965 Trypsin-like peptidase domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_109]

MAPDKDGPQREDLNTGGGSEYTAGGYLTEDFEETRARRPLLTRI VALAT
VLAFGLI AATSWPGHI LPMADLVEKSFQLKKDANTGLTQAGALI SVVSR
VPGSSVSVEQKTGTGFNVDPGGVI VTNNHHVVENALNVTI KFPDGVKYKAE
RWLSKPESDLAVI FLRAEGLPAATVNMAGPPAPGDKI RVAGNPSSLNNI V
VEGKVGRYLRI KDMQGI FSLDAPVYPGNSGSPVFDMSGRVVGGVFGVLA
GNEGSGDKAAGLAVTI DEAMGLAVSATE

>2617920563 Ga0073689_10964 Exodeoxyribonuclease I subunit D [pelotomaculum Ga0073689 : Ga0073689_109]

MRI LHTSDWHLGRI FHGVHLTSDQAHVLDQFVRLAVEEKPDPVLI AGDVY
DRSVPPVEAVKLLDETLSRI LLEANVPVLI AGNHDSPERLAFGAGLLAR
QGLHI AGRPEDGLAPLVI HDHSGPVYFCPLPYAEPVVRERLAAPDAADH
NRAMFSLVKHVTASI PRGVRTI ALAHAFVAGGAGSESERPLSVGGSGTVD
ASCFQPFQYAAAMGHLHQSQNTGGGNI HYAGSLLKYSFTEADHQKSVTLAD
MDGAGGI TMKNI PLSPRRDVRRLLEGI SEI LAGPRDGENREDYI MVTBKD
YGA I LDAAGKLREVPNVLHI ERPYLSGGGDVRGPGGDHRRLEI DLFSS
FFEQVTGVPLSDGQALVFNETVEALNRREREVFPL

>2617920562 Ga0073689_10963 exonuclease SbcC [pelotomaculum Ga0073689 : Ga0073689_109]

MKPLKLTMRAGFPYAGTOI LDFTELGGRSFFLI HGPTGSGKTTI LDAMCF
ALYGDITSGAERDQKMRSDHADRPVI TEI TDFFAVGDDQTYRI KRNPQER
PKRRGEGTTMGADATLWKRTGADEGEGETVLENGWRRVTEAVEKLLGF
KSSQFRQVVMPLPQGEFRKLLTAGSGERQVI LETLFRTEFYRRLEEALKEA
AKGI KNNFELAAAQKTWVLKEAGADSREELEERYRLHKKQAAEAAI RI EA
CENAYKEAQERLAAGRKAQDRLTEKKDAARVVADLDAKI PVMDTKRAELA
RARQASGLADAENI LKTRRREAAGAAGYHGEKLRLRETALAAKEEAAEKL
ASEKEREPEREAGREVRLGELTAKVAALAEARKEADAAQKGLLSAEGV
QSAHRALTGI QASLEEI SKAHLEAVSRAALAPALEAAFKEAGAI SGKRO
ELEEVVRGELLKI RKEFDTAGKTLRQAEVNYAGARQELLRLQEAWEYKGQAA
I LAGSLTAGAPCPVCGSPSHAPAAAAEAKLPSEQDI KAKQQETAAFEKLR
DSARDKQGA I ATQMAVI TGKTESI AKELGVNAGVDPVLRKAALKAGELW
KKAGEAMETASLLAKKLDDLKNEI NAGEQLEAANKAFLEAQAAREAA
VVKEREFSLPEDLRDPVSLQKAQKAAGEKREQLMSAYEQAAKNADEAVRV
FTKADTAVNEAFGVLLTAEKRVEDEERSFYLRLEAAGFKDQADFKAAVRT
REDI QLEKTVKEFDESRAAGDRLELAVRAAEGLEPDMGKLI LVVNEA
ENMWKQALSQGTQLSLTGRESGWLNNLMEI EGALKDLEGRYEVLGRI SE
VANGKNKYGMTFORFVMGALLDDVTI AATGRLKLMSRGYHLQRTLDRAR
GNAAGGLELEVFDITYGAARSVSTLSGGETFLASLSLALGLADVQSYAG
GI RLDTI FVDEGFGTLDPESLDFALQALI DLQEGGRLVGI I SHVPELKER
I DARLEVRPTDRGSAASFRLS

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>2617920561 Ga0073689_10962 Glycosyl transferase involved in cell wall biosynthesis [pelotomaculum Ga0073689 : Ga0073689_109]
 LYQREI NPCFI SSYPKCEGI ATFTHNLFSTYQNLASAGKVAVDGLQL
 VDYPPPEVDYI FDKNKVTDYI SAAGYI NAADLOVVNLQHEFGLFGGPEGRH
 IARLLEELKKPVVTTVHTVLQEPSLGYTSLI EVI QRSQVVVMSDKAVE
 I LKEI YVPLEKI VMI PHGVPDLPFVETEFKKDLGLAGRFVLLSFGLLN
 PGKGI ETVLEALPEVVRDHPGLLYI VLGKTHPEVAKI HGEKYRESLQKLV
 YENKLENNVLF DKFVTNEELNYI SASDVYI TPYHSQEQI TSGTLAYAV
 ALGKVVI STPYWYAQEMLAENRGCLAPFNNSKALAGAMDKI LSNREDMWK
 MRRAAYKYGRSMI WPRVAGLYHDLFKEVYKEFSLEKLQKI SVVYKSI QDH
 LGRHNLYGMFKRLTDDTGI FQHTKYGI PCLKHGYSADDVGRALGI LMKTA
 SYDNEPGYYQLAKKYLAFVLYVQKEDGRFHNFFVGYDRRI LDEDGGDDTFG
 RVLMLGLSAAALSDPSVAVLSKEI FDRAI AGRRPGLPLSTYPKAMAYCI
 CGLSSYLKKHSGVSGAGELLRTGTDYLVLYRNNKRPGEWFEPSVTYAN
 AKLPYALMLAHGVLKDKSYLDTALATLNFLTISI QYNGAYFDI VGNKDWFT
 VGARRAVYDQQPI EI GCLVEAYCEALRQTHDKSYGDLANKAFGWFFGKNR
 HGVPVYNLKDDYPLDGLTETGVNANSAGESVLVFAQAI LSLKEI SVRCTL
 WRKMEPAKTQDLAI DW

>2617920560 Ga0073689_10961 molybdopterine-guanine dinucleotide biosynthesis protein A [pelotomaculum Ga0073689 : Ga0073689_109]
 MECSWGFSSCPCPLFTVGRGSTGVTDNKRKCSI NKEI I LMETLSAALVVG
 GKSHRMGYNKAFLLKI GQSNLVESI AARLKI SPFVFLVGNPEPYRSELE
 PVI ADVYKGCGLGGI HAALVTANTPYVFI TACDMPFLDVQLVAFMVGKV
 SGYDVVVPRI RGYSEQLYAI YGKNCLPAI ESQI CGQYKVAALFSTVRVN
 YLKQEEI EKLTVVEKTFNLVNTPKDMQRAI CLTKFQY

>2617920559 Ga0073689_10960 Repeat domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_109]
 LFRKVLVLMGFLVFSALLFFVYQKASRPVSLAGPGGAPGTVESGVALI RL
 EDVSPGTYDTADKLGLRAMADYLHKEGVPHVSVI PVYKDPANNVEI SI
 GDTGDPVRREFI ATI KYLRGKGGMI GLHGYTHQYLAQETGSGFEFMARG
 LPYAQPAYAEGRVKKALELMDRAGI PVDYWETPHYTASPEQYKVFSNYFG
 ILYEPNPWDALGNI SFRDSTGPDDRSVI FVPAPFLNVNGEQDVDR I LSR
 LDKKGPGLASFFHFPQEFRFMYKMKAPEGYEFYVHETESYLHRLVNGF
 KERGYRFVTYDMI GFLPAQRVENLSPTAGKVLLTGDFDGDGRWDL LAGD
 PAAGRWLVTSLI NRALPRNNPGVFSPAGEWLDNWGRGGGMNDFATGDFN
 GDGRSDLAYWDEKTGEI RVAPSDGNKFVPRLDAGGGFNPPGGVVEMLSGD
 FNGDGRDDLFRPLPGENKYYVMLGGESGFSPASLWLERWPGGGDLTAVAG
 DFNRDGKTDLALYDRVTGTVDVALSDGSRFAPFAEDRGRPWI KDFATGGG
 WRLLVGDFNGDGKDDLAAYDSAAGKWAFARSDGGEFSAEDRFSLTWGRAP
 GSRALAADFNGDGKSDLAVERRFAGGREPI DFAI SAQNYKEK

>2617920558 Ga0073689_10959 dTDP-4-amino-4,6-di deoxygalactose transaminase [pelotomaculum Ga0073689 : Ga0073689_109]
 LFQSSSTGSCSGGLPAARGRPVGD TYLPCASSWI DEEDI AAVERALRG
 GRLAGGPLVAEFEREFASYVGAGYAVAVSSGAAGPHI AAAAAGI AHREEV
 I TSP I APLAAACCALYOGAAVFADI DI HTYNMDPAEEVKI NPLTRAVV
 AVHFAGQPCDLDAI HLLAGKNGFTVI EDATRS LGAEYGGRRVGALSDLTV
 FSRHPQGPVTGEGGMVTTNSEELYGWLKLFRRNGI VTEPGMMTRYEGPW
 YFEMQELGFNYRMSDLQAALGLSQLKKADRFLKRREEI ASFYNEAFQGM
 TLNVPGLAGVRPAWQMYVLGLRLERLKADRLEI FNALRAENI GVEVHYP
 LLFRHPYFVWQGHKDI CTLEGLCPRAEDLYQTFI SLLVFPAMSDRDAED
 VVTAVKKVMAYYSL

>2617920557 Ga0073689_10958 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_109]
 LI I GVLTVELFLGEANSLKEKRRVLKSVI DRLRSRFNVSAEVDQDTWQ
 RSTVGVAFVSSERARVDQVLAADVRFI EAQGTVVI TNYHTELL

>2617920556 Ga0073689_10957 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_109]
 MGKFNPFKNKKPAPNKVKKSTSGELRMEKPVENWLEI RVNNI LLRI VRSS
 AAPPQNELSAFVPRVEMRFRRYENGRLVAEEVI FSGTLVLDTPRRNSDG

>2617920555 Ga0073689_10956 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_109]
 LRI YALGDI HLSFSRPVDPSPRWDEVTRTHKPMDI FGGEWHEHYRKI YDNWS

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RVVGGGDAVLMPGDFSWALKLEEARHDLAFLGLLPGLI VGVAGNH DYWWQ
SLARVRRALPLNM RVI QNDHLP LGEVAVCGSRGWACPGDEQFSEADLKI Y
RRELI RMENSLRGAGSKKI I VATHFMSVNSRHEKNEFI ELFQKYGVGT VV
YGH LHGAAAGLR LPDRAWGI DFHLVSADFLNFTP VLI METG

>2617920554 Ga0073689_10955 chemotaxis protein methyltransferase CheR
[pelotomaculum Ga0073689 : Ga0073689_109]
LNSYKENQLKRRLDNLMAKQKLNPGDYAGFFKLLSDDRGVYVNFDTLTI
NVSEFFRDKAMFN FLEEKVFPALLAQKSVLKVWSAACSSGAEPYSLAI I L
NELTSNRRHRI EASDI DRNI LEAATGGRYNPDQVRNVPASRLAKYFRREG
NLFYI NDSI KKMVKFRRHDL LLDPLGQGYDLI ACRNVTI YFTRDAQVKLN
I KFHRLNPGGVLFVGASEMI FNYRELGF EKMAPCFYR KMI GSGKGWEAV
GYNF

>2617920553 Ga0073689_10954 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_109]
MAGGKLF PVVRRNPLFASGKRQMLPHEQDRLCLSQT LKRPGVRI LAEEVG
GNRGRI MI PDSAGQVFSRTVGSPLK

>2617920552 Ga0073689_10953 flagellin C-terminal helical region [pelotomaculum
Ga0073689 : Ga0073689_109]
MRI NNNI AALYTYRRLSLNES AAGKSLGKLSSGLRI NKASDDAAGLAVSE
KMRAQI RGLNQAYRNAQDGI SLI QSAEGALGETHSI LQRMRELAI QAAND
TATTS DRQEMQKEI DQLAQOI TOI SNNT EFNTKKLLAGGFGRTQEVRFHT
GANQDQTVGLRI GAMDAKSLGVAVDLKTGTMG NATGI KLVEI DSGGAI ES
GKTYT VTAQKI NSGTI I NAGTGSARAAQNDLSTTGADHAFNTTFKAGDYY
I EAGSGSVSGVKYTI KNAQGT VVSVADNVATNATNTTFQLNGDPTTTLTV
KLDGSLSTESRTKVTVADGSHSGAAAGKADTPTLNTFTGDPLTVGDKFSL
VTTLGGNGYTKYTL YDKNGNVFGSTEVDTTATSVTLTGQDAYTGRSTKFN
I SNTSVNQAYELEVD TGGNTFKTAAAESQLNTGT VAVNGTVQSGDYFAHI
I SDPANAGMYKI ELYDSAGSLVGTKDNFSI QGDASVVTI QAGKTASDNI S
FTVDGGTSASTGTI TLDNAVYTN I TNNGAAADQI SI VFKNNSEFGADAGN
GYKVI I DSTGAGAAVI DRNAKTI TVKVANAATTADVKTALDAVTDQYGNK
VFTTTLAGQTDDTWGNAATAATFN MAGGQSI I NNAAKLTVAKSTVNSVGT
YTQPLD TTTATDYVTNVI TTSGDYFLQAAQNV DGTKVDLRLVDGGGNTVA
QALGLTG HDI YDAAYGNQVTFTKDGADMI KLKFTGGAFNATAPAGMTADT
AKI NTVNGGLSDK VVI TAKDGS AI EGSFGNGWGI TLVDNAANAGQYTI DW
NSKTVSLNI NAGTTT SANLETYI EAI KDGSNQOMFDVTLTGND DTTWNDGS
LGTLSGGKFELDALYAKVSLNDVKTNGEDTLT FSLKDAASGTELEKVEGI
KTAEGV VTFATKGVT LTRDTGVT DNVRATVAVATTESKAAGLSARDEVVE
SAVAAKGI LI DTQTRA EKAI TI I NEAI DSVATERSKL GALQNRLEYTMNS
LDSTSENLT TAESNI RDVDMAKEMMEFTKNNI LTQAAQAMLAQANQQPQQ
VLQLLR

>2617920551 Ga0073689_10952 lysisine-N-methylase [pelotomaculum Ga0073689 :
Ga0073689_109]
LPGNHFLLPDYVDFQCRCTECCRW SI I FDWQSVKKYEQLAAQDQELA
ALLRERLKRDKSGRATVRLQNRVKRSPADPAGEI KEETEA AAVCPFLDQDG
LCLI QKKHGV EALSDTCKI FPRNI YLTERGWELSLTYACPQAAESLKNKT
PVEFYQDPAGDFDPALHGQY GKI GNLLERKKAGKTNYFEVEELLI DI MQF
REMDI DARLI LTGLI VNRLKDGDFPGI RRYLTSLDAGI I GQMOSMPGQPV
FMMKMVKEAVDRRLVARVAEKAMGRLLI MAYNELKLLDREVI SAEKAQRL
LEGYMKYYLPHTGAI SHVYENYFVNFI FSKKFFTHKYI DAYFLMVFFYI L
NRFFSI CACMAEGRHVEEDLLVNI SAVERSI GHNQAYYESI LHLVKKGD
YHRLPYVVS LI NLGCQPAAAVVRAGSG

>2617920550 Ga0073689_10951 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_109]
MVGQI KLV LGVLTASVEAGERSAALQAVAQFAVL FDEFLHRNNQYI FAHE
AASLNNCLKEMLAAVESNDFHGLTG LI RSTFLNFLDEWDFENKPLH

>2617920549 Ga0073689_10950 flagellar hook-associated protein 2 [pelotomaculum
Ga0073689 : Ga0073689_109]
MNSI YSNLRI GGLASGI DTDSMVKDLMAKRI PVDK LKQDQOI LKQQED
YREI NKTLRGFRDKVFNMKLOSTYLAKTAASSNEAAVTATATGNATQGI Y
SVTVTQLANGVAKGSQAALAEETNADGTTRTL TGQFGLSGSI I FTLEGSK
GSAKAFADTSTATI NTVA AEI NAADLGI SAGYDSTLNRFFLSATTI GNTA
KI KVTDDTANFLSDAAGDGNNTLKL LLLKGDGTVYSGQDALFNFGDATGLT
STTNSPTVNGI SLNLKQGGGASATI TVNSNTDAVFNSI KEFI TSYNDTVA

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KINDKLAETRYRDYLPPLTGEQKDAMSEKEI EKWEFFARSGLLRNDSSLN
 AVEKMRVTLYGAI SGLAGFKNLAEI GI TSGTYAEKGKLYI DEAKLKDALP
 KDPEGVMGLFAKSADSYNEKGLAARLYDDVNNAMSSI SAQAGGSDSFSLA
 DNSI I GKRLTAI DKS I DTREERLKKI EDRYWKQFTAMEKAI SQMNAQSAW
 LSQQLGRS

>2617920548 Ga0073689_10949 flagellar protein Fl i S [pelotomaculum Ga0073689 : Ga0073689_109]

MSI PAPYQQVQQNAVLGAAPQLTLMLYNGAAKFI NLAVQAVDKRDI TGA
 HNAI VRAQDI I LHLMDTLNEEFVI SGNLAGLYDYMHRRLI EANA KKDPEI
 LREVKMAEELKDTWDKAVKLARS GPRG

>2617920547 Ga0073689_10948 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_109]

MRVLI PVEAGKI LAALPALAERKKALVEEI FNLTRDCLAALETALERGPE
 EAPGLNRLLEERRQI I KKVDEL DGI KDLHOTVARI RRNDQFPAGWPPEE
 QPQWRI LEQI RI DTRSLLLKI REMDTSI GEYLNQQKQTLASSFRNLQLSK
 QGARVYTQONI QI GGVFVDENK

>2617920546 Ga0073689_10947 flagellar protein Fl a G [pelotomaculum Ga0073689 : Ga0073689_109]

MKI GAGGLOSLAVQEVLPVKKI EPVQTQKQQENVRSEMVSHSRVDPEAL
 NKVVEKLNKTSELFNQLTFKVHEETKRLI VKVI DDRTGEVVKEI PPKEM
 LELEESI SEMI GMI LDKHV

>2617920545 Ga0073689_10946 flagellar hook-associated protein 3 Fl g L [pelotomaculum Ga0073689 : Ga0073689_109]

MRVTNSMVTAAFLNNLSRTYRELAKVNNQI SSGKKLERI SDDPAAVDRVM
 RLRTTI DKHENYLRDI DSQI GRLGGSDDALEKANELLQRVSEI AVKGSSG
 TYNLSDLKNMSFEI DK I I DDMVI AANTTPGAGRNAVFFTRDADGNVVVNP
 VASPGWAVDEAADGSI FTASLLTETVDPVGVFWGETGSDGVFAVLQNLRD
 SLAAGDTRGVNSAI TALA EKT D VVLQQRSAVGAKVNHLSLKDQLEEQL
 RLTEFAAGLEGTDI AEA AVELQQRQTAYEATLAAGVRLMRASLLDFLK

>2617920544 Ga0073689_10945 flagellar hook-associated protein 1 Fl g K [pelotomaculum Ga0073689 : Ga0073689_109]

MPGTFLGLEI ARRALQVNRQAMNI TGNNI ANANTPGYTRQEA VLSPLPY
 TDYSLCRQGGAAQWGAGVEI SEVRRVRDDHLDGQVRANLAEAGYWOARQD
 ALRRVEAVFPETSGNSLQNLMDKFFASWHDLSDQPESTAARANVRETADL
 LAGGI RFAYTQLVGI RRDQEQMLADGSAGKI RRI NELAGQVAELNKEI VR
 AERMGATPAGLMDKRNLPLEELAGLLNI DVI NKSGGAVTVNI EGRALVDG
 AGGTVNAI AVNDTGDGVVWRDDGAEI TAPGGSVGGLLAVRERI AGYLAAL
 DDLASNLAAKVNELNGTEFFKSGLTAAI GVSNEVRNDLGKI NGQKSLAI
 AGLREELTMAGGTATFESFYQGEVGEI ASAGRNAALNVEGRQAVQEQLE
 AHRQSVAGVSVDEELTRVI QYQYAYQASARMVTTYDQMLETLLNMLR

>2617920543 Ga0073689_10944 Fl g N protein [pelotomaculum Ga0073689 : Ga0073689_109]

MKSLFSELCRLLTEQREVI GOLLELARROSEALRRNDTASLAALAREMAG
 PAARLAENEQLRLAVQGRLLVLDLPEGAGLGELLRLSPDDI KELLA E V T
 PAI SDQLKNLVVNEI NRLLTRRAI NFNEKLLEVLNPGSGRTYRSTGEVR
 ENGGSVSLI NRTV

>2617920542 Ga0073689_10943 anti -sigma-28 factor, Fl g M family [pelotomaculum Ga0073689 : Ga0073689_109]

MKI GQYNGTGLI KAYETQLKNNRELKNDKPEAGKTLPGDALELSSGAREL
 QRYRSELARLPEVGEERVAALKRQI QEQNYRPDPEKI AAGMVRERLLDER
 V

>2617920541 Ga0073689_10942 chemotaxis protein MotB [pelotomaculum Ga0073689 : Ga0073689_109]

MKKNAHVEKENKERWLLTYADLI TLLMI FFVVMYALSNDVAQKFRAI AE
 TLNKALGGGGMALTNPGLNVVQPPSI SATPPI AANESQQL ENI VKELQD
 YLEKNGLSAQVTVVSEERGVVLSFMDPVLFPLGSAELTPTALPI I QRVGQ
 I LLQTSNYI RVEGHTDDLPI NNARYPSNWELSSARATRVVQELI REMGFP
 PRRLSATGYGEYRPRAPNDSEANRQLNRRVDI VVLR SKYQGS ESAPYMTA
 PEE

>2617920540 Ga0073689_10941 chemotaxis protein MotA [pelotomaculum Ga0073689 : Ga0073689_109]

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MDVTSI VGI I LGTVCLVTAFLVLEGGHI TALFAPTAAMI VFGGTI GATI TN
 FPKSDLLAAVKMTRMLLFLKLPNEVDLI EQI VQLAEKARREGI LYLENMM
 EOLEDPMRKGVLQI VDGTDPELVRNI LETEI YTLQERQEAGAGVFEAAG
 GYAPTMGI I GTVMGLVHVLNLSEPERLGPSI AMAFI ATLYGVSSANI VW
 LPI AGKLKNLSKKESRVRELMLEGLI SLQAGNNPI LI RERLTAFLDPKRR
 EKGGRAGGRADEEE

>2617920539 Ga0073689_10940 S-layer homology domain-containing protein
 [pelotomaculum Ga0073689 : Ga0073689_109]

LRKMKVLPAGLLAI VLAFFLSANAAMGAPGLTVKVNNGDVARGSTKLVND
 NTVI VSVYDNNGETGQVLVNNKKATSVTGEVYTWRI NYPLTLGKNDVDI A
 ARWGGTESFKFAI MYVNLPPVGLSYSPSLPAAGKI EVFNKSLTLTYPK
 NNI LVDQDGKVVWVGSGEDTSI TFEI VTPPPDLEDRRPDDFHYLASPDVP
 FVFHI EADPGAKMLQPGRLLTYDQNI SSTMADQLAI WYSPDNDWNGPDN
 QVLGGYTNPARRAVTAPFQFSEDGGGYAVFLSQREFNEFQSADGNAVKW
 SYSNVMPLWARGI AEANDQSVSGNI YKTVSDNWFGLI NDDGSPKEI TRLE
 FTTMMVKGLGLPLVEKPSDGEEI FSDVKYNDGPKDNAYFGPSYSTAVNYY
 KPSI VQYI ETAVQNGI I AGYPDRTFAPAAGLKRQEAABI LARTANLKLSN
 DDQKVRQDLDKI FEDADSI PLWAAPSVLEAQKAKLI VGEPGSDPKSKKLR
 FNPSGKLSRAEGI TFAYRLLKKLKKI

>2617920538 Ga0073689_10939 DNA-binding transcriptional response regulator, NtrC
 family, contains REC, AAA-type ATPase, and a Fis-type DNA-binding domains
 [pelotomaculum Ga0073689 : Ga0073689_109]

LAKRVLVDDAAAFMRMMI KNI LAKNGYEVVEADGEAAVELYKQHKPDLV
 TMDI TMPVLDGVEAVKAI RKVDPNANI I MCSSMGQOALVI EAI QAGARDF
 I VKPFKQERI MQAI EKVMAARAGAHVYI NGKVQGVYFRAETRERLQNLV
 RGWVRNLPDGRVEGLFEGDRRDVEKLI DWCRQGPPRAVVYDVAVEWRDYE
 GEFSGFSI TI

>2617920537 Ga0073689_10938 chemotaxis protein CheC [pelotomaculum Ga0073689 :
 Ga0073689_109]

LLGKECKKMI NOWQMSEFHMALQEVANI GLGNAATSMAELLNKKVDMAV
 PKAFFHEFEQVFALVGGMEDLVSCVI I GI EGGI AAAMVFLFDEQNTYRLV
 DLLMGREAGSTAGLDAMGESVI MEVGNI LAGSFLNAI GEMTGLALKATVP
 I FAFDMLGAI LSSSLI ASGCWDDKVLVETVFSQKQDPVVGHFLLPEIG
 SLGRLFETLGI TLNS

>2617920536 Ga0073689_10937 chemotaxis protein CheD [pelotomaculum Ga0073689 :
 Ga0073689_109]

MQFLPVRMSGASRAAPVTEFQVGI ADLKVAGQPDRLI TLGLGSCVGVTLV
 DPVTKAGGLLHFMLPDSTQFSNVTKPAKFADLGI PLLLSEI ERI GRRAGS
 LOAKMAGGAQMFSGLNGKFMLDI GDRNI VSARQVLKKLGLRI TAEVVGNN
 RARTMI LDTATGQLFI RTAGSQI KVI

>2617920535 Ga0073689_10936 di guanylate cyclase (GGDEF) domain-containing
 protein [pelotomaculum Ga0073689 : Ga0073689_109]

LSKQI LI ADKSPSLRALI KNI LSGTEYKI AAEAEDGI ETI FYYKNI LPDL
 VI MDI DMPDL DGI QVI KSI HRI NPRANI I VCSALRGKNKVLEAVQAGVKD
 FI I KPFHEERFLSTVEKVFADREPGGNYRPEI MDDI TEAYNSKGFRRLV
 SEVLAGQKEKRNP I SVAI FVI NSF EAI KEQSGVAGRHAVLRQFVEI VRRR
 TRQDDLI ARFAANEFAI MLLKTDKVHGKMOVATRI ENNVKEESDPPFSVSW
 GI GTFPGDGQDVALLEAARRNLNNAVEPEHLNV

>2617920534 Ga0073689_10935 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_109]

MSLERELFQI I EETFKDKNLSGGDI EEGKKKGAGQAPSLRRQTGAGESG
 KVVVEGGGVYVKDPVGEKMP TI TPCRGVNLI I DGVKRTERTI VHEGREV
 I VEAMCEEI PGEI KI VVSPDKLLAKLELKPQKI VKYEVI DQKPAEDLELQ
 VI SRVEEDYAI TFQOI NDQLEARGVVYGI KDEI I RNLVKEPKSGSFI VAA
 GDLPGDPVDERVEI LFPRETESGPRLSSNEKVDKKNVRPVFSVEPGTVLA
 KKL PSTAGTPGRAVTGEEI KPAPPKAVRLKAGPGA EI MDSGNKVVAKI SG
 RPVVEQYGNRWSFKVTPVLLI PGDVDLATGNI YFKGAVYVAGNVCEGMTV
 RATGNVEVRGMVTEAKI I AGGDVMI NKNVI SSLVRAGGARSYFKKLGPVL
 DELSVNLGEI MQATGI MMSHPMVKSGNI RYGQLVMI I VEKKFKQTPALVG
 EI LNI TGOADVEI PEEI AGLAHLRLKNTLTGI NLLKI KEPETLAGMI QEVN
 AVWSFI DRVAERKARMTLSYHSNSNI ESTGDI MVTGQGCNFSTI I SGGNV
 I VNGVI RGGMI I AEGNVVI NEAGSELGSKTGVRVPEGSLVTI NKAYEGVT

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IRIGKQMAEI KYPQSHLKAGLDAEGRVQLDSF

>2617920533 Ga0073689_10934 flagellar motor switch protein FlIN/FliY
[pelotomaculum Ga0073689 : Ga0073689_109]

MSDKLLLLQEEI DALLGKRDDGOAGRDNSI NVLPEKEKSTLI EI FRI AMAR
ATTDI APVLNEEVVRTGPALTFTI AENI GEKI QVPHAVMKVNFSGDFTGE
IFFVVKI PDAAAVANI LTGEVVTGPAGELTEKEAGAAGEVFGRMAGSI AR
TMGELLNGKTDFSVGPLVVRNDGNQVI PSNI PLVLLSYNMLAGDLLNAEF
FQVMLSECAGELAAQLLNDSDPADLDGEYSEPLDQPAVEPFAAPSGQPRG
LDYQGI DQKQLDLI LDI PLKVSVVLGRARRPI KEVLGLAPGSLVELTSLV
DEPVEVLVNGTLVARGEI VVVDENFGVRI TSI SPAERFKRLGK

>2617920532 Ga0073689_10933 flagellar motor switch protein FlIM [pelotomaculum
Ga0073689 : Ga0073689_109]

LSI CYYVI LWEGEKPVKEVLSQEDI DQVLAASFSSGRLSAEEKERRSRKQE
EIKFYDFRRPNKFSKEQLRTLHMLHDNFARLLSSFLSGYLRTKVQFSVTV
VEQLTYDEFVRSI PVPTVLSFFSMKPLKGAII VETNPQFLFPVI DLLFGG
PGI MPKRLRDFTDI ELSVI RKLNAKI LENLALTWADVFPVTPEI ESI ETN
PLLHQI VSPNEI I ALI TLSCLMGDSKDGI IALCFPI VLDPVI SQLSAHY
RFSESASPGGEDAQQLKHWLGRSTVEI TAVAGEAQI TVQDFLHLQAGDVL
PLERKI GRMDMLYI DDRLKFKVQAGTLGRYLAVQI VSLVEEGDADV

>2617920531 Ga0073689_10932 flagellar basal-body rod protein FlgG [pelotomaculum
Ga0073689 : Ga0073689_109]

MI RGLYSAAAGLVQOEKLDVSHNLANVSTAGYKKDTAI MGAFFFEFLVE
KRDPQVI SEPEKVI GSAGI GAAVVDVVTNLEPGPLQQTGNATDFAI AGD
GFFNI LLAGGQVYTRDGSFKVDAGGNLVTSSGDRVLGNGPI VLSRNDI
LVRNDGAI LSGGNVVDMMVI TGFGNKAGLKKAGNNYFSAIPGANPVAVEK
PAVKQGCLEKANTDLVGEMTGLI EALRLYQLNQRI LRAQDELLAKAVTQI
GTVK

>2617920530 Ga0073689_10931 Protein of unknown function (DUF2802) [pelotomaculum
Ga0073689 : Ga0073689_109]

VAAAVALLVGLTVFARAKRRGSKFGRELSGLVGKNALDPGSRLSNLE
ARLETI I SLNVHI KERLEGLNRLAAMQDRQELVEMKNDI LKI HEKI YRA
FDRGKKI DDLAQEFGRTRGEI ELI LNLRRMKE

>2617920529 Ga0073689_10930 RNA polymerase, sigma 28 subunit, SigD/FlIA/WhiG
[pelotomaculum Ga0073689 : Ga0073689_109]

MIYERLWREYRATKNPAVRQELVLSHLWLKRLAGRVAVRYPSSLRSREDL
EGYGLGLMDAVDKYDLKGVFEAYASTRI RGAMLDEI RKQNW I PRSTW
VKLRQYFSVKERLEKKQGGDAPEERLASEMGI TVDELRLKTGNLNRQAFV
SLEGTYTGNNGEAVNYAHYLEDYNPDPLEI VEKAEGHANLAQAI NQLAD
KDQLVLALYYQEELTLKEI GKI MDI SESRVCQLHARAI KRLKSI LEEMSD
ERNQSTGGPGGKI GSGGRSGCFGSSGWPDLRLPR

>2617920528 Ga0073689_10929 c-di-GMP-binding flagellar brake protein YcgR,
contains PilZNR and PilZ domains [pelotomaculum Ga0073689 : Ga0073689_109]

LAFFRDLSI NLRI QI AREGEEYYI SALQDI KEKEI SIAI PYRAGI PLAL
RAGDRVVNFAGENEAFRSTTVLGRRSRI PLYSLAFPETI ERVQRREH
VRAPVMLEAGI AEVI PGKEWNFEQARSLDI SAGGMKI FSPKPYPVNTI LM
VRFTLPKKGNAAARMTVKAKVVRQDAVLTGRRSYLLGVRFVDI TSQQDE
IFSFI FSKMTELGRRLRVKDK

>2617920527 Ga0073689_10928 flagellar biosynthesis protein FlhG [pelotomaculum
Ga0073689 : Ga0073689_109]

LRDQASKLRAMSGSFFKMGRERTSLRTI AVTSGKGGVGKTSLVVNLALA
LAKLGQRAVVFADLGLANVDVLLGLNPPYNLYDVLYGEKNI RDI I VTGP
LGVKI VSGGSGI QELANLDTSGRQLI TALSYLEQADFI LI DTSGGI SR
NVLGFVAAAAGEVVI VATPEPTSLTDAYSMI KVLATNRVHSEVNLVVNMAA
DEREARI TATKI I SVTKRFLQI KVKYTGSI CMDPVVGKAVKMQQPFVLLA
PHSVASAGLSAI AGALLGERVEPGRMGSLGKLLRLFG

>2617920526 Ga0073689_10927 flagellar biosynthesis protein FlhF [pelotomaculum
Ga0073689 : Ga0073689_109]

LKI KKYLAKEI KEALRMI KEDLGPEAVI VSTRKMRGKGLKALLGPSRLEV
TAAI DEI TGDGGPFELYRGNRKS I QAPVVNFPEPLDNLSSRELAELKA
LLRKVVTTTAEDEPEDGFFNKWRKI LLGLELDEI I VGKLI GELKDGLNPD
RSDRGEVTGVI LKNSAARLLEPI YNNGGQVQGRVLI FVGPTGVGKTTTLA

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KLAAQLTLFHQRKI ALVTI DTYRI GAVEQLKTYGEI I GVPLDVMMNPEEL
I YSLNRHQDKDLI LI DTAGRPSGNI AQALELKGFLFVI PEPKDVFLVLSS
TTRGRDLYKI VEDYNKI RFNKL I FTKVDETDTLGCI I NI AYYVSLPVVYV
TDGQNPDDI DEVYPKKVAKLVFKGVDQFEGSGV

>2617920525 Ga0073689_10926 flagellar biosynthesis protein FlhA [pelotomaculum
Ga0073689 : Ga0073689_109]

LGLAAQVKVKEQI KKYNDMI I AGLVI CI VLLVI I PLSPVALDI LLTLSI T
VGLVI LLI TMFTTEPLQFSVFPALLLVVTLYRLALNI SSTRLI LTDAAAG
KVI AAFGDFVVGNNYVGMVLF I I TVI QFVVI TSGAGRVAEVAARFTLD
AMPGKQMSVDADFNAGLI SEEGARERRRRRLQREADFFGAMDGASKFVRGD
AVAGI I I I AI NI I GGLAI GVI QKNMDVAEAELETYLLTI GDGLVTQVPAL
LI STATGI LVTRATSDASFGKDI SRQFLNFPRLVFLAAVI LLI LGLI PAM
PNLLFLTMAAGAGFLAHSLVREERRKTI EQQEI SARQARSRKQEPENVFG
YFOI DPLEI EI GYNLI SLTDESQGGDLLERLTAVRRQCASDLGI FVRPI R
I RDNLQLTPNGYVFKLKGVAASGEVMPGHYLAAMDPTGQGA EI KGI PTRE
PTFGLAAWWWSPAEEQAEI AGYTVVEPSTVI VTHLTEFI KRNAHELMGR
QEI KELI EVI KEKNSAVVEELVPDMLTLGEVQKVI QSLLKEQVPVRDLVT
I LEALADAAARFSKETDYLVENVRLALSRTI CRRYATPDKKLLVI TLHPEL
EQALVDSI QETRLGAYPVLEPRVARQALDSLKAVI EKLAMRGLSPVALGS
PRARLPFRRLI ERYFPNLAVLSLNEI SPEYEVEAVGTVTLD

>2617920524 Ga0073689_10925 flagellar biosynthetic protein FlhB [pelotomaculum
Ga0073689 : Ga0073689_109]

MAESNTAQKTEQTPRRLQEARRRGQVARSSDLNGALSLLAVVI FFYLF
KDHLLLSMQRYSHYLANFFQKSSLDNPLEALTSSALYFFWLMLPLI VLV
TLVGI FI NI I QVGFVSPEAARFKWDRLNPAAGFORVFSTRGLLELVKSV
I KLAALGGLTYWLKGYLPGI MVVEQGNPGRTLSGDAQFI LLVLGYGSLA
YLALALLDYLHRRHEHVRELRMSRQEVKDELKQTEGDPLLKSRLRERQRO
I SLNRM I QEVPRATVYVTPNSHLAVALRYEQGKMNPVVTAKGAGYWAER
I KELARENRI PVI ENREVARFLYRGVEVGREI PGEVYQAVAEI LAVVYRL
NSKKKKVM

>2617920523 Ga0073689_10924 flagellar biosynthetic protein FlhR [pelotomaculum
Ga0073689 : Ga0073689_109]

MDGLLGAGNLLDFAQLAAFFLVLLRATAFVVSGLPFALRGI PVPVKAGFA
FLLALALYPVLPVQDYLPDGLL YLLQAAGEVAVGFGLLASLVLQI VQ
MAGHLLDI QI GFSLANI FDPVSGAONTLI GHFMYLCGLLLFLNLDGHHM
LLALAKSYQLVPLTSASVTGEATEVAMKAFAGAFAI AVQVA API LAVLVI
TDLAFGFVARTAPI NVFMLGFALRI AI GLLI I SLLAPVFSI FSVI LRF
VENNLFLLMRGLS

>2617920522 Ga0073689_10923 Transposase [pelotomaculum Ga0073689 :
Ga0073689_109]

MPLDVEI YNI MI KGYKPYNPNI YLFPPSPQEWLPKEHLVYFI SDLVDNL
DLSI I FKEYEKGTRGPPFHPGLMTKI LFYAYSRGVFSSRKI ATRLFEDV
SFI VLAGGNKPDFRTI NEFRRRHI KSLPGI FVQI LNLCEKAGLVGLKHAS
LDGTKI NANASKHKAMS YGRMKTEEEKLDKEI KKLLEKANRLDLKEDKQF
GPNRRGDEI PEELVYREKRLAKI KEAKAALAEAKI AQKEDEEKKDDDDK
DPPATPPRARI KYSKKTGEPKEKTQLNFTDPESRI MKNSDKAFVQAYNSQ
AVVDFKNQI I LSADVTNQAADSQHLPMMEKI KENTGRYPKEFSADAGYF
SEDNLKWLKNKTDAYI PSGKTKHSHEQGPAPKGRI PVDLPLPDLMKRKL
TKAGRAKYALRKQVPEPVFGQI KEARGFRFMRGLLELVRGWLLCLTH
NI LKLFGNKKKVI FANG

>2617920521 Ga0073689_10922 flagellar biosynthetic protein FlhQ [pelotomaculum
Ga0073689 : Ga0073689_109]

MSETYFI HI I QEALLLALLLSAPALGVSLAVGLVI SVLQAATQVQEQTLT
FVPKI I AVFAVI I I LGAWLLNLLVNYTI NLFNQLPGLVR

>2617920520 Ga0073689_10921 flagellar biosynthetic protein FlhP [pelotomaculum
Ga0073689 : Ga0073689_109]

MKNKAALLFI VLLSLVI LPQVFAQPVVPDVLKI RQSDNPAEVDVSVK
LLVLLTLI SFI PAFLMMMTSFTRI I VVLSFLRSALGAQQAPPNQALI GLA
LFLTI FI MAPVYQDI NEQAI KPYLANQI TREEAQNAGAKPLRSFMLRQTR
EKDLALFVSLSKMEKPQNAADVPLTVVVPF I I SELKTAFQMGFLI YVPF
LI I DMVVASTLMSVGMFMLPPVMVALPFKLLLFVMVDGWYLVVKSLSVESF
R

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>2617920519 Ga0073689_10920 flagellar protein FliO/FliZ [pelotomaculum Ga0073689 : Ga0073689_109]

VNGELYWALI KLLVSLPLVLALAYFFLKYVLGRGSYFSPAGTRRMKVLEQ
LTLPKAAALSLVEVGGRYLI AHHEGGI SLLQEELEELPGVLEGTAQGEST
LDFGAI LAGKFRLFSNNYMPGHPGRRRAGGRGLSFAFRNI FRKKNKPGD
NDEE

>2617920518 Ga0073689_10919 flagellar motor switch protein FliN/FliY [pelotomaculum Ga0073689 : Ga0073689_109]

MMTEEEI KEFLRGAGKDKDSI KKVRFKPLSPGKGLNRVKTSI RHLEDVRV
TII AELGQTTI KVREI LALTEGSVI ELDRPAGDAVEI YI NDQKFGRGEVM
VINDI FALRI I KVYPPLI FKPEEA

>2617920517 Ga0073689_10918 flagellar FliL protein [pelotomaculum Ga0073689 : Ga0073689_109]

VPEAGEEKGNKKEKKGSRKVLLI I AAVVVI AVPAAAAFNFFGGGKAGSPS
PKNSAHENKKQMVDLSDI I VNLADKGSNRYLRKI VLEFPENKKLDEEI K
RKAPQI KDALI AI LRNKTTTDDI QAAGSDEI KKQI LQKLNNEYLTAGKVE
NI YFTDLLVQ

>2617920516 Ga0073689_10917 flagellar hook protein FlgE [pelotomaculum Ga0073689 : Ga0073689_109]

MI RSLYTAI SGMRNHQVRMDVTGNNI ANVNTTGYKTGRANFSEI LSONI K
GASVSHVGVNSYSPSQVGLGI ATSSI DNNFAQGGLOATGRVLDLAI VGDG
FLMI KDSADSEKTYYSRDGALYLNNEGYLEVNSAGLYVLDSSGAQI DLGTD
VESIRI DKDGN I YKNSETDPAATI GI RI FVNPEGLAKVGGNLYEVPTGSD
MEDYAVTKDDTNGESTVVOSENLEMSNVDLTTEFANMI I TQRGYQANARV
ITTSQMLQELI DLKR

>2617920515 Ga0073689_10916 flagellar operon protein [pelotomaculum Ga0073689 : Ga0073689_109]

MPPVLPVVGPAARNRTAGKVTGRTTSFKESLDREI RRQEGI KLSAHAEKR
LRQYNI SLAPEDLVKI DRALQTAAAKGARDSLI I YGDI ALI ASVPNRTVV
TAVEGRPAGEQVFTNI DSAVI I K

>2617920514 Ga0073689_10915 flagellar basal -body rod modification protein FlgD [pelotomaculum Ga0073689 : Ga0073689_109]

VQVASSPSLYYLPQNPAPDRELDKNAFFKI LAAQLSHQDPMNPQDGSDF
VAQLAQFSALEQMQLNLRNTEEFSSQGSFLQATGFI NRKVTLDDGNGGTV
TGVVEKVRNLGAAVELMVNGAFYNVGRVVQVE

>2617920513 Ga0073689_10914 hook-length control protein FliK [pelotomaculum Ga0073689 : Ga0073689_109]

LI I AGLTI EQVAGGDLPGKGPVKGQNPDMFL LLA VAAAGGMPQAMQAGGM
APVEATAGGI TVRVGEVSL LHDKTGRAPVSAGLRQQGRDLAVGAI PAMEA
PGTAAGRGLQSEVDYAFRRAGADPGASGREGAPPVSAGLRQQGRDLAVA
AVPAPEGPGTAAGRDSPGVVREVNTGDTVPLTQLGDRVAAEVI RSI VGER
RKASVAQLQLEPERLGKLLI RLTVDKGEVTAHFFTESSQAKEVI ESSLKQ
LKEALLPHRLQLGEAAVFPGREGNHLKVPEGEYTFPVAANTEKPEPFADI
HKANVSGYRLNGFNLFNGFNKQGPLPELAASNMPAYRLSGEDI KGPAPGEV
DYAFRRAGADPGASGREGAPPVSAGLRQQGRDLAVGAVPAPEGPGTAAG
RSGSPGVVREVNTGDTVPLTQLGDRVTAEVI RSI VGERRKASVVQLQLEPE
RLGKLLI RLTVDKGEVTAHFFTESSQAKEVI ESSLKQLKEALLPHRLQLG
EAAVFLGQGGSRWPGREQQWSMGSRATFHGNQSPGSLQGAVESDPFQA
PDWSKVNYLI

>2617920512 Ga0073689_10913 flagellar FliJ protein [pelotomaculum Ga0073689 : Ga0073689_109]

LFRFRLERVLEYRAGLEKAAEQKLAVALEEKNRCSLALAEYRRRFEEAI R
SGYCELRLAANI HLDIFYRETLKQI KHGEELLEAAGROVELCYHNLVSA
RQERMALEKLKEKQMRGYKVRLTQAEQKI NDEI AAALFKHKKDV F

>2617920511 Ga0073689_10912 type III secretion system ATPase, FliI/YscN [pelotomaculum Ga0073689 : Ga0073689_109]

MDFASGDLSI DPVRRRI AAAGI I KLAGRVSRVI GLTI EVKGLNASI GEVC
DI YYPGEENPVRAEVVGFKENTFFLMPLGELKGI CPGCKVI PEGRSLTVR
VGDHLPGRVLDGLGPEMDGRPI NKGVEFNI NNSPPNALQRRRI TEALATG
VRAI DALLTCGRGQRMGI FAGSGVGKSTLLGMI ARYSYADI NVI GLI GER
GREVLDFI ESNLGSEGMARSVI VAATSDQPALVRLRGAFVASAI AEYFRE

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QGKDVLLMI DSI TRFAMAQREVGLAI GEPPATRGYTPSVFALLPRLERS
GTSSRGSVTAFYTVLVEGDDMNEPI TDAVRGI LDGHI VLARELAARNHYP
AI DVLQSVSRMLPDLAAGDQLRQAGRLRDLLATYRQAEDLI SI GAYVDGS
NPKI DEAI RMHDKI I DFLRQSPDERSDFEVTI SELMSIG

>2617920510 Ga0073689_10911 flagellar assembly protein FliH [pelotomaculum
Ga0073689 : Ga0073689_109]

MLSSSRVI KGARFREDAAAYLLEVRNVTEEGGDADEERVAGKMRELLDNAG
REAGEI VRKARAEAEI ARETRRAGYEEGYRDAFDKAGEEAESLRAEARD
VLROAERI YREKLGSLKDDI I SLALDI AEKI VAAQLSLDREMLNI AAEA
LRMVSDRERVTLFVHPSEGELFRSRKGDLEKVMTRAVI QVVADPAVSPG
GCLVDTEQGTVDASLDARWKNLLDAVYAQEG

>2617920509 Ga0073689_10910 flagellar motor switch protein FliG [pelotomaculum
Ga0073689 : Ga0073689_109]

MAALQGLTGLKAAI FLI SLGADLSAI VLKRGGFYDDEI ERMSYAI TNL
DRVQSVREKVLLEEFSELROAQEYLVQGGI KYARELLVKTFGSQKAEQI L
EKLSQHSKETPFRSLRKTDPRLNFI RDEHPQTI ALI LSYLDPEQSSVI
I QSLPPDMQGEI ARRI AI MERTSPEVTQVEKVLERKLSSLVQQDQTVVG
GVKALVNI LNMVGRSSEKTI MEDLENDPALAEVVRKRMFVDDI VKLDD
LSI QRVLRVNTKELALAMRGTEAVRMRI YKNQSKRAADMLRDEI EFMG
PVRLKDVVEAQLKI VKI I RHLDEI GEI VLSRGGEDAI VV

>2617920508 Ga0073689_1099 flagellar M-ring protein FliF [pelotomaculum
Ga0073689 : Ga0073689_109]

LSNRWRSFSPARKTAVVLLAVGLI VSI FYLGQLLVRASYAPLFTQLDPKE
AGAI VEKLGKMKVQYRLADOGETI LVPKSQVYDTRI RLASSGALEGTGKG
FELFDQKKLGI TDFEQVYYYQALQEELRRTI TQLEGVEQARVHLVLPQK
SVFVEDKGAPSASVVLKPLAKLKSEQVGI SDLMVGSVEGLMPENVHI
I DMDGHVLSQVSGESAGLAQKAVDQQQVKRNYEKEMEKRVQEVLERI L
GPGKAVAMVTADMDFSQQQVTTNVPFGNPAVVSEKTVTERNAGAVQGGMA
GTDNSI PPNYPGLANAGAAGGYARDEAVKNYQVGNRQETLI QPPGTMRR
SI AVVVVDGNPGAADVQTI QGMI GAAVGS DPARGDOI SVSNMAFDNSLRDS
LNEEMKVADAALKEAQKRKFYGYLGGAALLLFFLGFGFLRLLRARGSAG
EELVAAAGGDVPLKVLKLEKGLQLEGEELQSGI TLRQESVKELAKKSPED
VARI LKWLAE

>2617920507 Ga0073689_1098 flagellar hook-basal body complex protein FliE
[pelotomaculum Ga0073689 : Ga0073689_109]

MQI GOI PKLLQTPLEPGKSEQVNATPGFGEVLNKA I EKLDQARERADEV
ARQFLAGEI QDLHHVTI AMQEAKLTMQLAVEARNKVI EAYQEI SRMQI

>2617920506 Ga0073689_1097 flagellar basal -body rod protein FlgC [pelotomaculum
Ga0073689 : Ga0073689_109]

MGI FDSFSVSASGLTAERLRLDVI AHNLANVNTTTRTATGGPYRRRGVVFA
ERLRLAREAEETPPRPGAGVQVVAI TEDPGPPRLAHDPSHPDADQNGYVA
YPNI NPVNEMVDMI TATRAYEANATVLDAAKGMALKALEI GRG

>2617920505 Ga0073689_1096 flagellar basal -body rod protein FlgB [pelotomaculum
Ga0073689 : Ga0073689_109]

MTLLRKELDAGALRQV I ANNI ANVNI PRFKRSVVRFEESLQEALGKDTL
PLLTTDPRHI GGAKPPDEL RPEVERDEGTTMRADGNNVDI DQEMALLAAN
TI MYNAAQELNERLALLSYVI TGR

>2617920504 Ga0073689_1095 phosphate ABC transporter substrate-binding protein,
PhoT family [pelotomaculum Ga0073689 : Ga0073689_109]

VSTGLSGAI KMSGSTSVQPVAEELAQAFMAKNPDVRI TI AGGGSGVGI KD
AAQGVNI GNARALKDSDPKNI VGTTI AKDAI VVVVNPANSVSALTKEQ
VKKI YTGGI TNWKDVGGNDAPI I VNSRTAPSGTFDFSEEFGLKDVKVVA
TAKQHASNGLVRQAVANENAI GFI SMGYLDNSVKAPTMDGI EPSMENS
K NGAYHYVRPFNMVTNGEPEGLAKEFLNFVLSEEGQTI VDKEYI RVK

>2617920503 Ga0073689_1094 phosphate transport system permease protein
[pelotomaculum Ga0073689 : Ga0073689_109]

MKMGKASELSVLEVSFLKGVSVSAKRQSI KENVI EKLLFLFTLMSSI LI F
FI I I FVVNKAVPVLKASGI NFI LSGGWDEQFVSAWLASAAPVWEFGALP
LI AGTVYTTLGALLI AVPLGLGAAI FLTEMCPVWLRTPLESAVRLLAAI P
SVI YGLVGLMVVVPFI NAHFI SNELALKMI NTVALDGTSLLAGMVVLSMM
LSPI FI ALSSDALRAVPRQYKQASLALGVSHWRTI VKVMLPVARKGI MAG

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AI LACGRAI GEAI ALSMVSGSVANLPSPAHGLVFFLEPLRTLASTI VDNG
EGMGVVTCEALFACGTLLLLSSVI LSVFARLVAGGVRRGDTAHV

>2617920502 Ga0073689_1093 phosphate transport system permease protein
[pelotomaculum Ga0073689 : Ga0073689_109]

LPGWSPAAYAGEI PPMFNLRRKNLLGHGLCWFSGLTLAVCLLI LFMII
KGVDSLSWRFLI EDPRPSLDEALSGGI FTPI GTI LLVVMGTLFALPWAL
ATAI YLSEYADDNHWTNLTRTGI DVLSGVPTI VFAI FGLSI FTFPGLSI F
STMVEGVDNAKAFGRSFFVSSI TMAMMI LPFVI KSI EEAI RTVPESYKAA
AYALGVSKWRTI SKVVLPAAMAGI TGVVLGI GRI AGDTAI VWLCLGGSM
GFTGPQPWWEPQNLSTLQNTGSTLTSYI YYSSPAGEGNPNKAFGAGLV
LI I I I LALNTVVVDYLSRFTRLKED

>2617920501 Ga0073689_1092 phosphate ABC transporter ATP-binding protein, PhoT
family (TC 3.A.1.7.1) [pelotomaculum Ga0073689 : Ga0073689_109]

VQPSNNRAKI VENLSCWYGSFPALNKVNMEI YARSI TGLI GPSGCGKST
FLRCLNRLNDLI KSFRKGGGAVALLEGQDI YQPEADVMMVRRKVGVMVFQQPN
PFPMSI YDNVAFGVREHNQQVKKGALDDI VRESLKQANLWDEVKDKLNQS
GLSLSGGQQRLCI ARMLAVMPEAI LLDEPCSSLDPVSTAKI EELLQLK
DSYTVVVVTHNLGQARRI SDHLGFFLDGKLVEYAETLSVI TNPGERATED
YLAGNFG

>2617920500 Ga0073689_1091 two-component system, chemotaxis family, response
regulator CheB [pelotomaculum Ga0073689 : Ga0073689_109]

TPPGRDGAAGNALMRRRAAGAARVTSPGEAQGPASPVARTVGRAHPAGAEA
PSPSGGRDVPVQLPGRGGHAVSTLVTRPAAGRTRLVVI GCSTGGPAALQQ
VVPALPRDFPAAVVVVQHI PVGFSKPLAEHLDRKSRLEVRHAQNGDAVTP
GRVLVAPAGFELTFRGTAGNPTVALEKKGKGPVPPGGFRPSVDGVMTAAAR
FFGDSVVGVLMTGMGRDGAVMREI KQAGGRTI AEAESTSVFVGMPRAAI
EAGAADRVSRLPQI ASEI MAML

>2617920499 Ga0073689_10873 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_108]

LHVDI LKGSFI PAPEI RELRDMVRRRPTLMRETTKGNSWLKSALTEAWA
ASHTKDTYLSALFHKLVPRLGKKKSLVAI AHVI AI AI YHI LTEGVPPYEL
GSDYFSKQI NKKLERLI RRLEELGYKGKRQKK

>2617920498 Ga0073689_10872 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_108]

VSGNNFVI SRDDWSLHRKGEI DRQRHQEKVRDAI KKNLADI VSEESI MH
DGRKVVKVPI RSLDEFHFRFDYGKQKHGGQGEKSKQGDI YSDPQKGQG
KGKGAGEEPPGVDDYEAIEI TVDELAEMI FEDLGLPNLEQKKKPEI ASERVE
FKDI RKKGI SSNI DRKRTI MEAI KRSI KGEPKLAGI TPEDLRFRTWETT
FKYESNAVVLAMMDTSGSMGPFKEYI ARSFFFWMVRFRLTKYNNVQI VFL
AHHTEAKETTEEEFFTKGASGGTRCSSVYKLALAVI EKRYSPQDYN IYAF
HFSDGDNLASDNENCVKLI NELLOVCNMVGYGEI EGPYYTSTLRTAFKK
VTDSKFVVTI RDKSGVYPALKKFFSQTPAQAAASK

>2617920497 PrkA putative serine protein kinase, PrkA [pelotomaculum Ga0073689 :
Ga0073689_108]

MDFLKRLEEYRSLERQLSWEGTFQDYLA I VKERPWVSQLAHARI YEMI KS
AGVEEKDGVKHYKFFSPELYGLDKTLEKLVEEYFHPAARRLDVRKRI LLL
MGPVSGGKSTLVAMLKRGLERFSRTDDGALYGVKGCPMQEEPLHLI PKEL
REEFQREYNVYVEGELCPSCRMVDAEYGGNI EKVPVERVFLSEDNRSGI
GTFTSPDPKSQDI ADLTGSVDFTI TEYGSSEDPRAIRFDGELNI ANRGL
MEFQEMLKCEKFLWNLLSLSQEGNFKAGRFALI YADEMVVAHTNENEYK
SFI SNKKNEALQSRI VMKI PYNLKVAEEVRI YEKLI KQSDLRNI HI APH
ALRVASI FSVLSRLKESKKQGM DLVKKMKLYDGEDVEGFKQKDLHELQVE
AI DEGMSGVDPRYVI NRLSSALI RTSTQCI NPLDVLRLALKEGLDQHPSI T
KEERDRLLNFI SVARKEYDEMAKKEVQKAFVYSYEEAKVLF DNYLDNVE
AYCNGVKLKDPI TDEELDPDEKL MRSI EDQI GVSES AKKAFREEI LI RLS
I YARKNKRNFYNYSHERLREAI EKKLFADLKDVVKI TTSTKTPDAEQLKRI
NEVSARLI VEHGYCPNCANELLYVGSLLNR

>2617920496 Ga0073689_10870 adenine deaminase [pelotomaculum Ga0073689 :
Ga0073689_108]

LLSEKLTQLI RVALGTERADLAI VNGLLVNVTGELLSGYSVAVKGERI A
YVGKDI HQAI GPETVVI DATGKTI APGFI DGHTHMCYMC SI DQFLRYAMR
GGTTTFI TELMEPAFPLGYLGI LEFLKSFKDQPVKI FSVAPPMI TFSPGA

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RARAI NI EQI RELLOREDI LGLGETYWFVAVQAQDKKI LEFFAETGKARKK
 I TGHSAAGAKGNKLAAYVASGVSSCHEPI TVEEVI ERLRMGMVYLVREGWF
 RKELAAI APVKDLPLDLHQLI LATDSMSPQQI VKEGYLEVVLQKAI DLGF
 DPVSAI QMVTI NVARYFNLDERLGGI APGKYADI VI LPNI QNI RAEYVI S
 NGRVI ARDGELLVPSRKHSFPEWVRSI RLKKKFI PDDFLI HVSDVDSVK
 VRI I EQVTELVTRI HLDVPVFQGTVKI DLERDLLKVAI DFVRPEKQFV
 GLI KGFKI KRGALASSLAWDLTNI I TVGAREEDMALAVNRI VELOGGAVV
 CADGQVLAELSLPLGGYLTDSPI EELVQKTDDFQRAAAGLGAPFSDVHLT
 LATLTTPAI PHFRI YEEGLVNLREQRRVGLLV

>2617920495 Ga0073689_10869 homocitrate synthase NifV [pelotomaculum Ga0073689 : Ga0073689_108]

MRPVYFVDITLDRGEQAPGVAFTVFEKVRI ARMLDYLGVAAI EAGI PVMG
 SPELEAVTEI AGLELKAVVSTWNRMTI GDVKASLACGVKNI HVSVPVSDI
 QI KYKLGKNRVWVLERLKRTVSYAREHQCRITVGAEDASRADMNFLI HFA
 HQADLAGAERLRFADTLGVLDPFRAEQVI RQLI EETGMDVEFHGHNDFGL
 ATANTFAAWKAGAHYLDTTI GGLGERAGNCSFEEI I AVLKRHGGVEPATD
 DRLLAKVSRVAAAAANRLKAGGTVPRKSADNVVYLCPGGEGASPAI NSG
 LTNNG

>2617920494 Ga0073689_10868 Fe-only nitrogenase accessory protein AnfO [pelotomaculum Ga0073689 : Ga0073689_108]

MSKDI AVCI GENGETATLYDKGKI AVYRKKRGI WSVI KEEKYFSFSGGLM
 QELRGKMAELI GFLNGCRVFGVLSVTGVPYFELRKSLSFI WETVGKPVFI
 LDYVLQKEEEAPEPEQEKGI QLAPI EVFKGCYRI SLKEI QEKNTGVTSK
 QALLPFLRQGFHSLEVLCSHVPPWLEAELTTGKLSGTVEKI RNNELKVT
 ITR

>2617920493 Ga0073689_10867 nitrogen fixation protein NifB [pelotomaculum Ga0073689 : Ga0073689_108]

MTTVKVEVRKMDCLTSKQSSARI PADTAGMTERHPCFSFDAHHKYARMH
 LPVAPRCNI SCNYCNRFKDFCLHESRPGVTSEI LSPETALLKYKFVKEKVE
 NLSVVG I AGPGDALANWEETRTI ELFKQSGQDVI FCLSTNGLMLPEYAG
 RLVELGVKHVTVTNCLPKTGKI YKYVHYGKRFEFVGKAAI LI SNQL
 AGI EYLAGHGVAVKVI VMLEGI NDLHI PDI VKKVKELGAFI TNIMPLI P
 AKGCAFENLPQTPMKEI NRMRSI CRADLPQMYHCRQCRADAI GLLDDDRS
 LEFRNVAGNKEAV

>2617920492 Ga0073689_10866 nitrogenase molybdenum-iron protein NifN [pelotomaculum Ga0073689 : Ga0073689_108]

MSYRNVNENPCNMCMMPGGI LPFKGVEQSMVI HGSQGCSTYMRRHI AEH
 FNEPVDVASSSLNEKGTI YGGEDNLI KGLDNVMRVYNPGLI GVLTTCLAE
 TI GEDI ERI TSEYLKEKGLQDFPVVNVSTPGYGGTHTEGYFLATKKI I AR
 LARSTKHSKI NVI VPNLSPADI REI KRI LHLMKVEYTLMPDFSDTLDRP
 FERPYKKVPGGGTKLTDI AGMPGAAATI QMGMTVEDSLSPGKYLETGFGV
 PLYNVPI PMGI ENTDLFI NLLKQLTGNDVPDSLAEQGRLLDCMI DSHKY
 NFQGRSVI FGEPENVYAI VKTCMENGVPVAVATGGKSI KLRELLNQFN
 ELRREHVHLNETDFSQI REKSKEMAANI AI GHSDGRYLTEREGL PLVRYG
 FPI HDRVGGQRLLSVG YAGTTMFLDRI TNTLLENKYKNYRSSMYQQFYHD
 AASDR

>2617920491 Ga0073689_10865 nitrogenase molybdenum-cofactor synthesis protein NifE [pelotomaculum Ga0073689 : Ga0073689_108]

VI VVKAALKSDAVI KERTDFI RTKGKQKHQLKCDTDSI AGCVSQRACVYC
 GARVVLNPVTDVHLVHGPI GCASYTWDI RGSLSGSDLYRFSFSTDLKE
 HDI I FGGEKKLALAI GELVQKYCPFLVFYATCI VGV I GDDLEAVCRTAA
 KKHGI EI I PVQSSGFTGNKAAGYRAACDALLRLI QPGHQFI SKKNKCVNY
 LGDFNLAGEVWI I KNYLKQGTGI DVNVAFTGDSSCAALKTATGASLNI VQC
 AGSMSYLAEMEELYGI PYLNVSFLGI EDTSQTLRRI AKAFDDPDI MCKT
 EEFI QRETAKVDTAI QSYREKLKGKAAI FVGGGFKAI SLVKQFREI GI D
 VVMI GTQTGRQEDYETI NDLVDDGTI I LDDANPSELEKFMVEKGAHLLVG
 GVKERPLAYKLG I AF I DHNHNKHPLSGFVGAVNFAGEVYSTVCSPVWNY
 I

>2617920490 Ga0073689_10864 Mo-nitrogenase MoFe protein subunit NifK [pelotomaculum Ga0073689 : Ga0073689_108]

MLSYPKEI I ERKALVI NPAKTCQPI GAI LASKGI HKCMPLTHGSQGCSS
 YLRMLLARHYREPSI AATSSFTEDTVVFGGRENLEAVENI VSLYHPEVL
 AI STTCSTETI GDDVPSFMEEI KMESFFDPKI KVI I SNTPSYVGSHI TGY

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DNLVKS I AQTI PKKGAPNGKLN I I PGFVEPGDI REI RRI LEVMGVASI I F
PDTTDFVDAPLASDPCGLYPPGGTTI PDLEDTANSVGTVALGRTAGASGS
LVLKGRFGLPAVI GPTPI GI TNTDNFVMNVSRLTGAEI PKELEDERGRLV
DMMVDAHPhFHGKKVAVFGDPDLVSGI VGMLVDLGMAPVFALTGTPDKQF
I PEI NOI APECEALI GDLFLLHQKI KNKPVDLLI GNSYGYI ARAEDI PL
VRLGFPI TDRANLHYFPSVGYMG TARLVETI GNTMLDRQDRDADDSHYEL
I L

>2617920489 Ga0073689_10863 Mo-nitrogenase MoFe protein subunit Ni fD precursor
[pelotomaculum Ga0073689 : Ga0073689_108]

MSTAADNKKPVTLEESRRVVEEMLAAFP KKAGEI RRRHI VVRNTGKERQP
I QANDRPVPGVLTNRGCAYAGTKGVVFGPVKDI LDLTHGPVGCAYYTWGT
RRNLSRPEEGQND FAGYCLTTDDMMETDI VFGEAEKKLAQAI REAYSI FKPE
CVGVYATCPVGLI GDDI EMVCKKAEEDLRLKVI PVRCEGYRGVSQSAGHH
LASNSLMEHLI GTEELEDPGPFDI NVFGEYNI GGDYMMI KELSEKI GYRI
I SSFTGDASFHQI AKAHRAKLSVLLCHRSI NYTNRMMEKFGVPWLKI NY
VGI DDLI KALRDMAKFFDNQELTNRTeeVI AQEMTWVGPI I EEYRKRLAG
KRVMLLVGGSRAHHFKNMFELGMEVI VAGYEFARDDYEGRAI I PEI VH
TGRSKI LEDVI YERDPSVVSAYDDEE I KKKKEE I PSLMNYEGLYPHMKDG
HI AVDDFNHFECEYLKELGI DLFCSGI KDKYVFQKMH I PSRQMHSYDYS
GPYTGFEFGI KFVRDI DMAI NSPTWKFI TPPWREKKDA

>2617920488 Ga0073689_10862 nitrogen regulatory protein P-II family
[pelotomaculum Ga0073689 : Ga0073689_108]

MKEVVAI I QMNKMECTKDALATI GFPSFMAYKVYGRGKQRLQI VYPSEF
KDEAVKERRMKFLPKRMI TI VVEDEFVPAVVAVLTKI NRTGNI GDGRI FV
CPVVDARI RTGERGKEVI S

>2617920487 Ga0073689_10861 nitrogen regulatory protein P-II family
[pelotomaculum Ga0073689 : Ga0073689_108]

MKMLRAI I RPEKVDEVAKALDARGFTALTKI DVFGRGKQKGI QVGSVVYD
SLPKTMLMI VVEDPOLEQAI DI I EESSRTGNI GDGKI FVTTVEEAYTI RT
GERGL

>2617920486 Ga0073689_10860 Mo-nitrogenase iron protein subunit Ni fH (EC
1.18.6.1) [pelotomaculum Ga0073689 : Ga0073689_108]

MROVAI YGKGGI GKSTTTQNLTAALAVLGKKI MQI GCDPKADSTRMLMG
KROHSVLDLTLREEGDVKLEGVLETGFGGI KCVESGGPEPGVGCAGRI I T
SI GMLENLGAYTDDL DYVFDVLDGVVCGGFAMPI REGKAKEI YI VVS
GE MMALYAANNI CKGI QKFAETGGTRLGGI I CNSRNVHREEELVN VFAERI G
SRMI QFVPRDNV VQQA E I RKQTVI QYAQDSTQAQAYFGLAKNI DQNELFV
I PKPMGYDEFEQLMI DWGVEE

>2617920485 Ga0073689_10859 16S rRNA pseudouridine516 synthase [pelotomaculum
Ga0073689 : Ga0073689_108]

MERLQKI MAQAGVASRRRCEEMI ASGMVKVNGRVI TKLGTRVDPARDKI Q
LGGETLFLSPRKYI I LMNKPRGYVTTLSD EKGKKTVDLLKGVTTRVYPV
GRLDYDSEGLLLLLTNDGDLTYALTHPKHHVPKTYLVRVSGAPTPDKLEQM
AGGLVLDDGPTAPAGVRLI GEOEGKALLEI TI FEGRNROVRRMCEYI GHP
VLRLQRI RFANLSI EGLRPGQYRHLTGDELKRLKEKAGLRYGLRKN

>2617920484 Ga0073689_10858 spore maturation protein B [pelotomaculum Ga0073689
: Ga0073689_108]

MFEI I AELSRWAI PVVLLVPLVAVLRGVRVYETFDVGAEGFATAI KTI
PYLVAMLVAI SI FRASGAMEVLVVALSPFLNAVGLPAEVLPHAI MRPLSG
GAALGI ASDI I KTHGPDSFLGRLVSTMQGSCTTFYVLTLYFGSVGVKRY
RYAVI SGLAADLTTLAASVFI VRTI F

>2617920483 SpmA spore maturation protein A [pelotomaculum Ga0073689 :
Ga0073689_108]

MVNFVWLGM I VFGI VVAGAEGNI DVVTKAALDGANNAVKI SI SLI AI I TF
WLGI MKLAEEAGLVRLAWLVRPVMRFLFPSVPKDH PAMGAMVMNLSANI
LGLGNAATPMGLI AMRELQKLNHGRDNASDAMCTFLALNTSCVTLI PTI
I GI RLLYGSADPTEI VGPTI MATAFSMAVAI VVDRLLRLFYDGRGR

>2617920482 Ga0073689_10856 Glucose inhibition divison protein A [pelotomaculum
Ga0073689 : Ga0073689_108]

MVVVI VGGWAGCAAAYAAAAAGADTVLI EKTDMLLGTGLVGGI MRNNGR
FTALEE VWALGAGDFVRVI EGVVTHRWLDFPGHRHAMLYDVTRI EPAI RV

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ALRFAGVRLNLQKI MTGA AVNKGRI TGI ETAGEI I EGDVFVDCTGTAGPV
KNCSRFGSGCAMCI LRCPTFGPRVSLTDRAGVAEI RAGDGFPHFEAMSGS
CKLEKKSLSPALVRRRLERDGMVI PLPEHLHKKEQLGRKACQYAI NDFA
ENLI I LDTGHAKLMTYPFPLEI LRTLEGFQDARYADPYSGGKGNVSRFMA
MAPCDDSLRVQGVNDLFCAGEKTGLLVGHTEAI VTGFLAGHNAARLLAGG
EPLVLPVELACGDI I SYMHREMKKPEGLGKKYTFSGSVYFHRMQELGLYT
TDVASVRERVDRSGLSGI FKQRLI NI KK

>2617920481 Ga0073689_10855 stage V sporulation protein R [pelotomaculum
Ga0073689 : Ga0073689_108]

MKINPQEEI KLLLEEALGKI SI KAREFGLDFYDI YFEI CPADI I YTFGAYG
MPTRFSHWTFGKAYHKMKTQYDYNLGRLYEMVI NSNPCYAFLLLEGNSPI Q
NKMVMAHVMACHDFFKNNAYFKSTSRDMVESMAAADRFGRGYEFKYNRDK
VESFI DAVI AI QEHVPEPRLLVKEKKVEKEKKKKKGCRERPETPYDDLWG
LDEKSQCECTGCEQPKKFPPEPEKDI MMFI I QHSKELEDWQRDVMSVI WQ
EMLYFWPOMETKVMNEGWTYWHLR I MREI EVDEAEAVEFAKMHSGI I QT
SRTRLNPTYTLGLKI FEDI EKRWDNPPQEEKEKYGRPGGEGKQKI FEVRAT
ENDI SFLRNYLTKEI EEMDLYLKKTGFWDKI VDKDWEKVRDGLVNNLT
NGGYPII VVQDGFNKRGEIYKHA FEGNELDVYILEKTLPHVHTLWGRP
VHLETVI DNKPVLFTYNGEGSKKFL

>2617920480 Ga0073689_10854 Histidine kinase-, DNA gyrase B-, and HSP90-like
ATPase [pelotomaculum Ga0073689 : Ga0073689_108]

MNSGRPVTRFAPAERASDKFVAEQSKI ENMFGSCSFFDALPNI VMVLNR
HRQVI LCNRLLLDLLGVEDYESVKGLRPGELLHCVHACETAGGCGTTEYC
SSCGAVNAI LESQQGREVYHECRI SVNNGRGLEAMD LGI TAVPI NI NGED
FTVVMVDI SAEKRRRVLERI FFHDVMNTAGGLMGLVELLESTADSDLVR
EFTLDI MSSAKLLVEQI REQHDL LLAENNELRVDMTPLRSLDLLTEAGH
FNGFETSGGREI VI DPAAENVFVSNNRLLHRVLGNMLKNAHEASQDGEA
IRLGCRLWNGQVEFWVNNPGMPREI QLQI FQSFSTKGKDRGLGTYSMK
LLTESYLQGTVSFTVSEKEGTTFFAWYPLKPDQLDSGQTS

>2617920479 Ga0073689_10853 curved DNA-binding protein [pelotomaculum Ga0073689
: Ga0073689_108]

LSVSYQDYIKI LGVDRNATEKEI KTAYRKLAROWHPDLHTGKDKEEAERK
IKQI NEAYEVLGDKEKRVKYDQLGAGWQTGQDFHPPPDMEGI HFYTTSGE
GAGMDGFSDFEFMLFGGGGFGARGFGRRTTRPRSPVRGQDVESELELSL
EEAYRGGEKSI QI STQEVCPACGGAGYENNSFCPRCGSGI KTGFKTLTV
KI PTGVGEGNRI RLKGQGGEGLRGGERGDLYLKVRLLPHPVYKI QGRDLE
TEI TLRPDQAVLGDKVTVPTLDGPVTMKVPAGTRAGRLRLRGKGLPLEG
GGRGDQYVLVKI DI PERLTAE EHHLYKQLAALRKGA

>2617920478 Ga0073689_10852 MerR family transcriptional regulator, heat shock
protein HspR [pelotomaculum Ga0073689 : Ga0073689_108]

LEKRFYLQVHYHHALTPGEEDVWVDVQSLDLHPEVI KHLAEMGI VEYREG
LI PARQVARLOKI ARLRRDLGVNLOGAAVI LDLLDRLERLQEEELRLRKR
FP

>2617920477 Ga0073689_10851 fructose-bisphosphate aldolase, class I
[pelotomaculum Ga0073689 : Ga0073689_108]

VTGKEI RMKRLFKRSKRLFI VPMDHGVTVGPI AGLEDI RRVVKSVAQGGA
DAVI LHKGLARQI TEYI TPGGCELI VHLSASTALSPDPNRKELVSSVERA
VRLGATAVSAHVNLAGSYETQMLKDFGR LAEECDLWGI PLLAMMYVRDGS
RESEYDPVKI RHAARI AEELGADI I KVNYTGSPETFARVTSAVNI PVVI A
GGHKMDSTADLLAMI ADALQAGAI GVAI GRNVFQDNNPALLASNI RNI LD
GDI PRL

>2617920476 Ga0073689_10850 3-dehydroquinate synthase II [pelotomaculum
Ga0073689 : Ga0073689_108]

MGKKQREI WFDGRAVPLKRQDI WGLI NNSPI KKVVVSAEQHREGHYPHKT
ELI TEI QNVEDLDDI TTEETV LSENQELLEI ARQCGYKTCGLFSVKGWDS
LQSWQDAGKYNIAI VDFDLPTNI PLELI I ARLODRRTVLLRRVDTFADM
EVAFGVLEQSGDGLFSVTDMMEI QKLSNYLTRKNI HKI ELHPLI VREI R
HI GMGARACI DTTSHMTPEEGMI VGSTSGGGI FI CSETHYLPYMNLRPFR
VNAGAI HSYVWMPNDTAEYLTDLAAGSKVLCVNI NGEARELSVGRVKI EV
RPLLLLVKGEAAGRELNNI VQDDWHI RLMGADGKPKNATMVRPGDKLLAYV
CDPGRHVG I KVDETI I EK

>2617920475 Ga0073689_10849 hypothetical protein [pelotomaculum Ga0073689 :

Table S2

Ga0073689_108]

VDKKEI KAAVDVFKGKI DDALKGNDVVQDI QEAVWDLKDLGVELQSK

>2617920474 Ga0073689_10848 phenyl acetate-CoA ligase [pelotomaculum Ga0073689 : Ga0073689_108]

LKPQNKLEALNRVLERCKSSPFYKERI TGRPLRSLEELKHLPLTTKEDLR
RCSPFGLLCVPRSELYQYHETFGTTGNPVSTWFTRDDI RDNARQI TALGV
KLNEDDTVLVRFPYAI SAVAHMCHAAAQMKACVI PVSSRSVSPFPRVI
NLMRKLEVTVLACLPLQAVLI AETTELLGFKPKQDYPHLRAI CTAGEPLT
HGRRLLEDI WGVPI FDFYGM AEI GTAVVDCEFCRPHPLEDYFI FEVLGN
DLKTDVKTGETGFLVVTTLNWRATPVI RYLTGDRARVVEEEACGREFSL
EVRGRLEDTI TI NNRELDRLDDI VSNFSCRRFWVAGPAPGGLHFVVEE
EKTGDKI SPELI RMLESRYNMKLRVDVVPKGTLYDRSELDDVGVGPKPF
IYSAREMEQKAYMKS AKI

>2617920473 Ga0073689_10847 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_108]

MVLI DAHAHI SDTTYGNVEI YLEQLKEAGVNRGVVPGMLDVRKI TDYI
TGKLTENPAPDNRYVEESCQAHSGLWSFVCVNP HDLDALQTMESFKQG
CRGLKLSPLSHQFSFASKAVASLASCCGDYGYVPVYTHVVFSPGASTTRFV
ALAKQFPKTNFI LGHMGFGPADQEALAAAKLDNLFLETSSGSFLHI QEV
VRKAGPGKVI FGSEFPLSHPAVELKKI LLLDLK DGERDKI LGNNI RALLC
LV

>2617920472 Ga0073689_10846 phenyl acetate-CoA ligase [pelotomaculum Ga0073689 : Ga0073689_108]

MNSLFEKKLQRLNKP AI LDKYFSDEEFDPGMP LTKLVDFQKESI REI VSL
VYERSPFYREK MTRAGI I PDDI KEFSDLARFPFTTKEELRGK PWLLAYD
KEDI ALVQVSTGTTGEEI YI MYTWEDFYLHELSPGYPKLVPVERGDI VL
NALPYEMSSAGLAFHKTFMEGCRATVI PAGKGGAYSTPAKTVKLI HDLRP
NVVI TTPSWAI TLAEAAEQSFELNSVPLKKMWLTGEGCSPA FRERVEKI
WRATANFYYSLECGAVGMECDAHNGYHI PMGHVVVEI VDPETGYVLEPG
EI GEI VVSCLVRYHTPLLRYRTQDLGYI DDPDCSCGVALPRLFLRGRLVD
QVLI QGI SFSPFYLEEFLMRI PEVGNWFQFVDPAGSDI LKI RVELAEGV
QPSAELADSLASKMEFGTGLPCQFEI VDKI SRPRGKTVRVVHS

>2617920471 Ga0073689_10845 Tetratrico peptide repeat-containing protein [pelotomaculum Ga0073689 : Ga0073689_108]

MTKFQPWLFKPYWFSRQREKENDVMTDSGQSNQGEKELSTCEGGEKRKS
SNMAVEKKI NPVEI GNVENLKI HESVVCNEQLDKGDCSERTPASFA
GKSWAELFAEAVKLHQYGI AGNKDAVKEAYELLKKI RGMDPNNNLVEAYY
GSATALLGRDLVDPMERFKKAVKGLKI LDRTVSNDPENTEI RI LRAYVSY
RLPEMYFHRTATAVEDFSYLSRYEQDPSVFSEEFYWQI LFDLGFANKTL
GONQEAESVWLKLLSI TGDTKYKGLLKQHG I KTI QDQEPEQVTDLTGPYK
TESTFEPEAKLLSQKKEKLLQEG I KLHALALSGDQEATKKAFFFTDALE
I DHDDQLI KAYHADCMSMTGRDGADVAEMFTSAI KAMKVFD SAVNTDPDN
I KI RFLRANHSYRLPEAFFRRTVTAI TDFEYLI QRYENEPTI I SEESYQQ
I LHD LGVAYQRLGLEEEAFAWEKLLSLDPNSKYKPI I EKQRGYDLPGSP
FEHLSLDHREAYVEEGHQLHELGVAGNKA AVKALDLWEKAYEADPKDTV
AQAYYGSC LALSGRDSTDPNI I FSNTI KGLKLLNRAI SRNWKNPKI RLLR
AYLAYS LPESFFHLTERAI KDFRQLK MAYEQDNNVFSRELYHQI LYDLGI
AYQRTGNPNPKAKKVWSKLLKESEDPKYKALLHGKVENQG

>2617920470 Ga0073689_10844 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_108]

MGGKLNSLTDVLKKT I FFFEALSVAELAPHVQRKMLKD YALPQVEEKVSL
CLGQNP CFYKEKDNWRNLNLEGDKENDQFYSLLLKKGQPLN LREI LKSANS
KKKKAKKI LSEEAGLI SDGRFI QLDNGYWGLTEWEVETSHYSFKHLVI KA
MKI HPGGLSLQQLHQLI NSWRGTDI KTL EEVLHKFPYFEPAGEGVWSYNP
TTRVI YEDLLKKFLNLTGKHKDRWRRDRARWKNKI ETAQKQLQEAVAGQK
EAAAALAEKLELAGQHDYLLTQMAEKD LLLSLRKREI I RYREHLKKLEAK
ANSI LHQCRLWVKRTREAEQETAKLRESLEKNQGNLEGLFKKLOQYKEKD
RENKARLAELKEQHSI RVAELQTEI VELKQRMERERTLAAAEEERRLQEEI
NDLSNDLKKALRVEEEQQRSYLMAQHELA AAREGYKNLERRMRHPLVRLV
MRI CSFFDGYSRQSV

>2617920469 Ga0073689_10843 IMP dehydrogenase [pelotomaculum Ga0073689 : Ga0073689_108]

MWPEKFEKI GLTFDDVMI I PAASEVLPRDVT TTTCLTKNI KLNI PIMSAG

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MDTVTESRMAVAI AREGGI GVI HKNMPVERQALEVDRVKRSEHGVI SDPI
YLAPDNLVREALVLMERYRI SGVPVTVEGKLVGI LTNRDLRFERDFTKKV
GEVMTKNNLVLTAPVGTTLTLEQAKEI LQQYKI EKLPI VDDDFNLRLGLI TI KD
I EKSROYPYSAKDKRGRLLVAAAAGVTGDVMERVDALVRASVDVI VMDTA
HGHSRGVLDVTQI KERYPEI DVI AGNAATAAATRDLI RAGADAVKVGI G
PGSI CTRRVVAGI GVPQI TAVYDCAREAAAYGI PVI ADGGI KYSGDI AKA
I AAGADVVMGLSLLAGTEESPGDI EI YQGRSYKVYRGMGSLGAMKEGSKD
RYFQEQAESEKKLVPEGVGRVPYKGS LAETVYQLI GGLRAGMGYSGCRN
I HELKTKSRFMRCTAAGLKESHPHDVVI TKEAPNYSLO

>2617920468 Ga0073689_10842 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_108]
MI DDQDTFFQSRVPWSI VPSLKEMAHEVGVDFRFI DGI KDDKTNAEMAR
EFDVSEKLI YHLRDHFYAHGVHSI MGQD

>2617920467 Ga0073689_10841 alpha-ribazole phosphatase [pelotomaculum Ga0073689
: Ga0073689_108]
MSCRI YLVRHGETEWNALMRFQGQTDVPLSDKGRLOADLLGKRLAREKI Q
GFYASDLKRAYETATI LSDFHGLEVKTVPELRELNFGVWEGLTKEI KAS
FANELLLKWWESPLSTRI PGGETLGEMVERSULAI KKI VGRHCEGNVVVVT
HGGAI RSI VGS LGMDLNKYWRLRLDNACLN I DFPEWEKGI LI LFNDCS
HLYNPVSCA

>2617920466 Ga0073689_10840 L-threonine 0-3-phosphate decarboxylase
[pelotomaculum Ga0073689 : Ga0073689_108]
LOHLEHI HGGNVVRASLKYPEDKMI DFSANI TPLGPSEKVI AALTDSL
SLI SRYPDPCGELKATLSAYLGPESCLLMGNGATELI YLLVRVSGARR
AMI PAPTFCEYGLSVLSHGGEVLEI VMDEEEGFRLPVEKI LNRLREVDLL
FLCNPNNPTGRVVDGETVKLI LEEALPRGVTVLVDEAFMDFVPRREFYSV
MTLAGKYPNLAVLYSMTKFFGI PGLRLGAI AAPEELVRRMGGAADPWNVN
I LAQVAGVAGLRDREYMLETNRLVREEKQFLFHGLSGI SGLKPLPGAANF
I LLDVSHSGLTSAELTDLLGKRG I LVRDCAGFTGLAGRYRLAVKTRPEN
ERLLOALKDI LETDSI AVGGPTASTTRDNVAP

>2617920465 Ga0073689_10839 cobalamin-5'-phosphate synthase [pelotomaculum
Ga0073689 : Ga0073689_108]
LKGI LFAFYQLTRLPLPAVPFDEVACGRSI AFFPAVGFFLGS I LAALEWT
AGWFYPTQVRAALLVAGMVVLTTGGI HLDGFI DSI DGLFSGRPRERKLEI M
RDSRVGAFGVI GI I CLLLLKYSLFQGLTDQALTRLLPVI PALSRWGMSLA
I VAFPYARQEGLGKFYVAYAGNKELVVATI MAAAAAALLGPPGI WMTTA
GAVTLLAGWKI KKELCGLTGDTYGF I NEFLEVLLLAAYPI LKTEI I

>2617920464 Ga0073689_10838 cobyri nic acid a,c-di amid e synthase [pelotomaculum
Ga0073689 : Ga0073689_108]
MNNI PRLLI AGTHSGVGKTTLSTALMACTGLGYRVQPYKVGPDYI DPGY
HGVATGRVSRNLDCWMLGEEAVRELF I RSALDADI SLVEGVMGLYDGLGA
TSFSSSAHI AKI LNTPVLLVLDARSMARSAAAVVLGYRELDSEVI I AGVI
LNRVGSQRHFRI LREAI QDACHVPVVGYPVPRQAGI ELPERHLGLLPTAEK
DGLTGHVGAMAEAVKEGLDI QOI LALADDAGSSPEPLHQVFPGVKADCRV
RLGI VRDRAFNFFYYQDGLDVLALGAELVECSPLDGGGLPGNLHGLYI GG
GFPEMFLEEI SQNEPFKKDLRAAAAAGMPI YAECCGLMYLVS AI I DFAGN
EYPTAGLLEGRCRMGGKRAALGYVTATALSNSI LCTEGSSLRGHEFHYST
LVMDQQYAGAYRLTRWGE GPAGEDGI AAGNI LASYVHLHFAGCPGAAARF
LEHCKEYRDCKEL

>2617920463 Ga0073689_10837 adenosylcobi nami de-phosphate synthase [pelotomaculum
Ga0073689 : Ga0073689_108]
MPEI TGLYVFLAYLVDLAVGDPRVLPHPVVL I GKAI KRLESVMRRI ARSS
AGLRVAGVV TALVVVAGSWFSTSI LLHWAFTFNCWLGAALSI WLI STTMA
ARLAGAAGEI FALLAGGDLVEARRKVGWI VGRDTGNLTAGDVTRATVET
VAENI VDG I I APLFYAFI GGAPLAMAYRAVNTLDSMLGYKNKRYI DFGWA
SARLDDL TNYVPARLTGLLLLGAAGLAGLNAKRALATI RRDASGHPSN S
GI PEA AVAGALGVRLGGLNHYQGGASFRAYMGEDLNPLEPVHI KQTVKLM
YLTSVLAVSI GALI AI LAEYLPVKDVL I

>2617920462 Ga0073689_10836 adenosylcobyri c acid synthase
(gl utami ne-hydrol ysi ng) [pelotomaculum Ga0073689 : Ga0073689_108]
MVQGTASHVGKSVLVAALCRI FARDGYRVAPFKSQNMALNSFVTKDGGEM
GRAQVVQAEAAACVEPSVDMNPVLLKPTGHASSQVVVLGRPVG NLSAGQYH

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TEYAPKALGI I EGALNRLRSDHDI I VI EGAGSPAENVLQEREI VNMRI AR
LAGAPVLLAADI DKGALAAVVGTLLEI SPEDRERVAGI I I NKFRGDLRL
FQPAVDLFLEKKTGKPVLGVPYFQDFRVQEEDTVSEDRSRAELVEEQGWV
EVAVVHLPHI SNFTDFDPLEDELDI RLRYVGRGDGLGKPD LVI LPGSKNT
I EDLAF LKHSGMADQMAELYRAGTPVI GI CGGFQMLGRELNDPLRTESVI
PRMEGLGLLDSTTFAPEKVTTQVEAEAAGAGLFLNGAPAGLVKGYEI HM
GRTELVSGVRPAFTVLARSGEKVFFPDGAVSQDGLVFGTYI HGI FDNDEF
RRHVI NTLRI RKGLEPLASGWTVSTVEQRHRDFDKLAAVVRGSLDI SKI Y
SLLGLAGR

>2617920461 Ga0073689_10835 adenosyl cobi nami de ki nase
/adenosyl cobi nami de-phosphate guanyl yl transferase [pel otomacul um Ga0073689 :
Ga0073689_108]

MRGKLI LVLGGSRSKGSEFAEKI AGHMGASVI YI ATAARDGEMAERVRL
HRARRPRSWETVEEEKDI FKVLKDGREGDVFLDCVTI WLTNLLLDERI P
GPGVEQAEKEAYVLKLA I RLTDTVRTGAHLI MVSNEVGLGVVPEYPLGRA
FRDLGKVNKVLAEADQVYFTVAGLPLAI KSLARVELG

>2617920460 Ga0073689_10833 protein of unknown functi on (DUF3842) [pel otomacul um
Ga0073689 : Ga0073689_108]

MKI AI VDGQGGGI GKHI TEKLRLRELDPNVEFLALGTNALATSVMLRAGAN
EGATGENAVVYNAGRVDLI VGS I SI LFPNAMLGELTPGI AKAI ASSPARK
I LPLTRSGI DI VGLKSEPLPHI EELI KVKELLI HQETD

>2617920459 Ga0073689_10832 hypotheti cal protei n [pel otomacul um Ga0073689 :
Ga0073689_108]

VEDNADI PNLMKRI RELEEKVEQLRLSRRVLMNLI EKI EKDKNGCLSHLE
KENRKLHRDNYRYARWLLCKNRQI VELESKLRSI SRNSAK

>2617920458 Ga0073689_10831 hypotheti cal protei n [pel otomacul um Ga0073689 :
Ga0073689_108]

MSVDLHI HTTASDGVNSPEEVVGRAKALGLKAI GI TDHDTLEGVEPAFAA
GRLHKI DVLPGVELGAEROGEEI HI LGYLI KLHHRFLDKLAFFRETRI K
RMEEMVKRI GKLGFLVTMERVREI AGSGSVGRPHLAAALVEAGVVENTTE
AFEKYVGNCPAYI PRYKLDPVEAVHLI RAAGGVPLAHPGLNNTARLLE
ELI EVGLAGLEVCHPVHTREQVSYYFRLAGEYGLI ATGGSDFHGPGHKAG
CLLGAETVPYSVVEELKKAER

>2617920457 Ga0073689_10830 membrane di pepti dase [pel otomacul um Ga0073689 :
Ga0073689_108]

MVEEMLI GKAAALHRESI VVDAHCDTLTAMPGQRRRLGELSCLGQLDLPR
LRAGGVKVOFFAAFI APEFKTAPLRKALELI DLFYKEVDANKQDI ALVKN
LSEI EKAVTSDKI AALLSI EGGEALEGSPGVLRLMYHLGVRS LTLTWNSR
NELGEGVGEEPTYAGLTPFGRVVVREMNRLGMLVDI SHLGEKGFWDVLGV
SRQPIV ASHSNCRVLCHEPRNLNDQOI RALADKGGVMGI TFVSSFLGGGK
PGI GAVLDHI DHVVAVGGI DCVGLGSDFDGADEPPLGLEDCSRLCGLTEG
LLERGYGNI EI KKI LGGNFWRV I GQVLK

>2617920456 spoVS2 stage V sporulati on protei n S [pel otomacul um Ga0073689 :
Ga0073689_108]

VEVLKVS AKSSPNSVAGALAGVLRERGC AEI QAI GAGALNQAVKAVAI AR
GFVAPSGVDLI CI PAFTDI VI DGEERTAI KLI VEPR

>2617920455 Ga0073689_10828 hypotheti cal protei n [pel otomacul um Ga0073689 :
Ga0073689_108]

LQLLMI GDI FGRSGRRAVKANLSGLKKEHDLDLVVANGENAAGGKGI TRE
VAQELFASGVDVLTMGNHVWNKREAF EYI DQEPRI VRPANYPPTPGI GA
NVYETR RKVKVAVI NLAGRVFLQAI DCPFRKAEELVGEMKKKARVMVVD
HAEATSEKNAMGWFLAGKSAVI GTHTHVQTADECI LPGGTAYI TDLGMT
GPRYSVI GVKKEI I I NKFI TOI PORFEVATGPFQFNGVI I DVNEETGEAT
FI RRI QNHERE

>2617920454 Ga0073689_10827 hypotheti cal protei n [pel otomacul um Ga0073689 :
Ga0073689_108]

LGFRYKANRDAVTDVGLLI SI LVRYPEVATI NFDPEKQLLKFTFMYSKV
LGDNELENL KQRLMSDI EVYNFLEEKDTRMVSLSHQI CDNLTLI EVQRDV
DTLAQEEI ALI VELFRQHLNANLVTEENEQLI EEDLI AQEEI I EHMLES I
KCSNQDKFLFAFREEGKVLVFNK

Table S2

>2617920453 Ga0073689_10826 ribonuclease Y [pelotomaculum Ga0073689 : Ga0073689_108]

MNVNTI LI VI GAALAAFAVGYLVRKYLAELAKI ASAESEAKKI LDEAGKEA
EAKKREAI VEAKEEVLKLRNDMEKENRDRRSELQRLERRLVQKEETLDRK
VDLI EKKEDALNRRESEI EAI RTOLTEVYNROLSELERI SDMTSEEAKQA
LLSDI EKEI QHEAALMI KDMENKAKEEGEKRARDI I SLAI QRCAADHVAE
TTVTVI PLPSDEMKGRI I GREGRNI RAFETLAGI DLI I DDTPEAVI LSGF
DPI RREVARI ALEKLI VDGRI HPARI EEMVEKAQKEI NTQI REAGEQATF
ETGVHGLHPELVTLLGRLKFRTSYGQNVLKHSI EVAHLAGLMAAELGVDI
QVAKRAGLLHDI GKAVDHEVEGPHVTI GVDLARKYRETFEI I HAI AAHHG
DEEPKSI I AVI VQAADTI SAARPGARRETLEAYI KRLTKLEEI ASSFEGV
EKSFAI QAGREVR I MVKPKVDDLGA I RLVREI TKKI EKELDYPGQI KVV
I I RETRVVEYAR

>2617920452 Ga0073689_10825 RecX family protein [pelotomaculum Ga0073689 : Ga0073689_108]

MESLEDYGYI NDET FALLWVEQRLAKRGLPGLKRELLKKGVDTWVI SEIM
AELDPEVEFGAALEMAKKR

>2617920451 RecA recombination protein RecA [pelotomaculum Ga0073689 : Ga0073689_108]

LSDROKALELALMOI EROFGKGS I MKLGEASAKLNVEVI PTGTLALDVAL
GVGGVPRGRVI EI FGPESSGKTTVALHI I AEAQKMGGAFAFVDAEHALDP
VYAGNLGVDI ENLLVSQPDTEQALEI AEALVRSGAVDVI VVDSVAALVP
RAEI EGEMGDAHVGLOARLMSQALRKLTGSI SKSRTTVVFI NQI REKVG
VYGSPEPTTGGRAKLFYASI RLEVRKQENI KQGA EI I GSRTVRKVVKNKV
APPFKQADF I MYGAGI SREGSI LDMAADLNI I SKSGAWYSYGEDRLGQG
RENVKEYLKEHPMTKEI ELKARQVLNVGGQKAPAAGAPGGNGVASED
N

>2617920450 Ga0073689_10823 ATP-dependent RNA helicase DeaD [pelotomaculum Ga0073689 : Ga0073689_108]

MTLKDTVNFGLSEVNRRVAHALTDMGFEEPTPI QGKAI PLI MEGKDLI GQ
AQTGTGKTAAGFI PI VEMI NTRYGGVQALI VTPTRELA I QVAEEI SRI GK
YRRARTLPI YGGQSI DRQFRGLKQGVQVVI GTPGRLLDHLNRKTLRLNI
KMVVLDDEADEMLDMGFI DDI ESI LQATPAGRQTLLFSATMP E EI KRLSRK
YLOSPEFI TVSKNNLTVPQI EQVYETREHNKLEGLCRVLDSI SVTLAI I
FCRTKRGVDEL VAGLQARGYPAAALHGDLSQYQRNHVMRQFRTGQI DYLV
ATDVAARGLDI ENVSHVI NYDVPQDAEFYVHRI GRTGRAGKSGVAVTLI T
PRDYKQLRLI ENLT KTRI RREKLPSLADI HERQKEGVRERLQRM LAEGKL
AYYRTI VGTLLDDYDPVDI AAAALKLSLDLDGERDEPDVDSFGNTGARPG
MVRLFMTLGRKDNVSPGELI RI MAESGI PENSI GNI NI YEKFTFVEVPE
EWAGCVI GCLHRQTVKGRRMSVEPARGG

>2617920449 Ga0073689_10822 competence/damage-inducible protein cina [pelotomaculum Ga0073689 : Ga0073689_108]

MKAELI FTGSELLLGHMLNSHSQYLGMLSEI GI EVI LHTTVGDDWGR LG
QVLROAMERSDLI I TTGGLGPTTDDLTKKT VANVLNLPALDEKALAAI R
GFFNNRGLVMPESNKKQACFPASAVI LPNSRGTPAGALI ERENKI I AMLP
GPPGELTAMFEESLAPFLFKKI RGGTVTRYKVFKLTGI SESAVYDRVKDL
GGQGNPGI AYVAKPGEVQVRI MAWASSEQA EKMVADLSEKVRRLVGYI F
GYDEEVLEDVVGKLLLEKGLSI AVAESCTGGLI TARLTDI PGSSGYLKGG
VVAYSNEVKNEVLAVPPDVLGQYGAVSKQTAVAMAEGVKKLTGSNLGLAV
TGI AGPGGGSAAKPVGLVYI SLAADDGTCCREYRFPGERPAVRQGTANAA
LNMVRHYLLAK

>2617920448 Ga0073689_10821 vesicle-fusing ATPase [pelotomaculum Ga0073689 : Ga0073689_108]

MLKEI SI GLGLAAI I SLAVMGYDI TPFLFLAAAAGGLYYI ARMRGLVSAR
NFESGSLSRREVSFGDI GGQESAI QELKEALDFI KNHQDI KRLGI RPLK
GI LLTGPPGTGKTLMAKAAAAYTDAAFVSASGSEFI EMYAGVGAQRVRKI
FQTAREASALRQNSNALI FI DEI EI LGGKRGQTTSHLEYDQTLNQLLVEM
DGLKVDDKVRVLLVAATNRADMLDPALLRPGRFDRRVKVDLPDKEGRLEI
LKLHTRNKPLAEDVRLEI I AKETFGFSGAHLESLANEAAI LAMREGCGEI
SQHHFNESI DKVMMGGKLDKRPSEAEQMQRVAVHETGHALI SELVRPGSVS
TLTVTPRGDALGYMRQVPEDDTYLYTKDYLENQI AVMLAGAVAEV I LGN
RSTGSSGDFEQAVRTADTMLRSGMSELGVVCPDSLPRDLKHRTLTGI VRE
QEERVRSHI TSSKHVFTRVVEI LLEREKI NGGLFRSVLWNNEREQEPVH

Table S2

>2617920447 Ga0073689_10820 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_108]

MRWQGLKI PVI I L SLLAGMAFI FGVQWLYQKYSLOEPLNAALSRNNAVES
FOVNSDGRLLRVNVVLKYDADLMQAYKEVRKELAGTLGKRPFQTLTGDSR
DDVLNKNVWYNSQYAI YQAI EOGSYQDMAAVVHREAGATGAEAKI YI DEEN
I YLRLKHRGHTLDQVI PRGAGRNSGNVRAPAAGGGADAQGN

>2617920446 Ga0073689_10819 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl transferase [pelotomaculum Ga0073689 : Ga0073689_108]

MNLPNKLTARLLLI PVFLI TASMRYQYADYI AAVFI LGAATDGMGGYI
ARKRGQVTLGKFI DPLADKI LVSAALI ALVELSRLPGWVAVVI I SREFA
VTGLRAVAAAEGVVI SASGLGKVKTVTQI VAI AVMFVNGYPFNLLHLPFG
GI AMAVALI FTI WSGLDYFLKTWKI LKKGGF

>2617920445 Ga0073689_10818 SSU ribosomal protein S12P methylthiotransferase [pelotomaculum Ga0073689 : Ga0073689_108]

MSVKVGLI SLGCPKNLVDSETMLGLLKDAGFEI TGREREADVLI VNTCSF
I DDAKEESI KTI LELARLKEEGKCRALLVTGCLAQRYPGELQAEMPEI DG
LI GTGLLPVPGVVRRLAGEKVVAVGAPGYLHSARLSRI LATPGYTAYL
KI AEGCDNRCSYCTI PAVRGPFERSREI DDLLAEAEELAGRGVKELI LVAQ
DTTRYGKDLYGRPVLDGLLGRLLAAVEGLVWLRLLYTYPTLLTDELI RLMA
REKKI CRYLDLPLOHAANPVL SRMNRGGREEAARLVEKLRSEVPGI TLR
TSFI VGFPGETEEDFRELLDFMAQVRFDVRGVFAYSREEGTAAEMSGQA
PEAVKVERRERAMALQEI SLEKNRRKI GEEI TVLVEESGLKERGFYTGR
SEGDAPEI DGRVYFKADRI LNP GDFVKVSVKGARPYDLTGELVP

>2617920444 Ga0073689_10817 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_108]

MAKENSFDI VSQVNLQEVNNAVDQALREL RARFDFKGSKSDI TNDGEQI T
LI GDDEFKLNKVVVDI LEAKLVKRG I NLKALRYGKVEPAANDTVRQRVSLV
QGVDRKAKVI TKLVKESKLVQTSVHGDQVRVSGKNRDDLQAVMQI I KD
HEFDI PLQFVNFRTF

>2617920443 Ga0073689_10816 protein RodZ, contains Xre-like HTH and DUF4115 domains [pelotomaculum Ga0073689 : Ga0073689_108]

VDI GNKLKEARAARGLTLEVVEQETKI RRKYLNAMEEGQFHI LPGPI YAK
AFLKNYAKFLNLDLEEI METYDRQFPAETVPEVPTTPASTSPGHVRKNA
SGKPRPWLYFAVAVI I TGLAFSVYYGVLGAAFRSANKPKGEPAPWTSLOP
DGOAQTPAGQPQAPGQI LPTRTNGI NMVLNVKNAESWI RVDADGSPVFQ
I VPAGOSKNFDAREKI YI RLGNAAGVVEVLVNGQNLGLGGPGAVVDREFR
SGSQ

>2617920442 Ga0073689_10815 tRNA 2-selenouridine synthase [pelotomaculum Ga0073689 : Ga0073689_108]

MYREI TVEEAVEMEEALLI DVRSEGEYGEDTI PGAVNI PVLNDEERA AVG
TI YHHQGPAPARRLALVELVSPKLAEKVAAVDKLADGRKLAVFCWRGGQRS
QFLASVLDTMGYDVYRI I GGYKAYRRHVNQYLDQEEELNQRAVVLHGLTGV
GKTEVLVRLGEKGLPVLDLEGLARHRGSVYGKI GLPPSPTQKAFENSI VQ
FLTGI GQNSVFI VECESRRVGNLLAPLALMNSMKKGYRVLLYTSLENRVK
RI REVYTKPGENI KELQEATYSLVKRLGKARVEELNRLLAGRKFTVFA
YLLKNYYDPLYKYPDGPSSGGYHLFVDTADI EKALDEI YDFVI NLREKKQK

>2617920441 Ga0073689_10814 DNA translocase FtsK [pelotomaculum Ga0073689 : Ga0073689_108]

MGSQSQI KEERRYEI I GI TMAALGVLGLVSLI SPSSGLVSEFVDRVLSI
AGEGRYFLPLI LI LAGI RLVRKRNRTKVSEMYGAVLLFLAVLTFHLI I
PLDDSFKAGAAGDGGVGLGALFSYI FRKSFGI AGTYI I LVTAGLVALLLI
TNLSLA AVAKGLAVRAGGI FKKMANGLTGFLFTEVEEKKENVGTGPVI I D
HASGQFTVETQPVVKEQAESEKEQDHVI SSPPAKKKGPVSRTGGKDERGN
PVKDDNEPVFLNRDVLSDGYYYQLPPLSI I SRPYRTKNVRLSKDI NENI R
I LEETLESFGI KAKVI QVSRGPAI TRYEI QPPAGVKVSRI VNLADDI ALS
MAAPGVRI EAPI PGKAAVGI EVPNKEI SMVHLRDLLETQEFVQARSRLSM
ALGKDI AGNP I VADLNKMPHLI AGATGSGKSVCLNTLI ASI LFKATPDE
VKFLMI DPKMVELATYNGI PHLVSPVVTDPKKAATSLRWAVREMENRYEL
FAATGVRDI TRYNKMFKTGGADGGQPLQVVL I DELADLMMVAPADVE
DAVCRLAQMARAAGMHLVVATQRPVSDVI TGLI KANI PSRI SFAVSSQI D
SRTI LDMAGAEKLLGKGM LFFPVGA AKPV RVQAYLSDREVEDLVEYLK
KQAEPPVYNEKI LI EEPREEEQPEMEDELLPOAVQI LI ETGHASI SMLQRR
LHI GYARAARLI DI MEKRG I VGGYEGSKPRSI LMTLEQFDQTFGKR

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>2617920440 Ga0073689_10813 undecaprenyl -di phosphatase [pel otomacul um Ga0073689 : Ga0073689_108]

MVEVLI MTVFOALVLGI VQGLGEFLPI SSSAHLVLPWALGWTYAGLTFD
VALHVGTLI SVVAFFWKDWLI LASDAVRRRRRTHEASLFWLLLVATI PGAA
VGYLFEEQAEVFRNPHLI GI MLI VMGI I LYWVDTRAPRGKSI RAVSPGD
SLLI GI SQAFAI I PGVSRSGVTMTAGRALGLTREAAARFSFLLSTPI I VG
AGI FKMKDI VTGDI NAAFI TGVSSAVVGF I SI GLLRLYLEERSFGI FVW
YRFVVGGLAVI VLAVFRSV

>2617920439 Ga0073689_10812 Yl zJ-like protein [pel otomacul um Ga0073689 : Ga0073689_108]

VI LYTPMQLELVLEGFDQNKYPDYGETHI NGI PI LVEDAGFGRKRVVKLL
STNPF DY LKPELSPGSLI EC

>2617920438 Ga0073689_10811 ATP-dependent protease Cl pP, protease subunit [pel otomacul um Ga0073689 : Ga0073689_108]

MKTFNFDPEPNVFPCTPKPGDPDAEPKPQRPEERLPDEHEKEPGGKKV
VGKAKGALEAMREMGSTQI PEVKSNI HCLTI VQGI EGHVLVLPQNKTTKY
EHI I POLVALEQAPEI EGI LI I LNTVGGDVEAGLAI AEMI ASVSKPTVSV
VLGGGHSI GVPVAVGAQYSFI ANTASMTI HPI RLNLVI GVPQTYEYLDK
MODRVVRFVTEHSRVTEEFRELMFRTGELARDI GTVLI GKEAVDVRLI D
AVGGI GEAVKKLNEMI EEWKRNRKEVPLQ

>2617920437 Ga0073689_10810 ribonuclease J [pel otomacul um Ga0073689 : Ga0073689_108]

