

			Harvesting times (see Fig. 1) and applied proteomic approaches																									
			2D DIGE										Shotgun						Membrane proteins						Exoproteins			
			Fold change in protein abundance (as compared to 30 h)										Identification metascors						Identification metascors						Identification metascors			
			15 h 20 h 40 h 60 h 70 h 80 h 90 h 100 h										15 h 20 h 30 h 40 h 60 h 70 h 80 h 90 h 100 h						13 h 18 h 25 h 30 h 40 h 51 h 60 h 70 h 80 h 95 h						13 h 30 h 50 h 80 h			
Accession (PGA1_)	Gene	Functional prediction																										
EXTRACELLULAR PROTEINS																												
RTX-/Hemolysin-type proteins																												
262p00640		Hemolysin-type calcium-binding protein repeat protein																									224	
262p01050		Hemolysin-type calcium-binding protein repeat protein																									350 295	
262p01140		Hemolysin-type calcium-binding protein repeat protein																									317	
55p00350		Hemolysin-type calcium-binding protein																									412 203 196 175	
c16980		Hypothetical protein																									255 183 156 143	
c17480		Hemolysin-type calcium-binding repeat-containing protein																									515 258 145	
c18150		Hypothetical protein																									84	
c26140		Hypothetical protein																									2057 1478 1343 464	
Proteases/peptidases																												
262p00920		Putative protease, M23 family	2.6	2.8	1.2	1.2	1.7	2.7	2.3	3.3											121 294			65 32 58 84 71 127 322 449 326 417	883 1219 1267 1080			
c08290		Putative peptidase M75											340 204			91 194 159							217 298 375 107					
c21610		Putative serralyisin	1.0	1.1	1.4	-1.5	-2.0	-2.4	-1.8	-2.4															81			
c25160		Putative peptidase, M23 family																					74					
c32810		Peptidase, M16 family											117 202 345 496 540 490 486 350 241			79			101 101 57 50 161	548 890 309								
c32820		Peptidase, M16 family											178 327 479 493 472 515 562 457 352			116 86 146 278 255 342 315 281			453 419 133									
Periplasmic solute-binding proteins																												
c02710	ugpB	sn-Glycerol-3-phosphate-binding periplasmic protein	7.6	4.6	-1.1	-1.1	1.4	1.8	3.4	2.0											416 333			59 111 222 139 237	1500 1637 1847 1216			
c07420		Extracellular solute-binding protein	3.3	2.4	-1.2	1.1	1.5	2.3	3.9	2.6											69					130 377 673 343		
c07860	aglE	alpha-Glucosides-binding periplasmic protein	7.3	5.5	2.3	1.2	1.4	1.8	10.7	2.6											401 284					940 1177 918 498		
c11570		Putative nopaline-binding periplasmic protein	2.5	1.9	-1.7	1.1	1.2	1.6	2.3	1.9											96					355 394 579 403		
c12890		Periplasmic solute-binding protein	-1.1	-1.4	-2.4	1.3	1.2	1.7	2.5	2.1											88	133	143 217 228 148 78	385 702 819 799				
c12960	dctP2	TRAP transporter, periplasmic solute-binding protein	3.1	1.5	-1.7	-1.3	-1.1	1.2	2.5	1.6															722 642 747 820			
c15890		Extracellular ligand-binding receptor	6.3	4.1	-2.2	-1.2	-1.2	1.2	2.4	1.4											393 383 132	101 148 160 187 125	49	621 799 933 726				
c27930		Putative sugar ABC transporter, periplasmic binding protein	2.1	1.6	-1.5	1.0	-1.0	1.5	2.3	1.8											130 208	191 98 143	832 1165 1160 1067					
c31410		Putative receptor family ligand-binding protein	2.3	2.3	-1.0	1.1	1.1	1.4	2.6	2.0													76 91 76	618 1045 1035 1324				
c33920	dctP8	TRAP transporter, periplasmic solute-binding protein	2.7	2.0	-1.4	1.4	1.6	1.9	2.9	2.6													108	926 1154 1121 1178				
c34050	thiB	Thiamine-binding periplasmic protein	3.5	2.7	-2.2	-1.5	-1.1	1.4	2.7	1.5											241 242 82			182 147 163	1076 1272 1183 1055			
c01980	bztA	Glutamate/glutamine/aspartate/asparagine-binding protein	2.3	2.2	-1.0	1.6	2.4	4.3	5.8	5.6											659 697 588 528 625 850 700 652 575	425 203 316 524 496 624 976 1143 1086 1235	1452 1737 1817 1469					
c16270		Putative periplasmic dipeptide transport protein	-2.1	-2.5	-2.2	2.2	2.4	2.6	2.6	2.9											339 360 260 102 283 260 200 237 125	35 93 60	1156 1321 1720 1868					
c20180	dctP5	TRAP transporter, periplasmic sol																										