LAKEPKLSLI PLGGGLGEI GKNMMVVRYGENI LLI DCGLMFPEEEMLGI DI
VI PDI AYLLNREFVRGI VLTHGHEDHI GALPYVLRQLNVPVYGTKLTLG
LLQGLKLEQNLAGDVTLYTVKPRDI VQI GPFKVEFI KVSHSI PDAVAI AV
HI PLGVVLHTGDFKI DQTPVDGQVTDHFRLAQLGERGI LVLLSDSTNVER
PGYTMSESVVGNFTDETFRQAKERI I I ATFASNVHRLQQA I QTAHRHNRK
VAVVGRSMNVVNI AYELGYMNI PDGI MVELDEANRLPKNRVVI LTTGSQ
GEPMSALTRMALSDHRQVEI VPGDTI I I SATPI PGNEKLVAKI I DQLFKQ
GARVI YESVSGI HVS GHPSQEELKLM I NLVRPKFFVPVHGEYRMLI KHAE
LARDMGI SPENFVAENGQVLEFTRRSGRVAGRVTAGKVLVDGLGVGDVG
NI VLRDRKLLSQDGI LI VVI TI NRETGLVI AGPDI VSRGFVYVRESEELL
EEAKI KVKCALDKCADRGI SEWSSI KSQVRDALGKFLYEKTRRRPMI LPI
I MEV

>2617920436 Ga0073689_1089 4-hydroxy-tetrahydrodipicolinate synthase [pel otomacul um Ga0073689 : Ga0073689_108]

LTSDFGCVLTAI VTPFNKDLTVNYNQMRKLARHLVQSGSDGLVVTGTTGE
SPTLTKEEKI ELYRVVVEEVGGEATVI AGTGGYSTAESI TLTQAAQKGV
DGVMLVAPYYNKPSEQGLYQHFKAESTNLPI VLYNI PGRTSVNI LPQT
VVRLAQI NNI MAI KEASGSLDQVSELKRLLPDHFVI YSGDDSLTLPI LAL
GKGVI SVI SHLAGRRI QDMI NAFTSGNTTLATEI HLELFP LFKRMFI TT
NPVPVKAALNLLGWQGVPRPLMEATAAEKETI KNLLESMLKI

>2617920435 Ga0073689_1088 aspartate kinase [pel otomacul um Ga0073689 : Ga0073689_108]

MNFI VQKFGGTSLVDEEMRGKVVARVVEARQQGYLPVVVSAI GRMGDPY
ATDTLLALARDCNRELSPRETDLLMSCGEI I SGVVMAATI QKAGCPAVFL
TGTOAGI I TDNNYNDARI LK I NPENI I KHARDGKVVVVAGFQGI SGEGEI
TTLGRGSDTTAAALGVALDAAWVDI YTDVEGI MTADPRI VSDARPLEAV
TYNEI COLAHEGAKVI HPRAVEI AMQKNI PLRVKCTFSDAPGTLVTSHGE
VYKEAI DI NRDRTI TGI THI PDI TRI KVVTDAGNI PDFQRI FKALALA
GI SVDFI NVHPEVVLFTVKSSVAARAVQVLENMGI DPEVLDPDAKVAAGV
AGMTGVPVGMKI VEALAGEDVQI LQSADSYTTI WVLVKGDMMVKSI RAL
HHQFGPGQNNRTI

>2617920434 Ga0073689_1087 aspartate-semi aldehyde dehydrogenase [pel otomacul um Ga0073689 : Ga0073689_108]

LKKYNVVVVGASGAVGQELLRVLEERDFPVGELRLCATSRSGKEFPFRG
RSYKVEVTSPESFSGMDLALFAGGAASKEFGTAAVERGAVVI DNSSNFRM
DPAVPLVPEVNPDDVKWHKGI I ANPNCSTI QMVVALKPI HDAARI KRVV
VATYQAVSGAGLEAMEELTVQTRAVLDGGETVPRVFPYQI AFNLI PHI DV
FMDLDYTKEEWKMKETQKI LRDESM I TATTVRAPVYRSHSEAI NI ETE
KKLI AAEARRLFEEFPGI VVDEPAVKKYPMPPLFASNRDEVFVGRI REDN
SI PNGLNI WVVADQI RKGAAATNAVQI AELVVGYGCLLKA

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>2617920433 Ga0073689_1086 dipicolinate synthase subunit B [pelotomaculum Ga0073689 : Ga0073689_108]
MRLEGVRVGFALTGSHCCLDQVMPQLRKLVDGEVLPVI SSAVDASNTK
YGTSEKWKGLI KEI TGRDAI ATI VEAPEI GPQKLLDVMVAPCTGNTLAK
LANGI TDTAVLMSVKAQLRNQRPVVLAVSTNDGLSMNARNI GLLLNKNI
YMPFGQDNPAKPNLSMAKWELI ADTI LEALQGRQLQPVLVAI

>2617920432 Ga0073689_1085 dipicolinate synthase subunit A [pelotomaculum Ga0073689 : Ga0073689_108]
MQPDLGGTGVAVLGGDARELVLEELAASGALVNVAGLPVKDGMTGVVWR
REPLQCLAGVKAVI LPVPGVDEKGFYLCPLVEQPLVFTMELAAKI PAGAP
VFVGMARSALVELASREGLRLI ELMKLDEVAI LNSI PSAEGAVQMAMEML
PII I HGSNAFVLGFGRTGMTLARLLGAMGAKTRVVARKEHLARVLEMNI
I PVPMQLMAGCLGEADVFNFI PAPVLTAEVLKEI SPEAVI I DLASAPGG
TDFRTAESMGI KAVLAPGLPGKVAPRTAGRI LARVVTRLLVEEMAGS

>2617920431 Ga0073689_1084 dihydrodipicolinate reductase [pelotomaculum Ga0073689 : Ga0073689_108]
VIRVMVTGAYGRMGREVMKTVWNADDMELVGAVDRQGDGVDAGTLLEAGE
TGLVI EKDLEGALARTRPDVAVDFTGPGAVYQNTI NCLNRRVRPVVGTG
MSPEQI REI I NLSERVGVGGLI APNFVAGALLMI KFAREAVRHFPHEI I
ELHHDQKLDAPSGTAI KTAELVEQRDSEFRQGLAAEI EKI PGARGGEFG
GGMRI HSVRLPGLVAHQEVI FGGLGQTLTI RHDSI TRESFI PGVLLGI RK
AI HLEKVVYGLDKLLFEQI

>2617920430 Ga0073689_1083 HSP20 family protein [pelotomaculum Ga0073689 : Ga0073689_108]
VNVNPVI HGNQNHSYPLMNGWPNFTSAMPNPWLQNAAGTI I PRMDI I ET
DAAI VYI YDLAGADSTQLNLLEVSSSEVVLTAPLVVANKYPDI KYI YQERO
KGSYARI VMPPAGVNMDEVKADLQNGI LEVTFPKHI KSK

>2617920428 Ga0073689_1081 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_108]
MKKWYSLI DKVYRLDNLEEAYQAVRANKGAPGKDGVTYVK

>2617920427 Ga0073689_10797 SCP-2 sterol transfer family protein [pelotomaculum Ga0073689 : Ga0073689_107]
MKFGSNEWGNAFKEVI NNDTEFTNGLADPENFTLNMEFAVPGTKFHLRFE
SGKLI YTGEPKYKEELALI I TTDSETWQKI ASGQEQATKMLDMGKI TVQ
KGPMDAVLGNAGAFNCFMADVGVKVPTEW

>2617920425 Ga0073689_10795 Transposase [pelotomaculum Ga0073689 : Ga0073689_107]
MAVRKRYPAELKAKSVLEI I KEEKTI SQVSSECGI HPTQLNRWKNQVMED
LPKLFSDERNALEVVSAGYEKQI QELYAEVGRLTTQLNLWLKKI RHLT

>2617920424 Ga0073689_10794 diaminopimelate decarboxylase [pelotomaculum Ga0073689 : Ga0073689_107]
MKLNGTMRVNEKGYLEI GGCDAVDLAKEFGTPLYVLDEAYFRQNCRDYYH
SFTFKYSADVI YAAKTLMTLAVCRMVDEEGLGLDI VSGGELYTALKAGFP
VNRLYFHGNNKSPAELAMALEAGVGRI MVDNMYELELLDQMAAGEVNKKA
VI LRLTPGI EAHTHKYI KTGQI DSKFGLVI ENSQAMTAVKRALEMDNI SF
KGLHCHI GSQI FELESYTHATEVMMAFARRVYDETGYYVEELDLGGGLGI
YYAEGDRPRPVRDYASVMGTVLDRAAKYGLPAPRVI VEPGRSI SGPAGT
TLTYVGAI KEI PGI RKYVAVDGGMGDNPRSALYQARYEACLANAGRPPV
ELVSVAGKCCESGDMLI WDI ELPAAEPDI LAI PCTGAYNYSMSMNYNRL
PRPAMVLADGGRADLI VRRESYEDLI RNDLI PERLAKK

>2617920423 Ga0073689_10793 tryptophan synthase, beta chain (EC 4.2.1.20) [pelotomaculum Ga0073689 : Ga0073689_107]
MNETKI LLTEEEMPTAWYNVQADMPNLPKPLHPVTRQPVGPEDLKPI FP
MEMI NQEVTRERWVEI PEEVREI YRLWRPSPLCRARRLEKALDTPAKI YY
KYEGVSPAGSHKLNATVPQAYFNKKEGI KRLATETGAGQWGVALSQACNF
FDMECTVYMKVSYHQKPYRRTMMQI FGSEVLASPSDRTNTGRQI LKADP
DSLGLSLGI AI SEAVEDAAGRPDNTYALGSVLNHVI MHQSI I GLEAREQLT
KADAYPDVVI GCCGGGSNFSGAAPFAHDKI VKGAKVRLLAVEPTACPTL
TRGYFGYDFGDVAGFTPLLWMYTLGKDFMPPGI HAGGLRYHGDSPLLSQL
VHDGI VEARAYGQSAVFQSAMFFARSEGI VPAPESSHAI HGAVEEALAAAR

Table S2

EAGEARTI FFNLSGHGLLDLPSYDAFLEGKLVDPLEEDLKKALEKLPO
I

>2617920422 Ga0073689_10792 CoA-substrate-specific enzyme activase, putative [pelotomaculum Ga0073689 : Ga0073689_107]

VQGYLGI DVGSVSTNI VFMDDDGVI REAI YLRTMGRPI ETVQKGLKELKE
RLPSGVKVRGVGTTGSGRHLSGVI VGADAVKNEI TAHAVASLMLVPGVQT
I LEI GGQDSKI I I LRSQVVSDFAMNTVCAAGTGSFLDQQAARLNI PI EK
GEI ALQAKSPVRI AGRCVFAESDMI HKQQMGCSLPDI LAGLCEALVRNY
LNNVGKGEMLAPVVFQGGVAANVGMKAFAFEKALGLPVAVPPHFGVMGAV
GAALLSREAAARKGPSSFKGFKVAETEFKAGSFECGCPNLCEVVEI AEN
GDI I ARWGDRCGKWSNALNQEEKI G

>2617920421 Ga0073689_10791 Predicted nucleotide-binding protein, sugar kinase/HSP70/actin superfamily [pelotomaculum Ga0073689 : Ga0073689_107]

MRVTTFPHMGNLYI SVKAMLQYLGVDVVPPSSKRTLTLGAKHGPEFACL
PLKLNNGNFI EAYELGADTI I MAGGCGPCRFYGYAQI EHAI LRDI GREMQ
LI VLEPPERHI SELLVKI KWI AGNRSWQVI QAI RFGYMKAAVDEVERA
AFRRSPRELAPGSTDAAYRHGVELI DRAATSRELAEVGKKTVEI MAGVAV
DNRRPVLVKVG I VGEI YTLLEPFVSQQVEWHLGRLGAEVDRSI YLSEWI ND
HLFLGLVKGLRSNKEACRAAPYLRHFVGGHGQETI GNAI NYARAGYDGL
I QI FPFTCMPEI VAESI LPGAISTDFGI PVLTLI VDEHTGEAGMVRLEAF
LDLLARKKETKEACCPCKDI WG

>2617920420 Ga0073689_10790 Predicted nucleotide-binding protein, sugar kinase/HSP70/actin superfamily [pelotomaculum Ga0073689 : Ga0073689_107]

MPLKI GI PRALFYHYHYPMWRVFFEGLGTVVAPSSLSTKGI LAGGLKYAV
DEI CLPLKMAFGHVLDLAMKRVDYI FLPRLVSLARREYI CPKFLGLPDMV
RRI DGLPPLI DVTVDLYKKKRGAYLAAREVGKLTGSGLKVYMAYRRSLK
AHKRYFRLLQMG I PEEALAVMEDRVKEGPLLHPDGLTVALLGHPYNI YD
PYI SMNMI KRLRAMGVTVVTAENLSEKVV RDCAARLPKKLFWTLGQWMI G
AAFYYLERPDVSGI VHAAFGCGPDSMTGELI ERRARAAGKPFLNLTLE
HTGEAGVVTRLEAF LDMVRWKKTGGM

>2617920419 Ga0073689_10789 stage V sporulation protein AF [pelotomaculum Ga0073689 : Ga0073689_107]

VLFNRRKERVEKKEKDKDKTRI SPDLEENI RLLDAEMGI KKNFDVLTREL
VI GKKVITLLFVDGLTNDQI VTLVLQNLTLEREEMTPDGLKKLFRGHVG
YTEVEEVEYLEDI VTKVLSGPM I LVDGADKALI MDARI YPI RSPEEPDL
ERVVRGSRDGFVETLVFNTALI RRR I RDPKLRMEYI QVGLRSKSDVVVCY
I EDI ANPELVKSI KEKVEYI KI DGI PMAEKSV EELI TPGSFWNPFKVR
TERPDAAAMHLLLEGHVLVI VDTSPSVI I APATYFHHLQHAEEFRQNPTVG
AYLRWVRFVGVAVSLFLLPLWFLANNPELRPPWLAFI GVSKEGEI PLI F
QFVLAEVAI DMI RLATI HTPAALATSTGI I AALLVGELATRVGLFTQEVV
LYVAI AAI GTFLT PSI EMANANRLVRLALLI LTALFRLPGFALGLVATFV
FLALNRSFGVPYLWPLVPFNLKALGGVLV RTPVPVRNTRPSVLKPQDPDR
QVVAAPARKRLDRNRK

>2617920418 Ga0073689_10788 stage V sporulation protein AE [pelotomaculum Ga0073689 : Ga0073689_107]

LTDLPTGKRKVI I VTDGDRI AKRAVEVAARNVGARCI SSSAGNPTRSGE
ELVELI RRAHMDPVVVM LDDRGYNGMGRGETALAYI ARHPDI QVLGVLA
V ASNTEKVRGCTVDASI TCGGGI I DGPVDKWGWPEGGELQEGDTVEVLDSL
NLPLVI GI GDVGKMGGADEAEKGAPLTTSALKTI LDRSGYSVI QQKKGK

>2617920417 Ga0073689_10787 stage V sporulation protein AE [pelotomaculum Ga0073689 : Ga0073689_107]

MEFFWAFVVGAI CVI GQLLMDMTSYKFTPAHVLVTFVSAGAI I SALGLY
QPLVNLGAGATVPLSGFGHLLAQAI QGVEQKGVLAGFSGGVAAAAAGI
TAAVVFYLAALAFRPRG

>2617920416 Ga0073689_10786 stage V sporulation protein AD [pelotomaculum Ga0073689 : Ga0073689_107]

LTAPKKNGLQTVWFQNPVLI ATASI VGAKEGEGPLGKTFDKVVYDSYYG
ENTWEKAEQRMMLDAMRKALQKANLQEKDLDFI LAGDLLNQI I SANFTAR
AMAVPFLGLYGACSTMYEGLALGAVLVDGGFADHVLVAASSHYSTAERQY
RFPTELGVQRPMTAQWTVTGAGVALLAREGSGPVI THATI GKVI DMGVD
SQDMGSAMAPAAADTVTRHLQDTGRSPDYDLI I TGD LGVFGKKLAEQLV
RQNGYEI SDRYDCGI LI YNGSQDVHAGSGCGCSAVVTCGYLMQQLQSR

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RYKRFLGI GTGALLSPCSVQQGETVPGI GHAVVI EMR

>2617920415 Ga0073689_10785 stage V sporulation protein AC [pelotomaculum Ga0073689 : Ga0073689_107]

MPEATVSEKQKREYQKMQVQAKPGPRI WRNVFWAFVVGGLI CLVGQFI LN
FYRARGLELNEAGAATAATLVFLAAFLTGLGVYDEVSRFGGAGGI VPI TG
FANSMVSPAMEYRAEGLVFGVGSRLFTVAGPVLVWGI VTAWAVGI LYYFF
K

>2617920414 Ga0073689_10784 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_107]

VHI KVSELVGESPDWKGAVQSAI AEASRSVRNI VAVEVNFNTANVENGO
LVEYKANVKI AHTD

>2617920413 Ga0073689_10783 RNA polymerase, sigma subunit, RpoX/SigF [pelotomaculum Ga0073689 : Ga0073689_107]

MNLPRFPLLKDQEMRELLKKARVGDSYARDKLVNCLKLVFNLVKRFQNR
GYELEDLFOI GCI GLMKAI DKFDSSYNVKFSTYAVPMI VGEI RRFLRDDN
PVKVSRSVKETAYKVQVVRDLTLARLGKEPTVGEVAAELGI SREEVNNAM
EAAQTPASI YETLHQDDGDPI YLLDQLKSEEHGDTWPWLESLSVKELLNRL
PERDRLI I TWRFFEDKTQSDI AGRGLGSQVQVSRRLERQALKKLRDL MANG
DD

>2617920412 Ga0073689_10782 stage II sporulation protein AB (anti-sigma factor) [pelotomaculum Ga0073689 : Ga0073689_107]

MOYI NQMKLEFLSI PANVAFARVTATFASQLDFTLADLEEI KVAVSEAV
GNSI I HGYGNAPDRFVRVHAALTMDTLEI RVEDDGKGVNRNI ERALRPAFS
TDSERLGLGFVFMQSFMDDFRVNSTPGRGTAVI MI KRVGARVARPGPEQ

>2617920411 Ga0073689_10781 anti-anti-sigma regulatory factor, SpoIIAA [pelotomaculum Ga0073689 : Ga0073689_107]

VLFWDSSELSDTLVVRPSGEMDLGVANYFRSVLEEALDREQVRNLVFNLA
RVSF I DSSGLGVLLGRYKRVAKNGGKVF I VSPQPVRRVLDLSGI LRI MN
EYPSEAAALEKI G

>2617920410 Ga0073689_10780 D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5/6) [pelotomaculum Ga0073689 : Ga0073689_107]

MLCKKRLVSI LVALLMAGLAAGAAWAVPEGAGEKKPAKGAVPAAMETTA
ETAI LLEPVTNKI VYEKEPHKKLPMSVTKLMTLLLATEAVDQGKFKLTD
KVVTSENAWEMGGSQI YLEPGEEMSLWDL LLA I GLOSANDASVAVAEHI A
GSEEAFFVRAMNEKAASLGLQNTNFVNCHGLTADNHYTSAYDMAVI LKEGL
KSPLFRKI TAMKEYDLRGGAFLWNTNKLLWWYDGADAGKTGWTEAAKYC
LAASAERNGLRLGVVLGTPEPRSHFREMTKLFYGYARYKAVNLAPAGA
VAGAVKVGKGTDSVKALTAGKVSVVVPRGEDKGFESKI ELPAHI NAPVQ
KDQELGWYVVTNGQEV LKVKLVAAAGDVPKASLFRQI KKV I DSVY

>2617920409 Ga0073689_10779 Putative ATP-dependent DNA helicase recG C-terminal [pelotomaculum Ga0073689 : Ga0073689_107]

LHHEI PPEALREAVI NAI AHRDYHI PAQI RI FI FDDRI EI I SPGKLPNTI
TLENI RMGVHAERNPAGHRFTI KKPVVVKV

>2617920408 Ga0073689_10778 Signal transduction histidine kinase [pelotomaculum Ga0073689 : Ga0073689_107]

MKVVSI LTSI SEEQRREI EI KKLSDENDI LRKNNRLKNEFI GNLSHEVRT
LLTNI I GFAELLLDNSRAGDLNPI QREYVTFI LESGRQI RSLMNDAI DLA
KI EAGKLELKHEEI FI ENI I DSSVQI FQEQLTNKGI FLSKKI PGKTI KI K
ADPLRLKQVNNLLANAVRHPTPEGKI GI DARRESSCLOQTVWDTGTGI P
PEQQKRI FI PFEQGFHSFSASETGSGGLGLAI VKTLVEKHGGKI WVESQPG
WGSRFSFTI PI VQPELSQEQRV

>2617920407 Ga0073689_10777 two-component system, cell cycle response regulator DivK [pelotomaculum Ga0073689 : Ga0073689_107]

MKNFI LI I EDNAMNVKLMRDLLQAKGYQTKEVETAEEGI ALAREEKPDLI
I MDI ELPGMDGLQATGI LKADPLTKNVPVLAVTAYAMKGDREKALAAGCD
GYI AKPI EI LDFLEHI RTAFK

>2617920406 Ga0073689_10776 Signal transduction histidine kinase [pelotomaculum Ga0073689 : Ga0073689_107]

MI SNFELPFLKSLAGRI LI PCLAVFVSVLVVVTWGI AFWHFSQESRQKTNO

Table S2

NLAQTADI FENQI QNWLLTRERAAQFLASDPFLQKGLAQLAAGGTEAEEA
 KKLCEFYLLKLSI HI PMYEEI YFADKTGRI YLSTNPDRI GERRPVDDLI K
 KPLESggi YFNEGYI AFSTKEPSVAYAVAVNGRGVNGDYLGVLVFR I NTR
 EI LESI EFKGVGLGETGEALLVRKDGLYLTSRLYNSGARLKMHASAEPEV
 RSLRGEEGVMRTARDYAGHRVLAAYRQI PYANWGLVVKQDLEEVMAPLRRS
 LI TSLLPAGI GLLLI VFLVVPQVRKNTLPLASLVEGAREFARGNFAHRAP
 AGDERRDELSI LAQTFNEMAQDLOGHFLAREROSTVLOALVSTI HLTMPV
 EKALGTI AEEYDFQVGAVYLYDQKEMLRKTAAYCPGEKLLLLQEEVPAGE
 GPAGEVRRTOQKPFLLDI PVDTVYTVRAVSGEMLPAHVLYLPVI FGQELL
 GI LVLGSLRKPAPVTLAQLETI CTMLGVAVNNARI FEQVNELSGTSLCLN
 EELSAQNEELOVQAEELQTOERELREKNI QLERATRSKSEFLARMSHEL
 TPLNAVI GFSEVLAEGI FGGLNAKQKEYVRDI LTSGRHLLNLI NDI LDLS
 KI EAGKI DFQPVAVNPVLPRESLAFMLPDVQSKQLNLEI GI QYDENTVK
 ADPERLKQI FTNLLSNVKTFTAGGRI KI CSVPFGKDLRI SI ADTGI GI P
 PEI QTEI FEEFKQGHHLHRDQGTGLGLAI TRRLVEMHGGRI WVESEPGR
 GSTFTFTLPMTEEGKGATREI GPEAAAAARERAAGEAGPGLRGEGAGCRG
 KSLVLLVEDEPAAI KLLTDFLSEKDYSVTVTSEGESAVIDRAKELRPELI I
 LDVLLPGRDGEVLELKVAPETRDI PVI I VSALDEKKGKFSLGALDYFV
 KPVNKNLLLDRI ESLRLSRKPTGPAI LVVDDEPQVVEYLTAI LRAAGYKV
 SQAYGGKEAVELAI KERPEVLI LDLVMSDLTGFDVVEELSGCPEI AGTGI
 FI LTARDLTAAEKRRRLNARVSAI ARKGELTKDQFLAQLERVRLK

>2617920405 Ga0073689_10775 chemotaxis protein methyl transferase CheR

[pel otomacul um Ga0073689 : Ga0073689_107]

VKSNMSDSRRI FRPDPFLELLEDVCARGDPDFRLYRRETVERRLARRI LS
 AGCAGYADYI SYLREKPGEYRRLI DSLTI KVSSFFRDPPVFEVI ATQALP
 ALLNVKAKNERYLTI WSAGCAHGQEAYSMAI LMRELSRQKYAGLTARI I A
 TDI AEDALAKTRRGI YGEEDLAGVKEDFRSKYFHRGNLYQI NEEI KKMV
 I TGRYNLLTGASGGPPEAVFCSDLI FCRNVVMYFORQAQEKVLQSLWKM
 LVNEGVLVLGAAECLPVSLASRSREYGGTRI YRKLF

>2617920404 Ga0073689_10774 thymidine phosphorylase [pel otomacul um Ga0073689 :

Ga0073689_107]

VNWKI FHPGCPFMRMYDI I LKKREGRELTGEEI KFFI DGYTAGGI PDYQA
 AALLMAI FFRGLSAGETAGLTMMCDSGDRADLSAI PGI KVDKHSTGGVG
 DKTTLLVPLVPLVAAAAGVPVAKMSGRGLGHTGGTVDKLESI PGFKVVLEPAE
 FI DQVRRVGAAVVAQTGRLAPADKKLYALRDVTATVDSVPLI ASSVMSKK
 I AAGADAI VLDVKTGSGAFMRDVDSAFSLARTMVG I GNWVGRRTVALVTG
 MDQPLGRAVGNALAEVREAI ETLKGEGPADLVELCLALGAVMLLLAGKAAS
 I PEGREKLAGLLDSGRALAKCEEI AAQGGDPRTVREDGLLPAAKLLEE
 PAPAAGYVQAI HAERVGRAAMLGAGRENKESKI DLSVGVLKKKVCNDRV
 QAGEPVAELHAAGPDRLAEVREI I QKAYNI GDKRPEPRPLVCGTVPEKV

>2617920403 Ga0073689_10773 4-carboxymuconolactone decarboxylase [pel otomacul um

Ga0073689 : Ga0073689_107]

MEEADVKKRTQEMASKLFGKGI NMDPPYKTWREFDKELANDFSKFI TGNL
 YSRTVLTSPERQMI TVAALLAALRAGEELRLHVNAALNVGCDPKKLAIEI FF
 QI GTYAGMPAVNEALQVYREVLHERGMWPI E

>2617920402 Ga0073689_10772 phosphopentomutase [pel otomacul um Ga0073689 :

Ga0073689_107]

MVKSRLPLVVI LSI RGVFLVKI RRVVLFLDSVGVGELPDAGKYGDTGSNT
 LGNTARAVGGLKMPNLGRLGLGNI I EVTGVPLVENPEASYGRMAERSAGK
 DTTTGHWEAGLI LERPFVYPNGFPPEVI KAFEKKI GRPVLGNKVASGT
 VI I EELGARHLETGYPI VYTSADSVFQVAAHEE I I PLEELYRYCRI AREM
 LVGEHAVGRVI ARPFGGSGNFRRTTNRHDFSLKPPSRTVLNLLQGN I P
 VTAGVKVEDI FAGEGI TMAI HTRGNVDGVEQALQLLQSGLEGLI FTNLVD
 FDMLYGHRNNPRGYADALEELDRRLPELLAALREDDVLI I TADHGCDPTT
 TSTDHSREYVPLLI YGRAVRGGVNLGVRETFAVAAATVTEI FGLAFGVGK
 SFWPEVREL

>2617920401 Ga0073689_10771 tyrosine recombinase XerD subunit [pel otomacul um

Ga0073689 : Ga0073689_107]

LEKLLDEFI YHLAVERGLAENTLVSYRADLAGYI SFCRKYGLVSLEQVGK
 DAI MSYLFQLQLDGRSPATI ARHLAAI RTFYRYVVGEGFLQKNPTADLES
 PKPAHKLPKVLTVEEVDLLLQGPRI SEPTGLRDKAMLELLYATGI RVSEL
 VALDMEHVNTENGFRVRCFGKGAKERMI PLGDVAVRFLKEYLERGRSKLKK
 SSNEKALFLNQHGRRRLTROGFWKI LKKYVCGAGVKMEI TPHTLRHSFATH
 LLENGADLRSVQEMLGHAD I STTQI YTHLTRRKLKEI YDRSHPRA

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>2617920400 Ga0073689_10770 stage II sporulation protein M [pelotomaculum Ga0073689 : Ga0073689_107]

LAKRLREFWANSRQNPAYLVVLI FTLGLAAGAFGVQKLPADQAQELG
RYLDRFLQQAGGLEVDASKALRDVFCNDI I VFLAI YLLGLTVI GI PVMLG
I I FTRGFVLGFTVSFLTMEKSFSGAI LTI AAI LPQNI I LI PSLLMGGVAS
LSFALLLTRRFYNSKI LI WPSFLVYSALMLGVVI CSAGAGLVEVYLTPLV
I RLAAGYLI

>2617920399 Ga0073689_10769 peptidase T-like protein [pelotomaculum Ga0073689 : Ga0073689_107]

MVNSSRI VDEFLEMVRVDSVSGKERRI ADLLKSKLSGLGLEVRDAGRA
VGSDTGNI I GKLPGSGGGPVLLLLCAHMDTVEPGRAVNPRVADGVI RSFGD
TVLGADDKAGI VAI LEVLRLLI REHRI EHGGLEVVFTEI WEEGGLQAKNLD
YSLI TARI GFI LDSDGPPGTI I I RAPSQDRI GATI RGRAAHAGI NPENGI
NAI QVASHAI AQMLRGRI DHETTSNI GTI SGGKAI NI VPDSVNLOGEARS
LDASKREAQTAHI CRI I RDTAEKFGAGVDLVTEI YPDFNLGEYAAPVRI
AVAAAGGAGFTPRLEKTGGGSDANI FNSRGI AAVVLGI GMKNVHTNEEYI
TVADLADNARYLLEI VRTAQNTDI

>2617920398 Ga0073689_10768 2-oxoglutarate ferredoxin oxidoreductase subunit gamma [pelotomaculum Ga0073689 : Ga0073689_107]

VLEEI YI AGFGGQALSMGQLLAYAALTEGKFVSYPFYGVKEKRGGVANC
GVTI SDROI SSPI VTEPSVLVMMNSSLERFENAVI PGGLI I TNSSLVET
PVKRVDPKLAPEI PANEEAEI LGDSMVANNVI LGALLELTGVVSI NAVEES
LKKVLPKQRHNM I PVNVKALERGAALAGEYKKNREE

>2617920397 Ga0073689_10767 2-oxoglutarate ferredoxin oxidoreductase subunit beta [pelotomaculum Ga0073689 : Ga0073689_107]

LKKVFSRPKSLKDMPPHYCPGCTHGVHRLVAEVI DELGI QGI VI VVGPI
GCSVFI RDYFDI DMFQSGHGRAPAVATGI KRVLPGRVVFTYQGDGLAAI
GAGEI VHAAARGEKI TVI FI NNAVYGMTGGQMAPTTLLGQKTCTTPYGRD
KDI NGYPVKVCEMLTPLDGAVYVARVSLHSPKEI I KAKKAI KAFETQI N
GLGFSLVEVLSACPTNWGLSPAESLKWLEDNMVYYYPLGDFKTPAGVV

>2617920396 Ga0073689_10766 2-oxoglutarate ferredoxin oxidoreductase subunit alpha [pelotomaculum Ga0073689 : Ga0073689_107]

LSKI LMKGNEAI GEGAVRAGCRYFFGYPI TPOSELTHYLAKRLPDVGGLY
LQAESETASI NMVYGAAGAGARVMTSSSGPGI SLMQEGI SFLAGAELPCV
VVNMRSRGPGLGNI APAQADYFQATKGGGHGDYHLI VLAPNSVQEI LDLM
KMAFDLADRYRNPVMVMADGI I QMMPEPVEMEGGGEVEI PPRPWAASGMI
DHGGKNI I NSLYVI PEQMEALNLKLLDKYNLI RREEPLCEEYLMGAEVL
LVAFGTASRI CRAVVEKARAGGI PAGLI RPI TLWPFPSDFI VRATGTVKC
FLTVMNMGMQVEDVRLAVNGRAPVHYGRTGGI I PAAKDVLEEVKRLYS
GGKTS

>2617920395 Ga0073689_10765 2-oxoglutarate ferredoxin oxidoreductase subunit delta [pelotomaculum Ga0073689 : Ga0073689_107]

LPRLI FREDRCKGCQLCATVCPKGI I VMSGRI NDMGYHPAALEEQERCTG
CTLCALI CPDLVI EVEREEKTV

>2617920394 Ga0073689_10764 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_107]

MVLVNSWRLSI FTGNFGSGKTEVALNYALKI HADGNQVSI ADLDI I NPYF
RTRMVRECLSMGI TVVSPWGKLAGADVPALPAAI YGVLOGNAGYGV I DV
GGDDI GATVLRGRFKNLPAAGFNLFLVVNVCPRPFTRDVEGI TTVLRSI EK
TSRLRVNALVSNTNLGPETDVPVI LEGHRVVQEAARQLGLPVAFACARRD
LAASLGDLNI PVLPDLFMKPPWYDGGEPESDPHLRI PPGLK

>2617920393 Ga0073689_10763 two-component system, response regulator, stage 0 sporulation protein A [pelotomaculum Ga0073689 : Ga0073689_107]

MTRKAI QLLI ADDNRDFCELLKEFI NEQEDI NLVGI AYNGLEALNMI RET
SPGVVVLDI I MPHLDGI GVLEKLLKGNPGNPKPI I MLTAFGQESVTQRAV
ELGADYYI LKPFDFNVLATRI RQLAEGVNI SQYI TPVKPKNLDAVTNI I
HEMGVPAHI KGYHYLRDAI LMVI GEVNLLGAVTKELYPAI AGKFQTTPSR
VERAI RHAI ELAWDRGNVEMMTKFFGYTI NLERGKPTNSEFI AMVADKLR
I EAKVS

>2617920392 Ga0073689_10762 stage IV sporulation protein B [pelotomaculum

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Ga0073689 : Ga0073689_107]

LRGKRNVLFLGALMI FLYI I LACQMOGVTLPHDKQFI SAEENVLAFPAMEG
NLI KVI PGGQSI GVLI HSQGV VAGYAAVLDEAGNKVNPVAVDAGLKEGDI
I LKVNNGAVKSDGQVREFVARAGAAGQSVTLVVRGDEI FQTRVNPVFCK
ETLRYRLGLVI RDSAVGVGTLTFFYEPGSLVYGALGHI I VDPGTSRPVELQ
DGKI I GASI QSI HRGKRQGPGEKLGVLRSDFKI CGDI SKNTKVGI FGYLQ
KTPESPAFSESI PVAAVNQI HEGQAEI LTVLNGDMVEKFNI EI VKI NPLA
THDGKGLVI KI TDHRLLDQAGGI I QGMSGSPI I QDNRLVGAVTHVLVNDP
ARGYGVPAEWMLQEGEI LPGAQYGEKTRKI AG

>2617920391 Ga0073689_10761 DNA replication and repair protein RecN
[pelotomaculum Ga0073689 : Ga0073689_107]

MLLNI YVKNFGI I DLLKMDFOAGLNVLTGETGAGKSI I I DALQLALGGRA
HTDMI RAGAEKAVVQATFDLGGAPSLVSLLEEQGLEAPEDGI LVLSREI A
RSGKNI CRLNGQVAPLGFYRNVGRSLADLHVQHEQNSLI DQEMHRQLLDR
FGGTALLEVLGEVDSI YARWKEARRNFEKLRDSAAERAGRMDLLRYQVEE
I KRAGLRSGEDEELETEKRVLANAEKI NLLATRAYSMLEYEGGRPSAVDL
LAGAADSLRNLLTLDQRPENI LASLESALYQVEDAARELTCYRAGAIEYSP
PRLEAVEERLELI KNLKKKYGETI AGI LEYLD SAGNELAGLENVEENAE A
AARELRELEEAYNRAAGLLSAAARREAAALEEAVAGELASLEMGRVEYRV
TFSDLEGPSPGGLEQVYFLI SPNPGEPLKPLAKI ASGGELTRI MLALKVL
LARADEI PVLVFDEADTGI GGRALQAVAEKMAQLSGRRQVI CVTHSAQVA
CYADAHRI VKEFDGERTVTSVGLLEPRERLEELARMLGGREVTEI TRRH
AGQMLRMAAQTK

>2617920390 Ga0073689_10760 transcriptional regulator, ArgR family
[pelotomaculum Ga0073689 : Ga0073689_107]

MKAGRQRKI LEI I RREPVTQEDLAAALKKNGFAVTQATVSRDI KELGLI
KI PGEKNLFRYAI PGEPLHRGEERLRRFLRDTTVGMDLSENLI I I KTHP
GSAQAVASAI DQAGWQEI I GTVGDDTI LVVVKPKRVTA AVI KRFEG LNR
G

>2617920389 Ga0073689_10759 Putative rRNA methylase [pelotomaculum Ga0073689 :
Ga0073689_107]

MSKGLGSAVYLVQLLI SGAVRAGGTAVDATAGNGKDTLFLAGLVGPAGRV
YAFDI QEELRSTGALLEKDGLAERVTL LHAGHEEMERLI PGPVDAVFN
LGYLPGGNHTLI TRAGATVRALRSALNLI RPPGRTGLVVTGHPGGGEEY
RLVEGVAASLDGKLF RVI KI SFI NRAAHAPVVI VI EKAGASDEGRAATQN
S

>2617920388 Ga0073689_10758 NAD⁺ kinase [pelotomaculum Ga0073689 :
Ga0073689_107]

LRTFGLVI NLEKEKVHELVGQI VHWLED RGCTVLI SEDTARSLGFSRLGV
SODYLVGQSQCMMVLGGDGTLLRTARKVAAAGTPI I GVNLRGLGFLTEI D
I PEVMFALGKI MDGQYHI EERMMI EATVHRQGVVVEHSVGLNDAVI TKGA
FARLI RLDAYVNDEYI NTYPADGLI I ASPTGSTAYSLSAGGPLVTPALDL
MLLTPI CPHSLWARPVVI APESVI KVVVHARQGEVMLTMDGQHGFNLCDQ
DOVMLRRAPWKARFLRLKGRSFFEVLRKKLKEEEERYDV

>2617920387 Ga0073689_10757 23S rRNA (cytidine1920-2'-O)/16S rRNA
(cytidine1409-2'-O)-methyl transferase [pelotomaculum Ga0073689 : Ga0073689_107]

LSQKKQRLDVRLAGEGYCPSREKARAAI MAGLVFVDGARVDKPGRLVDPG
AAI ELRGNPVPYVGRGGLKLEKAI KAFGPDLTGKVVLDAGASTGGFTDCA
LRHGARLVYAVDVG YQLAWRLRNDPRVVVLTNTI RHLTAEVLKETPDF
ATVDVSFI SLSKVLPPVGVLTTPDAEGVALVKPQFEAGREKVGKKGVVRE
PAVHLAVLGNITALVKELGWSVGGLDFSPVTGPEGNI EYLI YFKKSGEGL
DCDAAAVVEQAHALLG

>2617920386 Ga0073689_10756 1-deoxy-D-xylulose-5-phosphate synthase
[pelotomaculum Ga0073689 : Ga0073689_107]

VSI LEQVHSPRDI RSMTYAQLHELAGEI RGKI I KTVAQTGGLHAPNLGVV
ELTLALHRVFNSPVDKI I WDVGHQSYVHKLI TGRREEFATLRQFGGI SGF
PRPCEI HDPFGTGHSSTSI SAALGLAVARDLKGEHAYVAVI GDGAMTG
GMAFEALNHAGHLKKDLI VVLNDNEMSI ARNVGAMSGYLTRLRTDPKYSR
GKEEI EQLLRKI PI GSTLLRI GERMKDCLKYLVVPGMI FEELGFI YLGPV
DGHDI KAVTTVLQHARAI KGPVLVHVLTKKGNRYRPAENNPGRFHGVGAF
DMTSGEI LKSGDI PSYTEVFGRTAVRLAQRDKNVVAI TAAMPDGTGLTNF
ARLFPGRFFDVGI AEQHAVTLAAGLAAGGFRPVVAI YSTFLQRAYDQI I H
DVCLQNLPTFAI DRAGI VGDDGATHHGLDFAYLRSI PNMVVMAPKDEN

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ELQHMFTAVNHSGPAAFRYPRGTGTGCKMDGDLKTIPIGQAEVLREGVD
ATLLAVGSMVRPALEAAGVLAGRGI EAAVI NARFVKPLDEELI LHYAGRT
GRI LTMEEHVLHGGFGGAVLELLAARGLNGVKVQCFGI PDSFVEHGKPAL
LMARYGLTVERVVRAVTDGFDKGRPRKLRVASESV

>2617920385 Ga0073689_10755 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_107]

LGNNKSTVSGRYI FLVGI GSFI LAI VFTLLSETFSSKLSNLI LSFI FLFF
IMI NI SADLVGTAVTAASHVFPNAAKRVGAPQGLQLI RNADKVANI
TNDVI GDI TTTVSGALGI SI VVQI MRAGPQLDQFWLNVLTALI SVLI VT
GKAAGKKI ALSHPDEVI FVVGRLLAKVENTTGYSFPQKRRSPRSRKGG

>2617920383 Ga0073689_10753 geranylgeranyl diphosphate synthase, type II [pelotomaculum Ga0073689 : Ga0073689_107]

VDFKEELKKKAALVDDALDRFLPSGDAYPPLI HRAMRYSAMGGGKRLRPA
LVMAGAEAVGGGEDVLPAAAI ELI HTYSLI HDDLPAMDDDDYRRGKPT
NHKVYGEATAVLAGDALLTLAFKLLTESKSPRPENVLVRI REVAEGAGTF
GLI GGQVVDTFSAKEKI DENTI EYI HRHKTGALYRVSVRSGVI LVGAED
RLAALTEYAEQLGLAFQI RDDI LDVEGDENKI GKPVGSDVKNKKATYPAL
FGLNRAGEKARQAAARAGEALSPFGPEAGFLRALAQFVI DRDS

>2617920382 Ga0073689_10752 Exodeoxyribonuclease VII small subunit [pelotomaculum Ga0073689 : Ga0073689_107]

MATEDKEMDLEANMKKGPTGGRETSSLDEPLAREMTFEEAI TRLEAVVRE
LEDGRLPLEKALELFAEQI RLSRI CGRHLEAEQRI CI LTEDKGGI TLR
EVDTL PSTGGGNRGG

>2617920381 Ga0073689_10751 Formiminotetrahydrofolate cyclodeaminase [pelotomaculum Ga0073689 : Ga0073689_107]

MGEFFNKSLEVI EVSASNSPTPGGGSVSAMVAGFGVAMCAMVCNLTVGK
EKYKDVEPQVKEI LDTANGLI KRLEELVDSDMAEFNSFMAAYRLPKGTDE
EKAAREEAI QKALKSATDTPMEI ARVCLKALEI TDKLAPI GNKMAI SDAG
VAAVVAEALNGVLLSADI NI PSI KDQDYVSKI VAEKEAMVAEAKRLKDN
TMAVAQERMK

>2617920380 Ga0073689_10750 methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase [pelotomaculum Ga0073689 : Ga0073689_107]

MATLI DGKKVAASI REEVKAEVAQLREQGI APKLAVI LVGDDPASVVYAR
SKEKACGNVGI DFELFVMPGTTPEDEVVALI EKLNKDDNVYGI MI ELPLP
KGMKQVRVLEAVSPLKDVDGVHPI NRGYI LSNSEGLFPATPQSCI EIMLR
SGI EIKGKHAVLVGRGETVGKPLI FMMLNQNAVTVI CHTKTKDLAYHTRQ
ADI LVAAVGRAKMI TADMVKPGSI VVDAGI NEKEGGGI CGDVDFENVEKV
AGAI SPVPGGVGSLTTVLI QKNVLKAI KLQKQNK

>2617920379 Ga0073689_10749 Exodeoxyribonuclease VII large subunit [pelotomaculum Ga0073689 : Ga0073689_107]

LRVLTVRELTGHI KGLI EKDYLLANVWVKGEI SNLRAAASGHFYFTLKDD
SSCLKVVMFRSRLVHFRPENGMGVTVRGYVCVFERDGTQLYAEEMEP
DGAGALYLAFEQLKERLQREGLFDRKHKALPLLPRRI GI VTSPTGAAIR
DMVKI I GRRWPGREI VLAPVQVQGEAAPPVARGI RLLNRLGGVDLI I VG
RGGGSLEELWAFNTEI VARSIFQSAVPVI SAVGHETDVTI ADFVADARAA
TPSNAAEMAVPDRREMERHI RALRARLTRAIEKAGEGRRRLTACLAARV
FVRPVDI VCGPGQOTLDSLNRRLAQGTRGAVEQEKGRVLAVLAGRLQALSP
LATLARGYSI CTPDPSGRI I SDAGSVGVGESLAVHLHKGLLKCVVQNKSM

>2617920378 Ga0073689_10748 glutamate synthase (NADPH/NADH) small chain [pelotomaculum Ga0073689 : Ga0073689_107]

MADEKKEKKAI I PNKNPMPAQDPVERSRNFNEVALGYSEEVAEANRCL
OCKKEPCROGCPVEVYI PQFI KLVAERDFAGAI KKLKEKNALPAVCGRVC
POENQCEKYCTMGKKHEPVGI GRI ERFCADWELANGVLPQEVAPSTGKKV
AVVGSPPGLTCAADLAKLGHKVTI FEALHVAGGVLMYGI PEFRLPKAVV
QAEVENLKKLGVDI QVNAVVGKFATVDELMEEGGFDVYI GTGAGLPYFM
RI PGENACGVYSANEFLTRTNLMKAYRFPEYDTPI RVGKKVAVLGGGNVA
MDAARTALRLGAEESWI VYRRSKNELPARHEEVEHAE EEGVKFSFLTSTPT
RI LYNEDYVWTGMECLRYELGEPDASGRRSPVPVKGSEFVMDVDNVVVAI
GQGNPLVPRTTKGLEVNKKGNI VANLETGATSKPGVYAGGDVVTGAATV
I LAMGAGRTAAKSI HAYLMEK

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>2617920377 Ga0073689_10747 ferredoxin--NADP⁺ reductase [pelotomaculum Ga0073689 : Ga0073689_107]
 LVLMYKI LKKEVLAPTLNLFEI EAPMVAGKAQAGQFVI LRNHEEGERI PL
 TI ADFDREKGTI TCVFQEVGKTTKELGTFNEGDCI KDFVGPLGVPSHI EN
 YGRVVCVGGGVGVAPVHPI ARALKEAGNEVI GI I GARTKELLFWEDKMRA
 ACTELRVTTDDGSYVRKGFVTDVLKEVI EEKKDVALCI AI GPLPMMRAVC
 NLTREYNLKTIVSLNSI MVDGTGMCGCCRVTVGGETKFACVDGPEFDGHQ
 VDFAEMARRSVI YKPQEQLAVERYANVDAYKCS CSCSCGCGGGK

>2617920376 Ga0073689_10746 NusB anti termination factor [pelotomaculum Ga0073689 : Ga0073689_107]
 MSRRQARERALQVLFQVDMGGAGPAEAFKNMDENFGVLTKNKEFAQRLVL
 GTLENLKSI DRI I AGI SKDWDI SRMANVDRNI MRLALYEI FCCEDTPNNV
 SI NEALELSKAFGGEE SVRFI NGI LGRVLEDPDKFRLATLAREGI

>2617920375 Ga0073689_10745 Small integral membrane protein (DUF2273)
 [pelotomaculum Ga0073689 : Ga0073689_107]
 MEVI REI LDKHLGKI TGVLGLVFGWLAI KYGI FKAMFVAVCAVAGYFI G
 KRLDEKLDFREMLARLFRER

>2617920374 Ga0073689_10744 Uncharacterized conserved protein YlO_U, alkaline shock protein (Asp23) family [pelotomaculum Ga0073689 : Ga0073689_107]
 MGLFDRFLLTG YTLF LTVLFI LWGTVM LGWPAPLSLLREL FYPGRPEVFW
 SLLVLLI LAGGR LFWVSLRRSGGRYV VLAESALGQI KVS LQAVENLV EKV
 VFQVKG VREV KPRI FSTPEGVGI RVRASVTPEI NVPEVSVEI QNLVKERV
 FEVTGI SVSAVKVSI ENI TANNPRVE

>2617920373 Ga0073689_10743 Uncharacterized conserved protein YlO_U, alkaline shock protein (Asp23) family [pelotomaculum Ga0073689 : Ga0073689_107]
 LDPKEI I REEKTGLGSI RI ADEVVKVI AGLAAI EI KGVAGMSGGLVGGI A
 EMLGRKNLPKGI KVEVGEKEAAVDI YVI MDYGI RI PDVAAEI QEKVKDAV
 ERMTGLAVVEVNVNQGI AFAPDSREEEHRVR

>2617920372 Ga0073689_10742 acetyl-CoA carboxylase, biotin carboxylase subunit
 [pelotomaculum Ga0073689 : Ga0073689_107]
 MFKKI LI ANRGEI AVR I RACREMNI HTVAVYSEADQDSLHVWVADEAYC
 I GPASAAKSYLNFTNI I SAALVSGADAI HPGYGFLSENADFAEVCSTCGI
 TFI GPPVKAI QRMGAKALARETMI KAGVPVTPGSDGVI EESAQALRVAEE
 I GYPVMI KASAGGGGRGMRVAHSRDEL ANAI STAQAEQA AFGNGEI YLE
 KYVEEPRHI EFQVMGDMHG NLVHLGERDCSI QRRNQKVI EEAPSI VLTPE
 LRDKMGEVAVRAAVDYYSVGTVEFLLDKYYNFYFMEMNTRI QVEHPVT
 EMVTGI DLVKEQI SVAAGEKLSI SQADVDI RGHAELECR I NAEDPNKNFI P
 CPGRI TTYMPPGGPSVRVDSAVYDGYVI PSFYDSMVGKLI VWGRDRDEAM
 ARMQRALQEFVI KGI PTTI PFHQKVL RNAFFRRGEI YTNFI RRR I LGDEE

>2617920371 Ga0073689_10741 oxaloacetate decarboxylase, alpha subunit
 [pelotomaculum Ga0073689 : Ga0073689_107]
 MMKCRVKI TDTTLRDAHQSLWATRMRTADMLPVAEKLDGI GYHSLEWVGG
 ATFDVCLRYLNEDPWERLRLKKHI RRTPLQMLLRGQSLVGYHHYPDDL V
 DAFI AKSVENGI DI I RI FDALNDI RNLA AAFRFSRKAGAHVQAAI VYSVS
 PVHTNQYYLDLATQLAEMGADSI CI KDMAGLLAPYQAYELVKLLKEKLN L
 PLQFHSHYI GGLAVGAYLKAAEAGVDVI DTASVPLAFGASQPPVETVVRA
 LQSPYDTGLNI RELFEI AEYFEI LRKASGFERGVTRI NDMRVFDHQVPG
 GMI SNLVTQLEEQSLYRLGEVLEE I PRVREELGYPLVI PVSQI VGTQA
 VLNVLG ERYKLVPGEV RNYFQGI YGRPPAPVNRDI ALKLLSDREPI LCR
 PADLLEPKMVKI REEAKDLAASEEDVI SYALFPQVAKRFLEARGGGGKME
 PGPPAAKDEDKTRDKKADDASRENI KNEVAVSLKAGSKVAAGGAAAGREV
 NKLNLSDI KELI KLI NETDI SEVSLESAGFKVAI KKGADRESEPAAGEPA
 QPFPALPREKLEAAPVQTPKEARPDLTPVVAPVVGTFYSAPAPEEPPYVK
 VGDRVQKGQTLCI I EAMKLMNEI AAEVAGEI VEI MVENGQPV EYSQTLFL
 I KEQI I

>2617920370 Ga0073689_10740 stage III sporulation protein AH [pelotomaculum Ga0073689 : Ga0073689_107]
 MLSI I I KKRTFTLVVLGLAGLVLLLLSWRGELLKDAPVPGTPVSAPVTGA
 VNFENGGRPVFEENKTGATGEGKEDGVESDFFVEYRLERERTRGQRV EWL
 REVI NNNNSAAETROKQAQEHLMVI SSNMAKEI ELENLI RAKGYKDAVVLV
 DDRAATVI VAARSLSAEEAARI TELI SRGTGVDSKNVVI I KKS

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>2617920369 Ga0073689_10739 stage III sporulation protein AG [pelotomaculum Ga0073689 : Ga0073689_107]

LQKI LEFFGLGGPGKDQVPPKNQGRRLWLAVLGI MMLVFSGLSGGK
APDQSSRQAPVPPAREQVKSNSLEEEQLGQKLCAMLGRI EGAGQVEV
SVRLSGSTRNEYAVNTTTGKKTTOERDQSGGTRLTNETDGSQGLVMNRNG
TGGEQPVVERELAPQVAGVLVAGGARDAGVRAKLFEATRVALGI EPHKI
I VVPMERRG

>2617920368 Ga0073689_10738 stage III sporulation protein AF [pelotomaculum Ga0073689 : Ga0073689_107]

VEI VRNLVQSLI VII I LAMFLEMLLPSSGMKSYVKMVMGLLVI I AVAQAV
GNLARFDFSGELPSL TRQDDRALLAGI MEGGKKI SGSQKEKAI EQYRRGL
ANQI MALARI NKEAPVVGVEVKVQSERGAPDYQGLREVLI VDGARSSE
KEAGRGVVAEVEPVTVRVGDPGQAGGTEPEAGPPREAAAGLVNTVAGFYN
LKPEQKV VYK

>2617920367 Ga0073689_10737 stage III sporulation protein AE [pelotomaculum Ga0073689 : Ga0073689_107]

LKRYYLFLALLLLFCFPVAVGAEQTDTVGMNGQTPAPDLTAVQEYI DRMD
AEI KNSVPQLNFRMVTRLARGEMNWRPAEI FKNI LEQLFKEVVANFDLL
GKLVLAVI CAVLQNLVSSFEGAVGRLSYSVSYLVLI SI AI GSFSLAVS
AGREVDTMATFI QALLPVLLTLLVAVGGVASAAVSPVLLATLGI FGTL
I KDVLPLLLFFVAI LEVSNL TEKFVSNLADLLKTAMGLMGVFSTI FL
GVLAI QGVAGAVGDSVVFKTAKFGVDAFVPVVGGMFSDALEAVSSSLI
KNAVGI AGMAVI GTVMVVP LLKI I TLAFI YKLAGALI QPI GDGQMVNCLN
GLGNNLLLI FAAVATVGLLFFFAI TI VVGVGNI TVMLR

>2617920366 Ga0073689_10736 stage III sporulation protein AD [pelotomaculum Ga0073689 : Ga0073689_107]

MDI I QI VAI GLI ATVLI VVVKSQRP ELAVLLSVAAGMLLFLVLGKI GAI
MDI ARDLADRAGI SMVYLGTI LKI VGI AYI AEFGAQI CRDAGEGAI ATKI
EFAAKVLI MVLAVPI VVAVLQALLKLP

>2617920365 Ga0073689_10735 stage III sporulation protein AC [pelotomaculum Ga0073689 : Ga0073689_107]

MGNNI DLI FKI AGVGI LVAVLNSI LKHAGKEEQGHI VTLAGLAI VFI WVI
QLLGSLEQVKS VFCLF

>2617920364 Ga0073689_10734 stage III sporulation protein AB [pelotomaculum Ga0073689 : Ga0073689_107]

MLKLVGAAMVVAASGLSGLAVAGGYSRRPRELRWLRSALQMLETEVAYGA
TQLAEAMARVANRCDQAVAPLFSRTAAELSAMSGI TAAEAWEKSLEGYYP
GSALKPQDLSI LRNLGSSLG I SDRTDQI KHLRLAMEQI SSEAAAAGEEAA
RNVKLWSYLGFLGGLMVVLI LY

>2617920363 Ga0073689_10733 stage III sporulation protein AA [pelotomaculum Ga0073689 : Ga0073689_107]

MFOADSLAPDRMPGGDRAI NETLPVLP GNI RRLVASLPGTVQGKI EEI RL
RQERPLVLCSS EDVFLDAGGRAVRRAGEAYRVTS LDMERLVQLI SGSSL
YALEEEELRSGFI TLPGGHRAGI TGRAVLEGGKVRTLKYLSGCNI RVAREA
PGAASGVLP HVLVDKNNGGI YHTVLVSPPRCGKTTMLRDLVRQI SDGVPGL
GLPGQTVGLVDERSEI AGCYWGV PQLDVGI RTDVLDACPKAEGMMMLLRS
MGPRVI AADEI GRQEDVVALEEV LNAGVKI LVTAGGASPAELAERP VLEK
LYSRKMI ERFVI LGRSRGVGTVEE I DGKNLLPLEVKRC

>2617920362 Ga0073689_10732 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_107]

VEPAAFI FPLPEHLKEHYARWARSLRQSTGEKTTGENDEGYAPVFVPVYP
AYPGFMPYPFPSSGSPSGI CPCCGKKTTSFWPPGVNPF I FLI LI LLLLG
TRKDQI LSAI RKLLKTDQKPEE I H

>2617920361 Ga0073689_10731 NADPH-dependent 2,4-dienoyl-CoA reductase, sulfur reductase [pelotomaculum Ga0073689 : Ga0073689_107]

MSANLKI VVI GGVAAGTKAAARARRLAPNADI TI I EKDKYI SYAGCGMPF
YLSGQVRELENLFTTSYGVRNEEYFLNEKGI NVLTGAEAVAI DRPNKRV
EVVNLATGERSFI EYDKLVVATGSTPLI PPI EGLDLKGI YRLNHPEDALS
I KAALEEGVGEAVVI GAGLI GMEAVDALMKLVFVNVVELRDQVLPGLLD
PDLAAPFALRLEENGVELSLGRKVLKLEGEDGKVAAVTDQGRLETEMVI
VAVGVRPNVKLA AEAGLT I GETGAI AVNEYLQTSYPDI YALGDCVENTHL

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VSGRKVYI PLASTANRQGRVVDNVTGGKTKFRGI LGTAVLRVMGI NAGR
TGLGEEQAKSLGYDVI TSLNPTLDATHYHPQHGKVFVKVI ADAQTGRVLG
AQGFPGGEVAKRI DVFAAAI TFGATLDDI ADI DTGYAPPFNTPI DPLHHS
VNI I RNKI AGI AEGI TPARVKEKFDRGDDFVFLDVRTEQQFKPKHI DDPR
VMLVPLGEI RRRI DEI PRDKEVVTSCVLGVRAYEALRI LKGAGFDNVKYM
EGSLEAWPYELD

>2617920360 Ga0073689_10730 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_107]
LDPSALYLI SQDSRFYKWEFPLLLLYMEWNI RLKYLCLV

>2617920359 Ga0073689_10729 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_107]
MKDLKARVAYLQGLSAGLDLNAESKEGKLLSGI I EVLDEFASMGDLEEA
QGQLEDYLESI DEDLYQLEDDI YEGDEVDDGGACEGDYLEVNCPGCGETVC
FDSEVLEDDDVVEVTCPCNDEVVFVNDGEYQAADMPMELEGRLTAGKAAA
EDEDI

>2617920358 efp elongation factor P [pelotomaculum Ga0073689 : Ga0073689_107]
LI STNDFRTGLTI ELEGEVFQVI EFQHVKPGKGAAAFVRSKLRNVRTGAVV
EKTFNAGEKI PRARI ERREMQYLYNDGKDYNFMDMESYDQVAMTAEQLGD
AVKYLKENMNI QVLTFQGKSI GVLPNFVELEVVEVETAPGI KGDTASGGSK
PATLETGAAVQVPFFI NVGDKLQI DTRTGNYI KRV

>2617920357 Ga0073689_10727 Xaa-Pro dipeptidase [pelotomaculum Ga0073689 :
Ga0073689_107]
LRRRLESLRELFGGAGVEALYI TNPENRYYLSGFSGTAGALLI SRDRQRL
LTDFRYI DQAGRECPEFEI VRVKENPPYPEALQEI VKGDGFTVLGCEGHH
LTYNQYI GLADKLAGVELKPAGELVEELRLCKEAEI HRI SEAVRLADEA
FGRLLPAI RPPGVPEREVALRLECLMRSMGAEAAAFKFI VASGPRSALPHG
VASARTI RAGDLVTLDFGAVYRGYHSDI TRTVALGEPDQKQEEI YSI VLE
AQLKAI AAVRAGI PASAVDRAAREYI EQRGYGECFGHGTGHGVGLSI HEK
PRLSAKDDTPLRAGMVVTVPEPGI YLPDWGGVRI EDTVLVEEGGCRVLTGA
PKEKLLVLS

>2617920356 Ga0073689_10726 3-dehydroquinate dehydratase [pelotomaculum
Ga0073689 : Ga0073689_107]
LKI LVLHGPNLNLGKREPAVYGRILTLEQI NRKLEELAAELGVELTCROS
NHEGELI DI LHSAAAADAVVFNPAYTHYSYALRDAVAI GVPTVEVHL
SNI HAREDFRKQSVI APAAAGQI SGLGVTGYLLALRAAAALAGD

>2617920355 Ga0073689_10725 PmbA protein [pelotomaculum Ga0073689 :
Ga0073689_107]
VDNEDLFLDAAGAAVRKAVGLGAQLAEAYI SNARELNI EVRDGRVETMKL
AADRGLGLRVMREGRTGFSFSTDLSPOGVVEEAAGQALANCGKTAADPFHR
LPPPGPAYPGLDI YDSAI REATVEQKI DLARSMEEAARAYDPRVKVI ETS
TYQDGEALVTVVNSLGMRLAYKGAYCGVYLALAAEGEGDSQTGFALDFSL
KYKLLKPEEVGREAAARRAVRMLGAAPAPTRRMAVALDPYVATGFLGLI GP
ALTGEAVQKGRSLFAGKVGARVVS DKVTVI DDGALAGGI ASAPFDGEGAP
TSRTVLI EGGI LKGYLYNTYTAAKDGVQSTGNGVGRGSFKGTPEVGVNTFF
VEAGPTPVEKMI KDVKAGLYVTEVMGMHTADPI SGDFSVGVAGLLI ENGE
FTKPVRGMAMGGNI I ELLAGVDAVGDDLRFEGGKGSPTLRVAEMTVSGQ

>2617920354 Ga0073689_10724 YabG peptidase U57 [pelotomaculum Ga0073689 :
Ga0073689_107]
MKI GDI VTRKVVYGEDMQFCI I GFYTNQDTGDRVAI LALLDPTLI VEASVE
DLAPI SARRLFSLTTPVFVH

>2617920353 Ga0073689_10723 Tld protein [pelotomaculum Ga0073689 :
Ga0073689_107]
LVDKEVLKEVLDAQALANGGDFADVFI EHKRTTGI GCEAGKI ERVQSGVDS
GAGI RVLSGDSTAYAYTNDLSRESLLEVAKI VSHAASGGKKEVNLDFFKKV
EPLVDFFEFKERPGDVPTDRKVALVEAADRAARAVIDADRI KQVI VGYGDVA
QRVTI ANSAGDYVEDERI RTRLLVQAVAAAGSLI QTGYEAVGSLCGFELF
ESYAPEEVAEAAAKRAVAMLVARPAPAGRMPVVMAGEAGGTMVHEACGHG
LEADLVQKGLSVYAGKKGVVASEEVTVVDDAAMDRLYGSYRFDDEGAPA
RRVNL I ENGVLTDYMYDRLAAGKDGROSNHGRRRESYQHKPI PRMGNTYI
APGKTNPKEI I RGTKEGLLVKKMGGGQVNTTTGDFVFDVAEGYLI EDGEI
GPLVRGATLTGNGPEVLRI VEMVGSDLGFTI GTCGKDGQGVPSDAQPTM

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AI RQLTVGGTTHGEPNGNI RRL

>2617920352 Ga0073689_10722 Copper amine oxidase N-terminal domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_107]
 MKRKFSI VVI VCLVFTSPALTMAADFSLNVNGVPLYSDVRPVVEGRNVLL
 PLRAVAEALGAEVI YDEFQRTVTI SKPALEARI SPGKYGGI KNGSLVLFV
 TPPKI I NDRI FVTREELTKI LDVKTFLRVPEYSI TVEN

>2617920351 Ga0073689_10721 type IV pilus assembly protein PilO [pelotomaculum Ga0073689 : Ga0073689_107]
 MWQRLKPREKI MLALLGVAGLCFVLLKFI LLHQFDITYADKTRLKDLQSK
 VQAAEAVVKSQDREI ELANKAAEQLENI KPLFNHEMGDGLALVHI GLKAA
 ESRVEI VSFKPSNI VDKRMYLELPSNFEVRGDYRNV I GFI DRMEALPDLS
 ELRTLKI QPEEKKAAGAGAVQQASPKDEDVPI QDGI V TATFDI VTFTN
 PTPGARFNLEQVLRWAVGRYNAFQTAAVTPYPGI KPVRKI EPLGTPEA
 I DI PKPGSLRGVPSDTEKGTTPQKPSGEQTGSPTGTWGVVPLAAMENVK
 S

>2617920350 Ga0073689_10720 type IV pilus assembly protein PilN [pelotomaculum Ga0073689 : Ga0073689_107]
 MYKI NLLPSELQRDLSI DVRKLVKRAAVSLVAVI LLAGYGSFLYSSYST
 KEI AKTEKYLNELNVTYKKEVEI KKQRETSEQSAQKLKELLNNRLAWSSV
 LEDLNHNLPVDVWLERI DLSHI DLQASTGASGQPKGQADAQAPQSQSQA
 PAQPNPAQAGTGAVPEGKPPSGSGTPAPSSPPVPNTLTI EGYSTRVPSI
 GVVFNNLSRMPYFTRVTLNEFAEDEKMGAI KFKVTAAI KEGGR

>2617920349 Ga0073689_10719 type IV pilus assembly protein PilM [pelotomaculum Ga0073689 : Ga0073689_107]
 LKGFNGI KLI GRWVKNVEEKENI TGGKKPGQAGGLRFPFGKGFSSSELL
 RKLAPKKTRFAAVDI GSREI KVVEVSTAGGDPEVTAFGRI PTPPGALDGP
 VDEEALVNALNEVLLTSGI QLNEVI TTI SGDRVI TRHI MI PLMPEKELKA
 AVRFEKTEFI PI PVQELTI RYLKLGQVSDGVKYL LLLAAVPTTFI YKY
 YGLFARAGLI VAAI DLQSLSLWRVFCGLQTHSAGTVGLLDI GASTTQFLV
 VRDRALQFTRSLPVGGNLLTSSLAHYGFEEEAQRVKETEGLLSTEEAA
 ATASPAAMQI DFSLRYGLSGLVREI RRSI DYMSQENATAI ERFI I SGGT
 SKLKGRDFFAEAMDVPVDFGDPSSLGQPGDETEAAPDPAFAVLGTAL
 REVVE

>2617920348 Ga0073689_10718 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_107]
 MRVI KSQSGQALVLI MI MTSVFLLMGSSMLAQT SQGLKASYEERNI VQAY
 YI AEAGA EKAVAEI KNNPFWLKG LASNI DVMYI GNPAMDYAGGQI TSVKV
 KRTSSTDNPTLFSI TSI GEYQAKRTI EVQGMYPDI AFSRGVWI SSADS
 QFDQNSVLDSDVTVQEPGTI YFENNCAI YRTI TAVGDVVL RQNMATKVV
 TSGSVKI ENNAQVTTDVEAGGNVTLDNNTRI NGATNAVGNVTLDNNAVI G
 GDVYFDGTLTNGSGTGALHPGEAHAVNVNVPFPALDQYWFCKNADRTL
 SGNLSGSFNV DGI SYI PGDI SI SGTYFGKGAI VAGGKVTI SGNLTRGNTD
 SSLAVI AFGSPVGI ETSNNLSVYALLYSPNQI I LANGTYLYGSAVCNQI V
 I SQGVRVND DDL LQDKQOWI TTVVRI TSWKEKFSVF

>2617920347 Ga0073689_10717 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_107]
 MYDSLRI SLDRMGRELRYTKGVTASSNSTSLSFVNAGGI TVRYYCSSLAL
 YRVEGGSPQPLASDI QSVSFTYI DDTGSVVSDSHI PARASSI RQVKI TIT
 AKKKGSRVDPVVLVLKVKLRALP

>2617920346 Ga0073689_10716 prepilin-type N-terminal cleavage/methylation domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_107]
 MFKDERGLTI I EVLMSVAI LSI I MVPMMNSFI I GGRLNDAEGYSTALT
 AQSKI EELKGLNFSSI VDI PQTDFSGESDYSQYDGYYSI TVAASGLNTK
 TVTVTVFFYSQDI SI TAEI AKR

>2617920345 Ga0073689_10715 prepilin-type N-terminal cleavage/methylation domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_107]
 MI NVFI TDRDLI KKTFLNNSAFTLLELAI VI AVLGI I VTSMPKFSGI I S
 GYRLDSSAREMTLNI RSLQQAII KSENTGFKVVFNTSTGSYHI YHFI NNA
 NVLYKTVELPSNVQLVFVNFYNSTLEFSI NGNPI YRI GGHI SLRDKVTGE
 FLYVI I DSI GRVRVSAEPP

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>2617920344 Ga0073689_10714 type IV pilus assembly protein PilC [pelotomaculum Ga0073689 : Ga0073689_107]

MAQTFLYKARNPAGKLVSGKVEAESRNSAVALLRERKFFVVELKEASAGS
FSFKSEI FFRKKVGARDLAI LCRQFATMVQAGLPI LQCLNI LI QQSDNI T
LKETLKKVAGNLEKGLSLAESI RNFPGVFPQI FI SMVEAGEI GGSLDNVL
ERLAFNFEKEHDI KEKVKSAMTYPAVVI LVAVVMAALLI FVI PSFVAML
NDMKAPI PAPTOI VI NTSNFLKSFYI AI LSI AGAMFGYKQAVKKGGQGN
MMDRLMLKLPVFGPMI NKI I I SRFCRSLSTLLMSGVPVLQSLDVVKNI VG
NTVI I KSI KETQNSI KEGQNI SLPLQKSGVFPPMVTRMMAI GEETGSLDT
LLERI ADFYEQEVDLVSRLSSMLEPI LI VVMGGI VGFI I LSI MLPMYSI
VTNVKR

>2617920343 Ga0073689_10713 twitching motility protein PilT [pelotomaculum Ga0073689 : Ga0073689_107]

MMTCNEI LALAFKLGASDVHI TVNSAPAFRLHGSLLPFDAPWQGRLGAE
ATAI GKLTPEDSMDLVRQI MTGDOYRKFOETGELDYSYAI PGVCRFRVNA
FKQQGNVSFVVR LI NSRI LSFQELGLPEVLADLSFKPRGLVLVTGPTGSG
KSTTLASMI DLI NREKSHHI I TLEDPI EFVHQHKKSI I NQREV GKDTRSF
ASALRAAMREDPDVI LVGEMRDPETI GI AI TAAETGHLVFGTLHTSSAAQ
TVDR I I DVFPFHQQQI RVQLANTI QGI I AQTLI PRVDRPGRVAAI EVMV
ATPAI RNLI RESKTYQI VSQI QTGAKYGMQSLDMALRTLYTKMI SREEV
LSRATDPESLSKML

>2617920342 Ga0073689_10712 type II secretion system protein E (GspE) [pelotomaculum Ga0073689 : Ga0073689_107]

MAAVPVTQKKLLGEHLI ERGVI TREQLWEALRVQSRTELMGKI LVKLG
VAEEVI NEI LEI QQI KLDNLDPALI KTI PEQFI RKYRAVPLKKEGNYLSV
AMADPKNV LAI DDLRLI TGLEI EPVQFGARDI DNVI QKHFGMPEVDEI FE
DLELLSEEREPEAMTLEEEVFDEAPVVRVNSI FI QAI EHNASDI HI EPM
EGQVRI RYRI DGMLREV MKFPKKI QSALI SRVKI MANMDI AERRI PQDGR
VMLKFGKKEFDI RVSSLPTVYGEKI VTRI LDKGSMKCKI ESI GFGPASL
KRFLSALRAPYGM I LI TGPTGSGKTTTLYAALNEI NTLEKNVI TI EDPVE
YMLEDI NQTQVNTRAGMTFAI GLRAI LRQDPDI I MVGEI RDGETADI AVK
AATTGHLVLSTLHTNDAAGAFTRLVDMGI EPFLVASSVLI AVAQRVLRLI
CRKCRRSYQLAPEVPERTFLGI GPDEPVTLYKGECCNECGNTGYKGRMAI
LEVLP MNAGLRQLI LRNADANVVKQKALSDGMI SLKMDGI RKALEGLTTI
DEVMRVAYI EETGD

>2617920341 Ga0073689_10711 Tfp pilus assembly protein PilO [pelotomaculum Ga0073689 : Ga0073689_107]

MRQLTTLKLNFKFNKREKTLASVFLVFI VFFLYCQYVYI PQEKKI AAI KN
DI KKKEDMI NQMI SQGYGNVSDLDKI QGMDAEI EKLYQKVPNTENKSG
LVDFYN LAI KNHVVAQTI TFGKLAHNSFSRFQVSLEVLGTKQDVNF I K
GI EDYPRQSMI SKI ELEPKEGNMI SAKI LDEFYVLQEVKNDPLEYPFMDK
KQGLNFLDFVFEQYNVTGEVYQSEDPTVKKNLDELPAI ATPARSNGVSE
LI FNSGGQSGSSVNDEKSKRRGKAQTLI PGLSR

>2617920340 Ga0073689_10710 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_107]

MVQMLQI I VFI I ALVVI LLI LGLAI PVDLI GTWQLLKSDYPELGI LFLI L
GGSFVAYFTGYLLKKGTQK

>2617920339 Ga0073689_1079 Tfp pilus assembly protein PilN [pelotomaculum Ga0073689 : Ga0073689_107]

LKLATVKDI DFLPQRI KVPREKKRNL I LTAALI I LAFLAGLAVWI PI KL
EKDYLAQVVLDEKI TELKKGEPI YRQVLAKQEEYQEKQALDTLKRND
KI I PFLEKVKEVTPPGSYI SKI SVTADEGANI TFVTRDPVETAALVGLR
SLDI FKNVDLATVPFI DYSKPVQFDLRFKWAREKPKEGTKEEVNKEVDKG
AEI NAAI KEAERKI KP

>2617920338 Ga0073689_1078 Tfp pilus assembly protein, ATPase PilM [pelotomaculum Ga0073689 : Ga0073689_107]

MI AKLGLKLYYDMRGSAVRLVEGRTLKSGAI VVDKFGSVLFEGGGDFPP
DNDFI SNNAALLKNYLQEQGI KTKKAVLCLGRTGI I ARAVKVPKMTLADL
KTHMELEMSDYI PVSSEESYDFDKVNGVI TEGERDYFNI LVAAVLNKHVE
ECVCTVEMAGLKPLVVDI YPNVWVWKLASKYQDI AVVDSGRDGT RLLLCR
GEDLVLYNDLPCQFEDQDDDLAQL TRELGGYLDFFASRHF GKTVDR I CI T
GELAASSNAPLI LERFFNI PVSPSLQEAGMPEI KGDVERFKLMASVYAGN
I GLMLREV

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>2617920337 Ga0073689_1077 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_107]
 LLKYLNTKGVAI LI VMLVLLVMVIMNI LI YAATQERLATNSYDNSKESF
 YIAEAAANLAI NRWVDFI NDAHSSDTTKQVPEKVDI TSTNNGYLKKYLDD
 GSTNSGNVRYDLERSFKDNLGTSNI SI SYSVDPSSVDNNGMLYDDDKYPS
 GPYNLLTI NI QATYNGTMFPYKVNLFCHHGKTL SYKGNATY

>2617920336 Ga0073689_1076 prepilin-type N-terminal cleavage/methylation domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_107]
 MVKII CTRSGFTLI EVMMVTAI I GILLTI VYNFLGFNFKFQHDRDYEYNS
 YLNARI AMDGI VYLLEQYEKI DI PSTGKVNGYKI DNTTDLPI DFNKNTTV
 VTGCKYYYFFPTGSSYGQI I NKDGSVLADGI LSFNLEKDLNSKYI SI ELD
 VVPTENPNAI PLKLYTSLGLSRKFVPLTG

>2617920335 Ga0073689_1075 prepilin-type N-terminal cleavage/methylation domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_107]
 LRAVNKSLRDNRGMTI VEIMI AVFGI FLTTGCSVYHFI GKFNADTLDO
 LMMTELAQSEI EKI KTGAKTVNYPSTSTVNYPNDVSPQQSYTVRYDSQNV
 SAAAVGGS I LKI TTGDSNDYVFGAWI PPQKTLHLYVENPTGEGGTYNLG
 SWTTDPNTNTNI NGWEI I TSPEPALTTVQGAHGGSDPI FYNQYYFNPPFS
 YTVDAI VTSLENGHCETGMAI DDNSNNDKYLFLYLSVDNSDRGDLVVKYP
 GGSFKPMTDI AI QEGRKYFTVDFNSGDPGTI I LNFGYYGTGNSKI AI LN
 NDYPDNKSHFSRTGHNYLGLHDTTAQTQMTYTLPTLLGEECYL

>2617920334 Ga0073689_1074 type IV pilus assembly protein PilC [pelotomaculum Ga0073689 : Ga0073689_107]
 MPEFSYRAI DTRGQLI TGTGGDSVPGVRLNLKERGLLPVRI EDGRVFSI
 PNLPGLKSKREI NGEALSQFCRQLTVI I SSGVNLLKGLEI MAEKTDPKQM
 RSEI RRI HREVQKGRTLAEAMGDRGSLI PGLLTNMVATGEASGLDEVLR
 SMAEFYEKDHRI KQKI KSASVYPI VMVMAAGLI AFFFNFLLPQMVALI T
 TSGGKLPLLTRI VI GI SNFTTRYFVLI GGALAGLAFLKLYFKTPGGRLN
 RDKLI LKI PLLGKTMRDVATMRFAHTAH I KSGLPLLQGLEFI KQNVNN
 ALAERAVEYAVEGLQRGESLAVNLAKAGYFDAMAI QMI SI GEETGELEKM
 LSEMADYYNQESDAGFTKLLALVEPVMLLI I GSI VSTVI I AVMLPMLDMV
 SHIKR

>2617920333 Ga0073689_1073 type II secretion system protein E (GspE) [pelotomaculum Ga0073689 : Ga0073689_107]
 MNI SFNQTKKLRLGLDLLHAGLI TEEQLKDALSQRGLGKRLGEVLLDGG
 YI SQQDLTSVLETLGI ESI NLKQTAVDPKFARM I PENLARRHVVI PVQV
 AKGHLYLAMRDPLDLAI QDVRLLVQMPVTPVLATRDDI I DSI ERVFSQA
 AAARAADDFVHSQAGLLAGLEDLSLVNSAPI VRLVNSTLENAVRSGASD
 VHI EPDHDQMRVRI RVDGI LQESLVTGLGAHGAVTSRVKVMAGLNI SEKR
 VPQDGRMTI TVDRREI DLRVSTMPPTYGEKVMMRI LDRANFMLGKEKLG
 SPADLEKFARLAAKPHGI I LVTGPTGSGKTTTLYSMLAELNDSKKNI I TL
 EDPVEFDMKGI NQTQI NVKAGLTFAAGLRAMLRODPDI I MVGEI RDSETA
 EI SARAALTGHLVLSTLHTNDAPGAVARVDMGI EPYLI SSSLAGVVAQR
 LVRKI CPFCREEYEAGEREKRI LRLPLDMPLKLAGGKGCDYCNRTGYKGR
 VGVFEI MEVRKELRLLI DKGPPTELDRI AI ELGMVPLWEDARQKVLEGI
 TTLEELLRVITYS

>2617920332 Ga0073689_1072 type IV pilus assembly protein PilA [pelotomaculum Ga0073689 : Ga0073689_107]
 MGKFI KNQKGFLLI ELMVVI AVI GI LAAVLI PKI GGTKNAAKLSGVDANA
 RI VQAQVESMI GRYQDKSATQMDKFADALVSSLSEVTSPFDVNYVGASKD
 ATETNGVVFVANKAVTVNTKEAAPATESNKKGLI YVLVDETKAGTPDKFS
 I TSI TI YPYDNDGNPMPTI TVNK

>2617920331 Ga0073689_1071 Type IV leader peptidase family protein [pelotomaculum Ga0073689 : Ga0073689_107]
 VTGVLYVLAVAKYGPTPAALRALLVSLVI PAAVI DLRHKI I PDKLNLG
 AVLALPLLLLSRDVFLLSGVAGLLAGGGLLLLI AI ASRGGMGGGDI KLAAY
 MGLLLGWKYLLVALFLAFTAGGVMGVLMI LCRVKKLKEAVPFGPYLALGA
 LTAALAGDKI VLWYTGLVRL

>2617920330 rpsJ SSU ribosomal protein S10P [pelotomaculum Ga0073689 : Ga0073689_106]
 VKSQKI RI RLKAFDHHMLDQSAQKI VDTAKRTGAAGVPVPLPTEKNI YT

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ILRSPHVNKDSREQFEMRTHKRLI DI LEPTPKTVDALMRLDLPAGVDI EIKL

>2617920329 Ga0073689_106128 large subunit ribosomal protein L3 [pel otomaculum Ga0073689 : Ga0073689_106]
MPKGI LGKKI GMTQI FTDTGLAI PVTVI EAGPCI VVQKRTPEKDGYSAIQ
I GFGEKRESLFNKPLKGHFNRAGMRPLRFLREMRVEDPEAYQVGQELKAD
I FARGEKVDVVGTSKGRGFAGGI KRHGFHRGPMAHGSKYHRRPGSLGAKG
PARVFKGRKLPGHLGVERVTQNLLEVI KVDPDNRNLLAVKGAVPGPRGGLV
LVKPTVKGR

>2617920328 Ga0073689_106127 large subunit ribosomal protein L4 [pel otomaculum Ga0073689 : Ga0073689_106]
MPTVALYNI NGEQVGELALKDEI FGVEVHEAVLHDAVVMQLANRRRGTHD
TKTRAEVSGGGRKPWRQKGTGRARHGS RSPI WRGGGTVFGPHPRDYGYS
LPGKVRRLALKSALSAKVNAEII LVLEDELRLDQPKTKDMARI LDNLKVDD
ALLI TAEKDEAVEKSARNI PNI KPLAAGGLNVYDI LAYDKLVMTRDAVAK
VEEVFA

>2617920327 Ga0073689_106126 LSU ribosomal protein L23P [pel otomaculum Ga0073689 : Ga0073689_106]
MKDPRDI LRRPVI TEKSTSLLODNKYTFLVAPGANKTEI KQAVEKI FKVK
VEKVNTLRVKGKFKRVIRGI PGKTPDTKKAI VTLKKGDKI EIEFGM

>2617920326 Ga0073689_106125 LSU ribosomal protein L2P [pel otomaculum Ga0073689 : Ga0073689_106]
VTVSDFEEI TSTEPEKSLLEPLKKSGGRNARGKVTVRHRGGGHKRMRYRI
DFKRDKDG I PAKVASI EYDPNRSARI ALLYYSDEKRYI VSPVGLEVGRT
VVSYPEADI KVGNCPLPLRNI PLGTMI HNI ELYPKGGGQLVRSAGSAAQLM
AKEGKYANI RMPSGEMRLLLDLCRATI GQVGNVEHENI TVGKAGRKRWLGI
I RPTVRGVVMNPVDHPHGGGEGRSPI GRNPVTPWGPALGARTRKKKTS
KLI VKRRTK

>2617920325 Ga0073689_106124 small subunit ribosomal protein S19 [pel otomaculum Ga0073689 : Ga0073689_106]
LGRSLKKGOPYCEEILLAKI EKMNETGDKKVI KTWSRRSTI FPQMVGHTVA
VHDGRKHVPVYI TEDMVGHRLGEFAPTRLFRGHGRHETERSTALK

>2617920324 Ga0073689_106123 LSU ribosomal protein L22P [pel otomaculum Ga0073689 : Ga0073689_106]
VEARAI AKYI RI SPRKVRQVVDLI RGKKVNDALAI LKYTPKRASEAVTKV
VESAAANAENNLQMGDEL FVKACYVDQGPTLKRYQPRARGSADI LRKRT
SHI TVVVGDKKEDR

>2617920323 Ga0073689_106122 SSU ribosomal protein S3P [pel otomaculum Ga0073689 : Ga0073689_106]
VGQKVHPKGLRI GI RDWEGKWFADKKNYATLLHEDI KIRKFI KRKLYAA
GVSRI QI ERAANRVKI SI HTAKPGI VI GRGGAEVENLRKQLEKLTGRQVS
VNI VEI KAPELDAQLVAENVAAQLEKRI AFRRAMKQVVSRSMMKMGAKGI K
I AVGGRLAGAEI ARTEWYSEGVPLHTLRADI DYGF AEANTTYGKI GI KV
WI YRGEVLPEVRTSAKAPERGGKAAQEGGGQ

>2617920322 rplP large subunit ribosomal protein L16 [pel otomaculum Ga0073689 : Ga0073689_106]
MLI PKRVKYRKQHRGMTGKAKGGKEI NFGEYGLQALEPAWI TNROI EAA
RI AMTRHI KRGGKVWI RI FPDKPI TAKPAETRMGSGKGTPEYVAVVVKPG
RI MFELAGI SEEVAREAMRLASHKLPI KTKFVKRGEVGEVNES

>2617920321 Ga0073689_106120 large subunit ribosomal protein L29 [pel otomaculum Ga0073689 : Ga0073689_106]
MKVKELRELDAELNKRLSDSKDELFLRFQMATGQLDNPMKLKDVRRI
AQVKTI I RERELGI KRA

>2617920320 Ga0073689_106119 small subunit ribosomal protein S17 [pel otomaculum Ga0073689 : Ga0073689_106]
VENRGMRKVLTKGVVSDKMDKTVVAVETLVRHPLYQRI I RRTRKFAHD
EKNTCRAGDKVRI METRPLSKEKRWRVI EIMERAQI

>2617920319 rplN LSU ribosomal protein L14P [pel otomaculum Ga0073689 :

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Ga0073689_106]

VI QVQSI LNVADNTGARRLMCI RVLGGALRRYASVGD I VI CSVKEATPGG
VVKKGDVVKAVVVRTRKEVRRPDGSYI KFDENAAVVI KDDKSPRGTRI FG
PVARELRDRDFMKI VSLAPEVL

>2617920318 Ga0073689_106117 LSU ribosomal protein L24P [pelotomaculum Ga0073689 : Ga0073689_106]

MANPKLHVRKGDVTLVI TGKSAGKKGKI LSVI PDKGRVVVEGVNVVKRHT
KPTRKMMQGGI MEKEAPI HSSNVMLFCGKCNAPTKVGGKLLSEGEKVRI C
KKCGEAI

>2617920317 RplE LSU ribosomal protein L5P [pelotomaculum Ga0073689 : Ga0073689_106]

MARLKDKYKNDVSPAMMQKFNYKNI MQVPKLEKI VVNMGLGEAI QNSKI I
DAAVSDI MTI TGQKPVVTAKKSVAAFKL RAGMSVGAKVTLRGERMYEFV
DKLNFVALPRVRDFRGI SPKSF DGRGNYS LGI KEQLI FPEI EYDKI DKIR
GMDI I FVTTAKTDEEARELLRLMGMPFRAA

>2617920316 Ga0073689_106115 small subunit ribosomal protein S14 [pelotomaculum Ga0073689 : Ga0073689_106]

VAKKSMVLKAQRPPRFKVRAYNRCKLCGRPHAYMRKFGI CRI CFRELSYK
GEI PGI RKASW

>2617920315 rpsH small subunit ribosomal protein S8 [pelotomaculum Ga0073689 : Ga0073689_106]

MVMTDPI ADFLTRI RNANTVYHDKVEAPASRVKKAI AGI LKNEGFVKDCE
FI DDGKQGI I RVYLKYGVNKERVI TGLKRI SKPGLRVYARKDQVPKVLGG
LGVAI I STSRGI MTDKQARREGLGGEVI CYVW

>2617920314 Ga0073689_106113 large subunit ribosomal protein L6 [pelotomaculum Ga0073689 : Ga0073689_106]

MSRI GRQPI PVPAGVDVRI DGNTVLVKGPKGQLEKELHRDMI I RYEDGRL
LVERPSDNKI HRSLHGLTRTLLNNMVVGVTSGFQKNLELVGVGYRASKQG
NKLVLAVGYSHPEI EPEPGLI EVPAPTKI SVKGV DREKVGALAAAI RA
VREPEPYKGGVRYEGERI RRVKGKAGGKGGK

>2617920313 Ga0073689_106112 LSU ribosomal protein L18P [pelotomaculum Ga0073689 : Ga0073689_106]

VLKKPDHKLAKRRRRVRKKI YGASGRPRLNVFRSLHNI YAQI I DDERG
VTLVTASTLAPELKGKLLSGSNTAAATAVGELLSSKATEAGI KQVVFDR
GYVYHGRI KALAEARAGGLEF

>2617920312 rpsE SSU ribosomal protein S5P [pelotomaculum Ga0073689 : Ga0073689_106]

MARI DASKLETSEKVVYI NRVAKVVKGGRRFSFSALMVVDGNGYVGAGL
GKAGEVPEAI RKG I EDAKKNI I KVPI SGTI PHEVTGQFGAGKVLLKPAI
PGAGVI AGGPVRAI LELAGVRDI LTKSLGSNNANMVRATI EALKSLKTP
EEVARLRGKTAEELLG

>2617920311 Ga0073689_106110 LSU ribosomal protein L30P [pelotomaculum Ga0073689 : Ga0073689_106]

VAKLKI TLVKSLI GRPEDQRTVTRLGLTKTSRSVI QEDNPQI RGMI NKV
SHLLKVEEA

>2617920310 Ga0073689_106109 large subunit ribosomal protein L15 [pelotomaculum Ga0073689 : Ga0073689_106]

VKLHELGPAPGARTKFTKGGGI GSGLGKTAGRGHKQKARSGGGVRPGF
EGGQMPLORRMPKRGFYNKFAKEVI AVNI DQLNCFEDGTTVTPETLLAAR
VI KKLGDGVKI LGNGTLEKSLTVQAHAFSKTAGEKI AAAGGKAEVI

>2617920309 Ga0073689_106108 protein translocase subunit secY/sec61 alpha [pelotomaculum Ga0073689 : Ga0073689_106]

LLDSLKSAVKVSELRTKLLFTLGMVFI FRLGAHI PVPGVNPDRAELVGS
GLI FGFFDVI SGGALKNFSVFAMSI TPYI NASI I MQLLTVVI PHLERLAK
EGEEGRKKI TOYTRYLTVVLA FVQGLGMVVGKGS LFNPGPLSYLMVAIT
I TAGTTFLMMGEQI TEKGI GNGI SLLI FAGI VSRVPSGVVRLVEYI NAG
TVNVLSI VLLVI I GVLVI AGVVAI QEQORRI PVQYAKRVVGRRVYGGQTT
HLPLRVNQAGVI PI I FASSLLMFPETI ANMFANSPVAI FYGKYFGWGTA
HTI FYALLI I GFTYFYTAVI MNPVDI ADNI KKYGGFI PGLRPGRPATAEYI

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SRI MSRVTLAGAI FLALIAI LPNFVLLATRI PNI YFGGTALLI VVGVALD
TMKQVESHLLMRSYQGF I K

>2617920308 Ga0073689_106107 methionyl aminopeptidase [pelotomaculum Ga0073689 : Ga0073689_106]

MITCKSERELNYMRDAGRLVARAHAE LARAVKVG VNTGELDR LAEDFI LK
SGGKPAFKGLYGFPSI CASVNEEVVHGFPGLRKL ENGDI I SIDI GTEI N
GYFGDSAVTLPVGDVGNEALDLLRATEEALYRGI EKARVGNRLSDI SHAV
QACAESHGYSVVRDFVGHGI GSKPHEEPQVPNFGKPGRGPRLKEG MTLAI
EPMI NMGTYEVRTLSNNWTVVTLDSKLSAHFEHTI AI TDDKPEI LTKT

>2617920307 Ga0073689_106106 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_106]

LVMSNDSIQI GRLVCSVQGRDSGRFYLVVGI ESGSRVRLADGEGRKVEKP
KLKNI RHLKI YDVMAGEVLNKSQSAKKI TNAVVRKELKSLVDNLD

>2617920306 infA bacterial translation initiation factor 1 (bIF-1)
[pelotomaculum Ga0073689 : Ga0073689_106]

MSKQDVI EVEGTVI EPLPNAMFRVELQNGHKVLAHVSGKI RMNFI RILAG
DRVMVELSPYDLTRGRI VYRYK

>2617920305 rpsM small subunit ribosomal protein S13 [pelotomaculum Ga0073689 : Ga0073689_106]

MARIAGVDLPRDKRVEI ALTYI YGI GRPTSQKI LTRSGVNP DTRVKNLTE
EEI NRLRDI I EKNYKVEGDLRREVALNVKRLI EIGCYRGLRHRRGMPVRG
QRTKTNARTRKGRKTVGVRRKK

>2617920304 rpsK SSU ribosomal protein S11P [pelotomaculum Ga0073689 : Ga0073689_106]

MARRVTRTKKRERKNI ESGVAHI KSTFNNTVVTI TDTRGNTI SWCSAGQV
GFKGSRKSTPFAAQMAAENAAKEAMEHGLKEVEVMVKGPGAGREAAI RSL
QAAGLEV NLI KDVTPI PHNGCRPPKRRRV

>2617920303 Ga0073689_106102 SSU ribosomal protein S4P [pelotomaculum Ga0073689 : Ga0073689_106]

LARYTESVCRCLCRREGLKLYLKGDRCYTSKCAVDRRAYAPGQHGOGRKKV
SEYGLQLREKQKARRI YGI LEGQFRRYFEKAESQSGVTGENLLRLLERRL
DNVI YRLGLGASRNEARQLVRHGHFDVNGRKVNI PSYLLRVGDMLTVRGK
SKESPRVKELLERAADRTPPAWLEYEADQARARVVALPARDQI DSPVQEH
LIVELYSR

>2617920302 RpoA DNA-directed RNA polymerase subunit alpha [pelotomaculum Ga0073689 : Ga0073689_106]

MLEI EKPKI EI VEMSDDSTYKGFVVEPLERGYI TLGNSLRRI LLSSLPG
AAVTSVKI DGVLHEFSTI PGVVEDVTDI I LNLKCLCLKI YGDEEKVLRI E
AVAEGPVKAADI I HDADVEI MNPDLTI ATLATGARLFMEI TVAKGRGYVS
AERNKKGDHI I GVPVDSVFTPVVKVNYTVENTRVGQI TDYDKLTMEVWT
DGSIRPDEATSLSAKI LNEHLRLFI GLTETVSDVEI MVEKEEEEQKDKI LE
MPI EELDLSVRSYNCLKRAGI NTVEELVQHNEEDMMKVRNLGKKSLEEVI
NKLHELGLSLRSSDE

>2617920301 Ga0073689_106100 large subunit ribosomal protein L17 [pelotomaculum Ga0073689 : Ga0073689_106]

VGYQKLG VNTGHRKAMLRNLVTSLFRDERI NTTEARAKEVKSI AEKLVTD
AKQGDLAARRRALAYI YEEEVVRKLFNEI ASKYMDRQGGYTRTI KVGYRR
GDAASMMVI LEMV

>2617920300 Ga0073689_10699 energy-coupling factor transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_106]

MNACGENEVFI EVKGLTHI YNRGGPGVYRALAGVDLAVRKGEFLAVVGP
GSGKSTLARHFNALLLPAE GAVLVEGLDTARPENLWEI RRRVGMVFQNP
NQI VSALVEEDTAFGAENLGLPPEEVRKRVDEALRMTGLAGYRRHAPHLL
SGGQKQRLAI AGVLAMRPTCLVLDEPGAMLD PAGRRELMATLNRLNRSRG
VTVVLVTHFMEEAAGADRI VVMSAGRPARVGT PAEVFAEVDLLEELGLEL
PVAAGI AHGLRRRGFALPDGI LTPDDMVSFLCRVGTGQRERSLVPGKNM
GRHT

>2617920299 Ga0073689_10698 energy-coupling factor transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_106]

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MSSI I SVKNLTHI YSPGTPFQVTSLDDVSLEI KKGQFYALI GATGSGKST
LAQHFNGI LTPTAGQVLVCGADLSRKKRRELWRRVGLVFQQPEQQFFEE
TVFDDVAFGPRNMGLGGTEVAERVNGALRLVGLDPDGI GKMSPFHLSGGM
KRKAAI AGALALRPEVLVLDEPAAGLDPRGRRQLMDRVENLRRERGI TVV
LVTHSMEDVARLAGRVAVLHKGRVMEGAPREI FNRAAELRAFGLDLPAP
AQLMHRLLAAGKQVRTGI LTSAAEEEEI ARLLKGGGR

>2617920298 Ga0073689_10697 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_106]
LKSWTPGWRRLKKVSRELKQGWKVKLWKKI RALFDDREVQNDRFDRINNR
LDKLTNDTTSTAKI KS

>2617920297 Ga0073689_10696 energy-coupling factor transport system permease
protein [pelotomaculum Ga0073689 : Ga0073689_106]
MLSNI TI GQFI PGESLMHRLDPRI KVAGVAAAGSVLTASNWQGFALAAG
FTLAAMALSGLRAGVFLGGLRSFWI LLAVTFLLI QALLTPGEAVLAMGSLR
VTWEGLAAGAQI FLRLTLII LVASLI TI TTSPMSLTAGLESLLSPLGRLG
VPAHELAMMMTI ALRFVPTLLQEAETLLKAQRSRGAGTAGRGPARTWTRGL
LPLFVPLFAGALRRALAVAMEARCYRGGANRTRMKALKFSRLDYTAGL
VTLAVSALVFMFRVIF

>2617920296 Ga0073689_10695 tRNA pseudouridine38-40 synthase [pelotomaculum
Ga0073689 : Ga0073689_106]
MSNI KVTI AYDGTNYGFEQRTDGFQTVQGVLEEKLAKLTGREI RVI GA
GRDTSVHARGQVI NFDPGDWPVPPEKVKYALNSLLPDDI VAVESVVVPG
SFHARFSAI SKTYRYTI YNGRMPSPFLRLYSYHVPLPLDVEAMRAGARHL
VGRQDFSAFRALGTPVKTTVRTLLNAGVTREGDI VYVDLKAEGFLYHMAR
LI TGTLI RVGLGKNPPEEVAI LAGRDSLKAGPTAPARGLYLEKVEYE

>2617920295 Ga0073689_10694 arginine decarboxylase [pelotomaculum Ga0073689 :
Ga0073689_106]
LFDROGCAPLFEALCRHAAKEPVNLHI PGHRQGRGLPEEFLSPGGPTPFS
FDLTEI PGLDDLHNPKGAI VRAQELAAELYGAGRSFFLI NGTTVGI QALM
LSVVSEGEVI VPRNAHRSVI GGLI VSGGDPVYVPEVI PEFGI DCGVDPG
EI QRALAENPDAAAVCAVHPNFYGVAGDLAGQVRI AGGVGRPI LVDEAHG
AHLRFHPVLPQDAMSAGAAASVQSTHKLGGSLTQSSLLHLREGRI DPAGV
AAALRLLQTTSPSYI LMASLDLARRQLALRGEVLLERALELARGVRERLA
RI RGLNI LTEEHLPDRCGLDPTKL VVSVRGLGLTGYQTGTLLAERYNVF
VEMADAVNI VAFVSI GTTREDCDALVRSLADI AAREGI PAGAAPRASLLQ
APAGCRKRI RPRDAWFSPSRRLPLTQARGRI SAETVAI CPPGI PAVNPGE
EI TPEVHEYLTAVSKLGLPCQGPSDPSLKI EVVIE

>2617920294 Ga0073689_10693 thymidylate kinase [pelotomaculum Ga0073689 :
Ga0073689_106]
MKGKFI VFEGI DSGGKTTQLNLLADNLAARGCRVLCCTREPGGTRVGERIR
ELLLDPRYGELAPLLEALLYAAARAHVAQVI LPALAEGLNLVLCDFVDS
SLAYQSGSGRMAI PLLEQI NETAAGLTPDLVLVFDI SSGSGLDRI SRSG
RGVDRLELEVREFHRKARLGYLALAARDPRRYRVI NADRPVELVRRDVLK
AVEEVLDAFFKGNRP

>2617920293 Ga0073689_10692 DNA polymerase-3 subunit del ta' [pelotomaculum
Ga0073689 : Ga0073689_106]
MRSLREI AGHKQI VRI LLTAVAGGRAAHAYLFSGPAGVGKKAAMAFARA
LLCSRPEVGACGVCRECRQVGGNHPDLYFVQPSGTSI KIEQIRGI LRN
CQYRSYQGGKRVFLI RQAEAMTADAANCLLKTLEPPGETVFI LVSSRSL
ALPATI LSRCQQFFFRGI PIPELVRGLI ELHGLAEELARLAAALSGGSMG
VALTCASGSYQEEEREAALRVAEVLGRSGSLEALELAEKVSGNKERAFTIL
EMLI CWYRDLLVHREAGPAGSLYNLDRMAAVVEEVERFETCRLVEIIEEL
EATKKKI EANANPRLALEALFLRLAGGSKTARAGGAGR

>2617920292 Ga0073689_10691 Cell fate regulator YaaT, PSP1 superfamily (controls
sporulation, competence, biofilm development) [pelotomaculum Ga0073689 :
Ga0073689_106]
VGI TVVGVRFKKAGKI YYFDPGSEMLAPGDDVI VETARGVECGHVVSGLP
KVAENEVAPLKNVI RKVTDTDCCQI MI NKEKEEKAFQVGLEKI AAHNLP
MKLVGVEQTFDGNKI IFYFTADGRI DFRELVKDLASVFRTRI ELRQI GVR
DEAKMVGGLGCCGRELCCSTWLADFASVSI RMAKDQNLNLNPTKI SGI CG
RLMCCLYENECYEYAREEFPEPGGVATPDGEGKVAGI NIFKKTVNVEL
KESKTI KEYS CGQI TLKNGPAKNYRGHKKEGRVI EKNAGGAADLPGRITGD

Table S2

PMDGLAP

>2617920291 Ga0073689_10690 Regulator of replication initiation timing
[pelotomaculum Ga0073689 : Ga0073689_106]
LQSLFKLTREMETKLHALLTELOELKNKARELEEENSRLRRELATVYRRG
FPEGSGGEAAI PGGGFFNLLGLYDQGFHI CNLHFGRKRTGDCLFCMAFLR
KEQEPAAAGAAGSEG

>2617920290 Ga0073689_10689 16S rRNA (cytidine1402-2'-O)-methyl transferase
[pelotomaculum Ga0073689 : Ga0073689_106]
LNENTRGTLYLCAPI GNLEDI TLRALRVLREVDLI AAEDTRHTRKLLSH
YDIHTPLTSFHRHNLKKGAHLELLVAGKNI ALVSDAGLPPI ADPGPEL
VTAALERGCVVPPGPSAGI TALVASGLSTESFVFI GLPAAERVRI KK
LKEI RHQRTLI FYEAPHRLRGALTDI I EVLGNRPAAAARELTKMHEEI I
RGTMEEI RARFGEIEPRGEFTLVVAGDAGEEDTRDEGADEWLHLDPAHV
ARLEAEGI RRKEAI REVARLRGI PRREVYRAVVEGRTP

>2617920289 AbrB transcriptional pleiotropic regulator of transition state genes
[pelotomaculum Ga0073689 : Ga0073689_106]
LKSTGI VRKVDLGRVVI PI ELRRTLGI DEKDALEI YVDAEKI VLKKYEP
ACVFCGSASDVQHYRGKLVCRECALAMFENAQAM

>2617920288 Ga0073689_10687 SSU ribosomal protein S6P [pelotomaculum Ga0073689 :
Ga0073689_106]
LRKYEI VFI LRPDLDEEKNAV I EKFKGMI EKQGGEI LKLDKWGKRRLAY
EVKDFREGLYVI I QMNAKSEI ANEI DRVFKI TDEVLRHI I VLVEQ

>2617920287 Ga0073689_10686 single-strand binding protein [pelotomaculum
Ga0073689 : Ga0073689_106]
MLNKI I LI GRLTQEPRLRYTPNGVAVARFTLAVNRSRANKQGERETDFVD
I VVWQKQAEVCANYLGKGRLLVAVDGRLLQI RSYDDSQGVRRKAAEVVAESV
RFLDRAKESGSGANGAAHGGEPPGYGSEI TFNEDDVPF

>2617920286 Ga0073689_10685 small subunit ribosomal protein S18 [pelotomaculum
Ga0073689 : Ga0073689_106]
LKRERGRRGKKRI CSFCVDKMDAI DYKDVPRLLKKYI TERGKI LPRRI SGN
CAKHQRLLTAVKRARNI ALLPFAAE

>2617920285 Ga0073689_10684 MazG-like family protein [pelotomaculum Ga0073689 :
Ga0073689_106]
MI PGSQEGGI AKNI KI I EWLKADLVTSVSALFRSMLKSSDHLLDALASL
LVTCYVLGRRLGI NFSSDLRVEAKLRQSI DEDHELERWYGDLSALLNYL
ADKKR

>2617920284 Ga0073689_10683 Uncharacterized conserved protein YybS, DUF2232
family [pelotomaculum Ga0073689 : Ga0073689_106]
LTSGEKTRALWEWI FFTGLVVTI GLAAVYLPVVYFPATVFLPVPVI LQVL
RKDI RYGI SSLAMAGI I LFI LI PQPVAVFVLI I HYGFLGI LYGLLFKNNV
FSGGVI VVGLLGAVALALLSAGLSYAFTGSNPFALSMETROAAEEWLTAN
ROAGTFNELPTEWQEI FDENI I NI FELLI PGQYLVTSGLSAATYFLARA
FLRRGNFPLPPEPAFTRMSFPWYSI WGLI AGLGLALAGDQFSLQLATKLG
KNI LFI AFYAYLVGLSVTVYFYRKI KFAPLI KVFLVFLALI YLPFSTML
VLLLGVTDPVLNFRRLPAGKG

>2617920283 Ga0073689_10682 LSU ribosomal protein L9P [pelotomaculum Ga0073689 :
Ga0073689_106]
LKVVLLKDVPGQGRRGDVI DVAEGYARNYLFPRLGAGEATKGKMKELADR
REAAALREKKLAEEAGELASRLNLTVVI KTKTGEGGRLFSGSVNNKDI AD
ALAEQHNI VVDKKKLVVREPI KQLGVYPVTTKLYPSVQAEI KVLVTGEQD

>2617920282 Ga0073689_10681 ATP-dependent Lon protease [pelotomaculum Ga0073689
: Ga0073689_106]
MKLFLEKFI SSARSESGKRGQEQNLNRQVI ALYGLLAELYGSDKLVLRA
GKLEALQLI RSEKLEERVLALQKLVFEDPTYDTLPVPEDI PGI LEEI EEE
I ADHI ARRI VEDQLEKKI TEKLOQRHEDI RDVKLQVI NENAGPENAQTL
KKLAI LEKLEHKKLSASAMEFLRPATFEEI VGQERAVKALLAKLASYPQ
HI I LYGPPGVGKTTAARLALAAKEARSTPFAGDAAFVEVSGATLRWDPR
EVTNPLLGSVHDPI YQGARRDLAETGVPEPKLGLVTDAGGVLFI DEI GE
MDPI LQNKLLKVLEDKRVFFESSYYDPHESNVPRYI KKI FEEGAPADFI L

Table S2

I GATTREPEEI SPAI RSRCAEI FFEPLTPRAI QKI LRQAAAKLEVEMDEA
APEVI SEYTI EGRKAI NI LADAYGLACYRGETQSGCLRI TVEDVQEVVQV
SRLSPYVI RKASPHREVGKI FGLGI MGFWGSVLEI EAVAFPARHQGQGS
RFNDTAGSMAKDSVFNAASVI RKLTD EDFNYDLHVN VVGGR I DGPSAG
VAVFLAI LSAI QDRPVPODLAVTGEVSI QGKVRVAGGVFEKI YGARQAGI
KTVL VPAENEKDVPHDLGGI RI I PVNTVEEVVRYVFP SAGVDSLVC

>2617920281 Ga0073689_10680 replicative DNA helicase [pelotomaculum Ga0073689 : Ga0073689_106]

LLERVPPQNI DAEQSVLGAI LLDREAI YKVMKMLQPEDFYREGHKT I YDA
MLFLNESGSPVDLI TVSEHLRORGELDRAGGVAYI ASLAEMVPI AANVEY
YARI VEEKSLLRTL I QVSTRI AGRGYEEGEEPEKLI AEAERMI I ELGSRR
VATTFYSI KEI LLDTFI HLEFLYNNRGGVTGVSTSF TDM DRI CSG LQPSD
FI I LAGRPSMGKTALGLI GYSAALKHNVPVAI FSLEMSREQLVQRI LCA
EAKVDQHRLRTGTLD EEDW RSLHETKDR LAKAPI YI DDTAAI TVRQLRAK
ARQLQAEKGLGLI VVDYLQLMOGSRRSENROQEI SEI SRSLKGLAKELNI
PVLALAQLSRSVEQRPNKRPVMSDLRESGSLEQDADLV MFI YRDEYYNPE
SEKKGI AEI I I SKHRNGPVGTVELGFLKEFTKFVPLVKNPGEYQPS

>2617920280 Ga0073689_10679 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_106]

MNKQYDVI I VGAGPAGI FAALELVKLKKGLKVL I EKGRDI EQRVCAARE
KNTHCNCPCSTI CGWGGAGAFSDGKLTLS TEI GGSLEQYVGEQNLSEL
I DYI DRTYVKFGAPEKVFGLEREEI LDMQRRAVLAELKLPVRI RHMT
GRCMEI LORMQEYLLSRGVEVRASCQVNEVLVEEGTVRGVVC RDGQALDA
KYVI LAPGREGADWLSREARRMGLETAI NPVDI GVRVELPAAVMEHLTRI
FYEAKFI YYSKSFSDKVRTFCMNPYGEVVQENNDGLVT VNGHSHAFKRTG
NTNFAVLVSKTFTFEPFKEPI AYGRYI ASLANLLGGGVI VQSLGDL LAGHR
STRERLAKCMTI PTLAEATPGDLSLVFPYRHLMAI VEMLKALDQLAPGI Y
SRYTLLYGVEVKFYSSRLALSGSLETEVN NLF AAGDGAGVTRGLAQASVA
GVVAAREI ANRI