[illegible]

[illegible]

Table S3 continued

			Harvesting times (see Fig. 1) and applied proteomic approaches																																									
Accession (PGA1_)	Gene	Functional prediction	2D DIGE										Shotgun										Membrane proteins										Exoproteins											
			Fold change in protein abundance (as compared to 30 h)										Identification metascoring										Identification metascoring										Identification metascoring											
			15 h	20 h	40 h	60 h	70 h	80 h	90 h	100 h		15 h	20 h	30 h	40 h	60 h	70 h	80 h	90 h	100 h		13 h	18 h	25 h	30 h	40 h	51 h	60 h	70 h	80 h	95 h		13 h	30 h	50 h	80 h								
Ser																																												
c36140	serA	D-3-Phosphoglycerate dehydrogenase	2.4	1.8	-1.2	-2.2	-2.5	-3.2	-3.2	-3.2		620	756	620	662	475	318	163	269			932	686	796	762	694	648	671	600	554	443	306												
c36150	serC	Phosphoserine aminotransferase	2.4	1.7	-1.1	1.1	1.3	1.7	2.6	1.8		181	311	220	249	343	481	249	235	106									25		79	333	54	421	538									
Cys																																												
c17690	cysE	Serine acetyltransferase											84	78											361	439	378	385	384	406	353	750												
c07640		O-acetylhomoserine / O-acetylserine sulphydrylase	-1.2	-1.2	-1.2	1.2	1.0	-1.6	-1.6	-2.3		475	610	697	818	946	954	267	113	68		124	119			72	80	159	427	622	1089	248		351										
c13950	cysK	Cysteine synthase	-1.1	1.1	1.3	-1.1	-1.4	-2.6	-2.5	-3.3		186	364	349	933	409	134	136				32							75	153	491	46		137										
Lys, Met and Thr ("aspartate" family)																																												
Lys																																												
c23510	lysC	Aspartokinase																	87			247	172	247	258	319	242	250	292	322	954	52												
c31480	asd	Aspartate-semialdehyde dehydrogenase	1.2	1.1	1.1	-1.2	-1.6	-2.9	-2.2	-3.0		250	313	476	666	606	169	161				110	125	303	182	52	110	184	189	332	437	202		163										
c28930	dapA	Dihydrodipicolinate synthase																																	113									
c36310	dapD	2,3,4,5-Tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase																																										
c36420	dapE	Succinyl-diaminopimelate desuccinylase	-1.0	1.0	1.2	-1.4	-1.5	-2.9	-3.1	-3.0																																		
Met																																												
c14560	metA	Homoserine O-succinyltransferase																									45		96	115	139	152												
c00860	patB	Cystathionine beta-lyase																				182	159	123	124																			
Thr																																												
c06310	thrC	Threonine synthase																																										
Ile, Leu and Val ("pyruvate" family)																																												
Ile, Val																																												
c08650	hom	Homoserine dehydrogenase																																										
c12350	budB	Acetolactate synthase, catabolic																																										
c20210	ilvI2	Acetolactate synthase isozyme 3 large subunit	1.6	1.3	-1.1	-1.7	-3.4	-3.7	-3.4	-4.9																																		
c20220	ilvH	Acetolactate synthase isozyme 3 small subunit																																										
c06580	ilvC	Ketol-acid reductoisomerase	1.4	1.0	-1.3	-1.1	-1.5	-3.7	-2.6	-4.2																																		
c29490	ilvD	Dihydroxy-acid dehydratase	1.0	-1.1	2.0	1.2	-1.2	-2.0	-1.4	-1.8																																		
c04020		Putative branched-chain-amino-acid aminotransferase																																										
c34950		Putative branched-chain-amino-acid aminotransferase, subunit B																																										
c34110	ilvE	Branched-chain-amino-acid aminotransferase	-1.3	-1.4	-1.5	1.0	-1.1	-1.9	-1.9	-2.2																																		
Leu																																												
c26470	leuA	2-Isopropylmalate synthase																																										
c29780	leuC	3-Isopropylmalate dehydratase large subunit	7.0	4.4	1.1	-1.1	-1.2	-1.5	-1.0	-1.6																																		
c29790	leuD	3-Isopropylmalate dehydratase small subunit																																										
c29830	leuB	3-Isopropylmalate dehydrogenase	1.2	1.0	-1.2	-1.6	-1.8	-2.7	-2.1	-2.9																																		
Aromatic amino acids																																												
Chorismate (precursor)																																												
c15860	aroH	Phospho-2-dehydro-3-deoxyheptonate aldolase	1.8	1.8	-1.2	-1.6	-2.0	-2.1	-1.7	-2.5																																		
c14100	aroB	3-Dehydroquinate synthase																																										
c35150	aroE	Shikimate dehydrogenase																																										
c14090	aroK	Shikimate kinase																																										
c04810	aroA	3-Phosphoshikimate 1-carboxyvinyltransferase																																										
Trp																																												
c04870	trpB	Tryptophan synthase beta chain																																										
c04930	trpA	Tryptophan synthase alpha chain																																										
c16860	trpE	Anthranilate synthase component 1																																										
c16890	trpD	Anthranilate phosphoribosyltransferase																																										
c16910	trpC	Indole-3-glycerol phosphate synthase	-1.9	-1.5	1.1	1.2	1.4	1.4	1.3	1.4																																		
Tyr, Phe																																												
c25230	tyrC	TyrC protein																																										
c00590		Chorismate mutase																																										
c30200		Prephenate dehydratase																																										
c29420	tyrB	Aromatic amino acid aminotransferase	-1.2	-1.1	1.1	-1.1	-1.2	-1.7	-1.6	-1.9																																		
Selenocysteine																																												
c18960	serS	Seryl-tRNA synthetase	1.1	1.3	-1.3	-1.1	-1.3	-2.2	-2.3	-2.3																																		