>2617920279 Ga0073689_10678 Adenylsuccinate synthetase [pelotomaculum Ga0073689 : Ga0073689_106]

MSTVVL I GAQWGEKGKVTDFLAQKANLVVRYQGGNNAGHTVVVDDREF
KLHLI PSGI LYPDKI CI I GSGVVI DPAVLI KELASLEERGVSTDNLKI SQ
RAHVI FPHYQKLDQAEEDRKGDEKI GTTCRGI GPAYMDKSARVGI RMI DL
VDRKEFAALLERNMEEKNHLLARVYGLDSL DYGSVLKSYTKYAGALEKYV
TDI SI I VNDAI RQEKNVLFEGAQGTLLDL DHGTYPFVTSSHPTAGAACLG
AGI GPTKI DRVVGAKAYTTTRVGEGPFPT ELVDELGAHI QKRGGEFGTTT
GRPRRCGWFDGI VGRYAVRI NGLDYLAI TKLDVLSGLEKVI CTGYSYRG
DVMEEFPASLKVLR ECVPYDELPGWREDI TGAGKLADLPYNARKYLERI
SEVSGRPI ALVGVGSKRSQTI LTAELYG

>2617920275 Ga0073689_10674 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_106]

MVI FKFFESVRFYFI YLVSGFSNGGSWKL NRI TELNSRETRRI LVRNMST
YEELFAHRDR

>2617920274 Ga0073689_10673 uncharacterized protein [pelotomaculum Ga0073689 : Ga0073689_106]

LLHKFLFDEMKI VLDVHSGAVHVVDL VWDI LEDYGRVTA EELARKWLER
YSPEEVAEGLSEI KELEREGMLFSPDPWREGYSPPEGSVI KSLCLHLAHS
CNLRCRYCFAGQGRFGGADELMTVETGRAALDFLLARSGVRKRLEVDFFG
GEP LLNFGVLKELVKYGRRAAARAGKECQFTLT TNATLLDEKVTGYLNEN
GI SVVLSLDGRPEVHDAMRPTPAGAGSYDVI LPKI KAFTESRRGLE YDMN
GVYVI RGTYTRNNPDFSNDVLHLADLGFDHI SVEPVVGPT EADYSLRAE
DLPLI LAQYERLARELPRRGQAGKPVDFHFNI DLDGGPCLPKRLSGCGA
GHEYLAVAPNGALYPCHQFVGRNGYLMGDVFAGI RRPDLVEAFRMAHLYN
KEGCAGCWAKFHCSGGCHANA EATNGSI LKPD PQCGI VRKRLECAI YLK
AVATGSTVK

>2617920273 Ga0073689_10672 Murein DD-endopeptidase MepM and murein hydrolase activator NlpD, contain LysM domain [pelotomaculum Ga0073689 : Ga0073689_106]

LPPEVEGLRRLPGQERSFLVAGFROWLTRQPVSR LVGMGA AI YLI LALMA
YAAF GGNACAVTVNGKVI AVAPDERSARGALDELVKL KSGQAGI PVTVVE
KVSYGGI RVAENEI LNQEDLKEKLVKALTFKARGTAI LVNGEAKVFLKEK
RDAEKLLAWLKT VYPVEEGEQLAFKEKVAVAEAPADPESI LDLEAAKKMV
LMGSNKI EQYTVKDGDNLDWI ARALKMDI DRI TLANPGLDPECLSI GQSL

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SLSREAPLI NVVATRQVTVDEEI PYPVEVKKDNKLLAGEKVVNNKGVPGL
RTVTYRI TRENGLETGREI LQONI VREPETEVTGTGALTMLASRGGSVRL
GRPCYGAI VSPFGSRGGRMHEGVDI GAGYGNNVVAAAGGTVI NAGWEGGY
GKAVEI SHGGGLVTRYAHLSSI NVSNGQVRVERGQLI GHVGATGHATGPHL
HYEVLVNGRPRNPAEYL

>2617920272 Ga0073689_10671 Tetratricopeptide repeat-containing protein
[pelotomaculum Ga0073689 : Ga0073689_106]
LFTKRSVKRNKFRKAVFI TI TVLI AI GLVI PLAGLFQNPQDNGGAQTAGL
TGQTPLERI NGLARVRENPADTAALLELA EAYRYAGKPDRALKTYEQVL
KLEPDNATARLEMAYI YFYSDKNDQAI AQLQELI KKEPDHKEAHLGYV
LGAGKKDYQAGVQELEKFVALAGEGQVEQVKQTI NEWKAAAK

>2617920271 Ga0073689_10670 Peptidase MA superfamily protein [pelotomaculum
Ga0073689 : Ga0073689_106]
MQPAVGKSANNSPDSI KNLFLIKI IRI SAAVFVLI SALAWKLPLGLKHYG
YSAVRELVKAHTVI GAWHMDKMTSEHFYI KFLSANRAQAELAETAERFY
RPVTQDFGFSRPFKI PI I LYSSREELNKSFGWEAKESAMGVYAGAI RVL
SPAAWVEVTEPERVKDVI KI DGVPYLEGGGRYPI I PDRI EAGTFMVAAAATGG
QYEEYKLTGFETAPAGSPQGRMYSMKELAENFDGLPDQSLAYRESLAAV
RYI VHNYGEDALHRLI EELGRGPDFNRALKTVTGLEEGQFEKQWMEWAAK
QCRT

>2617920270 Ga0073689_10669 UDP-N-acetylglucosamine 1-carboxyvinyl transferase
[pelotomaculum Ga0073689 : Ga0073689_106]
MDKI VI AGGKPLRGRI KI SGAKNASLALLCAAI LSRSEI VLENVPDI SDV
RVMI EI I NSLGAATSWEDRETLRI APPEKPAGEAPYHLVKKLRASNLLLG
PMLARFGSAGVALPGGCNI GVRPMDLHFKGLAGLGAELSLERGCVTGSAP
DWLKGARI YLDFPSVGATENI MMAACLAEGQTI I ENVAKEPEI VDLANFL
NSI GAKVRGAGTDVI KI DGVPYLEGGGRYPI I PDRI EAGTFMVAAAATGG
DVTLESVI PI HMEPLSAKLREADVDVHEEGDTLRVRACRPLRPI DI KTMP
YPGFPTDMQSQMAMLSTVPGTSVVVENI FENRFMVADELKRMGARI KVE
GRMAVI EGVPALHGTQVKATDLRAGAALI VAGLMATGETEI CNAAFI DRG
YHNLEDKLRLSLGATVWRK

>2617920268 Ga0073689_10667 23S rRNA (pseudouridine1915-N3)-methyl transferase
[pelotomaculum Ga0073689 : Ga0073689_106]
MYHI TI LAVGRLKERYLVEGTAEYLRKSAYARVDMAEVGDGFAENLPP
AGREKVKEKEGERLLSRLRPGTFLI ALDVKGKTRSSGEMAEVLNKLALLEG
KSDLTFVI GSGLGLTQKVTERRADLMLSFSKMTFPHQLMRLI LLEQMYRWF
KI SRGEPYHH

>2617920267 Ga0073689_10666 Helix-turn-helix domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_106]
MPQVRVANI NAHVLVWARQTAGYVLEEAARKI GI SPEKLQAWAGEDKPT
LRQLRI AANVYKRPTALFYCSTPPPEPDI ADFRVMPAAGLKYPRLLYE
I RI VLRSGGVCDLQETESESI ETYCNRVAGEVLVPRDALLCEETVVENG
NTWEDWRLKLLADRYMVSQEVI LRRLLAVLSAYHNEAI SSRDLSNSLGG
I KLEHVGR I EHAFGGEGSVEV

>2617920266 Ga0073689_10665 Type III restriction enzyme, res subunit
[pelotomaculum Ga0073689 : Ga0073689_106]
VPDFTERESFREALLKGRLAAALRKLNLRDGRPWLDEARI ARAVHKALTR
LOEGRTYAQGADRDERGGI I WHTQSGKSLSMVFLVRKMRTI PKLSRFKV
VVVTDRTDLEGQLRETARLSGETLRPNHDHKKLRESPTALTQLYRLPEMV
PEYASI I LSF AEEMLRGVLWAAGRI AQARPGLVRGALPEMTAFMDDPD
PVVRGYTLRLGI LGERMDFERHDLRLNDRSSVPI YENGRLEEVCVADLA
SRLTYLT

>2617920265 Ga0073689_10664 dissimilatory sulfite reductase alpha subunit (EC
1.8.99.1) [pelotomaculum Ga0073689 : Ga0073689_106]
VAFEPKREMKEI NYQENRI YDAELNNYTEELKNFKI KHEI PDVDELEN
GPWPSFVADAKRLALHRKKLADDRMLVGRETVEDLLGVLLQSFDDGETHW
KHGGI VGVMGYGGGVI GRYTDVAEKYPAVAHFHTI RVNQPASKFYNTNFI
RTVCDMWNYRSGGMMNLHGSTGDLVLLGTI TEQLEPI FFELTHVMDQDI G
SGSGLRTPSCCI GKARCEFACVDTQELSYELTNYQDELHRPAFPYKFK
FKFDGCPNGCVASI ARSDLAFI GTWRDDI RI DQDAVKAYKDGI KPNAGA
HAKDWGKFEI QKEVI NLCTGCMWMEDDKLM I DNANCNRCMHCI NTMPRA
LRPGVDTGI SLLCGAKAPI LEGAQLATLLVPFMKAEPYPYDNI KEVI EKVW

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EFWMEHGKNRERVGELMQRVGLPKFLEAVELPPAPQMVKKPRENPYI FWK
EEDVAGGWQORDI NEYRKRHKR

>2617920264 Ga0073689_10663 dissimilatory sulfite reductase beta subunit
[pelotomaculum Ga0073689 : Ga0073689_106]

MAEKLSLERLGRYNPDEPQKDRLTDLGPRHYWEYFPPVI KENYGKWAYHE
ILEPGVLVHVSETGAKI FTI RCGAARFMTVEHVREI CDI ADKHCGGYVRF
TTRNNI EFMVDSLEKVEELKQDLLSRKHVSGSYKFPI GGTGAGVTNI VHT
QGYI HCHTPATDASSMVKAVADDLFDYFTGMELPAKVRVSMACCLNMCGA
VHCSDI AMLGYHRKPPI VDHEYI SKLCEI PLAI AACPVGAI SPDKTPDGK
KTVKVKQDRCMFCGNCYTMCOALPLSDKEGDGVTI LAGGKI SNRI SEPKE
SKVVVPWLPNNFPRFPEVDSVKKI I EAYAAGANKYERLGDWAERI GWEK
FFEKTDLPTFTEHLI DDYRLAYDTWRTSTQFKFTDAAWAVSKAAGGI DE

>2617920263 Ga0073689_10662 Dissimilatory sulfite reductase D (DsrD)
[pelotomaculum Ga0073689 : Ga0073689_106]

MI EELKKTIVFAESSKSKFYFKDMEKAATAKVPAGKMRDVKKAATELV
NEGTLI YFSTGSSTMYGLKGRGI TEDPTEGDVEE

>2617920262 Ga0073689_10661 Tetratricoceptide repeat-containing protein
[pelotomaculum Ga0073689 : Ga0073689_106]

MKTPOSFGFEFI KQOVMDLNNENPECANASYNLGSMLMQQKYEAI RFFEE
AI ANSARAFEACVNLGYI YFKLGDLKVMANRRAVEMEPYARGYANMG
FAYLQLARTDEAI EALQRAI ELNPEI AQAWSNLI NAHLQNDLDDKAI ETG
EKLVSFAPTFALGYNNLGAYYLLKEDYEKAI RHVDKARELGFGAHPEFLA
ILEPYRTK

>2617920261 Ga0073689_10660 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_106]

MNRFRDI FOI YETLAAGADRTFVKI QKEYGSRVKCDVHSCDCCHSVFGLF
LIESLYLSHHFSKLDGKI RREALTRGDKADRDLLEI GKRLRAYDNDPRMK
ARAMARERI RCPLLVDAGKCLLYDHRPI TCRVYGI PAI INGEARVCWKAG
FEGGQYPAPNLDGAYQQLHRLSGELLERTGEMDGERAALLLSVSHSI KM
SEEELIKGR

>2617920260 Ga0073689_10659 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_106]

MQNYI EAGYAKRGLI RKSACPFCLSI EKPRELOTRRYGEMPVGSCSCGA
VYAYDATGHNLGAAFI EALVFGCDMNWDLAWELLPGEDYLEQVVENYDLE
SNLVVPGGSFEGGRI SGALYFVRLHRDI QKVTEGVRKKLDRATPI SAGT
PTERVPGRAFTKAEI EEMVKTYNYTPLLNMDRPGKRTLRYLQRLLCAGDE
LTRLRTAEI LGKVASI ARDEPGAVSNLLQELFNALTDTAASSWGAVDAA
GEI I RNSPGLFAGYI PKFYQLLEDDRFPRPGVLRAI GLTAETRPDLMRNAT
FRLLPYLRDPAPAARGYAAWI YGNLGVAEAERELERLKNDSHERVFLYSSG
SLKETTGVGHAAEALEKLRHPKN

>2617920259 Ga0073689_10658 putative regulatory protein, FmdB family
[pelotomaculum Ga0073689 : Ga0073689_106]

MPIYEFRCLECGSLFEKFFNNPEEKVEI TCPKCRSASFERRI SRASHI MG
SGKTGRKPAVTTKSCSSGSDCVTLEI PGPGE

>2617920258 Ga0073689_10657 4Fe-4S di cluster domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_106]

MYKVAVDRDTCGCGECAENCPVTMFEMVDGKAQVTGDMEECLGCETCVS
VCPSGAVNLEEA

>2617920257 Ga0073689_10656 4Fe-4S di cluster domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_106]

MYTVQFDEEKQCGCGECCDNCPAGI LSLVDGKAQVTGDMEECLGCETCVS
SCEHDAVTVTES

>2617920256 Ga0073689_10655 Nitrate reductase gamma subunit [pelotomaculum
Ga0073689 : Ga0073689_106]

VSFFI LQI LPYI TVVI FTI GVLYRLGRWAGARI VHNI TLSTPNFPKTPSE
AAVVAGTEI VLFKSLFQLNRGLWVGAWPMHI ALLSVLGGHFVGFYFLGKQ
FAYI PGI SESLSEQMSNFLGTTFGI LLFI ALLYLLFRRLTVDYMKRVNVT
SDYLHLFLLLAIVGVGNFMRLVPDTGI HYEPVKEYFTYLLTLQPI PVGAE
I LHKPLVAVHVLLVQI LLVVFPPFSKLMHLFGMFLRYI ENRPYQEPEPGV
PGVDLSKGI PDHSSRLQGAAGEV

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>2617920255 Ga0073689_10654 Fe-S oxidoreductase [pelotomaculum Ga0073689 : Ga0073689_106]

MPEYKGFQPLKANEKEI KAI HI VPVPDDKKVEVALQHLDEMRRKFRSFV
LAMESCVKCGACAENCHTYLGTDRPNNI PTNRAELI RKI YRRYFTMEGRW
FGKLVGAEDLTLDVI EQWYAYFYQCNECRRCAI ACPFGI DTCEVTMI GRQ
I LHWLGMVPKLHATTGAAMEKTGNHMLPKPGI VDTLEFMSEEI MDEFGV
EVEFPVDKPDSDVMI PSSADFSNLNPTLMGAGMFFNYI GANWTI PSTVT
EAGNFGYLFDRATQRGNVTRLLDAAEKLGVKKI VWGECGHGWRAAKMYI
PTLADRPVRWPI THVHDEVANYI RRGELKLDPTKNNHPTTLHDPCNYGRA
CGLAENLRTVI QAI TTDFREMTNPNRHYNFCCGGGSAI LFDDPEMYQLRI K
FSQKKADQVRATGVDANGDGI LCAPCSI CKAQLYPMVEEHQLGVEVKGLI
DLVGKALVWK

>2617920254 Ga0073689_10653 tRNA 2-thiouridine synthesizing protein E [pelotomaculum Ga0073689 : Ga0073689_106]

MPNI NIDGREI ELDEGFI VNPDDWTDGVAI AFASAEGI NALTDHVKVI
NYLRDYYKQFOI APMI RKLCKETGCSLKYI YELFPTGPAKGACKLAGLPK
PTGCV

>2617920253 Ga0073689_10652 cobyrinic acid a,c-diamide synthase [pelotomaculum Ga0073689 : Ga0073689_106]

LSELVKI PRLVI AAPQGRSGKTTI SVGLMAAFTARGLVVRPFKKGPDI D
PGWLTMTGTGROCRNLDSFMMGREALRRSFARHARDAGI SI VEGAMGI FDG
VDLEGGSGTGELAKTI QAPVI LVVDTTTRI TRSVAAMVMGFQHFDRVDI A
GVI LNKVARPRHESMLRAAVEHYCGI PVLGAMPNGI EFKI PDRHLGLI PA
SENEALHRAVEAVGEAAARHLDLDGLLRVAGCAPPLPAVEEGPPDRI SPA
GGDPSPARTGNPVI GVFRDRSFTFYYPENLEALVEAGAELTSVDSLNDP
GLPDVDALYI GGGFPEVFAAEI EANLSLRREVKERVEGLPVYAECCGLM
YLGRTLTWGERAYHMCALPFDVVMSPKPGHGYVLEVAGENPFPPVGG
VI KGHEFHHSRLVNLDRGKVDAAYQVRRGHGI DGEI DGLVYKSVLAGYTH
IHVVSQPGWAERLVGLAAEYRRMKS

>2617920252 Ga0073689_10651 N-acetylmuramoyl-L-alanine amidase [pelotomaculum Ga0073689 : Ga0073689_106]

LNNKPVFVKKMLVFLAGLLALFTAGTI PQVRRAAAQNPVLYWGAGDDV
LRVQQRLTQWGYTGPADGGYGYETFRAAQNFQLENGLNADGVVGRDWE
ALGFSAPPRAPEVSRGAATDRGEI ALLARVI EGEAADEPFLGKVAVGAVI
LNRTKSASFPRSVSSI FQEDAFESI ANGQAYRPLTQESVQAAQMAMGGY
DPTGGALFFWNPVKPSPWI WSRNI VNQI GSHVFAR

>2617920251 Ga0073689_10650 germination protein YpeB [pelotomaculum Ga0073689 : Ga0073689_106]

MRKRWI I PVI I GLLALALTGAWGYVQRQANRNLENYLSNKYQRAFFDLAD
QTQTLEVLLSKSLVAADPRLDSSLLMDI RQQAFAQSNLGLPI DDALAG
RTAKFLTQVGDYADSLARQVSRGGAI DPKHWDTLNSLYRQSAELNREFQG
MQYRVAQNNFYFGELVRQVRKNLQKPPDNLARTDFQALDKQMOSYPTLI Y
DGPFSHELTERTEPQALSGQAEI SQDDAKNRALAFMDKKPGVAYRAGVVG
ADGRI PAYRVEVETDGEKTVLDVSRGGKVI WMLNSRPVGERTVDLDRAR
QKALGFLKERFGEMFTYYMLHGNSATFNFAAVQNGVTI YPDLVKVTVA
LDNGEI TGAETSGYLSHRRRDLPESKI TMERAKVMVNPRLVSGGKLAL
I PAGATDERLAYEFRGKLGEDTYLI YVNALDGREENVLKLI ETPGGTLTM

>2617920250 Ga0073689_10649 solute: Na⁺ symporter, SSS family [pelotomaculum Ga0073689 : Ga0073689_106]

MI THTHYLSI I I TI LAVSVAGIYSARYVHTAVDFSVGGRRMPALVGGSL
I GSF I GGTSTVGTAQMAHQHI SAI WFTLGGGLACVVLGLFLARPLRERE
VDTVPOFLAGTYGDAVRPWVALYTSTGMFI QI AAQGLAAAPLLTGLLPVS
POWAVVI FTGVL I TYVLFGGFWGASLVGLFKLALI CVTLFTAGVLSYKLF
GGFAGARDVLPPTWFSMFPGGFTKEI ASGI SVVAGFI STQTYLQPVFAG
RDVRSARQGI LAGFLI ALVGLAAAVI GLYMRATHPEI KPGSALPLFLLD
YLNPLWGGAALATLLVSLVMTGAALCLGVGTI LARDI YGRYRPGAADGEM
LRI SRLLVLLVAAASLI F I LFNMDSMI LKWAYLSMALRGVTVFLPLLGA
FAARFLTPATGVRVALAPLLAVLWFLI FPGGGDPLYVGLCLSALFLTAG
ALRPGAASPRDF

>2617920249 Ga0073689_10648 Sporulation protein YtrH [pelotomaculum Ga0073689 : Ga0073689_106]

VAFEKKFVI I FFTAMGVMLGSSFI GSLAAVMVREPPFGTMLRLAGEI RIW

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AVVAAI GGTFFSTI EI LESGLLK GEMTAVI KQI FYI FSAMAGTHLGHMI I L
AVAGGER

>2617920248 Ga0073689_10647 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_106]

VKGEVFRLLSI LFLGAI LSGVFVTLRLGGEI DAATQENELLRRQLEESRD
EVNQLKRSI GEWEKEVVSSI EPHI TI VGENI SKLEEKNTLLALDKQVROW
LEPLKGQEVVRKLNHLLI PQI I DGRTAEVEGVSYQLKVNLVVVDNTLTVYL
VAKKGKMVRPVI RLQTN

>2617920247 Ga0073689_10645 DNA-binding transcriptional regulator, Lrp family
[pelotomaculum Ga0073689 : Ga0073689_106]

LKEI LELI ENDARLTPROI AAMLDMEEEEVARI I KEMEDKKI VLGYFTLI
NWDKVGEEKVSAMI EVKI SPQREVGFDVVAERI YRFPEVRSVRLMSGTYD
LAVLI EGQTMKGVAIFVAQKLATI EHVLTATHFVLKTYKHHGAI VEDGE
EDRRLVI TP

>2617920246 Ga0073689_10644 aminotransferase [pelotomaculum Ga0073689 :
Ga0073689_106]

VTTVTNWQERI NPI VRDI PPSGI RRFFDLVTEMKGV SLGVGEPDFVTPW
HI REACVYSLEKGYTMYTSNHGELLEREEI ARDLADTYGVVYDPRGEI LV
TVGVSEGLDLAMRALLCPGDEVLI PEPYVSYAPAVTLAGARPVYLKTSV
ENGFOVTAEMVERAI TPKTKALLCYPNNPTGATI DRERLLEI AEVARAR
DLLVI SDEI YDRLTYVGEHTCVPSLAGMRDRTVLLNGFSKAYAMTGWRVG
YAAGNSDFI SAMTKI HQYTMLCAPVTGQMAALEALRNGKPGMRKMVEHYN
RRRRLVLQAFREI GLPCFEPGAFYAFPEI RGAGLSSEFAEHLLKEEKV
AVVPGNAFGERGEGYVRCSYAASVEDLTEAFKRVSNI KRRAGRGI LTA
SFGKPEPKKEGI RRTL

>2617920245 Ga0073689_10643 prevent-host-death family protein [pelotomaculum
Ga0073689 : Ga0073689_106]

MSMI VTSTELQNNFGKYLMLAAREDI I I TRNGTAI ARLSAVKEAAYDHGA
ASGAVMERVEEYSYYGGRKASYEEFLELTKNSEERYEYI DGEI YLLASPK
TAHQI ALTELFGI FYNWFQGGKCVPLVAPYDI TLKRNPENI NVVQPDLMV
I CDI EEKLDENDYYKGVDPDLVVEI LSEGRSKDLI KKLDLYMSCGVREYW
LVNPLNREVTVYLFADREI SNNTTYRKPEI VQSYI FEGLSAELDRI FK

>2617920244 Ga0073689_10642 arginyl -tRNA synthetase [pelotomaculum Ga0073689 :
Ga0073689_106]

MSGI VEEVRAELAGALEGAARRSGAI KVDEI PDFAVEVPREKEHGDF
ATNLAMLLAKPARMAPRKVAELLAQNLAQVAFRVERVEI AGPGFI NFYLC
PDWVYLALPRI I DRGRDYGRI DLGGGKRVQVEFVSANPTGLLHMGNARGA
ALGDSI AAI LDFAGYDVTREFYI NDSGNQI ENFGRSLEARYMQLLGRDAP
VPEEGYHGEDI I DTVRGFMARHGDKYLERDPGERRRVLVEYALAEKLGAI
KKVLEDFGVRYDWFSEQSLHDSGAVRDTI DYKCEGYI YENEDALWFKA
TEFGVEKDEVVRSNGVPTYFASDI AYHRNKFQRGFHRVI DI WGADHHGH
VPRMKGAVAAALGYDPAALDVVI MQLVRLYKGGELVRMSKRSGQFVTLLEL
VEEVGRDAARYFFVMRSPDSDLDFDLAKAESNENPVYI QYAHARI CS
I FRQLGEEQGETPDPEQVDYSLGEEHELALARKLADFPGEVASAAKGLA
PQRI ARYLHELAGLLHSFYNSHRVI I PDRALSKARLALVEASRI TLRNAL
GLLGLTAPEKM

>2617920243 Ga0073689_10641 XapX domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_106]

MKEVLLTTATGFI MGMI FAWLKLPI PAPPSLAGVMGI VGI FLGYI VAVRL
GLSR

>2617920242 Ga0073689_10640 CTP synthase [pelotomaculum Ga0073689 :
Ga0073689_106]

MAKFVFTGGVVSSLGKGI TAASLGRLLKSRGLKVAI QKLDPIYI NVDPGT
MSPYQHGEVFTEDGAETDLDLGHYERFI DI NI SRSCNVTTGGI YWSVI N
KERRGDYLGTVQVI PHVTNEI KEKVRRAVESNADVVI TEI GGTVDI E
SQPFLEAI RQLKGDLAGRNVVYI HVTLPYLRAAKELKTKPTQHSVKELR
GI GI QPDVI VCRTERPLSKEMEELALFCDI DREAVI QALDAPSI YDVPL
MLEEEGLADI VMEKLG I ETGPPDLTEWREMTAKMKELRYLTTI GLVGKYV
SLHDAYLSVAEALRHAGFRHGS AI EI KWI DSEEVNRSNVKELLKDVDGVL
VPGGFGDRGI EGKI EAVRFARERQI PFLGLCLGMQLAVVEFSRNVLGWRD
ADSTEFNPATSHPI DLLPEQKELDQMGGMRLGSSYPCRLQPGTLVHRAY
QQEI I EERHRHRYELNNFYRAALAGSGMVFSGTRPDGYLVEI I ELPGHPW

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FVATQFHPEFKSRPNRPHPLFRDFVEASRKYKTAKIH

>2617920241 Ga0073689_10639 protease-4 [pelotomaculum Ga0073689 : Ga0073689_106]
 MKRKVI AGVVLGVVALSLI LAVALKPDDGTTAVTSGAKGDVGVYI DGPI
 MSGRGTGGLFETGTGSEDI AASLRKAARNPRLKAVVI RLNSPGGTAAAAQ
 EISAEVERLRQSDKKVVASMGDTAASGAYWI AAGADRI VANPGTMTGSI G
 V I I QYLSMODLYDKI GVGTEFTKSGPHKDMGSPSRPVTPEERVI FQSMI D
 DI YSQFVDVVARGRHKDAAEI KKLADGRI FTGRQAKEMGLVDQLGDLHDA
 VLLAGELAGI PGEPAVVELGPKNVWQEI FGGSGGNAFLDRGWPALPGMDG
 VCYNLR

>2617920240 Ga0073689_10638 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_106]
 MSRLFLAATNELGSLKSWKELFFLNGDSRWKGENAQENSGAGGPYTFEE
 RPPDKFSDEAAPLPTGTAPGDGPADGPAAEKDYQGFLFELVYGI LFEPAKT
 MTRVTRRPPLAAALLVVTI LSVLGSLMGLLTASRVLDQSLQEMAMGQFFP
 VMRALAPLGVVLGLFWGYVWFGYSAVLHLAADLLGGGRGSARGVFAAAGL
 AGLPGI FMI PAQFMAYWFGGKLAVALVGLI GLAVGI WSI VI LVI GVKQ
 VYGLSTGRI VLI VFSPYLALAAAMGIIII LALVAAASSMPVRQHLPGYF

>2617920239 Ga0073689_10637 two-component system, response regulator, stage 0 sporulation protein F [pelotomaculum Ga0073689 : Ga0073689_106]
 MTVDVDLSI LI VDDQAGI RHLLLEALSNEGYRLEI AASGPEALKKI SDRGP
 SI VLLDI KMPGMNGLDTLEELRKI APETTVVI MTAYGELDI I TEAKKMGV
 OHYI VKPFDLNEVRYLI KGLFAEMADI KEPLKEIG

>2617920238 Ga0073689_10636 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_106]
 LPDHGFHSAALGRFSAVLI ATNAALAMRCPECGKMGI HDFSRFAFAKGRAV
 HVNCSGGAALKLVVNTKNRSSYWFQVSCVVCEAKHLLI PGKSLWSGEVTR
 LVCQDTEFELGYI GPEPVVREI AFDYEELEALVKEFGCDGYFHNPEI MY
 DVLNCLHDI AEQDLYCQCGNHKI EVDI FPDRVELQCKSCDSI NI I YAET
 EEDLKVI QQVDTI ELARHGFKFLDSLSSI GKI KKSRRKRKNT

>2617920237 Ga0073689_10635 fructose-bisphosphate aldolase, class II [pelotomaculum Ga0073689 : Ga0073689_106]
 LALVPVSDLLKKAEEGGYAVGAFNCNNMEI VQAI I TAAEAENAPVI MQAS
 QGAI KYAGI NYI VAMARLAAERSRVPVALHLDHGTSFEQVMQCI RAGFSS
 VMI DGSKLPLAENI ALTRRVLDVARAVGVSVEAELGKI GGTEDDI YVSR
 EAFFTDPTTEAGVFVRETGVDAALAVAGTAHGQYKGTPELDFPRLEKI KSI
 VKI PI VLHGSSGVPDDAI REAVRLGVRKVNI DTNI REAFDAARKVLAEN
 PGEI DPRKI LGPAREAAAARI REKI RVFGSSDKA

>2617920236 Ga0073689_10634 transaldolase [pelotomaculum Ga0073689 : Ga0073689_106]
 MKLFI DTANVDEI REAYSLGVI SGVTTNPSLI AREGRNFAEVI REI ASI V
 DGPI SAEAVSAEALGMVAEALAAI HPNI VVKI PMTAEGLKAVKI LSQK
 GVRTNVTLVFSANQALLAARAGGAYVSPFVGRLLDVGQDGMELVCEI MEI
 LNNYQLQTEVI AASI RHPAHVTAAARAGAH IATI PYKVI MQMVGHPLTST
 GI KKFLEDWENVKEK

>2617920235 Ga0073689_10633 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_106]
 VFAEGLVFLKKKI VSLLVENFRAYYI KI I EVSDSPKRI ARGAAALGLAFDF
 LPI PVI SI PLSYVVARLTRCNPVAAVGTVVFFKLAVPFFYTLNVI AGNVL
 LGDLPRPEI TLSGASLPDFFLAKLVEHGYPFLVGSLVNAALAWLAVYTLL
 I HLLERRHNHRGV

>2617920234 Rho transcription termination factor Rho [pelotomaculum Ga0073689 : Ga0073689_106]
 LNYADLENKTMVELYKI ARELELPGYYKLRRKKELI FEI LKTQTEKHGLLY
 AKGVLEI LPDGYGFLRPFQYLPSHDDI YVSSSQI RRFDLRTGDLVAGQVR
 RPKETERYFALLRVEQVNGVDPEQAGERLHFDGLTPLYPMERI TLETPD
 KLSPRI I DLVSP I GKGQRL I VAPPKAGKTI LI KEI ANSVTTNHPMYLV
 VLLI DERPEEVTDI ERSVNGEVI SSTFDEPPENHVKVADMVLERAKRLVE
 HKNDVI I LMDSI TRLARAHNLVPPSGRTLGGVDPAALHKPKRFFGAAR
 NLEEGSLTI LATALI ETGSRMDDVI FEEFKGTGNMELI LDRRLAERRI F
 PAI DVLRSRGTKEELLSKDELEMI WQFRKATSGATPWDAMEMLVEQMKR
 TKTNRDLLQAFRSLRRAEATAAGRLESGRRGAPRAVKKWLT

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>2617920233 Ga0073689_10631 Murein DD-endopeptidase MepM and murein hydrolase activator NlpD, contain LysM domain [pelotomaculum Ga0073689 : Ga0073689_106]
 LFFMMAKMFKTKI KNI NAI ARSAAALATVAAVLWTAGPAAARLDELI RED
 APYFSPAAAVAGPQSLYTVRPGDTLWEI ARRNGI TI ELLAAANGLADRD
 NI RAGQVLTAPSDYVAHRVQPGETLWDI ARMYQVDARVI AARNGLSDI NK
 I I VDQSLYVPLGYPGAGLTARAAAVWPLNWPLVGA I TSPFGLRDGRPHEG
 I DI AAEEGTPI RAAAPGVVVFAGPRGAYGLAVI VDHGGGVRTLYAHCSRL
 LVAEGASVGPENI I ALAGSTGRSTGPHLHMEVLKNGI PLDPVTCLGSYYG

>2617920232 Ga0073689_10630 Pyruvate-formate lyase-activating enzyme
 [pelotomaculum Ga0073689 : Ga0073689_106]
 LYRLVFAGDDGRFLDHRNLLATGRTGDRFVEVAGEYMEKLPAGASLVLP
 GGVPGVI TRAGRFTALDNNPWTEGRAVAVGALLPQGYTRTLLPAYRRGKK
 EKPLPLLGYAAVACRGGEIYVAARRTDDPDRWDPAHYNTAGLPELVEKKL
 ARRPENRI LRQLARCSLEYSCFTAONI FYGRWEGGI PVSPACNARCLGCI
 SLQPAECCLSPQARI KFRPSPREVAEVAI PHLEGGEETMVSFGQGCEGEP
 ALAEGTI I EAI ERI RTVTGLGTI NMNSNGGHSAGVAEI CRAGLDTLRI SL
 I SAREDTYNAYCRPAGYGLADVRRSI KAAAARGVYVSLNLLVFPGLTDRA
 EEVETLLGLVRDTGVNLVQLRNLNI DPDFLFQHMPEGGGEI LGI PALI EA
 LREVPDLAVGSFSRPVR

>2617920231 Ga0073689_10629 Large subunit ribosomal protein L31 [pelotomaculum Ga0073689 : Ga0073689_106]
 VKEKI HPKYGKAKVTCVCGETFETGSTKKELRVEI CSRCHPFYTGSRQTI
 ETGGRAERFRKKYGLTK

>2617920230 Ga0073689_10628 Uncharacterized conserved protein YqhQ
 [pelotomaculum Ga0073689 : Ga0073689_106]
 MSAPFOYGGQAVI EGVMMRGPDSDRAVAVRRPDQTI VI DRKPVGSLTRRAP
 VLKWPLARGVVVLI EALVLGI EALTYSANQAAGEAEEEEKLTREI I MTIS
 FALGLAVLLFGVLPVAAAHLLOKI APGSLVQSLI EGI FRI VI FLAYVVAI
 GRLADI RRVFQYHGAEHKVI NAFEAGEELSVERAQRYSTLHPRCGTSFLL
 I VMVI SI LLFSLLGEOALWWRI LSRVLLLPAVAGI SYELVKLSGKYASAP
 LCRI LI APGLWLQKLTAPPDDGQVEVAI SAFGAVLKEGEQNAQ

>2617920229 Ga0073689_10627 bacterial peptide chain release factor 1 (bRF-1)
 [pelotomaculum Ga0073689 : Ga0073689_106]
 MLDKLAGLEEKYEQLGHMI GPDGVI SDLPRWQQYVKAHAELADVVTYRE
 FKKVVKEI REAGALMEEADAELREMAQAELDDLEEOKTALEQRLKVLLL
 PKDPSDEKNVI FEI RAGTGGEAAALFAADLFRMYSRYAERQGWKTEI MDT
 NYTDI GGFKEVI FMI EGRGAYSRLKFESGVHRVQRI PTTESGGRI HTSAA
 TVAVLPEAEEDVAI DPNDLRI DVFCASGHGGQSVNTTQSAVRI THVPTG
 I VVSMQDEKSOHKNKDKAMKVLRARLLDRARAERQEKMASTRSMVGS
 RSEI RTYNFPQNRVTDHRVGLTLHRLDGVLEGDLDEI I DI LI TTDQAER
 LKQVD

>2617920228 Ga0073689_10626 release factor glutamine methyl transferase
 [pelotomaculum Ga0073689 : Ga0073689_106]
 MPVTI REALELAGKKLRESGANTPTLDAGVLLAHVTGLDRAGLYRERERV
 LAEEVEARFFSLVGRRAAGEPLAYLI GHKEFMGLDFTVNPHVLI PRPETE
 LLVEKALELLPPAPVVVDVGAGSGAI AVSLAALCPKAVVYATDCSQEALA
 VAGLNAARHGVANRVFLCPGDMLEPLAGRVQAGGVLDI VANLPYI PTEDL
 LALPREI RLFEPPSALDGGAGGLELYRRLI PAAALLLKKGGYLLMEI GCD
 QGRRMVALLAPPVWEAI I LQDLAGLDRLVVARV

>2617920227 Ga0073689_10625 translation factor SUA5 [pelotomaculum Ga0073689 : Ga0073689_106]
 LKKKVATRYI KVDPVNPEPEAVQEAARI LRRGGLVAFPTETVYGLGANA
 LDGRAVAGI FTAKGRPRDNPLI VHVASMEQVTSLVENI PPAAGALMEAFW
 PGPLTLVLPVGKALPEEVTAGLATVAVRMPAHPAALALI GAVGAPVAAPS
 ANI SGRPSPTTAEHVLQDLCGRI EAVLDGGPAGVGVESTVLDI TTSVPLI
 LRPGGI TPEELRKTLGAVAVDPI AANGLPGGEEPRSPGMKYAHYAPRAPL
 FLVEGRPETVTAKI KELALERRAAGKRVGI LAYGGSGDFSFGVVVKTGS
 RDRPETVAAGLYAALRRFDELDVDLI LAGGLDEGGVGLAVMNRLRKAAGG
 RI I KV

>2617920226 Ga0073689_10624 Putative Mn²⁺ efflux pump MntP [pelotomaculum Ga0073689 : Ga0073689_106]

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MSFYTLMALAVALGTDAFSLCVGI GLAGVKKRQI LLLSVTVLLFHI FMPL
AGWVAGGLAGI VLGRATAI AGALLLVYLGVRMVDAWSNGGQTEPTTI KF
NTWGLLLLGASVSI DALSVGFTLGARQVNLTLTAGI I GLVAGTMTAGGLV
FGRFLGDWVGEKAQFMGLI LVGI GVKLFVTI H

>2617920225 Ga0073689_10623 protein-tyrosine phosphatase [pelotomaculum
Ga0073689 : Ga0073689_106]

MKILFVCTGNTCRSSMAEALTREI LKGRHGNKVEVSSAGVAAWSGDRATR
EAVEALAGMGI DLGGHRASRLTPEAVREADLI LVMTKSHREHI KHLAPHA
AGKVFTLTGYAGVSGDVPDPI GQPVENYRRCALNLRDLI VKALDKLEGSF

>2617920224 Ga0073689_10622 ribose 5-phosphate isomerase B [pelotomaculum
Ga0073689 : Ga0073689_106]

MRI AVASDHGGFRLKEEI I RLLREFGMEYKDFGAFSEDPVDYPDLALAVA
EAI RGGYFHRGVLCCTGI GVAI AANKAPGI RAAQCHDTFSARAAREHND
ANVLTMGQRFI GPGLARDI VKVWLQAEFQGGRRHARRVDKI CSI EQKYNRC

>2617920223 Ga0073689_10621 glycine hydroxymethyl transferase [pelotomaculum
Ga0073689 : Ga0073689_106]

MSLVRPLSEVDPEI YRAI ELETDRQRRTLELI ASENVASRAVMEAQGSVL
TNKYAEGYPERRYGGCEFDI AESLAI SRAHELFGADYANVQPHSGAQA
NTAVYLLALLKPGDTI LGMDLAHGGHLTHGSPVNI SGKYFNFVFGVEKDS
GRI NYEKVFAAAFEHKPKMI VAGASAYPRVI DFYKMEI AGEVGAFLMVD
MAHI AGLVAAGLHI SPVPYADVTTTTHTKMRGPRGGLI LSRDRGKYGAK
I DKAVFPGI QGGPLMHVI AAKAVALKEALEPGFKEYQRRVNNARALAAA
LLERGFELVSGGTDNHLVLVLRSKNI TGKEAQVLLDSVGVTVNKNAI PY
DPOPPNI ASGI RVGAPVVTTRGLGEDDMAQI AEI MDYAI AHREDRAGLDR
ARAVVAGLCEKYPLY

>2617920222 Ga0073689_10620 dCMP deaminase [pelotomaculum Ga0073689 :
Ga0073689_106]

MPRHSTTRVSPPASLFSTPPDPYPTSQRPGWDEYFMELAYVAKRSTCLR
ROI GAI I VKDRLLASGYNGAPAGLKHCLLEVGCRLDKLGI PSGERHELCL
GLHAEQNALI QAAVYGI AIGAI FYVTHQPCI MCAKMMI NAGMEKVVFQ
AYDPDPALEMFAGVDLVRYKEK

>2617920221 Ga0073689_10619 MazG nucleotide pyrophosphohydrolase
domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_106]

MQKKI VALPKLNNLSPTI ESTALKLMEEAGELAQAI GKLRGLSGEAEKCG
EREVMMI I TRELLDVAQTAVSMMFVLEEYQGVDLERARDEHI EKLI KKG
Y LKVGETQSDL

>2617920220 Ga0073689_10618 UDP-N-acetylglucosamine 2-epimerase
(non-hydrolyzing) [pelotomaculum Ga0073689 : Ga0073689_106]

LLKVMVAFGTRPEAI KMAPLVKEMEHRDEI DCRVAVTAQHREMLDQVLR
LFGI TPAHDLDI MRPGQNLFDI TVRALSGLQRVLESERPDLVLVHGDTT
TFVAALASFYLQI PVGHVEAGLRTRDKFSPFPEEMNRHLTGVADLNFAP
TATARRNLLAEGTPAGTI FVTGNTVI DALLATARPDPYRFADPLLDGI DYR
NRRVLLVTTHRRNLGEPREI YRALREVVEDHPDVEVFPVHKNPVARG
VVEEELGGDLRVRLI EPMYQPFANLI NRCHLVLSDSGGQLQEEAPSLGKP
VLVLRNTTERPEAVEAGTVRLVGTAREAAETNRLLEDRAFYDKMANAV
NPYGDGQASARI VQAI RYKFSLSEHKPEEFQ

>2617920219 Ga0073689_10617 Putative FOF1-ATPase subunit Ca²⁺/Mg²⁺ transporter
[pelotomaculum Ga0073689 : Ga0073689_106]

MPERKDRDKEKQDQGRGAVLQAFALTTTI GVELAI TVVLGYGGQYLDRO
FVTGPWLMLAGVLVGLAVGI VGVYKTLQGFRRERE

>2617920218 Ga0073689_10616 ATP synthase I chain [pelotomaculum Ga0073689 :
Ga0073689_106]

MRDWNFDGQLVRTKI SGFI LVFFCLSLVYRPEDPVAWGFLVGI VAGMWN
AFFLSRRLHAI VDMAAPRAKAQMRVGFVLRIT I LAVLFFVARTDWI NI Y
AAAAGLVVPCVFTFGAVGVLI REAREAKALGAGRGFKGENP

>2617920217 Ga0073689_10615 ATP synthase F₀ subcomplex A subunit [pelotomaculum
Ga0073689 : Ga0073689_106]

MLSLHEVEEKLNVGWPHHPWELTVGGAHLAFNPKTMI MTWI TMI LVAIF
AVAATRGMSMRPKGAQNVLEMI FEGI RNLVNQNMPPKGAALLSI VVTY
FIFI LFSNLI GLVPTLSSPTADYNTTLALALCTFILI YYFGI KYKGLGYF

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KHYI QPYVFFLPI TI I EDFSKPI TLTFRLYGN I YGGEVLI AVL LGLLGW
VHVFGGFI ASVWLAFSI FVGFI QAFI FTMLSI AYVSQAVADHH

>2617920216 Ga0073689_10614 ATP synthase F0 subcomplex C subunit [pelotomaculum
Ga0073689 : Ga0073689_106]
MDLAAAAAI GTALAVGLGAQGAAI GDGLVTGKAVEGI ARQPEAKGSI MTL
MFI SVGLI EALPI I AVVI AFI LMGKMA

>2617920215 Ga0073689_10613 ATP synthase F0 subcomplex B subunit [pelotomaculum
Ga0073689 : Ga0073689_106]
LPNSLKSDVLRPTTDDCYGYRLPFAHREMEGGEPLVLEFNATLLAQI VDFI
I LLI FLRLVAYKPLMKLLQERSDHI ANTI AA AEQERQQA EQLKAGYEAEM
RRAREQAREI VQKATKAGEEQAVEI I ENAKNEAARI KDAAMAEI QREKQK
AVAELRDQVASLSVLVAGKI I NQKLTDEI QHSMVQDFI KEAGDLPC

>2617920214 Ga0073689_10612 F-type H⁺-transporting ATPase subunit delta
[pelotomaculum Ga0073689 : Ga0073689_106]
MLRGAVAGRYAEALYDI ASKQKMVDKI EAELKAVEAVI EENADLQKI LYH
PQI TAKDKKELLDLLKKGKVS ETTGNFLALLVDRRREAFFGDI VAEFVNL
ANAARNI VAARVTS AVELNDREKGKLDQI LGRLTGKKVQTSYAVDPSLI G
GVVVRMGDKI I DGS I KTRLATLKERLKAI S

>2617920213 Ga0073689_10611 ATP synthase F1 subcomplex alpha subunit
[pelotomaculum Ga0073689 : Ga0073689_106]
MNLRP E E I S S I I R Q Q I D K Y Q A Q I E M T D V G T V I Q V G D G I A R V Y G L M D C M F M
ELLEFPGGVLGMALNLEEDNI GCVI LGPYTHI KEGDTV KRTQRI VSV PVG
ETLLGRV VNP L G Q P L D G K G P I N T D K Y N P V E K I A P G V I Y R K S V H Q P L Q T G I
KAI DSMI PI GRGQRELI LGDRQTGKTAI AVDAI I NQKGQDCLCI YVAVGQ
KQSTVANVQKLTETGAMEYTI VVAGASDPAPMLFI APFAGAAMGEAFM
AEGKHVLI VYDDL SKQATAYREMS L L L R R P P G R E A Y P G D V F N L H S R L L E R
ACKLSDDL GAGSMTALPI I ETQAGDVSAYI PTNVI SI TDGQI FLEPDLFY
AGVRPAVNVGI SVSRVGGAAQI KAMKQI AGRRLRLDAQYRELA AFAQFGS
DLDKATQARLTRGERMMELLKOGQYVPMPVEEQVI SI FAAANGYLDDMPV
EVVQPF EA EFLKFM RANKPQI GETI KKTGELKDVEKDLHAAVAEFKTQFK
TAHGLV

>2617920212 Ga0073689_10610 ATP synthase F1 subcomplex gamma subunit
[pelotomaculum Ga0073689 : Ga0073689_106]
MPSLRDLRRRI KSI KSTQOI TKAMKAVSAKMRKAQESVI SARPYAKRLK
GVLGRVAVASSGVKHPLLAVRDPKKVAFI VI TADRGLCGGFNSNVI RRAT
QEI KKF GGELNLI TVGRKSRDFFRRRGFNI AKQYVGLGEDI KYGAVRDI A
SFVI DKYSTEEYDEVYLVYSQFI NVLVQKPLL VKLLPAEPPAGEEGEEES
KKVDYI FEPSAEAVLT ELLPKYI ENAI YQGLLESKAGEHSARMTAMD NAT
KNAEMI AKLTL SMNRARQAQI TKEI SEI VGGAAALE

>2617920211 atpD ATP synthase F1 subcomplex beta subunit [pelotomaculum
Ga0073689 : Ga0073689_106]
MNVGHVVQVI GVVVDI RFPPGQVPKI YDAI KI KSDKEDMFGRKI DLTLEV
AQHLGNNTVRCVAMSATDGLVRGMEAVDTGAPI SAPVGRPTLGR LVDVLG
EPI DGKGPI VSDKRYPI HRPAPPLVEQSTKAEQLETGI KVI DLLVPFLKG
GKVG MFGGAGVGKTVI VMELI QNI AMQHGGI SVFAGVGERTREGNDLYRE
MTEAGVMDKTTMVFGQMNEPPGARLRVALTGLCLAEYFRDEEGADTLLFI
DNI FRFTQAGSEVSALLGRMP SAVGYQPTLATEMGQM QERI TSTQKGSVT
SVQAVYVPADDLTD PAPATTFAHLDGTVVLSRQI AELGI YPAVDPLDSTS
RI LDPLVVGN DHYACARGVQKVLQRYKELQDI I AI LGMEELSDEDKLVVA
RARRLQKFLSQPFHVAETFTGMKGKYVAI KDTI RSFQEI LDGKYDDL PED
AFYMVGSI EEAI EQKRLLAG

>2617920210 Ga0073689_1068 ATP synthase F1 subcomplex epsilon subunit
[pelotomaculum Ga0073689 : Ga0073689_106]
MSEKTQRLEI VTPQKKVFS EDVKFLVAPGTDGELGI LPEHAPLI TSLNI G
I LRI QQEGKNLKVVTGGFM EVRNSKVTVLANA AERADEI DLARAEAAKQ
RAEARLVARSPD VDLRAELALKRALMRLRAVQ

>2617920209 Ga0073689_1067 TATA-box binding [pelotomaculum Ga0073689 :
Ga0073689_106]
MLKKVYSNI KGVLASGEGEGI ARCLPALAAACWRALKGKLRFWREL PQKR
ELQAAALLLVAF LALALPVLAPLI RETLAAYREEK LLLRMVELPGAGLET V
I VTGWLKMPAGVPGAGDSAALVEGAAARLRLEEAGRQRESWQNRYARGVK

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LAGQTADGRVFSLLGQVLDLPGGEKATYLMISTAAAEEMNRARLSRREIGE
ALSGYGGGRVAVTCAKINGELSPPELRAGAEGMMALAGAAVREKTVKDN
LVSLTGLSPRLAGEISYAGREVNLNVALRSDPAERVTVYVYVASPVIYTEY

>2617920208 Ga0073689_1066 UDP-N-acetylglucosamine 1-carboxyvinyl transferase
[pelotomaculum Ga0073689 : Ga0073689_106]
VEKLI VRGGNQI KGAVKVSAGNAVLPII AATLLTDGVCVLQDVPALADV
TTI CNVI ERLGAGVSRGDGEI AVSPDLKVVEPPYEYVRLMRASFLVLGP
LLARAGRAVMPPLPGGCAI GTRPI DLHLKGFKALGARI VYGHGCI EAEAN
GLTGSRI YLDFPSVGATENLI MATSLARGHSVI ENAAEEPEI VDLANFLN
AMGARI KGAGTKI VRVNGVPRLLGGTVHTVI PDRI EAGTFLTAAAI TGGDV
LVDNVI CDHLKPVTAKLREAGVKVEEYENSVRVTGAGELRPVDI KTMPYP
GFPTDMQAQLMALLTVAKGTSI TETVFENRFMHANELKRMGARI RI EGR
TAVVQGVPRLAGAPVKATDLRAGAALVI AGLAAAGETEIANVYHIDRGYH
RLEEKLRGLGADIKRSC

>2617920207 Ga0073689_1065 prevent-host-death family protein [pelotomaculum
Ga0073689 : Ga0073689_106]
MSVRFSSGQMVSVTPELLRNFGVEAEKTGEEDFIIVRNNKTDVFLMNFAYE
EKLKELDEI EHI EIWNVGERIQQNDRMFPAGEVI EKLGLAAEDWKEIC
GEE

>2617920206 Ga0073689_1064 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_106]
VRSKLGVFDFNLLFYEGAVEDLLNLDLRIQKEALKQLVKIDRNPFAGQEPG
NRI GMNLTGYRKLYFHQKKYRI VWQVLADGKGLI SHI WGVGPRDKAQI YR
LVMERVKAQKNI KKFVDDFQKGDCTLLYCKSHLQLAGGLFI

>2617920205 Ga0073689_1063 stage II sporulation protein D [pelotomaculum
Ga0073689 : Ga0073689_106]
LRRLLVIGSLLLAALILSLPYFVKREIPARFFPGVTTVRVYLHGEDEV
MQLEDYLVGVAAEMPAEFPPPEALKAQAAARTYAVKRLVAGGVNPPHP
DADLCDDHRHQAALCREELKKRWGTLHYNYFYKI QAVDDTRGQVLT
QGQI EPAYHASCGRTEAGDVVWKFDPYLRVTCPYDDNPRPVQAASF
SLEQLDRALGASFAAPVPTGGKKTREIKVLEKTAAGRPKSLLLGGKQLS
AAVVRDLLGLRSTNFTWQVEGDKITFTTTGYGHGVGLCQYGAKGLAEHGY
NYRTILGHYYNGVEIVETGKK

>2617920204 Ga0073689_1062 putative DeoR family transcriptional regulator, stage
III sporulation protein D [pelotomaculum Ga0073689 : Ga0073689_106]
MQEYIQKRVLDICAYILETHATVRQAAQVFQVSKSTVHKDMTERLPSLNK
RLAQEVKNI LEYNKAERHLRGGEATRRKYKELA

>2617920203 Ga0073689_1061 rod shape-determining protein MreB [pelotomaculum
Ga0073689 : Ga0073689_106]
MFGGADIGVDLGTANLVYVKGKGI VLQEPSVVAIDRDSGRVIAVGSEAR
RMLGRTPGNI VAI RPLRDGVI ADYDVTEKMLRYFI SRADGGMKFFFRPRI
MVCIPSGVTGVEERAVRQAQVQAGAKEAHLIEEPLAAALGAGLDISQPSG
TMVVDIGGGTTDIAVLSLGGIVCSKSLRVGGDKLDENIVRYVRKKHSLAI
GERTGEELKIEVGTAYLPDSEDKTVEIRGRDMLTGLPRGVTVSRRQVHEA
IKETLDLVSSVKEVLERTSPELAADINKGIMTGGGALLDGI DRLISN
ETGLPVVYAEADPLSCVAKGTGRALSTMGVLSATGKRKGFKKIV

>2617920202 Ga0073689_105115 conserved hypothetical protein [pelotomaculum
Ga0073689 : Ga0073689_105]
MPKRFLILVAAAVLLPAAAAGAGGLDLAVSPGQVDIGLNFKGALLEIS
GSAPPDSDFLKLESPPGTMLNRKGKVGPFWMTVDNVKAENMPKI YEVE
TSGSLAELPRDAKDRMEINGYSYLKERARITRKHETGKEELGPDEAGTY
LDGLINIEYKKGYYINEGALEI ENGRFKAALQVPSGIPPGQTKITAYAV
QGGKVVASEEFPLQVNSTGLVQVVRTESTANGPFYGLIAVI VALVVG
LATGTLFNSLGRRKGTQADSGAH

>2617920201 Ga0073689_105114 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_105]
MTQVFLPI ARMPMSVIVLGMGGAVGLLSGLFGVGGGFLLTPLLMMAGVP
PAVATASDTNOIVAAASAGTLAHSRSGNVDFKLGFILLVGGILGGSYGTE
LVRI LRGMGNFDFVVKIAYVVMLLSVGMFMFIEGLHALRNNRRTVEKRES
GAARLLNRLPLQMDFPVSGIRCSVIGLFALGFLIGILAALMGVGGGFI ML
PVMI YLIGIPTIKAVGTSIFTVVFTSVNVTIAQSLNGTVDLVLAIIII

Table S2

GSSI GAQVGVRI GRMLKGEQLRVI FSVI VLGVAVKI LYDLLAAPSSLI VLGGH

>2617920200 Ga0073689_105113 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

MDKLLLDADKQKQKI KKFASAI TLVI AVLTLTLTFWI GVDFMRESVYKNYFN
PTRHVI VEQDQDSGVI LAWKDALGNVYTPEDRDVRLFPYGI MFLLLLLLMG
MAAGAYTI LVEHYAI LLLMQERTPQGYLDRMALNK

>2617920199 Ga0073689_105112 two-component system, NtrC family, response regulator AtoC [pelotomaculum Ga0073689 : Ga0073689_105]

LSNVLVVDDEESVRQMLKDI LEDDGHVLLAENGREALEQI DSRQPDVAVL
LDI RMPMDGLAVLDI VRGKGSNVPI I LMTAFGTTEMAI QAMRMGAYDYI
I KPFNI DELLLLTVKKAVNMQDLVSEVAALREELAQNLGDSLLI GRSPRMQ
ALYKDI GRVADRNVTCLI LGESGTGKELVAAA HRNSSRRRERPFVKI NCA
TI PENLLESELFHGKGAFTGADRRKPGKFELANRGAI LLDEI GEI SPST
OAKLLRALQEKEFERVGGTETI KVDVRI LAATNRDLAGLVKDGGFREDLY
FRLNVVTLOVPPLRERREDVPLLANHFI QKFCGEFNKQI TGLSQEAMELL
CRCDWPGNVRELKNACQRAVVMATGPVI LPDDI PFTVQAGTQGFETPAYS
PGMTLKEI VADVERQVI LKVLQENNNWRSVTAEALGI NRRSLYAKMKEYG
LI

>2617920198 Ga0073689_105111 two-component system, NtrC family, sensor histidine kinase AtoS [pelotomaculum Ga0073689 : Ga0073689_105]

LFIFRKGFGGQFLALI AVLLLLPVVLTVMYMLHAI KKTALALVENHKAKLT
KVMQQLDEHLPETFDEI LSRTVPPDAARRDKVQALNRELKKT I SDTGRSY
PGVELGFYSKDLVDI LDGDEHYGENFSSRRKKSFDOTI GARQTVMDSFQ
KPEGGYLESYKPLI RNGQTI GAVWARENLLMYTRVERAQRDSYLI I FIG
VVFGI GGC FYLI GNFLSNI NOVKKGVSLEYDLNTRLPPATGELGEI TGA
I NHLAARLMKVQNYNKVI LANI DDGI MAVDPAGVI VLLNPAFSKMFQI GP
EFLDKNLLEAFAPDSAPAEI I QAAL EERKL VKDCDI TWAQQGNGSKQI LM
STSLLTENDRMLGVVLNCRDI TERVRMREKMQRQERLAALGKLVAGVAH
EI RNPI TSI SGYI QFWQKKNSPSPGSI ATI YREVTRLNSI VDKLLQFVKP
SRLSPAPGDVNTLVNKVAQFFADTHQADNI RI TAE LGRDLPPAWI DPAQM
EQVLMNI MYNAWQALERGSGLI TLRTSFDPYADYLVLEVADNGCGI PAEN
I PRLFDPPFTTRPKGTGLGLAI AYEI VRAHGGNI EVDSGEETGTTVRI HL
QRAREV

>2617920197 Ga0073689_105110 CBS domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_105]

MPGTKKI KEIMI QI SEYPVYDDDTLKDAVKI LKNYLDGGKEHRSLLVFS
RTGKVGGEELI GI LTVRDI LNALKRNRTGYDNADLFTMSLASLGWAYLE
TAGKFVNVKVGVELRPLVEAFI RSDDNI TTAI ELMMNKNVNI LPVFDGKK
AVGI I RALDVLDI VEVL

>2617920196 Ga0073689_105109 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

MGWLP LFP E L N A P Q Q P V R P P G T A S R G Q F V K H S T F L K Y R P A E F S G I S R L E
Q I L W R G S C V R L K A I S I K I G V L K M P E V E E M L S H D E K D L L Q R F S L Q A V I L I I
L L Y A L F F W A G V N F L R E D I F K H N F N P S R H L I V S Q N P D T F E I L V W K D A L G N V
Y T S D D I Q V K L F P L A V C A L G L A E V V V F S G L Y Y L M K W H Y T I M L L F R R I A R S G
E R R A G A G I L L N R R P A A K

>2617920195 Ga0073689_105108 NADPH-dependent 2,4-dienoyl-CoA reductase, sulfur reductase [pelotomaculum Ga0073689 : Ga0073689_105]

MAKKI LVI GGVAAGPKAAARARRCDPEAEI TVVEQGNFLSYAGCGMPFYI
GGAVHDPRELMSTPVGVRDI PFFKNVKDI NVLTGVRADSI DRAAKQVRV
TNLATGEQSVLDYDKLVLATGSTPGRPPI PGMDLQQVFTLGSMSETVAI K
EAVKNCPDAKVVI I GGGMI GLELADALGSGGGRKI EI AVVELMDHVLPG
LDADMAGLVEKYL NQKGI ELYTAEKVQHLEGDDKGAVKRVVTDKLSLEAD
LVVVATGVPRPNVELARGAGLAI GDTGAI KVNQRLQTSDPDI YAGGDCVEN
I HLVTGHPVYTPMGSVANRHGRI I GDNVTGGSEAMPVGLGAAI LKVFDYT
VGRGLTEKEAGRLGYRAVSI I VPAPDRAHFLAGSKPVI I KLI ACAETRK
LLGAQI TGPGEVNRKLDVAAAAI GMGATVDQVALFDLAYAPPFSTALDPL
VHAANSLRNKLDGRAKSVNPLEVKEKLDRGDDFVLLDVRTPKFQEMRLP
YQNTVFI PLGKL RERAGELPRDKEI I I FCKVSMRGYESQLI LEGLGFDNT
KFMEGGI AAWAFETDTTPLPS

>2617920194 Ga0073689_105107 hypothetical protein [pelotomaculum Ga0073689 :

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Ga0073689_105]

MRMI LRKALLFLQVTVLGLAGALFLPVAALAAPSDLDLAYRWAPVHHQDT
 DSSDYDADYLSAVDFDGDWDAKNNWEHQDDNVNNLKAKVYYSVETSTHW
 YLVYSFFHPRDWVDYDPDFNLDDHENDMEGALMI VRKDGSTYKLEGMT
 VFHTNFYSFTPPGSPLRNGQEDI DGSVI MADYDGSQHPTTFQEAKEGHLK
 AWNGSGFPGGDGVVYPSRTTAEVPAGGNDQSVQYQLVDAFAGGGLWAHR
 NDSLTFASWGTFRGDNGKDANAANAAGWDDGDDGNVLRGEMATDPAKLVS
 IYFSNLGDFSAAAYLRNTYRQ

>2617920193 Ga0073689_105106 Metal -dependent hydrolase, beta-lactamase
 superfamily II [pelotomaculum Ga0073689 : Ga0073689_105]

LKNKPI TRTFVTLCLSLVLFAGFQAPALAAGSMVNI I DVGQADAIL
 VOLPDGKNMVDGNNADGPAVVNYLRGKGVNRVDYVVGTHPHEDHI GGL
 DDVI NNFDI GQVYLPDKTSTTQSYEELI NAI QNKGLTI TTAKAGVI MFNT
 TADGKTL SAVMVPNSNYEDTNDYSAVI RLVFGATSFLTGDAAVSEQ
 EMVNSGQNL SADVLKVGHHGSYSSTTEAFLNAVNPAAVI SVGLNNPYGH
 PHQETI DRLKAHGI DI YRTDMQGAITYTTS GSGYQVNVQPVWWSGGSPSPG
 AGLVI NEVFAPNKKQKHEWI ELYNPGDTAVDI GGYQI DDI AGGGQSPYT
 I PAGTVVPARGYVWQTDSYFNNSGDDARLI KPDGTVADSYTYDGSAYDK
 SWYRYPDGGNWSAGQDGTPTGAANN

>2617920192 Ga0073689_105105 Protein of unknown function (DUF3006)
 [pelotomaculum Ga0073689 : Ga0073689_105]

MDDKI KNLAI I DRFEGEWAVVEFEGRRTFDFPRSLLPAGVAEGDVLKFGV
 EVDKEETKRRRRKAEALAKELFVEE

>2617920191 Ga0073689_105104 Metallo-beta-lactamase superfamily protein
 [pelotomaculum Ga0073689 : Ga0073689_105]

LSLFSLMRGMILTAKRSRFLSLFAVLLAVSLALGGAGFFVSDAEAAASLK
 AHYI DVGQADAFVLVOLPDGKNMMI DGGDNADSSLVVDYLRNKGVS RV DYV
 VATHPHEDHI GGLDAVI NSFAI GKVYMPNKTSTSQSYTDLMKAI KNKGLT
 ATRAKAGVTLFNTAADGKTLKAYFVGPKDSYSNTNDYSAVRLI YGSTT
 FLFSGDAEVTPELDMYGRVASPAWVCR

>2617920190 Ga0073689_105103 subtilisin [pelotomaculum Ga0073689 :
 Ga0073689_105]

VKKYFLVI FLCALFFSFATMAYAEDGGRKI VVFKPGVKQELKEKVVREAG
 GFWAKHLDTI DGAAVTLPAGAEKI MKSSSLVEGI YPDAI VRPAEVAVAGG
 OEI PWGI TRI GADRAWATSTGEGVRVAVI DSGI DLDHPDLKDNI KGGYNA
 VKRKDSFDDGFGHGHVAGI I AALNNSYGVVGTSYNVSLYGVKVLDDTGA
 GRLSDLI EGLAWSVFNRMQVVNI SLETSEDLPFRKAI AKTYAAGVVI VA
 AAGNGGGETAYPAAYPEVI AVSAVDGEDNI APWSNSGKI ELTAPGVDI LS
 TVPVGFI PDSAYFSSSGTSMACPHVSGTVALLLASKI SRKYDFNHNGKWD
 PAEVKKKLQDSSETLPALTPAQGWGLVRADHALK

>2617920189 Ga0073689_105102 diguanylate cyclase (GGDEF) domain-containing
 protein [pelotomaculum Ga0073689 : Ga0073689_105]

MDI DHFKKI NDTYGHKAGDYTLKTVVDACRKCLREHDI FGRYGGEEITIF
 LPETSAEVALEVVEHLREKI AGTRLSLDHAEVAVTASFGVAGVERAGDVE
 LDDLLKKADQALYRAKEAGNRNVVLGAFADLAFTEKSG

>2617920188 Ga0073689_105101 magnesium chelatase family protein [pelotomaculum
 Ga0073689 : Ga0073689_105]

MI AI VKSTALHGLDGOI VEVEVDVSNGLPCFDI VGLPDASVREAKDRVRA
 AI KNSGLEFPVKRI TVNLAPADLKKEGPI YDLPI AVGI LAATGQLPPER
 GQFVYLGELSLNGSLRSVAGVLPNVLAARESSFHEVI VPAENAAEAGLVE
 GI KVFPVAVSLAELAGFLRGEI EITPHHQDLQDLMGGRGEEDFADVRGQ
 QAAKRALEVAAAAGGHNLLMTGSPGSGKTMLARRLPGLPEMTFQESI EAT
 KI HSLAGLLPAHRPLVTRRPFRSPHHTASAVSI IGGGRVPKPGEVSLAHN
 GVLFMDEMPEFQORDALEALRQPLEDGVVTI SRVNASFTYPARLMLI GALN
 PCPCGYFGDRERPCSTPHQVRRYVNRSLSGPLLDRI DIYI EVPRLSFEEL
 SRLEPGESSLEI KKRVEEAREI QRRRFTTGSGGSNVARVVNSGI SCNAHM
 GPREVRLCCRLSRDAAALI KEAFKRLSLSARTHDRVLRVAKTVADLAGSE
 IIEEPHVAEALQYRAADKVL

>2617920187 Ga0073689_105100 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_105]

MKLRCMLCGKPI EEEVSPDPFEEDDDMPKKKPLAVCLMCQAKLKHEAD
 ESQKI PKPV

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>2617920186 Ga0073689_10599 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

LQLKFRRAI SII I GLVFI LLVLT I AGARLYTDWLWFQSLNYQRAFI TII I
SDI GLRVAVGLAFFVLLFI NLMLTRGPLLRATEKASVLRGGI TI QNSP
WNQFLT PRLLLAVFAVLSLI MAFLFSFTVAGDWVTLQKFLHPTSFGNI DP
VFKLDVGFYVQLPFYQFLYKVASWAI I VI AFWVAAYLLVNATQGSPPG
LLQNI SARYHLSFLAALFFGLKALGYQLDQYALLFTHHGAVWGPYGTATH
ATLFAYKFLTFI ALI CALAI LI NI FLRRFKLVVYSI GVLLLASVLLGGI Y
PALVQKFRVTPNEI AMERPYLERNI QFTRLAYNLDMVERRDFPAGRVLSA
QDI RANRDTI NNI RLWDWEPLQQTYSQQLQELRQYYEFKDI DVDRIYI VDGR
YRQVMVAVRELNQAHLSPQAKTWVNQRLSYTHGYGVAMSPVNELTGEGLP
AFFLKDI PPAGSTDLKVARPEI YFGEATDQYVI VNTKSKEFDYPKGNENV
FSI YEGDGGVKLSDLFRRI MFAFSLGDYKLLLSNEVDNNSRVLYYRDI KO
RVPKI APFLQYDNDPYI VLSEGLFWMWDAYTI TDRFPYSEPFDRANNYI
RNSVKVVVDAYTGRVNFYI SDPADPLI KTYSRI FPGMFRPLEDMPEDLSR
HI RYPVDLFKVOAKMYTVYHMEDPQVFYNREDKWNLPTELYASEERQMEP
YYTVI KLPGENRPEFI LI LPFTPQNKPNMI SWLAARSDGEAYGKLLAYGF
SKQEI VYGPMPQVEARI NQDTTI SQI SLWDQGRGSRVI RGNLLAI PI KDAL
LYVEPLYLQSEQNKMPELRRVI LAHGERI VMEPSLEKALEKLFGEGTGVP
KPPEQTAEPDQPPVVDVAELAQAQANRLYDEAQAQKLKAGDWAGYGETLSM
LKQTLNELAEKAGR

>2617920185 Ga0073689_10598 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

MFFGTWWQGI I FGVTTI ALLAI GYAFTVMWRPYENGEKQRFPEHHDDHD
AHGSHDSHGCPVHH

>2617920184 Ga0073689_10597 6-phosphofructokinase 1 [pelotomaculum Ga0073689 : Ga0073689_105]

VSI SKI RRI GVLTGGGDCPGLNAVI RAVVKTAI RDYRLSVVGFENGFGGL
I QNRWELTGKDVAGI LHRGGTI LGTTNRDNPFHYPYMI KGQRVFRDVSD
RVVENI NI HDI DALI VI GGDGSLTI AKELYESKGLAVVGVPKTI DNDLSA
TDQTFGFDALTATEALDKLHTTAESHHRVMVLEVMGRYAGWI ALEAGL
AGGADVI LI PELPYSMERVI AKI TERRDI GKRF SI VVVAEGAKLAGGQMV
VQRVVEDSFEP I RLGGVGNVAGHI EEETGMESRVTVLGHLLQGGI PTAF
DRI LATRYGAAAVNMLMEGKYGEMVCLRTPNI ESPLAEAVGEMRLVPVN
SDLVRTARQVGI AFGD

>2617920183 Ga0073689_10596 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

MRYDPPVYRPPSEASSLI LQVSPGCSHNACTFCGMYKDKKFRKLTWPEI E
SDI MSAKQLFPGATRI FLADGNALTLGQSLLVKI LGKLVVEFLCLEWVG I
YAGPKDI LAKQPEELAE

>2617920182 Ga0073689_10595 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

MAYRI CI I ESGVPKLFKRAVI AVI VLSCLFTGI PGGFSI PERRSVEKDEA
EI VNVVKGAVEDTAWLHVSSROEMDRVLNRYYTAPLCRELAETAWNFVSK
PTDWDYI I KVENCKI TSLSGEQAAVLVDI VEKDDLADSCFPGRFEYTLI K
MADGWRI NKI CPSPEQ

>2617920181 Ga0073689_10594 Glycosyl transferase involved in cell wall
biosynthesis [pelotomaculum Ga0073689 : Ga0073689_105]

LKI GI FTDSYLPYTSGVVR SI QTFTEELSRLGHDVHI FAPSYRNCGQESK
VFRFASI PSPTNRDFTLAVPFSPRLRPTI RRLNLDLI HAHSPFLLGRLGA
RLARKLDI PLVFTFHTLYDQYVHYVPFATSFTRELAQRI SRDFCNQCDLV
LVPTWVI GEYLRGI GVRTAI DRVPTGI KLGDYRGGRDWRQYYGI DPRD
RALLFVGRLGHEKNI GFLMECFSLI NREI NETVLVLVGGGPPEENLKKKA
RELGLAERVVFTGTLPPEVAHCYAGADLFI FASLTETQGI VI AEAKAAG
LPVVAVGANGVSEMVEDGVDGYLTDPDAAQFAGKVCEI LDNDAMRREMI L
KAGQNAESLSLENCTARLVESYREALGQYKKMI KRPV

>2617920180 Ga0073689_10593 Fur family transcriptional regulator, zinc uptake
regulator [pelotomaculum Ga0073689 : Ga0073689_105]

MKNSDI I EQI KERGYKVTPQRRAI I DALLLPGRPRTAKDVLEKVRVLYPE
VGLDVTYRNLNLLI DMGLLI QI NLKNSETSRFEI I KNHHHHLI CLGCGET
LCLEQCPLNERELDKVTEKGYEI VGHAFEI YGYCPACRSAG

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>2617920179 Ga0073689_10592 zinc transport system substrate-binding protein [pelotomaculum Ga0073689 : Ga0073689_105]

MKRLTYPVVVLLVLFVFTAAAGCSGRQTGEDSEKLKVYTTI YPLYDFTVN
VGGDRVDVRNLTPPGAEPHEWEPAPRDLAALTAGDVLVYCGAGLEPWAGK
FLKNTSGSKLVAVNASVGI SLQEADGDNDHEHGHEAGGKEGHGSARVDPHV
WLDPLLAKQMVDNI KKGLSGVDPAGRDYYETNAARYKEELDRDLDAEYRAA
LEKAPRKAFVTSHAFFGYLTRRYGLRQI PI RGI SPEVEPTPSRI AEI VKL
ARQEDI RYVFFESMVNPKI SEVI AAETGARVMVLNPLGSLTRDEI DAGKN
YLAVMRENLNKALGVNDEP

>2617920178 Ga0073689_10591 zinc transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_105]

MNPKTI LDFQNVFSYGCHPVLDNI SLTVSAGEAVGI TGPNGSGKSTLLK
LI LGQLKPAAGKI TLFGARPGKSGDFGRI GYVSQKAASFNSGFPI TVEEV
VAAGRI TGRSLFRPLNREDHRLVLRLEQI GLAGQGNRLLGSLSGGQQQR
VFI ARALAGNPELLLLDEPANGLDRI AREQLYTLLGKLVHEOGLTMI MI S
HGMEDI SSVI TRQVCLNRYLCTCKCHDAEQMKAPAGCARRLWPA

>2617920177 Ga0073689_10590 zinc transport system permease protein [pelotomaculum Ga0073689 : Ga0073689_105]

LIVEEL LLEI FTYSYMNKAMI IGI MVG I CPTAGLFI VLRRMSLI ADALA
HVS LAGVAAAGLLTGTHPI LSASFVAGAVLVEKLREKYKGYSELSI AIM
LSAGLALGAVLLSLGNGFNANVFSYLFSGI VI I EESDFWLI TGTGI I VLS
FVFLI FKELSYI TFDEEAARTSGVAVGAI NI AFTVLTSLTI AVAMRI VGI
LLVSSLM I I PVATALQMAKSLKGALYLSVLFGI ASVI SGLFI SFYLNLA
GGAI I LNAI ALLSGVLAYKGLAI QRVVHSTANGQKSREKDAAL

>2617920176 Ga0073689_10589 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

MKKLALI TAFSI LI LLAGCTPPPKGRTANETPTQPKRFEI I QEEGETKN
I GGFTVLRDNQTGKEYLVI TGLNGAPTVTNLQ

>2617920175 Ga0073689_10588 HSP20 family protein [pelotomaculum Ga0073689 : Ga0073689_105]

VKSGGESGSGI LKGI GELVEI VKKMDAEGKTEI KRTGTGFI FPESRRI
GGSYGFTLKMGLPGRKEPASSGI THSGVGQKPVQKEREPLVDI FDESNFI
RVVVELPAVADEDVLYMNNENVLYTI RSPNGPFSKTI VLPDRVKPGAMR
KSI RINGI LEVI VEVKD

>2617920174 Ga0073689_10587 transitional endoplasmic reticulum ATPase [pelotomaculum Ga0073689 : Ga0073689_105]

VTGQCTFKVI KAPAKDVGRGI ARLDPADI QALGVEI GDLVVI GSERRTAA
RVMPAYAEHRGKLLQI DGI I RENAGVSLGEAVPVSGVAGRMAQKI TLAP
LGP GPAPQLDAAFI SRSLQGVPLVKGDKARI SVLGLRNQEFVVEDTVPEG
FVLSKKD TVVEVLGAREAGFKRANQI TYEDI GGMGKELGRI REMI ELPLK
YPAVFQHLGI EPPKGVLLCGPPGTGKTLI ARAVAGEANAYFLPVNGPEVI
HKFYGESEAKLREI FEKAAQKGRSI I FLDEI DAI APKRVEVTGEVEKRVV
AQLLTLM DGLASRGQVI VI GATNI PDSLDPALRRPGRFDREI TI GVPDLK
GRLEI LQI HTRGMPL EDDVLERVAELTGGFVGADLLALCREAAMCRLRR
I LPQLDPDPEGLPELLI RLRVSMQDFLQALEEVEPSATREFLVEVPNAG
WADI GGLDEI KOHLRETI EWPLKYAALFDQAGAQAAPRGVLLYGPPGTGKT
LLARAVANEANANFI SI KGPALLSKWVGESEKAVREVFRKARQAAPCI VF
FDEI DSLVAARGTGGGAAAERVLSQLLTEM DGI EELRRVVVLGATNRLDM
I DPALLRPGRFDLQLRLELPGRASRREI LAVHI GKRPAEDVDLDGLAAA
TVGYSGADI RHL CNRAALAAVREYLARNSWPPPEPKI RLYDRHFR LALA
EMGPRTEPHGPDGA

>2617920173 Ga0073689_10586 Gas vesicle protein [pelotomaculum Ga0073689 : Ga0073689_105]

MLTGI QPKKQRDDDTLASLVDRLLDKGLVI NADI LVS VAGVELLGI KI RA
ALASFETAARYGLEFPSGTNI ETTAWKEAQI ERESC PQCDKRVSK EELL D
EGCPWCGWI SAKAKKRLEAMVSLPVE

>2617920172 Ga0073689_10585 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

LSQDDKRRRKM KQYLAALDSRSRAVWWHLCCCHGHAGI TGLAREAGLDSDM
EALLSI HRVI NPTATAI LGPAVEFVTCRVDQI TGEKI HHHWWLKP SLWS
PPDAGGPLVDVFETGDEMVI I VDHGGRI GACHPEVTCRNGVI MI RFDRSG
RR

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>2617920171 Ga0073689_10584 Gas vesicle protein K [pelotomaculum Ga0073689 : Ga0073689_105]
VALEI SEDNLKHGLLGLVI ALVEI VKDALKLQALERMEDGSLEESEI ERL
GGALLDLDRAI DEI KCEQGVTESVKSVRDGLDRI VDDVVDRI LNPRRWEE
NAD

>2617920170 Ga0073689_10583 Gas vesicle synthesis protein GvpL/GvpF [pelotomaculum Ga0073689 : Ga0073689_105]
MRALARLLI RAE LAKLDLEKELRAAAAREVVQTTVRDAVRAALDEMAGGRI
RPVTPEOHGGM AETANRTPPAVTEPGEPSPPAKLLTVPDREDLPPGHGVR
TVEPEPAGLYI YGVAAGEEEI GLGVSGI DGSRVYTI GAAGLCVVHDCPD
EPYQPDGDEQAKGWLFDHQEVLDRAKERLGAVLPMGFNTI VRAAGRPPRE
ALEEWLAREGSRLKTL LDR LRDKEEYAVKVLVVEEVLKQAVLREDAHLRE
LRRELEGKPEGARYLYRERLENAVKESENAVEVYFRKI YRSLGPLCTDI
QVEKTKRGAPGTRMVANLSCLVEKNRAPELGKALAEFEGWEGFTVDFTGP
WPPYGFVGE LAAPA

>2617920169 Ga0073689_10582 Gas vesicle protein [pelotomaculum Ga0073689 : Ga0073689_105]
MVGEGRQLQPVRRRETSLNDLLDRLLTKGLMLNSDVVI TVAGI PLLGLNL
RLALAGMSTMLRYGFM TDWDAAI RSLVQKERAGKESYLEKGEQVLI TQFG
SCWYSRGI YSAWRPGLI YLTDRRLFLFRREPAEMLLDVGLKLI SSV DARR
VPHFSGRERQEI WLTLTSGDVVRLHSAGGSQLLAALEKSRDRAGPKNSEL
PGDDDOETI WYLTDPDGKGGQSWQRGA FHVL DGGI CWRGGSGQGQSFRLAT
TDVLAVEFVAGDVPDSPGGRPMVEMRYLGR LNPEKAYFAGEME I LRSWVA
LLREARWDVLETCPACGAPAPANRLLDKGCTACGWI SARLKRRLP

>2617920168 Ga0073689_10581 transcriptional regulator, TetR family [pelotomaculum Ga0073689 : Ga0073689_105]
MAKAQQRRLLPI FEAAMAVFSEKGF EKATVDEI AERAGI AKGTI YNYGSK
KELFLSLVEEGI ERL ENAVKSEI ARRKSVPAKLES LI NVQLRFFDDYKDY
CKVLLSEVWGOETRWEETARRI RSGYLSI I REI I EDGKKEGVLKKELETA
TTASALFGMVGI AALDWFLFEKEYPYEDI LSTLQI LFFTGAGTGNI V

>2617920167 Ga0073689_10580 drug resistance transporter, EmrB/QacA subfamily [pelotomaculum Ga0073689 : Ga0073689_105]
MFSKWEKWL VLSAVI I GLSMDLLDMTI VNVAVPKLMAVFGVDI NKVQWVA
TAYMMTI GVVI PI TAYLTD TYGAKKVFI ASMLLFTAGSALCGLAWSMNSL
I FFRI I QGLGGMI MPLGI SI I YKTF SKNEI GLAMGI MGLPLLAAPAVGP
VLGGYLVEHADWR LI FLI NI PVGI LAVLLSFLVLKEFEKQRSKLD SLGFI
LSAGGLAGL LLLALSNGPN DGDWTPYI VYLLLI SGFLLLLFVPWELLHRQP
LLELR L FANPTFCI SI LLSAFSI MSI MGSFLLPVFLQDLRGYGP MKTGL
LLLPEAVAAALI MPVSGLLVDRLKPAFLSVPGLALLTCATFFLT KI ELAT
GNEFLTRLLVMLGLGMGLGVMPAMTAGLNAV SAGLTGOASSLLNMI RQVS
SSFSI AVLSSI QTRQDLHYARI AEGVTVDSPAVVSFLNRLATHFQEQGL
AGQDAQTLAI AFLHSQAGLQALVSSFQDAFGVATLFGI LGLI PALAFFAV
RVQKVEESKQSKGFHLH

>2617920166 Ga0073689_10579 heat-inducible transcription repressor HrcA [pelotomaculum Ga0073689 : Ga0073689_105]
MTLTRRRRKEFLHTI KI I YENTGVPVHYVTVADALGVSKWTAYDI LKELEK
EGYLRSEYAVSREEKNPGRSAI LFLPTPKAGELFLKEKEEI DHMKEWQVA
REKLLGMFEKVKKCGSKKI I DDI WREMPAI EAPI I I SAYTI AVLI VCI QN
LGDKSVKI MKNLLQSATKPDVL SLFAGTVLGATVKNVQDAI NGR LPAEV
GKFQKYI SEFSAKENKLLVKFLRDALERA I

>2617920165 Ga0073689_10578 ubiquinol biosynthesis protein [pelotomaculum Ga0073689 : Ga0073689_105]
MSGMQLGKKYKHLQRYREI MGVLLKHGFGHVLRLNLGLLDFLLTKGKLVFK
KDPVI ELLSPAQRVRLALEELGPTFI KI GQI LSTRPDLLPPDYI KELEKL
QDRVPPFSFTEVKRQI ENELALPVKELFTEFDPGPLAAASI GOVHRAVLA
GKEVAVKI RRPGI EKVI ETDI EI LYDVARFLEKRSKWAEMYSFVEMVSE
FDCTLHEELDYYTEGRNADTFRNNFAGDDDVVI PAVYWEYTSKKI LTMEY
VEGVKLSNLSEI KRVGLDREALARKVAGAVFKQI LI DGFFHGDPHPGNLA
ALPGGKI VFMDFGMAGHLPEETKNKVGNLMMALI SKNADAVMKAVLDLGV
ASKSVNRKRLRRDI DSLQRKYDI PLSRI KLGDALNDI MSTAYRHRVRI A
PEFALLVKSLLTLEGI I GELDPGLSI VAVAEPFGROMLRARFSPSNLSGI
AARQLLEMGNLLPLLPRVYDVLELAAEGELKLKHQFPQT EEVLT KLNIM

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FNRLAFGI VI AGLVVGSA LI SGRSNLLFGQVPVAEAGFVI AGVLGFWLLV
SI LRSGGF

>2617920164 Ga0073689_10577 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_105]

MSGLLEKSFLVGLGAI SLVGKRI KNTVDELAEKGR LAKDEI TDSTRKLEE
KGA AKMESLRASFCLKCRAFEQKQPLTRODI ERQEQKLEELKQTS

>2617920163 Ga0073689_10576 ABC-2 type transporter [pelotomaculum Ga0073689 :
Ga0073689_105]

LEFVI TARDLVKKYKGTRAVGGI NFAGRPRECFLPGPNGAGKSSVATAN
LLVVAAMGLVNSPWALLVPPVLGLAGLLFAALSMI WTGLAPNI DSFNYYF
ALVI TPLFLFSGVFFPLTSMPGA VQQVAWFSPLYHLVNLTRGLTI GDAGF
HLVGEVWVLLAAALLTI PVSLHLLRRLVI K

>2617920162 Ga0073689_10575 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_105]

LGKVKSAYEMALERLKQRGEVPQREI DRMENVPAGKALANFLREKESNI
LAEI GKOPENI REFLLLEGAREAF LNNI SLPTDSSTLETNK RAMEGLLQI T
NDKRGVGEI FSQLEYLFHYEQSLTQAYSQFKESYAAKI GAALEQRI GTK
VKVDPEKQPGFREEWMKYQSRLNSQYEGLLAEQKEKLFRI E

>2617920161 Ga0073689_10574 MFS transporter, ACDE family, multi drug resistance
protein [pelotomaculum Ga0073689 : Ga0073689_105]

LAENADTQKPVNNFWLAVAALSGVPFI MVLGNSMLI PVL PDI REALNLTP
VKVSLLI TLFSLPAGI I I PVAGFLSDRFGRKTVI I PSLI I YGLGGVI AAM
GAI LLKQYVYPTI LAGRVLQGVGAAGTAPI AMALCGDLFOGKERSRSLGA
LESSNGLGKVI SPVLGAAI GLI AWYAAFLFFPLI VI PI VL SLWI MVKEQE
AERAQQR LSEYLR SFTGI LKNKTGLLFSSYLAGATT LMI LFGVLFYLSEY
LEQOFGLDGVRKGLV LAI PVLFMSATSLVI GF I I KKKKNLMKI LVVTGLA
I MTAAMVFLPLAKGVVI YFVAI SI VGI STGLVLPCLNTLI TSATSTKERG
LI TSLYGSVRFLGVAFGPPI YGFLMTRGLGLMFWSSAGLALLSAALALI F
I KTRPENADGDKQAAI FI FRTAPAKKPES

>2617920160 Ga0073689_10573 fructose-1,6-bisphosphatase II [pelotomaculum
Ga0073689 : Ga0073689_105]

MDRELAL ELVRVTEVAALASAQWMGRGRKNEADGAATNAMRTI FDTVSI N
GTVVI GEGEMDEAPMLYI GEKVGNAQSPEVDVAVDPLEGTNI LAKGLPNA
MSVI AI ADRGNLLHAPDMYMQKLAVGPRAAGKVHLD API EETLKI VAEAN
NKRVDQCVVI I LERDRHKELI ETVRRAGARVRLI GDGDVGS AI STAFDDT
GI DI CAGI GGAPEGVI AAAAL KCLGGEMOAR LAPEDENEY NRCLAMGI AD
PKRI LTMDDLVKGD DAI FAATGVT DGELLKGVRFYGGERAETHSVVMRVR
TGTVRFVRAVHMLSRKPYP SLYRCG

>2617920159 Ga0073689_10572 Putative peptidoglycan binding domain-containing
protein [pelotomaculum Ga0073689 : Ga0073689_105]

LQRFRLYLAI I FI AVLFTCAGTETGAAA API PERVSVI VDMDKLTLTLFY
GGEPI RQYPVAMGRYETPTPVGNWEI VSMETNPPDVMGTRWMGLNI PYGN
YGI HGTNAPHSI GSFASHGCI RMFN SDAEDVFSRI AVGAPVTI I GTPFGA
PGAPPAVLKFGDKGPDVLEVQ RSLKRLGYLKWTPDGFWGKGTEKAVKKFR
EDNGLKGP FVI DEKVYKLLGF

>2617920158 Ga0073689_10571 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_105]

LRRKRSTAWTTAAPWRFPRKSSARLPVRRRQLKELEAKGGDPVRI NELKQ
CI NQDEDLLQAVKFELHGI SGI

>2617920157 Ga0073689_10570 phosphoribosyl formylglycinamide synthase
[pelotomaculum Ga0073689 : Ga0073689_105]

MKKPRVCVLRTDGI NCDEETFYAFTKAGAE CRMVHVNL RNGAERLDRYQ
I LALPGGFSYGDDVHSGKI LAVELTSFLKNQLLEFVEAEKLV LGI CNGFQ
VLVRTGLLPERNPGKI KASLMANDSGHFECRWVNL LVEHSHCVFTRGLEG
TVLSI QVAHGEGKFYTD PATLQGI ENRGQVVF RYTGPDGGPTVLYPANPN
GSLNAI AGI CDSTGRI MGMPHPERYVAKTQHPNW RRI PEDTMPHGLAI F
KNAVEYAGQM

>2617920156 Ga0073689_10569 phosphoribosyl formylglycinamide synthase subunit
II [pelotomaculum Ga0073689 : Ga0073689_105]

MI QEVRVI SKTGI PDSKGEKVL YEI RQALGI QNMERVKTARVFRFEGIGE

Table S2

DDAVYLAIEKLLAEDVFQFYRVNAPVI EDAAVVLEVAYKPGVMNPEASLV
KSAADLGI SGLMAADSSWEYGFYGEI TGADMERI VNSLLVNATVEYVVK
EKPTQLLI HGTPGPTEI I PVRKMSDEELLELSRDKFLNLEEMKVI QEYF
TRLRRDPTDCMETI AQTWSEHCVHKTFKAKLMVDGREKKPLFARLREAT
EESGHPLVLSAFVDNSGVMEFYDGTAVCGKVETHNSPSAI EPYGGAMTGS
GGVFRDI VGTGPGAKVLASTDMFCFAPDPTLEEDI PPGCLHPHYLLRRVV
AGVRDYGNRMGI PTNNGSAHFHRDFRAKPTVI VGAYGI LPAASCRKGKPA
AGDKVVVLGGRTGRDGI HGATFSSGEMTDRTI EVNSSAVQI GHPI EEKRM
FDAI LAARDEGLI RAI TDCGAGGFSSAVGEMGSEI GARI ALDRAPLKYPG
LSPWEI LLSSESQERMVLAVAPERLERLFELCRGYNVEATVLGKFTGDRRF
TATYEGRTVLDLEMDFLHDGLPRRVKAAWRRPGFREPETTGSADLAGLY
TRVLGHLNVCSKEPI VRLYDHGVQTSALPPFAGVGGDGPNDVI LAPLP
GKPYGMVI SHGLNPVLNMI DPYYSGLWAAAEAVSNAVAAGANPKELVLI D
NFI WPFDPDELLGALDLAVDACVDFVRATGMPFI SGKDSLSTYRAKDGT
VI KI PPVLCVSTFGRI PDVSRVTSADFCKTGNRI VLVGHRDTGEMAGSVY
YDLLGVMGNLPLKVPVRLMKVFTAI HGAVKSASLPACHDI SEGGLAAAL
AEMCFGGGAGARLEI PAGETPEHFLFNETAGCFLAELPAGAEPEEI FGDA
PCI VI GETTAGQSI TAHQAGKVLFDLDAELKEAWQRPMEKVF

>2617920155 Ga0073689_10568 L-seryl -tRNA(Sec) selenium transferase
[pelotomaculum Ga0073689 : Ga0073689_105]

MNGESKETLLRLLPSVDEVLRDGRLAEALAAAYPRGMVVEAVRGVLAGERG
AI LAGEAPEARVNNKESQLDI VAGTLEAVRRLVRSKLRPVI NATGVMLH
TNLGRALLSERARRAVNGVADSYNLELDLDTGRRGSRVYALLEPLLTALT
GAEAAALVNNNAAAVLLALGALAQGREVVVSRGQLVEI GGSFRI PEVMAQ
SGARLVEVGATNKTHPDDYKRAVNENTALLLVHTSNYRI I GFTREVSVA
ELVEI GRAFSLPVMSDLGSGFLVDLSRYGLSWEPTVQEVVRAGSDVVTFS
GDKLLGGPQAGI I VGGRHFI EKMKNPLTRAVRI DKMTVAALAEATLREYL
DEERAI EDI PTLRMLTLTDELERKAAGLARLLVGQI GDRAEVAVEKSSS
AVGGGAMPTVDLPTAAVAVRPRDMSAGDLQAALRQGEPAVMGRVQEGRL
LDVRTI DDSQFVTLAAVAGSLKK

>2617920154 Ga0073689_10567 selenocysteine-specific elongation factor
[pelotomaculum Ga0073689 : Ga0073689_105]

LKHLI I GTAGHVDHGKTALVRALTGI DTDRLKEEKERGI SI ELGFASMTL
PGRRAGI VDPVGHHERFI KNMLAGAGGFDLVLLVI AADGVMPTREHLD
I I ELLQVKKGVVLTAKDLVDEEWLGLVKEDVGEFLKGTVLEDAPVATVS
AVTGRGVPELLNLI EQVAQETQTKASAGSPRLPVDVFSI TGFGTVVTGT
LLSGVLRVGDVVDI QPQGLTSRVRSLOVHGEKVEAVEAGQVVAI NLAGLE
VEQI ERGSVVAGPKSLAPSHRLDVRLLLLKSAARPLKNRVRVHFYLGAAE
TLGRVLLDREELAPGAMAYAQMELEEQAVVAGGDRFVI RSYSPMQTI GG
GTVI DPRPKRRHKKRFREEVLDALATRERGAPAELEQYLSGNTGLPDSTE
VATGAGLPEDEVSEAAELAGEGKLKI I NGDGRAYLVLTDTYRRRAGEI E
KLLQSYHREFPLREGYPKEELRSRKFQALNSKI LQYMLQEMERDGLLRDA
ARAVALPDFKPGNPQEERRI SGI YKMLEDARFLPPAWGELCRKAGLGEA
AGTEI LQYLLRSGEMVKVAEDLYFHREVLREAREKVAGYLRKGEI SVGE
MRDLLETSRKYALPLLEYFDREKVTRRVGDKRLPGRALERT

>2617920153 Ga0073689_10566 SAM-dependent methyltransferase, Mida family
[pelotomaculum Ga0073689 : Ga0073689_105]

LYFTGARGKGRFAHPSGCFRTASPNCRLLGGVSVTNRLKLNLAIE I ADFI
QKEGPI TFERFMDMALYYPLGYYSARENI GPEGDFYTSPEVHPVFGKV
LAGQFYEMWTHLGEPARWQLVEYGAGKGLLARDI LRHLREKHSRCFDSLL
YCI I EAGPPFI HRQREI LVDAGVPVEKVAWVDGPAGAHGGEI TGALFSN
ELVDAPFPFHRVRRRPDGLKEI YVDYRDGGFEELEGPLSDPDLSTRYFAEEG
VALEPGQAAEVNLRARGWLKEI SENLRRGFVLT I DYGGAAKELYTEDRFH
GTVRCFRRHCLVENPFEAVGAQDI TASVNFSSLRWRWDQYGLKPAGLFTQ
AEFLI NGGI LELAGGRDDFRHDEDSYGAAGAVKKLI LPWGMGSVFRVLVQ
CKGFAEMPPLSGI TKRFGRI

>2617920152 Ga0073689_10565 geranylgeranyl reductase family [pelotomaculum
Ga0073689 : Ga0073689_105]

MMKYDVI VVGGGPAGAVAARDCAVAGLETVI LEKKYFPRPKPCAGGVTA
AI NLLNVPVPPEVVEARCSSFRSFYGDRCVEI DLDREFMI VVSREVFDLW
LI SLAQSAELRQGEKVSVDTTREGVSVRTPGGVYTGRLVI GADGVHS
TVAKTVRPPLKKNLAFVCVSDI VTGDRESGWQEGI DVHYGPLPMSYSWV
FPKRGRLSVGLGGWLAGI ANVRETFMEFLRVKNLPGDQGI RGYHI PLGGV
PRPVVADGVI LAGDAAGFADPFTGEGI RYAI ASGRLLAAATAVSLI SRGAS
LNRVNLEI YERNWSHQFGAELKNALFI ARLFKHFPTALFGLYFSCREPFQ

Table S2

KSLEI LQGRLEYRQLYRWLLWRI PGLFCRRI TAESVNSFSLR

>2617920151 Ga0073689_10564 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

VEQKVFTYTGEGRLGVTLOATI TDDGLVAQVFGGEKPHVGAVALSLPRPGL
ADPRKVSCNTTVPVLLGHKDDDEI AKPVAEEI VKAWGSPVVVVAGVHLDNA
SGEEVESLI NNCMEVTRTLI EYLRQLK

>2617920150 Ga0073689_10563 N-acetyl muramoyl -L-alanine amidase [pelotomaculum Ga0073689 : Ga0073689_105]

LFVCAFRFRKRYI LVLALAAALAVLAVFRSATALYGERIYI STLSWVVADK
LI VI DPGHGGEDPGALGTTGVNEKDI VLEVSKKLADI LRQAGARVLLTRE
TDRELSESGRSLRQAKVEDLTRRAELANSRRADLFVSI HVNSFPDRRED
GAQTFSQPGSTESRKLAVALI QQELNRFLENPGREAKQVDYFATRMAMP
VI VEI GFI SNPREELMLDPSYQSRI AWSI YAGI VRYLAQPGQVTAPAKK
IDGYH

>2617920149 Ga0073689_10562 arginine decarboxylase [pelotomaculum Ga0073689 : Ga0073689_105]

MLPTPTKFTLMAGSAEGRTGLNAFDHALLAAGVGNCNLVRVSSI LPPGAN
HVPGI HI PPGSLVPI AYGS CLNSPGELI SAAAAGI SDEKTYGVI MEYS
GRTTGEEAEKI I RGMVEEAFEMRGLPLRRYMVRSAEHRVVKTGCAFAAVA
LWY

>2617920148 Ga0073689_10561 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

MSVAGMI I AVI FFTMGVLGTVPALPGAPLI WLGMLI YGLFVKFHSLHWT
FFLGQGLAVALI FLI DYLAGI WGVRRYGGSRRAAVWGSVLGGLLGVLLGY
FGLI FGPI GAVI GELYQKSPLEKAFQVGI GTLI GFFGGTVLKLSEAVM
II WFFI TVL

>2617920147 Ga0073689_10560 PAS domain S-box-containing protein [pelotomaculum Ga0073689 : Ga0073689_105]

LHWSFGFKKVI FALPLLAMI YNWLYDLVVRHGDVTGFNLNLLI QNLMV
I FFTVFLSYGI NKYERLKNKNTLQSEI GLLKGV EGLSLGI VVFDNSGR
I VVFNVEGFKRI TGYGDDLRLDFTKVEEKI I PLPERKNPAVKKALAQQA
SGEYACSLI SKDGRVLSSRASLVPLKNDDGSLTGI LWLFNDMVNQLELWY
LQKQTKGFFLDFTTSCVI AVDNLLKI TI FNTAAEKLTI RKG NVLGRHI TE
I FNDYEAHYPI I KTI I TGEEFHNYDVTFFMNGQLRTLLFDTARI TDES
TVKGAI GI FTDI SERKRI EEELKKTVDYCKEKSFMNRVNLNLPVAI I TY
DNNLQPTYLNMMAEEMTGFRSEELPARRHEADGAADPPCDLFRNLVEDVL
ETGEPI LDEQKSI VSRTGTAI PVSFDVHPI YSVLGEKSGLLVI ARDI RER
REHKQLLFLSRCI LNSLNSAVVSI DSGYRVVFNPPAEKLFGRANEVVG
RKI AEI PCQI FNEELI LQKALEDDGGSRFMETAMRTGEEELVLLI NSDAV
RDSENNI VGAVAI FQDI TELRLTQNAVRERERLAI I GQMAAGMAHEI KNP
LTSVRGFAQLLKEKCPDNPTI VDYVKI I LEEVDRAVSI TDFLQLARPKQ
PVLKSQSVNSLMEEI LAI VTPQAFNLKI NVEYETSQGI PPCRLDRNQI KQ
VI LNMCONAMEAMPVGGLLKI CTGFLPARNEI FI QI TDSCGI PLEKI DK
I GVPFFTTKAEGTGLGLSI SYSI I GAHKGRVEVESKVHKGATFRVYLP

>2617920146 Ga0073689_10559 aspartate aminotransferase [pelotomaculum Ga0073689 : Ga0073689_105]

LAI SKKI ELFLSSASWI RKMFEGERLRKI HGPEKVYDFTLGNPNVEPPG
AFKEELKKLALPVPGMHRYMSNAGYPETRRVAVAGVLAETGLTFNENHI
VMTCGAGGALNVVLKTLDDQGEVI I LSPFFVEYKFYTDNHGGVCKI VPT
TADFTPDNLAI GEAVTARTKAI I I NSPNNPTGAVYDAESLVGLGELLEAR
EKELGRPVYVI SDEPYAKI VYDGI TVPSVFKHI KNSI VVTSHSKDLALPG
ERI GYI AVSPA ENLELLI EGLVFCNRTLGFVNAPALMQRLVAGLQRESV
DI AEYREKRDVLYDNLTTLGFMVKPRGAFYLFPRSPPLDDLEFVRAAQK
HNI LLVPGSGFGCPGYFRI SYCI DKKI I LNSLPAFKALAGELGMP

>2617920145 Ga0073689_10558 Antidote-toxin recognition MazE, antitoxin [pelotomaculum Ga0073689 : Ga0073689_105]

MLSDI TPEGQI TLPRSI MRSLGI DGGNEI LI KVENGRLVLKKVEGI EQEE
ENSPVYKAG

>2617920144 Ga0073689_10557

7,8-dihydropteridin-6-yl-methyl-4-(beta-D-ribofuranosyl)aminobenzene 5'-phosphate synthase [pelotomaculum Ga0073689 : Ga0073689_105]

Table S2

LI VNRENFRPVEEVRI LSLI DNYFDGLLPSSGGRVFRRRGLTGAPGVKPT
PPPLTAEHGLSLYI EVKENGNVHSLLLDFGGSPDGVVRI SPLRLDLSKL
EAMVLSHGFDHFSGMENLVRRFI PPEKLPLPLYVGREAFRRYLANPKG
ATMDLGALSKEKVTALGLEVREI SKPTAI LPGVLLTGEVPRVVPYEQGSP
LMEI EREGAREKDQFPGELSLI FHLAGRGLVVVSACAHAGI VNTVRWAGE
LTGVERVHAVLGGFHLSAPEEKVNKTVEALHEFNPNLI VPMHCTGFAAT
KLLSERI APSFALYAVGTEYRLDSKNQG

>2617920143 Ga0073689_10556 LysM domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_105]

MPLAI TELI WSREGLDGAVLVDWGRVACRRPDLVAAAGRNVLFTSSDPG
FPLSATVEAEGMVLSLAAGLPVLEQDNI VVGLADRVAVYGWRQRTLVR LG
ETEPEPDARFVDLALTDI DGDGREEI I AASGGKEAVYFYRLTGAAELRL
ELLAI RLLPGPAQKVVLGREGRLPVI TVAYRNDGSSGLLTLEYTEMGF
OEGPALES LPARVTS AAGDLRPGPGEEPVGWGEDGAVRI MEI DRQFVLA
VTSNGLGSSAPALTAGRLAGSGANTLI AGTPEGFLFGFEAPVEKSAPDWV
VSPGRPVNDLAVSGEGLLGLGTADGAVQVWLLPGGGGAVHTVQPGETLSS
I AGLYKTTVA AI AGLNGI ADTDLI YPGQKLLI P

>2617920142 Ga0073689_10555 ATP phosphoribosyl transferase [pelotomaculum
Ga0073689 : Ga0073689_105]

LKLRLGLPKGSLQEATFQLFKQAGFDLTVRSRSYFPMVNDPELEVLMRA
QEI PRYVNEGVLDAGLSGLDWI MENEADVVEADLVYAKNTSNPI RLVI A
VAKDSNI VVSDDLNGKRI ATELVRVTRKYLVESGVAHVEYSYGATEVKV
PHLVDAI ADI TETGSSLKANNLRVI ATI LESTTRLHANKVSWQDSWKREK
LQNLAVLLQALRARSKVGLKMNVPGDKLEAI LDVLPAMKQPTI SQLVHS
DWVAVEVLEDKQVRDLI PALKRVGAQDI I EYPLTKVI P

>2617920141 Ga0073689_10554 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_105]

VEDI NYHVLPPNYDENALFLMFQSPRVLYAYWELSPGLKKLLYMHKKVQ
I RLNAEGHKVCHTHDI ALSQKSFYFMDI EPGQSYCEI GI I NLGDQFYPL
LCSNTVTTPLDHPREGNI I TEDYTDVFSTAFI ASSWVFSRGEK

>2617920140 Ga0073689_10553 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_105]

MGNYHLKGDCMTTAMGI LPHTSI EEALDMVLSLDI PFWPQLPKYSFYEDM
YVQVSEHFPGI SLDEEEKRVRLDLEAFYEGLYEYVEKGEDEGI FKLSPKY
SAVLDAFLAKDLGHYPAI RGQSI GPI SFGSKI TDNDLKPI I YHDDVRPFL
FDFI AKKVNVOYRQLKEKNENAFVWI DEPGLEI LFGSFTGYSSARAKDDF
TRFFDNVEGPRGVHLCGNPDWSFLLTGDLDDI LSVDSFNWGH I FTRYFEE
VKAFLEGGS I SWGI VPTL TEEVDDQSDVLLVERLEGLWDYLAHRGI DRK
LI LDRAWLAPARCCLVNADGAVSVEKSFAFLRRVSLRLKEKYNLA

>2617920139 Ga0073689_10552 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_105]

MSLSTGGGI GGGI SGSFNLSFFFTFFLI I I I VVFFLFGGI I

>2617920138 Ga0073689_10551 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_105]

MTLLSGLLEHRGSDLLVREQVSFYVRDVQNGMMEMGR LI QQI ADAEHPDI
AGQCSRLLQLNTQVGNLTLEQVQKSLK

>2617920137 Ga0073689_10550 Prolipoprotein diacylglycerol transferase
[pelotomaculum Ga0073689 : Ga0073689_105]

MI DPVAI QI GPVSVYWYGI I MTAFI LGTALAYHHASKSGI DPEHI LNLL
I LVI PA AI I GARLYYVI FSWGSYRANPLEAF AI WHGGLAI HGGLI GGFLA
GLFYVKKHGLDFWQLSDI FAPSI I LGQTI GRWGNFI NQEAFGGPVSAEYI
SRFPFGI QHQMFI GGQYHHPTFLYESI WNLLVFTFLMVYRGKNHFGQI L
LLYLALYSAGRFFI EGMRTDSLMLGPI RVAQLVSLVLI VTAFTVI FVRSR
KKVKHKI R

>2617920136 Ga0073689_10549 protein of unknown function (DUF1540) [pelotomaculum
Ga0073689 : Ga0073689_105]

LEI FKNKI LFPGKNNTSFKGEVI SLPNI KCSVTECKWNNSVECHAPMI QV
DRNGASKADNSGHTKCETFKMKA

>2617920135 Ga0073689_10548 Carbonic anhydrase or acetyl transferase, i sol eucine
patch superfamily [pelotomaculum Ga0073689 : Ga0073689_105]

Table S2

LFYSFDGRQPEI GYETYVSEQALLI GDVKI WGNFYI GHGAI LRGDYGRIE
I GSGTAVEEGVI I HAPPNETCKI GEKVTLGHGAI I HATTI GD LAVI GMGA
VLSI RTKI GGGAI VEGAVVKMGQSVPEGVVVAGNPAKI I RNVEERDI KH
WSYKGQLYI DLAKKYLQI GMHVSDI RCPCHSKGDFR

>2617920134 Ga0073689_10547 heptaprenyl di phosphate synthase [pel otomacul um
Ga0073689 : Ga0073689_105]

VDEMLELFNDI RDDLOAVEKELRAVVQTQNPLLTETSTHLLNAGGKRLRP
ALSIFGAKFYNFNLEKVLPLAVALELI HMATLVHDDVVDVAMTRRG I PTV
KARWGNSI SI HI GTYLF AKSLI LI AKYEDTPLI SRVLSDTSVKMCEGEI Q
QI SASFDVYQSLKDYFYRI KRKTALLI AASAQLGAVACGAPGSI HLPLRR
YGHNI GMAFQI TDDI LDMVADQSQLGKPI GSDLRQGI I TLPVI YALANS
RREYLMELVNKVDKNEDEVQEI KI I KDCGAI EYSFEI TRKYI RRAKEEL
MSLPDI PTRWTL SLAADFI GI RKF

>2617920133 Ga0073689_10546 precorrin-2 dehydrogenase / si rohydrochl ori n
ferrochel atase [pel otomacul um Ga0073689 : Ga0073689_105]

MPDRYMI SLDLNGKECLVGGGQVAERKVRSLLECGARVWVSPEI SAGL
KSLAQEGGI SYRRGYRAGDLKGVFLVI GSTDREEVNRQVAEDCAARGLL
VNI VDDPTKGNFFVPAVVRGALTI AVSTGGRSPLLARRI REELEKTYGP
QYEKFLNMLGDLREDVI RKGVDGEKKRDI LESLVDDLVL SLLKEGRMDLV
KERI TSVYSGSGP

>2617920132 Ga0073689_10545 glutamyl -tRNA reductase [pel otomacul um Ga0073689 :
Ga0073689_105]

VFI VVVGLNHRTPAVEVREKLSFSGNSLKGALI RLKSNPLI EGCAI LSTC
NRTEI YAATLEMD EGLNAI RDFLSRWSGVDI SQI KNFTYCHTLYDTI RHL
FRVAAGLD SMLLGETQI LGQVKEAYRQAVQHEASNRVLNTLFQQA I AVGK
RVRTETGI DQNPVSI SYAAVELARQHLGDLNKC SI LI I GAGKMSEL TAKH
LVASGVSGVI VSNRSFERAEALAVQLKGRAVKFNELYKYMGVADI VI SCT
AASHCVVRTGEMSRVMEKRRGREI FMVDI AVPRDI EPGVGELAGVTLYDI
DDLKNAVDHNL AERKQAAVRAEGI I EEELDEFMKWLG TQFVVPTI TALKK
WGDEI KOKELRRALNRLGELSEHDKKVVC SLANSI I NQI FHVPVTQLKNY
ALTTEGHLYTEI LQNLFDLDVSGQPKKQTTVFDLGKKHLLVEKG

>2617920131 Ga0073689_10544 hydroxymethyl bi l ane synthase [pel otomacul um
Ga0073689 : Ga0073689_105]

MKREI VVGARESRLAMWOANVVAERLKEASPSYNYRI VGI RTKGDNI LEA
ALAKI GDKGLFTKELEVAMLRGEI DMAVHSMKDLPTLPEGLAVGAI CRR
EHPGDVLI SREGKKLAELPPGALVGTSSLRRCAQLLRYRGDLRVVNL RGN
I NTRLRKLEEEKLDAI VLAYAGVRRMGWEERI TQMI PFEI CLPAVGQGSV
GVEVRAGDEEARELAAGI DHRESRLAVSAERAFLKKLEGGCQI PI GALGT
I ANRRRLRLEGVVASLDGKQI RSFLEGEAEEAPKI GVRLAENLLRAGAGE
I LKNI RQENSPDE

>2617920130 Ga0073689_10543 uroporphyrinogen-III synthase (EC
4. 2. 1. 75)/uroporphyrinogen-III C-methyl transferase (EC 2. 1. 1. 107) [pel otomacul um
Ga0073689 : Ga0073689_105]

MNKGTVYLVGAGPGDPKLI TVKGLECVQKADVI VYDRLAGPRLLTFARPG
AEI VYVGKSLDRHTLKQDEI NRLLVEKAGEGKI VTRLKGGDPFVFGRGGE
EAEALREAGI LFEVPGVTS AI AAPAYAGI PVTHRDY TSTLAI VTGNEDP
LKGD SG I AWDKI ATGAGTLVFLMGMANLPGI TARLI ENGRSPATPVALI R
WGTRPEQQVL AGALADI AQKAGEADFKNPAVI VVGEVASLRDKLKW FENK
PLFGKRVLVTRSREQASALSAI EALGGEALEFPAI SVAAPEDYAPLDKA
I REI GTYGVVI FTSVNGVEAFFKRLRHQRDI RELGTARLCAI GPKTREA
LEKYGLLV DYVPGEYRAEEI I EELRGKMDRGERVLLPRADI ARKALPEAL
AEMGAAVTEVTAYRTVVG GDASMI KEMLKRKEI HVVTFTSSSTVRNFVK
MLDTPDVKNLLAGVTLACI GPVTA VTAGEMGLEVAVVAREYTI EGLVEAI
LEYYGRLN

>2617920129 Ga0073689_10542 putative heme d1 biosynthesis radical SAM protein
NirJ1 [pel otomacul um Ga0073689 : Ga0073689_105]

MI MI SVTKLLCGTDYFGDSI RYSHGSKDQAYGTTRGQGPVVVWNC TRCN
LKCI HCYSNSEARRYKGELTTEEALRFI DGLAEFKVPVLI FSGGEPLLR
DLI KLAAYARSKGI RPTI STNGTLLGLENALY LKNLGVGYI GVS LDGI GE
NDRFRGRKGAFSAALDGI RSCI ALNQRVGLRFTI NRHNYKDLNAI FDLI
EKENI PRVCFYHLVYAGRGSKMVEEDI TREEARAAMD LI I ERTLDFHRRG
LEKEI LTVDNHADGVYI YLRLKKS DPERAAQMLELLKLN GGNRTGI AI GA
VDWHGDVHPDQFTQNH T LSNVRERKFGEI WTDLSQHI LAGLKDRKPLLKG

Table S2

RCAACKWLDVCNGNFRARAEAVTGDFWESDPACYLTDEEIGI NND

>2617920128 Ga0073689_10541 porphobilinogen synthase (EC 4.2.1.24)

[pelotomaculum Ga0073689 : Ga0073689_105]

MPFPVQRPRLRI NENI RRMVRETGLSVDDLVPVFAHGEGI AHPVEAM
 PGI YNYSI DKLEKLEEEVAALKI PAI LPFGLPAAKDEVGSEAYSGDGI IQ
 QAVRAI KKAYPDLLVI TDVCLCEYTSHGHCIGI VKEGRVMNDPTLELLART
 ALSHAAAGADMVAPSDMMDGRVGAI RRALDENG YENVPI MAYSAKYASAF
 YGPFREAAGSAPQFGDRKAYQMDPANSNEALREVRLDI EEGADI VMVKPA
 LAYMDVI RRVKDEFGYPAAAYNVSGEYSMVKAAAQRGWVDERRI VLESFT
 GLKRAGADI I I TYHALDVAQWLAER

>2617920127 Ga0073689_10540 putative heme d1 biosynthesis radical SAM protein NirJ2

[pelotomaculum Ga0073689 : Ga0073689_105]

LI I SWNTTNACNMFCKHCYRDAGVKAEEELNTGEGALALI DQI AEAGFKI M
 I FSGGEPLMREDI FTLVARARERGLRPVLGTNGALI TGETAGCLKEAGAM
 AMGI SLDSVNPESHQDFRATPGAWQGAVDGMRACREAGLSFQI HTTPMDW
 NMPEVERLTDFAVEMEAVGHFI FFLVPTGRAVNI EAESLRAGQYEALLRR
 I MKKQAEVKI ELKPTCAPQFMRI ASQMGFKTRFSKGCLAGI SYCI I SPVG
 FVQPCAYLNI PAGNVREKSFVEI WREAEI FRVLRTEEYKGGCRSCHYRKV
 CGGCRARAYFYHGDYMAEEPWCLYHGRKGY

>2617920126 Ga0073689_10539 DNA-binding transcriptional regulator, Lrp family

[pelotomaculum Ga0073689 : Ga0073689_105]

MKLDQVDRKLLNLI QTNFPLAPEPYREI GEGLSI PENEVI ARI KRLQESG
 VI RRLGGI FDSRKLGYSGALCAMRVAEERI AEVAAVVNSFPGVTHNYI RD
 HSFNMWFTVLAQSKGGLDEI LSRI RERAGI EEI I I LPAENI FKI RVSFDL
 D

>2617920125 Ga0073689_10538 DNA-binding transcriptional regulator, Lrp family

[pelotomaculum Ga0073689 : Ga0073689_105]

MLNEKDKRI VRELQNGLPVSRPFKVMAGKLGMSSEEELI TRI KYFI ECGQ
 I RRFGAAVRHODLGYVANAMVWDVPDERAPETGRI MAGFEEVTHCYQRP
 RQPDWPYNLFTVVHGRSREECVKTAEKLSRATGMEKYRLLFSAAELKSS
 MRYFEQ

>2617920124 Ga0073689_10537 glutamate-1-semialdehyde 2,1-aminomutase

[pelotomaculum Ga0073689 : Ga0073689_105]

MPLSRRRQRKMRI SI FRVDTGHTASQRKGFLI RMHNGFAKSVSLYGEAQEI
 I PGGVNSPVRAFKNPVLNPVFI KKGEARI YVDVGNEYI DYVGSWGPLI L
 GHRHPRVVLEALQCLEGVGTSFGAPTELESVLAAMI VEAVPSVEMVRLVN
 SGTEATMSALRLARGYTGRDKI VKFEGCYHGHADFLI KAGSGALTLGVP
 TSPGI PAASTNTI I ARYNDLEGLKEI FAAGGEDI AAVI VEPVAGNMGVV
 PPAPGFLEGLRNLTAGYGSLLI FDEVMTGFRVAYGGAQELYGI TPDLTCL
 GKVI GGGLPVGAYGGKREI MKYVAPAGPVYQAGTSGNPLAVTAGI ATLE
 VLKQPDVYEELEKKSAELEQGLKQAAADAGAEVVSNRVGSMLCAFFTGA
 VVDYSSACSSNTARFAAFFKSMLLQGI YLAPSQFEAAFVSLAHDMEI ER
 MVAAARTAFRAAMEI

>2617920123 Ga0073689_10536 redox-sensing transcriptional repressor

[pelotomaculum Ga0073689 : Ga0073689_105]

VKTLRVPEATI TRLSI YSRFLERLDRRG I VTVSSGET AEGVGVSPAQVRK
 DLAYFGFEGTRGVGVYNKDLMHYTLKI LGLDEPWPLVLVGAGNLGFALCT
 YRGFNDRGFSI I GVFDNDLTKI GKKI VDLEVYPLEKMAEI I QKHRVRI GI
 I AVPPRAAQEVADLMI KNGLQAI LNFAPVALNI PESI EVRNVDSLKLEI
 LTFNLGMRESEPV

>2617920122 Ga0073689_10535 secondary thiamine-phosphate synthase enzyme

[pelotomaculum Ga0073689 : Ga0073689_105]

VALKI QTELESTRESTQLVDI TGEVERVVAQSGI REGACRLYPHTTAGL
 TI NENADLTVAADI LTQLNKI VPFDDGYRHSEGNAAHI KSSLTGVSLSV
 LI TGGRLLLLGAWQGI YFCEFDGPRRRKVMVKVVEE

>2617920121 Ga0073689_10534 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

MLDQYMSAFYLG I YI FAAVALI AAI FTGPI NREMAEVEEHSSGHNVAH

>2617920120 Ga0073689_10533 CRP/FNR family transcriptional regulator, anaerobic regulatory protein [pelotomaculum Ga0073689 : Ga0073689_105]

Table S2

VGLVMSKENNI EYLRKI YLFTGLNDGELNEI ASVLERRRYQKGRI I FVEG
EPGEAI YFLKSLVKVSKQDGEHREHTLHYVNPDI FGEVVLFDAGGYPA
TAEVVENAEVGLI RNRDMDRLLLKNPVMTLEMLKI MARRLRNSQQQI MEL
ALKDTRRLAGLLLLKLAEEHGVAGDKGMMI DLPLTNQELANLI GTSRETV
NRI LGEFRRRKAI TVVKQEGI FVNRERLETWL

>2617920119 Ga0073689_10532 NTE family protein [pelotomaculum Ga0073689 : Ga0073689_105]

VI SI I TRADA I FEGGGVKA FGM LGALHEAERRGYTWVNVAGASAGAI I GS
LVAAGYSAGEI KKLWELDFSRFKDRDWLDRI PYI GPALSLWFENGVEG
NFLEKWLLLELLAAKGI RTFKDLVLQEFANDPRCRYKLVI I ATDVSRKLL
RLPYDI REYNI DPDDLEVSKAVRMSASLPFFYEPYKLFYTDSGKRRKFSY
I I DGGVLSNFPVWLFDGNDI PPWPTFGFKI VEPDEI SAPRI NNPFDLFKA
I LSTMMEAHDKLYLLDPKSSVRTI SI PSRGVKTMDFETI HNYKNDLFNSG
VQAAVKFFEGWDFESFKI KYCQGMNC

>2617920118 Ga0073689_10531 Thiamine pyrophosphate enzyme, C-terminal TPP binding domain [pelotomaculum Ga0073689 : Ga0073689_105]

MTMQEI TTAVERYSLPVTVVVFNNGTYLLEKSRMEKEGLQPFQVDVKAPDF
AALASACGAVGI RVDDAGMLRREVDRLSLDRPVLDI I SNKEPI YPEN
I I F I F

>2617920117 Ga0073689_10530 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

LLFLLYKFFQHREDVDKLADFYFKNQDLLAQLKNRYPDWETYVDRLSAE
VRAKLRERGVPI

>2617920116 Ga0073689_10529 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

LI SEKAWWWEDNCADFSFDCYI I ERVLHWLEKEDSDI EKLAGTGLCLAAY
TYFFAKMLQALL

>2617920114 Ga0073689_10527 4Fe-4S di cluster domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_105]

LSEPAKKKFKFSFEVNPGLCMACQCECECAYNVSFI DDNVQYAI NKDTC
TRCSKCFRGC PADAI VKLPI S

>2617920113 Ga0073689_10526 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]

MSKKVKGFLKCYRVPDVTETGYRDTWDMGKASKAKKRWRVAGPNRPST

>2617920112 Ga0073689_10525 NADH-quinone oxidoreductase subunit G [pelotomaculum Ga0073689 : Ga0073689_105]

MSQKVTLT I DGREI SAPVGEKI LWAALENGI YI PHLCAI HENNTPFACR
LCFVEVEGYPRPVTCTKPVAEGMAVSTRSERVDHLVRTGFEMLMTNHRL
ECKVCPRNRSCELRQI AQERKLGRLPKRLPVLERNLPI DDSAPNI I YDPN
KCVLCGRVCWTCRI RGMGTLGFAIRGFDMMTTTFMNAPLGESNCSACAAC
AAACPVGSLSLKKKEV

>2617920111 Ga0073689_10524 NADH-quinone oxidoreductase subunit F [pelotomaculum Ga0073689 : Ga0073689_105]

VSNNDSVVVKTGLGELKSKKAVDLRQLQGKPLI LVGAATCGRAAGALAVMQ
AI KDELAQLNI DATLMEVGC I GHCYAEPI VVI YKPGFPGI CYGYVSEGI A
ARLVQDFVAGDDPCI EFALAALNTNDYI PTFADFPRGVVEQKVLEHCGF
I DPEKLGHYLAVGGYEALAGALQKPPGWVI EEI KASGLRGRGGAGFPTGR
KWETCAGAPEKKRYVI CNADEGDPGAFMDRTI LESNPHLMLEGLAI AAYA
VGANQGYI YI RAEYPLAVERVALAI KQAREAGLLGKSI LGGGDFDFVEI F
KSGSFAFVCGEETALI ASMEGEPGMPRHRPPFAVAGLWGKPTVI NNVKTL
SYVPHI I KKSASWFRGI GTPDNPGAAI FALAGKVNTGLAEVPMSTTLHQ
VI YEVGSGI ADGKKFKAVQI GGPSGGCLPEAVLETPI DFNSLTRAGAMMG
SGGMVVLDEDDCMVEI ARFFLDFTQKESCGKCTFCRLGTHMLNI LENI T
KGKGRPEDI ELLLELAEDVKAGSLCNLGTAPNPVLSI RHFDEYEAI
KEKKCPALI CKDLI AYYI LPEKCRSCDACVGSCPVEAI FSNEDRI KVI N
QEKCVKCNSCLVACPPQYKAVI KLSPELVAEREKGGK

>2617920110 Ga0073689_10523 NADH-quinone oxidoreductase subunit E [pelotomaculum Ga0073689 : Ga0073689_105]

MI LTDKEKLAAVEANRRVLEGVACNKGNI PI LQRI QEELGYVPRDAMEE
VAGYLNLPVADI YGVVTFYNQFRLTPPGKHQVKVCMGTACHMKGGNI I LE

Table S2

AWERRLKI KVGETTEDREFSLERVACVGCCTMAPVALVDETVHGRFTPTK
VDGLLFSYQLAKEEGKKAETGEQ

>2617920105 Ga0073689_10518 toxin YoeB [pelotomaculum Ga0073689 : Ga0073689_105]
MNKI FSDI AWAHYLYWQSEDKKI LRKVNELI RDI ERNGNEGLGKPEPLKH
EFSGFWSRRI TEVHRLI YSI DDENI YII ASCKGHY

>2617920104 Ga0073689_10517 anti toxin YefM [pelotomaculum Ga0073689 :
Ga0073689_105]
MI AASYSVRRKFKDYCDKAANDFETI I I TRERGDNVVMLSEAEYNNLLE
NI YVRSNPKYYNELLKSI DQLKKGRGRKKELLDE

>2617920103 Ga0073689_10516 prevent-host-death family protein [pelotomaculum
Ga0073689 : Ga0073689_105]
MRPVSI GI RDAKI NLSKLLKEVQRGAEEI I TDRNKPVGRI VPVSAVEDLP
LAERI ASLEREGLI QPAKKKKARNLPPPLPLPDESAHRMLEEDRG

>2617920102 Ga0073689_10515 PIN domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_105]
VHNNNPVVVWDASAVLSALFKDNSEEA I NWSRREGVHLI SSLSCAEVY
AVI SRI RREGLLADVLI SAACESLEEGPWRRILYLPDWGDFKALSQKWPL
RGADLWYLATAKTLOKRI PESYLLTFDNRLMAAAMGEGLHGGVVY

>2617920101 Ga0073689_10514 looped-hinge helix DNA binding domain-containing
protein, AbrB family [pelotomaculum Ga0073689 : Ga0073689_105]
MRTTVTKRGQTAI PARLRERFGI RTGDYLEWVDDGQTI KVI PVSGDPI QA
LRGCARGSLGRKLLVERREDVLNDR

>2617920100 Ga0073689_10513 Predicted nucleic acid-binding protein, contains PIN
domain [pelotomaculum Ga0073689 : Ga0073689_105]
MTAKTERFVLDSSAI I ALMEEEDGADRVAEVL SRQNV I LPYMLLEVVYI
SLRESQADADLRYVLMKQLPVKI LWNTDEAVLQTAARFKAFRI SLADA
VI AAYAKLHDAVLLHKDPEYEALADEI KLES LPFKNP

>2617920099 Ga0073689_10512 Topoisomerase DNA binding C4 zinc finger
[pelotomaculum Ga0073689 : Ga0073689_105]
LNAAGI I NAFNMTLAEI SYLQNEGGRLVALDGVLTHRGEGLFLYVFD
LEAEAFLLDGTAPRVRYGSREARGEVI AVRGFELTLALNESLG DYVERAK
I FCEPWFLAALQERLHEAPGKNLALMALAVLGNVPARPRRFLPPSAAAEA
QEEALRLADERGI TFI WGGPPGTGKTETLARI GKLFYGGQKRVLI VSHANV
AVDGALLRVAAARI GAPASSGLVVRGWARLSALQRSGLQASNLAAARRPD
LGERRRELEAERGALLAGLRAGRPPGNRLSGVEQALREVRTALKEI EAEV
ARKARVLGCTLAMAATDPVI HQGEYDAVLLDEASMAYI PQVFFAASLAGR
KLVVSGDFRQLAPVALAGSGEVERWLK RDI FDQAGI VAAFEAGQAPDI AV
LRFQRRMHPAI AGFVNDAVYGGI LYNAPETSGRAAMAAAAPCPGAALALV
DLSDLPALCYRHGSSRFNPLSAFLALTLAGKI RRGGLSVGLLTPYAAQAR
LMNALVAGLLGAGGSRSEAAGLVAATVHRFQGAEQDAVI LDLADTFPQRG
PGLLSRREGGSGQRLI NVAVTRARGKFFLLAHRDYLENRLPGDATVRRL
FHF I EQNGRVI KGKELLAELPPHMOGEELG WYTGRWTAQAWQAEADLSQ
AEAI QMDWPVTAGPPEKHVTDALQRASAEGRDLSLRAGRPSALPTALQPY
AVKHTPAKTPLTTFDRRLFWYGCWPDDGRVDHLSVRVSGSERVCRTLMYL
LEMDLRKEFLSGRFAGLKAYI ENKFNCPCGCSPLTVRTATDDGHFLGCTA
YPRCNRPAQKI SPEI LEGYLAAGLTCPAGHLLKAVPTRQGPVAVCSHQ
PCRCAYQVKDLL

>2617920098 Ga0073689_10511 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_105]
VQEI NQEI KNTTLDHAKALQDMTKVFFSDI FPQTRYRHSSGRDFDFNRRF
DSHTLGVVQHALTLQVYVESI SEMGARLKATNGVLVVRLPEDGPNFNEPF
EYAVKVATYLNKSSVNLTKTQORRRQESMDFPYPGSTEI MRLEGTVDDL
LSRKDDEQLVNGRLI WRTSWKI GLNNWMT

>2617920097 Ga0073689_10510 prevent-host-death family protein [pelotomaculum
Ga0073689 : Ga0073689_105]
METLDLTDDI QPVTEFRANTSEVLES LKKNRRTI I LTQHGRPAAVLESVE
EYQRKLEELRFMKGLVAGLRDI ESDQVVEGEDFF

>2617920096 Ga0073689_1059 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_105]

Table S2

MNKTAI KNVATFARKELI NQVALRAQSFGI TLKSSGKMEVGS DYVSI TAA
CSCKSSAAVTWGRPG

>2617920095 Ga0073689_1058 Rhodopi rellula transposase DDE domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_105]
MEPRDTNTAGPGSRSRVKPAI DPDFLENALTDMFRKLAPHLDERQCRLLL
AAEAQVLGWGGI SKLAGATRTSRQTI KNGI KELEQPPLPRGRVROKGGGQ
KPLTEHDPELLAALDALVDPI TRGDPMSPLRWTCSTRQ

>2617920094 Ga0073689_1057 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]
MELKEHLAECLACRRELSRLRLWLLELAQPEKVPLPHELPHLRQQVLAAA
SPAHGEPGKEKSSFNNI OKLAWYPLCLTTAYLPGVGGARELVRTAGREL
GLLRGSLAVTRSLRLRLGRTRKGRGAR

>2617920093 Ga0073689_1056 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]
VSI VI PVLLGVI FLPI I VLCLPVAFSGKVHMEKVMGEGEVWAWGLVAA
RLDVREGKTNFSLRLGPLNI RPRRREEQNEI KKTRKPRHPGQRGKNKRNG
PRAVSRWKS I AGFLDNRLI GKAFSFLRRLI RSLNLKFRLEGEYGTGDPAL
TGYVAGLLAALNSGRGEWSPRPNFTEAI LDLRGEFRGRVI PAGLLWHTGG
FFLAAPVRRLLWWSGI VKPKLNPRRI LENVKRKH

>2617920092 Ga0073689_1055 Uncharacterized spore protein YtfJ [pelotomaculum Ga0073689 : Ga0073689_105]
MLKENI EAI VSRLEKLI TTKTI VGDPI VSGNTTI VPI MSASFGFGSGSGE
GSDPKGAGKGGGGGAGAKVNPTALVVI QEGEVKVYSLSQKGTLEKLAGLI
PDVVAKFQKQQKAD

>2617920091 Ga0073689_1054 Rhodopi rellula transposase DDE domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_105]
LAKDTGLAVTVCHLPPGTNKWNKI EHRLLAHI TMNWRGHPLTSHDVVLNL
INSTTTROGLKVHAEEDTGHYPTGVKLSDEDMKKI NLKKHNFHEEWNNNI
YHKWYPVNNI

>2617920090 Ga0073689_1053 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]
MTLETTI NAQTRWLMEASLAGI I KOMEFPAAYAAQI YNLFADVPLADI D
RFAARYGI EDKI LKQYYSYI KPVYPNPELEEMLAYAD

>2617920089 Ga0073689_1052 Nucleotidyl transferase AbiEii toxin, Type IV TA system [pelotomaculum Ga0073689 : Ga0073689_105]
MPTEPWQLFCKARAI LADQNI SLNDWTFGGGTALALFLHHRVSI DVDI F
LSDAQLLTLLTPRLNNNVAGGVSDYTEGSSFLKLKYPEGEVDFI I APFLT
RHPWVLMEEGEKARVETPEE I I KKL FYRAETLRARDVVDTA AVFTARR
ENLLEAAPVLVPRLAALQRRWAKLQLVFLTEARTLQVKEGLI EKSPALLA
AFLDELSKRL

>2617920088 Ga0073689_1051 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_105]
ADV LKDLGWEMPVDFI KLQYLPDNRELNTTREAGKKLGAAI LAHPGK

>2617920087 Ga0073689_104143 Aspartyl aminopeptidase [pelotomaculum Ga0073689 : Ga0073689_104]
MSDSKEKHSASALAYRRQNAWDRMSEDEKSLVMAFSSEDYKNFLNTAKTER
EAVAAAMTYLKGAGFLSFEEAGPLKPGDRVFAVNRKSLI AAVI GKNPPV
SGFNI I AAHVDSPLRLDKPQPLYEEENMALLKTHYYGGI KKYQWLSVPLS
LHG VVVKDNGAVI PVVI GENPSEPVTVDLLPHLAKDQLDKKMVEAVPG
ENLNLVLGGI PLAGEDVKDRFKLAVLEYLGHRYEI TEEDLVSAEELVPA
WPARDI GLDRGFVGGYGQDDRVCA Y TALRAVVETAAPGRTALLVLADKEE
TGSNGNTGLEAAFFTNNVAEI VSRCVSGYSELALRRI LANSRALSADVNV
GLDPNYPEVVEKMNTARLGGGMVLTKYTGSKGKYSSNDAHA EVVAFI RRI
FNDAGVLWQTGELGKVDQGGGTVAHLLAAHGMDVLD CGVALLGMHSI FE
VASKADI YMAYKGYKAFYAN

>2617920086 Ga0073689_104142 Colicin V production protein [pelotomaculum Ga0073689 : Ga0073689_104]
LNWLDWFI I GI LVLSALQGLRRGLLAGI AGLAGLLGGLVVAFTYYRLLAQ
YLSGHWSI EERI RTLI DGVLKHWLPAGNNMPPAMLPD TTVSTGI YAADQF

Table S2

SFSGDYLSGI I VTAVLELLCFLALLLATARI I NLACMVLTKI ADI GFWGL
FNRLGGLFFGAI RGVVLAALFLALVSFLQQPFLLPGGYPGSPGTFQLPGK
TLQDSMLLPYFRSLDAI GRPLPDFPPGAGHHNEPEKFKNI

>2617920085 Ga0073689_104141 Fic/DOC family protein [pelotomaculum Ga0073689 : Ga0073689_104]
VGHGOAYDFMFTLI GERSI TVKDI KTMHRLFYKSI DEANAGTWRKESVI V
SGSQYVFPRPQEI EGQMRKEI MRLLEHI PFPKMV

>2617920084 Ga0073689_104140 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]
MNEKTVI YVNVANI AMSTNDFEI SVGLKKDRSPGTPVTPDDI DI VLLMSP
OHAKSFTI AI GKAVQI YEEMYGNI SI QADTEVQKKYTGEI KMEDLT

>2617920083 Ga0073689_104139 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]
MI HFSTNDPLGRTI LLPDHSWQHI QDRHHEFATWTSVETTVNKPNNVVKQS
VKKPDRDI YYKLGALGTYPPLYVAVVVGFKGDTGNVI TAHLTADYGVVSS
GGI KYVSKK

>2617920082 Ga0073689_104138 Protein of unknown function (DUF2283) [pelotomaculum Ga0073689 : Ga0073689_104]
MFQKNKTPKATI KYDKI NDVLYI TFGPPRPSFCVAEI DDVFVMKDI ETKE
YSGLTI LDFSERLNDGSLFTI DLPFEFNFKEVVMEVDANN

>2617920081 Ga0073689_104137 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]
MKAWVRVAGDSKFEDPYERGLADRFDRDFKELFKVVPKSHRRVLI RMLYT
TNGLYVRESFRYPHGFENGQL

>2617920080 Ga0073689_104136 Helix-turn-helix domain [pelotomaculum Ga0073689 : Ga0073689_104]
MTAYRWRKEGMPYKHKGVVRYEKAKVQAWLERKNGHKD

>2617920079 Ga0073689_104135 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]
MKTYFRDFSMDNEVLVDSSYELEELI ANRQEKFKCTLTGYTELDNKI KGLF
GKLAEFSPEARKI VDELKDDI SHLECACYSAAAYRDGMSDLMVAQTLNKLN
VTKVEYYATQKPSI TRSI

>2617920078 Ga0073689_104134 DNA binding domain-containing protein, excisionase family [pelotomaculum Ga0073689 : Ga0073689_104]
VVAEKLLTPETAAEALGI SPKTLKDWLRAGKI KGVKI GRAWRI READLQV
FI ESGI VEKDK

>2617920077 Ga0073689_104133 Resolvase, N terminal domain [pelotomaculum Ga0073689 : Ga0073689_104]
MKKAVAYI RVSTQEQAQGGVSLAAQEERI KAYCLMAGLELVAI I RDEGIS
AGKPHSVGI

>2617920076 Ga0073689_104132 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]
MSRDTQAEYLLMHLPI LWERASQGI DNALHGGNRDLSANNRRSDGGHADT
TGRRAI ALAEANELAROLAMVROWI DSRLQPGDRAFLATWRTYRFGGWP
MVAREI GWEASEYRQRWDALVTELI AFSRH

>2617920075 Ga0073689_104131 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]
MI VPKMLVTMEEDNMTQDARTCSSCEKLERNGKRKVCPLSPLVGLDRPC
WAWTDDPAWRI KLSRAI RGYQQGALK

>2617920074 Ga0073689_104130 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]
MRCLSCRVI MI LSDDHHLCPNCGGEFFPAEYFRRREDPGYMLWESCMVR
YVKAMRDGOETARI FARTKRLAGV

>2617920073 Ga0073689_104129 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]
LDELKRARLRKGI I QELRHRNNYHGTSFLFLVDI YLDMLLQREVLEHEI EG

Table S2

AAGDKAVLQDVLANLDADI KSYRERLCLLLLPK

>2617920072 Ga0073689_104128 Phage terminase, small subunit [pelotomaculum Ga0073689 : Ga0073689_104]

LYDDLQKKYTRLTKAAMKKLGVYKKQFDITIDTYAGLLAQYEILTQRLVD
SGMNI EAETQGGPKKTPTLLALEKLRTDMAIYADRLLLNPKALLGAGLS
VGKEQSKLTDILAQLDRRN

>2617920071 Ga0073689_104127 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]

MQVINKAAERQEAQRKEAVTRTERARTRVWLDEKEPGFYLGKRVFEQFVK
AQMGA SLKGVY GSEMSTGAQYINQQVEAAEQFFPLALRDRHRLTRI AVDN
YKPVGRDIPLNLPDDLINELRSEASSSGVSLEQYATGIVRSTVEMFVEQ
DRAAKEII EQNMIKVESRKITGGYISEALADALEAKYGVQKYGVWGFSPAN
NYPIFTYWDMMVKTCCEYLGIKK

>2617920070 Ga0073689_104126 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]

MAYFTAAGTSCREAQRPTVERLQKLTSEVKQLRSKGMEACAKAQEAIEQQ
LKRALGIDKPKKTVREFKNNLKERLTKCR

>2617920069 Ga0073689_104125 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]

MLKKTKKPWLVFLPSVGSIGHRRPKGGKFSRVPERCWKNNIKKKGEE

>2617920068 Ga0073689_104124 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]

MKITI CETA E GLK KLSYYREIKRRDCSITLLTPLGKILLIFNSPEVKGLA
GEVNYTFTPSVLGPIVTPPAKLLVDIEIPGRKAVKVYFHWNSGLPKALLE
TRFLVFLAAKRPKEMSDYFSPSDLFRFAKAGSLDVLDEIMRKNLEDVILP
TELSNLLMSSI EAVH

>2617920067 Ga0073689_104123 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]

LRIFTKAKITADGRRSGKYEYTDGRYLTVTGLRLEKSPLTIEYRQDEIN
AFHREYIAKQKPSREQSQGLVSVLDDDELLSKARKAKNKAI FEKLFSGD
WAGYPSQSEADQALCNMLAFWTGKNPDQMERIFRQSGLYREKCDKHPTYL
ERTINKAIEDCATVYMERLSVEQAFGGCEINWDGTI AGGEEAGQENASSP
DSEVNQQTPKVIQANNRFLASITKEALQALVASNYPPELFTRGGEIVKV
KIQDKDKRNOAFTIPVVKPVNEASLRGYLARSQAQYVNAREKNGEVKYSPT
SPPLELVLDIMALDNLPLPMLRGI VQAPVMRWGSMFAQPGYDDATSLFY
APEYGFSLPDI PDKPNWTDIKKALQLLNDTVADFPFDSEASRANIIAAIL
TPVLRDLIAGPVPMLLIDKPLQGTGASLLSDVISIATGRNSYMTTAPDG
REREEWRKRVTSLSDGRPVI VDNVEEVFRSATLCALLTSINWSDRLL
GRNEIVNLQHRTCWIATGNNIRLAGDLPRRCYKVRLDANQAKPWQDQSS
FRHPHLIGYVKENRATLLAAIYTLARAWIAGRPGPGGEAPPMGSGFEDWRE
VIGGILRFAGASGFLGNSTIEYENAEVNEGIEEFI EALYQEFGERAMSAK
QILHLVTWESKLQEVLPDWLDPGERGFTRKLGRVLARKAGVIFTNGYKLLK
KCGTTDRALLWKICRA

>2617920066 Ga0073689_104122 transcriptional regulator, AlpA family [pelotomaculum Ga0073689 : Ga0073689_104]

MEHNAEQLRQDAQTALQQA RPQRETI TAPEAAEVLGLSPWSIYDLVRRRQ
LPHIRIGRRVLFRRESILOWLEAHEQASVAAEPETERGRIRRLK

>2617920065 Ga0073689_104121 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]

MKYFWPVEEVGKLGEVNYSLRALGVMSDYTTEEINGEKYIKEAGGEVIQH
IKLPADNKLIISLLEIVKEISPDWAMLSVIVPFDNIKKWLLKYGLPGYD
EELFYKHGTLYSRLFEKHVITLFLMFKLYESIYFEKEEDIVKYWSILIK
HPDFVKRSQNEYQEQQNKFIGKTLENKKASVLDLLGIIVNHEVENIQLRF
LEYRKFHLSTASVFSICYQFGLMLSKNDKTIVWKNIKKCANENCQTYFW
AHGNRKYCDMCDRRTISKNNPKKKKVE

>2617920064 Ga0073689_104120 Site-specific recombinase XerD [pelotomaculum Ga0073689 : Ga0073689_104]

MAGYYEKTSGKYRLFASAGTGGGSRKRLTKTIEAKSDREA EKALAKFV
AEVEKGEYIEPSKLFSELVERWLRDYGEVHLAPKTLHRYKQLLDRAIQ
MGHLPIEQIKPLHLVEFYANLQESGVREDGRPGGLSGRTILHHHRAISAA

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LQDAVEWGLI SSNPAARVKPPKVTTRKPAACYDEEQI AAMLSALEKEELKH
QVLVYTALFTGLRRGEVMGLEWRHI DFEGGMATI EQSSQYLPQGQOI TKS
PKNESSARVI SLPLFLVDMRLQYKKEQLKHRLKI GDLWQGYDRI FTTWDG
RPAHPEWPSQWFSKFI KKYELPHLNFHGLRHTAATMLI NQGLPAKNI SGR
LGHSNI STTMDI YGHLLKSADKEAADRLQVYQKMKDNGQKNI KKGQA

>2617920061 Ga0073689_104117 Uncharacterized membrane protein Ykvi

[pelotomaculum Ga0073689 : Ga0073689_104]

LNROKDAI LLLTKVVTYI GTI I GAGFASGQEI MQFFI LHGREGLWGATL
ATFLFAYLGGLVMLLSI TMRSVSYREI LSFLLGARAGKFMDFLNLI MLLG
GLCVMAGSAAVFGHEHGLPDWTGAMLVAALTSIVI MRGLDGVLTANI VL
VPLKFLAI MI I SI SVLCNGVSQGEPOAAQHQSOGVGTGHWALAGFLYVSY
NI VVPVAVLSTLGRTPVPLKLGVAAGI LGGLLLGLTVFI VTAAGLPYMPKL
ASHOI PLLYLAGNLGDGLRWALGI LI WLAI LTTAI ADAHGFA SRLAPGGG
FRYRAWGI GACLLVPLSEFSFSGLVRLLYPLFGYAGMVLLLSLLLI PFV
NFFRKR

>2617920060 Ga0073689_104116 putative sporulation protein YyaC [pelotomaculum

Ga0073689 : Ga0073689_104]

MSAI NNI KEI HDLDKTM I HVEDPLATCKFAWDLVNRMQKFEI KRSSPRI L
LCI GTDRSTGDCLGPLVGSKLDRVQQDFVVGTLDSPVHAGNLMKLEK
I NSLYEDPFI I AYDACLGRI ENVGCI NLGDGSLQPGAGVNKDLPPVGRI H
I TGI VNVGGFMEYLVLQNTRLNLVMRLDAI ANGLNKATLEFARNARGL

>2617920059 Ga0073689_104115 Uncharacterised protein family (UPF0180)

[pelotomaculum Ga0073689 : Ga0073689_104]

VKKI I AVEEGLLSNI KEI LREGYTVVKPDAGENVDATI I SGLDENVMGM
QDI TVKPAVI EASGKTAEI LGDLKKRVWKY

>2617920058 Ga0073689_104114 Predicted phosphotransferase [pelotomaculum

Ga0073689 : Ga0073689_104]

MI FKDRVDAGRKLADALADLAGKDGVLAI PRGGVVGAEVAI KLGLELD
LI I PRKI GAPHNPEVAI GAVTQNGTTI LDRRLI EI I GVGKGDLEEKI NYE
I EEI RRR I SLYKDVEEKQSYEGRLI VDDGVATGYTMVAALRSARNLRP
RELVAI PVAPPETLEI LKKEVDWAVCLHTPEVFYAVGQFYRSFEQTEDG
EVI DI LYELKKKKKTHYLK

>2617920057 Ga0073689_104113 hypothetical protein [pelotomaculum Ga0073689 :

Ga0073689_104]

MNVPAVYI DPLFNHLTSGSAYI VQVLRKDKKFFAYRLFAFDDKKPVDYTW
VMAGI DLNPQNI SFTI GSPSGWFLCYSHRI SVYRFI PF

>2617920056 Ga0073689_104112 chromosome partitioning protein, ParB family

[pelotomaculum Ga0073689 : Ga0073689_104]

LNKRRGLGKGLGALI PVNEDLPAEKEMMRDLNVDEI KPAPRNARKI FDQD
KMTLASSI KEHGI QPVVRPLEEGGYELI AGERRWLACKI LGYKKI PA
LVKEYKDLEATAVSLI ENVQREDLNPLEEAQAYHQLI EEFGLTQEEVSAW
VGKSRPFVANMVRLLGLPGEI KEMLACGRLNAGHARALLTI QDGKKQLAA
AGKI ARKQLSVRAEEI ARVLAEKRSKKKY

>2617920055 Ga0073689_104111 chromosome segregation ATPase [pelotomaculum

Ga0073689 : Ga0073689_104]

MGKTI AI ANQKGGVAKTTTAVNLGAWLSLMGQRVLLVDI DPQGNATTGVG
VDKEYVEKCI YDVI NGMSMRDVI VSCAVENMDLVPSTI ELAGAEEVEMVG
VAEREKI LKKSLEI KRDEYI FI DCPPSLGLLTI NALTAADSLI I PI QC
EYYALEGLGQLMNTFKMVQHLNRELELEGVLLTMFDGRTNLAI QVVDEV
KRHFKEKVYRSI VPRNVRLSEAPSHGKPMVYDSRSGAEI YKELAKEVI
GI E

>2617920054 Ga0073689_104110 16S rRNA m(7)G-527 methyl transferase [pelotomaculum

Ga0073689 : Ga0073689_104]

MKSDMNVLVETLARGVGLNLEI TGGQLKKFEKYYCMLVETNKRNLTS
VVDEREVALKHFDLSLTCLKAVSFEDGI SLLDI GTGAGFPGLPLKI CRPE
I WVTLVESLEKRVSLRKVI LELGLEKVTVLHVRAEELGHDKNHREKYDR
VVARAVAELAVLAECMPAVKVGGYFLAMKGPKVDEE I EGARRAMEI LGG
EI KKN I NFKLPLMGDERNMVLI KKI RCTPEKYPRRMGVPLKKPLKLRKDL
F

>2617920053 Ga0073689_104109 tRNA uridine 5-carboxymethyl aminomethyl

Table S2

modification enzyme [pelotomaculum Ga0073689 : Ga0073689_104]

MI EYLAGKYDVVVVGAGHAGCEAGLAAARMGCRTLVI TMNMDNVALMPCN
PAVGGPAKGHLVREVDALGGEI GLNTDRASI QMRLLNTGKGPVQALRAQ
ADKYYYQI YMKKVLQDQGLDLKQGMVERVI VEKGRASGVVI STGARFEA
WAVVI TTGTYLKGRI I I GNLSFPGGPNGQFSPVSLSDSLAGLGLRLGRFK
TGTPARVDRNSI DFSRMSVQQGDNKTHNFSFI SKI TEREQI PCWLTYTNG
ETHRI I RENLYRAPLYTGEI QTRGPRYCPSI ETKVVRFSKPAHQVFI EP
EGRNTTMYVQGMSTSLPEDVQLAMLRTLPGMEKVEMMRAGYAI EYDYVA
PTQLKMSLETQVLPGLFTAGQI NGTSGYEEAAAQGI VAGI NAALYVKNEE
PLI LDRSEAYI GVLI DDLVTKEI DEPYRMLTSRAEYRLLLRODNADLRLT
EKGYRI GLVTPERYRVYERKKKLVEEEKERLERTVVPVSEEVKKI I KDMK
TVDLPKQGI TMAGMLRRPEI NYEKLHLPGHQDLPEEVKEQVEI QVKYE
GYI KKQQVQVEKFRRLKEEKI FGDLDYKGI RGLSVEAAEKLASI RPSVI G
QAARI AGVNPADI SVLMI YLEQI RRGKGK

>2617920052 Ga0073689_104108 tRNA modification GTPase trmE [pelotomaculum Ga0073689 : Ga0073689_104]

LYEDTI AAI STPLGEGGI GI VRI SGPKAVKI AKKVFRARSQDWTGSGHR
LI YGYVVDCEGVI VDEVLLGYMRAPHTYTREDVVEI NCHGGI VPLRKTME
MALAAGARLAEPGEFSKRAFLNGRLDLAQAESVI DVI RSKTEAGRLAVS
QLKGELSLKVTEI QERLMGLLAQVEANI DFPEDDLEEATGNKVI GESEN
LNEI ELI I KGAEAGRI YREGI SAVI VGRPNVGKSSLLNALLGENRAI VTE
I PGTTRDI I EEYI NI SGI PMKI I DTAGLRETDDI VEKMGVEKTREVI GPA
ELVLLVLDAERGLADEDYKI I SFI GEKKT I FI I NKADVEEKI EAEELKK
VTRGRPVLWI SVLEKNSLVLEKKT I VEMVLGGQVTVADEI LVANVRHKQA
LEKAARRLAEVI DGVRMAPVDVMAI DI RAAWEALGEI TGSTVTEDLLDR
I FADFCI GK

>2617920051 Ga0073689_104107 spoIIJ-associated protein [pelotomaculum Ga0073689 : Ga0073689_104]

VKYVEKSGKTVDEAI SQALKELKVSKEDEVI DVLEEPSKGI FGI I RVKQA
RVRVGLKEGI LYKVEI LLRNI FRTMQMEVAMNI EERDNGVFI NLEGSKLG
I LI GRRGETLEALQYLVLNLSVNKNOELRKKI I I DI GGYRSRREETLRKLA
KKLAEKARQGRSVLEPMNSQERRI I HTALQNMEDI YTFSEGDEPYRKI
I I SPKK

>2617920050 Ga0073689_104106 YidC/Oxa1 family membrane protein insertase [pelotomaculum Ga0073689 : Ga0073689_104]

LELFQALVDGMTWLLNLWLYQLTVKTGLPNYGLAI I LLTVI I KMLYPLSH
KOMKSMAMQLOPKI KEI QDKWKNKDPKKMQOLI MEKYKEHNVNPAAGC
LPLLVQMPI LI ALYRSLYQFPFI NEVHASFI WVQNLSYKDPYI LPVLGAG
VTTYLQSKMTTSTADPTQRMMLYTMPVFI AWI AGTVPAGLALYWVFNVV
GSVQQYFI NKQAMVVKGEAGGR

>2617920049 Ga0073689_104105 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]

MI AMKGTLLVI I RLYQLMI SPMKPPSCRFYPTCSHYALQAI KKHGNVKG
WMALKRI LKCHPFHPGGYDPV

>2617920048 Ga0073689_104104 ribonuclease P protein component [pelotomaculum Ga0073689 : Ga0073689_104]

MSDLTVI KKNAYRKVYGRGKSVADRNLVLFLENNLRI SRFGFTVSRKI
GNAVMRNRI RRLFRESCRLNMDKFPEGYDLVLLARRGI VGAGYRQVEESL
LKLLKRVKLDRE

>2617920047 Ga0073689_104103 chromosomal replication initiator protein DnaA [pelotomaculum Ga0073689 : Ga0073689_104]

MLRSEVLDLWERVLQI LAKKVNKHSFETWLKPLKPLGFYENTI I I EVPNH
FSREWLNDRYTPLI KSVVQDLLDQDHSVQFLLSSEI SEI HPYDTKSSFRD
AVEEI WPKVLNQKYTFNTFVVGDSNRFAHAACLAVAESPAYNPLFI YG
GVGLGKTHLMHAI GQFI LENSNI FKVSYYTSEKFTNDLI NSI RYDKPDSF
RNKYRSM DI LLVDDI QFLAGKERTQEEFFHTFNTLYEANKQI I I SSDRPP
KEI PTLEDRLRSRFEWGLI TDI QPPDLETRI AI LRKKAQLEDI FI PDDTV
VYI ANKI HSN I RELEGAL I RVI AYATVKKRKSFLSWRQKSLRTSFPKTSR
NKLPLN

>2617920046 Ga0073689_104102 DNA polymerase-3 subunit beta [pelotomaculum Ga0073689 : Ga0073689_104]

MKFI SNKEKLTNTI QVVQRAVSLKNPLPI LSGI KFETEEERVSLTATDLD

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I G I C C S F P A E I L E P G A A V L P A K Y I G D L V R R L P D L P I F F E L D R D T G G V N V R
Y G Q S E A V I N G F P V E E F P E F P I P E S E I N F S V P E T V L K E V I Q Q V V Y A A D T D E
N R P I Y T G V F F E I N G S F A Q V V A T D T H R L A W R R L P L D N F E N I D I N F L I P G K T
L N D L S K I I G E A E R S V K V T V A E T Q V L F A T D D I C L I S R L I D G K F P S Y R H V I P
G E H I S K A R L K T R D L E E A T E R A S L L A R D G F P V V K M D I G E N S L V V S I N T E A G
R V R E E M P I H M D G E P V Q I A F N A R Y L G D V L K V I G S E E V I M E F T G P L S P G I F R
P S G N K E Y F S L I L P V R L R

>2617920045 Ga0073689_104101 DNA replication and repair protein RecF
[pelotomaculum Ga0073689 : Ga0073689_104]

L R L K R E L T N F R N Y A R Q V I E P G V N L N I F T G R N A Q G K T N I L E S I Y F A F I G R
S F R T P R E R E I I K L K N D F S R I D C L F E T K R R Q I E V K I L L R P G R K T I E V N C A P
V R G Y P L G W P G V V L F T P D D L M M I K G A P Q E R R R F L D L E I G P F H P R Y G H Y L G R
F N R V L I Q R N N L L R E I R E K K L K S D S L Q A W N E Q F C R Y G A V L L S M R L E L L K K F
S P A S R A L H R E L T G G E E D L G I R Y L S T V K I E E P L C D E E I Y L R F K E E I S R M E G
E E I A R A Q S L I G P H R D D L A I F I N G S D A R I Y G S R G Q Q R T I A L T L K I A Q I R Q W
K E E M D E H P V L L L D D V L Y D L D G G R R R A L F N K A G D E V Q I F L T A T G E E E L A S V
V D C N K K I F T V A G G E L F D

>2617920044 Ga0073689_104100 protein of unknown function (DUF370) [pelotomaculum
Ga0073689 : Ga0073689_104]

M F I H L G G D V V V P K K E V V A I L D I Q A G L A P A T K E F I E I A G D E G F I K N I S E K N
K G K S Y V I T K K E I Y L S P I S C A T L K K R S E S F L D Y

>2617920043 Ga0073689_10499 DNA gyrase subunit B [pelotomaculum Ga0073689 :
Ga0073689_104]

V L T K N G N N S R Y S A E E I Q V L E G L E A V R R R P G M Y I G S T S A R G L H H L V Y E V V D
N S V D E A M A G F C D Q I E V T I N E D N S V T V I D N G R G I P V D I H P K V G R P A V E V A L
T M L H A G G K F G G G G Y K V S G G L H G V G V S V N A L S Q W L E V E V R R D G N V Y H Q K Y
S R G V P V T N L K V I D K S N G S G T K V S F K P D P E I F E D L V F N Q D N L A Q R L R E L S F
L N K G I K I T L R D R R A G Q E L I Y Q H D G G I Q D F V K H L N K N K T P L H S K P I Y F H R Q
R D D V L V E M S L Q Y T D A Y V E N I L S Y A N N I N T I D G G A H E A G F K A A L T R V V N D Y
G R K Y N L L K N G A G N L S G E D I R E G L T A V I S V K V T E P Q F E G Q T K T K L G N S E V R
S I V D S V V G E S L G S F L E E N P P V A R R I L E K A L T A S R A R E A A R K A R E L T R R K S
V L E S S T L P G K L A D C S E R D P A V S E L Y L V E G D S A G G S A K Q G R D R R F Q A I L P L
R G K I L N V E K A R L D K I L A N E E I R A M I T A L G T G V G E E F E L G R A R Y H K I I L M S
D A D I D G A H I R T L L L T F F Y R Y M R P L I E A E Y V F I A Q P P L Y R V K K G K I D H Y V Y
S D A E L E K L L K R I G R D G I N I Q R Y K G L G E M D A T Q L W E T T M D P D T R T V M Q V K L
E D T I E A D T I F S M L M G D R V E P R R D F I Q E N A R A V R N L D V

>2617920042 Ga0073689_10498 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_104]

M S N E T A L K R A G K I K L L F L V A L L L T M A F L G G A V A E R T A H F L Q D V I A A L P D V
L D G T K A F L R E R I I F K I R D A A D Q L K W A A A I T F A I I V E P A S Q L I R G P

>2617920041 Ga0073689_10497 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_104]

L S E T K I I V I S L R G S R L L W Q K I Q Q G L G L T P K K D G H R I F N T C D L L K V K R D R K
K M

>2617920040 Ga0073689_10496 DNA gyrase subunit A (EC 5.99.1.3) [pelotomaculum
Ga0073689 : Ga0073689_104]

L P S L T G K V I P I D I N E E M K H S Y L D Y A M S V I V G R A L P D V R D G L K P V H R R I L Y
A M Y T L G L T P D K S H R K S A Y I V G E V L A K Y H P H G D V A V Y D A L V R L A Q D F A C R Y
P L V D G H G N F G S V D G D S P A A M R Y T E A R M A K I T L E M L S D I E K D T V T F I P N Y D
D K T E E P T V L P A R I P N L L I N G S A G I A V G M A T N I P P H N L G E I I D G V I M L I D N
T E A G V R D L M G V I H G P D F P T G G K I M G R D G I W N A Y R T G R G G I K V R A Q V T V E K
T G S G K N S I I V N E I P Y Q V N K A R L I E K I A E L V K E K K L E G I S D L R D E S D R R G M
R I V I E L R R D A N P Q V I L N Q L Y K H T Q M Q E S F G V I M L A L V E G Q P R V L N L K Q I L
F Y Y L E H Q K D V I V R R T R F E L N K A E A R A H I V E G L R I A L T Y L D E V I K T I R A S R
T T E V A K K A L M E K F S L S E K Q A E A I V E M R L R Q L T G L E R E K L E Q E Y K E L L E K I
A Y L R A V L A D E K K V L V I I K D E L I A I K K K F A D P R R T V I S G E D A D F G V E D L I P
E E D V V I T I T N Q G Y I K R I P L D T Y H S Q R R G G R G V T A M G T K E E D F V R H L F I T T
T Y H F L L F F T N Q G R V Y R L K V H E I P E A G R Q A K G I A I V N L L Y I V G D E K I T T V I
P I R D F D P G Q Y L I M A T R R G I I K K T S L D Q Y D T S R R D G I I A I S L D E G D Q L V N V
K L T S G E E E I I L A T G G G L T I R F A E E E V R P T G R S A R G V K G I S L V G E D K V I G M
E T V R P D A Y L L A V T A N G Y G K R T R L A E Y R S Q S R G G K G I I N I K T T G R N G S V V A
I Q V K E G E E I M M I S A E G I I I R I K T E D I S T V G R I T Q G V T L M R L D P G D T V V A
V A K I D T K E

Table S2

>2617920039 pdxS pyridoxal phosphate synthase yaaD subunit [pelotomaculum Ga0073689 : Ga0073689_104]

LVEKGTWTVKKGLAEMLKGGVI MDVTTPEQAKI AEEAGACAVMALERVPA
DI RAAGGVARMVDPTVI LRI MDAVTI PVMAKARI GHFVEAQI LEALGVDY
I DESEVLTPADETHHI NKHEFKAPFVCGARNLGEALRRI GEGAAMI RTKG
EPGTGNVVEAVRHMRMVMGEI RRVQNMPKEELMAAAKEMGAPYEI LAQVA
EAGELPVVNFAAGGI ATPADAALMMQLGCDGI FVGSGI FKSANPAARAKA
I VAATTQYNEPQI LAEI SRDLGEAMSGLEI ATI TPEQRMQDRGW

>2617920038 Ga0073689_10494 pyridoxal phosphate synthase yaaE subunit [pelotomaculum Ga0073689 : Ga0073689_104]

MKVGVVALQGAFREHQKI LAGCGVDSI QI RKQEQLGGI SALI I PGGESTT
I GKLLNEFKFFDRI VSMGRAGLP I FGTCAGLI MLARGI VGSEQPRLGLMD
MSVERNAFGQVDSFEADLDI PVLGPEPFRAVFI RAPIYI LSVGNSVEVLA
SFNEKI VLARQGRFLAAAFHPELTGDLRLHCYFLKNCTQRFL

>2617920037 Ga0073689_10492 aspartate aminotransferase [pelotomaculum Ga0073689 : Ga0073689_104]

MMQDKHYLMI PGTPVPPAVVAAMSRPVI GHRTDDFAQI HRRI VEKLQSV
FGTKNEVFVTHSGTGALETAVANTVNP GDKVL SLI TGNFGERFANI ARA
YGGVEVEANFGYGDDVDLGVLEEKLNERPDVKVVLATQNETSTGVVNDI A
GI GALVAKTPALLLDGVSGVGAI EI KMDEWHVDI LCTASQKAFMCPGGL
AMVSVSDKAWEVVQSNKSPRFYFSLPAHKKAYEKWNTAYTPSVSLFFGLE
AALDMMMAEGLDNVYARHALLAGATRAAMKALGLKLLAEDRCASNALTAV
WGPEGI PADELKRVVKKRYGVTFAGGQSAVKGKI FRI AHMGFADKMDVI I
AVSALEMALVELGHPVRLGAGI KAAQESFLGANAR

>2617920036 Ga0073689_10491 D-3-phosphoglycerate dehydrogenase [pelotomaculum Ga0073689 : Ga0073689_104]

MKVLVMDGVAESGLETLRREKDI EVVI GKMMNEDELVEVI GDFYGLI VRS
ATKVTARVFEQAKKLKVVGRAGVGVDNI DLAAATAKGVLVVNAPGGNTI A
AAEHTMAMMLSLARNI PQANATLRAGKWDKKAFMGVELREKVLGI I GLGR
I GSAVAKRAQGMEMKVVAHDPYI TEEKAE LLGI RLLSLDELMRQSDFI TV
HLPLTKESRHI LNERTFSLMKDGVRI I NCARGGVVDEEALYNAMKSGKVA
GAALDVFEKEPNTE SPLFEFNNFI ATPHLGASTLEAQLI VACEVAEDI VA
ALKDGSVKNTVNI PSLSPKALAVVKPYLSLAEKMGKFTAQLI SGRVNKI E
I TYSGDLARQEVVPI TTAFLKGFLDTVLQEMVNFVNAPLLAKERGVHVQ
KQAEENG GYANLI TVRAMSDKEEI TVAGAI FGGVDARI VSI DGYHVDI P
EGHMLYI PHNDKPKI I GPVGNLI GDHNI NI SGMQVGRKKI SGKAVMLLNL
DTPVPEETLAEI AGI DGVLGVKNI SV

>2617920035 Ga0073689_10490 seryl -tRNA synthetase [pelotomaculum Ga0073689 : Ga0073689_104]

MLDMKFI RANPQVI REALVKRGSAA NLDEFLELDGRRRENLF EVEKMKNR
RNV I SEEI GRLKRS DREAPDMVLEMRRLSROI REI DEEVKDLEKRLQDI L
LGI PNI PHESVPVGEI AADNLVARTWGEPRNFVFEPKPHWELGEALDI I D
FERGGKVSGARFSFYKGC GARLERAVI NFMLDMHTTKHNYVEI FPPFI VN
RDSMVG TGQLPKFAEDMFKLEGLDYLI PTAEPVPTNLYRNEI LDGEKLP
I YHCAYSACFRAEAGAAGRDTRGLI RQHQFNKVELVKFCKPEDSYNELEK
LTI DAEVQLVGLPYRVVVLCTGDMGFS AVKTYDI EVWLPSYRDYKEI S
SCSNFSDYQARRAGI RFRDGRGRAELVHTLNGSGLAVGRTVAAI LENYQE
SDGSVTI PEALRLYMGLLARI D

>2617920032 Ga0073689_10487 Protein of unknown function (DUF2680) [pelotomaculum Ga0073689 : Ga0073689_104]

VKKRFVI FGVVALLLVALAAPALADNPALDWFKQORMEAKKAYVDQAVQ
NGQLTPEQGQVWKDHFQDMTRFHEENGFI CPGRQGGMGGGQGFGRWQNG
GPGNGFGPGAGMMRNWNGPAQNKQ

>2617920031 Ga0073689_10486 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]

MKDCPVCSI PMDEVPKSGVMI DI CPRCKGVWLDRGELNRLLESVRAYRSE
YEEFYEKRHDDDDHYHYDKHHYKSHHKKKGFFRMI EDI FD

>2617920030 Ga0073689_10485 Glycosyl transferase, GT2 family [pelotomaculum Ga0073689 : Ga0073689_104]

MKRKDVGSKPFI SI I I PCKNEGPNVRMTVDSI LATAPGNDKEI I VVDDGS
VDCCCRFL EEDKTYCGI NLI PASGLGAARARNLGASVARGRYLI FCDAHI

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TVPAGWLDQLETFQHPGVDVSPAI GSLKNPAATGYGQTWNKRLETLWL
 PPPAGGGI KAVPLLPGGCLAVRAGAFRRVGGFDDGFI VWGHEDVELSLKL
 WLFGLYI NPTMKI LHLFREKHPYPVI MDHVHYNLLRLAYSHFNNEVRG
 KVLRLI EPSGRPEKLI RRVLDGAMDQRLRYDLRKYDDDFMERFGI DF

>2617920028 Ga0073689_10483 O-methyl transferase [pelotomaculum Ga0073689 : Ga0073689_104]

VKSLPYLNHDPFRAGGPQYLEDLATAYWYSEALFTAVELGLFTLLEPDGKT
 PAEI AGGLGLYREGLERFLQALCALGLLGRHGEI YFNTNI SSKFLVKGAA
 DYQGDSI LWRKNLFPNWRSLGSLRKGGRVNFARRQEEPERLI RRVKYS
 RAMECVAKAKVREI LPFFRDVFLSGEI LDVGS GSGAVSAGFLEYFPGLRA
 TLMDLPEVLDHAGELQWEKGVDRDFEYCPANI LEPWPVREKRFDLVI LSN
 I VHVSETEI AELLDRAAACLKKGDFLLI HOFFFEHYPEKAALFDLNMFV
 NTFNGRVYPKWLEQLAWRKLYVTELLPLASDTALVI AGKSPESLQNLRL
 LDLPRLVSE

>2617920027 Ga0073689_10482 di guanylate cyclase (GGDEF) domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_104]

MRKFFYRMADLLGRLRLPLLSCESLMAQSRVTGVLRDGHVWVAMLYLDI VD
 FKLTEQI YGNFYCNKVLQNLSHFVDTQASDCLKHYKYI ESRRWGDDLVI Y
 YYDPGQSPPTALEMAGLAGRI RNI LTAGI NENCRHLI PTPI SFHTGYALL
 DPAGENI EKI FYEGFKEAVLVAKNGLSAGEI DRRRQFGRI LLEKDVRMVY
 QPI ASLEHGEI I GYEALLRGPEDPFFSKPVNLLLEYAEKTNQLYALEKLAR
 EKALAGI DENLNKKI FI NI CPQVVNDPSFRADEI SAHLAEVGASPRQVV
 FEI TERTSI EDFRAFREALAYYRQYGFQVAVDDAGSGYSSLQAI SELQPD
 YI KLDI SLI RDI DKNQNKRVLVETFLTFSGKTGSRI I AEGI ETCEELVCL
 RELGVPLGGQFYLAARPESFPGLSPRVAERLAAAHNVTSRRERLGRMI PV
 GSI SHAAVTVSYRDKTREVVDFFTRRPEVEGMVLEEQRVPVGLVMRDKLF
 NQLGTQGFQFAI YNDRPI SLVMDNQPLVVEDDTPVEMVSQTALSRPDHKVY
 DSI I VSKNGI YRGLVSVRGLLDTI TSMQVEAARFANPLTGLPGNRQI EEE
 LLSRLGSDQPFQSVI YSDLDYFKSFNDCYGFERGDVAVI KLTADI LKEKSAA
 AGKPDLDVGHV GGDDFI I I TRSGVAGVVCGEI I AAFDQRPVPELHDPEDRK
 RGYI DTRDRQDQPVRLPLMSI SLAVI DCRPGQYQSPEELSRVAAELKKYA
 KSI KGSVFKERRNRQAG

>2617920026 Ga0073689_10481 phosphate ABC transporter ATP-binding protein, PhoT family (TC 3.A.1.7.1) [pelotomaculum Ga0073689 : Ga0073689_104]

MSCKLI EELQAWYGEERI LNGI SLAMPANEVTAVI GPSGCGKSTLLRCL
 NRMHEVMPRTRI SGRVLMGDKDI YNGSSPVEI RRRVGMVFQTPNI FPNMN
 I FQNVAVGLSLNGLRERRLLQERVETSLRQVGLWDEVDRDLYRDAAGLSS
 GQLQRLCI SRALAVEPEVLLMDEPCSSLDPI VTI RI EELLRELKQKYTI I
 LVTHNLQQAARVSDYTAFI SQGDLI EYGATHEI FI RPRDRRTENYI TGRW
 L

>2617920025 Ga0073689_10480 phosphate transport system permease protein [pelotomaculum Ga0073689 : Ga0073689_104]

MGSVKCDNI RRI WQOI I VGLCALATGLLLTVLFI VSGYI VLQGI PGLSLE
 FFTGMPAPVGLSGGGVAHAI AGSFLLVGLACLLGVPWGVAAAGI FLAEYGO
 RTLLGQAAARFTADVLSGMPSTAGI FI YTLVVVKMOTFSALAGGMAMGI I
 MI PMVARNTTEEI LRLI PAGMREAALALGI PYWRI VLFI VLPTASRGI GI G
 I SLALAGI AGDPAPLFFFTALNNNYWSLSLTQPI ASLPMEI FRYVAAPFAA
 WHSLALTGALALI SVVLVPMILLARI LLPGYKI RR

>2617920024 Ga0073689_10479 phosphate ABC transporter membrane protein 1, PhoT family [pelotomaculum Ga0073689 : Ga0073689_104]

MVAGI WREAAPSI HRFGNLFVSREWNPVAGQFGALPYI FGALVSTALAL
 LLSGPLSLGAAI FLAEFAPVRLRNTLSFLVDVLAAPVSI I YGLWGNFVLA
 PFLLRHAEPWLGQNFGLPLFQGPPIYGI GMLAAGVVLAI MI SPVI TAVSR
 EMLEI VPASQREALLAMGATPWEVVRMAALPYARKGI I GAFTLGLGKAVG
 ETLAVTMVI GNRDPDI SWSLFAPAHTMTSVI I NEFTEAVEPLHVAALI HI A
 LLLFLVTLLVNI LARLMI YQLGRRKNKWDL

>2617920023 Ga0073689_10478 phosphate ABC transporter substrate-binding protein, PhoT family (TC 3.A.1.7.1) [pelotomaculum Ga0073689 : Ga0073689_104]

MFLDKSPLAAVAALLVALLLVAGCGPAGQGDRTGAGAEQGAPASGKAI
 LI NGAGASFPYPLYSRWI DEYGI ERNVKI NYQSI GSGAGI EQI SKKI I D
 FGGSDAPVSDEKLKAFRGEI I HI PTVLGAVATTYNLPELKQKI NFSPDVL
 ADI YLGKI TRWNRRLAAI NPGAGLPDRDI VVVHRSDDSGSTTNI FTDYLC
 NVSADWKS RVGKGT SVQWPAGI GAKGSEGLSRQVQATAGSI GYVELSYAL

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LNKLPYGLVQNKSGRFI EPTLESTTAAAAGFTSSMPDDLRSI VNAPGEN
 AYP I ASYTYI LVYRDQDDPGKGRALVKFLRWAI HDGENMAAELTYAPLPP
 EVVKI VEDKLNSI TCQGKPLF

>2617920022 Ga0073689_10477 HD domain-containing protein [pelotomaculum
 Ga0073689 : Ga0073689_104]

LNQEQQLRAFWDCYVRDFSSHDP E I RAAVALKDEHTRRVCDNI VRAGR
 SLNLGV EELHLAETI ALFHDI GRFRQFTSYCTFNDRRSENHALLGLRELE
 RAGVLSGLAE EEREVV TQAVRRHNL RDLPPDLADPALLFTRLI RDADKLD
 I LKI FTEALDSLNRPNPLLRSSLPDTPEYSPV FLENLLQGKLC SYDDMK
 NFNDRKLLMLSWYDI NFPHTLAEI DRQGYLERI AGTLPETGEI RQVYTR
 LRSFMTRRLAAAGKASF

>2617920021 Ga0073689_10476 Acyl-CoA dehydrogenase [pelotomaculum Ga0073689 :
 Ga0073689_104]

MDFELN EEQKLLQETVYKFAVKEFEPLAKECDREEKYPHELWKKACETGL
 VGCYI PEQYGGAGFGFLEVALI TEQLCRVDVGLSLVMAATFGSENI LLF
 GTEEQKQKYLPLLVSRAI SAGAYTEPNAGTDVAGTKTLAI KDGSEYI I N
 GSKMFI TNGTI CDFMVVLCVTNPKAEKRHRHSLI LVEADRPGLTRNKLK
 GKMGI RASDTAEVI FEDVRVPVENLVGEEGKGFYQLMRFFDVTRTMVAAQ
 GVGLAQGALDKTLKYVQERKTFGQPLASYQGI QFQLAEMATRI ELARTLT
 YKAAWKVDQGRLDPSLNAMAKYSAGEMAVWVCDKALQLHGGYGYI DEYDV
 QRFYRDAKI LEI YEGVKEAEKLT I ARRLF

>2617920018 Ga0073689_10473 DNA polymerase-3 subunit gamma/tau [pelotomaculum
 Ga0073689 : Ga0073689_104]

MAYLALYREWRPRI FGEI I GOEHI TRTLKNAVSAGRVGHAYLFCGARGTG
 KTTTARVLAKALNCP RREAAPCNQCEVCRAVDEGF SMDVI EVDAASNRG
 I DEI RELREKI NFAPATGKYRVYI I DEVHMLSND AFNALLK TLEPPRHG
 VFI LATTEPHKVPLTI LSRQRFDFRRI VPADI I RRLKEVAAGAGLAVEE
 EALRLI ARSADGGLRDALSI LDQAAAFGGMKVTAEDVRDI LGTVRGDALA
 RMTGHLAAGEAGPALRLAAELAGEGKDLRLFAKELAGYLRALLLEKI APG
 AAAGETWDDAGQMAAWAAAFTEEGLLRAVEI MAGVEQGMRFSTLPGVVLE
 VALVKACRPGSFNDVSALAARLAVLEKKLGEPAGRPSEI MDFPCTGKGWP
 PGATFLPPKQI REPAAGEKAARPGGAGQGPVAPAPFAAEVDGAARPAAPG
 ROETMATGTSPPGGESTKSRPAPLGREDVAVKQAALLGREEVAATRTAP
 PRREEAALKGGI GEGGSLEQVRESWYNI METLRSERLPLYFNFTKAAPM
 AVKGRGLVVGFP EGEDLSREMAEQNKYLEELLGRFFKGEWQVAFSTYQG
 KVGLPGKRPAAGKEPVADV KRRFGGEEI NLEEGSGGTLF

>2617920017 Ga0073689_10472 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_104]

MMGGNMNKMVKQVQKMQQDMLKMQEELGDRTVESTAGGGVVKVANGRNE
 I I AVEI KPEAVDPEDVEMLQDLVVA AVNEALKKAQEMVSREMSKI TGGLK
 I PGLF

>2617920016 Ga0073689_10471 DNA replication and repair protein RecR
 [pelotomaculum Ga0073689 : Ga0073689_104]

MNYARPVARI DQLAKLPGI GPKTAQRLAFYLLNAPAEVALNLAGVVEE
 ARKTI RHCSVCGNFTDEDPCFI CGDQRRRRDVI CVVERPRD VVAMEKARG
 FKGLYHVLOGAI SPMEGVGPEQLRI KQLLRLEGGEVKEVI LATNP NVEG
 DATALYLAGLLRPLGLRVTRI AHGLPVGADLEYADEVTLSKALEGRRELK

>2617920015 Ga0073689_10470 inhibitor of the pro-sigma K processing machinery
 [pelotomaculum Ga0073689 : Ga0073689_104]

LEWKLVFI GLAVLLGLYLGVTVFFHPLRFLI HLAAWALLGGVLLVAI NAL
 FGHWGFHI AI NPVTVLTAGI LQLPGVALLVLLNFFLT

>2617920014 Ga0073689_10469 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_104]

MPDRI VETYVGEYAGGKSENAVNRAL ELARLGRRVTLVDLDI VEPVYTLR
 PI REELKALGVEVI AWKTPETTGLGEAGTLI KPEARWALRREGDVI LDI G
 YGVEGAKTLNLLGARTDPDLKVFAVI NTSRPMTAGVADI VEHVREMGRV
 DGLI NNTHLADETTVEVVQEGAGVVTRA AEI LGLPVI ASVAEKGI AEKMG
 PVDCMGNPVRPLDRFMPGAFW

>2617920013 Ga0073689_10468 2-oxoglutarate ferredoxin oxidoreductase subunit
 alpha [pelotomaculum Ga0073689 : Ga0073689_104]

MADKLI REEKRAFMTGNEVV TWAAMAAGAEI MYGYPI TPQNEVMHYWTRL

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APKYNKGFLQTEDELSAGFTTVGGVMAGRKAFTATAGPGNTLMQEPMSMA
EMMLRLPTVVVVQQRGGPSTATVI YSQQEVTLTTLGGNGEGMRVVYSTATH
QELFDYTI KAFNTAWKYRFPFTFI LGDGYQAKMREPLTVYDPEARGVELVG
PAPFVGLAGTPGEDRPPAQHRNTFSLEEELEYKVTRDMKEYERLVP E I AE
YQSDGAAGADLVVVAHG VVFRAVREAVENLRERGLKVG YFRPVTLRPLPV
SRI REI VAGTKKI LVVESACGQLARLFKEAAYGAAAEI QTLFKPGI GI TA
GEVEDRVKNI MGKG

>2617920012 Ga0073689_10467 2-oxoglutarate ferredoxin oxidoreductase subunit
beta [pelotomaculum Ga0073689 : Ga0073689_104]
LYPQPVMPRCWRVDTKPHKFCPGCGHGLVLKCLGHAI DDLGI QGRVVFGC
DI GCSLLSWDFFNI DTVQTHHGRTPVMTGVKRARPELI CVAYMGDGGGY
SI GAQHLVGAAARNEKI TVVLANTQYAMTGGQMAPTTMPGQI TETTPYG
RDPETTGFPLOGP EMI AAI TREGAYVARGSI ANLGQLRKFLKKALENQLA
NGGFSFVEALSACPTNWRNAAETWNFI EKKMAGYFNVGEI NVPTPSGGR

>2617920011 Ga0073689_10466 2-oxoglutarate ferredoxin oxidoreductase subunit
gamma [pelotomaculum Ga0073689 : Ga0073689_104]
MAERMAGKTKI VLAGEGGQGVQAMAEI LAEAAANEDGWQVLYI PNFGVEQR
GGVSVAFVQI SDSRI GSPKFRTGDI VVALSDRAVRRARRYVSGTTFVYD
SDI RGM EGA I PENAARVLAI PAI EVAKKEFHPRVFNII LGVVMGATGVI
SPERARAAI EKKLG YKI EKQPELRNLNFKAMKRGMELVKGI AR

>2617920010 Ga0073689_10465 2-oxoglutarate ferredoxin oxidoreductase subunit
delta [pelotomaculum Ga0073689 : Ga0073689_104]
MTI EI KPRTLELAKASWTLFPGFCKGCGLCI EKCPVKCI NWADVLGVYGT
PSVEADDGCI ACGI QNVCPDCAI RVDKKKQDKQ

>2617920009 Ga0073689_10464 Inhibitor of sigma-G Gi n [pelotomaculum Ga0073689 :
Ga0073689_104]
MMDVKSPVCI LCRRLRQE EGRGLWVKGYI CPECEARI I VLARDDPDYDY
YKWGLKKI WY

>2617920008 Ga0073689_10463 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_104]
VAGGLSWKVDEKALSKKYRADVGR LI RAWKKGFSDQEI TLKTGVKASTLF
LI RODLELAHRRFRLAQKKDAPVQGRAPGQYQI FFNPHL

>2617920007 rplM large subunit ribosomal protein L13 [pelotomaculum Ga0073689 :
Ga0073689_104]
MKTFFMAKPQDI KERK WYVLDGEGKVLGR LAEAAARI LRKHKPTFTPHVD
TGDHI I VI NAEKVLTGNKLNKKYI RHSGYPGGLKVMNYETLMKNRPEL
AVEKAI VGMLPHTRLGADMAKKLKVYRGSEHPHQAKPEAWQLQ

>2617920006 Ga0073689_10461 small subunit ribosomal protein S9 [pelotomaculum
Ga0073689 : Ga0073689_104]
LAKVMFYGTGRRKNAVARVFLVPGEGRVI I NNRPVSEYFGRRTLEMI VRQ
PMELTGVASRFDI QAKVLGGGI SGQAGAI KLG I ARALI QADPNLRI PLKR
AGFLTRDPRMKERRKYGLKKARRAPQYSKR

>2617920005 Ga0073689_10460 Protein of unknown function (DUF2837) [pelotomaculum
Ga0073689 : Ga0073689_104]
VDRLLFVFLLTAFI NLI NTLTRSSRLSGVRTGRLATAI SLFGVVYLAASF
ANTLOAPLLASTVEQI I ESAYDQDLAEAPAAGVTGSPAYQAALADLEQKL
RFVMLGATTGTI AGMLI VPSFVTSFSNAI KAFGRTGSVFKVLLLLLSLV
KPGGGI LKI RMTAPGTVREI LGRRTL SRGFLFWNLASYSLWTVNVLSGL
YAGALFPDFRQTAVLMASI VGNAAI VVNVLMVDPVLAGVTD AVARGEREE
I ELKQI I FYLAFSNLLGTLLSQI I FEPVARGLQLLTGLVA

>2617920004 Ga0073689_10459 N-acetyl muramoyl -L-alanine amidase [pelotomaculum
Ga0073689 : Ga0073689_104]
LSPVVI KSFVRVRKRI AGLVALVFLFFASRLVEAGARRAVEAMSWVA
GKVVVVDPGHGGI DPGVVGKSGAMEKEI ALAVARRLADNLGQAGAMVLLT
RETDTDLAGSGAVGI TARKREDLKRRVALANDNKADLYVSI HVNSFPSPD
RRGARI FI QPGSAQSNKAARFI QEELAKI LKNTGRLPMEVDYFI TRNTTM
PAVI AEI GF I TNLAEEKLLQDPAYQGVAVAI HAGVVKYFAQRDSSPMGR
PDKENTI KTFKEQAPVDLGEPI

>2617920003 Ga0073689_10458 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_104]

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VSTSVTKWGRMTVI LALVALSCFI FAGMALAQDFSI YGGENPVTGESTNV
 VKAAHTYDYTVEASGLNI DLNLFCEDDI NNPPLNQLI I DFPFDQEFNTLD
 GLOGKTVPVYI KVGKDYLVVPEVLENTTSLNGSVVDRVYMTI ERQSI
 PTNGKVTGFNI EGLRVLPDQPGSGYCVSVTHTQNCFOVACLNLNVETV
 GEI GI DSI I GCPVGGSKI TVI GHLNDTMGNPWPHTTWPVI VEFVNTKNVA
 TEAPCELCPPPSI TFTPADVNDPTKGQFVSSDCVPNQLSYYI EKYQNPQS
 GVPI APVVTHANNGYFEASI TVPAVAGTYQI I ARTVEVKDNQEDTGI EYT
 FTTADYLVPAEAI EDRTYLQRTNDNHYYRSI FHNGLEQFEHAWVMSDPTD
 VSPI PGDPKFI TLEPVGSQVDCDNCETLTI VLRDKYGI ETTNATPCGPD
 DPLKVDLKAFI ENGVEKLYGRI HGDAGNGSQI SGGCDAPEI DHVFI APG
 ESRAYAYFKPKDGGYVSI QASAI I GGTPKI AKI CNLEVNCGHCM I ETTPL
 VECDNSGYAKAGWPVKVSVHYDPKLTGTVLANNRTSADLRVELLDASGQP
 VSDATWDTVAKVDPKRLAFDVTGGKQSGNTYTHPGGVSYDPI KSDFYVYV
 PKSYCGPLTVKI VDEPVNVYDTKVI NYTSPTELVRVLSPTWQLLSTPKE
 LAGDGTMTSLLGGVAFSDMLVYDKNAPGGPWVQVTDSSYKLPQYGYLLN
 MKQNWNTEDNCRDKETCGKQNCVKANYVFGGRATGPVLPGRPLNLGWNMV
 GPSFDENLPEQNAEQI PTEYGEI TLPPHCSESGCNCDAELAQGDNL SRM
 LGSACADCKALVNWGGKGLDGDVNLSTSGTPVKI TFSGSPNAMGNLGNFQ
 AATVNNGTLLGGWGI DPTTI YGFNGDAYWLYI SSPQTLTSNTTLDVVDI QP

>2617920002 Ga0073689_10457 S-layer homology domain-containing protein
 [pelotomaculum Ga0073689 : Ga0073689_104]

MVSKLRRHGFAL I CFVLI LFSFGPVALAEDAQPPQMYPALYGTVKT
 ETGRPQAAGTVKAYVEDELCKI SFQEENFGMPAEDPYVGR LI VYSADRD
 LTGKEVTFKVEVAGREYPAKTD PVKI VWESRTKQAVNLI VAVEI PDGQSS
 PAGKSFSPFDLAGHWAEGTVSRMVYQGLLSGYEDGTFRPDNPVTRAECA
 AI LSRALNLPVAGPEGLSVYGDAGAI PGWAQKTVAQAVAAGLFSGYPEPD
 GSTTFRPDKPVSRLAAVL SRVLLQKGLAQDSGQAGFTDQDQI PEWARE
 AVRVVAAAGLAQGYPDGSGFQPKQEVTRAEEASMVERLLGSL

>2617920001 Ga0073689_10456 S-layer homology domain-containing protein
 [pelotomaculum Ga0073689 : Ga0073689_104]

LKKTSKLTALALSCLLFGLALPALAAEMPLVPMMI MGQVVDKNGNDLA
 EGTLLVFI GDKLVTEAPI LKGQVDI ALDAADEGNLSPI DRSDLDKTI RFS
 AVL DKGHEHDATAAKEI TFQEGGI EGADSR LI I TADVSSSSGQQNGGNPG
 GASGGQNTTQAPAAPVASPVAGTYAKGAKVELSSSTTQAVI YYTTDNTDP
 KSSATRKEYKGPVTI EKDTVI KAVSYKSNLYSAVVTFSYKVNQPAQQANN
 PPAQQGGQAGNSSVQLSDLOQHWAA SVI QKL VQQGVVSGYEDKTFRPDN
 QI SRVECAA I ARALALSSGSAGDLAGFSDAADI PEWARGSVSATVYAGL
 LKGYPEAEGKI VFLPQKQI TRVELASI MARVVI SKSGQQAQAQAAFTDSQ
 EI PQWAAEAVDLAAWKGFVKGYPDGTFQPKQSVTRAEEAAMI DRLLDSI K

>2617920000 Ga0073689_10455 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_104]

MGLARMKKI AFI CLSLVFLGLGTGI AWADDPLDNFDYFYGYVKNQQSETV
 SKGTI EAYI NNEERGEVNFQNGQYGI PMEDPFVVKLLVHGTNDNRDKPI Q
 FKVKI GDVSYTAQTD PETVTYQGS MNKRQVNLI I PTAGI NGFAKLEKVKP
 SDPEPDHAGTEVKASQGGSLVETVTTSSDGSYTVTGVAAGDSVLVFTNPG
 GSWKKVAKTVNVKAGEI TNAGTVTLYLGD MNADGSI NI LDLLWMAKMG
 VNEQSQAADVNSDNI NI LDLLRVSSNI GK

>2617919999 Ga0073689_10454 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_104]

VVQKMGAVI LSAVLFAVLLAAGQQKALAGSI EEI SSTDCVEALGEVWDG
 LAI LDADKMEELVNI NKEI NKALFI GI NGNPSVLTEQQQALMNKFHLDF
 GGTRWPWTI EEYVQSHQSGGQTYAGFVNSI QPGRDL DYLAGLYEQLRL
 TFPNDYRVEMNDTWGGERERLDFHVQMFKKI RFDAAGNLLCPPDFESV
 NOYI LAVSSI TKQDLDEVGFSCGMHQA AI EQLTDDQRLAQAEI AAKMGKG
 EGGI SGYYVLEKVPSPDPEPNHAGSEI I AKRNAQQAANAI SNSAGRYSL
 GGLTAGSYQI SFDNPGASWKEVDTQVSLGEDEYKQLPPVTLRLGDMNSDK
 AI NI LDLLWMAKMG PASGESQWADV NKDSQVNI LDLLRI ANNI GM

>2617919998 Ga0073689_10453 Cohesin domain-containing protein [pelotomaculum
 Ga0073689 : Ga0073689_104]

MLNRKI SLLFI ALLLAML MALPAWADGLSI GPQAPSTVNVGDQFEVNI VV
 NAAAALMGVQFDLQYDPSKLEAMQI TKGSVFESPFEPKTI DNNAGI VKY
 GAI VLTPAEAFNGSGAAAKI KFKAKAAGQVNLAFA PGSTI LGGESGVGFE
 HTTSQDTLTI NGTPPRRWKNPLYHSFNRQPGHRA

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>2617919997 Ga0073689_10452 Ig-like domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_104]

MNVTAVDLSGVTI KDAGDNPVAGVNASLGADNRTLNI AHANFAYDTSYSV
TI PAGAVKNAQDAANDPI TWSFTTAAEPPPETLTVTVNLEGDNI SSDRPL
TI SGAKEGENPVSVGWLVRVKDSAGNVVATYAPVSGATFTQI YPPALDL
PVVADYTAQVTATPESGDPVTVNKTFKI YNYPLKLSGI SI TGSGANRTVA
AGLTNFSASGVDGAKVFCQVTKGTDEGWI VVQSPQI KEANVSAGGTENI S
FDI NAPAEPGTYQVELFVWSNADGYWVTLGQQVEADLVL

>2617919996 Ga0073689_10451 Ig-like domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_104]

MRVTGKKTLII LCLASII LLI TGVGLSLAAGAPDYQVVI DDLSGLLDKVVK
LSPEQAEQAVGI SGQLANTLFNGGVLSDSEKTALENTLNI TYATYTETRS
ALEGYI ADYASGGKTGYAGLLNAI NPDNPDTEYLMGLVLQLYNALGPETR
AQLESRGITFDELVSI TTKLGQI QFEPGLEI TDAVROQI AAI LQEI I TKS
DGKLTQEDLTACGLTVENI TELYGKLTDPQKI QLEGI LETMGLI AGGDQE
KPRVTTYQPGNDAQDVPDVAVSATFGRDVTAVDLSGVKI EAGGSALAGT
GASLEGRVLTVSHPEFQYGTNYTVI I PAGSVQAGDI LNDGI SWSFTTLHE
ELGDYKLTLDVQYDSNNNKVTVSGSLKKNDEAQTTPVRDVAI GLVI EKGNT
QYALAQGLTDESGAFRKTFTSTASFDPGTYTVTATANLLTRQGSFTI PAQG
VVSPVVEITNSVTI TTSSATLNGNI TNTGGENCQDQKQYRKQGTTEWTD
AGVESGSFGTGAFSALTGLSSNTAYDAKAMAHNSAGWSEGAVVAFTTTL
EGVTLPVETGAATGI TTSSATLNGNI TNTGGENCQDQKQYRKQGTTEW
TDAGVESGSFGTGAFSALTGLSSNTAYDAKAMAHNSAGWSEGAVVAFTT
TRSSGGGGGGGGSTPELTVDITYEPAKDAKDVSLDAVVKI TFKQNI VEKD
LTKVTI KDDQNNNEVKNVKASVSGKVLTI NHDNFSYDSKYTVTVPKGTVKR
ENYSTVENKEI VWSFSTLKETPELPACDFKDVPAHWAADVI KELCKKGI
LSGYPDGTFKPDNDI TRAEFTKVI VTAI GLAEEETATPSFRDVSAGDWY
GVVQAAKAGLVIRGYENGEYRPNKI TRQEI AAI LVRALARENLAATGSG
DKTAFLDDQLI APWARSSI VI AVKEGLI AGYPDGTGPAKNATRAETCAM
VQRFLAKK

>2617919995 Ga0073689_10450 Subtilase family protein [pelotomaculum Ga0073689 : Ga0073689_104]

MYCLKVTVLMMFLI FIRDPTVQAKNLDLSAEHAKQVEDTLNQI PAAEKME
HVLNRFLVNGI GEGI AQKEFEQRHKLDLKNQI RVVVELKDPDPDLSFLK
SYGAQVEAAWKDRVQVMAPVEKLAVLAGDKNVNYVRRPFRAHYHGGLSYGG
GGGAGGSASQYI SEGVARI NGDQLHAAGI NGRGVKVAVI DSAFNGYRTNP
ELPPDRI VAVKSFRLDGKMEDQEDQGGDHGTACAEI VLDVAPEADLI LLA
CQTGVFEVAVDYAVNHGVEVI SHSAGFLVGPFDGSGFI CDVVDEARQKG
VLFVNSAGNYAMGHYEGWFNNPDNDHWHNFTEKDETLDLGYLPAGYPVDL
LLSWNDWPVSGQDFDLVLLRETYDGVLDVYSLNTQNGSQPPYEI I NYLT
KKAARYLVAI YKESANRSVHFELYAPTTLTQEYNHPESLGI PADAAGTL
AVGAAYWQNDALFVSSRGPTNDGRI KPDMPAPDGVSTRSYGI GKFFGTS
AAAPHAAGAAVLVKSMPHGLTAEELQKRLEEDAVDLGAPGKDNQYGSGRV
DLGGEI PAGAGI SGI VRLEKVRPADPEPDSPAADHSGTEI SI SQQDKQVK
NGFTEKNGSYHLDGLNAGTYSLDFI RPGWTRVEKDDLVL TANSTLDLPAI
TLYVGDMMNQDTQI NI LDLLWMVPGI GLSPEKPGWPEHQLADVNDYSI NI
LDLLRVAKNI GKPK

>2617919994 Ga0073689_10449 Dockerin type I repeat-containing protein [pelotomaculum Ga0073689 : Ga0073689_104]

MKGGLFTKALATFLI I TFAGGFI FTGGASAQTLTPLQEHYQELVEENKNL
FDRLLKTNLVNEDQI YLFVVDLESELSNRI I NQANADRI I KDVTI DEI FK
NQAVFSVAVKKAYSKEI MDHLI TGQLPADI TGLLSKVKTLLSSVVVARPA
GGGHPSCCTGVDLNSYVKGVCFYTLSSSQPTNASKQYADKI SLPGWNGPV
TLKAI AWKNGVSSDI AAFNYEI TGNPCQGR I RGYVYLEGANQFNPGDDRT
GI LI KVAGDHQENGSSAAPDGSYTVNDLCPGKYTVNLQPTAGTWKGVEL
PVTLTDCVKLEVTVTLMGMNGDQOI NI LDLLWMATMI DWKPGDQGW
EGKKADVNGDGSVNI LDLLRVAKNI GK

>2617919993 Ga0073689_10448 Ig-like domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_104]

MDKKARFYWKLVI CLAVLLSFI NLTI PAGQWYAEANFHPLQDKYDELKL
NYGLI NKLLATNKTGLTDKLLKAWVADVENELDDQI I NQKVDLSNLNTL
QDI VVSTFDLTI SPLAAKKHKEVFNAI AVYGKEI KECI FNGADLPADI K
HFLDRVKTI LI SYI VVADPPPGEYTGGLVTLKSFTEGSVI KYTTDGSDP
TYFGTMYQSPLLEDDQSDSPVSLKAI AVKNNVKSELVEFNII LPPPPAPQ

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AKSFI PAKNAQGI AI NTEVSVAFDLDI VDNDLSGI NI KGGGKTLNGTSAS
VSGKVLKI EHPDFEYGYKYYTVTI PAGAVKSKAYNTLNLTYWSFKTI QDT
QPPSGPAAPVLEKPANWSTVDSLTPSFSWQAVS GEGVTYALQI ATSPSFG
GSTLVVDASGLTGATYTSPKLAPQQYYYWRVSADSDMGATPWSSAWRFRT
PSGPAAPVLEKPANWSTVDSLTPSFSWQAVS GEGVTYALQI ATSPSFGGS
TLVVDASGLTGATYTSPKLAPQQYYYWRVSADSDMGATPWSTAWRFRTPV
NNGNV

>2617919992 Ga0073689_10447 Rhodanese-related sul furtransferase [pel otomacul um
Ga0073689 : Ga0073689_104]
MVMYENVMYENKYGPRFKPWTI FI VKI KYTRRI LDKI VEFANLKRVSFKI
FYKGVRLVLLKKVI I VLAGLMLLATI CVEAAETTI KLVI NGQPASVEPEPT
I REGRVMVPVRFI AEHLGAQVKWDDANKTVNI DFKQGDSYLGQNNSSGT
STGTMSNFI SASELKDI LDDDKDNDLADYRQGHNGGDQI ANDPLVVDLRK
QDEYNAKHI PGAVWLADAENMAESQNLQKLKDLLDEHVAKGSKQEI VVYC
YTGNLSGLVAGVLGSQGLPVKSMKYGFDI AWQGTKKADKPI LVPMEDSNG
KAVQCGG

>2617919991 Ga0073689_10446 Endonuclease, Uma2 family (restriction endonuclease
fold) [pel otomacul um Ga0073689 : Ga0073689_104]
MSLPVKEI EI PPKEVYTYADYTQLPEGAPYQLI GGKLVMTAPPTYHQA
STRLLEKFLFFMAGKGLGMI YHAPI DVYFGEKETYQPD I FI ARDRFHI I
EPARI NGAPDLVVEI LSPSTGGYDLRKKARTYAGHGVKEYWI ADPEDKSI
EVYKGREEKFVLDQRVEEKGRVKS LI LDGLEI EVKDI FAQL

>2617919990 Ga0073689_10445 Putative DNA-binding domain-containing protein
[pel otomacul um Ga0073689 : Ga0073689_104]
VDVSEFKEI LRRGEDSKTQFKTRFTHVDSLASEI CAMANTDGGI I AVGVS
DQGDRLTEVRTKGHFQWVKFFLLAAYESALDAI RTI DELVKLHHKNT
I VKGTGKAAKTI MKVFNYLEGSP I DI KKTSEELGI SFNAASNAVNLKLV
LGI LKQTEENVQRNREFAYEEYLN I LRKDT

>2617919989 Ga0073689_10444 hypothetical protein [pel otomacul um Ga0073689 :
Ga0073689_104]
LNI SNEEFQVMALQQLKDLTEGQKTLFAEQKALAEQKEI RKDLARLEYR
MEHEVI NKI RALFDACEAHEDYFKRI FARLDNI EI DTRYLVARVTRLEQL
AK

>2617919988 Ga0073689_10443 hypothetical protein [pel otomacul um Ga0073689 :
Ga0073689_104]
MHSTQFFFFLQTFKKI PLFTGGTI RYFSLPLLFOELQLSKNVLFYLPF
QNKRFNLFLARYGSI RPD I TPLANKYYAAGKSLEAECDAQFYSLA AFEG
ELKANSFPLDAAAKAKATYEARKSARAGQLFPASPDAPRI GRRRKNGPLR
LLKKPGPY

>2617919986 Ga0073689_10441 Uncharacterized membrane protein [pel otomacul um
Ga0073689 : Ga0073689_104]
LKLEI KNEFPYI LLFSVALALLI VSGASGTVRVI LGLPFVLFPPGYTLI A
ALFPAREDLDGVERVALSFLSI AVVPLLGLALNYTPWGI RLYPI LLTLL
AFTGVMSALAI YRRKI I DPEKRFI I SI TVHTTKWGELTRVDKI LTVALVG
AI I FAVGSLYYVATTPKVGEKFTFYI LGPGGKAEGYPREMKVN EKEVI
VGI VNHEYRPVSYTAEVRMDGQVKKRLGPCELNHEEKWEGSVGFALQPH
ENLKVEFLLFKDGESEPYRSLHLWVNI HE

>2617919985 Ga0073689_10440 hypothetical protein [pel otomacul um Ga0073689 :
Ga0073689_104]
VRI QKCDPVFQSKI SVKDHLFLWLYAAGI TAAEVVTAYANPLYGI ACHVV
LMLALLVHASVTYKQDVNLVYLTLSLAPMI RI MSLAMPLAGVPPMYWYLI
I SLPLFSAAYASMRLAGFKPREVGLLAGNLPQLMVAFLGVPLGLVEYLI
LRPAPLAPELSFHYI WLPALI LLVSTGFLEELI FRGVMYRAAVEI LGRWH
SI I YI SFI FGVLHI THRSPDVLVVFVAVSI LFSVTVGFSRSL LGVT LAHG
LTNI GLYI VWP HI LK

>2617919984 Ga0073689_10439 geranylgeranyl reductase family [pel otomacul um
Ga0073689 : Ga0073689_104]
MTMRYDAI VVGAGPSGCCAAESLAREGFHVLVLEEHN RVGEPVQCAGLVS
PRTLQLAGVTGRVVI NSLTGARVFSSLGARLEVNGRKVQALAVDRSAFDR
ELAGRAKEAGAEI CNGARVGLLRI SGGYLVMAQKNGASCFAEARLLVGA
DGANSRVARWLGLKNNNPRAVMYAADVELRRDLTGLVDI FLGRGLAPGWF

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GWVI PMDDKTCRVGTGYAFSRI SRSPPRYFQQI VKQFPNQFKGMKI I RYT
GGTAPMGLMPKI HTPHAMLVGDAACQTKPI SGGGI YLGI RGARMCARVAA
AALREDNLTEKRLAQYQQMWEEYAEI TCGI SHRESFLNFTDEDI DQLL
RFLNRPYWQSMVLKHGDI DYPSWLARRLFSAGPWWQRFVKVALGLAGYGS
QVKNGLKNMFS

>2617919983 Ga0073689_10438 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]

MGKKI LLPVI LLLFTVFALGGALFYGHQAEKRKTI DGAPFRSNEEATGNK
TGDSGEAVNSQKSPMDAKSGGTSAPQSPPTTAENGPADTATPPATQGASR
SGGKETTTADTGRQPSSGGRTLSRI EQEYTGRLQSLASGYEARLGGLVS
AAKEYEQAKKADPSADI TPLI NKYYAAGKALEAECDQFYSLAAFEFE
LKANSFPLDAAAKAKATYEARKSARAGQLFSGKS

>2617919981 Ga0073689_10436 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]

MI STVTTVTTTTATTASTVTTATSMI AGFGLLATI TLI VLLI AKELAGAA
SENSSAREFTLPALDRVLNVGI VPLLVFVSI VVVKVANVL

>2617919980 Ga0073689_10435 S-layer homology domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_104]

LLKLKVRFLNLVLTVLLSVFAGATPSFAQPADI QGHWAEKQI GDWVAKGL
ASGYPDGSFRPDNSI TRAEFI TLVNKSFGFTVQARI YFNDVSSTGWFYNE
I AKAGAAGYI SGYEDGSMRPENI SRQEVAVI LTRLLKLKI PDSADELSK
FADAGSFPRWGGAVSAVVAGGYMVGYPDQTFQPAKSI TRVEAVATLDRA
KGAPEESGAVGKAFFDKAGI YGPESGAETI EGDVTVSAGEEVKKSTPGASS
GGGGGNSGGGGGSDI VDTVAPKI TAAAVTVGGHEI NAVI EGDGLSGGI DL
SGQOPENARI TEGTI DVTRDSTLTTLTVHNI PLSQKLTAGSNSLEAI NLLSK
FGKDI TLGEFEKLFGNPAVLNGTLKDNSSGNTYNVSLTI TLP

>2617919979 Ga0073689_10434 putative ABC transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_104]

LKQDVLI EAENLTKVYGKGESMVKALDI GKLEI RRGEFI ALTGPSGCGKT
TLLNLLGRLDMPGTGGKI YFEGKNI TGLGETALCRFRNRNVGFI FOAYHLI
PALSALGNVMAFAFPLGGGYRRRALELLGLVGLTGKEGRRPGALSGGEQQ
RVAI ARALLLDPELI LADEPTGNLDTANGSGI I ELI KQLNRRDKTVLVAT
HRRVAEACGRNFGMVDGRI VSGG

>2617919978 Ga0073689_10433 Uncharacterized conserved protein, DUF1015 family [pelotomaculum Ga0073689 : Ga0073689_104]

LMAVI VPFGKGLRYNPEKVDNLAEVTPPYDVI DTAAQDRYRRHPYNI I R
LEYGKTGPDGARDNRYTRAAACFNTWLAERVLLPEDRPALRYREQEFTV
NGERRVRGGFI CGVALEPYEKGVLPHHEETMPKHKADRLELMRACRANFS
PI FSLYADPAGEVDRLREAVKGAPPDI DFTDEQGEAHRMWVI TDSEAI G
RVRRAMADRRI FI ADGHHRYETALNYKRERETRCPPAPGEEAAAGAGSRHT
GPDGVTCCRSSGPEPACNYVMNTLVNLYDPGLVVLPTHRLI KNAVGLDKNR
LVERLKKDFYVEEYPLSEDRNFFQFLKLMAERGLARGGAGRPEQQPGPA
PHHHVFLYAGKGRLLYLLSLTDEKALARLMPEDKSPAWRGLDVSALHTLI
I EKHLGI CGELRARAHI TYTREEGALAAMDAGEYQLAFFLNPTLVEEV
TAVANSERMPQKSTYFYPKLI TGLVNVKL

>2617919977 Ga0073689_10432 NTP pyrophosphatase, house-cleaning of non-canonical NTPs [pelotomaculum Ga0073689 : Ga0073689_104]

MDVKEMQKEVDEWI GRFEEGYWSPLSMLARLTEEVGELAREI NHQFGEKP
KKPDEPMGDLALELADI LFI LI CYANSLNI DLADAFKRVMAKYRYRDSR
WTRKDNGETR

>2617919976 Ga0073689_10431 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_104]

LSALALALVLALVVCAGRFI SRGGARLPPREMLTGLERSAASACFRFR
AETRLI TGGKAGAEFFSLVEGERVAPDRVRI KGTMMNTPI EFVQVGDSY
FKDQPTGRWI ALPGNKLADSELFYSELNPLAFFNFKDVPDLKYI GEEKLD
GERLLALEMRPNLMDPFLELRLTDYRYKVVWLSVPDYRLRAVI QAKDKHS
SDSGVEVDLRLWDYDKNI AI EPPAGN

>2617919975 Ga0073689_10430 hypoxanthine phosphoribosyl transferase [pelotomaculum Ga0073689 : Ga0073689_104]

LHPDGERI LLTEQEI RARVAELGAEVSRDYAGRELLVVGI LKGAMI FLAD
LVRSI TVPTSFDMAVSSYGSSARSSGAVRI LKDLDHGI DGRHVLI VEDI

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VDTGTLNLMVDNLKSRGPASLRI CALLDKPSRREAPVEI HYNFGSI PDE
FVVGYGLDYNEHYRNFYI MVLSPRVYRGK

>2617919974 Ga0073689_10429 GMP synthase (glutamine-hydrolyzing) [pelotomaculum
Ga0073689 : Ga0073689_104]

MALPEQEMVI VLDFGGQYSHLI ARRI RELKVFCEMLPFSTPVGEI MARKP
RGI VFSGGPSSVYQAQAPVCDPSVYDLDVPVLGI CYGMQLMAHQLGGKVS
GAAHREYGRSELEVLEREGLFFSCLEAFEQCWMSHGDLEAPPPGFHVTAR
TGKAPVAAMAHPAKNLYAVQFHPEVVHTPKGREI LRAFLYDI CGCRGLWT
MGSFLERAVAEVREOVGDRRVLCSGGVDSSVAAALAHRAVGERLTCVF
VDHGLLRKGAEQVRETFQEKFKI NLVYVDARERFLAKLDGVADPERKRK
TI GEEFI RVFEDEAAKLGRIDFLVQGTLYPDVVESGTATAAVI KSHHNVG
GLPEDMRFEVLPLRWLFKDEVRALGEEMGLPEEVVWRQPFPGPLAVRI
LGAVTAEKVAVLQEADAI VEQEI RRAGLYRRI WQSFAI LPDMKSVGVMGD
ERTYSYTVAVRAVHSHDAMTADWARLPYEALAI SSRI VSEI KEI NRVVY
DI TSKPPATI EWE

>2617919972 Ga0073689_10427 5-(carboxyamino)imidazole ribonucleotide mutase
[pelotomaculum Ga0073689 : Ga0073689_104]

MSRPLVGI VMGSDSLPVMREAAARVLDELGI ASEVVI SSAHRAPDKTVEY
ARTAVERGLAVI I AGAGGAAHLPGVI AAYTLPVI GVPI KSGALNGVDAL
YAI VQMPGPVPVATVAI NGGKNAGI LAAQI I GATDPAVRAVAFAKERLA
AQVREKDTLLGELGVEGYLAQKRD

>2617919971 Ga0073689_10426 adenylsuccinate lyase [pelotomaculum Ga0073689 :
Ga0073689_104]

MI DRYTLPEMKEI WSEENKFRKWLEVEI YACEALTDLGRVPPEALAGI KE
KADFDVQRI VEI EAVTNHDLI AFTTCVGEYVGEAARYI HLGLTSSDVVDI
ALAALMREAGLHVLERLKLREALLAKAEHRATI MI GRTHGI HAEPI TF
GLKMLLWVAETERNI RRMERAVETVSVGKI SGAVGTIANI DPRVEAHVCA
RLGLRPARVSTQVLQRDRHAEFLTTI AVI GSSLEKFATELRSLQRTDI LE
VEEPFKKGQKSSAMPHKRNP I TLERI SGMARLLRGNALAAMENVALWNE
RDI SHSSVERVI VPDSAI TLDYMLYKLTGI I AGLOVYPENMLRNI QRTHG
LI FSQRVLLALVEEKGLSREQAYELVQRNAMRTWRAGENFRDLLLKDPDV
TAHLGEKEI EELFDYGYHLKNVDEI YRRFGL

>2617919970 Ga0073689_10425 phosphoribosylaminoimidazole-succinocarboxamide
synthase [pelotomaculum Ga0073689 : Ga0073689_104]

VRATEPGGLTPCTHGDRLSFTANGVMGKVDKFI FIDLSGLDEPDYTGVS
QELYFSKQNPWEI CKTMPGGSVFDVGTI FSI PGSDI CRTALRHKI YSSL
GAPGQWDRVQKI I GECKDNQEMLWFLNEGLLEDFRANGANTHHVGM I DK
DTGEVHRETFPRNPSPYVLVKRYRI I KPGRVSCFSKYLDYSDYRAADKF
VI PLENI VRFGVTSGSSI YKKYLSLDGRGRRDFLGLGLEQELVPWTFFA
KPLVDFTTKYEPEDRSLSLQEALYI SGVNGASFLNI I KMCLLGS I MVAEI
FREMGLLLWDLKWEI ARDGDKLVFVDI DTDSVRVTARVAYKDRVYFVNF
NKQAMRDYMI MSPRWCEAVKSAKAEAVDSGRSFHHYKAGQGKGSYPKT
PVDDEEFI RI QEQKFSALI DYI YGRSTAGEI TEKYKLI GREEI RYYDAKG
VLDEFGLNGA

>2617919969 Ga0073689_10424 aminodiphosphoribosyl transferase [pelotomaculum
Ga0073689 : Ga0073689_104]

MAEEYGNPCCGAPPLGDKPGEECGVFGI YGPGLDVARLTYGYALQHRG
QESAGI AVGDWKRI QLQKDMGLVAEVFNHEKLNFRGHLAVGHVRYSTTG
ASHPI NAQPLVFRYAGMI GLAHNGNLNI TELCSQLSSTGSVFQSSTDS
EVI VNLI ARYSQSRLVDAI MKCMI DI KGAYSLLI LTEKSLI GVRDPFGI R
PLCLGRRGDAHVLAESCALDTVGAELVRDVEPGEI I I I DEGGI TSRKVL
QARRKAHC I YEYI YFARPD SRMDGFNVSKVRREMGRQLAREYPVEADLVI
PVPDSGTAAARGFAEESGI PFEEGLMKNRYVGRFTI QPSQSMRDLGVRLK
LNPI RDVLEGRVVMVDDSI VRGTTSGKI VNMLRECGAMEVHFCLSSPPI
KKSCYYGI DTSNEEELI ASYKTPEEI REFI GADGLHYLTLEGLLGVFGER
REDFCTACFSGDYPVEVPVTREGGKYVLE

>2617919968 Ga0073689_10423 phosphoribosylformylglycinamide cycloligase
[pelotomaculum Ga0073689 : Ga0073689_104]

MESSGKGLTYAGAGVNI EAGNEAVRLMRGAVRSTYRPEVLADI GGFGGFF
ALDTTRYREPLVVSAGDVGTKLRVAMLTGRHDTVGI DVVAMCVNDI LAQ
GAELPFFLDYLAVGRLAPEKVSI VGGVAEGCRRAGCALI GGETAEMPFG
YGPGEYDI AGFAVGVERDRI I DGRDI VPGDKLI GLPSSGLHSNGYSLAR
KALLEVTGYGVDTYLDRLGRAVGEEMLEPTRI YVKTVLPLLERFTVKGLA

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HI TGGGLTENVPRVLPEGAGVEI RLGAWPVPPVFGLI AEI GGVAEAEMLR
TFNMGI GLVAVVPAAGAGAVMDHLAAVGEKSYLI GEVAGERKVKYI

>2617919967 Ga0073689_10422 phosphori bosyl glyci nami de formyl transferase-1
[pel otomacul um Ga0073689 : Ga0073689_104]

MSKLRLGLVLASGRGSNLQSI MDAAGAGKI NAGVAVVI SDNKDAFALKRAC
RAGVPAEFVNPNGFASKEEYERAVVALLKERSVDLVCLAGYMRLVGGVML
EAFPYRI MNI HPALLPSFPGLHGQEQARAYGVKFSGCTVHFVDEGMDTGP
I I LQAVVPVLDLDDTADTLAARI LEQEHRI YPEAVRLFAGRLRVNGRRVS
VI

>2617919966 Ga0073689_10421 phosphori bosyl ami noi mi dazol ecarboxami de
formyl transferase / IMP cycl ohydrol ase [pel otomacul um Ga0073689 : Ga0073689_104]

MPVKRALI SVSNKAGVVDFAAGLVELGAEI VSTGGTAKTLREAGAPVTYI
SEVTGFPEI LDGRVKTLPKVVHGGI LAPRNEDHLGQLANLGI I PI DLVAV
NLYPFRETVAKPGVTLEEAI ENI DI GGPSMVRSAAKNYGNVLVVNPERY
GEVLDALRRGEDGGELRLSLAREFAHTAAYDAAI TAYLEGLGDDSDAGLF
PPTWNI SVRRQAI LRYGENPHQAAFYTDPAVTGPCVGNVQLAGKALSY
NNI LDLNAAFELVREFNEPAAVI VKHNNPCGCALAAGLADAYRKAFEDP
VSAFGGI VAFNRVDAATAEEMTRI FLEAVI APGYEGNALEI LESKPGLR
LLQTGPLTGQTSRLEVRKVNGGLLVQEFDREALRPLDKI VTKRQPTKE
EMDELI FTMTVVYKFSNAI VVTRERRLI GVGAGQMNVRVGSARI AFQAG
EKARGAALGSDAFFPFDLHEAARAGI TAI I QPGGSVRDEESI KADEY
GI TMVFTGMRHFKH

>2617919965 Ga0073689_10420 phosphori bosyl ami ne--glyci ne l i gase [pel otomacul um
Ga0073689 : Ga0073689_104]

MKVLVVGGGGREHALVWKLKQSLRVREI YCAPGNAGI ARDAACVNI GAED
I PGLLAFARGKGI DLTVVGPPEAPLNAGI VDRFNEAGLRI FGPSRAAAEI E
GSKVVAKEI MAKYGI PTAGYAI FTDPGEAAAYI KEKGVPCVVKADGLAAG
KGI VAADELTALDAVRSI MVDROFGEAGARLVVEECLVGEEVSVLAFTD
GVNVAPMI SSQDHRKRVFNDRGPNNTGGMGAYVPVPLYTGETRRRTEAEI L
LPI VRALRSEGRSYRGI YAGLMLTGEGPKALEFNARFGDPEAQPMLSLL
ETDLVEVI EAI LEERLDRI EI KWKDGAACVVLASGGYPGSYQKGKAI RG
LDRVPAGVVVFHAGTAEKDGEI VTAGGRVLGVTATGPDI PSAI NLAYTAV
ERI SFDGMHYRDI GRRALERRDADS

>2617919964 Ga0073689_10419 Trp operon repressor fami ly [pel otomacul um Ga0073689
: Ga0073689_104]

MYP SRLKDHL DRLFEAI LELKDLDECYRFFEDLCTVAELKSLAQRLEVA
RMLQGSWTYGEI AARTGASTATI SRVKRSLNYGADGYKLI LARLNGQSSG
EAGEAARPLE

>2617919963 Ga0073689_10418 signal transducti on histidi ne ki nase regul ati ng
citrate/malate metabolism [pel otomacul um Ga0073689 : Ga0073689_104]

MSKRTGLNKKAFI LI NI I VAQAFVVLFMGI HTYVWI RGDHFLMPPLLPVE
SGLAI FTTAGLLFTVAALALVHEVERMATEEVRTRERLAGLEKAEDMVRV
LRSHRHDFLNHLSVI SGFI QLGKYEAEVGYI KEVTGDLKVSGQVNL SKP
GLAALI LTKMND AETLGVLQVEVETKLAGI NASSTELVSL LGNLVDNAL
YAVKDLAEGDRRVRMTVKNGEFYCLVVANRGPHI TEKL RKEI FKPGFTT
KGSESGYGLYI VKNI VQKNGGRI ELASEAGGETI FTVYLP RRAAAQ

>2617919962 Ga0073689_10417 hypotheti cal protei n [pel otomacul um Ga0073689 :
Ga0073689_104]

MCELSI RFLFLSEI PLTI AFTLLAFARLEFRMVPVLLI GTVEALLEFF
VRKYPFPGFNVVTNVP LLVASLAVMLYI YWRGDI FRLVTASFLACAI LLL
LELI TTFVALRLWPYLENAGQNDLLFALGSYPCTTVTLGLAFYI NSRNR
RL

>2617919961 Ga0073689_10416 hi sti di nol dehydrogenase [pel otomacul um Ga0073689 :
Ga0073689_104]

LFFAGVLI I MSLLRMVEAGDPALEKLLQRDVPGRTEVAAKVAEVLAAVRK
GGDAAVCRYTTRFGGPRFSPEKLRVTHEEVEAAYGQVEESFLDDLRLALR
NI TAFHEKQLVRSWFEPGEGGAI LGQLVRPLRRVGVYVPGGKASYPSSVL
MNAVPAKVAGREVAMATPPAADGSVNPHTLVAAA EAGVDEI YKMGGAQA
VAALAFGTASI PRVDKI TGP GNI YVTLAKQQVYGQVDI DMLAGPSEVLVV
ADETADPVFVAADLLSQAHEDEMASPVLLTPCRELARRVREEAVEQLSRL
PRGEI MKSALAGYGA VVI TRDLEDAFELANRFAPHELELMVAEPFRWLSW
VENAGAVFLGSHSPEPVGDYLAGPNHI LPTGGTARFYSPLGVDSFLKKI S

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LI AYTGAALAGVGEAI VRLAEVEGLTAHANAVRVRLKSYDDKRGKGACP

>2617919960 Ga0073689_10415 histidinol-phosphate aminotransferase [pelotomaculum Ga0073689 : Ga0073689_104]

MTI KEGKGLVHRMNTVFDI VSLAREDLKTLVPYDAPFYPDVI KLDANENP
YGFPPGLLEKVVQEAGRSNFGRYPDAAAERLREGLAAHTGLKPENI MVGN
GADELI LNI MLTFGAGAKFAVAVPTFSMYGVHGRI AFCEKI EAPRRDDFA
VDI PAMKQAAARPEVKVVF I CTPNNPTGNATPPEEI KDLLDSTDALVVVD
EAYGEFGGRSCI PLLERHPNLVI LRTFSKAFCLAGLRVGYLLASRPVI RE
LWKVKQPYNLNAFSQAAARVVLENPAPFRERI AKI LEGRDWLFNGLAALP
GVDVFPTDANFI LFRTPPLPAEKLYKGLLERGVLI RNMDPALPRCLRVSV
GTPEENGI FLEKLAGVLRG

>2617919959 Ga0073689_10414 imidazole glycerol-phosphate dehydratase [pelotomaculum Ga0073689 : Ga0073689_104]

LDGTRQGI I SRKTKETI NVTLDLGAGVFWI NTGLPFFDHMLQLFAKHS
SFDLELTARGDLAVDGHHTVEDAGI CLGRAFREALGEKHGI NRGHAFVP
MDEALTLVAVDLSGRGFLAFEAPMPSPRVGDFETELVEEFLRALALNGEF
NLHI RLLAGKNTHHVI ESI FKALACSLKEAVALSGGVGI PSTKGTI

>2617919958 Ga0073689_10413 glutamine amidotransferase [pelotomaculum Ga0073689 : Ga0073689_104]

MI AI I DYGMGNLRSVQKGFVKVRVAAAVVKEPHMLDRAAGVVLPGVGAFA
DAMANLRAAGMDGAVHRAVEAGKPLGI CLGLQLLFDASEEWGHTGLGI
FPGKVRRLPEGLKVPHMGWNQI EI LKKDPLLERVPDRSSFYFVHSYAVEP
AEEGLALALTEYGVKFTSMVGRERVYGI QFHPEKSSSLGLKI LENFGRVV
ERC

>2617919957 Ga0073689_10412

1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]
imidazole-4-carboxamide isomerase [pelotomaculum Ga0073689 : Ga0073689_104]

MLI I PAI DLREGKCVRLVEGRDLRETVDNPVAMAALWQEQGARMHLHV
DLGAFSGAPKNLEVI REI LAGVDI PVQVGGGI RSLEVVERLLELGVARV
I LGTVAI LKPTVSEACARYGEAVLVGI DGRNGRVAI EGWGLTVDKGTVE
LAREMKELGVRVFTDI RRDGTLRGPNI EAI GELARETGLKVVASGGVS
TADDLRALKLEPLGVDSVI MGKALYAGTVTLSETLAI AAGEV

>2617919956 Ga0073689_10411 cyclase [pelotomaculum Ga0073689 : Ga0073689_104]

MLLKRI I PCLDVTGGRVVKGTNFVNLRDAGDPVELAAFYDREGADELVFL
DI TASHGRKTTLDVMYRTAGEVFI PYTVGGGI STLEDI RAI LSAGADKV
SI NTAAVKNPSLVAEAGRFGSQCVVVAI DARRRGEKPDAAVEVYI HGG
TPTGI DAVEWAQRVESLGAGEI LLTSMDRDGTGDGYDI PLI RAI AGAVNI
PVI ASGGVGNLEHI LEGLTAGEADAALAASI FHFGEYSI RETKEYLRAGG
VPVRI

>2617919955 Ga0073689_10410 phosphoribosyl-AMP cyclohydrolase [pelotomaculum Ga0073689 : Ga0073689_104]

MVFDLGSLNYNEAGLI PAI VQDAGSGAVLMMAYMNREALAKTLATGETWF
WSRSRQAFWHKGETSGNVQVRKEVLYDCDRDTLLVKVEQGAACHEGYYS
CFHYRVERDGGVTAVGERQFDPDEVYGKK

>2617919954 Ga0073689_1049 phosphoribosyl-ATP pyrophosphatase [pelotomaculum Ga0073689 : Ga0073689_104]

LGEKDI I RELYEVI LDRRERRPQGSYAAHLFQRGEDKI LKKI GEEAAEVI
IAAKNGGPPALVSEAADLVYHLLALLARHGLTPDDVLAELAAARREKKG

>2617919953 Ga0073689_1048 AAA domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_104]

MYTVDELVTKTFLHGWFTQWPFPI AQPDNAFEDNRI EGALNSLQQLLV
TREVGVVVGAEAGSGKSTLLDI FLNKVSNTRYRVI HI PI PQTRPRELYRSI
AAALGVNTSWFRADALKVVDLLTYSYLESNRPNLLLI DEAH I LTPACLNE
LRLLTNATGKNEAVTVLLGQPALSTTLKLPVLI PLA

>2617919952 Ga0073689_1047 small conductance mechanosensitive channel [pelotomaculum Ga0073689 : Ga0073689_104]

VGVI TI LAKQMETVLAVGKWLTPENI QTFLSDLVLSGLVLAVTYI LI KI
LSRLLDRVLREKEPDGKEQI GSPADQGM I SSGFI RSLRVLLQTLLLYGGY
FI AAVI I LETFDFKI I SPDDLKSLGAKALKI I GVLGAKLATNFGHLVVK
QVFAKQELQDHPTASRAQTLEVLLRSALTYI I FVAGI MI LQI FNVNTS

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AI LASAGI LGLAVGFGAQNVLKVDVI SGFFI LFEDQFGVDYVETAGVVGA
VEEI GLRTCKI ROWTGQLSVI PNGEI TRVTNYNRGQMLAVVTVGI AYEED
I DQAVAVLKQECDTAYREI DAVLDTQPQVGVTTELADSSVNI RTVAPTLP
EHWAVERELRRRFKYALDRAGI EI PYPRRVLYQRDEASLEEKAAEFHFSG
EGSGTAEG

>2617919951 Ga0073689_1046 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_104]
MDVGDGI SGETGYAGFTRNPI FHFSRPTSQTGFTPKI GSPALPFREDSAL
TEQSFVHRLS

>2617919950 Ga0073689_1044 lysine 2, 3-aminomutase [pelotomaculum Ga0073689 :
Ga0073689_104]
MNAKILSI KARDSEDWSDWRWQMQRHRTVEELAGYVNLTDDEEKLNI QKA
CDVFPMAI TPYYASLI RGGDPGCPVRKQCVPVSHRELI RGCGMDDDPLHED
ADSPVPGLTHRYPDRLVLLVTNECSMYCRHCTRKRKVGDDGRPVTSRDVD
RGI EYI KSRPEI RDVLLSGGDPFI LPTLHLERI I RKVREI DHVQVI RVGT
RTPVVMQRI TDQLVKMLKKYHPVWVNTNHNPREFTADSVRALAKLADA
GI PLGNQTVLLRGI NDCHVI I KKLVLHLLVKNRVRPYLYQCDSLRSRGI EHF
RTPVAKGI EI MEALI GHTSGFAVPTYVVDAPGGGGKI PVLPNYQLSATRT
KMVLRNYEGVI CVYEEDPADQEGGCPACKI CEGSGLKNPVGQLKLLDPD
NGI VSLVPEGNRRRKARHAARKGDARGC

>2617919949 Ga0073689_1043 putative beta-lysine N-acetyl transferase
[pelotomaculum Ga0073689 : Ga0073689_104]
MRHEKVMRVAEIKNFYRARPDRREVVEGCDFSCRVLVSPYNRRITICEF
DLARDDGAGEMVRTLAERAI AEGLDKI WLKTGSKWRRALAGAGMRLEATI
PGYYRGEERALVYAMYSARRQTPSNPAGMDLVKKLVDPAGAGGGERDLP
AGITLQWGGAEHCLELAGLYGGVYATYFPVFDPGYVRYTMEHDVCYLTA
WHGGELVAAAASAEI NRREKNAEMTDFATLSEWRGRGLAGCLLARLESRLA
GEGFRCLYTI ARSGSVGMNKVFAGAGYAFHGVLVNNCNI GGGFEDMNVWV
KLINPAAAV

>2617919948 Ga0073689_1042 extracellular solute-binding protein, family 3
[pelotomaculum Ga0073689 : Ga0073689_104]
LTMVMAALALFAAGCAGSPDKGGAPGEKKDFSWSCSGQYRPFNYDENNN
LTGFDVEI GKALSEKMGMEPKPVTAPWDSLINGLOAKRYDAI LGSMTIR

>2617919947 Ga0073689_1041 Predicted transposase YbfD/YdcC associated with H
repeats [pelotomaculum Ga0073689 : Ga0073689_104]
SSDWQASYGHPVLVVFVNHNRFKGTCYRAAGWVQLGKTSYGRKAGIY
YYHGETKTVFLKPLHKDARVLLSAPFLPPEFAGGKKAMVDLNVASI ETRG
GLIDCLAKVSDPRKKRGI RHTNLSI LAVAVCAI LSGELTFAAI GEWAANL
TQDLLEFECRRRPDTGKYI PPSEPTIRRI LQKVNAEEVDRAVGKWEIQ
ANDGAVAVDGVLRGSKGTGDKRVYLVSAFLHNVI TVGQTQVDKKSNEI
TAFQPLLKPLNLEGI VTADAI HTQVKNATFVVEKKAGDKRLLGLIRGH
LSI ENSSHYYRVDVAFGEDRSQI KTGSAPRVFATMRNLAI AILLNGVKNI
AKELRNLI RKSGQAAELIGI

>2617919946 Ga0073689_103148 phosphoglucosamine mutase [pelotomaculum Ga0073689
: Ga0073689_103]
MGVMFGTDGVRGVANRELSPMAFKLGRAGAHLAGGGLNTRVVI GKDTR
ISGDMLEAALVAGI CSAGVDVLKVGVMPTPAI AFLTRELKAAAGVVI SAS
HNPVEDNGI KFFGPSGYKLSDEVEAEI EALFMDDCANVPYPVGAVGRAY
RMHDAADRYVKFACGAI ATNLKGLKI VVDCANGAAYHVAPRI YQELGAEV
TPI FHRPDGVNI NECGSTHPEALMKAVVSHGADLGLAHDGDADRVLA
VAGGGLVDGDI MVACARHLKSKGLLAKDTVVVTVMNMGLHLALRDCGIR
VVETRVGDYVLEELLRAGARFGGEQSGHI ILLDHNTTGDGI LTALQILA
VMKESG

>2617919945 Ga0073689_103147 YbbR domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_103]
VARLDWRKNSIKLLSLLAFVLWVYVSNEQNPVREKILNVNLENKGLAQN
YIITGGIPESVRVRVQGNRNQLANLVPADFRAVVNI PEGKTGDI ALPVQV
TSPPGLRVAQVSPEEIRITVDRLVDRQVAVAVSLRGTPAPGYTALAPASQ
PDVVI VRGPSRVVNEINQATVAVDI QSAVKDVEQTPVNVGQHNVSLSPS
SVRVVPI VSETVTKTVPLPQLTGSPADGFTVKRSYAEPATVQLSGLAD
VLGAI TNIKTEPVDI RGVDKNLSRDAGLAPPQGVTVQPNRVI VRVEIEK
EEAPPRPLPESEPSRQRP

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>2617919944 Ga0073689_103146 diadenylate cyclase [pelotomaculum Ga0073689 : Ga0073689_103]

VEQFWLPNLDYLKAVLKFNLSV DI LI VAFVSYRLMLLI KGTRAVQLI K
GLAVLLI ATALSSLFNLYTLNWLRLROAMTALVVALPVVFQPELRRALEKL
GRGKFLTHHTYAPGEFDRGKVI AEI VRAATVLSKNKTGALI VLERETGLE
EHI DTGVKI EGLVSAEFLVNI FI PRTPLDHGA VI I QGDRVAAAACFLPLS
ENPYLTSDLGSRHRAGI GI TEHSDAVAVI VSEETGAVSVAVEGAI DRYLD
EAGLQERLARLLDSRANNSLSSFWPRR

>2617919943 Ga0073689_103145 trk system potassium uptake protein TrkA [pelotomaculum Ga0073689 : Ga0073689_103]

MKQFAVI GLRGFTSVAMTLSKMGFDVLA VDSNEERVNNI MEHVTHAVQV
DAMDEQALKALGI RNFDVVI VAI GQDI QSN I LATVI LKEMGVRKVVAKAI
TGLHGKVLERI GADKVVFPERDMGVRVAHALVSKNI MDQI NI SPDYSI I E
LMAPRI FTGKLTLEVS NVRSKYGVTVLAI RRGNEVI I SPGAGQVVEEGDVL
VVVGRDDRI RNLEDEE

>2617919942 Ga0073689_103144 trk system potassium uptake protein TrkH [pelotomaculum Ga0073689 : Ga0073689_103]

LEKNPVAGFRLTAVSTGWVKYWRPSPQI LVTGFAAVI LVGAVLLTLPFS
LQPGKTPDFLTSLFTATSACVVTGLVVVD TGTHWSTAGQVI I LLLI QVGG
LGFMSMATFFSI LMGRRI NLRERLLI KEALNQLNI EGI VRLAKYVFVTF
GTELI FALI LGLRWSADMGFRGMWYGLFHSVS AFNNAGFDI FGGFKSLT
EYKEDVVVI MSI TTLI I LGGI GFSVI ADI YRSRKGLKRLSLHSLVLT I T
TI LLAAGAI LI LLEWSNTLAELNPAGKLLASYFQSVTPRTAGYNTLDI A
ALHGSTQFLLI VLMI GASPGSTGGGI KTSTFGALSLAVLSQVAGKDDAE
VFGRR I PKWQI YKSLAI AFMALALVMFMAFLLEI TENASFLKVLFFETVSA
FGTVGLTMGLTPELTSAGRI LI I LTMFAGRLGPLTVALAMAKRRKR A VFR
FPEENI I VG

>2617919941 rplT large subunit ribosomal protein L20 [pelotomaculum Ga0073689 : Ga0073689_103]

MPRAKSSVSRKRHKKI LKLAKGYRGAKSKLYRI ANQQVMKSLVYAYRDR
RVRKRDRFKLWI ARI NAAARMNGI SYSRLI NGLKLAGVHI NRKMLADMAI
NDSQAFGRLEVMAKDKL

>2617919940 Ga0073689_103142 large subunit ribosomal protein L35 [pelotomaculum Ga0073689 : Ga0073689_103]

LPKI KTHRGA AKRFKKTAGGKLKGS HAFHSI LGKKS AKRKRNL RKATI L
SPADADRLKRLLP

>2617919939 Ga0073689_103141 translation initiation factor IF-3 [pelotomaculum Ga0073689 : Ga0073689_103]

VVDGDGAQLGI MPTRDALRLAE EKQMDLVEI APTARPPVCKI MDYGKYKY
EQSKRDKEARKRQKI VEI KEVKLRPNI EDHDFEVKAKNVI RFLKDGDQVK
ATI I FRGREI VHTQLGHQLLKKLA EHV KDFSTVEKQPKLEGKNMI MFLAP
KQDRQEN

>2617919937 Ga0073689_103139 K(+)-stimulated pyrophosphate-energized sodium pump [pelotomaculum Ga0073689 : Ga0073689_103]

VOESMTLAMYGAAAGAI ALLFALATMASI MKESMGTPKMKEI SEAVQEGA
MAYLNKQYKTLI PFTI VVAI LLVLVLPQLDSRVQGVPLMVSVLVGAVCSA
I AGYI GMNSTTKSNARTAEARSFGLGKALNVSFRAGAVMGLSVAGLGLL
GVSVLFLI YKDAVVI NSF AFGASAI AFFARVGGGI YTKAADVGADLVGKV
EAGI PEDDPRNPATI ADNVGDNVGD TAGMGADLFESYAATTI AAMI I GNT
I FGPKGALFPLVVGAI GI I ASI I GTFFVRTGEGGNPQAALNVGLWSTNVL
TAVGVYFLANWTFGNEGLGI FLAVASGLI VNVAI GALTEY TANNKPPCL
RI AEASKTGPATNVI HGLSVGMESVFFPMLFFAGAI YFAFWVASWVEPGH
AI YGI AMAAMGMLSTAGI VVAMDSFGPVADNAGGI AEMAELPPEVRQKTD
KLDAVGNTTAAI AKGFAI GSAALTALALFQAFAD EAVARNPKLTHI LQGGH
LVI NLNDPNVLVGLLI GASI PFVVGASTMRVGEAAYGMVNEVRROFREI
PGI MEGKAKPDYARCVSI ATGSAI SKMI FPGLVAVVGPI VI GFGLGALS
AGYLAGLTATGVLMAFLANAGGSWDNAKKWI EAGNLGGKKI DGNPNPI H
QAAVI GDTVGDPC KDTSGPAMNPLI KVAGTI SLI I GSVLFH

>2617919936 Ga0073689_103138 preprotein translocase subunit SecE [pelotomaculum Ga0073689 : Ga0073689_103]

VLKI I VTALHVLLSI ALI AAVI LQSGKSAGLSGAI TGAETI FGKKKGLD

ELLGKVTI GVAVFYAATALVLVI WK

>2617919935 Ga0073689_103137 enolase [pelotomaculum Ga0073689 : Ga0073689_103]
 LSTII DEI LAREI LDSRGNPTI EVEI YLEDGTMGRAAI PSGASTGAFAV
 ELRDGDQNRYYGKGV LKAVENVNSVI APEI MGYDATDQLGVDRAM I ELDG
 TPNKGKLGANAI LGVSMARAAAE SLGLPLYQYLGGANAKVLPAPMMNI
 LGGKHADNNVDI QEFMI MPVGAPSFTEALRMGVEVYHQLKGVMMKKGLS
 TAVGDEGGFAPTLGSNEEALAVI VEAVTAAGYKPGEDI FLAI DAAATEFY
 KGRYVFEAEKSRTAGEMVEYYAMLADKYPI I SI EDGLAEEDWEGWAKL
 TARLGKRI QI VGDDLFTNTERTLARGI KNGVANSI LI KLNQI GTI TETLD
 AI EMARQAGYTAVVSHRSGETEDATI ADLVVATNAGQI KTGAPCRTDRVA
 KYNQLLRI EGELGDLAVYKKGGSFYNLKF

>2617919934 Ga0073689_103136 phosphoglycerate mutase [pelotomaculum Ga0073689 : Ga0073689_103]
 LASDKKPLVLVLDGWGLNPRVKGNAI ARANI PNYKSFLAEYPHCSLVCA
 GEDVGLPEGQMGNSEVGH LNI GAGR VVYQELTRI NRDI RDGSFFRNEVLL
 EAVEHTQKNKALHLMGLLSDGGVHSI NHLFALLDLAARENMRNVFVHA
 FLDGRDVPANAK EYLQPLSRKLAELGFGVVATVMGRYYAMDRDRRWERT
 ERAYNAMAFTEGI PAGNSMEAVDLGYGRNETDEFI QPTVLSDGAGAPVTR
 VSGGDAVI FFNFRPDRARQI TRAFVDRDFTGFTRRPNHPAVHFTCMTLYD
 KTI EAPVAFQOTLHNTLGEVLSKNGI KQLRLAETEKYAHVTFFFNGGVE
 EPSPGEERI LI PSRVATYDQKPEMSANEVTEKFLEQLQAGKYGI I MNY
 ANPDMVGHTGDMAATVKAVETVDACLGRLVRAVLAKDGT VLI TADHGNAD
 MMQDEEGHVQTAHTTNPAPFI MI RRDAAGVTLRDGRLEDI APTI LQLLGI
 PKPEEMTGETLI KGI VSN

>2617919933 Ga0073689_103135 triosephosphate isomerase [pelotomaculum Ga0073689 : Ga0073689_103]
 MYKTVPEAEAFALQLKGAVAGLDGAEVAVCPSTALAAVARVLRDTGI AL
 GAQDVYWEDQGAFTGEI SPVMLKDAGCRYVI I GHSERRQFFGETDDKVN R
 KVKAVLAYGLTPI MCVGETLAERDAGVTERVVRTQT VAGLADI GSEQAAG
 LVI AYEPIVWAI GTGKTASEEDAQQMI GF I RSLVKELYGAGVAGGVRI QYG
 GSVKPGNAAGLMARPD I DGALVGGASLDVESFTGI I RAVVGR

>2617919932 Ga0073689_103134 phosphoglycerate kinase [pelotomaculum Ga0073689 : Ga0073689_103]
 MAKKTVRDI EVAGKRALVRVDFNVPLDKSGDVTDDTRI KAALPTI NYLI E
 QKANVI LVSHLGRPGKGVDERYKMDPVARRLSELLGRMVVKI DDCVGD I P
 REAVEKMQPGDVI LLENVRFYPEEEKNDEKFARRLAELADI FVNDAFGTA
 HRAHASTEGVAEFLPAVAGFLMEKEL AALGKLLAEPEHPFVAI I GGAKVS
 DK I AVI SNLLGKVDTL I GGGMANTFLKAQGYDVGKSLLEVDKVDLAKGL
 MNEARGRGVNL LLLPVDVVVAPGASLDAEQKVPVDQI PAEWMALDI GPDS
 I GRFTEALKTAKTVVWNGPMGVFEMAFARGTGAVARALAEI DATTVI GG
 GDSVAAVKKAGVADKVTHI STGGGASLEFLEGKQLPGVVALQDK

>2617919931 Ga0073689_103133 glyceraldehyde 3-phosphate dehydrogenase [pelotomaculum Ga0073689 : Ga0073689_103]
 MGWKI GI NGLGRI GRDVLRGALKRSDLEVAVNHKSRI PANENYAYSVA
 HMLKYDSI HGTYDLDRSGDNTI LVNGHEI KLLAEGDPALLPWGELGVDI
 VVESTGKFNNPAEAAH LQAGARKVVL TAPAKGGECLTVVMGVNQDKYDP
 AAHHVVS NASCTTNCLAPVVKVI NEKFGI VKGLMTTI HAYTNDQQLDMP
 HRDMRRARAATLSI I PTTTGAAKAVALVLP ELKGKLN GFAMRVPTPNVSV
 VDLVVELVKPATREEI NEAFKEAARGPLKGI LDYCELP L VSI DFNGNPHS
 ATVDAPSTMVI DGSMKVVAWYDNEWGYSQRVLDLVAYMASKGL

>2617919930 Ga0073689_103132 RNA polymerase, sigma 54 subunit, RpoN/Si gL [pelotomaculum Ga0073689 : Ga0073689_103]
 MRMGYGLNVVQTQNL I MTPELRQAI TI LQLSSLDLSTYI EQQLQENPLLE
 LREEGNESEGGAAAEKGPVDTGEEKPDYDL DWEEYFQDGS DLGTARRGKQ
 EVRQEYSYENFLSQSATLSEHLLLQNLSTCRGRDRAI GEYLI GNI DENG
 YLQMSLQEVAFRLKADPSEVAGVLTMI QGFDPPGVGARDLVECLSI QVKQ
 LGI KNEI LNKLI NNYLMDLAKGKLNRI AHN LGVPVQEVQEAADI LKTLDP
 KPGRNFTSLNETRYI VPDVVLEKVEGEYI I LVNDVNI PRI TI NSTYRSVL
 SKDKNYDSGTRRFVESKLNAAWLI RSI EQRRLTLYRVTNCLVELQRDFL
 DYGVKYLKPLNLKVAEMVGLHESTVSRATSNKYI QTPQGVFEMKYFFST
 GLNNDAGTATSTESI KKMLQEI VTGEDTRAPLNDQRI AELFRQGI KI SR
 RTVAKYRDELGI PPI RKRKRY

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>2617919929 Ga0073689_103131 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

VSFSAVTKNELARVI GQRPCCHLAELAALI RMDGSI QI CGGQVALNI I TE
NAAVARKI FSLVKKLFGLOTEVLVRRKTRLRKNNI YLVRVPSQRRTEGI L
ROLGLVDGAGLPEDAAPDNLVRRECCRRAYLRGI FLGGGSVNSPEGTYHL
EI I TENERFARFI GRMLKKFQLTAKVSRKKNWYVYLKESEKI I SFLNI I
GAHTALLNFENARI YKDVRNRVNRLVNCETANLNKTVNAAVROLENI I LI
RDAVGLARMPESLREAAELRLKHPDASLKELGDMMRPRLGKSGVNHRLRQ
I EEFAEGI RSKGLEKS

>2617919928 Ga0073689_103130 Heat shock protein. Metallo peptidase. MEROPS family M48B [pelotomaculum Ga0073689 : Ga0073689_103]

MNTLKVWLLMGVLSI LLVLMGNAVGGKSGAMLFFLI ALGMNFFAYFYSDK
I AI KMTGSYPVSQEEAPELYAI VGRLARQAGI PMPRLYI TPSPQPNFAT
GRGPTHAAVAVTEGI LHLLDRSELEGVLAHELAHI KNRDVLVGAI AAALA
GAI TMMANVFQWAAI FGMGRGEDDEGGGGLI GGLI MAFVAPI AATI I QLA
I SRSREYQADATGARI ARSPAGLANALLKLESGAHRI PMQVNPATSHLFI
VNPLSGASLARLFSTHPP I EERVERLRKMRV

>2617919927 Ga0073689_103129 DNA-binding transcriptional regulator, MerR family [pelotomaculum Ga0073689 : Ga0073689_103]

LVEQRKYKI GEI ARLAGVSRRTI DYYTNLGLLKPVRSSENYRYYSGETLV
RLKLI EGMKKKRLTLEEI GERLNLLEYGPVDGVEERRSGAVNI DFLLEQI
RQFENQLARLQPVAAPEANKGVLPTRQALVQSI ALLHSLMQYI SEMAPD
LTTLL

>2617919926 Ga0073689_103128 conserved hypothetical protein, cofD-related [pelotomaculum Ga0073689 : Ga0073689_103]

MI LLKWLYPGMRVKRWLWALAGLLLAALGVDLI MEGGLLGDFARSI HRL
EEKI LGKTYLRAVGFI I VPAGLSVI AAGLLKVHFSI AGALAPEQEGRAAE
I I YARYSLRRGPKI VVI GGGTGLSVLLRGLKEYTSNLTAI VTVADDGGSS
GRLRGDLGI LPPGDI RNCLVALADKEPLMEELLQYRFSTGELAGHSMGNL
LLAALTELSGGFDRAVRSMKVLAVRGQVLPATLTDVTLCAEMADGTVVQ
GESNI SRGAGGI KKVFLRPSRCLPLPEALAAI KEADAVVLGPGSLYTSI I
PNLLVRGI PEALTRTGAI KI YVCNVMTQPGETGGYTASDHLRAI I AHAGR
FLDYAVLNTGQVPRLQARYRQEGAEPVAADVA AVAKLGVRAVGEDLI HQ
TEVVRHHPDKLAQAVLHLVFSARREYERVFLNGRRKDGEEDCFPGAKTH
RP

>2617919925 Ga0073689_103127 UPF0042 nucleotide-binding protein [pelotomaculum Ga0073689 : Ga0073689_103]

MVTPKLVI VTGLSGAGKTQALRSLEDLGFFCVDNLPPALI PKFAELCAQA
ASKI NKI ALVVDI RGGEFFNTLFEVLSDLNNGRI HYEI LFLEASDETLVR
RFKESRRRHPLSSHGEVLVDI REERSLLQELRGMANKI I DTSNI GVQQLK
EEI AAVFVGNAGTARLHI TVI SFGFKYGI PLDSDLVI DVRFLPNPHYQTA
LKALTGNDPAVRDFVFGSAVTGEFMEKFSGFVEFLI PQYI KEGKTTLMI A
I GCTGGMHRSVLANRLGEI LSEKDFRVTVRHRDI NRG

>2617919924 Ga0073689_103126 putative hydrolase [pelotomaculum Ga0073689 : Ga0073689_103]

MMELFADYHTHTTYS DGRGAPAENI KAALGRGLKEVAI TDHGPKSI GTGV
AGPETFLAI KEEVAGLAPRFPEI KVLVGVEAAVVGDRDLDPKEI I GQL
DLLI AGHHPYI PENLGDALHYTLPNLMARLRRSAREKMRNTNTKALLET
VRKYPVDI I SHPDLMPVPEDELARACACKETALEVNTGHHYNKEDI VRA
AARRGARLAI NSDAHYPESVGD LASGAALVERLGFAEMVI NAVH

>2617919923 Ga0073689_103125 bifunctional phosphoglucose/phosphomannose isomerase (EC 5.3.1.8; EC 5.3.1.9) [pelotomaculum Ga0073689 : Ga0073689_103]

MENFDLNCAEGLCRI DSTGMLTALEGLPAQCAEACWDLTRHVELPKI EAI
SNI VVTGLGGS AI GGDLLRVYAADKVAVPI VVNRDYELPGFVGPDTLVFA
VSYSNGTEETLSAYGEARARGASI VVI TTGGKLGEMAQRDGPVI GVPCG
I APRAATGFLFI PSLRVLQRLGLLPDNVDEI TEMI DFI RDKRKKLGPEAP
EEDNPAKQI ARKLYNRI PVI WGSAGTTEVVAQRWKGQI NENAKAPAYWNI
LPELNHNEI VGFQFPLELLKKI HVI I LRDERDHPRVHKRVEI TKDVI KDV
VDGYTEVWASNGI LSRLFSLI YTGDFTSVYLAALYGI DPGPVKVI DYLK
RELQNDGAVCGLPHPHNL

>2617919922 Ga0073689_103124 glycogen debranching enzyme, putative [pelotomaculum Ga0073689 : Ga0073689_103]

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MYFFGKSDWRTFERGI EKEWLVNNGI GGYASSTI I NANTRKYHGLLVAAH
NPPGWRVLQLVKLDERFVAGOCAYNLAANETRSGYTEFGFI HLQQVRI SP
I PTFTYSFGDI TLEKTVFMVHGRNTTVVLYRLFNGAEPGMLYLTPLVNSR
GYHFI TNRGEI EFTQOEI PGGVSI KGREEVPPLLLNCGQAVYKNGGYWYE
GMAYAI EREGENPYEDHYI PGHFEI ALAPGENKTI TVI ASTVEFNDYDG
EKFLEEEI TRNKKLVERAGYRDHLAARLVRAADAFI VQRRSTGKKTVI AG
YPWFTDWGRDTMI SLPGLTLVTGRHQEAGEI LI TYARQCKKGLLPNSFRI
GAREAI FNTVDASLWFVYAVYKYLVTADLDFVRDEVYPVKEI I HWYME
GTDfNI GMDedGLLSAGSPDVQLTWMDAKVDDWVVTPRHGKAVEI NALWH
NAVRVLEGLAGLFGDKFPHDPDLPRI KESFLKKFWNGSYLVVDVI SPEGI D
CRVRPNQLLAVSLPYTMLGGEQGRLLVAQRVWRELYVTYGI RSLSPMDCEY
KGVYAGDRVRRDGAHYHQTAWSWLI GPFI TAYRRAHDYSPASLTQAWRFI
APFRDQLREHGVYI SEI FDGDEPAVPRGCI AQAWGVAEVLRAYVEDVLE
I RPPAENI MERGRA

>2617919921 Ga0073689_103123 glucokinase (EC 2.7.1.2) [pelotomaculum Ga0073689 : Ga0073689_103]
VSQFVI GVDLGGTKI YTALATEDGGVLVEI KLPTGAGKGLAHVVDRI VE
SVERVREAAVPPPEAVRVLALGAPGLDTARGI I HFAPNLGWKNVPI SRI
LEERLSLPVFLDNDANLALGEHAFGAGRGEENMVYI TVSTGI GGGLI LG
GKLYRGSSDGAGEVGHMTVPFPGPRCSCGNLGCLEAVASGTAI ARKAGEL
VAGGKGRGI LEAAGDPPRI TAAVVAAAASKGDPGAAAI I GEAARFLGI G
I ANI LNLNPSLVVLGGGVMDGGPVWENVHREVRTRALEAARI GARLAP
AALGGRAGVMGAI ALALGSET

>2617919920 Ga0073689_103122 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]
MSKFKLVAVDLDDTLSSRDFQLTGRVRETI AAVRAAGVHFTI STGRMYRS
AVPFAELEI NI PLI TYQALVKNSLSGDTLRDYLPLPHYAREI I ARI HQ
LGYHI NAYLDDRLLVERDTPGGRGYTAMAGVEAEVVGDFLEFLDRDPTKV
LVI SEEPDLLDRLEKEELTPI YAGKVHI VKSKPHYLEFCHPCATKGEALAYL
ARYFEVKREAI MAI GDSYNDEMLEFAGLGVSANAREEVKKRSGYVTAA
SNGDGVVEALEKFVLEGRSA

>2617919919 Ga0073689_103121 Helix-hairpin-helix domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_103]
MDTARRDDAADALTELARELELELPPIRMECYDI SNTQGSDSVASMVFE
EGRLANDQYRRFKI RTVEGPDDFASMREVLRRRFRTRVREERELLNTGQIS
SREAKFHHLPLDLVI I DGGKGQLSARQVMRELGFahi PAFGLAKEEELLF
SEDRPAPI ALPAGSKALHLVQRLRDEAHRFALAYHRNLRGKAGLKSFLDE
VEGI GQARRRALLKAFGSLSEI EKATPEQLATVPGMNKKTARAVYEFFHD
RRSG

>2617919918 Ga0073689_103120 Excinuclease ABC subunit C [pelotomaculum Ga0073689 : Ga0073689_103]
VRI DEKLKLLPDRPGVLYLDGGGKI I YVGKAVSLKNRVRYFQPGAQHP
PKTRVMLGKVADLDFI VTDSEVEALI LEQNLI KEHRPRYNVLLKDDKSYP
YLKVTLEEDFPRVMI TRRHVKDGSRYFGPYTRVGAVHETMRI LKKLFPFR
SCKQKEPPVRGRPCLNHHI QRCLGPCCGLVDREKYRSMI NEVCLFLEGRQ
KELI KRLAAGMEEAAEKLEFERAARLRDQLQAVREVVEKQKI VTGGFEDQ
DI VAMARAFDEACVMVFFCPGRQAHRPGETFYFKGDGSGSPGGGDDRLHQA
VLFGRGLYPGRNPPFGRNTGGKGGYRKVAFGQAGRPGDPENTQAGGEEEA
GGNGGQKRPPHPGTVPDGYGPPGRRGGCPDRTGPGA

>2617919917 Ga0073689_103119 excinuclease ABC subunit A [pelotomaculum Ga0073689 : Ga0073689_103]
MLDKI LVKGARAHNLKNI NVEI PRDKFVVI TGLSGSGKSSLAFTDI YAE
QRRYVESLSAYARQFLGMDKPDVDI I EGLSPAISI DQKTTSHNPRSTVG
TVTEI YDYLRLLFARVGRPHCPRCGRSI TRQAVEQMVDQLAALPEGVRLQ
I LAPVI RGKKGHVKVLEDI RKNGFARVRVDGEVLDSAEI KLDKNKKHT
I EVVVDRI I VRPGCARRLADSLETALKAGGGLAVAVPADGEEI TFSENFA
CVECGI SI SEI SPRLFSFNSPYGACPECTGLGI KKEI DPDLVI LDRRKS
ASGAI QGLSVGGYYYQFI EEMARQYGFSLDDSVKLAPEHLAVVLYGTGG
KRFHFVVESELYGRRHEMYTSFEGVNNLARRYKETASEHQREEI EQYMS
SRPCPACGGARLKPEALAVKVGGRSI TEVTRLSVLEARGFFHTLELTGRE
LLI ARQVLKEI NERLGLFLVNVGLDYI TLDRGAGTSLSGEAAQRI RLATQIG
SGLTGVLVI LDEPSI GLHQDNHRLRLTLERLRLDLGNTLI VVEHDGDTML
AADHI I DI GPGAGERGGQVVAAGTYKEI AENPSSVTGQYLSGKKTVPVPT
VRRRPNGKTVVELGAAGNNLKNINVSFPLGVFTCVTGVS GSGKSTLVNDI

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LYRKLAQELHGARTQPGPHREVRGLEHLDKVI DVNQSPI GRTPRSNPATY
TGVFNDI RDLFAQTPEARMRGYRAGRFSFNVKGGRCACQGDGI I KI EMH
FLPDVYVPCVCKGLRYNRETLEVRYKGRNI AEVLEMTVDRAVEFFQPI P
KI HRKCLKTQDVGLGYI RLGQPATTLSGGEAQRVKLATELSRRSNGKTFY
I LDEPTTGLHTADI DRLLKVLHRLVEAGDTV VVI EHNLDVI KTADHI I DL
GPEGGDRGGMVASGTPEEVAAAPGSYTGQFLRNVLKSPRAGAGLWEDT
EEDPLELAQGAN

>2617919916 Ga0073689_103118 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_103]
MRTTI EI STEMRAKLLALAARRGLRGQGHVKVI SRHNI YGLLSQASI Y

>2617919915 Ga0073689_103117 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_103]
LTDPCLRGYSEI VNEALNLYFEQAVKKDHDLEEI LSLAGSLSGTEAEEAV
KNTP

>2617919914 Ga0073689_103116 Excinuclease ABC subunit B [pelotomaculum Ga0073689
: Ga0073689_103]
MRSFQLKSEYTPRGDQPRAI AALAEGLEKGYRGQVLLGATGTGKTYTMAQ
VI QAVQRPTLV LAPNKT LAAQLCAEFKEFFPNNAVEYFVSYYDYYQPEAY
I PQTDYI EKDSAI NDEI DKL RHSATC ALFERRDVI I VASVSCI YGLGDP
EMYSALVLSLRKGESYDRDAALRKL VSI QYERNDI NFVRGKFRVRGDVLE
I FPASATEKAVRVDFFGDEVERLLEFDVLTGEI LGERSHVSVFPASHYAT
SRESMERAI VSI EAELVERLAVLRAQ GKLL EAQRLEQRTNYDI EMMREMG
FCNGI ENYSRHLTGRAPGQPPYTLLDYFPKDFI MFI DESHVAVPQVGGMY
EGDRSRKAALVEHGFRLP SAFDNRP LTFPEFVERVGQV VYSATPGPYEL
KNSVQVVEQI I RPTGLVDPEI TVRPTRGQI DDLMRI RLRVRRGERVLVT
TLTKKMAEDLT DYLREVG I KVRYLHSDI KTI ERMEI RDLRLGVFDVLVG
I NLLREGLDLPEVSLVAI LDADKEGYLRSESLI QTVGRVARNAEGRVI M
YADKI TDSMDRAI RETERRRKI QTAYNAAHGI TPETVRKAVREVI EATRA
AEPKAPYEAGAPGGGKRMTKAQLKKYI ATLEKEMKEAARRLD FEQAAQFR
DMI I ELRLELRGVKGAGPAVPDAEALG

>2617919913 Ga0073689_103115 monosaccharide ABC transporter substrate-binding
protein, CUT2 family [pelotomaculum Ga0073689 : Ga0073689_103]
LGGFSKSRGYLPLI I I VI I FI PLLYGCAKKGQPKPAGKGGGQEI KI AV
SLVDMERDGNKI I KNTI EGRTGOGDRGGGQDQGGEGGQGGQQAQGGGQR
VNI TWLDAKNDPARQAKDLEQLAGQNVRAVI LQVVDPSGPGLVKRLAQA
NI KVI ALDALPANSPLDGYI AFDHTRAGELQARYLLSAARERSVPLKV VV
FOGDRDDQASREVAASVLENLKNQSR AQVVL VKDHPRGDPQMAVATLDQV
LASTNNQI DAVVATDSRI TAAVAKVLKNRGLDQ RVI TLGVGADQQASRAL
EAGEHDAEVDI MPEMVAQYAFDAAVGLATTGHWQYEQLRNGDFDVPKAV
TPVRLLTRSEAYLLEQRWGKPAGREGQGGGQGGQPGGQKQGGGDDGGKEGE
GDQGGGGKKTTLRI TTQDGKTVEMQI NGEI KKI ETLEGAAGGQGGGGS

>2617919912 Ga0073689_103114 Protein of unknown function (DUF2508)
[pelotomaculum Ga0073689 : Ga0073689_103]
VKI I STLKTVALMEMSRLKDALNGPPAPT LAHTVENARRDWOQAI REMDQ
I DGELTEYVI FKVNAAE RRYMALLEQAKREGVTAWPPPAVFTVSEFCTG
NCAGEMENTPVCSS

>2617919911 Ga0073689_103113 DNA polymerase [pelotomaculum Ga0073689 :
Ga0073689_103]
LNNVI YSEDHNL SGVENLDDLKEMALGCTRCGLRAGCSGVVFGE GNPAAAG
LMLI GEGPGAEDRLGRPFVGKAGQLLDRI LAACGLERFTHTYI ANVVKC
RPPGNRAPRPEEAEOCLPWLHRQI ELVSPGLI VLLGSTALQNL I DPAARI
TQMRGRWL VSKSGI KI MPTYHPAALLRDGSKKKPVWEDFQKVRDEYLRI A
SI

>2617919910 Ga0073689_103112 Predicted RNA-binding protein [pelotomaculum
Ga0073689 : Ga0073689_103]
MCEANAYLRKQGEQDEL FLEMVDRVTPHEDGLLLEDI FGRRKI VKAKI I E
LALVDHKI I LEKE

>2617919909 Ga0073689_103111 PDZ domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_103]
LFPFVEVI PLI VKSFFLSFLDSQFLLLFLVVLALI AMQYSRMERI RAGFF
GMGTGRTRTDI LAATGFGLLGLAGSFLV VFI GLTI SGSGLAYLWPVAL L

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LMLI NMRFLCFAYAGGVLALAHFLDFPQI NVPQI MALVAVLHMVESFLI
LAGGHLGAVPAYVKPGGGRVI GGFTLQKFWPI PI MALVVMAGGMVEGGVE
MPGWWPLI NPGVPGDPRALDYI LLPVVAGLGYGDVAI ARSPAESRLSSL
HLGVYSLALLVMAVLAEQSRGMALAAALFSPLGHEAVI YAGRRI ELKGKL
LYVRPDRGVKVLDPGPAWRAGLRSGDVI LAVNGVDLAGRSDLNMRLO
NAFLPLAVDYSSRRVGVSSRRVTI RPPCPGESWGI VTVPEGNEDQYLELLT
TGPLGRWLRSFWRKFKS

>2617919908 Ga0073689_103110 carboxyl -terminal processing protease

[pelotomaculum Ga0073689 : Ga0073689_103]

LRYSFRARSGGGRWLTVLAVLMFAFFLVAGGLANNYKHFGNLLKVI SL
VRTQYLHPVDPTRLVDGAI KGMVNSLDDPYSVYLEPKTFSQLQEQI KGSF
GGLGI LVGI KEQRLMVVRAYKGTPAARQGI DGDVI TRI DDREAKGI DLE
TAVNLMRGPVGSKI VLTVERQGEPPGLQFTLI REEI NVPTVEGRVLPDTQ
I GYI AI SQFTERTAGEMRETARLQEGGLKGI LDLRDNPGGELNAAVNV
AKYFI PKGPI VHI DYRVGKDHTFYSDGRTI QLPLVVLVNGGSASASEI LA
GAVKDTGAGTLVGTKTFGKGI VQTVFPLDNGAGLKLTTARYLTPNKNDI H
EKGVEPDAPVQPLEERSRDVQLDRAVEI MNQKMAG

>2617919907 Ga0073689_103109 Septal ring factor EnvC, activator of murein hydrolases AmiA and AmiB [pelotomaculum Ga0073689 : Ga0073689_103]

LLSGSFGKKI LALGTALALLAGSFGVAYGDDLEQQLRETRDQLGQKKSEA
DOARGMI RDYSRQVSLNRSI SERTLOI RDI EANLARARENLRKAEDLK
DAEVKLDKSI GI LNKVRNMYEVGNVSYLEVLLAARDFSDFNRFELLMR
VVEQDVATI KQVEADRWSLDNRKAGLQAQHDRLTSMLEAEQAARRELASK
QDEKNALLREARGELWDLEAEADRLEAQEQEI LREI ARQRSKDRPRSEGG
FTWPVPGHSSI SSYFGARKHPI LGTTRMHNGI DI PAPTGTTVVAAQDGTV
I DVGYSYSGYNI VMI DHGGGVTTLYSHLSAQLVGNGQDVRKGEAI GRVGS
TGLSTGPHLDFSVRVNGNPVNPLSYL

>2617919906 Ga0073689_103108 cell division transport system permease protein

[pelotomaculum Ga0073689 : Ga0073689_103]

VLNANNI AATMESSVEI SVFLKEKTTHAQAKDLENQI KSLPDVAQVQFVP
KEQALEEMKKNFQDKKDI LAGLEEKNPDPADFVKSGAVEDVAPLAGRLK
SLAQVDQVRYGQGVVEKLLALSRRWVRAAGMVTMVLGI AAVFLI ATTI RL
SVFARRKEI GI MKFLGATNWFVRFPFLLEGMFGLAGSLLAVAGVYFGYF
SLI RNI KI SLPFI QVVERTSLI I PLLEGLLVGLVI GALGSMI SMRRFLR
V

>2617919905 Ga0073689_103107 cell division transport system ATP-binding protein

[pelotomaculum Ga0073689 : Ga0073689_103]

LI QFYNSKI YPNGVKALTDI TLRI RKGEFVFLVGPSSGAGKSTLTLLLYR
EELPTRGQI I FNGKNI VRMRSREVPHLRRI GMVFQDFRLLPRKTVYENV
AFALEVI GASNREI RKTVPVMMNMVGLSEKASAFPDHLSGGEQQRVCVAR
AI VNNPVL I ADEPTGNLDPETSRELMKFLDI NRQGTI I MVTHAQDI V
DAMKKRVVALAGGSI VRDEEEGVYCHEA

>2617919904 Ga0073689_103106 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

VLRTLASLI SVLRTHRGNTI GLAGKKLKD I LPHLKREVI DVEVDVSFKGG
ALLDSMTLTKI WGYCSI VKFRAKNLPQSG

>2617919903 Ga0073689_103105 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

VSEKLDLI LPKI ERLVENLDDLHREQSSMRQELAEVRQGQSSMRMEMSQI
QAAI FELLDGQKELAAQVEI MRRVDMLAEMYGRHELDI RELKRAI VLKY

>2617919902 Ga0073689_103104 transketolase [pelotomaculum Ga0073689 : Ga0073689_103]

MNKKI ATREAYGDVLVELGRENQDVVLDADLAKSTKTI NFKEVFPERFF
DMGVAEQNMVGTAAGLAAAGKI PFCSSFAI FASGRAFEQVRNSVAYSALN
VKI AASHAGI TVGEDGGSHQSVEDI ALMRVLPNMTVFVPADAAETAGAVR
AAAAMKGPVYI RLGRSAVPVLHGTGFQFVPGRAVTLREGKDVTI I ATGVM
VSAALEAAGLLAGEGI EAGVLDVHTI KPLDVEAVVGAARRTGALVTAEH
SI I GGLGGAVAELGEHHPVPLKRVGI QDKFGESGKPAELLEKYGLTPAA
LMAAAKEVLARKS

>2617919901 Ga0073689_103103 transketolase [pelotomaculum Ga0073689 : Ga0073689_103]

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LEI EQLKTKAREI RRHI I RMLGEAGSGHPGGSLSADI VTALYFHEMRLLR
PEEPHWPDRDRFVLSKGHAAPVLYAI LAERGYFPVEELLTLRKLGSRLQG
HPDMKKLPGVEMSTGSLGQGLAAANGMALAARLDRRGYRVYALLGDGELQ
EGMVWEAAMAAAHYKLDNLAAFVDHNLQI DGPVAEVMSPPEVADKWRAF
GWH TLCI DGHDPGQI LDALAEARTVKS RPTMI VAETMKGKGC SFMEGKVD
WHGTAPKPEEMEKALAEALA

>2617919900 Ga0073689_103102 Uncharacterized membrane-anchored protein YitT,
contains DUF161 and DUF2179 domains [pelotomaculum Ga0073689 : Ga0073689_103]
MALKI VWEI LGVSLGVLLTALGLDMFLI PNKI AAGGVSGI ATVLHYLI NV
PVGAAMLI LNVPLFAMAVYRLGLKFGFRSLYGTVALSVAVDALAPLAPVP
THDLLLASI FGGVLVGLGLVFRYRGTTGGTDLAAAI LRSYTGANVGQL
LFLVDATVVI AAGI TFDSEALAMYALI TIFI TAWLI DLVQEGFSYAKAFI
I VSEQAAQI APAI LKELDRGATAWMARGMFTGAEREVLLSVVHRSEVTRL
KDI VYGVDPRAFVI LADVHEVLGEGFKRYE

>2617919899 Ga0073689_103101 Endonuclease, Uma2 family (restriction endonuclease
fold) [pelotomaculum Ga0073689 : Ga0073689_103]
MSVPTPPAGEI I LTIEDYLRLPDDGKRYEI LEGVLHVVPSPTRHQRVSR
ELEFMI YEYVDLHGLGEVFDAPLDI VFSRTSI AQPDLI YVSQERQAVI TE
KHI AGAPDLVEI LSPSSSSDRVTKAQVYARYGVYYYWLVPDKRAVEE
FRLERGI YMLI RSWEEDEVFAPEI FPGLOVELSRI WAK

>2617919898 Ga0073689_103100 peptide chain release factor 2 [pelotomaculum
Ga0073689 : Ga0073689_103]
LEKQI LADGFWDDEKAQKVLQRLAGLKDVRVAAFQELTGELEDLEVLVEL
GEEEDAAVAGEARGALTSFI RRVEEMELAVLLSGPYDRGDAI MALHAGA
GGTEAQDWVEMLLRMYRWAERHFRVEVLDI LPGDEAGVKSATI EVRGT
CAYGYLRAEKGVHRLVRI SPFDAAGRRHTSFASVDVLPEVEDDVEVRI DQ
EDLKI DTFRSGGAGGQHVNKTD SAVRI THLPTGI VVSCQNERSQI ANRQA
AMKMLKAKLI DLELRKREAE LAAMRGDQOEI AWGSQI RSYVFHPYSLVKD
HRTGEETGNVQAVMDGEI DNFI AAYLKEKARGGRV

>2617919897 Ga0073689_10399 preprotein translocase subunit SecA [pelotomaculum
Ga0073689 : Ga0073689_103]
LRRVPALI KGV I YLLGFI KDWLDDNVREVKKLQRFI NEI NTLEEKFTTMP
EEELKGMTTVFRERLDRGRSMDDI LPEAFVVREVSRRVLGMRHFDVQLL
GGLVLHQGR I AEMKTGEGKTLVATLPVYLNALTGRGVHVVTVNDYLARRD
SEWMGQI YKYLGLSVGLVHGLDWDERRKAYRSDVTYGTNNEFGFDYLRD
NMAI HPEQLVQRELHYAI VDEVDSI LI DEARTPLI I SGQTEKSTDLYYTF
ARI VPRLVRET DYNVDERAHTVAI TESGVVKVEKI LGLENLYDDKNI ELT
HHLNQALKAHGLMKRDKDYVVKDQQVI I VDEFTGRLMFGRYS DGLHQAI
EAKGKVI ERESQTLATI TFQNYFRMYEKL AGMTGTAATEEQEFKKI YGL
DVVVI PTNKP MI RKDLPDVI YKTEQAKFRAVVEE I AVRHTKGQPVLVGTI
SI EKSEI LSNMLKKKI PHQVLNAKYHDKAEI VAQAGRLGAVTI ATNMA
GRGTDI LLGNGPEFLARHELHQVCDPELLDSVERGEQTAATAEGAFQNG
TNPDKGVI PPGEVFRLYKELLEKLQRETGEERRRVVELGGLHI FGTERHE
SRRI DNQLRGRCGRQDGPSSQFYSSLEDDLMRLFGSDNI AGI MDRLGI E
EDMPI EHSMI TRSI ETAQKRVENRNFDI RKHVLQYDDVMNQRELI YRQR
RQVLTGENLKDSI LEMI NAAVERAVNAHASEGVYPEEWDLKGLLDYADQL
FLPGHTLTPEDLGGMGRGELQNF LAERAREAYEAREQELGPETMRI ERV
I MLRI VDDKWMHLDAMDQLREGI GLRAYGQKDPLI EYKFEGYEMFQNM I
DAI QDDVVRYI FRVNLVQQRQAPRRVMENRYAEEGPRQPVRRRENKVGRN
DPCPCSGSKKYYKCCGRAEAV

>2617919896 Ga0073689_10398 putative sigma-54 modulation protein [pelotomaculum
Ga0073689 : Ga0073689_103]
MKMQVRGRNI DVTDAKDYVEKRLGKLDKYI DNFGDAQVTMTVEKGSRI
EVTI PI NGMI LRGEESTGDMYASI DQVVEKLEKQI ERYKGKLQKKGARFV
NGPRGAASAI PEDDENGPRLVRTKRF AI KPMPVEEAI LQMNLLGHNFFVF
SNAETEQVNVVYKRKDGNYGLI EPEF

>2617919895 CspC cold-shock DNA-binding protein family [pelotomaculum Ga0073689
: Ga0073689_103]
LLGKVKWFNQEKGYGFI EREDGGDVVFVHFSAI QEDGFKTLNEGQKVEFDI
VEGARGPQAANVI KL

>2617919894 Ga0073689_10396 comF family protein [pelotomaculum Ga0073689 :
Ga0073689_103]

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LLNLI FPPKPECPFCGETVPGGGTCGRCRELLAGYGRERYCGRCGRLP GK
GALLNCSAAPLCPECHGRDWPFLARAAGPYEGVLKGAI HRFKYAGRSL
AGPLAGLMAGI VRAEPLMAGADLI VPVPLAGDKLHLRGFNQAFLLAREVG
ALLRMPVNGRSLVKVETPAQAGLSRTAREWNLKGAFRVTNAADI QGKSI
LLVDDVFTTGSTMSSAAVLSRSGAGQVFGLSAAAGRWF

>2617919893 Ga0073689_10395 di guanylate cyclase (GGDEF) domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_103]

LRAKTGVWHI FYSWL VVGLAVWQLDLLFHALDMDRVREMLVFVFLGVLA E
WLAVSFPHGQLSGCFALVLASFLI YGPAATAWI SGLATMFGQGI ANRGNP
LRTTLFNAGQYVLA AVAAGYI FNLSGGAPGLVGAANALPLAAFTASYI AV
NHLLVYFYLLPGRRRRLPHPAWPDAMKWDGLTYLFTVPLGLLMTMI YGYTS
LTGI LLLFSSVLALQFI LRFHVRLOVANRELTA FYEVAGFLEKNPAPAEL
LEFI LKNVGKAFSFTHTGVVYVLSRSGEKDI YLPVAEAGPYAEQLRSTVVYAG
EGFI GQSI TGREPEI I FDSRLDCRTREEAGLCQTLRSLLVPLLSGKEPL
GVMVLGDKRPQAFDDKHLHI I AVLAGQAAVAVENSVLGGRLAHLRSRDSL
TGLLNFTAFFERMEEVCI GDAPGGI PVGI I LLNI DSFRTFNRRYGRPAGE
RVLFEMAGLVEGFTRKGDLAARYGGDEFALLPGAGGTRLLGTAETLWEE
IRGHI FFKVRGQGGQADRQRRGRRVPPGRW

>2617919892 Ga0073689_10394 Glycosyl transferase family 2 [pelotomaculum Ga0073689 : Ga0073689_103]

MGKFI LLPLALLVI AGVYLLRRLSAGDWVDSAGSTKKVVI I VKDQEPWLE
CLI RKLFRVKNTPWVGVLVDDCSRDTPEI LARLSYYPFDVFSMEAV
GSDYGARGASGAQPAAGVEAAAFAGARCFDLRGLRGDDLRLAPLFCQLSGFR
AGNSRALSK

>2617919891 Ga0073689_10393 methionine adenosyl transferase [pelotomaculum Ga0073689 : Ga0073689_103]

MTRRLFTSESVTEGHPDKI ADQI SDAVLDSI LEKDPFARVACETLVTTGL
VMI SGEI TTNCYVDI PRVARETVREI GYTRAKYGFDCDTCABI TSI DEQS
PDI ALGVNRALEVRDREALVDELETTGAGDQGMFGYATNETPEYMLPTI
SLAHLRLARRLAKVRRSMVLPYLRPDGKTQVTVEYENGRPVVNTI VI STQ
HHPRMTL TEI RENVLEQVI KTVVPKEFMDDATRI FVNSTGRFVI GGPQGD
TGLTRKGI I VDSYGGMARHGGGAFSGKDPTKVDRSASYAARYVAKNI VAA
GLAERCEI QVAYAI GVASPVSI MVETFGTGKVDEPTLVQLVRTHFDLRPA
AI I RDLDLRRPI YRQTAAYGHFGRI DLDLPWERI DKAEI LKQEAGI

>2617919890 Ga0073689_10392 sporulation protein, YlmC/YmxH family [pelotomaculum Ga0073689 : Ga0073689_103]

MLFKI SDLGLRDI VNLVDGAKLGPVKDVHI DLETGRVSMVLSSGRKYFR
LMSAGQDVVPWEKI KKI GVDTVLVEVDAVARTL

>2617919889 Ga0073689_10391 putative peptidoglycan lipid II flippase [pelotomaculum Ga0073689 : Ga0073689_103]

MTI GKFI FKATLLI AFFNLMSRI LGLVRDMAI AHQFGAKGVTDAYQMAK
APNMI FAI VGGALATVVVPVFI EYAAKGQKDEAWKVFTVMI VVTLFFLA
ASVI GVGAPLLVKLVAPGFEEGRVLTVELSRI I LPI MI FSGLASLFAN
LLNANNI FGLPAFSNSVNNI I I I VSTLTGLSLYGI RGLAMGTVLAMAFMA
LVQFPALFKAGFSFNL SMDLKHGPKVKKVYYLALPVALGI SVNQVNVFVNG
VLASWLPEASI SALGYADRLI QFPVSLI VLALGTAVFPTLADRAEKDIE
DLSGI LLSSLKVVI I GI I PASI GLMVL SHPI I TLLKRGAFDQRAVELTA
PALLFYAVGLVGQAAGI LLTKGFYALQDTRTPVKI GMLTVLI NLGSSLI L
I RYLOHGGLALANS MANLASMALLMWYLGKKVPGLYRCGLLKFTLVVLAA
SGLMAAASYAVNSALAGLLPGTI GLFAQVGLAI AAGVAI YVAAFFALGLE
EAGRI LRAAQEAVHRRCLKPPTDR

>2617919888 Ga0073689_10390 phosphoglucosyl transferase, alpha-D-glucose phosphate-specific [pelotomaculum Ga0073689 : Ga0073689_103]

MKKI SFGTDGWRGI LAEDFTFDNVRLVTWAVARYI LTHKLAERGVVVG YD
NRFLSERFASEI AGVFSGRGI TVHLTGRATPTPVVAFVKLYSAGGAVML
TASHNPPEYNGFKFI PEYAGPALPHI TGEI EENI RKLQEA GPDGGERPEA
PGKAPVRQVDPFPDYARHLATLVDMAAI GRAGLKVAVDPMFGAGAGYLEE
LLKQAGAAVETI HNYRDPLFGGSLPEPTAI SLTGLRNMVTKGVARLGLAL
DGDADRFGI I DAGGEYI TPNQFLPLLLYHLLTVKGQRMVARTVATTHLL
DRMAERHGLPVEETA VGFKYI GOCLA EKGAVLGGEESGGLSVKGHVPEKD
GI MAGLLAAEMVAVHGKSLTELLEQI YREYGCLHSERLDVHTSPAGKERV
LVALRDLAPEALAGRRVTSRVTKDGVKLLLEGGAWVLI RASGTEPLFRI Y
VEANSPEEMKEI QGATRSLGL

Table S2

>2617919887 Ga0073689_10389 Uncharacterized membrane protein YcaP, DUF421 family [pelotomaculum Ga0073689 : Ga0073689_103]
 MNPYLEI LI RAVAAFAAVFI TRMI GKSQVGGLTI TDWNGI VI GSI AAS
 LVTELNEPAGYYAFGLMLFMI LTI I SQWMGI KYRPLHKI LTDEPTVVVHN
 GKI LEGNMHKMRYTVDDLTSQLRQEGAFNI SDVEYAI AEPNGKLSVLLKT
 QASPVTPRDLNVPTRYKGVPSSELVVDGVI I EQNLQRNNLDENWLLGELQK
 QGI QSLKEVFYASLSDSGNLVYDKKRDDL DYVDVTDKLPKMLQ

>2617919886 Ga0073689_10388 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]
 MENFGI LEKLSRKMFEEYI RRNKDQAGRQGTKKKEVK

>2617919885 Ga0073689_10387 CopG family transcriptional regulator / antitoxin EndoA1 [pelotomaculum Ga0073689 : Ga0073689_103]
 MVDGMTTGVI DLFOGVLVPTRKI TI SI PNELFDI LDALSI KWNTTRSGVF
 TRLLKEVEAKCPEQEMTEGYMMAERNI GDMEMYLPVQAEALTNDKAR

>2617919884 Ga0073689_10386 UDP-glucose 4-epimerase [pelotomaculum Ga0073689 : Ga0073689_103]
 LKVLVTGGAGFI GSHI VDILLVEDNCRVAVVDDLSTGSFENVNAGVNFYHL
 KVEEGGLEEA VAREKPEVVLHQAQVDVQVRSREPLADAEI NI LGSVNLL
 EACRRHGVGKVVYASSAAVYGNPAYLPVDEAHPVAPQSPYGVSKHTVEDY
 LRI YRENYGI DYTVLRYANVYGPQDASGEGGVVAI FVDRLLKGEPRI F
 GDGEQTRDFVYVKDVAAANLAAFRRGDGMVLNVSTGAGLSVNGLFQALKE
 TTGSLAPMYRPPRPGDI THSRLANAAARQALEWRPRYSLAEGRETVEY
 CKKAGI S

>2617919883 Ga0073689_10385 UDP-glucose pyrophosphorylase (EC 2.7.7.9) [pelotomaculum Ga0073689 : Ga0073689_103]
 VKRI KKA VI PAAGLGVRFLPATKALPKEMPLI VDKPTI QYI VEEAI ESGV
 DDI LI I TGRNKRAI EDHFDKSLEI EVQLRDKGKRTLLELVQDI GQLVDLY
 YI ROKEPLGLGHA I YCARQFI GDEPFVLLGDDI VRSWVPCLKQLMDLHE
 EVQSSVI AVMEVPPEDVDKYGI LDAVEERPGVYRI NDLVEKPRVGEAPSR
 LAVMGRIYI EPRI LSI LAETRPAGGEI QLTDALRVLCREQPMYGLAQFQ
 KRYDVGDKLGYLQAMVEFALARPDLAAGFREYLQMVCREI KEQGI VR

>2617919882 Ga0073689_10384 Transposase [pelotomaculum Ga0073689 : Ga0073689_103]
 LKVVYPI CCGVDVHKKFLVATI I TSDQLTPHYQKKRFSTFNNSI LQFKKW
 LLDNNCRDVCMESTKYWVPVFNLLSDI NVTVANPKWVKAVKGNKDDTK
 DSKWI GDLFRLGLVPGSFI PCKAI RI MREYTRYRFLVSKSSEKNRFQNI
 VFTVCNVALDAVSDMFGKSASSI TDYLVNSDSFDPQLCVSFLRSSLKKK
 ADEVI ESI EGYQMI PEQKYRARLI RSHLDFVENS I SKMDSMLNVLAAPYE
 SAI QLLCTI PGVDRTSAI TI I SEI GTDMTHFSSSKRLCCWSGLTPGNNS
 AGKKKSVRI TRAGI YLKPALVQVAHA AVKAKDDSYRI KY

>2617919881 Ga0073689_10383 UDP-GlcNAc: undecaprenyl -phosphate GlcNAc-1-phosphate transferase [pelotomaculum Ga0073689 : Ga0073689_103]
 VQI PVA AI LLA LGSALLVTPLI RKWAFKCGALDRPDQRKVHQRVMPRMGG
 LAI YLSFVI AVFLTWEI TPQVAGLLVGGSLI VLLGI I DDTRGVSPGMKLA
 GQVAAACAVALFGLRVEFLTNPFSDEMI TLGFLSI PVTVLWI VSI TNAVNI
 LI DGLDGLAGGTSCI AALTAAVWVI EASKMGDSRNQMDAI ALALI LAAA
 VVGFLRYNFYPARI FLGDSGSMYLGFSVATLAVMGLAKTATFI SVI I PVV
 I LGI PI LDTI FAI VRRYCGHRPI FQPDKEHLHHRLMQMGLSHRQAVLCI Y
 GNVVVLGLSAVAMTLATPKQAAI FLVALSTTI LVAANKI GVTGAGGRTTY
 LTRSNKQQRSSRM

>2617919880 Ga0073689_10382 REP element-mobilizing transposase RayT [pelotomaculum Ga0073689 : Ga0073689_103]
 LPRKNRI WYPGAI YHI TCRGNKQDI FRDEKDRLTLYLI LRDVKNNHHFL
 LHAYCLMTNHVHLHMETTATEI GQTMKLVNMQYAVYFNKKYQLTGHLFQD
 RFRSELVKNKDSHNLEI NRYI HLPVRAKI VDKPENYPWSSYRAYLGTSED
 DLVSKSKI LGYFQNRSPLLYQKFVGGRLVGDNY

>2617919879 Ga0073689_10381 3-hydroxyacyl -[acyl-carrier-protein] dehydratase [pelotomaculum Ga0073689 : Ga0073689_103]
 LDI KQI QEI LPHRYPFLLVDRI EAVEDGRKAVGI KNSVNEPYFQGHFPG
 YPVMPGVLI VEAMAQVGAVAI LKMPFAGKVALFAGI DKARFRRQVTPGD

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QLRI EVEI GKLRGTI GKSATAHVGEELAAEELMFALQK

>2617919878 Ga0073689_10380 protein of unknown function (DUF4330) [pelotomaculum Ga0073689 : Ga0073689_103]

LGQAGVTGKVLVDEKGLFGLINI VDLLVLAALLLVLGGAAYKFKDRDSG
AGVAKTVRVTAI ATSI RPEMLTGI KPGDRMVSGSSFTDVVVKDI KIPAY
MI VTDSAGRRVEAVDPYLKDLI VTVEGKTVI SGGAI NLGGQEI RRNKDYF
IKSLDYEFGKGLVMDVVI E

>2617919877 Ga0073689_10379 Glycosyl transferases group 1 [pelotomaculum Ga0073689 : Ga0073689_103]

MLKGETI LCLAAADWAGMWARAQFMTI FARRGNRVI YVDPPI TLLSPLK
NPALRGSRGDRRLRLEENI YVYSPPIV LPFGNMYRPVNRVNQRI AAGLG
RVYRKTELRTPTI CWTYLPGTVDLPLPGEATLVYDCADEHTAFPGI NKET
VSRMERELFARAAVSLASAGELYRRKKEFAPGLVLPNGADVAHFKNALR
PDLAAPGELAAALPRPI GYVGAVSAWLDQEMLAARAHPEWSVALI GQV
DTDVSALAAALPNVRLGRDYSLSAWLKGFDAAVI PFRI DELTRGVNPV
KLYEYLAAGRPVSSDLPEVRPFAPAVI ARNPAEFVSRLEEELAADSP
KAAARLALAERHSWEARAAVEKTI EATGRRG

>2617919876 Ga0073689_10378 Glycosyl transferase involved in cell wall biosynthesis [pelotomaculum Ga0073689 : Ga0073689_103]

VAI LKVAHI IGGGEFGGAERHI LNLGAI DPGKVEI AVCCLFAAPFKEIA
SGAGVLALSVPMRHKADFGVVGKLAALLWDAGADLVHTHGVRANLLGRLA
ARQAGKKKVI TTVHSLRLDYPGFFTCANSWVERATRGITDHF IAVSRE
LKEKLVAGGLPEDKVTI YNGI PLEEFPPADPGAVRARLGI ARETPMVG
I FARLHTVKGHRYFLAAAREVLARRPGVRFLVVGDGPLRPALEEQARGLG
ITDRVFTGFVEDVRPLMAGDLLVI SSLWEGFGLTAVEAMALGTPPVAT
EVGGLPEVVRHGETGLLVPPANPEALAGSI VMMLEHPEAAGEMAGKGGEA
VRENFSAGVMARRTWELYRRMAGWERC

>2617919875 Ga0073689_10377 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

MLLNHLKTGNAYQVEI LRGDVKKYVHVTI EEETPPVPYQTHGAVGI DTNPH
GLGI AI ADYLGQYRGLWLRESEWYAGSNRRTNLI GEKAKQI VTLAKET
GYALAAEDL

>2617919874 Ga0073689_10376 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

MSHGFI WSKFLEHVDRCAAREGVPVI KVKPVFTSI IGI LKYQHMYGI SYH
ESASYVTARRGLGFNHEKI PKI LLDKLI KNKPKFNLMMNLKQWSAVQKAA
LAKI KKI TKRQVKSLSVWQVHRKNI LGI G

>2617919873 Ga0073689_10375 O-antigen ligase [pelotomaculum Ga0073689 : Ga0073689_103]

LI SAKAWQESLTGRFALLRRSGRQSLFFRWAAGSAGYSRQNTVRRSMTG
GALAAARLAAQPLERAGAAVRRGLPGSLFLKI KPHPVLSHTLAWRSLAG
VRAETLLWVFSYI LVDYALRRSPATAFWAGNWDLELLI FAFLAWPVQMA
LRGNLTLYRLTPLDLPI LLYLAVAVFLFLI RSPQTSI AVEGLRVYVEYLFW
YFVAANLLLNNQARALVNWLVALGAAVAVHGVYQYI LGVPI PSTWLDAA
ESDVRTRVFSI VGSPNVLSGLVLVI PI TI SQFLSAPGRLRKLYALCLV
PMALSLFFTYSRGAWLAI AGAMAI YGLI YNWRLLLALAAAAYAAPKLVP
IASRI GYMLSPAYLVSSARAGRVARNMALERLNNRPLAGEGFRFGGAV
AARHI PSSAYVDNFYLTAAESGLVGLAAYLWLMFSGVRCALNSYRRITD
PYLKGLAGGLI AGLLGVLLHNTVENI FEVPMMSYFWLLLGVTAAALPHLE
GQASPPAE

>2617919872 Ga0073689_10374 Protein of unknown function (DUF2442) [pelotomaculum Ga0073689 : Ga0073689_103]

MLYDKNVKTQHEI RSAYPVKDFHLI LEFDDGEYRVVDLRPFLNGPVFEP
LKDFSHEFVLPTYAS

>2617919871 Ga0073689_10373 transcriptional attenuator, LytR family [pelotomaculum Ga0073689 : Ga0073689_103]

LRTRRRKLKRKTPFI IFSVLLLALLAGGCVLARDI LFPGDSI GEI VDEEG
MPRKDQRI NVLLLG I DARQGETMARTDTVI LASVDPKDKQI ALLSI PRDT
RVNI PGHGWDKI NSAAVYGGPELSTRVASDLLGVPVRNYVLTNFSGFKDI
VDALGGVTLDVEORMYHEGDAEYGGAYGI NLQKGVQRDLGEKALQYVRYR
DYPMGDVDRTRAQQKFLTALAREI LQPGTI PKLPKLVEI NRYVKTNLNI

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GEMYKLAAASKNLENGNI LTQTLPGRPVEVAGGSYWGVDPSEARRTMEKL
FNGETTTAI VLNAPLNSRYLGTAAKPVEPPKSEGTAPAAEQGNKAI PP
AKPGQGGQKSGSRGSSVI TPGGKDTGTGKDTGTSTGKPSAGTQTGKDTGA
KTGTGTGTGKTSSTDGSAAGSDTSGTDGSTGNRTGSDVNPPI PGTTTG
TNTTSS

>2617919870 Ga0073689_10372 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

VRLNRNVI TLVALAGVLALCLLGYTAFAGAEGEPGGSGDPLVAQSYVDQY
VKWQVAELRTGOVLAARTGAEFI VRRGQVAVDATGNGI PDVTGGADI SN
GSKVPLNHLLVFPREDGRGI KALAPAVVMYRGGASQ

>2617919869 Ga0073689_10371 polysaccharide pyruvyl transferase CsaB [pelotomaculum Ga0073689 : Ga0073689_103]

MI MPRVVI SGYYGFYNSGDEAMHLHAMLQALGDAI PGLEATVLSKDPDYTA
RAFSVRAVPRDNPVRVLKALREADMLI SGGGGLLQDVTGPKSI VYYLGTV
TLARLLGKPVFFYAQGI GPVNTAAGRALVRLVADRVNVI TVRDQDSREEL
AALGVTRPPI HVTADPVLGLDPERI DRRRGRTVFASLGMGSGPVAGI SVR
PWKGLDGYKKVI ARVAGDLAAEGWQVLLAPMHSLLDTAVCREVATLARGK
I FLMDDDPDFMDLLSVTANLDLAVGMRLHFLI FSALFGVPLVGI PYDPKV
NRFLOAMGLPPGLNAEDLEYNELSARI RQVLAGEEI SAGLKKRVAPLRG
EALRNALLAAELLRSI LKR

>2617919868 Ga0073689_10370 N-acetyl glucosaminyl di phosphoundecaprenol N-acetyl -beta-D-mannosaminyl transferase [pelotomaculum Ga0073689 : Ga0073689_103]

MKVDLLGAGI DALTMEETVERVAGFI GSGRPHRI I TLNPEFLYRAQFEKR
LLDLVNRADLVTPDGVGI VWACRVAGDPVPERVTGI DLMLRLVERAAREG
WRVFLGGAAPGVAEEAERLRRVYPGLRVAGVHHGYFKEDERAANLVR
EARADLLFAALGAPKQEFWI DSHLTATGAAAAGVGGSFVGI AGRVRRAP
RWVRRHLLEWLARLLREPSRWRRLALPLFAGVVLRYKFNFRQD

>2617919867 Ga0073689_10369 drug resistance transporter, EmrB/QacA subfamily [pelotomaculum Ga0073689 : Ga0073689_103]

MANTVTGGEAPGARDVSGYPSGGI PVAALLTLVI GGFMAI LDGSI VNVAL
PKMMAI FGVGPEVDQWMTAYLLTSGVVI PVTGYLGDYGLKKI YI FSLV
AFTAGSAVCGLAWSNNSLVAARVLQAVGGGMI MPVSMAMI YFI VPREKI G
TALGI WGI AAMAAPSI GPTLGGYLVDFNSWHWI FTI NI PI GI AAVFLALV
TLEETPRRAGLKADYPGI LLSAAGCFALLAMSEGQDKGWTSLYI VNLMI
FSGFSLALFVI WELLAPHPLLDI KLLKNKTFASLLATSI VTVGMFAAI F
MVPLFAQNVQGYTPMRTGLMLMPMALTMGVMMPI SGRLFDKI GALPLCLT
GLTI TVI TTYQLHAI TYDTGFREMQLLAHRAFGGLCMMPLTTAGMNTV
PHFLI GRASALSNLARQI SASFGI AFLTYVMLHRQDYHAARLADTVTWS
PAAVETLRQI QI VLGQAAGLEQAGARDAAAVLQGLVRREAFI SGI ADAF
VVS AVI VALAI PLVFFFLSKRVDRAVEEYRRYVHLI PPGGTPGGSRPGG
APPGGGAPAGGSAVI

>2617919866 Ga0073689_10368 Barrel -sandwich domain of CusB or HlyD membrane-fusion [pelotomaculum Ga0073689 : Ga0073689_103]

MKKKVI I YVVLAAAMVLALAGASGYWYKGNHFVDTEDARVDGAI VRVSPQ
VSGRI QEMS VSEGDTVKEGQI I ARQVDF TATPSMSI GANPELYVVKSPI G
GTVI KKI GNVGEVGPQPVVMVADLNSLYI TANI EETELYKVKAGQQVD
FTVDSI PGVKFSGQVKS I GDAAVSTFSLPSQNTGGNFTKVVQRPVKI S
I RNYQQORLLPGMNAVRI YVR

>2617919865 Ga0073689_10367 membrane fusion protein, cobalt-zinc-cadmium efflux system [pelotomaculum Ga0073689 : Ga0073689_103]

LRKWFGI I MAGLLAVSMLALAGCGAGGRDAGAGERDNVAVTRAVAGAGKI
TGGAVVSGKLEALDSAEVAPKMAGRVAI SVDVGSRVAAGDVLAQLDAE
LAALVDLYAAQLDKARNSDLPAQKNQAEALANAEATYKTAEADYERSKQ
LRDASVI SQQQFEQAEKMYTQAKAAYEAARNSLDI LVNATI PETI RQCEA
QLNKARADYANSVI KAPI SGVVTARNVNPGETAGPTRPVVTLVNLDTVVF
RANVGEEQI NYLKVGQEI KVKVGSVQDEPFTGTVANI ALAADPSTKAYPV
KI QI PNPQGI LKPGMFAEVYLDAGEEEGI VI PKEAVLREGEKSFVWLI KD
GRVTRREVATGRSDGSNI VKSGLNEGEAVAVTGLDALREGAVVI VQE

>2617919864 Ga0073689_10366 DNA-binding transcriptional regulator, MarR family [pelotomaculum Ga0073689 : Ga0073689_103]

VVEHPAEDKYFARLEEVFQEMI RRLHGEMAYRMVSGI TGSQFFVLKKI QG

Table S2

KGRMTVTEVADALGVSLSAI TALVDRLVKSGFVVRNRDEQDRRLVWLEAT
EKGREI LMQCEVRRNVAI KYFGRLPEEDI QKLI EI YEKVLTVMRKEEKD
G

>2617919863 Ga0073689_10365 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

MI ALLI LAFLLI MVQEVPGLLKKRAWRELAFFFFLALGFALALPOALDI
EAPNPNTLI EAI FKPLARWLEY

>2617919862 Ga0073689_10364 spore germination protein KC [pelotomaculum Ga0073689 : Ga0073689_103]

LGKKAACLLLI I LPLVLLGGCWSRRELSEI AI VLGAGVDRTDPDNQVRLTL
QI ARPSAFAGAAEAGAGAAKQNVVWVSGTGRTI YDAERNLALKVSRHI
YWGHEVI LVYGEEMARGGVVDASNFFMRNPMTGRGTI WWLVTKGEASRLLE
SHSELEKTSAQSMGYLVRARAGFSI MLKDFQMALASWGTNPAAPRVELQK
AGQPQPGMEAHEQHEEVAI TGTGVFKDDRLVGWLDDETRGLLWLRDEI
RKGAI I I PSPGQPKLI TFR I I RGGARVDPEYDGETVRFNVTLHVEGDLM
DQOSMEDLTTEKAAAVEEAVAGDI FRKCAATLEKAQGEYGTDFVNFGEA
FHRKYKKEWRKLRNWNNEEFARAEVDI AVEAHLRQTGQI TRRASQKE

>2617919861 Ga0073689_10363 spore germination protein KB [pelotomaculum Ga0073689 : Ga0073689_103]

VPEGGKI SSRQATFLMANAI FATATVFLSGFTI RHARQDAWI SI FLAVGA
GLLI GVLAAALGRFPDKTI FEYPVEI VGRWPGKLVGLLYVWWFLHAAAE
SSREFVEFMATTYMPETPLVAMLLMGI GGSAYI AKNGLEVI ARANEI FLL
VI FGATI I I FI LAADKMDFHRLLPVADVGAVQVFKGA AVTLSYFGEI AVI
AVLVPLYLDPKPREACRAVVA AVLSSGAFFLLALLGLVLA I YGPHI AGAYLFT
TLNEARI I SI ANFLERMEAVDI I I WI SGAYMKVSFYLLWVAALGSAQVLGL
KDYRPLVLPVGAVVI AMSI MLHPGI PDLLDFRGRVWPVYALSAFEAGLPL
ALLVTALARGKGR

>2617919860 Ga0073689_10362 spore germination protein KA [pelotomaculum Ga0073689 : Ga0073689_103]

MRKFI RPI RVNLPAAKRNPGRWGSQGLPEQLNKNPFLEPDLEAN
LARLREI FQDCSDI I YREFLFAQREDI RLALI YADGLVDKDQVSEI MRA
LTLELPMVPRSEI SKAGAYHLI KERSLCMHQVREKDRLEDVVEAVLSGD
TALLVDGRPOAI I SGARGWEARQVGDAETEVVVRGPRDSFVETLRTNTAL
LRRRI KNPALKI EMLKLGRVTRTDVAVVYI KGI ADGKLVEEVRRLQGI D
I DGVLESGYI EEFI EDNPWSPFPQVNHATERPDRLAARLLEGRVGI MVDGS
PFI LTVPCI FI EYLHAAEDYERFI I ATAVRMVRFVALFLSLVAPSFYI A
I TTFHQEMPLPTPLLLSLAAQREAVPYPPI VEVLLMEFSFEI LREAGI RLP
RQVGQAVSI VGALVI GEAAVRAGLAAPATVI LVALTGI SSFVFFHSASI A
TRLLRFPI MVLSATLGLFGLI AGI VGI VVHLCTLRSGVGYLSPVAPLSA
GDMKDLVVRVPPWSMLNRPRI GWKNRRRMEPGQEPAPPKTGPGYKGGGG
SAGRR

>2617919859 Ga0073689_10361 glutaryl-CoA dehydrogenase (non-decarboxylating) [pelotomaculum Ga0073689 : Ga0073689_103]

VDFGLTEEQQMVQDMARNFAEKEI APYVEEDEKNHYRREI LTKMGELGL
LGWSLPPEEYGGNGMGWMEGVI ALYEI AKVHTSWRLSI SGNNWGPAMTI NE
YGNEEQKQKYI PGLLDGSFI GSFAMTEPNTGSDVASMKTAVDKGDHWLI
NGTKTWI SGGHTCDI GLLYAVTEKGAGPKGI SCFVI DYNNTPGVTRI PI H
EKVGMWAAPTSSEI FENAVVPKENLLGPLNKGFI CMWQLNNTRMGCATG
GAALSRACLDGAVQYANERI QFGKPI GKHQMI QAQI AEMI LEDEAAKNLV
YRAAWLKDNKLPSQQATSI AKLAGCNAAVHAANLAMKI YGSYGYSNEYPC
GRWLDRSKQFETLEGTSNMHMQI I ANI ELGYAPNR

>2617919858 Ga0073689_10360 6-hydroxycyclohex-1-ene-1-carbonyl-CoA dehydrogenase (EC 1.1.1.-) [pelotomaculum Ga0073689 : Ga0073689_103]

MAI PAQI ETWQMI EPGKLI KTSVDMPELKSGEVLVEVAGCGVCHTDI SYF
YDGVPTVTKPPLTLGHEI AGRVVAGEERLLGKEVI VPAVMPCNNCPI CAS
GRGNRCLQAMPGNLSGI YGGFSTHI PVPAADLCVVEDRKGMPLEHLAVV
ADAI TSPYQAAKRADVREGDI AI I TGATGGI GVVYVTOI AAVMGAREVI AI
ARNKEKLESLQYGATHVI STQDKSVKDVREEFRAYAKSKKLPSYGLKI F
ECTGSKMGQEI CLELLTFVSKLLVVGYGTKVEYMLSRMAFDAEI I GTW
GCLPKYYPEVLQVLDERI KVEPFVEVKPMSQI EEAFKASHAGKLSKRVV
LTPDF

>2617919857 Ga0073689_10359 cyclohexa-1,5-dienecarbonyl-CoA hydratase

Table S2

[pelotomaculum Ga0073689 : Ga0073689_103]

LNYQYLKVKNDGGVASI TLNRPPLNVLTI SMMEELI SAFNWASQEPCHLI
LLDAEGKSFSAGVDVADHTADKVESMI DVFDRLFLTMDGI DKPI VAAVNG
AALGGGCELALFCDLVVASEKAKLGQPEI AVGVFPPI ACHVLPRLLSWPL
ALELLLSGEVI GPSRAEQLGLVNKVFPAESFADYLKEYLQKFLAHSPVVL
ALTKKAVRAGLNKGFGEI KDI DRI YLKELMRTKDAVEGLTAFMEKRKPV
WQGR

>2617919856 Ga0073689_10358 6-ketocycl ohex-1-ene-1-carbonyl -CoA hydrol ase
[pelotomaculum Ga0073689 : Ga0073689_103]

MELFKWPRQTDI KDHDLFSEEHFGKEAPCVI YEKKPVLDPNGNPVEGLYN
AWI I LNNPAQYNSYTTEMVKGVI AGLHRASMDRSVVAVFTGTGDKAFCT
GGNTKEYAEYSSANPSEYALYMDLFNGMVDI LMCKKPV CRVNGMRVAG
GOEI GMACDI SVSSDLANFGQAGPKHGSAPVGGATDFI FWYMGMERAMWS
CASCEMWSAYKMEQLGLI TKAVPVLKKDGKFI RNPQVI TDRYI DDGAI VY
GEPVQGOAAAEAKKLVECEVDFTLLDNEI NKI I YTLANTFPHCLMMTI D
SI RQKKKFFWDQAKLPSRHWLAANMMGEAYLGFNAFNNKLTGKNEGDFI
KYRQLLAKATPFTQELI DAVLPPRTE

>2617919855 Ga0073689_10357 hypotheti cal protei n [pelotomaculum Ga0073689 :
Ga0073689_103]

MGFEKFGYKSFAAHTKVAAFVDYLEOGELRATQCHACGQVYFPPRADCAA
CLSNMMEWVKI EGSGLI SYTTANYAPTGFADVPYTLALADFGKVKVFG
RI KSEVKKEDLVGLAVKAVVGKLPDQI TYDFI PA

>2617919854 Ga0073689_10356 acetyl -CoA C-acetyl transferase [pelotomaculum
Ga0073689 : Ga0073689_103]

MPKDVAI I GVGQTAFVRGYQGS I RELAFDAFREAMDAGI STKDVGASMV
CSAPEYDKQSPAGLI AEYLGLNPQPTFVLENI CSSSTTGI RVGYSMI KS
GLHDI VAVVGFQKMSEI SSADSQERMGRGADI MWESPFGTMMPAYYAMHA
QAHFTRYGTTEKDLALI RVKSTKYGV LNDRAVYRKELNLEQCLNADYVSS
PLKLYDCCANADGASCVI MASADKAKEI SKKPVVVI GLGAASASMTLTGR
ESLDGLSCARLAAEQAYEMAGVTPQDI DVAEVHDCFTVAELMAYENLGFA
EPKGAEI REGQTYI GGI PVNV DGGLLSKGHI GATGGSQVRTI VLQL
RGEAGDI QVPGAEI GLVHNI GVG I YSNVI I LGR

>2617919853 Ga0073689_10355 3-oxoacyl -[acyl -carrier protein] reductase
[pelotomaculum Ga0073689 : Ga0073689_103]

MLLKGVKVAI VTGARQGI GEGVSVGLAEAGADLMLVSRSI KEDDDVVKACL
AAGRRVLTMOQDVSKRSQVQEMVDRTI SELGRVDI LFNNAGI SKPGMLWK
LTEEQWDLVI DVNLKGTFNCI QAVAGPMMEQKSGAI I NVTSSAGLLGTI G
QVNYTAAKGGVYALTKSAAKELARYGI TVNTI APMAETEMTKTI ATDPRF
KDKYLERI PLGRFAKPDEI APAVVFLASDGARYI TGQTLCDVGGMVML

>2617919852 Ga0073689_10354 phenyl aceti c aci d degradati on protei n [pelotomaculum
Ga0073689 : Ga0073689_103]

LAI YEFEGKRPQI GRGTYVHPEATI I GDVSI GEDCYI GSGARI RGDWGA I
TI GSRNI QENCVI HVNLNVA AVLGRSHI GHGAVLHTPTLGEHVFGMG
SI I MDYAI GDGCC I GAGALI LERMOI PPNKLVLGVPKI VCELNEAI RS
RLEWATKCYI ALPPRCLRGMREVPLEACLSERED

>2617919851 Ga0073689_10353 Sporulation and spore germi nati on [pelotomaculum
Ga0073689 : Ga0073689_103]

MKWFGGKAAKI TI SLAAMALI LFLSAACDSFSKTEFREVPASGATGAENG
NTPPERKLNLA VYYYKMT PGDVYLVREI HKVPFTREVARAALEELI NADP
I TPGAVRVLPPATKI RGI NI RDGLATVDFSREALRANVGASGEVLGI QSI
VNTLTLP GVRKVSFLVEGKLDQEARDWWGHVGLYTQPFERDVVMVHEPA
I WVI YPOSGQKVRSPLEVRGSARVFEEAVSARLRDGS GKI LAVAHGVATR
GAPERGDFVI SI PFNVAGPGSGNLEVFWGSPKDGREMDLI KVPVTW

>2617919850 Ga0073689_10352 hypotheti cal protei n [pelotomaculum Ga0073689 :
Ga0073689_103]

VLVI VTWVEGEEVFYRLMSEEEI NALEEDDKNYI I TGLLN

>2617919849 Ga0073689_10351 hypotheti cal protei n [pelotomaculum Ga0073689 :
Ga0073689_103]

MLSVCHLYCDLLNLYGDRGNI I AFRQRCRWRDI PVTVRETNLGDKI DFRE
FDFVFLGGSDREONLI AADLMKRRDELKGAVEDGLVVLAI CGGYQLLGK
YYLTREGGNI PGLGI LDFYTRAGERRLVGNTVVETDLGGRAVKVVG FENH

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SGQTYLGEI QPLGRVLYGNGNNGWDGREGARYKNVFC SYLHG PLLPKNPG
LTDYLI SLALARRGMDPELKPMDDSFEDRARGVMLQRLGFRNGRT

>2617919848 Ga0073689_10350 UDP-N-acetyl muramyl tripeptide synthase

[pelotomaculum Ga0073689 : Ga0073689_103]
MLKFRLSAAI LAGKLA A WLSRLRGHKSSLPGLVARKI YTGCLRDLAGQV
RRGI I VTTGTNGKTTTNNMI AGVLTGAGHKV VANLEGSNMI TGV TACFI L
DAGI GGGI ECDYAVLEVDEASMPAVLA EVKPGVVALTNFFRDQLDRYWEI
DKI AGI I RDSLREQKQ GALVLNADDPLVAQFGR TTGLPAVFYGLGQHGRA
TGTGVGVREARFCPFCGSAMEYNFFHYGQLGNYRCPGCSFARPDPRVEGL
EPRVEDGVSGCRLVYDGREVFLT I HTRGLYNLYNALAAFTASLHLGI DVA
DI LSGLVNYPVTGRMERFI YEGREAYLNLVNPTGFNEGI AALSAAPGT
KDVFI AI NDNDADGHI SWLWDVD FEI LGLDHGSFLHFVCSGRRGEEMAL
RLKYAGVPVEKI MVRLELPAI ESALSGGAGVVYFFPTYTALWPVHRI LG
QLADGGGAHAQRMPFVL

>2617919847 Ga0073689_10349 Glyoxylase, beta-lactamase superfamily II

[pelotomaculum Ga0073689 : Ga0073689_103]
MLEI HKI TVPTLYPI GPVNCYMKVKNRPYTLVDPGPKTAEAKKALLDGLAS
LGLTPADI ARVVI THSHSDHSGLARWLGETAGAAVYVHRLEVRKLA FDYD
FYQEKMHFLK DAGLPFEVLKEI QGDRDLVVKSGLPRSWVALEGGEELF
EGGSLRVMHLP GHSSGHI CLYEPESKI FLAGDFI LKHI I SSPSMEVDPAD
FTRRI PTLAQYMEGLKVMEELDI DLI MPGHGENI DDSRKAARAQTHYAR
RLEEVC SI LEGNSLSAYOI MRLLYPGLRGFQAFLGI SAVFTHLDYLRSLG
KVSMERRGEVSFFSLG

>2617919846 Ga0073689_10348 Uncharacterized conserved protein, contains GH25 family domain [pelotomaculum Ga0073689 : Ga0073689_103]

VETEKEGAGPGRVLWLEPAHLHFHHGHP I RVKVLWGEAMKPGGAVFDAGD
LTASVAGPGGSRPVVRVDGPESGQFVLT FNAGEEGMYT VTVEAAMGTARV
MVPVGHVHSGRGVAAGRGLEI VPLDCHEFH PGETAEMQVLWDG SPLPGA
VWTTFHLYEGALLYPWRPETGDGGVFRFTFGEKGHWLFVVEHNQKFATLV
VPGVH

>2617919845 Ga0073689_10347 cobalt/nickel transport system ATP-binding protein

[pelotomaculum Ga0073689 : Ga0073689_103]
MADI I EVEELSFTYRDGTRALDGLSLTI REGARVALLGPNGAGKSTLLLH
LNGI HLARQGVVRVMGREI TPKNEKWVRGI VGLVFQDPDDQVFSSTVRED
VAFGPVNMR LVP AEI DRRVDEALAAVKMEKYRDKAPYHLSYGQKKRVAI A
GVLAMSPQVI VLDEPVAYLDPRGRDVLMEI LGR LNEKGATVVI ATHDVDL
AAQWAAQVLI MKDGKLLA QGDTSLLSDAAVVQEAELSFPVVTRI FKKLPG
LNLPRMPLTVDDAVFEI KKI MEKAEKDR

>2617919844 Ga0073689_10346 cobalt/nickel transport system permease protein

[pelotomaculum Ga0073689 : Ga0073689_103]
MEQI FTVPVGRTSI I HKLDPRVKVVAI FSFAFTSTMSSLTVLAAAALFV
LALAGLSRVP AI YLLKRLVWVPFGGI LVLI FPF I TPGAPLFELKAGFVS
LAATAEGVNRAGTFFLRVFTAVSALAVLTATTGFREL MNAFREL RAPHVL
VALVEFTVRYVFLADEAQRMRARRARGFDGGGSLFNRHAKTI GOLI G
VLFI RSWERGERVYNAMLARGYSQVDRVSGRI PGVRDI CAGAVI PI FAL
SLRFI ESGGQI WLI LLK

>2617919843 Ga0073689_10345 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

MMRKI EELKEI ETLI DALDVALREARTI AQGYQTGDQRLNANLEREK
RFLDLWNKLRGGNKEV

>2617919842 Ga0073689_10344 Predicted DNA-binding protein with PD1-like DNA-binding motif [pelotomaculum Ga0073689 : Ga0073689_103]

LQYQQGNI SRVFVARVEHGEDFLGELKKLAARETI R SAVFFFMVGALKSAS
VVVGPREPVLP PQPMWRDFDNTREL VGTGTI FWDEKEPLPHVHG VF GKGD
TVLMGCLRK GTEVYLI LEVI I FEI TGVNAVROFSETLGLKALELK

>2617919841 Ga0073689_10343 DNA helicase/exodeoxyribonuclease V, subunit A

[pelotomaculum Ga0073689 : Ga0073689_103]
LNNQWTD EQREAI FSRGGNLLVAAAAGAGKTTVLVERVI SLI TDPANPVD
VDRLLVVTFTNAAAAEMRERI GRALAQEAARRPGVKRLRRQMVLGRACI
STMHSFCLDLLREYFYRL ELDPAFRVADETESALLRMEALDFERRYAA
KDNLPFTALVDCYGGRRDDTQLQELVLDAYKFARSTPRPEEWLDRLPENF

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HLPEDASLDRLPWCADLKKALEMELTEALAADLALKI SRRPGGPGAYLD
 NLEAEREMVARLLGACSAGASWELHASFGGAGFGRLLKQCKRDEADPGLV
 EQVKLLRDGARKKI TGLQEQHFPRLLPEELLADLRAVAPLARELAGLVQDF
 ADSYRRAKAARGVVDVDFSDLEHYALGI LTERGPDGPAPSRAALEMRERFAE
 VLVDYEQDTNDVQEAJ LQLVSRQEGKPNLFMVGDVKQSI YRFRLAEPGL
 FLNKYRSYPAGGGGRERRDLTRNFRSRRGVVEAVNFI FRQLMTPAVAE
 AYEDAAALVYGAGYPPPPAGAGPDEAVELRLI ERDDAGAGFPVKSAPEDR
 AVSEEGEGGGNGPDEEDDLDAVQREARLVAGRI KELVTGAGGDPLMI YDR
 DLKAYRPPAYRDVVLLRATAGYANSFI EEFRRREGVPAYAETATGYFEAT
 EVETVLSLLKI I DNSRQDVPLAGVLRSPVVGKKAADLAGI RLAAGKGDYF
 EAVVAAAALGRGELSDRLTDFLAKLENWRTAARQGGGLADLI WSI YRETGY
 YDFVGGPLPSGGQQRANLRSLYHRRARQYESTAFRGLFLFLRFI ERLREGGR
 DLGLARALGEKENVVRI MSI HSKSGLEFPVVFVAGLGKKFNFKDLNKTML
 FHKSQGLGPOQVDEAGVTYPTVARLALKHRLKLEALAEEMRI LYVALTR
 AREKLI LVGSARKLAECARRWCGPVGADGPCLPDGMLAGAASYLDWLAPA
 VARHRDGAAL RELGRAGEEPPESVASGPSAWKVI DAGRVVPGAGGEAEP
 ELFSRVKMEPLEPGPLADTVKARLEWRYPAAAVAGRAAKASVTEI KRRF
 DLRETEEGHRLPDDFHPVPGRPRFLQEEGLTAAEAGSALHLMQSLDL
 DRVSGAAAI KEQI AGMVVERELLTHEQASAAPVERI AAFAGPLGRRVLAG
 RAVRRELPTLALPAGELYPDRLAYPGEVALAQGVVDCLVDEGDGYLLLD
 YKTDRVARDOVAAAVDRYRAQLSLYTRAVEEI LGRRVKEKYLYFFNPGLG
 VRCD

>2617919840 Ga0073689_10342 DNA heli case/exodeoxyri bonucl ease V, subuni t B
 [pel otomacul um Ga0073689 : Ga0073689_103]

VTLRFI VGRAGAGKTRACLDVREELRARPEGGPPLI LLAPEQATFQTEY
 ALAATPGLKGF RVHVL SFRMAHRVLOEVGGAARAH I GELGKRMVLSRL
 LERRRDQLKVFRRSAGQPGFADTLARALGEMKTYCI GPDELAASGLRG
 AGDGLADKLADLRLLYCDLEEYLADRFTDPDDYLNLLADRLEMSEAVRG
 AEVWVDGFTGFTPREYRVLAAALLRAAGRVNVTLCAGAGDLGAGGDETDLF
 YPVRETYNSLCEMAARERVAVERLLALDGHPRNFRSPGI ACLEGGYFDH
 AAPSTPCSGEGVTLAAAANPLAEVEGVAREI TALCRDGGYRYRDI VVLLR
 DLESYAHLI ARVFADHGI PVFI DQKRTVTHHPLVELVRSTLEVAAGDWP
 DSVFRFLKTDLAPLAREEADLLENYVLAHGI RGSRWTDGRPWEYVRRLTL
 EEKREI MGTETEELAEI NRI RNRAAAGLAGFCRAVERAGNVREMTAALWG
 LLERLAVSEQLGWSLRAAEEGRLEAAREHI QVRDGFADLLDQVVEALGD
 EALTPAEFAAVLDAGFESMRLGLI PPGLDQVVVGS�DRSRSPPEARAVFI P
 GVNQGLVLPARVSGQGLTDGERERLAAVGLNLAPGARRKVFDEQYLYI A
 LTRPSELLYLSYPLADDESGALLPSPVVARVKELLPGVAERVWPVEPVA
 GEGTGQGEPPAGAGDLAFVATPGCALAHLAVQLRQARAGRPVNPLWWDV
 YSWFVRGERREOCARVLSALFYSNREERLPAGMGRALYGRTLKTGVSQVE
 RFRACPFHFSLQGLKLERAVFKLDAPDLGRFFHAALKLFGERVADGL
 DWGRLDREOI AGMAGEAVELLAPRLQSEI LLSTARRRYLTGKLERTVRR
 ALVLAHHSRRGRFRPVGLELAFGPGETLPGVTFTLADGSEMLVTGRI DRV
 DAAPGEAGVYLRVI DYKSGRMTI DLSDI YHGLRLQLLAYLDVALCHAGRF
 LGDTGKGGGGRRGPEAPARDRAGGSGLPGAI LYFRVDDPLI RTVGGV
 PPVEELEKMI LKELRMTGMVLADPAVVDMMDNGLTGDSALI PVYLKRDGG
 FGARSVLTREQFDLLRAYLRFQI SAGEGI VGGVVDI SPYRRGTRRPCR
 YCSYKPVCRFDI LVDGNVYRI I REEDRET VWGKLAELVGGEDI E

>2617919839 Ga0073689_10341 Cal ci neuri n-l i ke phosphoesterase [pel otomacul um
 Ga0073689 : Ga0073689_103]

LRLI YLTDTHI QSGRPEYRRDDFLEALFNKFAEI I GLCRRLKI DFMI HGG
 DLFDKPCPDQSRDLFRWLLKELDLPVYCVAGNHDLI NQRLDSLENTALG
 RLARERLVRLKPGKEVYLTNSSCVVQLSGQHFYEGI DRWKNGRDYVVEK
 NRCDLAVHVVHGMLLPRAFSEKVPTTLI SEVAATGADFTLGAHAHLGYHE
 TAGGKFFLNPGALARLTGLKKELI RI PQVI YLDFTAPASYNFI PLRAVRP
 GSEVLEI KPSGEDG

>2617919838 Ga0073689_10340 Predi cted thi oesterase [pel otomacul um Ga0073689 :
 Ga0073689_103]

MAQKLKAGI QGETRVAVSEENTAI AYGSGSVRVFATPAMVGLMEKAALSS
 VDPILLEPGLTTVGARVDVKHLAATPVGMNVVATSRLVEVDGKRLVFVEVA
 RDEADLI GAGVHEQFI VKLDSFI KRAEGQAKE

>2617919837 Ga0073689_10339 Uncharacteri zed membrane protei n, DUF441 fami ly
 [pel otomacul um Ga0073689 : Ga0073689_103]

MFTPKKWAASI PKAERCPAYPEMKRLNGNFLGLSPPELI LI I LLFLGI FG
 RSNLVVTSACI LLSLRYFNLDHI I LPVLEERGLEI GLVLLMLHI LSPIAT

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DKLSRQDFLSVVSGKGFALVAGALATKLNGDGLLELMNASPEIIFGMTVG
TVMGILFLRGTPCGPVMAAAVTAVLLQIAGLFNR

>2617919836 Ga0073689_10338 Anti- σ factor N-terminus [pelotomaculum
Ga0073689 : Ga0073689_103]

LETRGVVVKIKGNTCIVLTPAGEYRKAPLPKGGTYCVGREIELGKRNNFL
WLKYLMAAASFLVIAAGLLYQGRTOQAAAYLTI DINPSIELAVSADGK
VVSARGLNGEGEKILGKVKVNGCEVREAVCLVVAQAVADRYLGEGDEDNV
LATVTVEGGGEPVVDLELVYEAIKKSVESGGIQARVIEPVEPEMRREA
ARSGISTGRYFLMQSAQKGVFPFAAEINSMSLGKLEKEKKINFVRLLEE
DTRENGFIEKEHGNSHGEERAGGRAKQGIYVELWNREAGPDTKPAGREI
VPGRPQKDDRDKTTVKKREGEKEKEKRSALPGRGSVKITSEDDDGKGKNG
RNHGKKYDE

>2617919835 Ga0073689_10337 RNA polymerase σ factor [pelotomaculum Ga0073689
: Ga0073689_103]

LFPVQDMEERIKEIKGDRDLAREVFLESSRPVFKVACKYSRRI LEWGRD
DELAVALIAFNEAIDRYREGSGVPFPAYARMVIGSRLTDHFRRENRNATV
NVPLPSPGDGLNEAEFARAREIYWEEMAARERGEIEREFKELLNAYGVSF
EDLVKCSPRHSDTRRSLLLAARTLAEREGLLAELMEKKKLPLTELVKSTG
LGRKTLERGRKYIAMTLLIHRREDFLYLSSYLNLPAAG

>2617919834 Ga0073689_10336 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_103]

VADLEEKGISVREFVAACVGMVIALII LLGAGLGI LLDLPYALTGLVVG
VIATWAIAGSFAGTVNVKCEPCGNRERVVGTVGSYQCSNCGKMAPIKHE
EPEVILYSAPTD

>2617919833 Ga0073689_10335 UDP-glucose 4-epimerase [pelotomaculum Ga0073689 :
Ga0073689_103]

MNIVLTGGAGYISHSIKELLKRKHVVTLNLDNLKGHREAVTGGVFVLGD
CGDAVLVKELVDEYQIGAVVHLAADSLVGESMAKPKYQNNLNGGVNLF
TTLVETGMRYFISSTAAVYGEPEYTPIDEAHPTRPVNVYGGTKLMLEEI
LRWYERAYGLRYISLRYFNAAGADPDGNI GENHNPETHLIPLVIQAALGK
REKIVIGADYPTPDGTCLRDYIHVSDLAVAHILALEALQDGRPSAVYNL
GNEQGHSVRELIHTVHRVTGRDFVVEDGPRREGDPAALVASSKKIQEELG
WRPVYSDELEKIVRTAWEWHRHP

>2617919832 Ga0073689_10334 4Fe-4S di cluster domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_103]

LEGVSGVAPRKIVLRFSDISDKPIIFRLVKDYDLVNIKANVNPKEG
TMVMELTGEKYDQGLEYLGSQGVVRVQPLAEVFRNEDKCTSCGACTDIPC
TGALHMERPSMEVKFDESCEVCQICLKVCPVKAMEVRF

>2617919831 Ga0073689_10333 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_103]

LKFTDRSYRQSFQDDLVHFQVVRQTDLAI GVRERFSPALTRWVEELV
REQRALLEKYIKQDPSFLRSLTPCGLKPGAPPMVDMAEAAARAGVGPMA
AVAGAFHYVGRALVRRSKDVI VENGDIYLRSTRLRRI GIFAGKSSLSN
RIALEIPREDTPLGICTSSGTVGPSLSFGKADAAVILSPSAI LADAVATA
AGNLVQDETVDQKAAEHAMGITGVTGALIMGDRLAACGNLKLAPMAASN
RLREK

>2617919830 Ga0073689_10332 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_103]

VLMARIDFKKVREEKDLSYLENWYCLERTGERDLNPASGGHSPVVSATH
LIPWLSLNRVQFDLAQKQAMAGF

>2617919829 Ga0073689_10331 phosphate ABC transporter ATP-binding protein, PhoT
family [pelotomaculum Ga0073689 : Ga0073689_103]

VSDNKISVRKLNLFYKDFQALKDVNLEVGVNVRTSLIGPSGCGKSTFLRT
LNRMNLDIEGVKEGTIFMDGRDIYQPDVDVSLRKRVMVFQRPNPFPM
SVYDNVAYGPRI HGERNKRRLDEIVEASLRGAALWEEVKDRLFKSALGLS
GGQQQRVCIARLLAVEPEVVLMDPTSALDPLATMKIEELIRLLKKDYTI
VIVTHNMQQAARVSDTTAFFLNGELVESGETETIFTKPVDQRTEDIYITGR
FG

>2617919828 Ga0073689_10330 phosphate uptake regulator, PhoU [pelotomaculum
Ga0073689 : Ga0073689_103]

Table S2

MQKRI LENELEDLQFEI LRMSALVEKAI FESTKSLLNDQVDLANQVI AED
DNI DKLNI EVQDKCLRLLALRQPMAYDLRAI QTDLQI ATDLERMGDYSEG
I AKSTI RLYGKRTI TKLTYLPQMAEMVREMVHDI I TSYI LADVEMAKNSV
I LEKEI DSYLYREYFDI I MDTI KKDVENKADMAVQLLFAGHYLERI ADHATN
I GESVLYMVTGQVRSLND

>2617919827 Ga0073689_10329 methyl -accepting chemotaxis protein [pelotomaculum
Ga0073689 : Ga0073689_103]

MEKI KPVVLI KQNELLI KSI KTVRGKI RFGKPI YRGWSNLRFI TQMTVL
FTCLI VFI VSALGGATYFLGKGGTEKMQDNLVFSTKNMAEKI ELFTTTV
DSRELKNKALYQLSKEYSHYKSNGLRAKLAVI DQDGKI VLHMGDGDGQEF
LPAGLI SEAVAKKSGTATFEI GREQYVAAYENI AGKSWVYLSCLPEDDYL
APVYKMRNI TLAVGLSALI PAFFTCLVLSRRI TVPLDDVLQVAEKAGAGN
LAVRAREEGAGWELSRLGKSFNKMMLDLSSLI RDFKGVAEGLFARSGKMQ
MVAVNQLTSVEQTCAQVDEMAASVTDI TGKI GETQRAGEQMLQAVENGKE
ALDVI LKNMNNNF TLVDEQTRSVALLGENLGKI GKVLNMI KEI SDRTHLL
SLNASI EAARAGEHGRGFSVVAEEI RKLAGNAGSSVKEI DELI RAI DSEC
KVLGKVEESRLTAREGAQMI GRASEYLNNI YSAVCDVGTHVDDI SSAVE
QI AAGTEQVVATI QMMAGDAGGSKDVSAREVADQARELAATAQELKDQLM
KFKIA

>2617919826 Ga0073689_10328 phosphate ABC transporter membrane protein 2, PhoT
family [pelotomaculum Ga0073689 : Ga0073689_103]

MNARLADKAATVMFWI GAGVVI VI LASMLSYI LYHGLKSI NLEFLI LPAE
VI RAGGGI GPQI FNSFYLLFLSMLFTVPI GLLAGVYLAEFARASKWTEI V
RLSI ETLNSLPSI VVGLFGLLVFNMTGWGYSI SGALALTVI NLPLMVR
I TEEAVRSVPVGI REASLALGANRWOTI CKI VLPALPGLLSGAI I TSGR
VFGEAAALLFTAGMSSPPLDFSQWNI FHPASPLNPFPAETLAVHI WKVN
TEGLI PDLRRVADGSAAVLI I VVLGFNL TARWFGRI VKRLTAT

>2617919825 Ga0073689_10327 phosphate ABC transporter membrane protein 1, PhoT
family [pelotomaculum Ga0073689 : Ga0073689_103]

LGLGLNKNKTI NKLDLTRSELTGRI LTTFAAALAI I TTVVI I FFI ASKG
LSLFFVDHVSUGHFLFSTEWPPDRPPEEGGPQGVLAFLI FGSVVVSLMAV
AFSAPLSVTCAVMVEI APYWGLRVLQPAI ELLAGI PSVVYGYI GLSLLV
PFI RENFGGLGFSLLAGFVVLVSMI LPTI VSVSTD SLKALPREWKEASYA
LGSTRWQAI RLVLPAARSLI TGMVLGLARAFGEALAVQMI GNTRKI P
DSI LDPLI TLTSI TMDMGYTPMGSLLWNNALWTMGLLLLLMSCFFI LVVR
FVVRKGGVVE

>2617919824 Ga0073689_10326 phosphate ABC transporter substrate-binding protein,
PhoT family (TC 3.A.1.7.1) [pelotomaculum Ga0073689 : Ga0073689_103]

LFKKSQWLLFAVLCLSAVVVLTGCGSGGKDSGKQPAGEQKLSGNVTAVG
STAMQPLVEQAAQFMSKNPDVKI VVQGGSGTGTLTQVSQGAADI GNSDV
FAEEKSGI DASQLTDHQVCVVGMAAVVNPVDKI NNLTQQLI DI FTGKTT
NWKSVGGPDQKI VLVNRPKSGSTRATFKKYALDNEEAAGI EEDSSGTVR
KI I KETPGA I GYLALSYLDGSKALKLDGVEPTKENI TAGKFPI WAYQHS
YTKGKPLGAVDAFLKYMMSDDVQKAI VPQLGYI PSTEMKVVRDVSGKI TN
K

>2617919823 Ga0073689_10325 two-component system, OmpR family, alkaline
phosphatase synthesis response regulator PhoP [pelotomaculum Ga0073689 :
Ga0073689_103]

VPLI LAVDDVNI LELLKFNLTKEGYQVI TATEGQQALKYAREEKPDLI I
LDI MLPGMDGYDVCRI LKADRETAGI PVI MLSAKGDVLDKVVGLELGAED
YVTKPFSPREMARVKVHLRRNAQLAGGQASEPLNEI KVNNLVI RPDKYE
ALLDGMKLDLTPKEFELLHLLAVNPGRVFTRDVLLERI WGYDSVRETRTV
DVHI RYLQKI EQDPAKPDYI ETVRGVGYRFKEQA

>2617919822 Ga0073689_10324 putative hydrolase [pelotomaculum Ga0073689 :
Ga0073689_103]

MRI EADLHVHTI ASGHAFSTVKEVAEAAAAGRGLKI I GI TDHGLNMPGGPH
EYFYAQLLGLPGVI AGVEI LRGVEANI I DPNGNLDMPERFLAELDLVLG
FHEGCGYESGSVEANTRAMI RAI RNPYVHI I CHPGNPAFPVDI EKVVLAA
KLAGKVLEI NNCSFFLSRPGSAPRCRI FAELARRHKVMVAANSDSHFCDT
VGWCDHALDLI KAVGI KNEAVLNTSAAMVRNYLHRHKKVLQRTS

>2617919821 Ga0073689_10323 Ca²⁺-transporting ATPase [pelotomaculum Ga0073689 :
Ga0073689_103]

Table S2

LSDTV I I THHLPGR I RFSVRGLKRNQSLSKELASFFLQMKGVVDYRI SPV
 SGRVLV FYNSNDLNP GALT GALCLFLFTSETTSACREQLTEAVACSEREI
 YEPI PLNQKPGWPQMSPEEALQI MGVT PGWGLGNEEALARLEYFGPNKLLK
 EVEKRGFWSRLLDQFRDFLVQALMGSTAI CLI MGEFI DACAI LSI LVI NA
 VI GASQE QRAAGAVEAL KELSAPGARI LREGRPVQI PASRLVPGDI LLL E
 QGDI VPADARLLNVTGLSVEESAMTGEPPFPVAKQAGAI GSCVQLFDCDNM
 VFQGATVVKGRARALVTATGMETE I GKI AGLLOEGNEDRQTPLOEKL SAT
 GRI VFKSSLLLSGAVVALGI LRGGRVFNVFLTGVSLAVAAI PEGLP AVVT
 I ALATGAHRMAKTN AVVKS LPAVESVGATTI I CSDKTGTLT TNQQTVRMV
 YVGGQWWALTGTGYNPDGGEVVS LARDGGQGGAGLVFALAAASLCSNASL
 KKKPDDASDDPGPDARWQFTGDPTEVAI LAAAVKAGLDLEEVNQRYTRLN
 EI PFDADRRRMSVI CSGAGGNVLFVKGAPDTI LDMCRGA WHDGVVAPLSE
 TERRSI I RANDKLASRAMRVLA VAYRPLSDNSAGEADELERDLVFI GLLG
 I LDPPRLEV KESI ARCKHAGI KVAMI TGDHPNTAVAVGKELGI LKPGEND
 VLTGRQLEQMKDEELLAALDKTRI FARVPPRHKLRLVRAFRER GELVTMI
 GDGVNDAPAVKEADI GI AMGGAGMDVT KKSALI I I I DDNFSTVLNAVEQG
 RGI YANI R KSI RYLLATNTGEVLLMFGAI ALGLPLPLLPI QLLWLNLLGD
 GLPALALAVDPLQPLMNNKPRAGDNEVLDRELKVKVLSRGLTI GASTLG
 AYI LGLRRGNLPGARTLALATLTSGQLLHALDCRAEGKERSARNPFLLKS
 VLLSGALLAGAI YLPI GRSI FRTPPLGPADWGVALGGTAVSSLLDRLLLK
 TRKNKENL

>2617919820 Ga0073689_10322 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_103]
 LEQLEQARAKLAEASRLVREAVDLSLEVMCRDVKPDPAVTRLWEDFLGDF
 LKYI QI KGKEKKRNLFASI SFARVWRR

>2617919819 Ga0073689_10321 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_103]
 LLDNFNLYRI DVGLDKVLQYYKFSI EYEVFFMQRGGFDSRSDGYLLDEL R
 EELLAELEERSERQKVRRRRYPRRDLGRLRREVYNELNAMRAI ENRLRRS
 RVSPEARVLLNELMDEAADQGLTI DDLFRSLPRQPLTERLADFFQSRNGM
 YLLLAMLV I LATPSTREMVKPA LKKVAGEVNELADQVRGLLAKI KEGLED
 VVAEARFEKMKAMEQAI YEDLNNEETRPGPQPDKE

>2617919818 Ga0073689_10320 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_103]
 MLNRLVLRTSPWG LTTGLVVG I AASPVVRKSLRAAVVRTTMVALSVTDA
 VKSAGEKMGQEFGGI VSEAKSRKETQTEAVESKVRSAVAVGSGLAADV
 KVKEVAGGAKQKWDELVAEARES RKETVEKAEPVVETTGEKALT LREPPV
 QEEP

>2617919817 Ga0073689_10319 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_103]
 MKQGAARKDYSKI I HRLPGRLWI ELAGLRGAKSLSGQLAGEI TGVKGVKL
 ARANPCTGSLLVI YERQMYTETEI FELARACWQRVRQGGYGPREGAPA
 PEERKEHPNNNNEGNQEDCPLRAVS AVSKPLAGFVRPENI SYRRQLFNNT
 LVTVI MGVLGLRRLVWGASPLAGSPGLFNLSSAMTI LSGYPLLRRLRTL
 TAGGPVNSDLVMGAVGLTTAVLREGMLGLLVTWVGNVTALI NAAVREEYA
 RQLPQAVKPAGAEADPLAGETAASP VQHTSLPEEAVAGGYRRVFRRRSSP
 PGAGPSGDRFAPORTGGSRGFQQPRRPGLLV

>2617919816 Ga0073689_10318 ATPase, P-type (transporting), HAD superfamily,
 subfamily 1C [pelotomaculum Ga0073689 : Ga0073689_103]
 VVSNNPGGPDCLFEADVGI VLNNSQPAVAAAVLI PEQGLEKLGTLFKLSL
 I CQSKI RQNL LLMRTANSLGLYLGA VRRRLTPQLAAMYN SAVTLAVGLNTL
 FFVKRNGFYRNSGPKCGKKEQRPI TDRREAGDTPEKAPKPLLT LVKKNG
 DPPSAPEAALAPGKPACGNGWPRLTAGEALLKL GSDQLKGLTGDEVAKRL
 LTYGYNKLAESKRPGMFSRFI NQLNNFMVQALLGSTVVCFFLGEI SDALA
 I LAI VI MNAI FGMLQEQAENALAALQOMTAPGARVLREGQMI QI PAEL
 VPGDI VFLEQGDVVPADMRLLT VNSFEVEESSPTGEPCPVGKKTAVQKH
 DLI HECVNMAFMGT TVTRGRAVG VVVATGMNTEMGGI AGLLAADDNETTP
 PORRLEAI SKSVLKACLT VSGVVVLAGI LRGQPPFAMFLTGVSLAVAAI P
 EGLPATVTVALAAGVRRRLAREHAI VRRLPGVETLGCASVI CTDKTGALT
 K NQLTV

>2617919815 Ga0073689_10317 ATPase, P-type (transporting), HAD superfamily,
 subfamily 1C [pelotomaculum Ga0073689 : Ga0073689_103]
 VSGVGYEPGDFDFEDGKPVYHTLEDGLI STLTAGVLCSDARVVSEEEYTP

Table S2

NGAYDNRRVSTGRWLVLDGPLEGALLVAGMKAGLKPDKLRRSFPRLAEI
 PFDSERGYMAVSCASGEGETTLYFKGAPERI LSMCSRVLERGRVI PLDR
 RKEKI LAMNEYLSGQALRVLATAYRPAGEDPGLGLEEHEKELI SLGLVGM
 RDPLRLEVRDAVDSCRRAGI KVAMI TGDHRNTALAI GRELGI LDLAGPER
 VI TGPELEI MSNEELKAAVGDTNVFARVLP RHKMRLVNVFKERGEI VAMI
 GDGANDAPAVKSSHI GVAMGLSGTDVTVRESSTII I TDDNFATVVTAI EQG
 RGI FDN I RKSRYLLATNVGEVVLMTMTGMPLALLPI QLLFLNLLGD
 GFPALALGLDKPAPDVMQKPRSPKSRFFDRDYSNKI I SRGVS I GLVGMG
 SYI WGLRGGNLPLARTTTTLATLTLSQLLHALDCRWEHKVNGRNSGNKYLT
 GALGLSTLLLAGAVYLPTRAVFKTWPLGPLDWGVVGLGVGMSSVLDRLV
 WGLI NQFRPETGEDDRNTGQI EGI KTPAGI AYGEPTGHEI SPI MVDGSQP
 TCLTGSLPAPRVGGAPAGMGAD

>2617919814 Ga0073689_10316 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

MLCNAI AMEKYRKMI GDSI FTANGSDLLESACVTVDKCVQVI NEQVDRI
 DEKI REVPAFVVKALFEKTGVVEI FHRLVTSYDILI CLQRKVI TVLKQEI
 LPGGYEELKPPQVPI NTGPLNDVFSRTRAVI SDTKVSGI EKWASEKVL
 GLAMQGI PGEEI LGRFI GGI FQKTFEEARQAEETALI HRLYSVAGLLET
 VGSQI KEQLSYKVAVLVYSDYDLGEGSTCEGYENVNI PA

>2617919813 Ga0073689_10315 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

MYRYRRNKDLDREREAYEI LAEDLLAEI ESRRRWEDATRHRRAGLWGQI R
 DRGDYNRAASRLRADLARELRAI RAI EGRMGRSRDPVVRELLANLLEEAH
 ERGI TMDELARYYNGGGLOQLASLLPGGGAGGLSWALPLLLLLLALPPV
 RQGLKPLTKKVKGAMDI SEKI EELFTTAKEEMEDI VAEVNFEDI KNSLS
 VPEDPPPTS

>2617919812 Ga0073689_10314 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

MRWMRMGFLHQMSPGLTLVAGLAI GAVGI PI LRNGVRKLAYTATKGAI AV
 SDTVKNTGGKI GEEWKQI VAEI KAEKLKEKAAVKTGLRGAGVGI RTGMN
 LAEQAKDTI EGI KGEWRELVEEARS DLKEAGAAVTAASGTVKPTAVEDR
 EEQVEETGQYDNRYDNKNEI

>2617919811 Ga0073689_10313 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

MVLGHVNENNL SGI CAGLLSEQLSARVI YNI LLEI TACKI VEDCHQVVAI
 NVNRHFSYFQDMAPVLSSQI FNNATFAEELI QSTI GNGLTMLI ADI HRDL
 AEKLKI NI FHCEENSATPLI DVLPGVESLKSDEI I MESCKFSRLTSKI S
 FHLCEKALDQAVPKTLGCFLLKKTSM LALSECFRI AGRDAQLAGEMKKRL
 KGFI NNI RFQLI NAI NDAI SEFVFHCLDQI CGLPEEAEDRGELALTA

>2617919810 Ga0073689_10312 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

VFADAAEDI I VKHYLTGRARLFVPALKKDKNGFPWI LARLKKLPGVKRAE
 VNFTTGRLLVYFEESLLSLGELVAFRLTVLAEETGERDSSGTRNNI PSPI
 RAVKEPEDLPVWROVLNVALGGVLFWTLKHVLVGKSALAQSORLFNLA
 AVTAI I SGYPI FKSGLKNLAVKGRI NHDLMGALSLGI LLMRESVPGLLV
 VWLVNLNSLFQSLALAHSRRI VEECLAGNCGGEALLNEDAPSGLSPGTT
 PAEEYAEKI VPVSLGLAAAGAGATGQLNTALASLLAASPAPAGLARPGAL
 GAAMALARKKI LVRRPAAFARLRDNDLVFTGPGLPGCRPEVVEALPLP
 GFHKAELI SVAEAAFOEYRLKDMKEWPVSGEPPGGI SASCGGRNI LI GG
 KDYI SSAGVSTYPALLKEKRL LRRRNPLYVAVDGRLAGLLGLRPQI AAE
 TRSAI YNLRSRGVSGI YI VAGEGDLAALSLASELGLTI I PALPEEGVADF
 I QELRRDGGVVAAVGHGPGMEGLGNVDVRMVFKQAGGPCLKEADI I LAG
 NNLDLAGEAVALSFI ASERERRGVEI TGVLNI LGLVLALSRLSPGGAAM
 YNNLI SI AVSLNSLSMLRETGSAAGVGS

>2617919809 Ga0073689_10311 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]

LI RENRGHSYCRRLMNYLPKKI WELNI RQATVLGI AGAGGAGFKLI TCMP
 FLQYKDLLTI LI MI SVMVTLVDTVSSRI RDRI I

>2617919808 Ga0073689_10310 PhoH-like ATPase [pelotomaculum Ga0073689 : Ga0073689_103]

LTVRVLDNTI LLD RPMEEI I OSFPPCKI I LPLAVI HELDGFKGVDDQRGL
 YARSAI RFLDGLRPKLHEGVPLKSGHFLKVELNHTDVQLPDFLSRNKVDN

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RI LAVCKGI MEEELRLI SQDI CTRLI ADVLGI PAENYI VENI ELGNLYS
GWCEMVI SDREVQEFYQLASFSPDRPLMANQYLKLVDKTGGVHYGRYCAE
REI VVPLRRDLQAFGVGPAEGNMEQHFLMDALLNPEI ELVSI LGPAGTGK
TLLALAAGLHQVVNQDKYTKLI VSRALI PHSRDI GTLPGGKEEKLSPWMG
AI FDNLEFLTRNFAGSKYDKKLTPAEQVDRFMEEGFI ELEALAYI RGRSI
PGQWMI I DEQNLTKENI KTI I TRAGKGTI VI TGDII QQI DNCRLTATNN
GFVTLI EAFKEQKLYAHI TLNKTERSSLAALGVLELLP

>2617919807 Ga0073689_1039 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]
VSKI LSHKKI KSLEELHFKPVNACKRKTVEDQFANPI I KVDVSSGDVI CN
RLRLVWDSELVEYKGCPCDN

>2617919806 Ga0073689_1038 N-acetyl muramoyl -L-alanine amidase [pelotomaculum Ga0073689 : Ga0073689_103]
MI TI VLDPGHGGTDPGAAAFGLNEKDI NLDI ALRTRAALGFYEAKVYLTR
DTDQDVGLGARAAVANKLGADYFLSI HVNAGGGAGFESYVHTYAGEKSRA
I RDVI HARVSDFYSSAGFGDRGKKSANFAVLRLTAMPAVLLENLSI DRKE
DAARLAEPSPFREGLAGAI ADGLARALSLRPVDAWDPVAEI EKLKADGLI V
SDHEPGEKVPWGEFAAVI NRYRGKSSAADPWDPGKEI SKLKSGLI NSVH
DPVMEVLWGEFAAVLNRLRGR

>2617919805 Ga0073689_1037 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]
VANI RDYYRKNFLYEGHRLI LPELRDKVTHTCSECKFFI RVVGRTESTRAG
CAALI PRYANLARRVPRELDVMDVLKAVGREGLERVLGAGPGRQACGLF
HPGEYCNK

>2617919804 Ga0073689_1036 DNA polymerase-4 [pelotomaculum Ga0073689 : Ga0073689_103]
LGVI VLRCPTLLADMNSFYASVHQAMDPRLRGKPI VGGDPARRHGI VLA
ASYEAKARGVKTGMTVWEAGELCPEAVFFKPRHGHYVNFSAI VRI MKDF
SPLVEPFSI DEAFMDVSGCGRFGSSPGI ARKLKERI KGEVGVLCSSVGVG
PNKLLAKMAAGMQKPDGLTLLDFPDVPARLWPLPVRELFGVGGRLKRLR
ELNI HTVGELARYPLPALRQRFGLVGHVHLHLSANGI DYSPVDPHSLERVR
SI GHQI TLPRDYRGYREI EVVI LELCEI VCRRVRLGGYVGRTVNLI LKDV
DFLWLSRARTLARPTASTNDVHRVAVDLLHRHWPAPKVRMVGVSAGLV
KNTVEQMDLFGAEAKARLHAACDRI KDRFGEQSI LRAI SLTPEGVLDR
NGEAGRG

>2617919803 Ga0073689_1035 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]
LTPFERKAMRCQNCALI EI PSPEI QPEEI RDYI AI MGKI HFPCPECES
HQPLVSEAI TI LRKF

>2617919802 Ga0073689_1034 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]
MYCWNEKQMWVDSAI FI GGSGAVLCENCNEYRLPGDGGPACRTCPEAI RQ
FPDQPEEHFNROGCTCANCRELOKKYLPKQGR

>2617919801 Ga0073689_1033 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_103]
MVSVYPLNKLRYGTDI AGRKPGNSHSAPLQNKGI LQQFLLCAELMKFK
KSGAKQLLFFVGI GLEVEQRLKGSKEKRRTESSGLI AWYGI TAPASAGTS
FATPGSSRMCLAG

>2617919800 Ga0073689_1032 selenium metabolism protein YedF [pelotomaculum Ga0073689 : Ga0073689_103]
MSARVVDGRGKACQPVI ETKKALEEEVGKDI LVI VDNEAARENVSRAF
NAGYQVTVVVEKGLYHLNI TGSVGRVPATGPVAEEAVGCMPATGGVVYFI
TTGAI GQGSPLDGLVALMKSLMNTLVEQQPPRALLLNLTGVHLAVEGSPVL
EQMRKLAGAGTEI LVCGACLDYKMKELAVGVVSNMYEI NSRLAGPYKV
ITVA

>2617919799 Ga0073689_1031 Nitrite/Sulfite reductase ferredoxin-like half domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_103]
VEI NQEMPKNLDERFQHSTPGRDMLEKGI LQRDGAYAI APhi PGGVI TD
PELLI KI ANVAKKYNCPI KVTSSQRLAI VGLRQEDI DAAWQELGLSPGA
AIGLCVRSVKFCPTTFCKRGQQDSVGLGMEI DRRYHGMLTLPKFKI SVS

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GCPNKCMDAMVI DFGVMGAPKGFTI YVGGNGGI NPRFGEKLAHQTEQV
LDI LDRTVSFYKKEARTNERLGRFI DRI GFDRFRQEVLKEEFIH

>2617919798 Ga0073689_102157 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

MALVNENYLKLPGSYLFSEI ARRVNQFKKDNPDADI I RLGI GDVTLPLPP
AVVEAMKKADEMGRQETFRGYGPEQGYEF

>2617919797 Ga0073689_102156 Radical SAM superfamily enzyme YgiQ, UPF0313 family [pelotomaculum Ga0073689 : Ga0073689_102]

MI REGNPLKVI LI YPEFPDTFWSFKHALKFI RKKASSPPLGLLTVASMLP
SDWGKRLVDLNVKRLTKEDLTWADYAFVSAMTVQRQSAHKVI ARCKEEGV
RVVAGGPLFTTEYEQFETVDYFVLNEAELTLP AFLNDLEQGRANRI YTTA
GFADI LKTPAPQWELADLDYATMSVQYSRGCPYNCEFCNVTALFGHRPR
TKSARQVI AELDSFYNLGWRGGI FFVDDNLI GDKRRLKTELLPALI EWRK
NRAGLSFNTOVSI NLADDKELMOMMVEAGFCTVFI GI ETPEEDSLAECSK
KQNMHRNLVEDVRRRI QQAGLQVQAGFI VGFDSDSPATFQRLADFI QKSGI
VTAMI GLLQAPPPTVLYERLKQAGRLI ERMSGDNVDGTTNI I PVMNLDVL
RNGYKNLLQYI YSPEAYYQVRKTFLEYNLPRLDVPLDFEHLLEYI LAFI
HSVYRLGVVGKERVQYWKLFWWTLFRRPRALPLAI TLAVYGHHRKI SEL
RVL

>2617919796 Ga0073689_102155 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

MQYLRTELLTLKLYKYYSI VKKVNI PLI ASTLLFVEFHVDRALQGNPEW
VTEWWVDRI GVFDSEGGI KREYCREFAEQL

>2617919795 Ga0073689_102154 mannose-6-phosphate isomerase, type 2 (EC 5.3.1.8) [pelotomaculum Ga0073689 : Ga0073689_102]

MKI AMLSPI AWRTPPVGYGPWERVVSLLTEGLAAEGI DVTLFATADSATR
AKLHAI APRPYEEDKTELEPKWECLEHI SELEKAGDFDLI HNHFDLPLT
YSGLTDPVLT TI HGFSSPKI LPVYRKYNHKTYYVSI SNADRSPEDYI A
TI YHGI DI ENFTFQEAPGDYLLFFGRI HHDKGAAEAVQI AKLTGMKLI LA
GVI QDI DYYKSAVVPHLDGVMVRYAGVAGPELRNKLGGARALLHPI NFN
EPFGLSVVEAGACGTPVVAFFNKGSMPEI I ESGANGFLVGDVCSAAEAVRS
LDTI SRRKCREI VEERFSRARMVEDYLGVYRKI I EKK

>2617919794 Ga0073689_102153 Predicted glycosyl hydrolase, GH43/DUF377 family [pelotomaculum Ga0073689 : Ga0073689_102]

MSFKKRAPVVKRYAGNPI LTRDDVPYPVATVHNAGVVKVNGRYMMI FRSH
LLNGRSI LGMAESVDGYGKVRPEPFMTAPARDGVWGEYEEYGVDPRI CQ
I DGDFLI TYSAYSRHGVI GLARTRDFRSVERI SLI TQADLRNVALFPQK
FGGRYARLDRPHSEI SPWSMWI SYSPDLI HWGDSKVLVKPAGYHWDEMKI
GPGATPFRTEGWLNI YHGVFRTMDGAVYRLGVI LHDLDPSRI LGVADE
WI LQPEDPWEI TGYVHNVVFTCGAVSEEDGTVKI YWGGADKVMCAGVASI
SDLVAMCLERSRDPM

>2617919793 Ga0073689_102152 Predicted glycosyl hydrolase, GH43/DUF377 family [pelotomaculum Ga0073689 : Ga0073689_102]

MDVGQSKDLEMPFNEI VKDVVEQAKVFGEVHVVI GI PFYFNEKELLPEV
LKMLDEGLTGLQDPGKSLI I CVGDPGSAETMESVRHLDLKVPHEFLMKH
GI SGRGASI RAI LEI ANI LEADAVI FAADMVREEGRGMQSDWI KRLI EPI
RGEYDFVVTSFQKHFFEEELLSLFLSPLLEVFYGYNVKGSLSGI YAI SHD
TVEEFCADI KFWNNI TREFGI DPWLVSAMRWKNI CEVEFNARLEGI SI
EKLKVI FKDRARLLFECI KMDEDYWPGGKFI I RTPDI YGSKI NDATLRPF
YSSQDLALFRDI HI QEKNLFNATYI DYLYEGI GGI ESVPDKDLRI EGKAW
TEI VYRLLLLKYWFASGVHRDDI LSALTFAFSGRVSSI ESI QSMKEQLAG
AKNVDI NFI VSSGVTSKAEQAKRDFLRLEMF I QI WKQRDLEMKPPLI PA
HYLEFI PGVPTVLPKRI EGQGRVVSSEEI FNRFSQRYQEAFFSHFI GDGL
GTPESAGSGTI TQRMKEFMSELEKTMWLLPGDLYTVEGTRQVVDGLFRF
FHSPTVFSLKDDFLRELLLRFPPLNFM I PAECRTPRELI KKLGI RDAATL
ANLVEARNYVNKI LWI QDNLRPDGMGEVELKPI VLGEKAPGGTVELGNI
SVFNNTLSRI VVRPLDKGMGGDYPRLRFSLFVARHI MMAENYGVLRMYA
KERKNLGEKI RNSVAVHYETI PFSAHSI FENFHHRALVGQLRALSQLAD
AGQNEQARLI KMMCDSYGLSQVLADGTF LPCSAWSWASYSYKGGKSI PTP
LSCHVEEKWFNHDFFLEI YKELGYDPGQI VKTVFQLI GEGRAGQNL I NVL
LGI RPKKDVTVVQEQQDYPPAKPLVRYAGSPLLSPI KEHPWESKYVLT
AALRVKDRVYLLYRAYGDDEVRSI GLAVTDGCNVLERLPDPVFPQDRAE
KKGVEDPRVTI I DNKI YMLYTAYDGI I AQI AAAAI GLDDLLNKRFDKWER

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KGLAFQDI WDKDALLFPEKI NGKYVI YHRI EPSI WVLQDKLEFPAPKI E
HSI I LGPRSGWMMWSLKI GAGSQPI KTKYGWLLI YHGVDNRNVYRLGVI L
I DLANPERLLYRSPNAVLSPETEYEI GKEGESWVPNVVFTCGAAPAKDKE
VLEAGDEI LVYYGAADTHI CLATGLVGDLLPESVRQE

>2617919792 Ga0073689_102151 Radical SAM superfamily protein [pelotomaculum
Ga0073689 : Ga0073689_102]

VDLSFEQGPI RPPSEATSLLLRLTRNCPWNKCGFCKTYKGEKFSRRTVDE
I KEDI DTVTRI CWSVRDFSSARGFGGTVNEEVLAHI YGSGQFQLFHVAW
LYNGAKTVFFQDANSLI MKTADLLEI LKYLKERLPSVERI TSYARSETLL
RKSVDLAELGRAGLSRI HVGMEGSDDEVLFKI NKGVTAAQHI DAGRRVR
EASI SLSEYVI LGLGGKQWAQGHPLETARVLNAI NPDFI RLRTLTVVKG
TPLYQKMLNGEFEEQPEEDVVRGERLMI EHLDDGI QSNLFSDSHSMNLLLEEVN
GSLPGDKPAMLATI DRFLALPDGEKQNF I LGKRWAMYRRLDDMLDLARHS
EVRKAI DRLKKEGKLGETI SFLKGQLI

>2617919791 Ga0073689_102150 L-ascorbate metabolism protein UlaG, beta-lactamase
superfamily [pelotomaculum Ga0073689 : Ga0073689_102]

MKI QWLGHACFLVTLNKGKTI I TDPFDSNVGYPPQGLYADI VTVSHQHFD
HNAVKTVPKSAI VQKEGRHSYEGVVI TGVLSFHDTAKGSQRGKNI I F I I
EAEGRLI CHLGD LGHVLEPDQVDKI GAVDVLLI PVGGYYTI GATEAI KVV
EOLKPKVVLP MHFKTSYI DFP I STADEFLKSYPGHRVERELVLSADSMVP
SQQVVLLELKKI TRGGCDPGC

>2617919790 Ga0073689_102149 exopolysaccharide biosynthesis polyprenyl
glycosylphosphotransferase [pelotomaculum Ga0073689 : Ga0073689_102]

MGKPNGTEKKNF I FRAVLVPMDLALVNLGYLLAFWLKFGWKI PEDNFAA
YLSTCPWLTAAAMALLYFYRLYSSYRWRWTEVFASLVCVFFQGLAAMAV
TFFLRGFSFPRTVLLAPLI QLALLSLWRAAWHVERRLENPRRVVVVGQ
PSDALALADKLEAAPGGI LKVAGLVVENGEETDDLVPGLPLPRFLPPGS
DLPPVAGSGTALAEAAAGADLAVKVAGSRDAGLPGRAVRAESGVGRAEDS
SGAGFPWPASAMADARRLSEYHRLCNI LGRWPVLGGVAEFCECLDAVRP
DQVFVCSALSPEAKAEVYACVARDNRVFLVPGLYEI MLAQARLDQVDDV
PVFTVGR LAI PEEAKFVKRATDI LI SLATLVAAAPLFALVATAVRDLS PG
PVFYRQKRLTLOGKPFYLYKFRTMVADAERESGPVLASENDPRVTRVGRF
LRATRI DELPQLLNVLKGNMSI VGPRPERPSFVDELMKETPEYVYRMNI K
SGI TGLAQI AGRYSTSPENKLKYDLLYTKSYSPARDLAI LLQTVKVI LMK
DRAS

>2617919789 Ga0073689_102148 YvrJ protein family protein [pelotomaculum
Ga0073689 : Ga0073689_102]

VSNVGFPI AI SAYLLVRI EGKLEKLAVSI AKLAEALAGERQEVKR

>2617919788 Ga0073689_102147 Protein of unknown function (DUF2922)
[pelotomaculum Ga0073689 : Ga0073689_102]

MRLATTTQTRMVFNRQAGRNVTI TLDNPRDNLTAEEVEAMDVI ARNI
FTSSGGDLVSKQDI RI I DSTTNDLYDPQA

>2617919787 Ga0073689_102146 Protein of unknown function (DUF1659)
[pelotomaculum Ga0073689 : Ga0073689_102]

MAVSKI PANSALRLELRVGTDPENPVYRNRLNNVKPAATDQDLFDVAN
ALAGLQEYPLNGI SRFDSAQLAQV

>2617919786 Ga0073689_102145 Glycosyl transferase 4-like [pelotomaculum
Ga0073689 : Ga0073689_102]

VVYHVAAGLSPEQFEI TVACAPGGELVQWLRELPOKVRVI EI PELKRNI S
PLKDLKAFWKLYTLI KKKGFDI VHCHSTKAGVLGRLAARLVGVPKI FFTV
HGWGI NKYQSWPVRF AKRRPTVVPATGNCTWMGWKNFCLDFGYKPANTGW
KOMTRDGNQFARFVKTVAPLSFTTPGVFPGI WGVSLNMRQGYNRRNMWK

>2617919785 Ga0073689_102144 Nucleotidyl transferase [pelotomaculum Ga0073689 :
Ga0073689_102]

MKALI LSGEKGTRLRPLTHTMAKVVLNPRPDSPTKGKI TAFHMGQLNPV
LLRI PPFVHHGFTAEGGQMAI I VNYPTELYNYVEPDEFRLPYNDPSI PYD
WEVKHG

>2617919784 Ga0073689_102143 dTDP-4-dehydrorhamnose reductase [pelotomaculum
Ga0073689 : Ga0073689_102]

LKVMVTGATGMLGRQVALEYRRRGAAVYGLPRRELDI TKPGQI DTI I QKI

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KPDVVLNCAAYTNVDGAEKEEKAFLI NGLGPRYLALACRRYGATLAHI S
TDYI FDGWANRPYQVYDTPRPI NTYGASKLFGAAVRETGGNFFI VRTSW
LFGPGGKNFVDTI LNLAREREELKVVDQDQGCPTYTI DLAEALI HLVESE
VYGTYHVTNTGETTWYEFARKI VSTAGLKI QVNPCKTQDFPSPAPRPAYS
VI DLFPFKQVTGYSLPAWEDALERYI K

>2617919783 Ga0073689_102142 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

LHYPPSCI TLSI TNCLVI GQPSI KDTMDLTNYSCHLFGKAVRLSPGLF
RVVVMFLLAWFRKTRRDNPPI KGTSPDHVQKCSPRKSARNSPAAPRVSP
SI SSASSRRSKI STAFRLPAQLFQQPGMAVTAIEVPVRHPVEELSHI PI I T
THWTCPARAEKPLTPVI PAI LKP

>2617919782 Ga0073689_102141 Glycosyl transferase involved in cell wall
biosynthesis [pelotomaculum Ga0073689 : Ga0073689_102]

LGQMKVLLVI TLSELGGAQRVYHI AAGLSPEQFEI TVACAPGGELVRWL
RELPOKVQVI EI PGLKRNI SPLNDLKTFWKLYSLMKKKSFDI VHCHSSKA
GVLGRLAARLAAVPKI FFTVHGWGI NKYSQPARFFYTWAERLAGAVSTR
VI CVSESDLLKGRNLRVAHDKLYVI YNGVTDSQKKGALRGELNI KKED
I I I GTVARLAQQKDLPLFLELAEWMI KHPKNDLSEVRI YFVFI GDGPLKA
ECEKFVI RKGLDERVFLGAREDAVELVRDFDVFAFWSRWEGLPLTI I EA
MLAGVPVVATDVGGVDELVVDGETGFLI RGLDPEAAERALLKLLADGELR
RRLGEAGRKRAREKFSLEEMVRRYRELYLEGLER

>2617919781 Ga0073689_102140 glucose-1-phosphate thymidyl transferase
[pelotomaculum Ga0073689 : Ga0073689_102]

MKALI LSGGKGTRLRPLTHTMAKQLVPVANKPVLHFVMEQVAEAGI KEVG
I I I SPETGEQI KASI GTGDSWGFNTTYI I QDKPAGLAHAVKTARDFLGDD
PFLMFLGDNLI QGGVKELVAQFNTDI TDALI LLKEVPNPRAFGVAVVDSE
QRVRLI EKPKDPPSNLALVGI YLFSPVI HKAI DKI KPSWRGELEI TDAI
QELLNMGHKVTARRLTGWMLDTGKKDDI LEANRVVLDEYAKVEI TSSSDV
DKSQVVGVRQI GAGAEI I ESVI RGPVVI GENCKI I RSFI GPFTAVGNGSI
LEDVNVEHSVI LDRCELQQVPRLEDSLLGTGAKVSKKNSAHKALHLFLGD
DAEVI L

>2617919780 Ga0073689_102139 dTDP-4-dehydrorhamnose 3,5-epimerase [pelotomaculum
Ga0073689 : Ga0073689_102]

LDLI KDVVVKQLKI I PDDRGYLMEMMRKDWPEFMQFAQSYMTACYPGVYK
AWHYHKKQYDHFVCI TGMKVVLFDPRPDSPTRGKVNAFHMGLNPI LLR
I PPFVYHGFTAEGGQTAI I VNYPTELYNYAEPDEYRLPYNDPSI PYDWEV
KHG

>2617919779 Ga0073689_102138 RmlD substrate binding domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_102]

LKVLVTGAAGMLGRQVVLAYKRRGAAYGLSRRELDI TKPDQI NI I IQKI
KPDVVLNCAAYTNVDGAEKEEKAFLI NGPRAALSSI GLPPACSSAGAYK
H

>2617919778 Ga0073689_102137 dTDP-4-dehydrorhamnose reductase [pelotomaculum
Ga0073689 : Ga0073689_102]

VHI STDYI FDGRANRPYQVYDTPRPI NTYGAGKLFGEAAVREAGGNFFI V
RTI WLSVPGGKNFADTI LNLAREREELKVVDQDQGYPTYTTDLAEALI HL
VESEVYGTYHVTNTGETTWYEFTRKI VGAAGLKTQVNPCKTQDFPRPPAR
LFCYGSFSFQASDRF

>2617919777 Ga0073689_102136 dTDP-glucose 4,6-dehydratase [pelotomaculum
Ga0073689 : Ga0073689_102]

MKLLVTGGAGFI GSNFI RLMLAESDWEI VNLDKLTAGNLENLADI KDNP
RYSFI RGD I ADTKLVDEI FNQHKFNAVI NFAAESHVDRSI QDASPI ATN
I MGTQVLLGASRKYGVQVSTDEVYGSLEDEEGFFTEDTPLAPNSPY
SASKASADLLCRAYHKTYNMSVVI TRCSNNFGLYQFPEKLI PLI I TNAI E
NKPI PVYGDGMNVRDWI HVLHDCQGLKLA I EKVPGGEVYNI GGGAQVPNI
I LVKKI LEI VDKPELI TFVKDRPGHRRYAI NPQKI RHEMGWEI SFNFD
RALADTVEWYRENRTWWERVKSGEYQYQWYSRLSKEE I FNNARQTL
EHKNLTKRGGI KALSKDMEND

>2617919776 Ga0073689_102135 Glycosyl transferase involved in cell wall
biosynthesis [pelotomaculum Ga0073689 : Ga0073689_102]

MKVLFEVENTAVRSPRPSDLPRI VKRLEAALFRTAGRNGELLPENLAVYSP

Table S2

LAVPLPYNKAAVAWNFSLI KGRVRRFLEEEKLRPDEVLFITYLTTPALRL
LI EAFPWARVVYDVSDPKKVESRLAPFEERFLRRADLTLFASATLLEQY
RGHTKKPVLFDRDGFSTGLLDVEVETPDELAGLPLPRFLYI GGI NRKLWVE
AI EALCATVPHGSVMLMGPVAHGEVVLKLPNLHLLPPRRRYVELAGVLR
AADAGLI PYRPDPYAGAMHPAKLNEYLVFGLPVVAAATPELEKLAREFPF
EFI YFGTTPHEFAEAGLRALDGRTRLSQEKI SGFI TQFGWAARLKEFLKL
CEGDY

>2617919775 Ga0073689_102134 Glycosyl transferase WbsX [pelotomaculum Ga0073689 : Ga0073689_102]

MNQELYQYLKRI YWNLPLPENVKKSI I CRARALAFI FQHKFI LSEQSLQH
ELELLRAYI DHVLA I PEKPGPEHVGLAKDCYNRCGDGPKVLAYYLPQFYF
TPENDAWWGRGATEWNNVSRAPQYI GHYQPRLPGEGLGYDMRI KDNLKR
QVELAQMYGMYGFAFYFYWFDGKRLLKPLDMFLESSDLDFPFCLCWANE
SWTRRFDDGTGCEI LMKQNDTAESYI AF I DSVI PYMRDCRYI RVNGRPVLV
I YRPSFVPGCAAI LRI WRTHCRNAGI GEPYI I GVREHTWDADLLTHGFDA
QSEFHPGTI FRYCENI TEKI KFMRRDFGGLVLDYRDI VENKKYFRYSYPK
LHRAVMPAWDNTARRNNMGM I FEGATPELYKRWLKDVLVETKSNHELDEP
FVFI NAWNEWGEGAYLEPDRRYGYAFLQATREAI EEEYR

>2617919774 Ga0073689_102133 Methyl transferase domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_102]

VSEI NSQAYWDYRFSSDWEKCGREQSRFFI ELTI QAFPEWFWKEVRFHR
LSI CDWGCALGDGTEVLSDFFQGS DI TGVD FSSI AI QLASKEYGKI RFLY
EDWLKRELE TN I TCYDVVFSSNTLEHFNDPSI PMDVLFRHANLFVVL TLP
FREI NRI AEHHYTFLTNNI KVNPFKNFLLVHSKI I NSAI LQPNYWPGEQI
VLI YARPDWLQANSLTSELNI DSEQTI FLKEKLEDSKQEI ENI I QTLAE
HEVKI VDFKDKLANRDTRI SSLI HVI AEKDGEI ASLNDTVAERDMQI VNL
NHAI TERDGOI ANFNRAI AERDGOI ANFNRAI AKRDGOI ANFNHAI AERD
GOI TLLQROI QDI FESTSWRI TVPLRAVSRI MRDKLSSSGEVTANQHALT
STTSEPTDGLPYWVRHGHYYLQRFNRGVRRYGF LRSI PRSVRALYMLSSA
WLKKVVRHRQYEQRMVELAAMI KSHRGFI DLFHVPMGWNTPLFQRFQHI S
QQAARLGALALYGGHHQVDRDLLVFERVOGNVVVFDALDDR VVKCI FDKL
RGTFQKKI LRLQSI DLVTRI EDI EQFLADGI TVVYEYI DEI SEEI TGTIP
NFVKERHKALLQDERI LVVATSDKLFNEVKQQRARNYLLSTNGVDLEHWR
KTPRKPPVDMEPALQSGRTVVG YHGALAKWI DYELLHMI VDNGKYELVLI
GYEHDSSFEEKSLI QQPRVHFLGSKPYFELNQYAFYDVG I LPFKRNALT
ESVSPVKI FEYMAANKPVI TTDLPECTKYKSCLVAKSHEEFLEKLRI ATV
LKQDETYLI ALAEDAERNSSWAQKVAEVLHLAGVQI K

>2617919773 Ga0073689_102132 Lipopolysaccharide transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_102]

MSSDDI AI RVSNSLSCYFI YDSSQDR LKQYI YPRLQRF LGRLPKNYFREF
WALKDVFFEVKKGETVGI I GRNGSGKSTLLQI I CGTLTPTCGTVETKGRV
AALLELGSGFNPEFTGRENVMNGGVLGLSKEE I DARFDDI AAFADI GEF
I EQPVKMYSSGMYLVLAFAVAI NVSPNVLVVDEALAVGDVRFQAKCI RCI
KQLKESGTSI LFMVSHDI SSI RTLCDKAVWLDGGGI RMQGSVFPVTGSFME
YMADECPETVPLSETRPI VPVI PEAKLPATPAI DSKPVTHWGSHVGC I
TAGI YNLEGQRCDVVRYGEHLI VKI VFHPPEI ANMHFLSAAFSI KDMRG
TDLFVSTTFDKGQYFTTDAQDSI I EVVFKFANYLVNGRYLLI AALED RSSG
TI HYYEYI EGAQYFASLNNEKLFGI FHPEI KQYI KYFSGNTVRVVO

>2617919772 Ga0073689_102131 Lipopolysaccharide transport system permease protein [pelotomaculum Ga0073689 : Ga0073689_102]

VNPHQAHPSSPLAMFTSFWRNRWLI WQMAQREVVG RYRGSV MGLAWSFFN
PVLMLFVYTFVFSVVF KARWGVSGEESRADFAI I L FVGMI VHGLFAECI N
RAPGLI I SNVNYVKVVFPLEI LPWVVMWSAI FNSLVSVI VLLI GQFI I N
QSFPWTSVLI PLVI LPLVLAGMGFTWFLAALGVFVRDI GQVTGI FTTVLL
FLAPVFYPVSALPVEYRGLLQFNPLTLI I EESRKVLI YNSLPDWPSLGFA
LLASLATAAAGFWWFQKTRKGFADVL

>2617919771 Ga0073689_102130 Tfp pilus assembly protein PilF [pelotomaculum Ga0073689 : Ga0073689_102]

LPKATAKPKEKKKSAQPKKPP EVKKAPEI KKTAE SKKAPRNEPWEFSHAI
AFWGLAI LLFLPPYFRGLFFQPEQERALI FAAVI FWF A WLKWSKRDNSF
LSHPLDYFVPAPVYVI I SAFQTANYGLAVDEVKTTLYFLVYWLASRLV
RNDKDI VTI LHVI YI SAI GVALAGLATATGI I EI KDGFLNGRI YSSFQYP
NALASF LGAAAFMGI YLWRRAGSPELSGGAGGVAI KGVDPDLNWN NAGQY
LYAAGNFLLLAVFLGTKSQGGFLVFTVV FALFVLGLPRGNRLPVVFHI AL

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LAVPSLI AI WRFLAAVAGGKADPAWLWI FAGLALAVAGQALYSFAERKGL
 FOWI AGHRNVFLAAALLVVVTAGI GSGVYAGGHSDTI KAAVEEI RLRNAT
 ERMYYFODALKMFKDRPPLLWGSGGGWQEA YRSYQGYLYNSNQVHGHYFQI
 MVETGLLGLLAI LGI WASFLYLTHRLYHGARENPATRFLVWTI TMAAVSI
 GLHAVI DFDLSLSALALVLWTFMGFARGI GLYSGAGAEKKSRKYVPPNN
 TVLAGI SVASFI I I VFAGSLAAAGSYI TQAGQYLQRRDFNKGTELI RKAI
 SCNPSNAEYHSSLARVYQMOGKPEEGI TEALKASELSKYNAQRYSELASL
 SFSLKKNEEAVNYAEKALALAPFQVQWYELLARTYFMVGYNELTGGNREA
 AKQYFEKAAGVPNKI EKQMTSLDETEKRLWKDAPLMTDTPAVKLNVGASQ
 YLLGQWSDADANLOVALSDDKTKEASLWLAVLRNKQGRTEAGELLAQS
 QMLVPELAKGYQGLQGLEVFK

>2617919770 Ga0073689_102129 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_102]
 MMDLAGEGAPAEAGRAWNGAASAKRGGAVGSGKATAGSGAAATGDGAGRR
 PPVAAATATGDRALYGGGADGGTAAAAGI TGEGEAAAGHGDEPAAGHGGGG
 GI SPGSDLVVATCRLARLYRREPI KLLYDSLHG

>2617919768 Ga0073689_102127 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_102]
 MVYVNSYANRI VMKFYRKNQRLPPLTCYLVGSLSLWQGLLHYFFKDLTSI
 VELTSEKHRTRLGLFPFI EFTAQI VKSLMLYYHASLI PYVRVLDVI REAA
 I AGI CFNTHAI EELAEMLDVNPVTVTRWWRI FRDKAGVLMALTAYASNH
 FI H

>2617919767 Ga0073689_102126 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_102]
 MNI GREI EECPYCLAI HSLKYESMATVWRWDLELPGDWQFPQWEAVRLF
 P I QVPQVLRCSQCGEHI KVI PSFI QHGTTLTLPAL I FVAFAYEFSGLTWW
 DLPQKFCASNRI THSTLYKAVHGLGQLI HADSEFRKLCEQHLPAL KTI P
 SWPI PNE

>2617919766 Ga0073689_102125 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_102]
 LLDI TRI TQNKI HLQQRLELNELVROTLEDHRALFEKNGVHLEI GLAPS
 ALFLDADRARLAQVI GKRSYPNMDI VKSDEYRPGD

>2617919765 Ga0073689_102124 PAS domain S-box-containing protein [pelotomaculum
 Ga0073689 : Ga0073689_102]
 MSGARI LI VEDEGI EALDLQHRNLRLGYI VPDTASTGEEAVKKAGETSPD
 LVLMDI MLRGEMNGVATAGQI RARFDI PVI YVTAYADEDTLQRAKI TEPY
 GYLKPFNDGELHI TI DVALYKHKMERKLKESERWFATTLRSI GDAVI AT
 DKNALI TFMNPVAEKLMGWKLGEVLNKKLTEVFNI I NMYSRKPTGNPVTR
 VLLEGI VI AGLANHTLLI ARDGKEI PI DDSAAPI KDDKGN I NGVVLVFRDV
 TEREQAANALRESVERYRALAEELREADHRKNEFLAVL

>2617919764 Ga0073689_102123 Two-component sensor histidine kinase, contains
 HisKA and HATPase domains [pelotomaculum Ga0073689 : Ga0073689_102]
 LKEI WLEPLEPGHCEMVSYI LNSPLSQTALSDFGALTEGNPLFVSES
 LSYLYNQDLLFLDEDRQWRWDLDKI RRFPMPTNVVALFNTKI QKHTADLI
 NMLEYCACMGNTFSPAELSLI RGMSLLETYEI LKPVLGQGLLI ESKDRLO
 FI HDKVREAVLSSI PAERRCRI HRQVGNHLLAAVPEDGADI EKLDNLFTI
 VAHLNLGRNEHPDAKTAYLLSDLNRYAGNKALDSLAAEVANEYFNLSRAL
 LPDDCWDHDERI FRI FOKAAKTELI CGNYI KSERLLNELLDHAKTDLD
 KAECLAEQTTSLSSI GNFI KAI ETANRGLAYFGKSI PKSPDEADKRRLEL
 MAGI TSKNI DI HDAI LDMPTTDRKSKVELAFYSELI PDLYMSGLAPQLY
 LAAAQSTRHCLSGGMDESIV YSFSI MGLHLGEQEEFEQAFRCEDLARDLC
 SKYPNTFGATRGMNGI VWCNMHSRSHPEEI ADYCLKSI QCGKNCGDLYNA
 GLSYGPLMWNLQVQADLSLI DDYAGECLQFSNRYHLAFSAGLAEAMRAG
 WI EPMKKQYAPI PMEEKLKAWEQDNHI ASAGSYVHMAHAYYLGEYEEA
 GKYLEGVRKYL SGLTDNVLKRWVHFQVLNALKLCEKGLRFKSKQELLAE
 I RPI I EKI KKWASLGPLLKPYLAFI HAELERVAGEFRNARSLEYLDAI EAA
 HKQKYTFLEGHNECLGEFLLQAGHCSERVYFAEAARLYKKCRAGRKEDN
 LI KRYPEYFEEDI TSCPSTEAGSVSRI LPDLDAEYLMKSSLAI SAEI EQD
 I LMKKI MNVVI ESSGAQRGYLLVRERGDIFI RAASHI SDKRVVQTFNQTL
 EEAADI CKAI VRYVYRTGEKLI LSNASREGMFRDNPEVQKMLRSVLCPL
 VI QQSRTI GI I YLENRLSDSVFTSEKTQMTTELLTSQAAI SLENSRLI EEM
 KEAEGQVKKSLREKEVLLKEI YHRVKNNLQI I HSMNLNLQLPYI KDEQAEE
 LFKESQNR I HTMALI HEKLYQSESLAKI DLSGYI KSLTANLFLSYGVSER

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AVKPNI I VEDLALNI DTVI PCALI I NELVSNLSKHAFPGSPGRTGKSDEI
 RVDLRRGAGNKF I LTVGDNGAGLPEGFKI QNCETLGLKLV I VLGKQLRGA
 I NLNTCGGTEFTI TFTEQKKERGNAMNVRKDTDC

>2617919763 Ga0073689_102122 Protein kinase domain-containing protein
 [pelotomaculum Ga0073689 : Ga0073689_102]

MLLPNYKI I EKLAESRQTVVFKAYHQKNPDRLLALKVLKTI SLSEYKEAQ
 FRQKI EHLRVLKDPLI I TPI EFAAKDGI CFI AHDFFDGTPLNKLTEAHTG
 FRPDI FFTI ACQLARALDKAHEAGI I HGGVKPHNI LVNPGTLDI RLI DFF
 SVVDVRDVSHFI YDRSFI RETLSYTSPEQTGRI SHMVGFSDDLYSGLI VF
 YEMLTRRLPFLSGDPLELI HSHLAEAEAPLVNELNPD I PPVLSKI I AKLML
 KEPEKRYQSSNGLLADLLLCRDEYSATGI I REFPLDSLVRTQKVTFSKM
 VGRNREAGI VLEEYEQVARGAFRSLFI SGLSGI GKTRLLQELQKPI VKRK
 GYFTSGKFDI YHKNI PYSSLVQAFRNLI RAFLTESNERVALWKKRI LQAV
 GONGKLLTEI I PELELLI GPQPVVKQLPPVESLNRFDLSDGRFLGCLASE
 SNPLTLFI DDLQWCDTASFNFLAYLFDNYMDYPYLF FFLGAYRHNEVDSSH
 HLAGLI RKAKKTDGY

>2617919762 Ga0073689_102121 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_102]

MRI GVDI DGVLADSLPLWVEELNRRFFNKGKRLEE I HLFDI CQTYEI TGEE
 LSKFLDRRGRYLMTAPPPVAGAPYYLSRI KQYHEI YI I TAREEQYGRETQ
 EWLKKHELPYDDL LLLGNHDKKEACLAKKLHVMVEDTLEI GVDVSAAGVP
 VLLMDAPYNRGPLPLGVYRKRSWREYRAVVAESRQI VPQRPGGGAAMKM
 KTPLVGLAET

>2617919761 Ga0073689_102120 LysM domain-containing protein [pelotomaculum
 Ga0073689 : Ga0073689_102]

MSLVTRVLMGFFALLGVFVAPAAAHAAVHTVSLGESLYTI SLDYGI SLDK
 LMEANGI WDSLI YPGQKI YVPDSASNGSSYTVREGDSLYI GRRFGMDY
 RDLMAANGLSGTEI YPGMSLYI PAGQVSRGGHFGRYDPREVDLLARLI TA
 EADGEPYEGKVAVGAVVLNRLTSTDFPNSI SDVI YEYGDGTYQFEPVMNG
 WI ERPASAESI KAAWDALKGWDPNTGAVYFFATYVDNPWLWARTLSKI I G
 DVAFTY

>2617919760 Ga0073689_102118 Protein of unknown function (DUF2512)
 [pelotomaculum Ga0073689 : Ga0073689_102]

MI RNKYFNAI I TKFLLI VAVLGMLPPVAKVSTATAVVAHVATI TAYFI
 ADLLVLPPQYGNRAAADAACLLTMAVTWEMAWVLENALI PLPGLALLALI V
 GLGEWYYHRYLARLI FRGKMKP

>2617919759 Ga0073689_102117 zinc-ribbon domain-containing protein
 [pelotomaculum Ga0073689 : Ga0073689_102]

LLELYNKMNGGGVVVEI FKKVSEGARS I GEGAKTLGKKSSDLVGAALKKF
 EVAKLEKEMENNI AALGKLVFMQYKGEQGLEDEI ERLLTSTKAI ENDI DD
 LOEQI ARLHPKPPVPCPKCQTELPLTAKFCFNCGSKVI QEEPEEEK

>2617919758 Ga0073689_102116 ribonuclease HI [pelotomaculum Ga0073689 :
 Ga0073689_102]

LKVFI NI DGGSRGNPGPAAAAMVI TDGGGNVLATKSKFLGPDLTNNFAEW
 SALEGAVTALVHLVGRYKLEAEVRADSELVVRQFNRYKI KEPSLQEI A
 GRVWKNLAGAPGLKLTVRHVPREKNKLADAAVNRELDYQQQLKEDG

>2617919757 Ga0073689_102115 Metal -dependent hydrolase, beta-lactamase
 superfamily II [pelotomaculum Ga0073689 : Ga0073689_102]

LTVKFGVDPGATAGLKEDI ENMVDKLLRI DHRMRQFKKI FVLFLVLLFLA
 GCAGI GVDPPSPAGRAALDQTSPAVRLEVHFLDVGGQDSI LVRFPDGRN
 MLVDAGTNDSSAAVVGGLKNGVKKLDYLVGTHPHEDHI GSLDAVI NGFQ
 I GELMMPKATTNTRTFRDVLAAVEKKGLRI TTARAGVDVAEGADWQVKI L
 APNGDGYESLNNYSIVI KVRKYKDVSLTGDAAELSEKEMLAAGADVGAR
 VLKVGHHGSHSSTSPAFKAVNPRYAVI SVGAGNDYHHPHREVLNRLKKA
 GVEVLRTDQRGTGVFSTDGGEI TVTTEK

>2617919756 Ga0073689_102114 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_102]

VKRRTGKKKEPSLAPGNKEVLEKGVGKEDI RRGNFTWVTSLSYDEMPS

>2617919753 Ga0073689_102111 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_102]

Table S2

LEYI ETHKI RYRLANI KAMFEEERKSLNPLPLVPMEEAAKTVTALVNSDLT
VLLDGTTRYSVPLDYVGKRVTLKVSPFTVAVVWRGEEVCRHTRALQKGDHQ
CFEEQVTV

>2617919752 Ga0073689_102110 putative ABC transport system ATP-binding protein
[pelotomaculum Ga0073689 : Ga0073689_102]
VQTDVLI AVKNLTKVYGKGLAVRVLDI KNLEI RRGEI VALTGPSGCGKT
TLLNLLGLDRPTAGDI FFENKKGFALKSETALCRFRREKI GFI FQAYHL
IPTLSALKNVLAPAFPLGNNYRRRALELLKLVGLAGKEGRRPGALSGGEQ
QRVAI ARALLLDPLLI LADEPTGNLDSATGEGI MDLLKKLNQRGKTVLVA
THDQ RVAEKCDRNI RMMDGQI GI YRDAQDPLPSGEHKGHV

>2617919751 Ga0073689_102109 putative ABC transport system permease protein
[pelotomaculum Ga0073689 : Ga0073689_102]
LTLLFFSI QNAFRKKVVAALAVLGVAFGTALMTFLFSLAAGMDRRVEGTF
SELSNRI MI SGRDAI FGGLYLGMGTRPI PFSHI DYI RNI PHVKKI YSQVS
VVLRPQNGNYVMPLFGYGSEAI HDLDDNPYNKI I EGAAPGNEKEI I I GKS
LQEYMSLLNFPYEI GNSYPFI I MEGGQAKELDLKVGVYQGTGNEVLGDGA
SGSEKLAREI GKI PEGSVSAI NVAVDLDNVESTAGAI QQELLGKKPELQ
VVVPRDVLNPVKNI LDVLGKFLMAVSLVAVVAGGLSI MVMMLLSVNRMR
EFGI LKALGWTPVNI I FMVLVESLTLSMFGAI LGVAMGYAGI VAARI FIA
ADI AFLSRQVTVSVFLAGI LI GVAGGI YPAWRANSAAPAKI LREV

>2617919750 Ga0073689_102108 Surface polysaccharide O-acyl transferase, integral
membrane enzyme [pelotomaculum Ga0073689 : Ga0073689_102]
LNRMKEFDYI RAI SI I AVI MI HI GTSGFI I RYGNEI TLKHPMSTYYI YHQ
VTAFAVSAFVCI SGAVLCLKYKDI NFNYLKFI GTRI WYVI VPFVWTFI Y
FNLKNLI TVEESGKI NLPDQLVKALLTGESYYHMYI PMI FSLYLLFPL
FRLFVKKFKSPWWLVLLLLFQHYVQI RLNAVYTPDALKYLQFRYFVFLFV
AGCYI GEYYQEVKI FI NKYI NAVI GLLGVVI LYKI VYFYYSVYHLNVFFK
DVPQTI TFDNRI YTLI I VALI I YI TPQVKNRAI DLVLDRLGKNSFGI YLV
HPLI I KGI DDI VKQNKWFNLSSEAVFVI LLI TLVVSYAI SELVNLVPYGY
LFVGKNDKSTGTLKLTGLNDI I KI KMNK

>2617919749 Ga0073689_102107 Membrane protein involved in the export of
O-antigen and teichoic acid [pelotomaculum Ga0073689 : Ga0073689_102]
LANHVRGTSLAYRSRI VLDLYLKWRNKPLYSNAYLMLNNVI TCLFGFAFW
NI MARYFLPSQVGI GASLI AASSLI GVLAEGLRI GLI RFVPDSGENTGL
LI NSAFTLAGLSSLI GGLI YI AGI NI WSPALSI I QENI LLLLQFLI FTI T
NTLSGLTDSSLI AGRSSRYVLLKNTLVSI LKI PLPI YVFANLEGYGI FTG
NGI SFAVAVLI TWLFFLPKVYKGFPLPRAVI SKDLLQKVLPPYSSANYMANI
LNMSPQFI YPLMVLNI LGPESSAYFYI AWMMTMVLVVI PNGVSQSLLAEG
SHDPKKMGRDGRGVLYLSLALSVPAVAVMVMAGWLLHFFGPGYAENGTE
VFRFLALAI I PQCVNTLYI TVNQVRKQVYLI I I QTGFLAI VAI GVGYYWF
GHAGLPGVGMAYLLAHSVLALAVI RPLLKVLKEKGATTVPGL

>2617919748 Ga0073689_102106 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_102]
MI I KKYSNI I TTASFMFAYI LYLDYMLFRKGI NVSI EYFWVI LI VLI I T
LFYQI I KYDGTKLSENVLLFEVYI I AI GLLLMYAMPHTGLFSDPHWDYS
VLKAI SEYGWPLPNI ATI I ETRNLSEWPLLHI LTLI VSKVI YI DSKGI A
KYFPVI I TSLTSI FFYLI VKNLYGNVVAALLGTLAFCSLFWHTFFHSLFI
RETMAFMLFMMI VYI KSKRQNI SSQI I FI I SI I AVVI SHHLTALVLI LFS
FTLLVAKYLFYI I I NSNI LI KYRENFFSNKLMRFSNTAFTLI VVCI LAYW
MYVGDFTFKVLGI LYRDFVCGSYGSYSLNHYFTASSRMI FGSYGNMLFI I
FVFI CLLYSI I KGKDNKNFTDI FFLMWGGLI I AI SYVSTFLMPRI EFSRF
I LFGYPFLLMSSTVAI VKFKNPI KYMYI LFVFFQLMLVPPYLYNSSFTPE
YEYGRYREYFLPEEYI AASWFKNNVPQKNKI VGDWTSFELFGSQQFNVYH
DTENAVRI FKGDLEI LEPYQWLI I RKEDFFAARVGKPRATNPI VVTEETF
GKI NGDWRI AKVYDNKEI MSFKLN

>2617919747 Ga0073689_102105 Polysaccharide pyruvyl transferase family protein
WcaK [pelotomaculum Ga0073689 : Ga0073689_102]
VYNYKNKKLYVNKEQLTKI I LWNMNYVLDSKDPNVGDKALLSSI I KAI K
SNI SNAHI I VFARNPEVI SDEYGVGVGYNI GNI I NI I KKI YI CDYFVFA
GGEVI VDRGSLLYTFPMHAAFLAKLFKKTII I GYGI GVGEI NEI SSLGKI
LSRI I FAKCI I SVRDPKSKETI ESFCRPGKI YCTADPVI NLKQSKDEDIN
KI FSDI GI YI EEHTI I GI VPROPLMPI KKLSERI LNI FPI KLREKLKI TP
PEYNEKLN I YKKKLAEI GDYLI QKYNVKI I FVPMYNGFMSYKDNALCEDI

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I KNMHYKNNTTELI SNNYSAEI LKGI FGKMH LVI GVPLHSI I FASSMEVPV
I AFSYESKVNRYMKLLDFEQYSFI I EDI NHEI DLQKVYYGI DYI MENREQ
VKEKLNRI DHLRKMELRNME LFSFN LGN

>2617919746 Ga0073689_102104 Nucleoside-diphosphate-sugar epimerase
[pelotomaculum Ga0073689 : Ga0073689_102]

MKI LVTGATGFI GTKLVKLLDSYTVHI FSRKPATYYNVRWSKEVI TI Q
GNLTNKDSI SKAVKD VDAVI HLAAQLGSWWVKENYYYDVNVEGT VNL FKE
AKNAGI KHFI YVSTAGVFGK LKQI PANELHPCSPRYPYEKT KYMAERYI S
DAASGGFPATI LRPSHVYGPGLNTVPLI RLLQKMHFFPLI GGGNSLFQP
VFI DDLVDGI I LVLQHFKNTCGKLYI MAGKDTVTFKEYLSLI GKI LGLRI
LTPPI PYSVAKI GAQI NESI AGLLKGEPLLTKFRVDFFGGHQCYDI RQAQ
NDFNYFPKI I LNVGMNNAI NWYKEEGLI L

>2617919745 Ga0073689_102103 Radical SAM superfamily enzyme, MoaA/Ni fB/PqqE/SkfB
family [pelotomaculum Ga0073689 : Ga0073689_102]

MI KVSFLTEVGSRL LGYKTQC VFGFPKTKPLSLTVSI TQKCN SKCKTCNI
WKDKRSNPQTNELSI DEYETI I RHLGKTVI WYTLGGEPFLRSDI VEI VR
LI KKYSNPKVLI I PTNALLTNRI I KNTELI LNTI SPGTSLI VNLSLDGVG
EKHDDI RGI KGNFLNLETFRALKDLKKAYPNSFELGVHSVSRFNVGFL
LDI FTYI KNDLGPDYSI CEI AENREELLNVTDDI TPPI DFYEKSI RPLQQ
EI RDSLLQNKGLTGI I QAFRLKYDYVI TEMREKKRI I PCYAGRVS AQI S
PWGDVWPCCI LAYKADMGNLRDFDLNLKLWYSEKATQVRNQVFKGECYC
PMANVHYTNMI LTPKAMMGVMSNYLGAKLARK

>2617919744 Ga0073689_102102 Glycosyl transferase involved in cell wall
biosynthesis [pelotomaculum Ga0073689 : Ga0073689_102]

MRI CI VGSSKFFSGI SAYTI VMANAFAERGHRSVI LLRNLVPLFLYPG
RTRVGKGECQI DFHPGI EYDGM DWNAPL TWGAYRFLQRQKPDALI MHW
WTSSVAHLQI FLALAKHMNGAKFRLALEMHEVVD TLEEKI LPI RLYSRI G
GKTL LKFCDI YTAHSDEARKAI ADTYHI PHNKI HI VPHGPYNI YESLDKK
AAKKELNLAGYVLLYFGMI RQYKGVSLI KAFNKLPADVANDI CLVI AGE
DWGDDTGI OKALSNSPYREKI I FKSEFI PDDLVPKYFAASDTVVL PYLRT
CGSGVVNI AVAQGPVI TADLPTMRECLKGYEGARFFPVGDI DSLCAELT
EVYQNKFFTENKYYQFHTVSWENI I DKYERI FHK

>2617919743 Ga0073689_102101 Glycosyl transferase involved in cell wall
biosynthesis [pelotomaculum Ga0073689 : Ga0073689_102]

MYNNSKI HHLDPKI KYSI VI PAYNEEAGLPVVL RDVFWLI DESFEVI VVD
DGSTDRTEVAEKFPCRLVSHVQNSGKGEAMKTI REARGDNVI FI DADN
TYPPEGI I EI AKALDRFDMALASRKM GQKHI PAFNRI GNAI FRNSI RYI Y
GFGKYDPLTGLYGLKKAFLKVMNLESNDFGI ESEI CI KAARMGLKV KDI H
I KYRDLGEAKLNL RDGYRI FATI LRHFPLLFRLEKPGLYR

>2617919742 Ga0073689_102100 geranyl geranyl reductase family [pelotomaculum
Ga0073689 : Ga0073689_102]

MNYDVI VI GGGPAGCETARI ADKGYKALVVEHRKI GEPMQCAGLVSPR
TLKAAAI PEGTI TI NQI HGA FVHSPGGETLSI RGHEVYALVI DRSEFDSKL
SEKAQGAGAEVL TGVRASVGEFFSDGI SI KLKTGNRESTVKTCLLI GADG
ANSRVARRI NVPEAENVI RMCAAEVELECPEKDMVHI FLGGEI APGWFGW
VI PVDEKHARVGI GVSGRDKRPGFYFKKMVD TNPGI FKG MNI VRGTGGVV
PI GLLPKI YGERTLLVGDAACQTKPI SGGGLYLGLLGAKLCAKVATKALA
KEDPSPELLSEYQRLWEWEMAEI Q TALWYRNI FLTMSDKEMNALVRFFR
RPLWQNI I SRYGDI DYPSLLAGRLSLARPWAERFFMAGFKKI LNYC

>2617919741 Ga0073689_10299 two component transcriptional regulator, LytTR
family [pelotomaculum Ga0073689 : Ga0073689_102]

MKI TVLI AEDDPDMRHVI RKVVEQVEGI KVI GEAGDGLEAI KLI EELSPQ
VVFVDI DLPKGNGI ELAREI FDI NPWTFI VFATAFNEFRREAFDVYAFDY
LVKPFKMNI RQTMERVKQVLSGKVAGRHSY LKRLHENVGRKQFFKSDS
KFI YLDLDDI I YVTKEGRKCTI YFI GGQI KTNDNLSALEEQLEGYPFFRS
HSGFI VNLKMKELVPI GRSSYELVMEN TKRPLI TVEKFKELEEMANAK
VSNRGRVVLG

>2617919740 Ga0073689_10298 cyclic lactone autoinducer peptide [pelotomaculum
Ga0073689 : Ga0073689_102]

MMRLVKKLMFTPI VMVALLVAAAGI KPASFFWLYQPAPPI KPK

>2617919739 Ga0073689_10297 accessory gene regulator B [pelotomaculum Ga0073689

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: Ga0073689_102]

MNLNQLAGKTANYLSGELALDNSKI DTLRFGLEI I FGVLFKGI I LI SLAH
FFGI LPEVTFALVSGAI YRI LSGGAHCNGYWRCLLLGLFI YLGVGALALF
AEPYLSI DLMVYLLLAGYSLSLI CI I LWAPGEVPFKRI ANI SERI MFKFL
SLVHLSLWLG SI I VLLYSSSSLAFAGLI AVI TQTI SFSPPGYKVI HKI D
YFLEGLFKERRCQANDAAR

>2617919738 Ga0073689_10296 Sensor_kinase_SpoOB-type, alpha-helical domain
[pelotomaculum Ga0073689 : Ga0073689_102]

LDEMNLVSLLLVSFPEAI LVATLGFLLVGLKPWWRDLLI I GVAQAGFAYL
IRLSPVPFGVHSI LEI FLVFLNI RLVTSLPFRI VI LVSLGLI FYGSVET
VAI PFMLHI TRFSMI DVLNYYVKI FFFLPQALI MLMI I AACKI FNI SLI
GYSQEYNRSDYSSRKEFQENLKSDI VNKHNLII FVVVLLPVLLVI I NSV
FNASRLDI FPKHEHLNI LTGFI GIFI I VLTALSTVAI KKI VQYI ERDYEAK
RAEENLQI KQI DSSRKQRHDFHHQLQTI YGLMEGGSYERARDYI SRVF
GDI SKTGELI KTDNFSI SALLHTKI GLAEARNI EMEVTVECSLKEI PLTP
HEASSLLGNLI DNALAEVESKTGEHRWVNVKMTREERGAYVI MI SNTGDPI
VPGI RENI FKPDTFTKNHSGGLSI VKDI VTKHRGSI GVNSDAEKTFTT
VKI PLKKRGEVK

>2617919736 Ga0073689_10294 phospholipase C [pelotomaculum Ga0073689 :
Ga0073689_102]

LVARLHQI TSTVGLI GKYLLATGRI SWTVDLGFCVTHVQCNRQARLI LEA
DGYVGPAALLESYRRELDLGVCPDSCWGSLLHHFYHARTGNGLLGRTPAD
VVGERYRRALNLWRRGKFGKAMFFLGAVTHLLQDVCEPHHANCCFGSGH
HHYEKWWQAHKDDYLVDQRI YKKYREPARWLKYCARRSFGALELVHERS
NVKFYNQATGHLLPFTORI TAGFWLNFLEQAGVI PDSKLYFI FQVPGLKP
SAFSRRALASVFTPV

>2617919735 Ga0073689_10293 UDPglucose 6-dehydrogenase [pelotomaculum Ga0073689
: Ga0073689_102]

VKVAVVGAGYVGLVAAACLSRSGHEVI CI EKDEQKLAVLQAGKLPPFEAG
LEEI MYDGLKSGNLKFGKRVTECLDAEMVMVAVGTPARPDKRI DLSQI YE
VI SDI VEQARKPLLI VMKSTVPPGFGVDLKERFLAVAKVPLGYLANPEFL
REGLAVRDWYHPERI VI GADDDAAVAKMAGLYAGI DAPVLTMDI GSAEMV
KYAANAFLATKI SFI NEI ANLCELVGADI LPVARAVGMDRRI GGEFLQAG
LGYGGSCFPKDTI GLDFVSTCNGYAFNLLKAVI EVNSRQRLALRKLKRA
LGKLHDKI VGLGLAFKPGTDDVRESPALEI I NLLLDGARI KAYDPAAG
KNAQKYLDPDEVQFAANAMTAVVNCHALLI ATAWPEFI TMDWARVRSLMRP
PFVVDGRNCLPEGEMAKHGFNYLPI GRPGI QREVREI VSLVG

>2617919734 Ga0073689_10292 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_102]

MKI LKADFHCYKLFSGHGRFRPAQLRRRLNWAARLGLDVQAVTEHFDVPD
FWEI YSCLETLCNGRGGLEWRGVTVLAGEVSI DEGGDI LLI GSI EALK
GLEKRLGRLTAGNMPFFKDLLDASEDLGFLRI GAHPCRPDKELWKMGSLL
KRLDALEI NAGELSMARWVQQAQHTNMVLAGSDAHHWLQMGVFNLLP
FGGSFTI AELKRAVAERKVAWRNEGAFSVLVRGLI KGGFAR

>2617919733 Ga0073689_10291 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_102]

VREVCAATGLLGESI ASI FPDYGGFFVDFFTKYTDLEPGSALVVEAEGKV
VGYLLGCTDGKRHRRFQGLLRRAAFHVI GNLCRGSYGPQARRFLWWLVW
RGWREI PAAPAGAHFHFNI LKWRDAATTRLLVDVLELLRREHPGVKLV
WGQMETFGARRSRDLFRRLGWEFYDQVRLGKYRYLFGETPPPHLRKI ASG
EYVLTITI YRRL

>2617919732 Ga0073689_10290 alpha-1,6-mannosyl transferase [pelotomaculum
Ga0073689 : Ga0073689_102]

MKI CDI TNFYHEKSGGVKTYLHQKMEYI GRCRSEHLVI VPGPVNAERWI
HKSLLCRI KAPELPLARPYRLI TDLWRVNYI I ERFQPD I EVGCPYFLPW
AI AARRKNSFCLVGFYHSDFPRAVVRPAAGRI GKMPAALLEKGAFAYVRS
MYRRMDLSLAPSSFASALYHGVKSVRVLPGLVDLDFHPRFRLRQFGT
RLGI PPGSLLLLLYVGRFAPEKGLEVLRRAFESLADREPGRYHLLLI GEGP
LGDCLREWAAERGDVTGGYLOGRMLAEAYASADLFVTAGRAETFGTLI L
EAQASGLAVVAAAASGAPEAVAPRAGVLVEPGDPVALAAVAGMAGQNL
ELGWKARKHMEVYVGWDTFTRLFTYYEQLMSQPLLQAAAAAPSGATVRR
I AGE

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>2617919731 Ga0073689_10289 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

VYVNVSLHDVTPHYESEI RLLFSLI RQAGVAKGAI LVVPNYHGI SLMRPE
SALACWLRELAGDGWEI VLHGLTHFEPALSRNGSRGNPVAQYLVSRWYTN
GEGEFYRLAGAAARLQKGLSVLAACGLNPSGFI APAWLLGEESATVLG
EFNFAFTTLLGGVCDLKSGAFYRAPAVVFSSRSFLRAVLSRMI VPVLAGEY
WGRRELVRVLHPLDARRPAI MEI I ERLCOGMLACRRQVTI GEYLAATRK
EKPALVGVDK

>2617919730 Ga0073689_10288 Glycosyl transferase involved in cell wall
biosynthesis [pelotomaculum Ga0073689 : Ga0073689_102]

LKLAI FTDTYLPQVNGVSRITARI SSHLQKQNI PCLIFAPECGPLPEDCK
NVHTFSAFDLPFYPECKI ALPSYPVVREI LDSFKPDLVHLVTEFSLGLCG
LKYAKDHRLLPAVASYTTNFPQYLAYYKVGFLKNWAWRYLRWFHNQCRLNY
CPSPAI QSLLMKKGFFHNLTVWGRGI DTGLFSPDKKSEFLKKLAPGKNLFF
LYVGRLAPEKDLVLFNAWRTVSGRLPGAQLVI TGDGPLAGELKEKNVDG
VVFTGYRHGEELSTI YASSDI FVFPSTTETFGNVVLEAMAAGLPVVGPA
GGVKNLLVDGHNLACRPRNHHDMAAAMLKLARHDELRAQI GSRARQYAI
ERSWENLLRSLVESYRAVI TPPEKVKTISI GA

>2617919729 Ga0073689_10287 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

MPEITLGLRDGI I I KEAPGGGAELQSDTGWVPLKEASPGAARALVRLVAG
GATKEELEEI ACEADWFLGDEPLKKASYRQLGDDAVHLTPASTSAAASTG
GGR

>2617919728 Ga0073689_10286 DNA-damage-inducible protein J [pelotomaculum
Ga0073689 : Ga0073689_102]

VAETTNLISI RMDKKLKEQAEQLFSELGMNMTTAFNI FVRQAVRQGKI PFE
ISLNI PNAETI AAI EEADKI SRDPNAKRYSSFEELVAEVQNEV

>2617919727 Ga0073689_10285 mRNA interferase YafQ [pelotomaculum Ga0073689 : Ga0073689_102]

MKYEI LATGRFKKDLKAI I KRGYNI QLLQDVVSLLATGSPLLVKNKDHAI
SGNWTGHRECHI TPNWLLVYKI DDDI LVLTLTRTGTHSDF

>2617919726 Ga0073689_10284 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

MSSPPVFYAI QNRTAGFFNPALYLI AVGFRLRCYDVVVVRAARGVHVGI AT
SMTFI FI HHLCTGGTVRKKI KLOSFCHTTQ

>2617919725 Ga0073689_10283 possible tyrosine transporter P-protein (TC
2. A. 45. 2. 1) [pelotomaculum Ga0073689 : Ga0073689_102]

LPEHYQVI FAI AVFLLTYAVI VSEKI HRTVAAFAGAALVVMGTI MTPEAA
VHAI DFNTI GLLVGGMI I VGVTRQTGVFEFLAVKAAKGSNGEPI RVLAAL
CLVTAVLSSLLDNVTTVLLI VPVTFAI AKQLEI SPLPFLI AEI LSSNI GG
TATLI GDPPNI MI GSATGLGFMDFVI NLTPVI VVVYVPTI FFLQLI YRKQ
LVVKPELKGNI MKLNERDEI KNRVLLRKCLAVLFLTI LGFVVHQYVHLES
SVI ALSGAGLLLVLTREDPEHSFOAVEWPVI FFFI GLFVVVGALEEVGVI
EAI ARWSLEVTGGNI LPTGLLI LWLSAI ASAFVDNI PFVATMI PLI QDMG
RLGGI TDLNFLWWSLSLGA CLGGNGTMI GASANVVVVGMAEKRLRI SFI
GFTKI AFPLMLMSI VI STAYLYFWYVFHTMTAMAATLCAGI VLALLLKP
TNMLTRERTPALEDYDKSRSC

>2617919724 Ga0073689_10282 CBS domain-containing protein [pelotomaculum
Ga0073689 : Ga0073689_102]

MYKPRRVMDI MLPPDGYPGLKLDLGLI RAWQNMTDFYKKMSAPPPTEERI
ALVYDDDECLAGVLAQKAI MMTI TPAARESVDRLRGFLEEGGGFFSCI L
NPDI KI KEVMPVEQVAVKSTDTI VKDMPVLLKNNLSAFPVNI WGKVI G
MLRRGDVFHHLGLNSAFCKLGFSGCDWDHYGVFDR

>2617919723 Ga0073689_10281 solute carrier family 13 (sodium-dependent
dicarboxylate transporter), member 2/3/5 [pelotomaculum Ga0073689 :
Ga0073689_102]

MSDHAI AI QQPQATNLFGLVPGRRPMI FGFLVI LFAI MVLLPPPASMVSL
MTETKPAGAKLESGTTNFVDSYNKTMKYKEAQKI DAVQVAQRAKAAVAML
FFTALLWGTEAI PLGATNFI VAI I CYI FALLPI DRI SQSFFKDAVFFI GG
VLCLAAGVSVTGLDRRLGYLLLGRI GGMKSFAFI FFPLLGLLAFFSEHA
LVALMI PI LMLVYAQACKKAGVKHDKNLAVFLFLGI CLAANI GGSGSPAV

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GGRSAI MVGYFSYDGMPI SFGQWMMYGLPLVPI LAI TVAVFMWLI CGRKV
LAKDFS I ARTMKNVEGI GPLRGKELI MAVLFGLOVI LWMFFSGSYGLGG
TTI MI VVLMMLLLGVVWSDLRVAMDVLLYAAACCI GTALNATGGALW
MARQFLSGLVSVLPGLTEGSI I I AVSLI TVI I TNFMSDGATVGAVGPV
LPMAAI GGHLWKVGLACSFSSFAHAMI VGTVNNAI AYTMARDPETGEP
LI TVWDFLRI GAPFVI I SLI VTWVTCFWGYWNFLPWPTFK

>2617919722 Ga0073689_10280 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

MFFRKI TCRSNGKEYAYVKLI ENYREGGKVKQRVVANLGN DNLTPERVE
GLVAGLRKI CGCPHFSSQVCSAAGKADVSEAGLSEMRGLPGDSAQLKAN
KVLRYGEVFI I HKI WEI I GLRDAVEETFSGRSSDLNI TLLVELMVMNQI I
KPLNKQVI SDWYHCLYLPELEGKELLPHHFYRALDLI ARDKKVLEKRVLE
KMKSKDTADTDI VFYRLTTATI EPSPHDELNMSSYGKYFFAEPKEI NVD
LGI LI SRNGMPFGGRMLQKTADETGYSYTVNYLKSNGYVQHCI FVGERN
TVKRDLDVLI ALGYEYLVRKRPWRREDI ELI KTEAAPGRDNYLPI NDELW
FREVRKGEI RFLFCFNPQVAESHRALLKERQEA VESELKAI EQAVDESRY
GI PGQPFKNASI FKDEYCLRYFDWRYDKDSKFTYRRRDDLLERDLDA
GLFVLESNSSALSGRELVESEI NSTQI GEFFRKI KNFEVRPNKLKANLDI
SANI LVCVLAII I EKI LERI VRGAGVNLSPGQTLQVLEEI KVTVNQVGGR
EVKSI TRI DKI QAEI LRAVGVI NL

>2617919721 Ga0073689_10279 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

LDEVG I LRSLSNKEQLI QFI RELGWGDMKI RVENGQPVLI YEAI KTI RL
EDKPLNQGS I YKKPRESLKK

>2617919720 Ga0073689_10278 Response regulator receiver domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_102]

MSAGKI LI VDDEYGVWALEKALREEGYEVVSAAKGMEGLEALASQTI SL
VLLDYKMPGI SGLEALERI KEAQPELPVVFMTGHSSI PTAMDSL RMGATA
YI TKPFHLADLKATI KKVLTGD

>2617919719 Ga0073689_10277 Signal transduction histidine kinase [pelotomaculum Ga0073689 : Ga0073689_102]

MFKLWSQGRFQI MVI VSVLLI TPALVTI FDMLEFSKTDI LVKDLERKL
AGI VSSMSVKI HDQVVALLEVEPGRDLPSAMEI YFNGI AAPKAESYKGV
LGI YI VEQDRI LI QGFLHDYRPPGGEEQRQREORI YQETFAGI RAVVVG
API TKLGQTDWDDQFVEYLVI FI DSKLVAVI WAEERI HPI FAQSARAHV
I RLVTVI VFGFI GATLI STI SLFGQVRNI KNGLLNLERDFS NVLPDMPG
EMGI AGAI NKMVLSLKEQLAEQLRASEHLASLGRVTDI AHELNP I
SI I QCAVDLMPEKVSHPDNECI FMSQEQLKRLSLLTEELLD FGRPLPM
NMEPLDLRGLLSLI DTTETLLQKNRI TLHFI NPVQLPDI I GNREKLTQV
FVNLI I NAI QAMPGGGALTVQFTTENMVCVFI RDTGEGI SEEDLSEI FQ
PFFTCKAGGSGGLAI SKKI VEAHQGS I TVESRPGEGATFTVCFPNQLTG
GGFKECPPEKS

>2617919718 Ga0073689_10276 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

MI DWKFLPRQGHVFFVPSGDSLDTYRDKNLGGI KMSSLSHSCRRNLI PA
FSNPTAGI KKALERFFRSKTI ARLARI YHGKFSYDLVPTAI STFENMAR
VTSVDSGDLYI CVFEDARYQGQYHI VSPGEKAQI GCCGSVVI SMRPI PVD
VFRNNARSPAWCWELPGSMYVWHFSPGCKYT

>2617919717 Ga0073689_10275 Benzoyl-CoA reductase/2-hydroxyglutaryl-CoA dehydratase subunit, BcrC/BadD/HgdB [pelotomaculum Ga0073689 : Ga0073689_102]

MTTDYRGMWKS I GLDLEAHDQLLRALPPAYGEVYLSQANRPAGMEYFDFV
VNEI HGLRI QELQEHKAGGKVVGAFCVFVPEEVVRAAGGI CI GLCSGVE
I GLALAEKALPRNI CPLI KSFMGFKLAKVCPYFESCDMVVGETTCDGKKK
AFEI LNDYVPVHLMETPQMKREKDKSLWRGEVRDFVSKMEECAGNKI TAG
ALRQSI KEVNGKRKALLRLAELRKNDPAPI SGKDSLLI TQI AMYDDVERF
TAKVNALCDELETRVRERKGVREPGALRVI VTGTPLAI PNWKAPHI I ESS
GAVI VAEELCTGLRYFENTVREEGEI VDDLVDLSLAERYLGI NCACFTPNE
GRMERLVQLAKEYNADGVI HCSLAFCDPYLVEANRVERVLKEHGVPLLKI
ETDYGQEDSGQLKTRI EAF FEMI R

>2617919716 Ga0073689_10274 CoA-substrate-specific enzyme activase, putative [pelotomaculum Ga0073689 : Ga0073689_102]

LFCHLPPGVSVTATGYGRHAAGADFVRRVVTEI KAHALGVSQI YPEARTV

Table S2

LDI GGQDMKVI LLDGNGGVEDFQMNDKCAAGTGKFLEVMASALGYSAVGD
FGRDALAGGPGTRI SSMCTVFA

>2617919715 Ga0073689_10273 Copper amine oxidase N-terminal domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_102]
VFFI FRVRFVI LAAVLFFSLLLFSRQPAGAEPGI VIKGTNQLAFFVDGY
LLDVFPVATGRLPQFTPEGKWRVVRKLI YPAWRHPRGGPLI PGGVPENPL
GPRWLGLDALGTAGGSYGVHGNNNPGSI GSHASLGCVRMHNRDI LWLYDR
APLGMEVEI I NSGEDLAGWKKI ARVTVNGAEPEFAPHLGPVQAGETSYLP
VRPTATALGYRLSWQDPAGTI LLANI DREVLLTLDSTVTVNNNVYTAGE
API FLEGI TFAPDYYFQSYLGVEAHYDHI SRTLAMTAPVDPSSGRLVRYN
LTVQVDGKALHLPEDLAPLNDGENLLVPARPFCAVLGAVARWHEELKAVE
I TTRGKTLTI PAGGAPARLNGAVVDI PSGI FFRNGYAYVNLRLLTGAFGF
PAELDDSSRTLRI STFNI AEMFFNPFQAKSPGTGPVSTVFFYRRO

>2617919714 Ga0073689_10272 cation diffusion facilitator family transporter [pelotomaculum Ga0073689 : Ga0073689_102]
MAHDSESAVKAALLANGLI AAMKLFGLI LSGSASMMAEFKHSLGDWGNF
FLLVGI RQAQRPGDERYQFGHGKRVFFWSFI ASLGMLFI GGALSI YGGVL
KI LHPEPLEHVELNLI I I GFSI LFELYSFTMAVKAI MHETGEEARGLRMF
ARAVPALVKTTTPATRFI FLEDTAALAGLTI AGTAI LLARNTGNI FFDGLA
SI I I GVLLFFI GFGTARENASAI LGESADPALI KEI GDFVMTI PGVVDVH
NARSMCVGPNKYLLLEMVVEANERTRLCDCDDI GFTVNKLVDKDFKEI AFA
HI SI I ADDKKROWKRQYQPGFWPGGRG

>2617919713 Ga0073689_10271 methylated-DNA-[protein]-cysteine
S-methyl transferase [pelotomaculum Ga0073689 : Ga0073689_102]
MAGVWTGAGLKALALPRENPEAALENLAGALRPAPGALRGALPLTPAAPA
GAATVPQALHLLVDEVEKYFEGEKVAFTAPLDWSGYTPFQRRVLELVRTI
PHGEVHTYGRVAREAGSPLGARAVGGVMWANRTPLVI PCHRVVAANGSVG
GFSGPPGMKKYLLLEKTACLRGLPLLR

>2617919712 Ga0073689_10270 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]
MAEGROWN I ROVLYLI CFATLMMLI I GLVQLI MGVDLVYPDPNMESQY
LDTKI KVSEMQRNNEI TREDI ERQI QEDQARQKVSRYKYSQI KSFI NSLA
LVMVSLPVLYLHWRKI QRGGLPA

>2617919711 Ga0073689_10269 cysteine synthase A [pelotomaculum Ga0073689 : Ga0073689_102]
MSQNYLSCEALVC I MPI YEGLTELI GRTPLVRLKRVAAGLPAEVAVKVE
FFNPGGSVKDRVALAMI SEAEKRLI DKDTVI I EPTSGNTGI GLALVCAS
RGYRLVLTMPETMSEERGRLLKAYGAEVVLTPGAEGMRGAI SRAAELAGE
FPRFSI PQOFANPANPAHRKATALEI WEDTGGRVDI FVAGVGTGGTI TG
VAEVLKKKKPPVWAVAVEPAGSPVLSGGQAGPHRLQGI GAGFVPEVLNRE
I I DEVFRVTDDQAF TVARRLAREEGLLVGVSSGAATHAALETAKRPENRG
KLVVALLPDTGERYLSTELFQQPD

>2617919710 groL chaperonin GroEL [pelotomaculum Ga0073689 : Ga0073689_102]
LAGKEI I FREDARRALEKGVNALAGAVKVTLGPKGRNVVLEKKFGSPMI T
NDGVTI AREI ELPDPFENMGAQLVKEVATKTNDVAGDGTITACVLAQAI V
REGLKNVAAGANPMI I KRGI EKAVDKAVEVI KNSAKTI ESKAI TQVATI
SANDEFI GSLI ADAMEKVGKDGVI TVEESKGTITTTLEVVEGMNFDGYS
PYMI TDTDKMEANLSDPYI LI TDKKI SAVGDLPLLEKVVQTGKPLLI I A
EDVEGEALATLVNLKLRGTFOCVAVKAPGFGDRRKAMLQDI AI LTGGAVI
TEELGLKLDKASI EQMGRASKVRVKKEETI I VGGAGSADEI TKRVTQI KK
QI EETTSDFDREKLQERLAKLAGGVAVI QVGAATETEMKEKKLRI DDALN
ATRAAVEEGI VPGGGVVYVNAVKGLEGMTADSLDEKTGADI VRRALEEPL
ROI ANNAGMEGSVI VEKVKNSEEGVGYNALLGEYTNMI EAGI VDKVTR
TALQNAASI AAMI LTTETLVAEKPEKDKDPMGGMGGMGGMGGMGGM

>2617919709 groS chaperonin GroES [pelotomaculum Ga0073689 : Ga0073689_102]
VI RPLGERVVVKPLPSEERTKGGI VLPDTAKEKPQEGEVI AVGSGRLLLET
GQRVPI DLKPGDRI LFSKYAGNEVKI DDVEYLI MREADI LGVI EK

>2617919708 Ga0073689_10266 myobdopterin adenyl transferase [pelotomaculum Ga0073689 : Ga0073689_102]
VYRI AI I TVSDKGARGERVDRSGPTVREMTQSLGEVVDYRVLDPDDL I LK
ETLI NLADQEKVDMI FTTGGTGLGSRDNTPEATLAVI EREVPLAEAMRL

Table S2

ESLKKTNRAMLSRAVAGVRHRTL I VNLPGSVKGARECLGVI MPALPHGLE
I LTGRGGEGCAG

>2617919707 Ga0073689_10265 cyclic pyranopterin monophosphate synthase subunit MoaC [pelotomaculum Ga0073689 : Ga0073689_102]

LVI SHKELLPVDEL SHLDERGEARMVEVGAKEATPREAVARGEVAMRSET
LELI LGGRVPKGEVFGTARVAGI MAAKKTAGLI PLCHPLMLTGVDVSFRP
DRERSRVEI EARVRTTGRTGVEMEALTAVAVAALTI YDMCKAVDRAMVI G
AVRLARKSGGKSGLFQREGEAEWA

>2617919706 Ga0073689_10264 FdhD protein [pelotomaculum Ga0073689 : Ga0073689_102]

MPDPGNKSI NTPVVMYKDHRLTPAEV VVREVPVTLFLNEREFVTLVCSP
GELRELA VGLFCSEGLRKREDLREVTI NEGEGLI WVEAAVEAPSEETFL
KRFI TTCCGRGRASFYFI NDARGI SPLTSDLRVAPRTVLSLVNQLEERSS
LFRLTGGVHSAALCTGGEALAFYEDI GRHNAVDKI FGRCFLEGI PLRDKI
I VI SGRVSSEI LI KTRRMGVPVMVRSAPT KLAVDLAEEMGI TVVG FARG
DRFNI YSRSERI VPDS

>2617919705 Ga0073689_10263 S-layer homology domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_102]

MYESKKMYFLI PLLALTLVLI AALGTAAAGGLKDI REAPWAQQAI AEMNA
GGI I I GYPGGVFKPYNEVTRLEAVTTLVRVLGLEEQARAKENARVDYKMP
PNLYWGRGYLI TGVELGMLRGDYL NQLQASPASRVEVAMLVYHALKLDP
SGSALTFTDAGEI PADYREGVAAVVKSNLMQGLPGNFFKPNDR I NRAQMA
VLLARI VEYRPSEVYRARI NGTVSSVDPGNRALALREGGNKFYTADCAV
FFDGAGAEP SALKAGDVVKMVL DKGGRVAFI NAVRTNADQKVEKYEGRVD
SLFGI GGEYWLGLSGFDGSKI I RPVAGGVK VNDAGGQ RDI SSLTQGSCE
I KVVDNKI AEI NVLKT RTAEGRV RTAGYANLSVRDDNGSSI ELDVPENVA
VVKNN TAMAYVEVREGDRVKVTAYENKAVRI EVLAGGLEGRI RELDTQGT
LGI TI RDENGDI EEYVDDNVRVERDGDRI DFDELDEGERVRL ELDGDDR
VI HI ELI DSKSTSEVEGEI EKLDTS GAWGI TI RDEDGDTEKYDVDDDDVDV
ERNGKNI DFGELDKGEVWRLELNSRDI VTRI EVDEEVSGI KGKVVDLTTD
SSRVVMRLI REDSGRTAQYDVA KDPVCI RDDKDI DLDEI LLGAEEVVRVR
DGKI DK I KMTNDEDI TVEGVTSVSASRERI TI KQI NGNKFTDFAVGYV
LKDKDGDRI TELEDVEGDWDVELE LANGEVKKMTRK

>2617919704 Ga0073689_10262 molybdopterin molybdochelatase [pelotomaculum Ga0073689 : Ga0073689_102]

MKRN VYLDDLPWEEALERYLSHLWDAGALEPGRPELI PAEGLTRVTAAP
VYARI SSPHYHASAMDGM AVRSDTYGASETSPKQLKVGEDAVMVD TGDP
LPDGYDAVI MI EDVHYVQPDVI EI I QAVPPWQHVRVVGEDVVATEMI MPA
NHLVRPVDI GAALAGGVNEI YVHPRPRVALLPTGSELVQPGAELKPGDI I
EYNSRMLGAMVERWGA VPLRREI TADDFPALRVAVAAVDEADVVLVNAG
SSAGSEDFTAGVI DSLGRVLAHG VATKPGK PVI LGEVAGKPVVGVPGYPV
SAYLCLEL FVKPI I FKKLGSVPPAAEKI EAAVSRKLVSPLGV EEFVRVKL
GOVGDRV VATPI SRGAGI LMSLVRADGMI RVPRLSEGYNAGETAPVELFR
SKEE I GETTVI I GSHDI ALDVLANFLRRKYPMATLSSAHVGS LGGLTALK
RGEAHCAGTHLLDEETGDY NVAYI KRLLPGRSVVLVNLVHREOGLI LAKG
NPKGI RGLADLAREGV SFVNRQRGAGTRVLLDYRLRELGI DPARI HGYDH
EEYTHMAVASAVOAGAADAGLGI RAAARALDLDFI GI VEERYDLCVPAEF
WDPHTRRLLEVM SMPEFRKEVEKLGGYDLRNCGI MWRN

>2617919703 Ga0073689_10261 molybdopterin molybdochelatase (EC 2.10.1.1) [pelotomaculum Ga0073689 : Ga0073689_102]

LSRPLSRFNRLEVVVAELFQALTVNEARAVLARHMPERRRPAARVALPES
LGRPLAAPADGDVP GDFDRSTMDGYAVRARDTYGATEGMPAYLDVTGEA
LMGOEPRGEVGI GQAWRI ATGGMLPSGADAVMMVEYTEELDDRTI GVTRP
VAPGENVVRRGEDI AAGEVALPAGHRI RPQDMGF LAAAGVTGVEV VTPVK
VGI I STGDEL VGPEENPD PGQVRDI NSYALYGAVEACGGAPRLYGI VGDD
YEELKGVLERVLGENDLALLSGGSSVGARDVAARVI DSLGKPGVLFHGI S
I KPGKPTVGAVVGGKPVFGLPGHPVSALVFDLLVAPLVRDSGYPPPGAA
PGEFPLRAVI TRNLRSAGREDFI RVRLSLWDGRLYADPVLGKSGLI STM
VKAAGLARI PAGKEGVEAGETVEVKMF

>2617919702 Ga0073689_10260 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

LAEVASEVLEAVKRAAKDGOI SCTVARKLAE ELEAPPRVVG EACNALKI K
I RACELGCF

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>2617919701 Ga0073689_10259 molybdopterine guanine dinucleotide biosynthesis accessory protein MobB [pelotomaculum Ga0073689 : Ga0073689_102]
MDKSVPI GLAGYSGSGKTTFLEKFVAELKKRGYRVGVI KHTHHQVEFDW
PGKDTWRVAGAGADVVALAAPGGVSLVRKFAADPRPEEVVSMVGEVDLI
CEGYKRGRWPKI EVFRRETTPRRPALPREELLARVSDTGPEDAVPHFGLDD
AAGVADLVERVSLKKS

>2617919700 Ga0073689_10258 MOSC domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_102]
MGTI KAVCASPCKGMRKKN I NEGLLVPEHGLEGDAHAGPWRROVSLLAIE
SI DKMRAAGLKVGPDAENLTTEGI DLVGLPLGTRLKI GPDAVGEVTQI
GKECHTHCAI YRLAGDCVMPREGI FIVLNGGKVEVGDI IETVET

>2617919699 Ga0073689_10257 cyclic pyranopterin monophosphate synthase subunit MoaA (EC 4.1.99.18) [pelotomaculum Ga0073689 : Ga0073689_102]
MQDTYRREI NYLRI SVTDRCNLRCVYCMPEGVWRWSPHGEI LRLEEI ETV
VRAAARVGI KKI RLTTGGEPLVRRGLEDLVRR I ASI PEI DDLALTTNGLLL
PPFLPVLKEAGLRVNI SMDTLEADRYREI TRGGDL SGAWAGI NSALDAG
LHPVKLNTVVVRGFNDDEVA AI ARLTLNRPLHVRFI ELMPI GSSSDWAAG
RFVPAVEVMAAI SAKLGRLI PAGOPTGGGPARYYHLKDAAGTI GFI TSMS
EHFCHRCNRLRLTANGGLRPCLYDRREI DLKAPLRERANI KEI TGLLMEA
VTMKPDHHHMLEGWRDGRVMSQI GG

>2617919698 Ga0073689_10256 molybdate transport system regulatory protein [pelotomaculum Ga0073689 : Ga0073689_102]
MADAKKSKGGLPGPFHVEYKI WLKKGDAI FGDGI YMLLSHI DARGSI SWA
AREMGMSYRAAWGKI KGLEKTWGVPLVI TQVGGEAGGARLTPEAGELMR
KFRRRLQDQDVFI HSAFQGI FGVRSGL

>2617919697 Ga0073689_10255 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]
MI GREETVSVI ETTI DDMNPEI YSYLLEKLI GEGALDAYATPVYMKTRP
GNLLTVI CRRENTEQLLEI FRETTLGVRLREEKRRVLKRCFAMVSTPW
GDVNI KI GYTGENERKI LQAAPEYEECKKI AENSGTPLKEI YTTALAAFE
KI KI DKGDDL

>2617919696 Ga0073689_10254 uncharacterized protein [pelotomaculum Ga0073689 : Ga0073689_102]
VNEPAEKLAYLKEI LKDCGSVLVAFSGGADSTLLLKVARDVLDGRVLAVT
AASEI HPPGEAEAGALARAI GARHLVVKTGGLASAAFTGNPPDRCYHCK
KELYAALWDI AWKEGI HCVVDGSNADDGADYRPGMRAAAEMGVRAPLREA
GLTKQEVRLSRELGLPTAGKPANPCLATRFPGAEI TREGLAMVHAAEG
CLRSLGI PQPRVRHHGNLARI EAPVEYLGLVVEKSGEVAAKLKEI GYTYV
ALDLQGYRAGSMNESLSLAERVI FPADVMHW

>2617919695 Ga0073689_10253 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]
MKI AYYDCFSGI SGDMCLGALAGGVDFERLKEELVGLAVAGYTLRREKV
KRNGI TAVNVFVDLLEVAQPARRLADI HRI I DGATLPEEVKEKSKAVFSR
LAAAEAAVHDTTPDRI HFHEVGAVDAVDVVGTVLGLHLLGVDRVYASPL
PMGRGLI RCGHI I PVPAPATLEI LRNVVPYGT E EGELVTPTGAALVVT
LAETFTGLPAMTI ENI GYGAGKKMMEHPNLLRLI VGELYESRAPGMPCH
DGYDRGNSPGRGRHHPDGGYSENEGRPV

>2617919694 Ga0073689_10252 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]
MVKDELRRLLLEDVKNKVKVG DALNRLKNLPYEDLGFAVADHHRALRKGF
PEVVFQCGKTVEQVAGI FKSLCGGKRSI LGTRATGEAYKAVWEI YPDAVY
HELARTI VVRRGWQPPRKG NVLMSAGTADI PVAEEAAI TAEVMGNDVRR
AYDVG VAGMHRLLDKLDLI RWAHVI I VVAGMEGALASVVGGLADRPI I AA
PTSVGYGASFNGLSALLGMLNSCASGVGVVNI DNGFGAGALADAI TRMVA
GADE

>2617919693 Ga0073689_10251 Protein of unknown function (DUF3232) [pelotomaculum Ga0073689 : Ga0073689_102]
LI KGI NKI I EKMEKKSSKEDI EIQGFI QDCSRYVDTVI NMENAI AVSR
FI MEADEYRKHLVSLDKNRKI AHD SLI LSTRLLNKLCLRYDI EPI YNGSD
SRI EVAEFAKQVVDEFFAERKTAR

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- >2617919692 Ga0073689_10250 4Fe-4S binding domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_102]
VSDGEGKKVI SMSRRTPRWHADTFI KTLREKYPPEKVHTLVI WTKFPMV
LTAPPYREVLVAYDQLYI HVTVTGFGGTPLEPGVPPDDALAAI PELI KL
SGDPRRI RIRPDPLLLALRKDGRI ITNI PVSGEI I VKAAVLGVVSFSTSFL
VEYPKVERCLRKSGYTVVELVQEKREI MSGLLKLGEKLGVTLNACCVAG
FPVSACI DGNLLTGLHPSRGVCRTDRAAGQRKRCGCTLCAKACENSAI IG
EKKEPHVI DQEKCVQCGECLAKCKTGSIVPAYFKNI LQQPGAGLQVARHF
YAGICRG
- >2617919691 Ga0073689_10249 Polysaccharide deacetylase [pelotomaculum Ga0073689 : Ga0073689_102]
MPSGI SNTLKKYGACWI GSPDEKVVYLTFDEGYENGYTPKI LDALKVNDA
KAAFFITGRKEMKYLRPPKGEYSDRTLAVTRELDYHNI FWSMALVDWAPM
PGGP
- >2617919690 Ga0073689_10248 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]
MDNLHNGAVILLHAVSKDNTEAIDRI LKDI KARGYTFKNLDDLKVS
- >2617919689 Ga0073689_10247 LexA-binding, inner membrane-associated putative hydrolase [pelotomaculum Ga0073689 : Ga0073689_102]
VFI FAHTGI TLGAALLDRLLPYKAVGTGVAAGAGNPAPAGGDEPPDRVK
GMDYRLVLLGSMLPDLIDKPLGLLAPGLGLGTGRGI AHTLVFALVLLVGG
LFFYGAGRRGLLHVALASAGHLVLDCLWQLPRVLFWPLYGFTFPTVGRSG
ILSQLAAWWHTLWTPGVFI PEIIGVAIILAFALRLRRRGVFSKFI KSGM
APWL
- >2617919688 Ga0073689_10246 UDP-GlcNAc3NAcA epimerase [pelotomaculum Ga0073689 : Ga0073689_102]
MKIVTVVGARQFI KAAAVSRAIAKHNLKNPI KQINEIIVHTGQHYDHNM
SEVFFEELDIPRPGHNLGVSGSPHGRQTGRMLEAIEKVLAEERPDWALVY
GDTNSTLAGALAAVKMHVPVAHVEAGLSFNRRMPPEINRVLTDHAATLL
FCPTAAVENLRRREGITGGVRRVGDVMYDCLLHYRSKIKDNTPTLANLGL
KPGGFALATVHRAENTDSPGALKEIFDAFNEISGQLPVLVALHPRPRKYL
DSYGIKTAPGVKLLPEVSYLQMI ELEYNARVILTDSGGVQKEAFFVGAPC
LTLREETEWVETVQCGANVLCGASRDRI VDAYVSLERKHFKRNYSIGIY
GSGEASRSIVNMLVDSFYEY
- >2617919687 Ga0073689_10245 dTDP-4-amino-4,6-di deoxygalactose transaminase [pelotomaculum Ga0073689 : Ga0073689_102]
MQVPQFSLTAQTAEIYDQLSAAVNRVILKGSFILGENVRGLEEETAAYLG
VKYGVGVGNGSDALYLALLACGIPGDQVITTPFTFFATAGSIVRAGAVP
VFADIDPRTYNLHSGLI EEKITGKTRAIMPVHLYGQAADMAPI MEMADKY
NLEVIDETAQAMGATYGRKTCFSGHASCLSFPTKNLGGFGDGMVVTG
DPEIAEKLRLRVHGSRKYYHEIVGVNSRLDEQLAAVLVVKMKYLDQWI
AARNKVAENYAQLFKQYELEGVVTLPFARTNSFHTYNQYTI RVPRRDELO
NYLKERGIGIAIYYPLPLHLQPSFAELGYKPGDFPEAERACREVISLPVF
PELAFKQQECVVKTI RQFYPLKL
- >2617919686 Ga0073689_10244 transferase hexapeptide (six repeat-containing protein) [pelotomaculum Ga0073689 : Ga0073689_102]
MVI KMNTNTIIAPTARLGAGCKTGFFTVI GENAVI GAGTVVGNNVTICPG
TVIGKNVYI GNNCVI GKQPRPARTSTIKNREPLPPLVLGDSCVTGENTVL
YAGATIGNSAFIGDLATVREKCRIGEVI IGRGVAVENTDSIGDYTKVQT
GAYITAYMTIEEHVFI ASMVTITNDNFMGRTERRFKYIKGATIKRGARVG
GNAVLLPGVTLGPESFI AAGALVTRDVPAQTLVKGVPAKPAGKVPEEELL
P
- >2617919684 Ga0073689_10242 protein of unknown function (DUF4338) [pelotomaculum Ga0073689 : Ga0073689_102]
MDKNRAKPGIIDQIESKDTNLSPLVVRPI TLNEVDKWDDLMSNHHLGFN
SKTLTGKTLKYVAVLNGQWVALLGWGAAALKNSNREKWDKYPISILRSWD
ANWAEITTFFSYPEQIRHLI YTTNAVEAYHRMVRKYTKIKSIFPTDDSI R
KVVFLSAREITKKWTQPSRDWAMAYSQIMIFFADRLTA
- >2617919683 Ga0073689_10241 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

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MI NNATSKQSLEQARLKMLNRAQVQVI QATLNKDQSAAAVI GWRREVEFT
WCFEPDL

>2617919682 Ga0073689_10240 NlpC/P60 family protein [pelotomaculum Ga0073689 : Ga0073689_102]

MFGRVKLIIFVAIVLIILNMSESLCLASTTSTI PNVSREMLKSDFWI EKL
AEPDELLMSQKEIAAFNKDIHKLPETIYDMTNPSSLNKDELTKLVTKR
PFPEEDRFLNDKKVDLSYYEILKKQMNLPQIEINQVYYALTI RRTNI RT
FPTSGVSLSEPNDWEFDMFQETAVGVAEPVLVLRSLDGQWYFVQVNYC
GWMPASDLAI AKNKADWLDYVNADRFLVVTDNRLRLGFNMYSPELSQLEL
TMGTLKPLADEIPKIVDNQSVAGNYVVKLPVRDSNGQLNI KQALVPVVS
VSEGYLSYTKANI KQAYKVLGERYGWGGMFNGRDCSAFAMEVFKCFGR
LPRNGDEQEQAAGETVKFDSLNTQRYALI DTLLPGATLHTPTHEMLYLG
KHGGYYVI HDVTSLGDTSNRNPDGSLGRLVLNEVVTDLSI PRRNGMLL
IDSLTSGKQIEYQKEPNLYNYSVYVNDI LVNFPDQRPFI DLSLTSRI YV
PVKFVSEAMGAKVKWVNKNRKI VMEKADKKI AFVI GDKTVDVNGKNYTL
AAITIVNDRTMVPPLRFVSEVLGAEVQWTVSDDGGRVDI KND

>2617919681 Ga0073689_10239 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

MQNNNKIYRENYIEELKRHFQDQRRINHAQKVLAYAESIMDGEVDEKT
HKIVTITALLHDVGIKIAEQYNSSAGIYQIEGPPIVTEIMTRHGEPED
FIWRVAYIVGGHTITKNNGLDFQIWESDLLVNI EEEGLYNHTEKLRI
IAKNFRTSTGTIRARERYLE

>2617919680 Ga0073689_10238 Cell fate regulator YlbF, YheA/YmcA/DUF963 family (controls sporulation, competence, biofilm development) [pelotomaculum Ga0073689 : Ga0073689_102]

VSELDKALELCVELGKILSETGEYKKMKRAEYDMLHDSVARGLMENLQAL
QMGMRKKQLAGMQITEENKKLKEVEMTLKNSSVVKASHQANADFQALMG
KVSARKIREGIRQNEPMQQ

>2617919679 Ga0073689_10237 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

MRLENRTLIVSAEVLKLSAGGKSLVKPGVLI SADNVHLFKASPTVNKAR
KSFEDI GFKTEGHSTGITLVGPALRFEEVFKISLSVEKAGGTQMAVSI R
GEPQIPAEKDFVEAVFPFPPPELLG

>2617919678 Ga0073689_10236 Subtilase family protein [pelotomaculum Ga0073689 : Ga0073689_102]

MAEEALKKKIPPIVYAEASVRSLLGGVSLFDFKEDVADNVNGFYSEQGLI
GEAVDKLRKYGFAPLWGGITITIAAPADVYEKVFKTRIIEEREAI KHF
GLKDTATFLDCPDTEKPLIDVSKSPLKDI LEGVALNEPVYFSPSAFPP
AQGYWRDLVPAGVSLGLRADLAHRLGYTGRRVRVAMVDSGWYRHPYFTSR
GYRFNPVVLGPAATEPEHDEHGHGTGESANIFAVAPDVNFTMVKMNFVNS
IGAFNTAAALKPHISCSWGSSKKEGPLSAADNALAAVASAVAGGITV
FSAGNGHYGFPGQHPDVI SAGGVFMKEDLSCEATPYASGFASNI YSGRNV
PDVCGLVGLPPRAQYIMLPVEPGDTLDSSLSGGSHPNGDETAPDDGWAFF
SGTSAAPQLAGVCACMLQAYRKLSPSNVKDILKQTARDITKGHCSPSTG
GNAAVPGPDLATGHGLADTFRATMKARGI GWGYRPLAPGPDNAPRERHYS
QDGGYQHSAGQDADWKKYFEDALAHYECYGTSATWDDCGVENFEREVIDE
HLAYYQEVLSQVQEQYQKLEEEVACLKRLKEGE

>2617919677 Ga0073689_10235 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

MANNEDYYNIQAYETALAEYEEALAENQNYIDQLI AYYENIITQYENAAP
YGGEDVVSYYEIGIAQYEDALAAAYDAIAQYEGALYGYEGYPAQYGGTPT
IPQPPIQPIVPRPPLVPVPPPLPRPPLVPRPPLPPIVPRPPIVPLPPRPP
LVPRPPLPPIVPRPPIVPRPPIVPLPPRPPIVPRPPLPRPPLVPRPPLP
PLPPRPPVVPVRPVVPVQPVMPVGRPR

>2617919676 Ga0073689_10234 radical SAM additional 4Fe4S-binding SPASM domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_102]

MGTAESEYDLRQLNERLNYWEKYLLVEILKSFPVHI ELPTGERCNVQCVF
CLDRSDEQKNKYDTFTAEVKKMAELLPLRFCSTLNLYSWGEPFFNKDYE
QIFDYITNNFPGICISITNGTLLNGKWAekli SHGNI MLNVSLNAAASRE
TYKRVMQRDLFEAVRENI NRLVSMKRETGADKLIISLSFVAIKDNI DELP
LFI ELAHRFSADVVQDMFIIDDKHKHAALHDEPELARRFFAKATGKAK
ELGINFCSYVYTPVEYFKQEEQSAADNFCYDPWQSFKVASNGDVGMCRRS

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DKVMGNI FEQGFQEI WNGDYRYRRTVNTANPPDECRI CPVKTGCG

>2617919675 Ga0073689_10233 Predicted DNA-binding protein, UPF0251 family
[pelotomaculum Ga0073689 : Ga0073689_102]
MARPPKCRRVEQFPQVTFKPTGVPLPDLPEVALSVEELEAI RLRDLTGL
EYEECAQRMSVSRPTFHRILASARQKVAGALVNGAALRI TGGNFRLTLHK
LECRACGHRWEGTI CCRRTVCPSCSSRDWHRVE

>2617919674 Ga0073689_10232 Predicted Fe-Mo cluster-binding protein, NiFX family
[pelotomaculum Ga0073689 : Ga0073689_102]
LLRFAMPHREGRVNEHFGSSREFI VVETENGVI KGKKI LTNEMLHDHGGL
ARMLGAEGVDVVI TCGI GRPMAEALQLAGFKVVTGASGEVERVVQEFSLG
QLVSLPVQSCSGHHGHHAHRHGHGHNNH

>2617919673 Ga0073689_10231 putative membrane protein [pelotomaculum Ga0073689 :
Ga0073689_102]
VFMPWTGNLYGWGLLAMLLHMMV WGAFI VGI AYLI I RI LRGPYDPRNNA
LDI LKRRYAAGEI SEEDFERMKDRVR

>2617919672 Ga0073689_10230 acetaldehyde dehydrogenase (EC 1.2.1.10)/alcohol
dehydrogenase AdhE (EC 1.1.1.1) [pelotomaculum Ga0073689 : Ga0073689_102]
MSEQRAEKVENNLSGDTGKTI DSLVEKAQGALRVFMDLGQEDVDRI I KAM
ALAGLDRHMEARMAMVETGRGVYEDKI TKNI FATEYVYHSI KYHRTVGI
I KVDEEEDYEEVAEPVGI AGVTPVTNPTSTTMFKSLI SI KTRNPI I FSF
HPGARRCSAAAAKTMLEAAVAAGAPEHCI SWI EHPSVEATRMLMAHPGVS
LI LATGGSGMVRSAVSSGKPALGVGPGNVPCYI EKTADLKRAVTDLI LSK
TFDNGMI CASEQGLI VDREVAEEVDALLVANGCYFVNPEELKLLERI ATC
GETCSMSPEVVGKSASTI AGMAGFSVSEETKI LI ARLAGVGPEYPLSREK
LSPI LAYVVNNSREGI ERCEQMVEFGGMGHSVI HTADEELVDEFARRI
MAGRI I VNAPSTHGAI GDJ YNTNMPSLTLGCGSYGRNATTANVSANLI N
VKRAKRRVNMQWFKVPERI YFERGSVQYLT KMPGMERVFVTDKTMAL
GFLDKI KYHLGKREP KPLVDVFSEVPDPTLDLVLEGRDLMSRFQPTDI I
ALGGGSAI DAAKGMMWLFYEHPEVEFEFLRLKFLDI RKRAYKYPKLGRKAR
LVVVPTTSGSGSEVTAFAVI TDRGRDI KYPLADYELTPDVAI I DPDFVDT
LPRSLAADTGLDVLHGI EAFVSVMSADYTDALAKAI ELVFKYLPRSWR
EGDPVAREKMHNAAATI AGMAFTNAFLGI NHALAHKVGGEFDI PHGRANAV
LLPHVI KYNAGPPSKFVSFPKYEHI APEKYRRI AAHLSLPAATPEEGVG
SLI GAVGELNRS LGI PATFAEMGI DRGRFAAKLPALAEKAFEDQTTTTNP
RLPLI GELEKI LREAYGVPLEAENEADLPVPAGVLTETGTEGEAGKYTLF
Q

>2617919671 Ga0073689_10229 hydrophobic/amphiphilic exporter-1, HAE1 family
[pelotomaculum Ga0073689 : Ga0073689_102]
VFLTNLSLKRPVFATVTI LALI ALGI I SYI GLNI NDYPDVEFPYVGVTI V
ORGASPGQVETKI AGKVEEAVGQI SGVKHI YTTAREGVCTVVAEFSLETK
PEVAAQEVDRDLKI RGELPQDI EEPVI TRFDPTAYPI MSLAVTGDLSMR
EMTTLVDDLLKKRI QTI NGVGEI SVSGAEKREI QI DLDKEKLAAYGLTTY
DVLESLRGENLDVPGGKLGAGREI TLRTDGGI DRVAEFANLPVARRDGT
PLYVRDVATVTDGTERESLSRYOGRPAI GVDI LKQSGSNTVVVADKVRK
AVEELRKELPPGVNVDI VRDINSVYI RDAVNDVLKTI LEGSALAVLMVFLF
LKDWRSTAI SAI SI PTSI I ATFFAMKLMGFTLNFLSLMALSLAVGLLI DD
AI VVI ENI VRHMR LGKTPLTAAREATAEI GLAVTATTLTVVAVFLPVGMM
TGVVGQFFKQFGLTVVFSVLVSLVSTLVLPLASRHLQGEERLPWGPPG
RFLAWFNRGFEGLTGLYARFI NVVLRNRLKTLGLAVALFAGSLMLVPFLG
STFI PAGDYGELNVVAELDSGLSLEAAGEVTGRLENI VLGYPEVVNI YST
TEPDKATI FI KTVDKNHRERTI NEI AADMREKLNTVPGVRMAVNLSGLN
TEKTVOFRLLGGDLDELQVYAEKAQWI MESI PGAVDVGNYSYKPGKPEGKI
QVKHDLAADLGVSTAQVADTLRTL FNGVVAGQFEDGEDRFDVRVRLAGEQ
RRNMDDL DNI YLQSSNEPAGGPRPMVALSQVTGRFTSTAPGEI RRFDR
KEI VVSANLEGI SLGEFNKAFI ERVNRELPLPPGYRI YAGGDSELMGETF
TSMGLALFTGVLF I FFI LASQFESYI DPFSI MSLSPMAVVGAI LALLALG
SDLSMMSMI GVI MLMGLVTKNAL LLI DFARQQRARGVERNEALAKAALTR
LRPI VMTSLAMI FGMLPLALGLGPGAEGRAPMAHAI I GGLI TSTMLTLV
VPVVYTLDDLKNKVYGLKGRLKPQASGGSQSTR

>2617919670 Ga0073689_10228 RND family efflux transporter, MFP subunit
[pelotomaculum Ga0073689 : Ga0073689_102]
VEKLKWKWL I PLAALLAFGLLKGGDI WGQKKGEELPPVHVQTVSVEEVA
KVKKENTLSLTGTLEAFSDATVSAKVPGRVSGVLVENGAAVAAGQPLVSL

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ESTEFENQLAI NRATLQKAEANLSSVRTNHVRFKELYAGGAVSKKEFEDL
ETALKVAEADVASAEAAVANAGDSLNTTI ASPLNGVVADRNVTGQVVS
PGVPLMTVKDLSSVYVLVNI EQKDLAVI KPGLRANVTVDYGDRTKFTGVV
EII NPVAEESARVFKTKI RVDNPGRLLKPGMFAKVEI KTGEAEEVLAVPM
NALVDKQGMVFVFAEGDTARRRQVEI GRVI DQRVEI KSGLDPGQRVVVT
NVNKLKDQDKI NI AG

>2617919669 Ga0073689_10227 DNA-binding transcriptional regulator, PadR family [pelotomaculum Ga0073689 : Ga0073689_102]

MSLQKAI LGLLTYPMTGYDLKQYFDQSI NYFWSAQLSQI YRELGALESE
GCVFHHTERODGGRPDRTKVYSI TKEGEAKFQQWLEKFPQTLSPVI RDEFV
MRVFFSSRVAPEELAFQLKRYI KEEQELLDSLAALEGMI DAYAREI SRPG
EKFYWRLTLKRGYI MTGAAI RWARECLDELEKNMKNHI NRAVEGG

>2617919668 Ga0073689_10226 4-alkylglucanotransferase [pelotomaculum Ga0073689 : Ga0073689_102]

MESGKMNEI PGI RFP LLHRLARLHGVEACYRDHTGRRRCAAPHI LLAALQ
ALGAPVENI SLDPAFRARVREKWRQCEPVAVVWEGSQGHLNLRLPATQ
TGCGADCI LELENGETRRWRCPVRLPLLAGVSVEGVKFERRRLLPPGL
PLGYHRLTLCLPARTEEALI I SAPRRAYDPTDGATASGWGVFLPLYALHS
GRSWGSGDLTDLAALLNWLKSLGGDMAGALPLLAFLDEPFAPGPYEPVS
RLFWNFEYLDVERVEELKRSPALDLLNSPEFRAAMEALRGSPLDVYSRG
MALKRQVLEHCVRTCFAGGSNRQAALRRWAENPAALDYARFRAVVERRR
AGWPAWPERMRDGI LREGDYDPEAARYHLYVQWLAAGQFREI AAMARENG
ORLYLDLPVGVHAGYDVWRERAVFAMEACAGAPPDFAFFSGGQNWGFPP
HPERLREQGYRYFI ACLRHHLRHAGI LRLDHVMGLHRLYVWPRGLPAREG
VYVRYHAEFFYAVLALESRRROALLVGEDLGVPVPGYI RAAMERHGI HRMY
VLPFETTGNPRQALRPAPAVALASLNTHDMPPFASFWLKQRRSDRAVLPV
FLYRQGLLGVPNTKAGPVRRACLAHLAAGRARFLQVNLEDLWLETAPQNV
PGTTEEYPNWRKARLSLEDFTDRPSVLEI LGEI NQLRKARGKAI LSRPA
PSPPAADFFTD RG

>2617919667 Ga0073689_10225 maltotriose trehalose hydrolase [pelotomaculum Ga0073689 : Ga0073689_102]

MTGNFTPGATYLGNGRCRFLVWAPLAETVAVRFLEPRERLAPLARGERGY
HYGELAEVAPGSLYLYVLDKKEKRPDPASRSQPGVHGSPRVDPGAFPR
PAHCWSPARRDLI FYELHVGTFTEPGETDAI I PHLEGLRELGVTAVELM
PVAQFPGGRNWGYDGVYPFAAQDSYGGPEGLGRLVDACHQRLAVFLDVV
YNHLGPEGNYLGDGFPYFTDRYRTPWGFALNFDGPGSDEVRRFFI ENALY
WI TELHLDGLRLDAVHAI TDKGALPFEELAGAVHQAERMGRRVYVI GE
SDLNDPRLI RSRVGGCGLDGQWSDDFHHALHSLI TGELGGYRDFFGGL
QMARAFREGYVYTGOYSPHRQRRHGRRPVLCRASQFVVFQNHQDQVGNRA
RGERLSVLTSDGLKLAAGLVLLSPFLPLLFMGEEYGETVPFQYFTSHTD
PALAEAVGKGRREEFASFGEDEVDPQDEATFLRSHLQHDLRHRGRHRV
LYEFYRQLI RLRRELPAELNRDNLEVVTYEDELALLI RRWHGEDEALA
I FAFGEGAVTI TLPVPKGLWLKRLDAAEEQWLGGGSALPGVLASPGKVRL
TLPPRACVLFERANSFSLH

>2617919666 Ga0073689_10224 Glycosyl hydrolase family 57 [pelotomaculum Ga0073689 : Ga0073689_102]

MERYVCI HGHFYQPPRENPWLEDI ELQDSAYPYHDWNERI TAECYGPNTV
SRI LDEEGWI RKI I NNYSKI SFNFGPTLLSWMEKKEPEVYWAVI ESDRES
GENFSGHGSAFAQVYNHMI LPLANRRDKYTQVWGI RDFESRFGRKPEGM
WLPETAVIDMETLDI LAERGI RFTVLSPHQAWRVRRTGAGTWNEVGAGVDT
TMPYRI NLPDSGRTI DI FFYNGDI SQAVAFEKLLANGERFAKRLLGGFNG
SNPSQLVNI ATDGETYGHHHRHGD MALAYALHYI EI NKLARI TNYGEYLE
QHPPTHEVEI HNNSAWSCAHGVERWRSNCGCNTGMNPGWNQGWRTPLRNA
LDWLRTDI ASQYEEKGRQFLKDPWAARDYI TVI NDRSPESVRQFLEKHA
ARELKPEEQI TI LKLELQRHAMLMTSCGWFFDELSGI ETQVI KYAAR
VI QLARELFNNSTEEHFLEMLTQSKSNI PEHRDGAHI YEFVKPAMVDLL
KVGAYHAI CSLYENYDEHSSI YCYDVNREDYQNRLAGAARLTVGKALVTS
VI TRESAGLTYGVANFGNHNVSAGVRFHQDDGAYQKMVQEVGTGAERADF
AGVVRMLMDHFFGGATYSRLRQLFRDKQRMVLDQI LDTTLTEI AEDYRRI YE
RHAPLMRFLKELNI PQPKVLYTAAEFVLNTNLROAFTTDI LDI ERI NALL
DEAKI SNVPLDGA I LGYVLEQTLERLGEQLRDRPTDHSI GHLDVAVGLV
RSLPFEDLGNVQNI YYSLLOSVYPGLREKAGQGGGARTWVDQFNALGD
KLQVRREQ

>2617919665 Ga0073689_10223 maltotriose synthase [pelotomaculum

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Ga0073689 : Ga0073689_102]

MAGPVI PAATYRLQFNRRFRFNDALVI VPYLNALGVSDI YASPLLAAGRG
SAHGVDVTDPARLNPELGSSEEF AALAGSLRCHGMGLLLDI VPNHMAAST
ENPWWRDVLRNGRHSAYAAAYFDI DWRPAQPGLAGKVLLPVLGEPFGKVLE
NRELTI EPDEGDFAI RYFORRLPLNPRTTAQLLARWAEAPAGASGTSGRC
LPPQWREFSEELKVLLDSMDKKESAASLGQLYEKFWRRLYGALPEVKAFVD
GELRLLNGRRGDPRSFDRLQI LAEQAYRLAFWWLAGEEI NYRRFFDVNE
LVALRGEEKQVFEATHAFVFRLLVEAGLVTGLRI DHI DGLADPQTYLERLQ
DRLATPGRRPGFYVVVEKI LAGGEKLPDDWPVYGTGTGYDFLNMVNALFI D
GNGTGELNRLYSKFSGFAEDFATVVYDRKRRVMAMLFAGEVRS LARRLI E
LAAEDRHGHDLTPAGLERAI DEVI ACLDVYRTYI RDTFTVSRDRRYI EQA
VHKATRLCPAAGPACAF LGRVLLLEFPDTPREKKETWLR FVRRWQOFTG
PVMAGKFEDTALYVYNRLVSLNEVGGEPTPGI TVGEFHRRNKDRKDRLP
HTLNATSTHDTKRSEEDVRARI NVLSEI SAAWARRVENWRRWNGPKKPVVN
GLPVPEDNTEYLI YQTMAGAWPLREDELPAFRERLQAYLVKAAREAKI HT
SWLEPDTGYEEALKNFASAI LEPGENNHFLRDFLEFORGI ACYGAVNSLS
QTLLKI TSPGI PDFYQGTSLWDFSLVDPDNRPPVDFGARAGLLET LKREE
ARGLPDLVKKL TASWKDGRVKLYLTYKALNFRDRHREL FASGEYI LVETT
GSGVEHACAFARRLTGFWVLVAVPRLPARLCLSVRASGEI ELPATGI LPE
PAVWKNGVLI LPGQAPTRWRNI LTGEELPATVAGAPPGEKYVLPLAGMFR
NFPVALLAEG

>2617919664 Ga0073689_10222 trehalose synthase (ADP-glucose) [pelotomaculum
Ga0073689 : Ga0073689_102]

MTRFKLQDYETAAGSAI IEEI RTLGESLKG YRI LHI NSTLVGGGVAEI LH
SLAPLMQEAALSPEWQVLEGNPEFFNTTKLFHNGMHGQPVSI TGEMLSEY
LTTAQKNKHLAEAEANLVVLHDOQPLGLTAFRGGNSARWLWYCHI DPRLA
VPEVWYFLAPMAAACDVAVFHLPEYARDLPVLQYFMPPAI DPLSDKNRDI
SPDEYERVLEKLGVDMDGPPVI LQVSRFDRLKDPVGI QAFKLVRENKRC
RLI LAGGSAGDDPEGMTI LEEVRAEADGDPDI NI LSLPPDANLEI NVLQR
RADVVVQKSLREGFGLTATEALWKGKPLVATPTGGLANQVLDGKTGLTAR
TVEETAARVERLLADPSLGRQLGATGREHVRQSYI LPVYLRNWLKLLLLL
SGRR

>2617919663 Ga0073689_10221 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_102]

LI GLDRI REAARRDKNLRFTSLMHHI TI DLLREAYKALKRNAAPGI DEVT
WQQYGEKLEENLSKPPACTKWQI PCKALKTDLVT

>2617919662 Ga0073689_10220 4Fe-4S di cluster domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_102]

MAAPPKDVNI TI GDKAFLVPAGSKVKDAAAAAGVVI PRLKI DPATCKGCT
LCAKACENGAI TGEKKEPHVI DQDKCVQCGECLAKCKTGSI VPA

>2617919661 Ga0073689_10219 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_102]

MKI SNI GLKPGNAPQKVAKKSAGGEFSANLDLARRENAEKNLAEI LKKI N
KLGEELKEKPSLEKNKEYKRRRI RAYLSFVLKHYYKLSPHYGRCSAQLLI R
VEVI NRKI EELTAEFI RRQKGAI DI VGRI DEI TGLLVLYS

>2617919660 Ga0073689_10218 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_102]

MI ROARNHYRI SPGRLLYAALLFCGAAAAALHLAEVEQVWRAVKHGAWG
I ALAAFLQFVFLNL SAFYSI YQALKLPERFTRLFLLVLA AFTTVVAP
GGSLSGAGLMYDATTRDLEAARVALANVLFYLLDYLAFLLVLTAA LFYL
FTRGALLEYQMTAAAVLAALVAAALLLVFSALRPEALPGFI GRVAGPFS
RRLPAAAGHRVRAWEEKI AGFTSRLAAAARTMRKDKGGLARPALHALLVE
I I GLFQLQALFLAFGGHPAPGQLI TGYALGVLFMI VSI TPSGVGI MEGAM
TAAFASVGI PLEQAALATFTYRALSFWLPMI GFLALRRVRES

>2617919659 Ga0073689_10217 phosphatidylglycerol lysyl transferase [pelotomaculum
Ga0073689 : Ga0073689_102]

LI SRSPRLRLAALLVALNGAFGI LSAWLVHHPARFTLLAHHLVPVLLRG
SWLTGVLGAVQLFLAWSLSRRKWQAWRI VVVVLLFSAGAQLLRELHYGQ
AAFSGLLLLLLLVLKPOFTAASDPPSVRHGALVFLGAALFTYLYGLLGFY
LLDRHFHONFNLLDASRQTLAFLAWLDTPALARPNNLARWFLDSLAVI EA
GGLAYGLVMVLQPVVYRRTVLAAERERARGI LERHGRSSLAHLTLLPDKT
YFFSRSGQSFAAYTLVGNVAVAGDPVGPPEEDI PRLI SEFRDTCGENDWY
PVFYQTLDPHLPGYHTAGFKSLKI GEEAVVELAGFSLAGSRRKSLRQSVG

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RMTRLGYTTELLEPPLGDDTLARLKEVSDQWLRLOTGGEKRFSLGWFDPS
YLKPCPVMVVLDTGRFOAFANLI PEYRRNEGTL DLMRRRSAENGLMDML
FI RLI EHFRERGYETFNGLCPLAGVGDEPGAGLQERAARFFYQHFNRLY
SFKGLRRFKEKFDPCWEPRYLI YNSALALPKI AVAVVRANAGGSLLTYAG
AWLEKVKSRRAASTRLKLS

>2617919658 Ga0073689_10216 stage II sporulation protein P [pelotomaculum
Ga0073689 : Ga0073689_102]

VFKNKI HRKWLVLMGI VAGLSLPVFWHAAMATRP I FSLNQLLKNTDDELG
AGKVCAI KDEEGLVMTVSRRLRVGCEI I TAGGKHVRVQTVRGNTATAGF
LGMDKDI LAYSELF SKMELPAVAPEQAAGPVAI YHTHTDESYPDGHVS
I PFNGGI LQVGDSYSSSLTHDGANVLHDKTPHDPHDNNAYRSRRTAVQL
LQKKPI AVFDVHRDGVDDPEFYRKVI SNEEVAQI RL VVGRENPNMAANLD
FAKRLMAYANQTHWPI VKEI FI GAGDYNQDLLPTAI LLEAGTYTNQKEEA
MRGI AOLADAVPAI LGI TGPSGRPEASEYEKPVTDP TARRPGVWSSSLGWL
LLTTLVGAVFVI I NEGSYRKARERMFHFLGWEMGDFNGFEVKKNGLAKW
VGDTGRKAKERLLHFLGRKSFVHGPQAKKI QSEGLDRDSNRYGKKP

>2617919657 Ga0073689_10215 TusA-related sulfurtransferase [pelotomaculum
Ga0073689 : Ga0073689_102]

VAI VRDARGLLCPEPVL I AKREMDQLGSGTFQVLVD TAVARDNI I RLANN
OKWEI SVEPNGEEFLLKLLK

>2617919656 Ga0073689_10214 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_102]

LNQKGLI I FTGAI VGGLAI LLVKLGNPANMGYCI ACFLRD TAGGLGLHRT
NTVQYI RPEI LGLVI GAFF TALFTRETRVTGGSSPLTRFVI AFFAMLGML
VFLGCPLRMVLRI SAGDLNALVGLI GLVAGVGAGI FFI RKGFSLGRAI AQ
NKSNGYI FPAVAI AI LVLFLAKPAFI FFSEQPGSMHAPI AVSLAAGLI A
GVLAQRSRLCMVGGI RDFVMFRD TYLLSGFI AI LLVALI GNLSLGSFKLG
FENEPI AHGDGLWNFLGMALAGFSGVLLGGCPLRQLI SAAEGNTDSAI TV
I GLFAGAAFAHNFLAAGPKGVPVPGQVAVLI GFAVVLLVALLNSKALFK
QGV I VSGDSQGCAGSPLS

>2617919655 Ga0073689_10213 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_102]

VARSKPEI I DYKVSRRTSFTHNI MEVGLI PDI RVLSPYCYAEKRDELKKM
MEEVDCGNVPLFI EHP

>2617919654 Ga0073689_10212 Endonuclease, Uma2 family (restriction endonuclease
fold) [pelotomaculum Ga0073689 : Ga0073689_102]

MSFORKRQTKVNYTYADYASLPEEERCEI I DGELYMQAAPSRI HQEI LME
LSRQI ANYLADNPDKTCKVYPAPFCVRLPDGDEKNDDDI RTVVEPDI SI V
CDQSKLNRRGCMGAPDMI I EI TSPYSARKDRLEKFYKYERAGVKEYWI VE
PEEKLVSFVLGGNNRYGRPNI YTEGDEVKVSMLPDLVNLQNVF

>2617919653 Ga0073689_10211 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_102]

LTAGVPAYGKMAFRRGVHLAYMFPLSRPVGSSRTATCGAAVKAAAYNI PR
NWFTLN

>2617919652 Ga0073689_10210 putative ATPase [pelotomaculum Ga0073689 :
Ga0073689_102]

MNLFESAMEKDLVKTAPLAMRMRPGTLDEFEEQNTVAGTGTPLRRAI EAD
KLVSVI FFGPPGTGKTTLAMI I ANMTRS RFVTI NAVTAGVADI RRVVEEA
KEARSLYNRKTI LFI DEI HRFNKAQQDALLPFVENGLVTLI GSTTENPMF
AVNRPLLSRSRLYRFELL SPEAI RRLI KALRDEKRGLGEYRAEVAPEAL
DHLAGVANGDARAALNALELAVLTTPPDDEGVRRVTLAVAEAEI QKRVLR
YDRVDEHYDVI SAFI KSMRGSDPQATLYWLARMLYAGEDPEFI SRRI MI H
AAEDVGLADPNALVVA AAAAQAVERI GMPEARI VLASAALYI AAAPKSNS
VI MGI DAAFSAVEKERAEPVPAHLRGTGYKGAASLGHGKGKCPHDYPGN
YVEQDYLPGNMKGKVFYKPSENGSESVI KNRLEKMK

>2617919651 Ga0073689_1029 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_102]

LRGRVGYCSAGGLGTAQRRPAGI I EAAARGAKENGGLTVGI LPDNSSCFA
CKHTDI PI VTGMGDGRNYI NVLSSDVVMALPGKAGTI SEI ALVLKNRKKV
I LLNFDVGKI FDFYMEVGLHTAGSPEEAI RI I KTR

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>2617919650 Ga0073689_1028 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

MDDFDRFLDYQQR I AEMTLEE I KKI RNRPVKTPRTYKLRI VEPI LKKAGK
PMHI PEI I RI AERDYDVTLERDSLAS

>2617919649 Ga0073689_1027 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

VTQGFARTLDRNI RMAPSKPLSGGEVAKKRI RALVDTACQLLNSAVPEVG
RDKI HRLDKADTI GGMGTI RALSVLGAPYAMLLYERFLGQPYAGHRDSVS
VLMNPQSGSLDQGRLLPSFI

>2617919648 Ga0073689_1026 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

MERGLSHFTGLSAVFI KMAFALKRGAPLVFTYHHNTI EAYLPI AVAVLD
AGLTCSAPI PCPAEMGASI HI NGTGSSVI DTVFVCRSTDSVPRRTI VFTP
EEI AGLAHEDLKLLOAGKVKLTRGDARCVAYGHLVRLAI WNLRRKKWSVET
PAVEKMKTVLALAI EQLGGWAGVERRLAGDMAGVPFRRTSLVREEQEYYGG
EEDEI SFLKHLSONLKPRTYTSPLFSPAWSQNSSSCPGGTGSRI FMPDR

>2617919647 Ga0073689_1025 regulatory protein, luxR family [pelotomaculum Ga0073689 : Ga0073689_102]

LSYREAOYYHGKWFYVQFKKI LDLVAVI GATRDI DEMRRI VLQELRRLI W
FDGANFGLNDPLTGLPQEKFAQLDTPVESI KPYLNYYI HLDEVLOAHRDS
GLLVARSTDLLLEYGOWTRRSEYNDFLRTFRTHYLLGLNI KKGRTGFAML
CLYRDKSTGNFRPEDVQVLQI LYPHLLNLQWRHALVEAAHRRRLRSCQER
PTLNVPGFSESLTHRELDVVQMVLTGLANREI AESLRI SVNTVRMHLQN
I FAKLGI KRRGQLLALYLKAERAAGEG

>2617919646 Ga0073689_1024 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_102]

MCRKHCLALLTFCVLLFVAGCGSGKGTGAPQGDAGGAKETAKGI VDPRL
LTAEVEAALREQVREPEFTDTKNPLGQRLCFYSPVSEKADKFI QLSVVQ
NEGMGKSLRDQGYNVEQLYKETKKNLADAKPVSGI GDEAFWGANGLHI LK
GNVYLN I SVGNTSI PENLELAKVLAEKVVPRL

>2617919645 Ga0073689_1023 Copper amine oxidase N-terminal domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_102]

LVLAMLLLSLI PVPAGAI NPQPEPPGEPDAI SVFVDGSPLTLDVAPLI EQ
GRTLVPRLAI FEALGATVGWNEATRTVTGKKGDTTI KLVVGLETAYVNDK
PVTLDVSGRI I QGRTLVPRLRFVSEALGAGVAWDSAARRVTI STAGSPGVP
GGAQEI PGLPGFSNGTQPPLASGDLARLLPVYLKLSVNDKRFDAFI YQD
KLLAKPLDKSLI LSA LPPKLDYSPYLTLTGNQDGWGGCI GRSMVHTI SI L
KEMEHPYSPDLSFWYLHARQAQLLESGVPDGI VSKTLLENHGLSSEVTMP
TDYDPAELI YDGQGNPVKWDIFSAMPQPTAAVNTEASLYRVKLFSDPVTPN
VDGVKSLLCRYGPVI AGGPLPLLLGPNPPEGHCI TI VGFDDSLDVFKCLN
SWGDTWGPNGNGFNVYPYNQLTENFDWVRYFENRPSDRSATGHAYTARI R
I RHQNERNDLTVKI GVEGKEPLI VWNRPNDEPKHPYDNSKELFI DVPLP
AYAPSNWPPGYHRWYVEADGVKDNLT AQI KEI TLARLYHNPGNLTVGK
FQTEYVPEQTN I TVPDGGS I KVVYPGANPAKPPLAPQI RSTYTLTI EPG
QTSVLPGNPVTLQGLTVSAI AGQSSPAAGREI HI YKYI GDPCVNKPGQW
AMVI KVTVPVNGPAEAGKVI TDSNGTYTVNLTPSAGRHI YAAALVDQNGKA
LASSGEAVVDAGI PQLKLPQVELYQQFPEI I PGP GPI MEQPDFDLKQGG
PLTRLR

>2617919644 Ga0073689_1022 Copper amine oxidase N-terminal domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_102]

MLKI LKNLKMFTAGFLACLMLTGLLSVAFAAEDLSVQAI LSNTVKLKLNG
KDWTPQDPATGDYYRPI I YNSRAYLPVRVVEAAGMPVDYDNATKTI WI G
GKNNVLQVNDTI YKDDYGTI I TTDEARLTSPDSVYKWGV TNDKELSMQY
FNFYLPKNGKYQRFRAFSLDRSAKDALT VNI RKESYDGGV LKSI VLQPG
ETLS DVEVGI GGI NQI YVEANI RI NHGTI KCLI VGEPVFYNGALPAKTPV
RS

>2617919643 Ga0073689_1021 Copper amine oxidase N-terminal domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_102]

MKFKTRRRRI CI LVLLMMLAALVPVPAASPSGLPGQI NVKTPPGGFKSP
PLPDSETTMI I I KLF I GKTGYEVNGEAKEMDAPI I REERTLLPI RYVVE
ALGGTVGWTASERKVTVTLNEKVI ELWI EKNI ARVNGQEKFI DTQNQQVA
PI I I PPGRTMLPLRFI AENLGCKVDWDAAAKKVTVTYFTTGSPGGTPGSQ

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GFSNATALI GQVQTPLSSEKEKFMQVNL TNRLTHPKYDTS LDF AATGPG
KPGQQPVVSFFQOVLPDVNGA QSTD AVGPLKNTNPHMQANLALLNQPGI K
PGLSPI KPFPASTGPVYSNADCAAFI DQSGDKKRWFAFKLNSDI QAVKVV
WQVSTSPFSGFRENWQKPSGLVSSGEVSPQAGEFVI DFGSFAPGQQTGGL
WNLKVKNNMI WNHSYREI PKTORKYYVRAAPVDANGNCI GDPGEGLQVL
YGKALTAPTASTQGKTVSFELWAARWTGEPYQVPEFPNTMEHKQLFGYS
PDETQPHWFMFOGFDPAATKMVMQVSAKPFTGSAADWEAPPGLVYAKSYS
PLPVSLTGYGNNI VPVPFKDFGPPKTALKPDEYLPFYVRAVAVKPSSTPG
CVDVDFSETI TVKYGYASPPKI YI PQNVTVPYSI PNI KVLHYQPQWENP
DWP HHYMFQAPK WNEI SCKWKNL NNGATLYPYSPTYSI SPQQYEQQV
I PTVLVPGTKALI RDREEDKSWWGE LWDGI CSFFSSI VDV I AKLTNWVSQ
TYANLKAGLI NFVANAFPVESWRDALKVALTAMVDTGLAAMGI PPTLPNF
DQLSNMSLDYMAEVALTEAGVPANQLTEELVKKTAAGLEGEMAKAAGTAT
PNPI NSPFLKADPDYLSRPAYI DVELSNPYDKPSLPGSLNI DAQWEWRET
GVTVTETWAHLPTDQQAEGLYAVHFFYGLSQGHEGYPI YYRI YEPVR
GQPI PSLQPGETRVRRI YLKEYVGKPYFAGGESVNSVDFANLYWGNCGKA
I FSVSTGDYDLPDPKAAAKAAGFQEDSDHLYTYHYDCFGHSKSDGFQQAP
CQPFSP

>2617919642 Ga0073689_101228 polar amino acid transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_101]
VVVPLLRCI NFLEETGGGEI WI EGKRVDRKKEDLNLLRRDVGMMVFQLFNL
FPHFTVLGNVMEAPVHVRGVDPKQAREEAMALLKKVGLDDKCDAYPSQLS
GGQKQORVAI ARALAMRPKVMFLDEPTSA LDPELVGEVLAVMKRLTADGMT
MI VVTHEMAFAREVGDWVVMDEGRI VKVGRPEQVFESPRDERTRAFLSR
VREPRQPSRNQARRSRMALRSHVEEGPGRAVNTG

>2617919641 Ga0073689_101227 CopG antitoxin of type II toxin-antitoxin system [pelotomaculum Ga0073689 : Ga0073689_101]
MSKNLPEFKGDRI PEFATEEEAAEFFDSYSFAEAVEKCLFEPEKVELEPE
LVMKI RERAKTKQFTLRLRVSQI EAAKEI ARKKDI PYQTLI RSWVAEI R
RERE A

>2617919640 Ga0073689_101226 DNA helicase-2 / ATP-dependent DNA helicase PcrA [pelotomaculum Ga0073689 : Ga0073689_101]
MDLLAQLNPAQVEAVTYGDGPLLVLAGAGSGKTRVLTRRVAYLLKEGGVS
PHRI LAI TFTNKAAREMRERVEALVPEVAGDLWI CTFHAACLRI LRRQQE
FFGRDRDFVI YDADDQLTVVKDCLKELDLDEKKYPPRPVAVAVSQAKNLL
MGEDEYARHVHDQFSRVVSDAYRLYQDKLRRNNAVDFDDLI FLT VRLFRE
YQVLAYYQDRFRHI LVDEYQDTNHAQYVLNLLARDHRNLCVVGDPDQG
I YGWRGADI KNI LSFERDYPEARVVRLEQNYRSTGAI LEAANQI I RNNAN
RKEKRLWTAAGPGAPLVDFYGGDERAEAD FVAGRI LRI KEAENRPYRDF
VLYRTHAQSRVI EENFVRGVPYTVI GGLKFYERREI KDALAYLRLI LNP
HDTLSLARI VNVPRRGVGEASLGKI VAFAREREI SPVEALARAAEI PGLT
AKVREGAAALGALLRGFSAAEPQLTVTELVRVLEERTGYRMELLAENTVE
SRTRENLDEF LSVTGEFDRQAEPEGLRSFLENVALVTDLDKYEAGADQV
TLMTLHSAKGLEFPVFLI GLEEGVFPHSRSLTDAGELEEEERLCYVGVT
RARERLYLTHCWKRTLYGTQRYNPPSRFLEEI PPHLVSADDSLDRAKGR
AAGTPAPAGRGTEPRKEKPF I LGDKVRHGKVGWGV I VGVREGADA EFK
VAFPDQGI KVLLARYAPLERAN

>2617919639 Ga0073689_101225 Protein of unknown function (DUF2837) [pelotomaculum Ga0073689 : Ga0073689_101]
MERLLLVAALTALI HFVNTLI YAVRI SGVRTGRLATAFSLFNVI FLLAST
ANSVQGFLLASI VERA I KAGQTGVGGI AAAENLV RHPAYQAQLGALELDF
RLI I AAATAGTMLGAMLI PAFVHI FSAI FLFEETGSVPGMMARFLFSPR
RVFGRAGRPSLSGRNLFKAAAARRLAI PSAFLVLNLVVTGVYTI GVLSSL
FAGALFPDFRI TAATMSAVVNGI ATVLAATVVDPTAAAI TDQALRGERSE
DDVKQMALYLT I TRLLGTVFAQLI FVPSAHLI KLAASLLA

>2617919638 Ga0073689_101224 DNA ligase (NAD+) [pelotomaculum Ga0073689 : Ga0073689_101]
LSEVPEYVRERVELREEI EKHNYHYVLDAPLI SDAQFDRMLRELELLE
KOYPSLI TPHSPTRRVGGKPGEGFASVRHLVPMLSLANAFDEGELRDFDR
RVROALPGEAVRYVVEPKI DGLAVSLYYENSLLARGATRGGETGEDI TG
NLKTI KSVPLRLRRPVPGLEARGEAYMSKEAFSRLNEAREEEAGETPFANP
RNAAAGSLRQLDPRVTAARRLDLFVYGI GYSTGVAPAEHVEVLELLKELG
FKVNP EYRLFNDMDEVRYCREWQARRFDLPYAADGLVVKVNSLSQQRERL
GATMKSPRWAMAYKFPPEQAVSTVKDI FVRVGRGTGALTPTAELEPVRLAG

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TTVSRATLHNEDI I REKDI RI GDRVLVQKAGDI I PEVVAVLPEKRTGREK
VWSMPGRCPSCGSPVERAAGEVAVRCAGLACPAKLHEGLI NFASRNAMDI
TGLGPAVI GQLLAAGLVDRPADLYALRHEDLAPLERLGPKSAQNLLRAI E
TSKI SSLARLI FALGI RHVGERAAKI LAGHYGSLEALMAATEEELVNI PE
I GPKI AASVTTFAGSQNRVTI EKLI RAGVNTREERDAGAGRKPLAGKTF
VI TGTLVGFSRQEARELVEKLGKVSASVSRHTDYVVVGKPGSKYEKAL
SLGMPVLNEEFREMTGVDLK

>2617919637 Ga0073689_101223 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]

MSEQLLI EI LGELKTLNQRVENLEEGQKVLTERFDKLEEGQKELTGRFDK
LEEGQKELTGRVGRI EEGLRLLETRLENEVVGKI GALFDGFSLRGDQI EH
LKKHLDERLDEI SLDI NYFI GKTARHETAI LDLKRAK

>2617919636 Ga0073689_101222 beta-aspartyl-peptidase (threonine type) [pelotomaculum Ga0073689 : Ga0073689_101]

MGKLLLLKI FMSDI I AVHGGDLTSREREFMAVLEEAAQGHGCLAAGRVRA
LEATLTVLEDSPKFNCYGYSVLNLDGEVEMDAALVDGPTGRFSAVAARI RN
VRNPI SVARAVLEKTTQVLLAGEGAVRFARRQGFPEAGCASDEQAQAWRN
AGDRLARGEKPEQNPF TGLEDHGD TVGCVVWDGRGLAAASSTGGCFLKLP
GRVGDT PCLGGGI FASAASAVI CTGVGESFVETLTAKYVDEQI AGGAHPQ
QAVESALKRLEDLKGKGGI LALDTRGRI GAAFNAGKFPVVI VRGGKI LA
AYEPVNLRSARPD

>2617919635 Ga0073689_101221 aspartyl-glutamyl-tRNA(Asn/Gln) amidotransferase subunit C [pelotomaculum Ga0073689 : Ga0073689_101]

LI TKEDVDHVALLARLELAGEEREMYTRQLNGI LEHFQSLQELDTENVQP
TAHVLP LKNVYREDWVGQHMPREDALANCPDRDENYFKVPRI I

>2617919634 Ga0073689_101220 aspartyl-glutamyl-tRNA(Asn/Gln) amidotransferase subunit A [pelotomaculum Ga0073689 : Ga0073689_101]

LQLFRLTAHELHDLI KKEI SAKELCRAVFERMESVEDKVGAYI TRI GER
ALERARTVDGQI KNGEEI SPLAGI PVAVKDNI CADGVPTTAGSKMLANFI
PPYSATVVKRLDAAGAVMVGKTNMDEFAMGSSTENSFAQATRNPDWDTGRV
PGSSGGSAAVAAGEAVCALGSDTGSSI RQPASFCGVVGMKPTYGAVSR
FGLI AFASSLDQI GPFARDVTD CALMLNAI CGHDPDSTSAAFDMPDYTA
FLQNDVRGLKI GAPEEYLAEGVEPGVRAAVEKAMALLES LGAVVEYTTLP
HTRYALQTYYL VATAEAGSNLARYDGVRYGYRAADAKDVDMFMKTRSRG
FGTEVKRRI MLGAYALSAGYYDAYYLKALKVRTL I KGDFDRAFEKYDLLL
SPVSPTPAFRFGEKTD DPLQMYLSDI CTLSVNLGI PGI SI PCGFVDGMP
VGLQLMGKHFDEGTLLRVAYTFEQNTAYHKEFPEL

>2617919633 Ga0073689_101219 aspartyl-glutamyl-tRNA(Asn/Gln) amidotransferase subunit B [pelotomaculum Ga0073689 : Ga0073689_101]

LARYEAVI GLEHVHELKTRSKI FCDSTTEFGGDPNTHVCPVCLGLPGVLP
VVNKKVVEYAI RAACALNCRI AEYSKFDRKNYYYPMPKNYQI SQYDLPI
ALDGHLEI ETDGGSRI GI TRLHMEEDTGKLVHQGTI TTPFSLVDYNRA
GVPLI EI VSEPDLRSPEEARRYMEKLRAI I QYTGVS DCKMEEGSLRCDAN
VSI RPVGSAGFGTKTEI KNMNSFKALQKALTYEI ERQVEVLEEGRI VQE
TRTWDEGKGI TLPMSKEEAHDYRYLPDPDLVPMVI DREWVEDI RRS LPE
LPDDRRDRYVRDYGLPAYDAGVLTNTKELADYFEACVAHPNPKT VSNWV
MGELTRLLNANNLEI TECPI KPEQLVALLQLMDKSTI SGKI AKAVFEEMF
ATGEDAETVVQERGLVQI SDEGAI AAVVEEVI AKNPKSVEDYRSGKEKAL
GFLVGQVMKATRGKANPELVNRLKERL

>2617919632 Ga0073689_101218 homocitrate synthase Ni fV [pelotomaculum Ga0073689 : Ga0073689_101]

VTQKEI I I VDTTLRDGEQTAGVVFANREKVRI AKFLDEMVGQQI EAGVPV
MGGDEKEAI KAI CRAGLKASI MGWNRPV LKDI EASLECGVDAVAI SI STS
DI HI KHKLMTTREWVLEQMVNATQFAKKEGMI SVNAEDASRSDMDFLI Q
FVRAAKEAGADRLRYCDTVGI MDPFTI YEKI KEI RNAVDI DI EMHTHDDF
GMATANLAGVKAGANYVGVTVI GLGERAGNAAMEEVMALKHLFKI DMK
I KTEMFVEVAEYVSASGRELPSWKAI VGSNMF RHESGI HADGVQKDPKT
YEAHPPEEVGLQRQI VI GKHS GTAALKAKFAEFGRHLTEHQAEELLPKI R
SHTVSLKRPLFDKELVYI YEDYFGKRD

>2617919631 Ga0073689_101217 3-isopropylmalate/(R)-2-methylmalate dehydratase large subunit [pelotomaculum Ga0073689 : Ga0073689_101]

LGQTI I EK I LSTHS GREVYAGEI VVAGVDYVMGQDGTAPLAI NAFNDMGG

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KEVFDPGRVAFVI DHSAPSPNEGVSAHKLHREFAEKKGFRLYDI GEGVC
HQLLPESGEVGPGLSVI GADSHCTYGNALNAFSTGVGSTDLAGGLI SGRM
WFKVPETI KFCVCHGTLPVGYAKDLI LYLI GDLTADGATYMAAEYVGGAI
AALSQEARFTVANMAI EMGAKAGLMEADDTMTWLRFTDKKFNPFADP
DARYARVLE YDMSNLEPOVARPHRDNTAPVSEVAGLPVQQAVI GTCTNG
RLEDLRI AAGI LGGRKI HRSVRLI VAPSSRWVFLDAMAEGLI QVLVEAGA
AVVTPGCGPCVGTHTNGVPSDGETVI STANRNFKGRMGNSKAGI YLASPAT
VAASALTGKI TDPREFA

>2617919630 Ga0073689_101216 3-i sopropyl mal ate/(R) -2-methyl mal ate dehydratase
small subunit [pel otomacul um Ga0073689 : Ga0073689_101]
MRFNGKAHKFGNDVNTDYI I SGKYKFKTLDMKELARHVMEDLDPDFYKKV
TPGDFI VAGANFGCGSSREQAPLAI KHAGI GAVLAKSFARI FYRNAI NTG
LPVVECDTDRI EPRDELSDLAAGVI TNKTRGI I I PI KPLPAVMI KI LND
GGLAPHFRKYGGFNFD

>2617919629 Ga0073689_101215 Starch/carbohydrate-bi ndi ng modul e (fami ly 53)
[pel otomacul um Ga0073689 : Ga0073689_101]
MAHPSRFGEGEARLKAMHGAGYPGGVVVDPTPI TAGQEVTVFYNGLLGRE
GDGQI YLHYGYGGHNRWRNI SEDRMEKTGWGWVSN I TAPEHEGRFNFCFR
DSAQNWDNNNGVNWSFEI HNGSQRY

>2617919628 Ga0073689_101214 gl ycogen(starch) synthase [pel otomacul um Ga0073689
: Ga0073689_101]
LKVLMLSWEYPPKNVGGGLARHVYDLTGALAENGVDVHLVTSGGMGAPSE
QVNGVKVYRVEPYRVSSPDFVTWVAQFNVALLEVI PLLTGNGEFHLI HA
HDWLVAAYAAARAVKHAGRLPMVVTI HATEYGRNHGLHNEI QKHI SDI EWWL
TYEAWRVI CCSRYMEGEVRHVFQLPADKI TVI PNGVDPGNFRAVNRAVQR
GDYAAPDEKI VFYVGRVLVREKGVQVLLDAAPEI LAHYPRTKFI I AGKGP
QDALKQQAVALGI ANRVYFTGYI NDEVNRSLYSWADVAVFPSLYEPFGI V
ALEAMAARTPVVADCGGLGEI VRHSEDGLKSYI GNSHSLAQNI LAI LKQ
POFAGELKENAYRRVLNEFNWQOI ARQTAAYRGVWEAHRSTPWSAAERQ
SGI FGRFNRLAKYS

>2617919627 Ga0073689_101213 nucl eoti dyl transferase [pel otomacul um Ga0073689 :
Ga0073689_101]
MKAI I MAGGEGSRLRPLTCGRPKPMVPVLNRPVMEHI VDLLKEHGFTDI G
VTLOQQPEAI RDHFNGAEYGVNLRYFVEETPLGTAGSVKNAAAFLEDTF
LVI SGDALTDLARAVEFHKWOQALATLI LTRVAVPLEYGVVI TSDDGR
I TQFLEKPGWGEVFSDTVNTGI YVLEPEVLDYFAPGQKDFDFSKDLFPLLL
RENRPPLYGLALPGYWCDI GNLOQYLEAHHDALSGKVKI KMPGEEVLPQVR
VEEGVFI SPSASI EGPAL I GANCQLGAGARVEPFVSVLGRGCLVRDGASI K
RSVLWNNVYVGSGAAMRGAVVGSRVQVQAKAGI YEGAVVGDDSI I RENSL
LKPVDVKLWPHKLVETGATVQVRSVWGTCSPKKI FGFEGVTGLVNVEI TPE
FAARVGAAFGSVAGTGARLVVSSDNYTASI MI KEALACGI RSVGAQTMDF
GAGI TPLHRYAVRSLDCKGGVHVKI SPDSPEKVALVFTNHRGGNI SRGQE
RKI ENALAREDFLRAESARVMPPPI TI DGI AEEYI AAVCTGPDTRLRDAG
FKLLLCYDRI NLEKFVAGLCRELGFVLENYGYDGGGAEYRSWRSYQEMLP
SLARAVAESGAGAGAVLDPNADRLI LI DEKGRVLQDDMLTALLSLI I LKG
QEGPVVVPVTAPRAI ETMAERYGRVVRTKTALQDFLEQVLVNDGGMEGI
SRFFLHFDALSALARVLEYSARYNI SLSLVEEI PAFFMDRREVPVPWEA
KGRVI RQI QEPPAGRLLELDGI KVIYHRDGLVLPDPDEPVCVFSEGC
SMEVAESLTDYFVKKI SEI AKC

>2617919626 Ga0073689_101212 1, 4-al pha-gl ucan branchi ng enzyme [pel otomacul um
Ga0073689 : Ga0073689_101]
MSKGYLCLVLHAHLPPYVRHPEDEHFLEERWLYEAI TETYI PLI QVFEHLV
ADNVQFRLTMSLTPPLI SMLTDPLLQERYVRHLAKLMELAGKEEGRTYGS
PFHEPALMYKKRFSEAMAI FCNRYGRNLVSFAKKFQDAGRLELI TCAATH
GYLPLMMNHPEAVRAOI GTAVDLHTRHLGRPPEGI WLPECAYVPGLDEI L
KENGLKYFFTDShGI LYASHRPRFGI FAPI YCPSGVAAFGRDI ESSKQVW
SAREGYPGDFDYREFYRDI GHELDI DYI GPYI HPEGI RVHTGLKYYRI TG
NMDLGRKEPYNPGRANEKAAI HAGNFMFNRLQARHLAAGLMEPPI I VAP
YDAELFGHWWFEGPQWLEYLLRKI AFDQDDLELI TPSDYLRFPVPCNQVAT
PCSSSWGNGKYHEVWLCRANDWI YRHHMHMAAARMTELADRYHAAGGLLRR
ALNOAARELMLAQSSDWAFFI MSTGTMVEYAVRRRTKTHLHNFRLRYEEI KG
GRI DEGR LGDLEYRNNI FPDLDYSWYRGSPPRARAV

>2617919625 Ga0073689_101211 hypotheti cal protei n [pel otomacul um Ga0073689 :

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Ga0073689_101]

MNVLPPLLLFI LI LVLAVGI FLWPARRVRPSGRPDFQALPRALFKEETSR
ELGPYI PVTTRARPSQLPEPQLPHNYGVDRMVLMDRPHWLAYWEI TAT
KQEAFFSSYGPAWSSSHPVLRVYDVTGVAFNGANANRYVDI QVDEYVDN
WHI QVEEPDRSFCVDLGRMFPDGRFVTLRSNI VTTTPRASLSDRLDEEWM
WI EGLYRSI DRFQYGVSSPMI I EELALRSI LPLGI GSPGFNKAVERES

>2617919624 Ga0073689_101210 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]

MFLNPDNDVI I GLLEESRTVAVVGLSAKPDRDSFRVARYMQEQGYRI I PV
NPALKREVLGEKPYASLAIEVPCKVDI VNVFRRSEDPPLVVEAALPLKPKV
I WMQLGI KNEEAERVAGEGTVVMDRCI KI EHGRLLGELCLGNK

>2617919623 Ga0073689_101209 DNA-(apurinic or apyrimidinic site) lyase /endonuclease III [pelotomaculum Ga0073689 : Ga0073689_101]

LEI NEGKAPEREAGARKEGGSGGAKKEKAARVLEI LAEAYPAAGTALHFR
TPFELMVAI LSARCADROQVNI TARLFPKCNTPODFAALAPEELAEI K
GCGLYRNKSKYI VEASRELLKRHGGMPQTRKELEALPGVGRKTAGVVLG
LAYGGSALPVDTHVYRVARRLGLSVAKEPGKVEEDLAGVI SPGERMAVHH
RLI AHGREI CSARKPRCGSCCLKELCCYPAQAGERSCT

>2617919622 Ga0073689_101208 tRNA (cytidine/uridine-2'-O-)-methyl transferase [pelotomaculum Ga0073689 : Ga0073689_101]

LHI VLVEPEI PANTGNI ARTCAATGSALHLVRPLGFSTEDKYLKRALDY
WRLVEVI YHDSFAEFAGRHRGGI FYLATRAPRFYSEVVYEPGSFLI FGK
ETRGLPPEI LDSYPERQI RLPMAVEARSLNLANSVAVI LYEALRQQGFPG
LR

>2617919621 Ga0073689_101207 MoxR-like ATPase [pelotomaculum Ga0073689 : Ga0073689_101]

MELTVAGLHRAFEEOGYI CEKDLVVTVFLALKLGKPLLVEGAPGVGKTEI
AKVLSRI FNGGLI RLQCYEGLDENKALYEWNYQRQLLKI QLLKESGGCEM
MERDLFGPEYLLERPLLKAI RSEEQVLLI DEVDKVEDEFEAFLFEVLSD
FOVSI PELGTLAARRVPMVALTSNGERELSDGLKRRRCVYLF I DYPSVEKE
VRI LQVKAPETGAKLANEVARAVHFI RTNLELRKKPAI SEAI DWARALVA
LGADSLSPVVAQTL SLVLKNKEDI DTLHREVGKGLADYAVRVAGAGPT
EAEPAAPAHSHAHTHCHCHTGG

>2617919620 Ga0073689_101206 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]

VAEVEWDGPDTFSHSLVKFATVLRRLGI RVSTAETRDALDALARVDMMDR
DOVKGALSAALVKSYPDQVFSLAFDLFFVPAEVKQERLRLRRERLVERE
KOI QNAEALARTI REGGRDWEETLERLQLSEEQRETARLPEPERKRL
LDI FSRMRGNPVPNSPDLI AGTI QASLDYWRYRLKKEEGESGGTPLEI T
PSGVEELDEI I EAVAAGVARERSDDQI LYEDMKNI AEKDLSRVTLI KKL
SRRLATRI SRRYHRSSKRDLDI RRTI RKN I RYGGALLELKYRARRVQKP
RLVLI CDVSAMARYAVFVI QFLYGLSSVI RNI ESFI FSEDLERVTPYFK
NGGDFAAI MASLMSRSGQWGRATNLHTALTTFAYHQRLLAPDVFVI VVS
DTKTLEAVQAAKDLDEI RCRVRDI I WLNTLPRKEWRELPAVAELQKHCRI
FECYTLAHLNKLVRGQI LGA

>2617919619 Ga0073689_101205 DNA polymerase-3 subunit alpha [pelotomaculum Ga0073689 : Ga0073689_101]

LFVHLHLHTEYSLLDGAARI KEAVDRAVDMGMPALAVTDHGAMYGVVDFY
KACKKAGI KPVLGCEVYVAPRAMDDRTPKVDDNLYHLVLLAENGEGRNL
LNLVSLGFTRGFYKPRVDKEALARHGKGI I ALSGCI AGEVAAQVLVGEN
EKARQAAGDYRDI FGPNFFLELQDHGFDEQRKANKELLKI HKEMDI PLV
VTNDVHYVRRENAETQDVLLAI QTGKSVDDPGRMKFQSEELYLKSPEEMN
LLFGELPRAMRNTVGI AERCHVEMFEGKYYPHYAVPEGYNADTYLAELC
YRGVRGI YGEPGDEVEKRLEFELGVI KQMGYSAYFLI VWDFI HFARQQGI
PVGPGRGSAAAGSLVAYSIGI TNI DPLKYGLLFFERFLNPERVSMPI DDI
CYERRGEVI DYVVRKYGADKVAQI I TFGTMAARAAI RDVGRALNMPYGEV
DRVAKLPVELHMTI EKALNDAAELKEQYDQKPEI KKL I DTAALLEGMPR
HASI HAAAVVI TKDPLTHYLPYKATDGPVTTQFAKDTVEELGLLKMDLL
GLRTLTVI SDALDI AESAGVKMDI DRI PI DDRATYEMLSRGETAGVFQL
ESSGMRSI LRDLPKEVFEDI VAI NALYRPGPLGSGMVDDFI I KNKHGLKKA
KYLHPKLEPI LKDTYGI LYQEQVMRI ASDLAGFTLGEADLLRRAMGKKK
PEI I SGLRSQFVEGAVKNGI DEVI SGQI FDLMEYFAGYGFNKSHSAAYAM
VSYQTAYLKVNYPLQYMAALLTSVKDNTDKVSAYI EECRRLGI EVLPDPV

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NESRESFSVAGNKI RFGLAAVKNVGLGAVNSI I RARKKDGPFSGYADFCR
RLDTKVVNRRVLES LI KCGAFDSL DHRR AQLMAAVDAGLGLAQQSQRERE
NGQLSLLDFFGDGARESVSI NLPEVGEYPEDELLALEKETLGLYI SGHPL
SRYRDDLRRLTTVTAAEI AELPEDSEVALGGLI TGVKKI NTRKGDMAFL
TVEDLTGTFEVVVFPRPYQONRLAI RVDEVVLI KGKSSNGE EVKI I GEE
I STLD SHLGGELHLKI DSVNSPLLDQVQI I LSGFRGESPVFLHF EKERKV
LKAGQDFQVDLSGPVMSRLQDLLGP ARVKI R RKNGAAGADAAEGAGDPEN
SAHALNSETKAKNTLSGRRRFFSI LEL

>2617919618 Ga0073689_101204 transcription attenuation protein (tryptophan
RNA-binding attenuator protein) [pelotomaculum Ga0073689 : Ga0073689_101]
LPEKCEI AGEYVVI KALDNGVTI I GLTRGKDTKFHHSEKLDKGEI MI AQF
TEHTSAI KI RGRVELLTRHGRI RTDE

>2617919617 Ga0073689_101203 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
VWTVVYI APNKKEAERLEKLLAMEGFLVKLR TVGLSQANNSCSLEI LVPE
SEVDEALEI I NTI

>2617919616 Ga0073689_101202 acetyl-CoA carboxylase carboxyl transferase subunit
beta [pelotomaculum Ga0073689 : Ga0073689_101]
VKNRDI PDGVWI KCDRCNEI LFNKELDSNHKVCRCG FHFRLSAFERI RL
TLDEGSFREMDAGLLPTNPFNMADYENKLAAACKNTGLNEAVLTGEGAI E
GYPVVVVMDARFMMASMGTVVGEKI TRAI EAAAEDGKPLI I FSASGGAR
MQEGI LSLMQMVKTVAALTRLGKAEQLYI SVLTDPTTGGVSASFAALGDI
I I AEPSALI GFAGPRVI EQTI RQKLPEGFQRSEFLKQHG FVDMI VPRPQM
KGT LAKLLELHLOGEK

>2617919615 Ga0073689_101201 acetyl-CoA carboxylase carboxyl transferase subunit
alpha [pelotomaculum Ga0073689 : Ga0073689_101]
MPASI LEFEKPI QELETKI SELRNFSREKGI DLGNEI AI LENRAREVREI
I YSNLNPWQKVL I ARHPERPNTYDYI KYLLTDFI ELHGDRLFGDDPAVVG
GI GRFRGRAVTVLGHI KGKDTKENLSRNFGMAHPEGYRKG I RLMKQAEKF
RRPVFCFI DTSGAYPGMGAEERGQSEAI ARSI TVMSTLKVPVLVVVI GEG
GSGGALAFVGVDHI LLLLEHAI YSI I SPEGYASI LWKDASRAREAAEALKL
TAQDLLELGVADQVLPPEVGG AHRDPEGAARMLGEALAAALDEL TGVDPE
VLVARRYEKFRVI GSPVNNAN

>2617919614 Ga0073689_101200 6-phosphofructokinase [pelotomaculum Ga0073689 :
Ga0073689_101]
LQRI GLLTSGGDSPGMNACI RAVVRKAI YHGLEVI GI KRGFNGFI EADMA
PMHLGSAVDI I HRGGTVLHTARSDQFLTPEGRSRANENVKRFGI QGLVVI
GGDGSFRGARI FNQEHGLPVVGPGTI DNDI PGADQTI GFDTAVNTVVEA
I NKI RDTATSHERTFVI EVMGRNHGFLALAAGLAGGAESI LI PERPFNYN
EI CERLLRGYRRGKLHSI I VVAEGAADGMEVGRKI KERTGFDTKVTI LGH
LQRGGTPTAADRI LASRMGAI AVDLLMAGETGKMVG VKAGEI VPLNFEDS
LAQSRSI DLDMYNLAGI LSI

>2617919613 Ga0073689_101199 pyruvate kinase [pelotomaculum Ga0073689 :
Ga0073689_101]
LRRTKI VCTI GPASDGVEVI KKI LLAGMNVARLNF SHGTHEEHGRR I TSI
RRAAGEVGKNAAI MLDTKGPEI RLGLLKEEPVVLSE GALVTLTTENI KGD
RDRLPVNYPGLPGDVRAGDTI LVADGLI ALKVLSTSDTEI RCRVENGGEL
TSQKGVNVPGVTVNLP AVTEKDI QDI QFGI EHRLDLI AASFVRKSSDVLA
I ROI LEEAGADI DI I AKI ENREAVNNLDEI I KVSDGVMVARGDLGVEI PV
EEVPLVQKAI I ERCNRAGKPVTATQMLESMI HNP RPTRAEASDVANAI F
DGTDAVMLSGETAAGKY PVEAVETMARI AQRAEAALHYEEMLGKRRVTP
QRTVTD AI SYATCATAQDLGAAAI I TSTESGHTAKMVSKYRPQAPI VAVT
PHARVMRK LALVWGVQPLL VGVGKNTDEMMAAAVEVSLSAGLI KGGDLVV
I TAGVPVGVHGTNNLI RVHTVGD I LARGTGI GHRAVTGVVRVSQTVREAL
EKMRPGDI LVVPATDS DYVPAMEKAGAVVTEVGGLTSHAAI VCLEFGI PV
VVGVEAATAI LPDGETI TI DGQRGLI YSGAARVL

>2617919612 Ga0073689_101198 membrane protein DedA, SNARE-associated domain
[pelotomaculum Ga0073689 : Ga0073689_101]
LLDLI AGYLSALGLSGLLVGVFI EAMGLPFPGGI MVI I TGFLVNQGR LNF
SSALAATLSGYTI GSLTAYFI GRNLGRPF FVRCGKLLHVSPERFDQTRAM
LDRSAPAFI I GFRFLPGLSNLTPYI AGVSRI GVAYFLFYNSI FALVWGTL
YLLLG VFFGHNYQFI AGYMNSKLPLVGLGFLGLYV VYLYLKKHLGRRV

Table S2

>2617919611 Ga0073689_101197 0-acetyl -ADP-ribose deacetylase (regulator of RNase III), contains Macro domain [pelotomaculum Ga0073689 : Ga0073689_101]
MFKVI KSDI TELTVDVVNAANNHLMGVLGAGTI KRKGGVI I EEEAVAK
GPI PVGEAVVTGAGALQARHVI HAAAMGQDLVTDVAVKRAATRNALLRAG
ELGLKSVAFPALGTGVGGDLDFDTASRVVMSETRRHLARGSRLEEVVFALF
DEAGFRAFSSI AGRDKVVCLGDSI TYGYPYGPASWVEI CAEKMSLEMVN
KGI SGGTTTGQMRKRFARDVTALDPAYVI I LGGANDALGGVTLAEVRENI G
AMVDDAFAAGVCPVLGLPTPVDSVI LGSFPLEDVAEFTGDMDSFRNWMKE
FADEWLLPALDFYTPLLDPETGRANPAYFVDDGHPNTDGYRI LARAAERV
LVELKGI

>2617919610 Ga0073689_101196 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]
MYKEI AFPEFI GETEQAVVLVVPALDDELSVLFKRFHESEEI NYWFTWEL
TSNNNDGYMVTLDLGDWQEDAVSI GFTMDMWKYLPIV TQRSNVVLMTDWR
LI KEGI AAGMDNMGRFRPRALI KDAGRAMEDLSGKVAEQVI FNQSSREL
AQLLEI LRRSCKEGLTLH

>2617919609 Ga0073689_101195 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]
MAFEVYKPRFEKEVTVAI SKNHI TLNKKLLDKFNTRCVELAYDPEMRTVR
I KPSVNESGLVLNNKI GARGFFKHFNI EQKGKYGAVYNDNEKAI YIRL

>2617919608 Ga0073689_101193 cobalt/nickel transport system permease protein [pelotomaculum Ga0073689 : Ga0073689_101]
MAGAKYGI LSSI YLAAVFLVFPROAHAMHI MEGFLPPGWAGFWFALI I PF
LLLGMRSI QRTVNLNPSLKMMLGLAGAFVLSALKI PSVTGSCSHPTGV
GLGAI LFGPLAMSVLGSV LLLFQAI LLAHGGSTLGANTFSMAVAGPFVA
YGI YKVCQRFSGSPLWLSVFLAAALGDLATYLI TALQLALALPAETGGVPA
SLVKFTGVFALTQVPLAVSEGLLTVVVFNI LVDYNKKELQELSI LPGEAR
AYERR

>2617919607 Ga0073689_101192 cobalt/nickel transport protein [pelotomaculum Ga0073689 : Ga0073689_101]
MKDANRNPVAI NLTLVVVLVLI I LPLVVRDAGFEGADGQAEKVI AEVR
PDYEPWLKPLWEPPSGEVESFFFSLQAAAGSGMI CLYFGYLLGRRKERE
HSKHVRH

>2617919606 Ga0073689_101191 cobalt/nickel transport system permease protein [pelotomaculum Ga0073689 : Ga0073689_101]
MFAI DQYAYANRLRSAHPGEKFAFSVLTMAI CLASPSALVYPVAVLLMAG
VAVLRAGI PWRYYLKLMTAPLSFLLVGVATVAVSVSRHPDGVVYGVTVLG
LTVGATPRDLGVAAGLLGKSLGAVSCLYFLALTTPMI EI I SVLKKLRVPP
LFI ELMGLTYRFI FVMEI ASKI YTAQSSRWGYASLRTSYFSLGQLASNL
FI KSYHRSRDLFTALSARCYSGLNVI EPAYAVSKVNI ALI VVI DLALTA
LALVDGNYLKM

>2617919605 Ga0073689_101190 cobalt/nickel transport system ATP-binding protein [pelotomaculum Ga0073689 : Ga0073689_101]
MLSPGVI LLAEYI LEAVDVEFAYPDGTRALKGVSLGI EKGKKVAVLGPNG
AGKSTVFLHFNGI LRPVRGRVRFAGRDVRYDHASLMELRKNVGI VFQDPD
TQLFSASVFQEI SFGPLNLGLSREEVEKRVREMAATEI TGLGKKPTHLL
SYGQKKRVS I ADI LAMEPKVI I CDEPTAWLDPKHSRQALELFDRI NRS
GTI I I STHDVI AYSWSDYVFI MSDGGVVGEGAPEAVFQNEAFLRATDLEK
PWLVEVYDELRVKGWLPDGPAPRTRGELLSSI LPAGPYSKPI KLVKAAN
QVK

>2617919604 Ga0073689_101189 Protein of unknown function (DUF1657) [pelotomaculum Ga0073689 : Ga0073689_101]
VTI GDKMHQTLASLEGAAANLKTALDSQDQTAKKMF I DI NHQLEGI VQS
LRGRVNYVEQQEPQYKMEQPKR

>2617919602 Ga0073689_101187 Nucleotide-binding universal stress protein, UspA family [pelotomaculum Ga0073689 : Ga0073689_101]
MFKKI LVAFDGSAHAVKALRI AVDLCKKYGASLSVTTVVNLPELPDMGES
NGGKPFHRDLERAAQI ANHEGVAVVTHLLRGNVANTI QRFAEENKFDLVL
VGSCGRNAVHRFFMGSVSTHLVKSLECPVMVVEKNA

Table S2

>2617919601 Ga0073689_101186 anthranilate synthase component 1 [pelotomaculum Ga0073689 : Ga0073689_101]

LNTPGRDEYLDLSRKYNLI PVCCEI NADLDTPI SVYKKI VREGPAYLLES
VEGGENLARYSFI GDFPFLVFTSRDEEAQLTGGGQQKTMPPPLESLERV
LSGFRVYRRSGLPRFYGGAVGYVSYDAVRFI ERVELPPDGI RGLPDCSFI
FAGTVLVFDHVRRTLI VVNSLTGDNPEKSYGETVERI EAI IQALGGNI P
PEVEYSROELHGNRVEASLSKAEYMERVLRAKEYI RAGDI LOVVLSHRI R
VSFSGEPFNVYRRLRALNPSPLYLFYLDFFGGVKVVGSSPEMLVRVEGETVE
TCPI AGTRPRGADPRADEALAAELLEDAKERAHVMLVDLGRNDLGKVCE
TGSVRMARFMEVERFSHVMHLVSNVRGRLAPGKNAFDALKACFPAGTVTG
APKVRAMEI I SELEPDGRGI YAGAI GYFGFSGNLDTAI AI RMVVFHEGSA
YI QAGAGI VADSDPEREYEETLNKARALLKTLGINV

>2617919600 Ga0073689_101185 para-aminobenzoate synthetase component 2 [pelotomaculum Ga0073689 : Ga0073689_101]

MVLMIDNYDSFTYNLVQYLGELGEEVRVYRNDRI TCDEI EELKPEHI I I S
PGPCSPNKAGVSLAVI ERFAGVI PLGVCLGHQAI GQAFGGAVVRAFRML
HGKTSI YHGRSVFRDI PSPFTATRYHSLI VDRDSLPECLEI SAWTGEG
EI MGLRHRAYPVEGVQFHPESI LTEHGHKLLQNFLARN

>2617919599 Ga0073689_101184 anthranilate phosphoribosyl transferase [pelotomaculum Ga0073689 : Ga0073689_101]

VI KEAI KKVVS GMRLSEEEAGAVMEQI MEGEASPAQI AALLTAMSLKGET
VDEI AGFARVMRQATLVRSI HPVLVDTCTGGDGSCTFNI STTAAFVVA
GAGLPVAKHGNSVSSRCGSADVLEEMGI KVDLDREAMEECLNKVGI AFL
FAPALHTSMGRVAGLRREI GI RTVFNI LGPLTNPAGAGAQVLGVYNPSLT
EVLAEVLARLGSSRAFFVHGAGGLDEVSLAGPSVI CEVKNGSVRKGVLDP
AKFGFTYAPVSSLAGGSARENAVI TRQVLEGEKGPRRDVLLNAALGLVA
GGKARDI AEGLEMAAI SI DSGSARAKLDELI ECTGRLATKKAVSK

>2617919598 Ga0073689_101183 indole-3-glycerol phosphate synthase [pelotomaculum Ga0073689 : Ga0073689_101]

MI LQKI I TCKKFELARRKEQFPLEDLKALLSGLSAPRPLVPALRRPGKVA
VI AEVKKASPSKGI LCCNFDPAQI AQAYEKAGAAAI SVLTEEKFFFGHPS
HLGFVREVTTVPI LRKDFI I DPYQI YESRVLGADAVLLI TAVLSDAQLVE
LRLAGELGLSCLVETHAVELARAVAAGAEI I GI NNRDLNTFVTDLSRT
FNLTGLI DNPEI TVVSESGI KSRADI LRLSEHGVHAALVGEALVRRDDPG
EALRELI GLPCGGPEAATGVAGDAETNRP

>2617919597 Ga0073689_101182 phosphoribosyl anthranilate isomerase [pelotomaculum Ga0073689 : Ga0073689_101]

VSATI PI KVKI CGI KDLDLTAALAAVEAGADALGFVFASSPRRVREI VRTI
CSQLPPFLSRGVFVNPAAGLVEETAAYCGLDI LQLHGEETPEYCRQLKY
RVI KAFVRVDATSLAEI KRYRCSAVLLDTYVPGMPGGTGCAFDWSLAREL
VPARPVI LAGGLTPENVQQAVAL ARPYAVDVSGGVETDGKKDI EKI RLFI
QRAREVF

>2617919596 Ga0073689_101181 tryptophan synthase beta chain [pelotomaculum Ga0073689 : Ga0073689_101]

LDLQNAVLPDGRGYFGPYGGRFVPETLMPALEEELEEAYSSVKGDPEFHRE
LAYYLQHYVGRPSPLYAEGLTRRCGGARI YLKREDLNHTGAHKI NNTIG
QSL LARRMGKKRVI AETGAGQHGVATATAAALFGFQCAVYMGEEDI RRQS
PNVYRMRLLGSEVI TVTAGSRTLKDAMNEAI RDWVTNVRDYYLI GSVAG
PHPYPAMVRDFQKVI GEEARQVLEQAGRPPDYI VACVGGGSNAMGI FYP
FLSETGVKLVGVEAAGRGLDTGEHAATLNRGSTGVLHGSLSYI LQDEDGQ
I LNAHSI SAGLDYPGVGPEHSFLKDSGRVRYTSATDPEALEAFKLLCRTE
GI I PALESAHALAEAI KLAPVLSREEI I I VNLSGRGDKDI PAVAGEPGVN
I

>2617919595 Ga0073689_101180 tryptophan synthase, alpha chain [pelotomaculum Ga0073689 : Ga0073689_101]

MSNRSPI TDCLDNLRSGKKGLI PFI TAGDPDLAGTVEMTRRMAAGADL
I ELGI PFSDDLADGPVI QRASLRALAAGATVPKI LDAVREI RKDCPVPLI
LMGYYNPI YKYG I RRFAGDAARAGVNGLI VPDLSHEESGPLYEAALAAGM
DLI PLVAPTTTTGSRLEI TADARGFI YCVSVTGVTGAREE I KTDLASFTE
RVRRYTNLPLAVGFGI AGPEQAARVARHCAVAVVGS I VKI I AECGKAAD
AGPAVDLLVGRI RAALDGLDG

>2617919594 Ga0073689_101179 3-deoxy-D-arabinoheptulose-7-phosphate synthase

Table S2

[pelotomaculum Ga0073689 : Ga0073689_101]

MI VVMASHRATDDEI ESVL I RLEKTGFQI HLSRGVEHTVI GAI GDKTSLED
MGLEAMPGEVKKVPI LQPYKLTSRTFHEEGTVVTVGGLEI GGDTLHVMA
PCAVESREQLLTAARQVRDAGATI LRGGAFKPRTSPYSFQGLEEEGLELL
AEAREATGLLI VTEVMDARTI SLAARYADI LQI GARNMONFFLLREVAKV
DKPVLLKRGPSATVEEWLMAAEYVMAGGNYNVI LCERGI RSFETYTRNTL
DLTAVPVVKHLSHLPVI VDP SHAI GKWRFPVPPMAMAAVAAGADGLLVEVH
PNPAEALCDGPQSLTPGNFAAMMAQLKKI AAVMGRKMP

>2617919593 Ga0073689_101178 prephenate dehydrogenase [pelotomaculum Ga0073689 : Ga0073689_101]

MNPEFSRVTI VGVGLI GGSGLGLALCARGLAGEVVGAGSRPENLRLAVEMG
AI HRFAESPAAGVAGADLVVI ATPVSAI I PVLKEI LPSI KPGAVVTDVGS
AKAAI VRRAEKLLPPGI SFVGGHPMAGSERAGVKGADPYLFENAFYLI TP
TAATAPOAVKTVKKLAGGVGAKVMEPERHDLVVAVSHLPHLLAVTLV
NTVAQLPESDLVPLAAGGFRDTR I VSGSPVMWRDI FMANRDRVLEMVR
RFRAELVSFETLI EQESGEAVRENLDQAREI RSGLPSTGKGYLPSLFEI V
LTPDRPGVI AAFTHLAEEGI NI SDI EI LRVREGEGGTI RLAFATVEER
EKALRVLGKKGYTVRKR

>2617919592 Ga0073689_101177 3-phosphoshikimate 1-carboxyvinyl transferase

[pelotomaculum Ga0073689 : Ga0073689_101]

LDLHVRPARSLRGTVAVPGDKSI SHRAVMLGALAEGETVI ENFLPGEDCF
STI SCFKKMG I EI TDPMAGVVRVRGRGLHGLSEPEDVLNAGNSGTTMRLM
LGI LAGQPFPSVI TGDSSLRRRPMARVARPLSLMGAWI DGRNGSLAPLA
VRGGGLKPVDFSSPVASQVKS AVLLAGLFVAGETAVAEPHRSRDHTERM
LRQFGAEVDVSGNKVVRVKGPPRLAGRKVTVPDI SSAFLMVAAAAGMPGS
DLTLVGVGVPNTRNGI I EALTAMGAGI ELLNPREEGGEPI ADI RVRYAGK
LSGVSVGGETI PRLI DEI PALAVAAAALAEKTEI RDASELKVKNRI AT
AAGLLAGFGAAVEELPDGLLVRRGRPLEGCVCESHGDHRI AMAAVAVAGLS
AAGTVVRGAECI DVSFPGFSGVLENI QVK

>2617919591 Ga0073689_101176 cytidylate kinase (EC 2.7.4.14) [pelotomaculum Ga0073689 : Ga0073689_101]

MDSKPNI AI DGPAGAGKSTVAKLVAKELGYVYI DTGAMYRAVALKALREG
I DLEDSEGLARLAAVI SVNLESGPEGRMKVFLNGEDVTGEI RGPVSRV
SLVAMAPAVRKRL TELQRAMAKDGGVMEGRDI GTVVLPDARVKVFLTAS
PEERARRRGEELAAKGYCMDRRRMEEELLERDRI DTSRETAPLSPAPDAE
I I DCSPLPAEDVVKMI VAMVQRK

>2617919590 Ga0073689_101175 1-acyl-sn-glycerol -3-phosphate acyl transferase (EC 2.3.1.51) [pelotomaculum Ga0073689 : Ga0073689_101]

MFYRFARLI CRI VLALLRRWEVLGAENLPVAGGVVLVANHVSYWDPVVVG
CAFDRQVHFMAKAE LFKI PLLGAVI RALGAFPVRDKSDRNAVRI AVRLL
KEGKVVGVPFEGARSQTGELMRPHLGAAMLAFKAGAPMLPVAVAGTKGI L
GKVKVHVGRPI LTTECGRASKADLENASDWMARI AALLVELTL

>2617919589 Ga0073689_101174 4-hydroxy-3-methylbut-2-enyl diphosphate reductase [pelotomaculum Ga0073689 : Ga0073689_101]

MEVRI AAKAGFCFGVKRAI ELARATVSDRAGPI FSLGSLI HNPQVVRCL
EKG I REI NDI EGVNEGTL I RTHGVGQALLDAAREKGLNI VDATCPFVRR
AQVLARDLAAEGYRVVVVGDRAPHEVQGI VDWAGGRALVVENPEAAALLP
REGRI GVLAQTTQPLVNFEAVVEVFKRTGTRVRVCNTI CSATAERQQAAL
DLARQVEVMI VVGGTNSANTRKLTGLCREAVTPTYQVETAVELEPAWFKG
AKVAGLTAGASTPDWI I EEVKSRMSEFEEMNNREESVQEEGMKDAVEVKA
VRHGOI VKGTVVHVQGDEVMDI GAKSEGI PI RELSCCEVTSPQDVVKV
GDEI EYVVLKAEDNEGKLVLSKEKADSEKAWVGLEALNSGDPVYGTVRE
VVKGGLLVDI GVR AFLPASLVERGYVEDLTKYLGQVI KARVTEMNRGRRK
VI LSRKAVLEEEYARLRQEMLENLQEQVVKGVVRRLTQFGAFVDI GGVD
GLLHI SEMAWHRI NHPSEVVKVGDELEVMLRVDRNEKI SLGLKQALPN
PWD TAKDRYPVGS I I KAKVVRLAPFGAFVQLEPGVEGLVHI SHLADRHVA
KPDEVVTEGEDVNKVLSDRDEKRI RLSI REVVKEKQDREYRDNVNVKT
QDNGDVVTI GDMVGDI FEKRE

>2617919588 Ga0073689_101173 Uncharacterized membrane protein [pelotomaculum Ga0073689 : Ga0073689_101]

LDRFPI GI I VLVI ASVI I YLGLAHRVLDRLSDRGALVVI GAI I VGGFI
NI PLPFI PFNTSVNVGGALVPAGLAI YLLI KAGSDREWI RALVGTVATAI
I VYAI GSLI NTGATVEPAGRYAVLDAI YLYPLVGGVVAYI FGRSRRSAFI

Table S2

AATLGVLLVDI FHYI WLLNQGAPGNYTVAI GGAGAFDTI VLAGI VAVLLA
EVVGESLERLAGGPSAKGRPEELVKGLKKPELDTGRKDRDLPGDEKSAV
LEKERGKRADLDEQK

>2617919587 Ga0073689_101172 stage II sporulation protein P [pelotomaculum
Ga0073689 : Ga0073689_101]
MSRNKSKI YI AVI LMLAGFSLFAYLKAANQYLMPALT TAGLFGKEETPDH
LTGRFTTI VDEQNTLSMMARMTFVGDEI YTAEGRSYRI EKVEGDRAQAR
FLGMDPQI TAHNDFYAGQEAPVAKELAEKSRGSFAVYHTHSDESYVPSDG
SETI PFKGGI YQVGAALVDRKGRGMDVNYDQTPHDPHDNNAYTRSRTA
ANLMKTNPVAI FDVHRDGVDPSPSYRATI DGKDVAKLRLVVGRENPRMDA
NMDFAKRMMAAANNLHPKVVEI FI GKGDYNQDLMP TALLI EAGHTNSK
EEAEKGMAMFAEAI PTVLGI APAAPAPTAPGAAGGAWKALGWI LGLTI V
GGLVFLLVSSGNWENAKRLSGI GREFTGFFGPRRAARKPGRQGAAGPGR
DKGKEVYDSRANDVLEDI KDDVTKD

>2617919586 Ga0073689_101171 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
MPDYI PDYLLVI LAGVVAGAAARI I MLRVDYRQYPGYPHGYLAHI SLGFI
AAALGAVAAPAI MKPDYAAVTFLLALAAQQFREI RNMERRTLESLERTEL
KRGLDYI EGI ARTFEARNYLVMGA AFVTS LAAQFGGVAAAMVA AFLALLV
SRFSMSG EVI GDI CDVVPARLSFEGAVLMVDEI GVMNI GLKSMREKI LKE
GLGVKI I PKGGNARATVHDI GQRTAI AFTAAVI VGTKKDVDI PEFTPLAR
KNPDTGEVGLYI LPVERDMEQLI AAVKLTPVLESARSKPLKAGAGI KQAK
KKVHEA

>2617919585 Ga0073689_101170 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
LSEKLSEVI LAVI TLNMDQVSGGAPI FFARDEAGREKI ARYLSNI LNGTV
HDLNGTYI VVRH

>2617919584 Ga0073689_101169 Protein of unknown function (DUF3189)
[pelotomaculum Ga0073689 : Ga0073689_101]
MKI I YHCYGGAHSSVTAASI HLGLLPADCLPDRETFWRI PLYDRQEADEH
GHI FFMGVDEAGNGVYLAARRSRPEVLENI FRGLAEI FNI PPEDYLLVNV
MHKVNLTMKLGGYLSRRWGF I KLGRPI VTAGTRAAYFNVELVTKVSRL
GGYGEENPVFQR

>2617919583 Ga0073689_101168 Protein of unknown function (DUF3189)
[pelotomaculum Ga0073689 : Ga0073689_101]
MVKRI LYFSDSKFPLAGLAGAI HTGRLPAGREPGDSELRSLPFLNSKKSG
EGKI I SLGEDGSGNKI YALSVKGERGMVPRLVESFLKI HRI PEDELSLLD
MGLRDNWFLLAGLLCRFDSLEPLGRFFTSI GLKRI YGRI TQLVRDVKTG
PANLP

>2617919582 Ga0073689_101167 putative radical SAM enzyme, TIGR03279 family
[pelotomaculum Ga0073689 : Ga0073689_101]
MTNRGLAI HRVEI GSI AEEAGLLSGDRI VTINGE PVRD LI DFRFLETDEN
LSI EVKKAGGEDWLLVEKDFDQSLGVDFGAGGFGRTI RCANKCVFCFVD
QMPPGMRETLYVKDDDYRLSFWNGNFI TLTNLGDEALRRI ARQRLSPYI
SAHATNPALREKI LGNPGAALI MEQLRYLAGAGI ETHQVVLCPGLNDGR
ELERTAADLAGLWPAVRSLAVAPVGLTRFRQGLHPLRVFTREEARGLVRW
I ALKQEEYLRDLDPFI FASDEFYLMSEGPVPPAERYADFPQTENG VGLT
RLFMDWEVEVLDGLPRETFPRRVTLATGLLGEKALRPVADRLNQI KGLEV
SVKVI KNNFFGRRVTVAGLLTGDDLQI QSEEAGDLLALPAVMLRKDEP
VFLDDI TPRELARRLKTRVAVAEGRGLVDLLDDNAEKPGI FYPEG

>2617919581 Ga0073689_101166 GTP-binding protein [pelotomaculum Ga0073689 :
Ga0073689_101]
MPKKPVVAI VGRPNVGKSTLFNRI VGGRVAI VEGEPGVTRDRLYQDAEWA
GRNFTLVD TGGLDFQETGEI VRGVRQAELAI NEADAVLFVVDARAGLTP
ADEEVAPVI RRTEKPVLLVVKVERFDATGHI YDFYRLGLGDPI PVSAAE
GLNTGDLLDRLVALLPPEAEDEYSPDVVKI AVI GRPNVGKSSLVNSI LGE
ERVI VSNI PGTRDAI DTPFERDGKHYVI I DTAGMRRRGRI DRPTEKYSV
I RSLRAVDRSDVVLTVLDAVEEVTEQDKRI AGYAHEAGKASVI VVNKDWL
VEKDDRTMNR YTERI RRELAFMQYAPLI FTSALTGKRVPVLELVDFVAE
QHATRI STADLNALI REAALQNPPPADRT RRLKI LYATQGGVKPPKFI LF
VNDPELMHFSYLRYLENQI RSAYGFEGAPI RFALRRRGKES

Table S2

>2617919580 Ga0073689_101165 glycerol -3-phosphate acyl transferase PI sY
[pelotomaculum Ga0073689 : Ga0073689_101]
MLDYWVVI VSYLI GSI PFSYLVARYWKGDI REHDSGNVGATNVWRNAGP
AAGVI ALAGDLGK GALAVMLARHYGGPLLEALAGMAALAGHSWPVFLGFR
GGKLVATGVGVI AAI SLPVGALAAAI WLLVVGVTTRYVSVGSLI AVVSI PV
LMLAFHLARPYLLVGVFVAAFVSVYKHI PNI KRLAAGTEPKI CRRKE

>2617919579 Ga0073689_101164 glycerol 3-phosphate dehydrogenase (NAD(P)+)
[pelotomaculum Ga0073689 : Ga0073689_101]
MSGKI GVLGAGSWATASVLLAQKGYQVRMWSRRPELADEI NKARENSRY
LPGVAVPSGI EVSVAMEYVLREAEAVVFGVPSHAFRDVVRAAI SHI PGRV
MLVNVAKGI EERSLNRLSVVYAEAEAGRDRLERFVVLSGPSHAEVGRSVP
TAVVAASTCMESA EYVQDLFMGETFRVYTNPDVVGVELGGALKNI I ALGT
GI ADGLGFGDNTKAALI TRGLAEI SRLGI VVGANPLTFAGLAGVGDLI VT
CTSMYSRNRAGMAI GRGRSLEEALAEVKMVVEGVRTTRAARRLAERHAV
EMPI TDQI YRVLFEGI SPREAVANLMTRGKTHEMEEVARVAAVVGKI NF

>2617919578 Ga0073689_101163 Putative peptidoglycan binding domain-containing
protein [pelotomaculum Ga0073689 : Ga0073689_101]
MKKVI RFFLLLLLAFGLFWCLPADTAYAEQPVFKQMSGDDVLKLQGI LKN
LGYHGA LDGAFGPGRSAVAGFQTDHDLVDGI AGPATLRALSFSSVVV
SRGSTYRDN SASGEQALKRDMSENVLKLQKRLREL GYYQGA LDGAFGP
GTGNAVI RFOADYDLVDGI VGPETLRTL YSNSSRPQPGRGRTESRQARA
I VSFARQFLGVPYVWAGSSPSGFD CSGFTRYVFGQHG I SLPHMADEQFKT
GI SVSKPQMGDLVFFTTYEPGSHVGI YI GDNQFI HASSGAGDVTVTSL
APYYRDRYLGSRRVIT

>2617919577 Ga0073689_101162 stage IV sporulation protein A [pelotomaculum
Ga0073689 : Ga0073689_101]
MERNDI FRDI AERTGGDLYLG VVGVRTGKSTFI KRFMELMVLPMKNVY
DRERAKDELPOSAAGRTVM TTEPKFI PNEAVEI QI TPNLNI KIRMVDCVG
YRVEGALGYEE EAGPRMVSTPWYEEPI PFQEA AEI GTRKVI SEHSTMGIV
I TTDGSI TDI PRENYI EAEERVI EELKDI NRPF LVI LNSADTAGEETARL
AAELSEKYDVPFI PLDCAQMTQADI LNVLEKLLYEFVPNEVNI SLPSWVE
ELELKH WLRQKFEESI QETVKNVRRLRD VNGAVESLADYDFVEQVNL RSM
DMGTGSASI NI TSAPELFYQVLSEQFGFTI DGEKELFRLVRELSGAKREY
DKVAQALGEVKEGGYGVVTPTLDEL VLEPELI RQGNRFGVKLKATAPSL
HMI KADI TTEI TPI I GTEKQCEELVRYMLNEFEENPQKI WQSEI FGKSVH
DLVREGI QNKLYRMPENAQVKLQETLQRI VNEGSGGLI CII I

>2617919576 Ga0073689_101161 chori smate mutase [pelotomaculum Ga0073689 :
Ga0073689_101]
MAGKERRFYLVQEDLLPDVMI KTVLAKELLLRGEATTVNEAVEKVELSRS
AFYKYKDGVPFYPYQWSPGMTVTLALVLEHRSGVLSAVLNTMAAARANI LT
I NQSI PVYGLANVTVT FETAGMKDGGDDI TARLGALDGVREVNPLGYDVG

>2617919575 Ga0073689_101160 homoserine dehydrogenase [pelotomaculum Ga0073689 :
Ga0073689_101]
LPENVI GVGLLGLGTVGRGVYRI MONNRAGI EQKVGI SIEI KKI LVRDVQ
KHGRVELPEGI LTTDPGEVLENPGI DVI ELLGGVNPAL EYSLRALRQ GK
SLVTANKDMI AMHGRELFEAAEGRDI FFEASVGGGI PII RPLKECLAA
NRI RQVI GI I NGTTNYMLTRMSGELDFQDVLREAQALGYAEADPAADVE
GYDAARKLAI LASI AFNTRI TLDQVYVEGI TRI TAEDI KYATELN YVVKL
LGI AKES EEGVEARVHPALLPKSHPLAAVNDVYNAI FVTGDAVGDMFFG
RGAGELPTASAVTADMNAARNLLWNVPGMI SCTCFTEKPVKSMGDTSTK
YYI RLNVADRPGLASI AFVFGNNDVSLASVI QKHTTGHS AEI VLVTHQV
LEKNLQDALKI I KELSTVNEI SSVI RVEGE

>2617919574 Ga0073689_101159 homoserine kinase [pelotomaculum Ga0073689 :
Ga0073689_101]
MI RVQVPTTTANLGP GFDCLGMALELYNVVEMI PTPRGLVI EVSGEGAVE
I PRDERNLVLQAARSVFSQVGYAPPGI RLRLQNI PVARGLSSTAAI VG
GVI AANLLAGGNLSVKEMI TLASSI EGHPDNVAPAVLGGV VVAVQDDDDV
KYLKFP PPPGLRGVVAI PDFPLATKTSREI LPAQVSFQDAVFNVGRVALL
VAALQQGDSL LGTAMEDRLHQA FRSSLVPGLKKVLAAAKLAGARGVTLS
GAGPAVI AFADANFDLI ARVMGDTFRQNGI KARVLI LKPSVPGARALEVK

>2617919573 Ga0073689_101158 aspartate kinase [pelotomaculum Ga0073689 :
Ga0073689_101]

Table S2

LKMLI VQKYGGSSVADAERI RRVARRVADVRAEGHRVVVVVSAMGDTTDD
LI HLVKEI TDSPPEREMDVI LSTGEQVSI ALLAMAVKELGLQVI SLTGAQ
VGI MTDNAHTKARI LNVNTGRLQEELERGNV VVVAGFQGI DSRNDI TTLG
RGGSDTTAVALAVALKADLCEI YTDVDGVYTTDPRVSEARKLDVVSIDE
MLELAHLGAVVLHPRSVELAMQYNMPLHVRSSFNHNLTGI VKEAGKMEKA
LVVTGVAYDLVDVAKI GLYNVYDRPGI AYKLFQSLAVEKVNVDMI VQSAMR
GERNDI SFTCAQGDLLKALAVVERLLPELGADGFTGDDGVAKVSI VGAGM
ASNPQVAALMFEAMAEEGI NLEMI STSEI KI SCVI KAEDAPKAVRALHKK
FNLAKGADY

>2617919572 Ga0073689_101157 2, 3-bisphosphoglycerate-independent
phosphoglycerate mutase [pelotomaculum Ga0073689 : Ga0073689_101]
MKYVI LLGDGMADGKI AELGGKTPLOYAATPNMDFLAHGEGLGTARTVPE
GFAPGSDVANLSVMGYDPQQYYTGRSPLEAVSMGLDLEDSDI AFRCNLVT
LSERGMAYAEKTMVDYSSDEI ATHEAAELI REVNARLGTGKLRFYPGI SYR
HLMVWKGPGSGADLTPPHDI SGRVI AGYLPGGEGGETLLNLMQESNAFLP
GHPVNRKRIVATGLRPANSVWFWGQGMRLPKFYDKYRLTGAVI SAVDLI
KGI GI CAGLDVVEGATGNI HTNFRGKALAALDELKRGKDFI YI HVEAP
DEAGHRGELENKVKAI EEVDGMLGLLLDGLSRFDSYKI MVLPDHPMPST
RTHSANPVPAFI YAKGRETGGKNAAYDEDAI KSNFNFPAGHELMDFI H
G

>2617919571 Ga0073689_101156 Protein of unknown function (DUF3006)
[pelotomaculum Ga0073689 : Ga0073689_101]
MKEESRGLRI DRFEGEWAVEFDERKI FYFPRFLLPETAAEGDVLRFEM
KVDREETEKRWQEI YAPAKKLFKD

>2617919570 Ga0073689_101155 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
MSNRELI LEVKGRFMMKLLFSPFRLGEI TLRNRI VLGPYQYLLCNPGFQS
DR

>2617919569 Ga0073689_101154 NADH: flavin oxidoreductase / NADH oxidase family
protein [pelotomaculum Ga0073689 : Ga0073689_101]
LAPTSTCFATPDSKVTDKLI RYYEKI ARGGAALLI VEPGVVSARGKLFER
SMGVYEDSAI DPLSRLTGAVKNTGRRLSSSSATPAQRRVQSWWGET

>2617919568 Ga0073689_101153 Xaa-Pro aminopeptidase [pelotomaculum Ga0073689 :
Ga0073689_101]
MRYTPKSELDQVQKLQDI MKKQGI DGAVI VQNAFLFYFAGTTQQSHLFI
PSEGI PI LMTKKSFDRAKQESTLENI VPI DNLKELPGI LKSYGYSSLKQV
GFELDVLPANLYLRYMKLLEPAELLDI SQYI RAVRAMKSPYELEI LRDA
RLNNI FFSHVQEFLEGI SEVELVGELEALCRREGHQGFVRTRAFNTVLE
YAHLI SGWNAGVPGAFPGPI VSGGI NPSFAQGPSAKVI GRDEPVLVDYVG
VI DGYMVDQARI LCI GSLPRKLVDHNTALEI QEI VKERARPGVLCGELY
DLAVRRAGSSGFDFHMGCPDPSFI GHGVGI ELDELPPVAKGVKTPLEE
GMVFALEPKFVFPEGAVGI ENTFFVTKDGLNLTVFDEAI IYT

>2617919567 Ga0073689_101152 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
MFMSMGFI I LDAVELI VFPI MHPNQVGCIFYQI I AQVLVAGADTFNI FGFP
LAGLLFI PHQTGELGKCLLVLPKPGD

>2617919566 Ga0073689_101151 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
LLLWRKSRNLRVKKVVPDTAVYAMVLNRI SNPLSKRGVNRWI EEVYRLDF
SELELHYFYRALDLAEHKKRSETGLFKRI QSLFKYESGYCFLGYHI CYN
PAQAEHDKKTRREEMVQKLKRLQENGVKSLVGNISGYRRYLLKKDITAVGI
NQDLLKEEARYDGKHVLRNTCQLDTDEVALAYKDLWHVERAFREI KFSLD
LRPVYHWKDSRVRGDI MVCFLALVL

>2617919564 Ga0073689_101149 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
MLI NI ELAKRLAKYLPWEPKVGDLTI VYGESGEDI I EPI I PKHEREKKI V
LSMRDVGDLVWLPRLTLMLYELKI RSI KGFTFSYDKDITDTRYKDERI ET
CEHSPEDAAAKALLELFENRDSK

>2617919563 Ga0073689_101148 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]

Table S2

MLKCKVRNVFLI LGPLMI LAAFKLTLPLVTLVLMAGVSVQVTLAFRGR
T

>2617919562 Ga0073689_101147 Putative zinc- or iron-chelating domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_101]
MLLPAAANLYTLI SSMKKGAFOELEKI YGQLPETVCEQCGACCTVPPPGY
FI EYLNLYRYLRDNOKEERAGI LQRLARYYFLELVDI GSRCPFLSGENKC
LVYPVRALSCRITYGLLNKKDRREDSGAMELLAREYRERHGI ELP AEI VEF
RLPAGCEKVKI KDGAI PPKGRI ERLI AEVAKLDTGI LPADFVEQDRSLMP
YATYLVFTVLGEGAQARRI RVMKEYLEKGSSELLEQYQEKASKFAF

>2617919561 Ga0073689_101146 Fe-S-cluster containing protein [pelotomaculum Ga0073689 : Ga0073689_101]
MTYGLKQTMVEKLESGELAEKL EDSFTFHCQDRCMGRCCAKI TILLDPW
DI EVMARHLGLAGRDFVERYCHLDFDPQI KWPYACLGHA KDGPACFLLEE
GKCEI YPARSRNCRTYPVGRAVRFDKDGSRMEERLFMVDRQQFCFGHR
GDRAWTVREWLEDGDAFLYYELSDLYFELI SYAATVLEGRRWMSERTAQM
MMTI LYS PDALRSRLGI STGEVGHEEFYRRRMKALKAVLTDLAAGFGFGP
LAVRFLEGDI PETRI MDWMKKI LVTGEEQSM

>2617919560 Ga0073689_101145 sulfate adenylyl transferase [pelotomaculum Ga0073689 : Ga0073689_101]
MSKLMPPHGGKLT PVL LPKEQRADALAKAKTLP AVMSSRESSDLLMI GM
GAFSPLTGFMNKADYENVSTKHLASGLAWPI PI TLSVSKEQAAALKEGM
EVALVDD ETD TYVGI LTVGDKYEYDKTKECKEVFFTD DMEHPGVQKVMAQ
GDVNVGGSVVTFSQMGYATKYAGYYATPEETRALFEEKGWRTVA AFQTRN
PLHRSH EFLCKI GNEVCDGLLI HPI VGKLPKPGDI PAEVR LDCYKVLLDNY
FNQKTAVMRVYPMEMRYAGPSEGI LHAI FRQNF GCSHI LVGRDHAGVGSY
YTSYQAQELFDQFKPGEI LCQPI KVTSAFHCFKCN GMTTEKTC PHGNEDH
LNI SGTKLRGMLAAGELPPAEFSRPEVLRI LMKYYQSLNDK

>2617919559 Ga0073689_101144 dissimilatory adenylyl sulfate reductase beta subunit (EC 1.8.99.2) [pelotomaculum Ga0073689 : Ga0073689_101]
MPAFVI AEKCDGCKGQDKTACMYACPNDLMVLDKERMKAYNRDTWMCWEC
LCCGKI CPQAI DLRGYADFVPLGASATPLRSSDSI MWTI KFRNGSVKRF
KFPI RTTEEGKAVPDGGFGPDKAEDI NSPYLFT EPASLGVELFTLKK

>2617919558 Ga0073689_101143 adenylyl sulfate reductase subunit A [pelotomaculum Ga0073689 : Ga0073689_101]
MAI PTFETVEVTTDLLI VGGGMAACGA AVEAAYWGKKHGVKVALVDKAAM
DRSGAVAMGLSAI NQYI NLGGKSQNASNTVEQYVDYVTQDLMGVTRQDQV
ADI ARHVDSTVHLFEQWGLPI WKDENDKYVNEGRWQI MLNGESYKVI VAE
AAKNALGMDNI YERFVI I EPLMDGDRI AGAVGFSVRENKFYVFKAKAVLA
VMGGAVGVFKPRSTGEGLGRSWYPPFSTGSSAYFTI KAGAEMTCQEVRFI
PVRFKDAYGPVGAWFLLFKSRATSALAGEY MVERRSELENWAPYGLVKPI
PANLRNYLGM LDCFEKGPI FMRTEEAI ANLAKKYEGDEKAFKKMKKELE
SEAWEDFLDMTI AQALLWAATNVEPDKRFSEI AAAEPYFI GSHSGASGAW
ISGPEDI QTEESKKDYFWGYGNMTTVKGLFAAGDASGASSHKFSSGSHAE
GRI AAKSAI KFI LDNNAQPNVDAAAVEALKEKTYKPLAVFDEFKGYTTTP
DVNPNI RPKMYMYRLQKLMDEYVGGVSANFSTNTPSLDRALELLNFLKE
DSEKLAAEDMHLMRCWENI HRTWQAEAHVRTVMFREETRWPGYYFRADY
PKMDEANWHCFANI TWNPKTGEWTCVKRPI HKI FA

>2617919557 Ga0073689_101142 putative adenylyl sulfate reductase-associated electron transfer protein OmoA [pelotomaculum Ga0073689 : Ga0073689_101]
MSKSI LVVGGGI SGLTAAVEAAEVGCEVFLVEKNPYLGKVTQLNQYFPK
LCPPNCGLEI NFRI KSNPRI KFFTMAEVDSI SGKEGDFDVTI KFNPRFV
NEKCTGCGKCVEVCPVERPNEFNFGLNRTKAVYLPHEFAFPNKYLI DGNA
CRGASCGKCVEACPYGAI ELEMETKTTSLKV GSI VWAAGWNSYDPCKLSN
YGGGQYANVI TNLMMERMASQSGPTGGKI VRPSDGOEPKRI AFVQCAGSR
DENHLHACS NVCCLASLKQATYARAQYPDAEI VI FYI DI RARGKYEDFYT
KVQDEANVTFI KGKPGEI KEAPATRNPPVVLVEDQEKQVMEEEFDLVVLA
TGMAPATRDVKI PAEVTYDEDFVASAAAGI YGAGCVNKP LEVASSVQDG
TAAALKAI QSVRRQNG

>2617919556 Ga0073689_101141 quinone-modifying oxygen oxidoreductase subunit OmoB [pelotomaculum Ga0073689 : Ga0073689_101]
MAKKVGVI CSGCI GDALDI VALSKVAKKECKAAI VKDNPFLCGQEGVD
SI KKDI ADEGVNVVVAAACSPRVCYDVFNFGPDVMVERANLREQVWVWCH

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PGDEDTQMLAEDSI RMI GVRANQAEI PTPYMPEDPSKTI LVVGGGLAGMT
AALETAKANYQAVLVEKEAALGGWLNKVYKNAPMNPFTDLEENNATALA
KEI EGNANI KYYTGATI EKTAGGPGMFDVTI NQGGNTVTERI GSI I VATG
AKPYEPAKLTKLENLGF GKSPDVI NNAMFEELALAGNGKVL RPSDGKEVK
NVAFVQCAGSRDKERLPYCSAACCVESLKQATY LKENDPEANVFI YYKDV
RSSGQYEHFYKKVQESGVVFI KTDTKTI CVVDEDGSLTVEADDVLLGGKS
RAEELDLVVLATGMVTTYAPEEVAETAGEAGQEA AAAAEGOAPAPAI PK
LDI LNLOQYRQGPMPSLKYGFDPDSHF I CFPYETRRTGI YAAGSVRKPMQ
VTAVEDATGAALKAI QCVECTARGEAVHPRVLDTSFPEFNMNRCTQCKRC
TEECPF GAI NEDEKANPLPNPTRCRRCATCLGACPERI I SFKNYSVPMI G
NMI KAI EVPEEDEEKPRI LVFACENDAYPALDMAGVNR LKYNAWI RI I PV
RCLGSLNLVWI ADAMSKGI DGVLLMGCKHGDDYQCHFVKGSELA EI RLSK
VSETLDRLGLESERV RATEVSI MDYTKI PAMLDEF A EKLDELGP NPMKGF

>2617919555 Ga0073689_101140 qui none-modi fying oxi doreductase subunit QmoC
[pelotomaculum Ga0073689 : Ga0073689_101]
MAECKI SPDSQKYDL SFAREI YALENGSQI KKCMQCGVCVVS CAARQEME
YVPRKLFNLI KL GKKEEVLKSN TMWMTSCCTCKARCPRI RI I DVMHDL
KKYCI EKGYVSYPOAEFYQAFWNE LQKAGRVNEG NLMKNYLLKKGI GYAI
KKGLEMYMGMEMI KHGRMSI KDMI PFI SPPKI KGI QSLNNI I AKAKAQQ
EEANK

>2617919554 Ga0073689_101139 heterodisulfide reductase subunit B [pelotomaculum
Ga0073689 : Ga0073689_101]
MRYSYFPGCSMEGSGI PYL KSI KAVAEELGMELEE I EDWNCCGATMASGV
I GDYI QQVVTARNLALAEQGLDI LVTCSACYMSLAI ADKRFKEDKHFKE
MANEALTAGGLKYSGALRVROI LDVMI NDVGLDKI RARVKRPLTGLKVAC
YLGQCI VRAMPWEFDDPENPVFLDRLI EALGATPVFPFPMKARCCGSSQAS
VAPEVVVS YGKKI LESAVAGGAHLI VTPCAMCQLNLDAYQDQLNKTYNTN
FSI PVLFFTQLMGLAFDLPPTAVGLNHNI VTPFHI LSRYWTKANYEGR

>2617919553 Ga0073689_101138 dissimilatory adenylyl sulfate reductase alpha
subunit precursor [pelotomaculum Ga0073689 : Ga0073689_101]
VVERVYI DTDLLI I GGGTAGCLAAWEARKMAGPDLKI TI LEKAFI RHSGC
LSAGMNALNMYI SQSPEDYVAYARYDI CGAPVREDI LLSVAREVNETVA
I MEKAGLPMKKKEDG SYLNRGKWN I EINGSHLKPI TASMAYEAKAI I I NR
VYVTNI FLNDGKAVGAAGFGVRDGK FYVARARAVLI TAGGAAGLWRPANG
GDAHHR I WYFPFNTGASYAMCKRAGCEMTGFDMLVTVRTKDTYSATGTL
QI GMNAPMVNARGRAFI EDPYYI NWGGHSAPTPI RVLGVCRETENHRGP
VYI DTSRGDPYKVTGI KGQYLDMSPCLVLYWGCNDI DPSKEPVEI EAADP
SLVGAHAGCTGAWTPDVDRMTTV PGLFVSGDALGATPSRF I SGSWTCGRI
AARHCVEYI KKNTGLAELAPAEI DRQEEI TFSPRANYEERSKSGFWTDGA
LKEGI CPKQMEEHMQRVMEDYCGGRSRLYYANETYLDI ARRR I NRLRKEQ
I QHLCARDTHDLQLAWDVI NRLDI CQLVI EHI SFRKETRYPGYVKRTDFP
EMSSDYDCFVNSVWNPETDELTFYKRPHYVKI VPGDRRKESI

>2617919552 Ga0073689_101137 adenylyl sulfate reductase subunit B [pelotomaculum
Ga0073689 : Ga0073689_101]
MPPKVD PVKCDGCRGDDVPVCEMVCPGDLMTLDSGVKKAYCREPGDCWDC
MTCAYCPRQAI QTQLSYQI ACFPCKLI PLVAHNSVTWTSI DCHGKVERF
AI KTVAGEDDDD

>2617919551 Ga0073689_101136 Carbonic anhydrase or acetyltransferase, isoleucine
patch superfamily [pelotomaculum Ga0073689 : Ga0073689_101]
MLRFSPATSWNHTEKLPRVHERAYI DRDAI LI GEVLVEKDAVVLPGVVI R
ADEGCPI I I GEGSNVQDGI MHALKSGI EVGRRCVAHGAVVHGPCRI G
DNSFI GFNVLLKADLGKNC FVSHGAMVI GVKI ADGKFI PPGQLI DSGDK
VAGLSNVAPEMNGFAHEVLEVN GELLEGYRRI AVREALGENDEFPCSLAV
CNE

>2617919550 Ga0073689_101135 solute carrier family 13 (sodium-dependent
dicarboxylate transporter), member 2/3/5 [pelotomaculum Ga0073689 :
Ga0073689_101]
LSAMPGYGG LMSKQKVFNLNDFRKKEI QPSNKFETSTPGGHTGYYGPLGK
AGEVLAERRWLLLGI ALLAVI CLMPTPEGLSDKGK YALGLWVFVI I CFLT
EAVPLPMTAMI I GSYQVI SGI GSFQEVPRTFMDDAVI FIMGVLMMGAMLV
KYN I HNKI ALYMLKI SGTRI DRVVLGI VAF CALSAGFVTEHATVTI MLPI
GAGI VSLSGI K KAPRLGKLI MLAI AYGVI VGGVASPSGGARNALMLSFL
STKGI NVGYGQWMLMAMPFTLI MI PVVAFWLLKLFKPEVNDLKDVLEAI K

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EEMDADGPMTAGAKVASGI FLAVLLSWVLSRDFGAGNI AMI GI VLATVL
RLVDWQYLQOKTQWGVVVL YAGAVSMGKMLVTTGAASWLAEQLLWVAAAV
GVTKNLP LLATTTAI TALTTNAMPDGPTVAVLGPI FI QAAELAETSPFAI
GVATSLGSALSYLLI I ATPANAI VYGPGLKVTDFLKAGAMLF I LSMLLM
I VVLGLWWRI LGI W

>2617919549 Ga0073689_101134 Transposase [pel otomacul um Ga0073689 :
Ga0073689_101]

MFFRKI TSRNGKEYTYLKL I ENYREGEKVKQRVVANLGSLENLTPDKVQ
GLI AGLSRI CGVSNKPSSLEAKKVLRYGEVLAVHRVWEMLOI PRAI EI SV
PEHTKDLNI PLLVELMAI NOVVKPQNKQAI SDWYRCLYLPGLDEKELLSH
HFYRALDVLAKAKDAVERNI FTRLTGI LPVSADLAFCRLTSGLFEPAPRE
ELNPSSYGRYFLEDQNELEKVRFGI MVTRDGI PFGHRMFREDSGEWEFRE
VLDYLKGNFGI DRCI FTGERSVTANPSLEVLVAQGYEYLI GRKVI AGQDQ
DLVDREMSSGRKDFREVREDLWFKEVKDGDVRYLLCYNPQGAEQKKTFL
ERLSAVEGELDAI RKS I DEKROKGI KTVI NKNTAVFKDEFCKRYFDWSYD
EESMDFI YRRRENLLAREKNSAGMFI LETNSRDLTGTEI LDSYTRLVRLG
DSLREI KNFEARPGKLYTELNI SANI LVCVLAI MLEEALERLVRRAGFNL
NSRQTLDLLLEI KLTVNQLDDREVRVTRI PEAQEQI LRAI GVGVI QRTI
I

>2617919548 Ga0073689_101133 hypothetical protein [pel otomacul um Ga0073689 :
Ga0073689_101]

MKFFKRVANGGLATGQFLTELSTOAKWELEMSRI I LGKRWKL LLI AMFP
VLLGI GMEVAAAALPEHI GGHKAYMPSFASTQMF I GSI FVGLMAGLI TGV
I GAGGGYVLTALMSI GVKGI MAVGTDQFHLFAKAI MGTVI HKKMGNVNF
WI AVWFVLGSVSGATVGGMI NRSI YOKSPALSDAFI SSVYVLI LGI LGAY
ALFDWI SSSRGKAKGEVSSTEATTKFAKWLQALPLKPRVGFHDHI VPGGR
SI SVYPLI I VGI VGFVAAI MGVGGGFLT FPI FVYCLGVSTFTTVGTDI L
QI I FTTAYSSI AQYAVYGYVFYSLAMGMLLGS LVGVQMGALATRVLKGST
I RAI YALTI VAGFTNRI CSLPPKLNDAGYMSVGKQTTNVL TNVGN I VFFV
LAATFSLWI MI SFFKGVGKFRAEAAAAGAESSLSTAAR

>2617919547 Ga0073689_101132 hypothetical protein [pel otomacul um Ga0073689 :
Ga0073689_101]

MI VNKKQFMI GLVMI I SFAVI FSVMMSPI I NGQTVI SYADDLFNQLTKGS
TYAI PGVQKKANGFEG I TFDI SLTAKSEEEVDKMTKLMAAAGAKVEADGL
KMKI SGDMGKVAKAALADADLEFNNGAQI EGKYGMESREALYQWWRAFD
GMAKFKRENKAQELAL TNNVLQKAI EPAYNFEG I QTVNI REKAGI TTFM
LLFYVVYTVWYGFAI MYLFEGLGI I ATHGEKAEA

>2617919546 Ga0073689_101131 CBS domain-containing protein [pel otomacul um
Ga0073689 : Ga0073689_101]

MEKKVKDVM I PVGRCP TI PVGSSVKEAVALLGRALEAGPCAAGASALVI D
NNTPVGVLMREI LQAVAPVAFKGGTYRGWTPADWSAPVFLKGI FTDKC
QRLSSI I VGEVMAPVTMTLNAGDPLSKAAHVLVAGGYPVPVWQEGKVVG
MVGYTELFAEVTAI LSGSEPGADSGRKQVAG

>2617919545 Ga0073689_101130 CBS domain-containing protein [pel otomacul um
Ga0073689 : Ga0073689_101]

LPHEKKVAEI MI PI EDYSSSVNSTVKEAI TI LKKSFCDLDTGECHGHS
ALI FDDDNKL VGI LNFRA LLLAI EPRFLKYEGGPSLYKEGFFSQRAREEA
ERKVGEI MQPVEFI TVDAGDAI LKAI HLMLKHLGALPVTREGMVGMVR
I NEVFNEI AKSVVEE

>2617919544 Ga0073689_101129 Do/DeqQ family serine protease [pel otomacul um
Ga0073689 : Ga0073689_101]

LVNWRRL LFI AVAAFLAGI MFTGGCYLV RDVFPDKQGP KGGGTAGADLL
PGVGPD AI ADVVTNSSPAVKI STRVSSGGAYDPFFNDPFFRQFFGLPSR
PRQEEGLGSGFI I SGDGYI LTNEHVVDGATEI AVTVTGFDNELTARVVG
ADYDLDLALLKI DAGKELPFLNMGNSDQI RVGNWVI AI GNPYGLDHTVTT
GVI SAKGRPI SVNDRHYENLLQTDTSI NPGNSGGPLLNL RGEVVG I NTAI
NAQAQGI GFAI PTSTVQGVLEDLKNSASQVRPWVGQVRSVDEETARYLG
LSGTGGALVVGMAPGSPADRAGLKQWDVI I EFNGNKI NNADELVTAI RAV
QTRKAKALVVRHRQVYTVNI MI VEKPKNI R

>2617919543 Ga0073689_101128 Peptidoglycan/xylan/chitin deacetylase, PgdA/CDA1
family [pel otomacul um Ga0073689 : Ga0073689_101]

MEVEASFLOI LLLI FLAYAVAPTVLI RLARLGAVYRARAGNLKI ALTFDD

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GPDPRTYTPQI LDI LRHYHVKACFFVVGAKAMAHPELVKQI ARAGHEI GNH
GFSHRAAWLLSPAATTREI MEANRALEELTGRKI RFCRPAWGLFNLFSI L
YCWLLKGMQVVLWITYMSWDWI SKATPESI TRKVLGRI KDGAI LI FHDSDST
PGAAAGSPSRVVAALPLI LEGLKNMGMQVPLEELLATKKVRRKI LKRL
RLLWNLLDPAI LRLAGVRDLGDDKTSI WRVALRHYRGRDWLMPDGSVLRR
GDFYMEHLI NNNRLI SLMDENTSLERMALI AMREVRGGLPALADLLNSDE
QFGKVKVI I GI TLLHRGARRI GFTVYDMKPVLF TWTGWYERWLLVLFHP
GGLKNLSYRHDLSPKYVVMTRQELI RRYPPVSPGTAPACRAVESAVK

>2617919542 Ga0073689_101127 Predicted arabinose efflux permease, MFS family
[pelotomaculum Ga0073689 : Ga0073689_101]

LRMKAI FSSRKESCLLLLLFLI EFTRGAFFLTFLPLYTVNYLSI SVVAV
GLAVSAHYLVETLFKGTAGWQLDRRGHPVLLFGLTLGLAALLMMKFYPSA
PVLMLGSAFFGLAVSPVWLAVI SGVAPVQLKERASRMGVFAVWLAGGGG
GPVVI NFFI ARNYDMAFWLLI ALWSAALVLTAVFFPGVAKTGDDSSFSFQ
KEVTRMARNPVAKKLLLPGMFVOTLAGGLLLPLMPI YAQI KI GLNPNQYA
VLLLAGGAAAVLSFLPMGRLADRI KLKI LLGTGFGMTALSLALFSTARQA
TSAYLLAALVGFSYAMVLPANNLLARVI SPERQATGWGVFATVEGMGVA
I GPALGGI VAKFLGI SAAPVLSAAVLASMSCFYFLYPVERLFEK

>2617919541 Ga0073689_101126 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]

MAEI DTKGMI AEISDAQFTQLREMEKKLNGAAGDKQEI YLLAVTRH

>2617919540 Ga0073689_101125 Fe2+ transport system protein FeoA [pelotomaculum
Ga0073689 : Ga0073689_101]

MTLDKAKKGQVI KI TGI PNELLRVQAI RFGI AEGSVVTCREVPAGPVV
ARSKQEI AI GRGLARSI AVEPCQPIN

>2617919539 Ga0073689_101124 NiT/TauT family transport system substrate-binding
protein [pelotomaculum Ga0073689 : Ga0073689_101]

LPLRLKKI I ALAVFI SLAAFLT VHFFKKPAPVREI HTVRVLESARSPYFL
POYLALNLGFFKEQDLVUNI STTSPEAI RTALADGRDI ALCGLQKI I FN
PHARGPQPRVFATMALKDGSFLLARKDDGYFQWEKLKERTI I GNSQDDSS
EI VLEDALRRRGLRPYRDVTYNNI PDLRLGAFSAGTGNCI QLLEPDAT
LAESKGYGLVAASVGEAAGDMVVTAYAALPGYLEARPDI QRFI NAI YKA
QLWLSHSAEEAAAVATPSFPNLNREI LLKSI ERYRALGI WTGSPLVSEE
PYERFCLAAAREAGEI I TPDPIYENI VVNDFAQAVETVKYSPEAEKEKKPL
LKRI FI SMVNPFAQNI

>2617919538 Ga0073689_101123 regulatory protein, gntR family [pelotomaculum
Ga0073689 : Ga0073689_101]

MENNGQSSLHI ARYI TI AMDVAERI I HGDYREGQKI SGRSTLAGLYNVSP
ETVRRALSLLQEAQVVKVI PGTGVFVDSVAAAREYLAESGQYKVI KEMQE
RLSWLVQERNKLNIAI EHLTAELLDYVLSVLSTRHKI

>2617919537 Ga0073689_101122 PAS domain S-box-containing protein/diguanylate
cyclase (GGDEF) domain-containing protein [pelotomaculum Ga0073689 :
Ga0073689_101]

MSETFQDKKSLVLI VDDSRFMRLKLRQMLNEEGYGV I EAENGLQALSV
FRERQPDLI LMDQVMQEMDGTACARLQELPGGSRAPI MI TSLEDDNAV
EQAFSAGATDYI TKPI NWAVLRQVRRLHARHTELSLDRSEAFARSI I D
HALDGI I TMDTDGLI QTFNPASEKI FGFSSTDI LGQKVNLLLPGFYQDF
RRYSADYRQDGENNFFGAI MEATGRRKDGSKFPVELTVSRLNVDEQAMFI
I I LRDI TDRKRYEETI RHQAFHDALTGLPNRTLFKDRLTLAI TNAKRKQ
RLAVLYLDLDRFKLI NDTLGHALGDQLQMAAQRRLRMTVRAGDTVARLGG
DEFTI LLTGTDKPEDAAKVAQKLI DAVKKPFQAGGHEFYVTSVGI VLYP
NDGEDAGTLLKNADVAMYLAKEKGRNNYQLYTPEMNTRALQRLELENSLR
RALERGEFLVHYQPKI NLLTGKI TGMEALVRWQHPGKGLVQPGDFI SLAE
DNGLI VSLGEVWLRTACSONKAWQDRGLPPVRVAVNLSAKQFHLQNLVET
VSRVLEESGLDPRWLELEI TEHVAFQNAEYTVKMLRQLKKMGI QLSI DDF
GI SYFSMRYLKQLPI DRLKI DRSFVAQI GKDRFTNI ASAVI TLGQSLKF
GVGAGGVENEEQLDFLKKHNCIEI QGFLFSRPI AAEDFETLLKREVM

>2617919536 Ga0073689_101120 diaminohydroxyphosphoribosyl aminopyrimidine
deaminase [pelotomaculum Ga0073689 : Ga0073689_101]

MDSHYMQMALNLAAGARGRTSPNPMVGAVVVKDGRVI GSGYHLRAGAPHA
ELHALNEAGAAAGATLYTLEPCCHHGRTGPCTEAVI GAGVAKVVVAMT
DPNPRVSGGGI RKLRLQAGI EVVLGVLEDEARRLNNEVFI KYI TTGRPFVVA

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KAAMSLDGKI ATRSGKSQWI TGPGARARGHRLRDWYDAVLVGI GTVLADN
PSLTTRLPAAGGATRRG

>2617919535 Ga0073689_101119 RibD C-terminal domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_101]
LTQSAAPTI I AATAGAPPARLEALRRAGAEALVVNDGPRVDPALMGI L
AGKEI TSVLI EGGAHVHASALAAGI VDKVAWFI APRI I GGREAPGPVGE
GSTTPPKRWNSGWK

>2617919534 Ga0073689_101118 riboflavin synthase alpha chain [pelotomaculum
Ga0073689 : Ga0073689_101]
VFTGI VEEKGVLRAVRRGADSARLVI GAEKVLEDI RMGDSI AVNGI CLTA
VQFSARAFSADVMAETLARTNLDAALRTGDRVNLERALRLGDRLGGLVSG
HI DVGVTI VEMKKYDI ATLVTI RAPFEVMRYVI KKGSI AIDGASLTVVDF
RAGTFQVSLI PHTAHATTGLRKPGDTVNLEGI I GKYI ERLAGFPSDAS
RESGI DLGFLAKHGFV

>2617919533 Ga0073689_101117 3,4-dihydroxy 2-butanone 4-phosphate synthase / GTP
cyclohydrolase II [pelotomaculum Ga0073689 : Ga0073689_101]
MKFNTI EEAIEDI RQGI I VVDDDEDRENEGLI MAAEKVTPEAVNFMAT
HARGLI CMPVEGKRLDELDPAMVNHNTDPHATAFTI SVDARECTTGI SA
QERAMTVKKVLDSNSRPEDLRRPGHI FPLRAKEGGVLKRAGHTEATVDLA
KLAGLYPAGI CCEI MKEDGTMARVPELMEFVRTHGLKI I TI ANLI QYRRR
TERLVRRVDSAKLPTRYGEFTAVAYESLLDGKGI ALVMGELDQVEAPLV
RVHSECLTGDVFGSVRCDCEQLARAMEMI AEETGMFLYMRQEGRI GL
LNKI RAYNLQDQKDTVEANLALGFPADLRDYGLGAQI LADLGLKKI RLM
TNNPRKI AGLEHGHLQVVERVPI VI RPKGCNCFYLATKQKKLGHMLNMSG
GEW

>2617919532 Ga0073689_101116 6,7-dimethyl-8-ribitylumazine synthase
[pelotomaculum Ga0073689 : Ga0073689_101]
MPKI YEGHLLGQGLRFGLVVGFRNEFI TNKLLSGALDNLNRHGAADENI E
VAWVPGAFI PLVARKMTATMKYDAVI CLGAVI RGATPHFDYVAGEVAKG
VAKVGLDSGVPTI FGI TADTI EQAI ERAGAKAGNKGWDAAVNAI EMANL
IRNMAG

>2617919531 Ga0073689_101115 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
LKI GVI SDTHGDAASWRI MEGVFRDVELI VHAGDI LYHGPRNPLVEGYD
PRELAGRI NSCPVPVLFARGNCDAPVDQLMLNPI QAPYLFLOVGDRLI M
AHHGDLGDLHAEMMLRLARLYHAGVFI SGHTHVPALGNDRDVEAVFLNPGSP
SLPKGDSRPTAALMECEEGSLKI KI I HI DDGSTGEQLAMGWVKGLFPER

>2617919530 Ga0073689_101114 large subunit ribosomal protein L28 [pelotomaculum
Ga0073689 : Ga0073689_101]
MARKCAVCGKI TVGMKLSHSI RTKRTWAPNLQVRKALI DGTPRRVLC
TRCLRSKGVQRAI

>2617919529 Ga0073689_101113 ATP-dependent DNA helicase RecG [pelotomaculum
Ga0073689 : Ga0073689_101]
MPDNYLEKSQYLKMGPRRAASLAKMI FTVRDLLYHFPRRHEDRTRLO
PAGSCAHGETATLRGTVLAARELKPGRGLTVTKLAVRDGLGI FYAVWFNQ
PFVKKNLPLGTLFI TGKVEKGYGVVQVLVEEYEVDDGGDSLGAAGRLVPV
YPLAGQLSQRLRAMVKSALDGAGEADGEFLPKKLEKFSPLRLDKALKG
AHYPDHEI EAGAARERFI FEELFLFOVALAARRKGLDGQKKAHRYLPEGR
LTA AFLNSLPYRLTGGQREVWREI SRDMDSPAPMRRLQGDVGSCKTVI S
VLALLKAVESGLOGALMVPTVLAEQHHLGMKRLAPMGVEAGLLTGGR
KREKELLERVRSGELKVLVGTHALI REDVDFQRLGLAVVDEQHRFGVRQ
RAI LQKHGHCPTLVMTATPI PRTLALTYGDLDI SVI GELPPGRRPVKT
HAVRPAALPKVYSLVKEQVRLGRQAYI VCPLVEESEKI DLKAAVDLAEG
AAGEFRDCRVGLLHGRMKAGEKEKVTDSFRGGETEI LVATTVI EVGVDVP
NATVMVI LDADRFLAQLHQLRGRVGRGGHQSICI LVAEPKTEEGI ARLK
AMAGTADGFALAEEDLRLRGPGEFHGARQSGLPGFKVADLLRDWQALQAA
REEALAWVGEDPRFQKPESRALLKEI RARFGGAGNYI GVG

>2617919528 Ga0073689_101112 PAS domain S-box-containing protein/diguanylate
cyclase (GGDEF) domain-containing protein/HDIG domain-containing protein
[pelotomaculum Ga0073689 : Ga0073689_101]
MSQHTVNKALI AGLVLI FTLLGGFVLFQI ARVMVNLDLLAVTVDKVAAAG

Table S2

RLHDYALRQSYAI EGYI LYHEPAYLEEFRRYAGLSRQEMEQLRQVVRPAR
KTLVEEI LARQOEYAELECEQEI VPLVDRGGTAGAARVARQSGAVTLSEEM
LDRI DELQRMRLADASAI TGRASGQVRQALRWGACGGLLALFAGLALGFL
VNRRLVLENLI YRLVLLNTRNAVI VARRGGRI HMVNRMAEEI FGCKREAV
TGRLEFAVFTGRRQPGELAFSYPVAAVMAAGKDVCNI EKSIVTADGWRYT
LLTDCLHLRDEGGRPHGAMMI I RDI TERKLVEEKLOGLVVRDSLTMLYNH
SYLKQALDREVTRAGEQGRLAFLMMDVDNFKGYNDQFGHPAGDELLKKL
ARLLEKHMROADI PGRYGGDEFDAVI LPGADQAVAVEVGERLRRFAEHF
PYRELMPPGGRI TVSVGVACFPGDAAGAAELI RQADEAMYNKRNKRNVE
VWFSSFKELESDWPDERDLLYSI GGLLAMVNSKDRYTYGHSEKVAHYAAV
LARAAGLSPEEVKKI KVA AFLHDLGKVDI PEEI LNKPGLLSAAERELCRD
HPVTGAHI VRQI KSL E E I APLI RHHHERYDGRGYPDGLAGGAI PLGARI I
ALADSFDA MTNRPYRRARTRQEI QETRKEAGRQFDPYLVGLFI TMDVD
GGGI GTSGGTESVREEPSPPAVNLDDYAATS

>2617919527 Ga0073689_101111 DNA-binding transcriptional regulator, XRE-family
HTH domain [pelotomaculum Ga0073689 : Ga0073689_101]
VSLAEVRKSONVSACKMAESLGLTVAEMRAI EEGKRTPLRCVAQKWANAL
GLTFEEFSRHYAKADPAQLDL DHI ESDQ

>2617919526 Ga0073689_101110 Small, acid-soluble spore protein, alpha/beta type
[pelotomaculum Ga0073689 : Ga0073689_101]
VAQGQKRNI LI R GANRAMEDFKWETARELGI QVPDNGYMGDLPSRMNGA
I GGNMVKKMI AAYENSLAAGTVPPPTQVTNANLNP

>2617919525 Ga0073689_101109 spore protease [pelotomaculum Ga0073689 :
Ga0073689_101]
LDLDFYKSGFI SVDLAVEAHD I VRGQTGKEI PGVI VDREKYAACSVTI VK
I VEEQAEQLMGKPMGNYI TI EAPALRDNNRVAQQEVAEI LARHLSSLFDL
PENANI LLVGLGNWHATPDALGPKVI DNSMVTRHLYKYAPEELKGGRLSV
SAI APGV LGI TGI ETAEI I KGVVEKI QPELVI VVDSLAAGSVDRI ATTI Q
I ADTGI SPGSGI GNNRAGI NKESMGVPVI AIGI PTVVHA AVI ARVTVEQF
LEQLQTSPLVYQI YKNLRPDFTOQVI NDVLQPFAGNLMVTPKEI DTLI LD
TSKV VAGGI SMALHPSI TLEEYNMYLN

>2617919524 Ga0073689_101108 16S rRNA (guanine(966)-N(2))-methyl transferase RsmD
[pelotomaculum Ga0073689 : Ga0073689_101]
LKVP RGLGVRPTSNRVKEALFNI VGGLVPGCRFLDLFAGTGNI GI EALS R
GADI AVFAENNAKNARI I RENLAVTGMEAKARLI CLDVAEALVLLGKEGK
NFDLI FLDPPYLKDFESGALAGI AGQGLLRPGGRVVVESSNKDRLPRETG
GLKMF RQEKYGD TLLSFYHNEQTTGEGN

>2617919523 Ga0073689_101107 Phosphopantetheine adenyl transferase
[pelotomaculum Ga0073689 : Ga0073689_101]
LRTAVCTGSFDPVTFGHLDI I GRASLLFDRI I VAVSRNPI KKP MFSI EER
MEMLKGV LAPYPNVEVDSFDGLTVNYALRQAKAI I RGLRVI SDFEYEF R
MALTNKKLACQVETVFLMTKA EFSFI SSSTI KEVASFGGSVRDLVPPLVE
EKLKEKFKTCHKVKEEL

>2617919522 Ga0073689_101106 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
VDLLSALNELEELI ESSGKI PLTKRVMMDEDRVLDI LDRI RTTI PDEI RQ
ARWI I QEREKVLDDSQEAMRI LEDAQKQVEKRADESEVTRQAKVVAEEI
VAKAEATAREI KESARQYADDI LANLQESLGRI LTQI EQGRAELKSMKQK
S

>2617919521 Ga0073689_101105 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
MI NLYI MGTAGSGKTSVAVGLALKFRQEGYRVAYFKPVGAAGWATSREDE
DALLMKQVLHMEQPLEAI APYLAGPSYLSGHRNSCDLTKTI RQAYESVAA
GNEVVI VGGAGFPHI MGCLGLDAPSLALELKAVSLFMI RI ENDYSLDQAI
FFNSYLECKGVPVLGNI FHSVPRPLLAKTEGI YRPVLEERGYRTLGI I PG
NPEMASPTVKEYEYV LGG E I LAGEEKLDRVVEDVVI GAMTI ESALGYLRR
AANKAVI TGGDRSEVALAALETSTSALI LTGGLYPDVKVLARAGEKDVPV
I LVHYDTFTTI EKI SEVSRKI RATDEKAI KMAVENI EKHVDWRSVLKALQ

>2617919520 Ga0073689_101104 acetyl transferase [pelotomaculum Ga0073689 :
Ga0073689_101]
VAVI GASKSPGKI GNVI VKNMI SCGYQGKI FPI NPKETEI EGLPCYPAVD

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KTPEPPGLAVVSVAAGALEVAELCGKGGVKNLVVI TAGFKETGREGLEL
ERKLLTTCRRYKMRMLGPNVGFMDTHAPI NASFATGFPRRGEI AFI SQS
GAMVLSI LDWSYQAGLGFSGFI SLGNKADLTEAHFI EDAAADPHTKVI LC
YI EDVENSHFLEVAGRATRKKPI I I LKSGASQAGAQAASSHTGALAGSD
LAYETAFFROCGVI RARSMPELFDLAVAFANQPAPGGERVAVVTNSGGPGI
VATDTI ELKGLKMARFTKETVAELRGQLPAESNI YNPVDVLGDARAYRYR
FALEKVLADPGVDSAVVLVCPAGVTEPLETARAMI EMREAHPEKPLFAAF
MGGERLSEGVKLLGEAKI PCFTTFPEPAI SAI SGLVSYGRARELPPEEALQ
ALDGI DAKTVKTVFYDVKKDNRLVLLGSEAAEVVGAYGI PAAPTVLATSP
EEAAEQAEKI GCPVALKVASPKI MHKTDVGGVKI GLDSPEKVRRGFVVI M
DNI HRYLPRAVVYGVGVQMMMPKGVLEI I GMSRDVQFGPLI AFGLGGI YV
NLLKDVSFRLAHGLTAREI ENMLAETKAYTLLRGYRGEKPADI RAI I EI I
GRVVKLVTDFFEI TEMDI NPVFAYSRGASALDVKI TIS

>2617919519 Ga0073689_101103 sporulation integral membrane protein YIbJ
[pelotomaculum Ga0073689 : Ga0073689_101]

MAGLGKKTIFFTDGRSDLVRLWTACALVFVAGMVVYPRITFEGAVTGL
KTWWNI VFPALI PFFI ASELLMSFGVVHFLGVLLPEVMRPLFNVPAGGSF
VVAVGFTSGYPI GSMVTARLRSQSLCTRVEAERLMSFTNNSSPLFMLVAV
AVGMFNPNPLGALI TGAHYLSNI TLGLLLRFYARRDPERVPGLPGHGNP
VI LAFHRMLAVQREENRPLGKI MADAVRNAVTNLLNI GGFI I LFAVLI RL
LTATGFI DLLASFLGVFLLPVGFAPEI LPALGSGVFEMTI GSKMASETAA
PLLQQVAVSMI LAWGSLSVHAQAAAMVAGTDI RMAPFVFSRLI HTCLAG
I YTYI FCHWAGPLI DPAAPAMTVAGEWQSLTYTYFNFKI FGFFI I LLTTI
ILLALLHLANSVRLRVLKI K

>2617919518 Ga0073689_101102 uncharacterized protein [pelotomaculum Ga0073689 :
Ga0073689_101]

MLLVDAKLKRSRPGDSARYDLQAEPLPELPGESASFAGLVRAGLEVI NT
GKTLAVEGVVSGRLRLNCGCCLEPYDYPFEVAVEETYI PASEGGGEEAVP
FSGDYDLTPEVLKSI I LTLPMKMVCREECRGLCPQCGRNLEGMCGCEN
EDI DPRLSVLKNLFKEKG

>2617919517 Ga0073689_101101 large subunit ribosomal protein L32 [pelotomaculum
Ga0073689 : Ga0073689_101]

MGVPKRKASKQRGRRAANMKLDAPALVNCPQCRALVMPHHLCPCEGY
KARKVVATK

>2617919516 Ga0073689_101100 Acyl-coenzyme A thioesterase Paal, contains HGG
motif [pelotomaculum Ga0073689 : Ga0073689_101]

MTRESLNRVERQRLARCLEKDLFLTDEDLARI FKVSQTI RLDRELEKI
PELRERI KNVARGSELRVRTMTGEELVGELVDLEVSRAI SI LLI TPEMT
LRKTGI ARGHHLFAQANSLAVAVI DAGAALTGI ARVSFKRPVYRGEKVLA
KAVI KFKKGNKYMVKVTSVHKDEVVLQGFVLVFAI PEEVSPQ

>2617919515 Ga0073689_10199 phosphate:acyl-[acyl carrier protein]
acyl transferase [pelotomaculum Ga0073689 : Ga0073689_101]

VKI AVDAMGGDYAPREI VQALQAVREYGLAVI LVGDEERLRAELAECEA
GDLVSVVHAPEVI EMREHPAVSVRRKKNSSI VRATOQVKEGKADALVSAG
STGAAMAAALLGLGRI KGI DRPAI AGVLPSEKGTVLLDVGANVDCKPHH
LLQFGVMGYLYAQKI LGI PNPRVGLLSNGEEETKGNETTAAFPLLQNAI
I NFI GNVGERDI FRGTVEVAVCDGFVGNV VLKACEGMARSLFKMMKEEI T
RSLLAKI GTVLAEPVLKGFQKRLDYAEYGGAPLLGVDGVS I CHGSSTAR
AI KNAVRVAAESVENRLVESI RDCMENVTKKRVGDDFAQGI D

>2617919514 Ga0073689_10198 3-oxoacyl-[acyl-carrier-protein] synthase-3
[pelotomaculum Ga0073689 : Ga0073689_101]

MTLPRELI RAGI AGLGTYVPERVLTNAELERVVNTSDEWI RTRTGI RERR
I VSPEQAASDI AVPAERALRDAGVAPEEVDLVI VATNTPDMFFPATACL
VQDRI GAKNVGAFDLAAGCTGFI YALAAGSQFVATGSCRTVLVI GADTLS
KVTNWEDRNTCVLFGDGAGAVVLQAPENSGI LAFKLWSDGAGGPHLHLP
AGGSRRPATRETVEGKHQYI HMNGREVFKFAVRVMGDAAEEVLAAAGLGK
ADLDFFI PHQANI RI I DAAAKRLGLPMEKVLVNVDRYGTSTASI PLALE
EAVHSGRI KKGDI VMVGFAGLTWGAVAMKW

>2617919513 Ga0073689_10197 enoyl-[acyl-carrier protein] reductase II
[pelotomaculum Ga0073689 : Ga0073689_101]

LFRTALCDLLNI EYPI I OGGMAWVSTAELAAVSEAGGLGVI GSGSAPPD
WLRGQLHKARELTAKPFGVNVMLHSPFVEEI MAVLREDPVAVVTTGAGNP

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GKYL PALREV GTKVI PVVSSVALARRL TRGGVDALI AEGMESGGHI GELT
 TMLVPQVVD AVDI PVI AAGGI FDGRGLVAALALGAVGVQMGRFI CAEE
 CTI PLKVKEFVI KAKDRD TVI TGASI GHPVRALRNKL TRKY EKMER NFAP
 PEEI EKLGLGSLRQAMVEGDI DYGTVPAGQVCAMVREVQSAREI I MDI LR
 SAAEI LI SLNERVVKK

>2617919512 Ga0073689_10196 [acyl -carrier-protein] S-malonyl transferase
 [pelotomaculum Ga0073689 : Ga0073689_101]
 VRCAFVFPQGGSQYVGMGKEFYLSLPEAAAVFKRADEALGFSLSI CFEG
 PEEELNKT VNTQPAVLATSI ACLTALRVAGGPVPSATAGHSLGEYTALVA
 AGSLSFEDAVRLVRKRGRYMQEAAPLGAGGMAAVLGLPGDAVVALCRKAS
 GAGVVEAVNLNCPGQVVVAGDTAGLKAAELAAKEAGPGRFVPLPVSAPFH
 SSLMMPAGERLAGDLDFI NVADPEI PVVVNVGAD FVRTGPEVKASLI RQV
 YSPVRWEESI RRLAAKVDTFVEI GPGR I LSGLI KKI SREARVYNVEDRA
 SLEKVLALTGEVG

>2617919511 Ga0073689_10195 3-oxoacyl -[acyl -carrier-protein] reductase
 [pelotomaculum Ga0073689 : Ga0073689_101]
 MVFNSRVAI VTGASRG I GRAI ALALARGGA AVVVNYTSRADAAAQTVEAL
 KDAGGRALAFRADVADPGEAAGLVKAAVDEFGRVDI LVNNAGVTRDNL I L
 RMKDEDWDTVFGVNLKGAFNCARAAVRGMVKNHYGRI I NI SSVVGLTGNS
 GOANYCAAAGLI GFTKAMAKELGSRSI TVNAVAPGFI NTEM TAGLAEEM
 KKKMLAQVPLKRFVPEEVAGAVVFLASDAAGYI TGQTI TVDGGMTCI

>2617919510 Ga0073689_10194 acyl carrier protein [pelotomaculum Ga0073689 :
 Ga0073689_101]
 MSVFDKI KDI I I EQLGLEEEVEVKVEASFVDDL GADSLDI VELVMALEEEF
 DI EI PDEDAEKI RTVGEAVKYI QDRR

>2617919509 Ga0073689_10193 3-oxoacyl -[acyl -carrier-protein] synthase II
 [pelotomaculum Ga0073689 : Ga0073689_101]
 LRKRVI TGLGVI SPVGTGLEKFWSSLAGGVSGI RRVNRFDPADFSTKI A
 GEVVD FNPVDFD FKKEARRMDRFTQFAVAATGMAI KDAALDLEKEDRDRI
 GVI LGSGI GGI ETLEEQARI LFEKGPRRVSPHFVPMI ANMGAGQVAI SY
 RLGPVNVT SVTACSSANAMGEAFRMLOWGYAEVMI TGGSEAPI TPLAMA
 GFCSMKAMSTRNDEPEQASRPFEAGRDGFVVGEGA AVL VLETLEHALSRG
 ARI YAEVAGYGCTCDAYHQVAPDPGGCGAANS MREALADAGLAPGAVDYI
 NAHATSTPLGDKA EVTAI KKVFG EHTCKMAVSSTKSMTGHLLGAAGGLEA
 MACALAI HSGI I PPTI NYQQPDPDCDLDFVPNVARAVVVNVAMSNSFGFG
 GHNATMVFKKFC

>2617919508 Ga0073689_10192 RNase III [pelotomaculum Ga0073689 : Ga0073689_101]
 MTKKNECLERLKKRLGFSWRDEGLLEQAL THGSYTYENHQNGLENNQRLE
 FLGDAVLELAVSDHLYRSPDRDEGDLTKLRAAVVCEPSLVRVARELELG
 LCLKMGKGEERSGGRERPSI LADAFEALLGAVYLDQGLGCAGELAVRCLA
 PI LKDVMEGRLERDYKTELQEMVQQRGGEQVQYVLLNEEGPDHHTFTAG
 VLYRGEMVGRGAGRSKKDAEQQA KVALVKDLFKKVEFGFGRKA

>2617919507 Ga0073689_10191 fused signal recognition particle receptor
 [pelotomaculum Ga0073689 : Ga0073689_101]
 LDKVMSFFGRLKESLTKTRQGLVEKI DNI VHRRKVI DEELYEELEEVLVQ
 ADVGVKTAMD LVTRRAVRERRVDDVGELKFI LEEHI KEMLGEDKAPLN
 SGSEPPTVVMVGVNGVGKTTTI GKLAHLYKSEGGKVVLGAADTFRAAAI
 DQLEVWANRVGVDLI KHQEGSDPAAVAFDSLQAARARRADI LI I DTAGRL
 HTKSNLMELKKI ARVLGREMPGAPHEVLLVLDATTGQNAVVSQARLFVEA
 AGVTGI ALTKLDGSAKGGVVI AVKQALDI PVKLI GI GEGI DDLRPFNAGE
 FVDALFTKAEI K

>2617919506 Ga0073689_10190 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_101]
 MPI CPVCNGLAMVDEKCLVCGRPMVDGGVLRDYYDNYSAYLEQDLYEDGY
 SCYDDSHCVHLFACPHCHYDTRLRFKKLAKEWLMD

>2617919505 Ga0073689_10189 5'-methyl thioadenosine phosphorylase [pelotomaculum
 Ga0073689 : Ga0073689_101]
 VEVKIGI I GGTGVYEPGI MTGVRDET VASPYGDVQLKI GSYRGKPVAFI N
 RHGEEHSI PPHLVNYRANI AALKKI GVKNLLATGAVGSLNPAMQPGHFVF
 VDQFLDFTKGRHQTFDFGGVSGVVHTDMTCPYCPEI REI LVRAARSLGFT
 AHQTGTYVCCGEPRFETAAEI KMYRLFGGDLVGMTGVPEAPLAREAMCY

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ATI AMVTNYAAGI SPTRLTHQEVVDVMMQNRENI RKLIMQAVAWI DQDRA
CACHYALEQSDG

>2617919504 Ga0073689_10188 methyl thioribose-1-phosphate isomerase
[pelotomaculum Ga0073689 : Ga0073689_101]

LDTMRWTEGVLLELDQTRLPSGI EYLRCTGHTDVAGAI KCLAVRGAPAI
GAAAAAYGLALTAALKI ESCSKEEFLAGVEASAGELAATRPTAVNLSWALDR
LLRRLRRVESEDNLNVLRLATLLEEAHAI YREDVAGNRKMGEGQEMI PDGA
RI LTHCNAGALATAGYGTALGVI RAAHEAGKKI SVYADETRPLQGARLT
AWEMLOEGI PVTLI TDNMAGYMLTLGKVDLVI VGADRI AANGDVANKI GT
YGVAVLAGEHRLPFYVAAPVSTVDLSLASGAEI PI EERDHGEVTHLAGLP
VAPAGVKVWNPFDI TPHRLVTAI ITDWGI VRPPYTENLKKMALK

>2617919503 Ga0073689_10187 adenosyl homocysteine [pelotomaculum Ga0073689 :
Ga0073689_101]

MSDYI VRDI DLAQDGRLLKI DWVREHMPVLNAI REEFERDRPFEGRLVAMS
IHLEAKTAYLAEVI RAGGAEVAI TGSNPLSTQDDVAAALAAAGI NVYAWY
DATDQEYREHLLHVLGARPRVI IDGGDLVNLHTERKEQAAEVI GGCEE
TTTGVRRLAEALEREGRLLFPMLAVNNAFCKFLFDNRYGTGESVWSGI MRT
TNLVVAGKTVVVLGYGWCCKGI AMRAKGLGARVI VCDVDPVKAI EACMDG
YQVMRSDQAAAYQGDIFITVTGCRDVLRLRHFTRMKNGAI MANAGHFDVEI
NKTELAGLSVERRTARRNI EQFTLPDGRKLYLLAEGRLVNLAAGDGHPT
IMDMSFGI QALSARYI KENASLEKRLYRVPEEIDRRVAQLKMASMGI EI
DNLTGDQEAYMNEWQE

>2617919502 Ga0073689_10186 5-methyl thioadenosine/S-adenosyl homocysteine
deaminase [pelotomaculum Ga0073689 : Ga0073689_101]

LSNII LRGATVI TMEGQDNVYGDGEI AISGNVI LAAGPKGSVPEGFTAER
VIEAPGMVALPGLVNCHTHAAMTLRSYADDPLMKWLSEKI WPLEEKL
PEDII YWGTMLCCLEMI KSGTTTFADMYFEMDQVALAVEKSGMRACLSRGM
IEGPNQAQRAI DENMSLI EDWHGGAGDRI KAFFGPHAPYTCPPDYLLKKI
DLAGRYGVI QIHVAETWDEVEI RDRYGASPVRLDNTGLFELPVVAH
CVHLDGDI GILAAKRVGVHCPESNMKLASGVSPVTRLFEAGAVVGLGT
DGAASNNNDMLEEMRSAALLQKVSTGDPMALPSFGALQMATSDGARVLG
LADVGQLKAGMKADLI LVDFRQPHLCPRHDLVAHLVYAAQSADVDTVI ID
GEVI MEGRVRLTMNEEVMAEAQRCLRLTGK

>2617919501 Ga0073689_10185 transcriptional repressor NrdR [pelotomaculum
Ga0073689 : Ga0073689_101]

MKCPFCGFYDSRVLDSRPTVEGNSVRRRRECGSCGRFTTYEKVDELPLV
VYKKDGRRETFDRRLKLLGLSKACQKRPVSTGKLEAMVDGI ERELNTME
PEIKSQYI GELVMDRLCRLDEVAYVRFASVYREFRDAESFMEELKDLLKK
NGDSLKGG

>2617919500 Ga0073689_10184 intein N-terminal splicing region [pelotomaculum
Ga0073689 : Ga0073689_101]

MFKTI QKRDGREVPFDETKI TDAI FEAARAVGGEDRQTAMELTI EVLKLL
KKKYNGNLFGVEDVQDI VEKVI EAGHARTAKAYI LYRDKRTRMREAKGE
LMDAVEEILEETNRENANI SNPSAKMLQI ASAASKYYLTRLI PEEIAQ
AHLRGDFHI HDLDFYGKTLTCVPDFEYTLI RDRQSEVRRVKFDYFNALVD
RNCEVNIIEGAEVLELEGYQILGRNGWTRI NKVMRRKLREGECLYRI KT
RKGPPLHLTGHEKVPVLRAGHEFLQVKDNI GDRLLTGRRDFEGSFAP
GRNLDPQDVVAIDPVKEYERFVFDLETAEHWFTVNDYI VHNCI QI PLYKL
LSEGFNTGHGYI RPPKRPTSATALAAI LQSSQNDMHGGQSFAFFDRDI A
PFVEDADDFETYQAMEALI YNLNSMHSRAGK

>2617919499 Ga0073689_10183 ribonucleoside-triphosphate reductase class III
catalytic subunit [pelotomaculum Ga0073689 : Ga0073689_101]

MTRPYLKGRVTKLAQVPFSSLNMGTTTSEAARRVKNLLLAYEAGLGKGE
NPIFPNIIFRVKEGILNLPDGPNYDLFKLAI RVACKRLNPTFSFMDSSFN
KEWGAQVSVMGCRTRVMANRRGPAVTDRRGNLSFTTINLPRVAIKERDL
DDFYRRLSDVMDLAI RQLYHRYGVQSKLKVRDMPFI MGQKLYLDSNLGP
DDPVAAEAI KHGALAVGFI GLAEALTSLTGRHHGQDEECQALGREIVAFMR
QKINEACEEYDLNYTFLATPAEGLSGRFVKLDRKEFGLIPGVTTREYYTN
SFHIVPDPFITSFEKISLEGPYHKYCNAIGHI SYVEMPSPPVHNPEAVEAI
IRHMRSDSMGYAGI NYPVDFCVNCLLGVIDEDNCPRCGSGNI RRVRIIT
GYLSTTDRFNDSKLAELRDRVSHNPSMRKN

>2617919498 Ga0073689_10182 anaerobic ribonucleoside-triphosphate reductase

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activating protein [pelotomaculum Ga0073689 : Ga0073689_101]
 LKIRIAGTIRESVVDGPGRLRFVFAQGCRCCKGCHNPDTWDLSSGGTPVT
 TEDLLEDIKATQLIKGVTFSGGEPFLQAAPLAWLGREVKKLGLDVI TFTG
 YTWERLLALAQEDRAVDLI LTSDYI VDGPI LAERDLTLPFRGSRNQRI
 IDVMESTRTGEVVEAGFA

>2617919497 Ga0073689_10181 protein of unknown function (DUF1992) [pelotomaculum
 Ga0073689 : Ga0073689_101]
 MDI VAVI AEGRI REAMERGEFKNL SGKGKPLELDDLSHVPEELRAGYI ML
 KNAGALPEEMLLKKEI VSLQKLI DCCHEEAARKSLRKKLNQKI LRFDMMM
 ERKRVSTALSYRDKI YTKLGG

>2617919496 Ga0073689_10180 LysM domain-containing protein [pelotomaculum
 Ga0073689 : Ga0073689_101]
 MARKYTVRTGDTLFEI ARRFGATVEKLARLNNI TNPELI YVGQELI VPEE
 GEAGTPGGTVPGGGGDRVSRRVDGLLYTI FTDKENYRQEDDVVI TLVKTN
 VRGREI TLRYSQRSYDFVVRGPGGGGEVWRWSRGRSFAQI TSVSLSPG
 ESQVFKVVDQRNNRGEQVAPGSFTI EGFNI AQDLGDEGI TTTI RIRRGV
 EPTPTPTSPPTATPCSENI LVNPGFERWPNPSLPPAGWSGSNLFIRSTLS
 HRGNFAAELGATHNERAVLSQRVEI EPGRI YDLI WHARENVQPGGVARFV
 LFVEI FYYNRAGEFVGRTEPRYSQENI PNNAYQRYSLSTGRAPAGARAAE
 VRTTFEPSAGNDNTVKI DDVELRCRF

>2617919495 Ga0073689_10179 putative regulatory protein, FmdB family
 [pelotomaculum Ga0073689 : Ga0073689_101]
 MPI YEFRCGDCGHRFEKLCPMGKNGKLCPCGAPSPGRVMSSFSAGT
 EGGRGDDSGCGTCGSHNCSSCGVH

>2617919494 Ga0073689_10178 metallo-beta-lactamase family protein [pelotomaculum
 Ga0073689 : Ga0073689_101]
 MRLOFLGAAGTVTGSCFLDTEAKIMI DCGMFQGPKEI RERNYGNFPVQ
 PRSVTHVLLTHAHVDHSLI PKLVKHGFRGRVYATAPTVELCEVLLPDSG
 YIQETEVERKNRKNRRAGRPLI DPVYTVNEAYKSLTSFKPVQYGEI IRLT
 PGI RARFVDAGHI LGSAMI ELWVGEGGSEVKLVFSGDI GNKDRPLVKNPS
 FI VEADYVI MESTYGNRLHEQCENI ELLHDVI WETYKKGGNLI I PAFAV
 ERTQDI LYHLNLLMEAKRVPPMTVYI DSPLAAAATAVFQKHRDVFDDQAN
 DLI NRGDPI NLPGLKI TQSAEESKTLNNI DRAII I SASGMCEAGRI RHH
 LKYNII WRPESTVLVFGYQPVGTLGROLLDGEKHVRI FGDEI AVKADVRFI
 ECYSAHADQAGLLEWAKSFTRPPREVFVHGEPEASETLARLLNTELGLO
 AAVPAWQQWVELI PAGGVAAAEDPVKLLCASLTAKI QSLLTRGVDESAYER
 ELLARLTELEAFI DQRMKKAVG

>2617919493 Ga0073689_10177 conserved hypothetical protein [pelotomaculum
 Ga0073689 : Ga0073689_101]
 LLTSGDLKFYTFPHFGETGLVI HGFTSRAGGVSGPLAGLNTAFHVGDR
 ENVLANRALACALGVDHRLVAGROI HGDRI EVVGLREAGRGALSHADA
 LPGTDALVTGTPGVPLASFYADCVPLFLDLPVRKVVALAHAGWKGAFLKI
 GLKTMRKMTAAFGSDPADCLGGI GPSI GPCCYEVDGRVMEPFRRSFAGFR
 ELARATSPGKCHLDLWEANRRTLLEAGLREKNI TVARI CTSCRNDLFFSF
 RAQGGTAGRMTALI MLK

>2617919492 Ga0073689_10176 two-component system, OmpR family, alkaline
 phosphatase synthesis response regulator PhoP [pelotomaculum Ga0073689 :
 Ga0073689_101]
 VVDDEKNI LELVRFNLEREGYHVL TAPGGVAGLELARRENPDII I LDVML
 PGMSGLEI CRELHRDPVTKDI PI IMLSARGEELDRVLGLEMGADDYI TKP
 FSPRELVARVKARLRRSRSEERREEPPEARLDFGRLI I DEDRFVAVYVDG
 KKQDFTPKEFELLRFMAHKQGVFSREQLLEQVWGYDYAGDSRTVDVHI R
 HI RQKLEHMPGGSRLI ETVRGVGYRFKEDWMC

>2617919491 Ga0073689_10175 PAS/PAC sensor signal transduction histidine kinase
 [pelotomaculum Ga0073689 : Ga0073689_101]
 VLTVLKNFKKI GWRPVASYFFLFLVFFALNQLYTVQALNMWGAVALAFTC
 SVFLAWI MYRRI I SPLEEMATI AQDMARGNLDREI RI YAQDEI GDLARSI
 NYMARQLKNNI DDVI SEKNRI QAI LSSMADGVI AMDNWGRVI LI NPVVEE
 I FGI TPAASKGKNI LRV I RNCLELRLNQALESGQAI QRQI EI LTPEPKI
 FRVHI TPLQNTGVDHGGVVALLRDI TERKRLDEMSEFVANVSHEMRTP
 TSI RGFTELTLLDGALEDTOAARKFLEI I NDETERLSRLI DELLNLSKI ED
 GRLAPKLQPLEMGDLI NRVVAI LQPRAQEKDLAI KVELSENLSVVQGDPI

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MI SQVLI NLI DNAVSYTQPGGEI RI RAATMQNELKVDVI DNGI GI PPESL
PRVFERFYRVDKARSREQGTGLGLSI VKHI I DVHRGSVQVESKVGSGSA
FSFLLPLNGSNNNS

>2617919490 Ga0073689_10174 putative membrane fusion protein [pelotomaculum
Ga0073689 : Ga0073689_101]
LKVLVYTASLVI VAFFAWGYLVAASRVEVLTMQEVARTVPLEGLLI KEE
KVI KSPAGGRLCYTARDGQRLEVGAAPARVI AAQDAGGTVDI FTPVAG
I FCTHLDGLES I LSPGNLDI LDPAGLEKI PQKPVCAEGRVEKGHPVFKI V
DNLSSVYLYARLPKDSFPAGLVDRPDWLPVAVRENLTLLI KPYKLADRGDM
WEGFI LRNYPEGI LHYRKVSLYLTVEKLGGLLVPGRAVVYRDGEPGI YM
AVRKRARWAPVRI EGEFAGKVAVSGRGLVEGARYVSYPLAREGGLVE

>2617919489 Ga0073689_10173 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
LSVQGNLI RVRERVTTAARRAGRDPGKI KLVAVTKTVPVEVI REAVACGV
TALGENRVQEFRLKI PLVPPGPEWHFI GYLQTNKVKKI I EKVSLI HSLDR
WALAEALSRAACEAGI VAGALAQNVAGEKTKSGLSPAEAEFVAASRL
PGLAVRGLMTI APWCENPEEVRSVFREMLARRLKDQTMGAEEYLSMG
MTGDFEVAVEEGANI LRI GTAI FGGRP

>2617919488 Ga0073689_10172 cell division inhibitor SepF [pelotomaculum
Ga0073689 : Ga0073689_101]
MALKLVDKMLGFI GFEEPLEEEENRGRDETPEEQQPWQRKRKDKKEKEK
GAVLNLHTORQVKVVVVEPRSFDEVQGI VDNLKNRRPVI VNLEQAEPDLA
KRVVDFATGATYALNGSSQKVGSSI FLFPNNVDI ASDLKDNKEKGI FS
WTRS

>2617919487 Ga0073689_10171 pyrroline-5-carboxylate reductase [pelotomaculum
Ga0073689 : Ga0073689_101]
MSLRGRKI GFI GGGAMGEALI TGLLRAGRMAPSAI FVSDVSAGRLEYLKE
KLGI NVTTENSGLNETGI I VLAVKPRVMAVLLLEEI APLI RPEQTVI SI A
AGI PTGFI EAYFKVPVPVVRMPNTPCMVGEASAVSAGKFAGRDSVESA
LAVLSAAGKAVEVPESLLDCVTGLSGSGPAYMYEI LEGFVDGAVRLGLPR
DVAI LLI AQTMLGAAMVLETGEHLGKLKDMVTTPGGTTI AGLFALEEGA
LRAVLMKAVEAATRRSRELSGVKQ

>2617919486 Ga0073689_10170 YggT family protein [pelotomaculum Ga0073689 :
Ga0073689_101]
MNI GGASI I LTAVNVAFQVYTI LLI I RI LLSWFRHNPYQPVI KFI YEI TE
PYLGLFRRI I PPLGAVDLSPI AAFLVLDYI I RPLVMYI LGFI FMRLV

>2617919485 Ga0073689_10169 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
MSI DRERMLARARDGEEKSSLARVLDRAMVLRSGLTQVTGFHDPYNTGL
VVTCAEGGYPI GPQGPPEGGRGERPLEKRAYGGNI KQVFI AAVLYFEKY
CSGRQDMSFFLSKVVFLLKTGPGVMKPC

>2617919484 Ga0073689_10168 cell division initiation protein [pelotomaculum
Ga0073689 : Ga0073689_101]
MLTPLDI QKKEFCRAFRGYNDREVDSDLRI NQEYENLYRENQVLKEKLT
QAEQNMARYREI EEVLKNTMI MAQKNADELRRNTEKETGLLMDRARLEAE
QI TREAEQEAVALLODTKRRAAGMLAEAEGRVNRVMEEYHRLERDARVFR
TRFRTFLEAQLRLLENQGENNSGLEGGMGVCPTGAKCLI ESELLETV

>2617919483 Ga0073689_10167 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
LGWKTLDYPEGSPGSSI I SSLSAGRNI FPDRRDLQPDPPI QYHFLVQPD
GFQLVSQPPHSGYDHYGDHLNPHCHRVSDPDALWSSGNRSQARI CMI RT
AKHI ETGEFSLLPRLRFPSPCPALHSCGTRFTEWTHELI SSKNGFVRLK
NCRRGTAGRNHFYRDGSGENQGRGFNLNCCM

>2617919482 Ga0073689_10166 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
LLYVKEDQDGVLFKVRVQPRAAKNQVAGLYEDALKLRLTAPPVDGEANEA
CRAFLAGLLDVPRSRVEI VSGHTGRSKMI KVTGVS AEKLSKAFSF

>2617919481 Ga0073689_10165 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]

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MPVDVQYI KEKLVGEFTGPQAGI PAEVI SEAVRAAGSELVKTSDFNELKE
I VCDLALAQQKI EL

>2617919480 Ga0073689_10163 Isolucyl -tRNA synthetase [pelotomaculum Ga0073689 : Ga0073689_101]

MDYGKTLNLPRTDFPMRANLPEREPEFLKFWDI DI YHKVREKNSGRPKF
I LHDGPPYANGHLHLGHVLNKVLKDI VVKFHSMAGYDAPYVPGWDTHGLP
I EQQAI KAFGLNRHDI HPVEFRRKCKEFALKYVDI QREEFKRLGVRGQWE
KPYLTLMPHFEARQI GVFGEAMKKGYI YKGLKPVYWCASCETALAEAEVE
YGDQKSASI YVRFPVLDGKGI LPEDDTYVVI WTTTPWTLPANVAI CLHPD
FDYVLVRAGKEKYLVAELRDSFLEAAGLRDAVVVKEFKGAELERLECGH
PFVERI SLLI LSGHVTLEQGTGCVHTAPGHGMEDFI VGKQYGLPVI SPVD
AKGRFI GEGGI FAGQFYLDANKAVLEELERRGHLLSHFTI QHQYPHCWRC
KKPVFFRATEGQWFASI DGFRQAALDAI RKVRWI PGWGEERI YNMVANRGD
WCI SRQRSWGAPI PIFFCRCGCKELI NDRTI GHLQELFREHGSDVWFARE
AGELLPEI KCPCQCGCEFTKETDI MDVWFDGSSSHMGVLDEPSI WPDLR
WPADLYLEGSDOHRGWFNSSLSTAVAVTGRAPYRAVLTHGFVVDEQGRKM
SKSLGNVVDPAKVI KOMGADI LRLWVSSADYRGDLAVSPKI LKOMTEAYR
KI RNTCFRLLGNLYDFDPAGDKLEYKELPEI DRWALTRLQKLI RRVLQAY
RDYEYHVVYHAI HSFCTI DMSALYLDI I KDRLYTAPARSAGRRAAQTVLY
ETLYALVRLTPVLAFTAEI WRYVPGDKGGAVSVQLTDMPEVREECLDE
ELDOKWERLLAVRGEVTRALEAARRDKVI GNSLEAAVELYAGDDLVSFLE
PMAGELATLFI VSRAALRRPGDAPEGLPRSESLPELAVLVKPARQGKCR
CWMYLEGVGADADHPTI CPRCLDVI KNME

>2617919479 Ga0073689_10162 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]

MVLVMGVI FPFVLVWLGLPLEMVLRPVFLLASLPAGLVVGWVNYLPARL
I LAVPLKSLACMLI MDARLKPWDQLL

>2617919478 Ga0073689_10161 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]

MAGKCVHEHCQRLLHVI TRAKDNTVGYTGPPPETGKRGQKPPVWGKKVK
LWKQFRNANEF

>2617919477 Ga0073689_10160 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]

LLWKPI KEKVRFVLVMDGTEKFI LTCSNLOWLP EEI LOAYSYRFKI EVTF
KGLKYLLGSFCYRFWTKAMPKLGKKTFFVDLGGVTDATKQRLI AETANAI E
I YTSRSGCLGNLI NSGKLKPLKTNFYKQGTFLKRGFLMLRARNDLRYSH
HTSLHSPRQSFDCRRPLRNP

>2617919476 Ga0073689_10159 signal peptidase II (EC: 3.4.23.36). Aspartic
peptidase. MEROPS family A08 [pelotomaculum Ga0073689 : Ga0073689_101]

MFFFI I AATFLVDQLSKAVVQLLMYQGESI PVAPSVFHLTYI MNPGAAGF
LLAHQTLFVAVTVLLVAVVLLGYKRLPPGRTPRLRYGLGLVVGALGNLV
DRLRYGRVVDLDFRI WPVFNLADTAI VI GACLLI WGLLKDAGKKAKEP
GC

>2617919475 Ga0073689_10158 23S rRNA pseudouridine1911/1915/1917 synthase
[pelotomaculum Ga0073689 : Ga0073689_101]

VPTVHSFEVDEGGAGKRLDVFLAGETAGLTRSHI QKLI QEGLVAVNGQPA
RASHRVGTGELI I LQVPEPEGLEVKAEP I PLDI YFEDADVI VVNKPRGMV
AHPAEGNYSGLTVNALLYHCRDLSGI NGVLRPGI VHRLDKDTSGLI MVAK
NDAHL SLAQQLKDRLVTRRYLALAHGRVKEQAGVVD API GRDPRNRQKM
AVVEKNAKRAATS YRVLKRFDYTFLELKLETGRTHQI RVHMAYI GHPVV
GDPKYGPVRPHFGLAGQFLHAAVLGFKHPRTGEYLQFEAPLPEVLQEI LK
GLAAEPAGKKWLK

>2617919474 Ga0073689_10157 Uncharacterized membrane protein, DUF441 family
[pelotomaculum Ga0073689 : Ga0073689_101]

LSGVNMLVALLI GI VAHSNLI ATAACVLLI LKFTNLNLVFP LLERRGLE
LGLLFLLLSI MYPLANGGVVSQQDI MYNLTSLPGVLAVAGGALATHLNTKG
LRLLLKDPEI VFGLVLGSI FGI VFRLRGVPVGPLMAAGVAALFMEMFRLSR
R

>2617919473 Ga0073689_10156 phosphosulfolactate synthase [pelotomaculum
Ga0073689 : Ga0073689_101]

MGGQAYANI WLEMLHFPLAGRSRKP RRQGLTMLLDKGLGVGETKDLLNMA

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GDYI DFLKLGFGTSALYSQVQLEEKI HLAKSFEVDI YPGGTFLEI AVLQD
KLKEYLALAKDLGYTAVEVSDGTI NLSPEVRERAI SMAAELELKVLTVEVG
KKDPGEKAPVENYVRQI LRDLANGAHKVI VEGRESGKNAGFYDHEGQFVA
DEI EEMLAAGVDPHLLI WEAPLKEQQQELI LRFQPNVNLGNI SPYEVI AL
EALRVGLRGDTLRSVCRDGG

>2617919472 Ga0073689_10155 Protein of unknown function (DUF2619) [pelotomaculum
Ga0073689 : Ga0073689_101]
MI LLTDKI VAGMAGLRFLSAAT EFTAAMLMLKAGRVEAAFKI NAVLALI G
PAVLLTVTSLGLI GLAGKVSATGMV I I LGVALI F I G I N K C

>2617919471 Ga0073689_10154 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
MGRDYLFYREYRKANKDEI I NFLRSRRSLLDYHPI QGGAELELKTGTVT
RYVVRDSEPKGELVLKAEKVVEKTLPFSPAGLMGELAGKNI VYGVKHNEI
REMLANPEDGLYNI RRGRSARGFR

>2617919470 Ga0073689_10153 Protein of unknown function (DUF342) [pelotomaculum
Ga0073689 : Ga0073689_101]
VDI SSGNI RFKGDVVVHGNVSEGMTI QAAGKI DI KGMVFQARI AAQGNIN
AGQNI TGSTI VAGGNSFFKSLRKI LGQLHADLAAAAVVPALARRPRME
GVKRGNWFNCWWTRNTPGCPA

>2617919469 Ga0073689_10152 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
VVGRGYI NTSI RAGGNVNI KGVFRGGEI I AGGDI FLNEAGSEMGARTFVK
TAEERKVVYKKAFFGI QI QVGDRLVSI TSQRNNI KAELEDEDGALLVNSLT
KV

>2617919468 Ga0073689_10151 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]
LSRI DAMSLI NEDI PI SVRFHFVPAI KRAYGMVNKYSYEFDWLNWPVGI D
I LGVLRVAVVEYELKKLI DRQKLPLKYI I APNAI DNCRHLVLI AKRCRLT
I SQI RSPRSI PRKAI YRTNYSLOGRQLQDFPDEFMDI NKKEEEQFYMI L
THSYSGPAPEFVSI SVPGPYVKEWLEQI DLLSEPHPVYLVEEDTLTEES
LLEFKKEVHEVLKGGKETVS

>2617919467 Ga0073689_10150 Zn-dependent peptidase ImmA, M78 family
[pelotomaculum Ga0073689 : Ga0073689_101]
VERKRSHKPNERHNTFVPERLRQARLAKGYSSTELADALGI TRQAVSRY
ELGLAVPSGEVLGKTI EI LQFPLSFFSKPVEQSHNSARVTFFRSLKSSTK
KSRESLI VRSGWVQEI YTYLERFLDFPKVNI PEPNI NKNI DELDLEDI EN
I ALAVRKAWGLGLGPI SNMVFLLEKNGALVTRTSGSTLKTDACSQWRVDR
PI VFLGSDKESAVRSRFDAAHELGHLLHMDI DQDQLSDSKI MARI EKEA
NRFAGAFLLPKESFAQEI I STSFHF I SLKKRWKVS I AAMLYRCEDLGI L
SDNQLLYLRRQMSANGYRTREPLDNELEPEKPTLLKQGI NMLI KNGVQTV
AEI I EAI KLPQI EI ENLCGLPVGTLSLGGQVI PLKI R

>2617919466 Ga0073689_10149 DNA mismatch endonuclease Vsr [pelotomaculum
Ga0073689 : Ga0073689_101]
VDNPGQVKFERDTSI MRKVHSSNTTPMTFRKALWSKGLRYKI CPADLP
GKPDVVLPSKRLAI FI DGDYWHGNQWRERNLSALEEQFGTSSKDYWLNK
I RRNMSRDCAATASLLSEGWTVLRFWSEVKKNLGKCVDLALEVARKSAM
PDPFSLATQKTFAEFFAGI GLMRMGLERQGTI SFSNDI DQQKYEMYEGH
FNGVDKHFI LGDI HQI PAESVPTVTLATASFPCNDLSVAGARNGLSGKQS
SAFWGFVRI LEEMEERRPPI VLLENVVGFLT SRKGADFKEALLALNRLGY
DVDAFI LDAARFVPSRQRLFVVGLLAGSEVWEVRETLRFYESDVRPKAL
ADFI FASPEI RWN I RHLPPQPRNSETLESI I EDI PETASEWWSPERA EYL
LNQMSPRHREI AETMI AGAEYSYGSVFRVRKQGSMAELRTDGFAGCLRT
PRGGSGROI LFKAGKGKYFARLLTPRECARLMGADDFRI TVPLNQALFGF
GDAVCVPVI EWI AKYYLNPVVNELI RGRPLRLNVKEG

>2617919465 Ga0073689_10148 protein of unknown function (DUF4928) [pelotomaculum
Ga0073689 : Ga0073689_101]
MKPKDRAI RAFKQWYDALPI HKPSGGPARGTI GAALVVLRLKGAFDLNL
DSHRAAGQSQI KGASGAAVARI LSRYGETRPF I KEGGRTNRGGPGDI GKM
LDAI GTARLDRLTVNERNEI LDELQRNGVPNAGCLRKQVQAKYRGGAQGI S
SRS

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>2617919464 Ga0073689_10147 pyrimidine operon attenuation protein / uracil phosphoribosyl transferase [pelotomaculum Ga0073689 : Ga0073689_101]
MAREKAOI LDREGI RRALTRI AHEI I ERNKGTEENLVVGI RRRGVPLAER
LAERI ROI EGRSAPVGVDI TLYRDDLGSLARRPLVRSTAI PFPVSGKRV
VLVDDVI FTGRTI RAALDAVI DLGRP KVI QLAVLVDRGHRELPI RADYI G
KNVPTSRKETVSVRLQEI DGEDRVVI LESP

>2617919463 Ga0073689_10146 aspartate carbamoyl transferase [pelotomaculum Ga0073689 : Ga0073689_101]
MGLGRKDLLGLRTVTAEEI GLI LDTAAPMKEI I KRRI KKVPTLRGRAVAT
VFYEPSTRTRTSFELAAKYL SADVSI AAATSSSVSKGESLKDTARTI TAM
GVDVVALRHPMAGAAELLAGAVDAAVI NAGDGAHEHPTQALLDLFTVREK
KGRLAGLKVAI I GDI LHSRVARSDI WGFTKMGAEVRLAGPATLI PPEI EK
TGARVCGSLEEALEGADVNNVLR I QLERQRQGLFPGLREYARLFGI NRER
LKLAAPDALVMHPGPVNRGVEI SPGVADGLQSAI NEQVTNGVAVRMALLY
LLAGGGAQSEVAD

>2617919462 Ga0073689_10145 dihydroorotase [pelotomaculum Ga0073689 : Ga0073689_101]
VKLLI KGGVVVDPVACKTAQKDI LVVDGKI ARLGANLGAGGAEVLDATGK
LVAPGLI DMHVHLREPGEAKETI YTGTRAAAGGGFTAVACMPNTNPAAD
NAALI SYI KNTAI AEGAVNVYPI GAI TRGGKGEE LAEMGDMKAAGAVAFS
DDGMPVSNAGLMRRAMQYARMLGMTI I SHCEDKDL SAGGAMHEGYVSTVL
GLKGI PAPAEVVMVARDI LLAAETGCRVHI AHVSTAGAVRLVREKAWGV
RVTAETPHHFTLTDEAVMGYDTSTKVNPP LRAAADVA AVKEGLADGTI D
VI ATDHAPHTAEEKDVEYDRAPFGLV GLETAVGLVWTEL VETGALTPLQA
VAKMSLNPARI LGI PKGALETGADADI TI I DPDNVWTVDAARFESKGRNT
PFHGRRLKGRACATVVGGRVVMRGGVMED

>2617919461 Ga0073689_10144 protein of unknown function (DUF4829) [pelotomaculum Ga0073689 : Ga0073689_101]
LI YVCTGQLSKPPVDI DALSP EQLVETYFKTLSSGNLATAEKCLSDEMKK
TI SLPDSDFKNLKSLSNLEVSPAHP I KLYGKNFTEVQVVVRYDAVYKEI F
SAPNGRQTRFI YVAKAGPGSPWRI I SI GAGP

>2617919460 Ga0073689_10143 carbamoyl-phosphate synthase small subunit [pelotomaculum Ga0073689 : Ga0073689_101]
MQAI LALENGAVFTGEAFGAAGEMWGEVVFNTGMTGYQEVLTDPSCYCGOI
VVMYPLI GNYGI MKEDFESGRSYVRGFV VREECKRPSNWRLSGTI DSFL
KKENVI GLAGI DTRALTRRLRSFGTMRGVI STGTTDVRALVKKARSCPHL
TGQELVPTVATTEI YTLPGNGRRRVLMDFGAKLNI I RCLRERGCEVVVAP
PNTPAGDI LALDPEGI VLSNGPGDPTDVPYAI ETVRALAGQKPI MGI CLG
HQI LALALGAKTYKMKFGHRGANHPVKDLETGRVYI SSHNHGFSVDEESM
KGLDI YVSHRNLNDGAVEGLKHKFLPVFSVQYHPEASPGPKDSEYI FDHF
LELMAGEGR

>2617919459 Ga0073689_10142 carbamoyl-phosphate synthase large subunit [pelotomaculum Ga0073689 : Ga0073689_101]
MPLRKG I KKVMI GSGPI VI GOAAEFDYAGTQACRSLREEGLEVVLI NSN
PATI MTDANMADRVI EPLTPGFVTRVI RREKPDGLLPTLGGQVGLNLAL
QLAEFGVLEEEGVRL LGTPLEAI KRAEDREMFKEMMRI GEVPESAI VS
TLEEAGAFAREI SLPLI VRPAYTLGGTGGGI ANTMEELRDI TSRGLKHSI
I SQVLLERC VAGWKEI EYEV MRDGADNCI TI CNMENI DPMGI HTGDSI VV
APSQTLSDKEYQMLRTASLKI I RALGI EGGCNVQFALDPDSFQYYVI EVN
PRVSRSSALASKATGYPI AKVAAKI AMGLTLDEI KNAV TGKTYACFEP SL
DYVVLKYPRWPFDKFAQGDRLGTOMKATGEVMAI NRTFEGALLKAVRSL
EI GLDHLALPGAENLSREELEARLACPDDERLFLVAEALRRGMTVERAHQ
I TGI DRFFLDKI QGI LHLEEEI RRTAGGELPAPLLERAKKYGFSDAHLAG
LTGSDRSGRLTMRKESGI LPTFKMVDTCAAEF EAETPYYYSSYDREDETA
I TPRRKVLVLGSGPI RI GQGI EFDYCSVHSVWALQEEGYEAI I VNNNPET
VSTDFDTADRLYFEPLVTENVLNI LDREKPEGVI VQFGGQTAI NLAKPLA
GAGI KI LGASVEDI DRAEDRERFDRLLI ELDI PKPPGRTAFSVEEAVVI A
SEI GFPVLVRPSYVLGGRAMEI VYNND ELLNYMASAVKVTPEHPVLVDKY
LFGKELEVDAVSDGTDVLI PGI MEHI ERAGVHSGDSTAVYPPQSLSREVK
ELVVDYTVRLARALHVKG LI NI QYVLHEGRI YVLEVNPRSSRTVPFLSKI
TGI PMVNLA TRLI MGRTLRELGYQSGLYPESRFVGVKVPVFSFAKLLQVD
I SLGP EMKSTGEVMGVD CDFKVALYKAMVAAGSMFPKKGAVLATI ADRDK
KEAVPI I KD LAELGYRI CATSGTAAALRAAGLPVEQVNKVGEGSPNI LDL
I RANKI NLVI NTLTKGAHQRDGFRI RRAAVEYGVPCLTSLDTTRVI LEV

Table S2

LAENKGGGDSGLVPLQEYLR

>2617919458 Ga0073689_10141 dihydroorotate dehydrogenase electron transfer subunit [pelotomaculum Ga0073689 : Ga0073689_101]
LSLLVDVRLTKQKEI APGYHRLTMAAPAVTEAARPGQFLHVRCGNTLDPL
LRRPVS I HTVDRARGEVTLLYRAAGRG TALLAGKKKGEAI SI LGPLGRGF
TLPGNNGKVAVVAGGI GI APLYFLLQVLGERNI HAAVFWGAATEEQLFSA
WKREKTGGKTI RTRHFPI I QEMEELGHQVVI ATDDGTAGFPGMVTELFEL
CLRDPSGGNI PVDSSGDAAPVPEFGTDRWPPGLVYGCGRGMLKNLCGI
I GRLGI PGEVSLEERMGCGVGACLSACKTGDRGGFAYRRACVDGPVFP
AGEVIWE

>2617919457 Ga0073689_10140 dihydroorotate dehydrogenase (NAD⁺) catalytic subunit [pelotomaculum Ga0073689 : Ga0073689_101]
MSGKTGGKSGGPALAVNI GGVKMKNPVT CASGTGFGGPEYAPYI DLNRL
GAI VVKGTTLLESRTGNPTPRLVETPAGVLNSI GLQNP GADRFI EEALPYL
ACFDLPVI VNI AGD TVEDYARLAARLD RAGGVAGLEVNI SCPNVKKGGMQ
FGSDPATAVEVTRAVKENTALPVI VKLSPNVT SI VAVAVRVAEAGADALS
MI NTL LGMAI DI RTRRP LLGNVMGGLSGPAVRPVAVRAVWQVYREVRPI
I GMGGI TCAEDAI EFI LAGATAVAVGTANFI NPRATMEVLEGI EKYLAEN
GI SDI NELVGAAQREGRL

>2617919456 Ga0073689_10139 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]
MTDGERI KEADMAI TAGD TDGI I LEKNEKDCKMFMKDGAGN

>2617919455 Ga0073689_10138 orotidine-5'-phosphate decarboxylase [pelotomaculum Ga0073689 : Ga0073689_101]
MFVFKNPLI VALD VDTGEEAAGLVDGLGPYAGGFKVGMQLYYAGPEAVR
KLREKNVPFFVDLKLHDI PNTVAGAARALTRLGASI LNVHAAGGGAMMRA
AAEAARDEAAKAGI HRPLVAVTVLTSI DQEVFNQEVGI GGPI QDRVVAW
ALLAREAGLDGVVASPREI AAVREVC GPDAFI I TPGVRPAGAAKG DQKRT
MTPGEAVRLGATHLVVGRPVTAAPDPVEAAKT VLEEI SREHDNNNQNKYN
GVK

>2617919454 Ga0073689_10137 Predicted nuclease of the RNase H fold, HicB family [pelotomaculum Ga0073689 : Ga0073689_101]
VKLPVTI SPGEDGWI I VEC PVI PGC I SQKTEDEAI T NI KEAI KLCLEVR
REEGLPLTLPVREVEVAI

>2617919453 Ga0073689_10135 2-isopropylmalate synthase [pelotomaculum Ga0073689 : Ga0073689_101]
MRRLYI FDTTLRDGEQSLGI TLNVKEKLEI AGQLVKLGVDVI EAGFPASS
PGDLDAVRTI AREI KGAVI CGLSRAVERDI DCCAEALRGAEQPRI HTGI A
VSPVHMERKLRLSPDQVI EVAVAAVKHARKYVG DVEFYAEDASRGEP AFL
ARVLENI EAGATVNVNPD TVGYATPWEYGELI SYVI NHVKNI ERTVVS I
HCHNDLGMATANSLAGI KAGASQVEGAI NGI GERAGNTSLEEVVMAI YTO
RGRYGVETGI NTREI AATSRLVSRI TGVT VPAHKAI VGANAFMHASGI HQ
DGVLEKKTYYEI I EPETVGVPRNAI VLSARSGRHALKHRLEELGYKPELG
ELEAVYERFLRLADQKKEVFDEDLHTLMGYHGGESNGI VI KNI SVTTTG V
SKATATVTLELDGEEVTD AACGN GPVDAVFKAI DRLVEKPVNLEDYTLKS
VSRGSEALGDATVKVRFSESGLVVGRAI SADVI EASAKAYVSALCKI KPF
SLG

>2617919452 Ga0073689_10134 Hsp70 protein [pelotomaculum Ga0073689 : Ga0073689_101]
LSWKFWVKDKKSEADNALNSLKEQLTRMG EVM D TI NDCLTGNNSQVAEI A
VQVGI AVLKEWKGI TI KQGGFHV I I PRNTTI PVTRTDKFYTAADGQAAAS
I EI YQGEGEVWKNNHRLGEFLLEGI PPNRAGAEVI EVTYRYNLNGI LEVT
ARCMSTGKEMSVTVQDALDRDSEEA FEESKAGLEALFSSAGDELEDKEDK
EEWDSLAEI LAGEVEEEMDEDVVSPTVLHEEASRLRGRAVGPAGGMQGR L
TAPGAEGY

>2617919451 Ga0073689_10133 Tetratricopeptide repeat-containing protein [pelotomaculum Ga0073689 : Ga0073689_101]
MESGSWVRRRRKRKEKVENYYKI LGAGANASQQT I KKKYI EAVKAFPPETR
PEEFQQVRLAYETLRDPVKRSEYNLLRKFGGQVEDI MKEAYELAEAGRYG
KAKELLSRAVHVSPDNSNLRALAH I LLLTGDEPGFQECCQAALDLVPAG
MKGMI MALKARMFLEI DRAQDALGVLEE I RSLYPEQVKDMQGLYFDVYLE

Table S2

LGMKEELWEI VRSMPLDQDSQAPEDI YLFI NWI NVMI ELEKWNLLSTVQS
 RVRKFLKSI KDGEDRLMVLTAQGEHDEYYEMGRFREAEI FIDLAYFVER
 SNI FIKQORQRTQEMMRVEKELLRMQRDGEFMSLLTAYSAEFYKDFAPE
 EEIRFFRESLMDQFYQPPGVDLAFDEALAEVYLRKRYPLVYRRFQDRW
 DEIFSERVARLNREARRRLRVKP

>2617919450 Ga0073689_10132 orotate phosphoribosyl transferase [pelotomaculum
 Ga0073689 : Ga0073689_101]

MLTRDEIISI FQKTGAMLTGHFRLTSGRHSDSYFQCALVLQHPNYTGTLG
 RELAAARFAGDDVSVVI GPALGGIISYEVARALGGRSLFAERENGAMTLR
 RGFSISPGERVLVVEDVI TTGGSVREVMEVVRKLGGRVVGAGVLVDRSNG
 MVDLGV RTEALLTTEVVSYALEDCLCRQGLPAVKPGGRNV

>2617919449 Ga0073689_10131 hypothetical protein [pelotomaculum Ga0073689 :
 Ga0073689_101]

MEINGTKPVI RDSRGLSTPATVRGAAESSRCKELWLPDPGEPAKGVRVF
 SNSAGQSEGRRHHTFLPPGFTAGRPCRQSGQSSRA

>2617919448 Ga0073689_10130 Predicted component of the ribosome quality control
 (RQC) complex, YloA/Tae2 family, contains fibronectin-binding (FbpA) and DUF814
 domains [pelotomaculum Ga0073689 : Ga0073689_101]

MPFDGLVLAADVRELAEKLTGGRIERI HQPDQDDLVLVHRPGLRLRLLL
 SANARRARVHLTTTGRENPTTPPLFCMVLKHLLEGGRILGLEQPLERVL
 VIKIESRDELGFPGKEYLICEIMGKHSNIVLVEPATGIVVDGIRRYSHAV
 SRYREILPGRPYLPSPSQGKLDPLAATEEQFRACLNPLETLPDLLQR
 RFEGFSTICTREIVHRANLPLDTILDRCGDYEFRLWEALRGVAEPTRRG
 CFEPCLLTGERGEPLDFAALDIDHTGOQKKHGEMNTLLDIFFGAREIEEK
 LNRERKALAAVVDKDAARLGKKLDIYTESMDETAGLEKLRLYGELLTANL
 YRLTESATSIVLENFYEKDRPPLTILDPRTPAENARAFFKKHAKAKNT
 RRILESRI TOVREELDYLEGI RTALELAADPAGLAEIQELLEQGYLKQP
 VPAPGARKGKKEKHI PAPLSFISPDSEFIVLGKNNKQNDYLTLMKAREND
 IWLHTKDI PGAHVIIRSEGREVPATLAQAAGLAAYFSKGRGSKSVVDY
 TLKKHVRKPGGARPGMVIYDHQRTI MAAPAEGPVERFSAGEPSRSGFH

>2617919447 Ga0073689_10129 Zincin-like metalloprotease [pelotomaculum
 Ga0073689 : Ga0073689_101]

VGKEKRAGKYRPAAGKKPALTDQFEFLATSFI DEIPAKLCAELNGGFLL
 LPEVKRDGEFYIMGEYVEDGVMGCSIILYYGSFVNLLLEGSSRGEWEKELR
 ETIHELRRHLESRAGVDDLAREETALEALKNK

>2617919446 Ga0073689_10128 Enamine deaminase Rida, house cleaning of reactive
 enamine intermediates, YjgF/YER057c/UK114 family [pelotomaculum Ga0073689 :
 Ga0073689_101]

MYEARLKEMGISLPGVPKPVAAYVPAVLVDKYVYTSGQLPFAGGELRYKG
 RVGGELTESQGCEAAKICAVNCLSAVRELASLDKVERIVKVTGFVNSAL
 GFTGQPGVINASELLGEIFGEAGRHARAAGVVAELPLGAAVEVEMVVKI
 K

>2617919445 Ga0073689_10127 Ca²⁺-transporting ATPase [pelotomaculum Ga0073689 :
 Ga0073689_101]

MAGRWYALTEQIEEHFKTDGKRGLTDKEVKERAARFGPNELAKVPKAPT
 WOLFINOQKDFMVLILLAATAISGFLGEYADAVTILVIVVNAVLGFIQE
 YRAERSMEALKQMTAPEARVIRGGQERKVPAPVELAPGDIVLLEEGDRVPA
 DMRLLRTVNLEVEESTLTGESVPVKKRKETLPDRDVPPLGDTCNMAYLGTV
 VTRGRGRGLVVHTGMATEMGQIAGMIQEAGQEEPTLQRRLAQLGKGLVGF
 CLLICAVVVAVGIMRGEAYQMFLAGVSLAVAAIPEGLPAIVTVALAIGV
 QRMIRRNAIIRRLPAVETLGCATVICSDKTGTLTQNEMTVRQVVLGGDTL
 EVTGEGYDPKGEFAGEGDKQGRPFKLFMKAALCNNAVLERGGISVAGLF
 RGLTRGRPAREWSVLGDPTEGSLLVMAAKAGYWRERIETKEVRVAELPFD
 SDRKRMTVVYRDPSGKVAAYVKGAPDVIDLCTHVYKGGMAVPLTARERE
 EVLERNSSLAGRALRVLAFAYRELPAAGNFSGEAVEQRLVFLGLAGMID
 PPRPAAVKAVQTCRRAGIKVMMITGDHQITARAVGGELGILTKGDQVLTG
 ADLDRMSVEQFREVAQRVSVYARVSPKHLRIVRALKHAGHVVAAMTGDGV
 NDAPAVKEADIGIAMGITGTDVTKEASAMVLADDNFTSIVAAVEEGRGIY
 DNI RKFIRYLLSCNVGEVLTMLAVLAGLPLPLAPIQILWMNLVTDGLPA
 MALGVDPYDRDIMMRPPRHPRESVFSHGLAWRIISSGTVILGLTLLAFRT
 GLSLGDVDLARTMAFNLTFLQLFYVFTCRSEFHTILEVGLFTNPYLVGA
 VAVSAALQLAVNYAPFLRPIFHTVPLSGLHWAFLVLLIAAPTVLSTLFRH
 FGGARKKVMYLRV

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>2617919444 Ga0073689_10126 di aminopimelate epimerase [pelotomaculum Ga0073689 : Ga0073689_101]
 LRFTKVHGLGNDFI LVNCFEESVNQEDFPGLAVKMCHRHFGVGADGLVPL
 LPAAADVMMRI FNSDGSEAEACGNVI RCAAKEYLHGVVRKEKI RVETL
 AGI MVPELI VENGRLVLRVDMGEPRLERAEI PMEGPSGRVVDPELEVDG
 VSCRVTAVSMGNPHCVI FVPDVEQVPLRVVGPRLETHPVFPRKTNVEFVQ
 VLSRGEVI MRVWERGAGETMACGTGACATAVAGVLNGRTGRRVTVRLAAG
 ELI IQWAENNRVYMTGPAEEVFTGEYPY

>2617919443 Ga0073689_10125 acyl-CoA thioester hydrolase [pelotomaculum Ga0073689 : Ga0073689_101]
 MDDKGPSCNI EMEVGWDCDAAGI AYYAKYFDWFSGR I HFFKKHGLPYM
 TI FHWQNI HMVALDAGCRYKSLRTEEI I I LETVLVTLSTRTRI GFKYKI L
 KKDGVLA AEGFTTHAYVDERGKPFDLKKRHPALWEEI NDVFCGQRAIR

>2617919442 Ga0073689_10124 DNA-binding transcriptional regulator, FrmR family [pelotomaculum Ga0073689 : Ga0073689_101]
 MRNTDGDKKS I SEQPGGSGGLETPVGENI TGKQKLLQGEVLNRLKKI E
 GQVRGVYKMI EDCRSCGEI VI QLAAI RAAVNRVGVTVLACHMADKMEKDI
 LEGQDTGESLNEFMSLFKKFS

>2617919441 Ga0073689_10123 4Fe-4S binding domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_101]
 MI RELKMRRRKLSLTLVGLPLVI I GGWFYPLLGFLLFGCMI GAVGVALF
 KGRAWCDDMCPRGSSFFDLVFSKI SPKKQI PPI LRTRAFRTFMLGLI I TVL
 GGQLYLAWGDPQRMGLAMVRVLTVTTVAGI ALALLYHPRTWCHI CPMGMT
 GNWVSRGKQPLAI NRSCVSKI CAKACPMQLKPYEFAPGGVMGDRDCI KC
 SSCVASCPKKALSFN EEGKSSPKKI A

>2617919440 Ga0073689_10122 DNA-binding transcriptional regulator, FrmR family [pelotomaculum Ga0073689 : Ga0073689_101]
 LRKKCNSGPPKGI DNSGAGLPATGEQI NI TGRNQVVQDGI LGRLKKI EGQ
 VRGVYKMI EDCRSCGEVI QLAAI KAAVNRVGATVLVCHMAERLESDLLE
 GKDI KESLADFTVLLKKFS

>2617919439 Ga0073689_10121 TusA-related sulfurtransferase [pelotomaculum Ga0073689 : Ga0073689_101]
 MTTEELKNI KADKVV DARGI SCPGPI LAACKAVVDVKAGQVMEI LATDSG
 AQKDI PAWAKKMGHEFLGVI DEAGTYKLYVKRLK

>2617919438 Ga0073689_10120 Coenzyme F420-reducing hydrogenase, delta subunit [pelotomaculum Ga0073689 : Ga0073689_101]
 MAGQVKEGKDLSPKI LAFSTNNI SDPGI DLAGSSHQHYPPSVLVI SMPCT
 SGI KPEWI LYAVEKFGDFVFLAADGEECAYLPDCAERTSHI VQEAQDLLA
 QKGYEPQRLRMTAI CSVCAEPFTNHMKEFSEALKKLG PARKG

>2617919437 Ga0073689_10119 heterodisulfide reductase subunit A [pelotomaculum Ga0073689 : Ga0073689_101]
 MNYDLLVVGSGI SGMESALKLGDMGYKVLVVEKEASVGGKMI LLSKVFP
 LDCASCI STPKMVATVHHPN I DVM I YSEVEE I KRI KNGNFKARVRRKPTF
 I NQALCTGCRQCEMTCNVAVPDQFNFDLVARRAAYI PFPQAVPKKAVI ER
 EGASPCSFTCPAGI KAHGYTALARGGKFDEAFNLVLENAPLVGSLGRACY
 APCEGECTRGALEGPVPI RRI KRFI ADRIYKKHARPEYGVPAERSDKKVA
 VVGAGPAGLTAAFFLTQKGYPTI FEAAPQPGGMLRLAI PAYRLPKDVVD
 RDI ENV TALGVEI KTGVRVENLEELKNEGFEAI FVAAGTHGNRRLOVEGE
 DLEGVTGALDFLRDNLGKKI SLKGKTVLVVGGGNVAVDSARVAVRLGAG
 KVI VQYRRSRAEMPAYAREI EASEKEGI EFQYLRLPVRFTGKGGKLN GVE
 SVRMELGEPDAGRRRMPVKGESRI AVDLVI TAVGLEPVLKPLAKQLR
 LNKNGTI QVNPETLQTPAPYI FAGGDAVTGPSMI VKAVGQGRRAAFYI DR
 YLRGEELAGVEFDHKLPPVDKAKVI ARQESYRTLPPVNGELLQEKVRDF
 AETEPPLTEEEVRY SAGRLDCGVCSECRQCNTCPAKAVELGMKEEERE
 FEVKS VI VSTGFKLFSAHQKPQYGYGKYKNVI TGMQMDRLLAPTRPYNTI
 LRPYDGKVPENI AYVLCAGSRDQLVDNPLCSRVC CMYSVKQNQLI MGALP
 LADVT VYYYVDI RAFGKGYEEFYRQAGDMGANFI KGRVARI EEGENGNTL
 YYEDI DNGGKLAAA EHDLVVLSVGLI PNTEAQNLFMGENLELDEYFFVRE
 VDEDVNPGRTSI DGVFVAGTASGARDI PDSI LHAGAAAAQAAAYVERARV
 RK

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>2617919436 Ga0073689_10118 heterodisulfide reductase subunit A [pelotomaculum Ga0073689 : Ga0073689_101]

MSDRRI GVHI CHCGNI SDYVDVAGVAKAVKDEPGVVVAKTAMFTCSDAT
QOEI I QDI REQNLDGLVVASCPKLHLHTFRDVARRAGLNPYQYTQVNI R
EQCSWTHTDHREATAKAI RLI RGGI ARTNLTI PLKPFKI DTVPRVLI VG
AGI AGLRAAVGLADI GMAVFLVERALAVGGWVSFRGSMYPNGKNGRKLID
QLI EEVWKRDKI TVFTGAELVEKSGNI GNFEAKI RTGGRDEI NI NVGSI I
VATGFDAYQPREGEYGYSLDGVVTLPEFKEMLDGAAGGLTRNGKAVKDI V
YI YCVGSRQSDMADANRYCSRYCCNATVHASTVAFEKSPGLHQFHLFKD
MRTYGRFELLYNEALKRGATFLKFDDSEPPMVERGENGRKLVTVKDLLTF
GEEI EI GADLVVLATGMAPGKNEKLEI LKLPGLGRDRFFNEI HPKLRPVE
TVVDGVYI CGACQGPKNSSSVASALAAVTRSASI LKKGYVELEPLI AVV
DPERCAWCGQCEKTCPYAAI EKDRYREKEVAKVNEALCKGCGGCVPCPV
DALDLRGYTDGQI RSMI DGF I KEI C

>2617919435 Ga0073689_10117 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]

MNGGVRDVRVI REEMLMRDKI LAVLGEKSKTVPEI ALDLGHPSHEVI FW
VMGMRKYGHAEDELDEGYKYRAAAREGS

>2617919434 Ga0073689_10116 heterodisulfide reductase subunit C [pelotomaculum Ga0073689 : Ga0073689_101]

MATANPGFVEEI RRSDEFNASSCMNCGVCSAVCPMGI ELLPRKLFYVLL
GI KDKVLENAEVI YSCLLCKMCEVNCPAQVRI AENVRTLRYMNNKKVYKL

>2617919433 Ga0073689_10115 Fe-S oxidoreductase [pelotomaculum Ga0073689 : Ga0073689_101]

LHMLPLVGDITGI LADNLKI RKSVLPI PARSGTEWAKGLNLPRGGETVLY
TGMMCQLI PYVDVANKAQEKI EDSWLANYI GLGRAVNKVI NI SGFMASPP
KOMLESYNKI LVNI ALLLKEAGVEFGCLYEDDLYSYGALVYDLGMDDVLEA
HARKVDEI FKKYGVKNVI TVDPHTTNMLRSVPSLVAGYGLEVKSYLEVL
AERHMEPKNRLDAVVAI HDSCVYARYENVLNEQRALLAKAGVTVREPAQA
GKYTYCCGGAESLFPKKARANAAKRVQLKQAAAHGVTMCPI CYMNLQK
AAGGEI HLEDI STYLVRAYCGG

>2617919432 Ga0073689_10114 Peroxiredoxin family protein [pelotomaculum Ga0073689 : Ga0073689_101]

LKKTII VFSGDLKVMMAFVI ANGAAAMGDDVTMFFTFWGLNVLRKPEKI
KTKKSFLQAMFGRMMPRGADRLGI SKMNFGGMGAKMMKLVI KQQNVSSLP
ELI QTAREQGI KMI ACTMSMDVMGI REEELMDGLEFAGVATYLGAEADSN
VNLF I

>2617919431 Ga0073689_10113 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]

MI AALPFFAPTWSSNPVLGNMI AITVI LTVAATVLLLYYRSKRIRKK

>2617919430 Ga0073689_10112 MoxR-like ATPase [pelotomaculum Ga0073689 : Ga0073689_101]

MDLFONTESI RKGLTAQGYLAERRTAATVYLAHWLQKPLLVEGPAGVGKT
GLAVALAGAMDTDLI RLQCYPLDEAKALYEWNYQKQLLYI NAGKNGETE
WEKI KKDIFSPEFLLERPLLRAFRTDRPATLLI DEVKSDDEELESFFLEA
LSDYQVSI PEMGTVPKAKHVPLAI LTSNGSRDFSALKRRCLHLYI PYPAA
EQELAI VLLKAPAI KKDLAGRLVEFVQKLRLPLKAPSI AETI DWARTM
ALMGAEFLETGLVADTLNVLLKYEQDVLKI RDKLPGLI PPEKPEERHLTG
DTGRYSAGSDDGAGAPGEEKTQPVKTRLEELLERFDF

>2617919429 Ga0073689_10111 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]

VKI EI LLTDI SRKNEALTRLAGEPGI KAGGGRLEI DGLKLEVGENYLLFT
I DRWERAEEI VPLLFSVNPASHTFRPESGLKALVTCRAKAI EDI I PGL
ASVSHDLAAGELAGDFQVTWSSHDVAVSARAGLMVQGGGLAVAKI KFTVH
ARDAEYHCRACI ELI SFKEI LKVFCREPLEAPLEPAPGPI VI EGEATVEG
NGWLEFFNARPGVPVYHARGAEELRLTFGPHDYI SFRKKGKAVGVLAHF
EDPGALTDDLAAGAAALLGLAEVKVSREI GGLPPDLRLRRELGFKLEEG
PARFVRTGEFTARYDAGRLAAVLTAEPDAPVRERLLRI YREMEELTRQ
LII YAG

>2617919428 Ga0073689_10110 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]

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LGKLAGFPGLRRAGI RVSPGETVDFLRSALLGLDREALVTAALAALAK
GETEERVTRKLFDFLYFTFSPGELAPAERVPPSVFDNPPRLAAGEFLERLA
DLRSTI RRELARCKTGAEEAAGGGGAGTGTGRGGVRPDQLPDLERAFRT
GDRGETRALAGYVI REVLEKTGADPVGYDELLRRVKVGLDWAGTVDCLEK
EDGGLPPEGGNI RDFEQI LI DELDREI RRRRPEALEEVAGRSDLAGVDF
NSLNLRQVEDI KRI VAGMARSLAARLSYRRARSRRGEVDMRRTARLAART
GGVPLI LCRRSKI PHRPELVVLCDSGSVSLCAGFMLQI YAVQERFTRV
RTFAFVDDVAEI TEFLKEGEPGEAI LRVI REARVARTPFSDYGAVWKEFC
FKYMEYLTPTKTTVLVLDARNNWRSPGLEYLEQI RDRSARI I WLNPAEAE
RWRDDSI I SLYSYCSKLFECRNLRQLAEAAARYLGKL

>2617919427 Ga0073689_1019 Hemerythrin HHE cation binding domain-containing protein [pelotomaculum Ga0073689 : Ga0073689_101]
VKWLSRFHDDHMAVVRLLPKLEGNLKDLEHGEAGVNAI WDLREFAEI I RN
VI I PHFKNEEKTVYPKASGVGEEAQKFMTGMYKEHEDLYEAFEGFFKALG
GEAGEKEATGRDKSATRI I SASVNAGREEAPKNI EKVAPVKYLDEEI NKG
EI LEYGYKI VQLLKEHI EKEETTVAELVKKTKESGRD

>2617919426 Ga0073689_1018 L-fuculose-phosphate aldolase [pelotomaculum Ga0073689 : Ga0073689_101]
MLEDFQRI GRDLFLTGLNNSHSGNLSVRRGDRI VI TRRGSMGLHLEEKDL
I ETGLEKNDGNTVLASTEI GVHRAI YRGSTLAVVHAHPVHAI ALSLMEN
EI I PVDAEGAYLLQKAPVLAVEKTI GSSEVAEKLPGLLKEHKI VVVRGHG
SFAAGQTL EEAYQWTSCLENVCRI I HLTDLRLTY

>2617919425 Ga0073689_1017 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]
LVVKTLSKI DGNVVRTFTLDNPQPVKHPI FMDYPVEGVLRVSGRDI KGSP
QVKRVTVENYKDLNKL LYNRTA

>2617919424 Ga0073689_1016 glutamate racemase [pelotomaculum Ga0073689 : Ga0073689_101]
MKEVRRLLPAEDLLYYADSANCPYGVKPKEMI RARAFAI CDFLLSRGVKL
I VVASNTTSI AALDALRERTGAPVVGVEPAVKPAVSVTRTGRVGVLATGV
TLDGERFNSLVDRFCEGVVYTPCPGLVELVEAGRWERPEAGELLGRYL
APLLARGVDTTVLGCETHYPFLRPLVEMLAGAGVRVI DTGEAVARQVVRVL
ECSDLLAPGTGRGGEQFFTSGEPKEVGQVI RLLWENPGLAVEQVKL

>2617919423 Ga0073689_1015 NADPH-dependent FMN reductase [pelotomaculum Ga0073689 : Ga0073689_101]
MTWSNKI I CLAVAGSPRRGGNTELLARRALEGAVEAGAQGEI I CLRDYHY
APCAACDGCFCKEGRCVVRDDASLI FEKI LAADRVI FAAP I FSMGLCAQAK
MLI DRSQQFWACKYVLHRPVI EDEEKRPERRGI FLSAAGAGLPGVFDGAL
RVTGYFFKI LDI KMDGAYCYPKVDRRGDI LKLPEAI TEVFEAGRKLASRR
SQGHY

>2617919422 Ga0073689_1014 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]
VPRKKYRVGDRVAI YLPDGSLLKAKI KEI I PATKSNCYLVQYNGAYALVA
ERDI I QRI

>2617919421 Ga0073689_1013 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]
MYCKDCVFFKQWKSFGAAMCEATSNPVQPLDRACESFTPKGRFNEWGEET
CGRSCL

>2617919420 Ga0073689_1012 hypothetical protein [pelotomaculum Ga0073689 : Ga0073689_101]
MGNKKI TVFSLVLF CMI I I AAFTAI I HFSWAEPTRTVQVGLLAGGRQAG
QEKLI LDAYEQALREEGFSYRPVSPGDLAEYGAAGVEERFDALVVPEYVN
SAMPEETANVI NSYVREQGGYVLLALDPASQTSGGAPRQAPLLAELAGVR
YCLSASGDQKPI YSGHWYFPSAATGREWGI TPGKLDKDNVSSYSYGKLL
FEHSQAVNVVDARVVAFDRTEGGETPVI TEKRYDSGGAAYANMPLGHYKL
RSDDSLRSVLRTFLI RHARVPRLVNSPGGGGGLVFNLHI CSGAYFRPI T
VMMMQGLFQDEL PFSI HI TAGPDTYKLGDMGFFAESKLGKRPVLEI LQN
YGEI GSHGGWVHNFFAYNLQYLPRKKALELVDWNAALAEAVTGKKVVEYS
APGGDHPFWVNRHLEEMGMKAYYYAGDTGSSPTHRLDEQYASQKMWAFP
I TPFQKFASLEEMERGHVPPAEVKRW MEDLVDFSAGERVI RMI YTHPSDT
RFCLDAI RAFEEKALSEQEGRI TVAPMSWFADFLNRHSKTVWQI KRMGR

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DYTI DLENPEGLKDI TVAVYVGGDDKNI VMGGDVKTSREDGWLYLTI TAN
HRKKHLEVRR

>2617919419 Ga0073689_1011 hypothetical protein [pelotomaculum Ga0073689 :
Ga0073689_101]

LKEWHVEDAGGGCRAFSEVLVLVCEQTGEI YSDKLPLTWNDGTSMEETC
SLMI EMMERAGVTGKDRLLVCSGNI FHTFHNWLTENGYHWGKAKI DGLAH
DTAEELFHRQVVEAGFPLDI NLKERNYREYYRAI EQWVNGDPGRQVFLKD
FAVRRKPAETRYLLKGNGSHTRTCLRCRQRI PPYNPVVVYRARENGRKI R
RYFHPACTPVEPLKSTLETITI NWDSSRI EGVI LNSHEDKRLCAVCGRP
EPGNRTFYAYLNGQVI AGHPACFKDEKSAVRGA