			Harvesting times (see Fig. 1) and applied proteomic approaches																																		
			2D DIGE		Shotgun										Membrane proteins										Exoproteins												
			Fold change in protein abundance (as compared to 30 h)										Identification metascors										Identification metascors										Identification metascors				
			15 h	20 h	40 h	60 h	70 h	80 h	90 h	100 h	15 h	20 h	30 h	40 h	60 h	70 h	80 h	90 h	100 h	13 h	18 h	25 h	30 h	40 h	51 h	60 h	70 h	80 h	95 h	13 h	30 h	50 h	80 h				
Accession (PGA1_)	Gene	Functional prediction																																			
Amino acid decarboxylase (biogenic amine formation)																																					
c03800		Putative lysine/ornithine decarboxylase	54																																		
Nucleotide biosynthesis																																					
Purine nucleotides																																					
c10810	<i>purF</i>	Amidophosphoribosyltransferase	75																																		
c23610	<i>purD</i>	Phosphoribosylamine-glycine ligase	100 113 123 85																																		
c13420	<i>purQ</i>	Phosphoribosylformylglycinamide synthase 1	1.1	1.1	-1.0	-1.4	-1.5	-2.0	-2.2	-2.0	122 84 156 100																										
c17120	<i>purL</i>	Phosphoribosylformylglycinamide synthase 2	76 170 190 166 152																																		
c13260	<i>purM</i>	Phosphoribosylformylglycinamide cyclo-ligase	262 285 456 381 369 331 112																																		
c24860	<i>purE</i>	Phosphoribosylaminoimidazole carboxylase catalytic subunit	155 153 251 262 237 271 256 172 180																																		
c24870	<i>purK</i>	Phosphoribosylaminoimidazole carboxylase ATPase subunit	-1.1	1.0	-1.1	-1.2	-1.2	-1.3	-1.3	-1.5	81																										
c13400	<i>purC</i>	Phosphoribosylaminoimidazole-succinocarboxamide synthase	109 139 164 68 127 132 99																																		
c13410	<i>purS</i>	Phosphoribosylformylglycinamide (FGAM) synthase	180 185 272 259 115 105 165																																		
c18780	<i>purB</i>	Adenylosuccinate lyase	1.0	1.0	-1.5	-1.2	-1.1	-1.2	-1.1	-1.3	178 377 344 426 449 218 75																										
c32860	<i>purH</i>	Bifunctional purine biosynthesis protein	-1.2	-1.2	1.1	-1.4	-1.9	-3.9	-4.2	-5.5	288 393 686 565 401 330 164 122																										
c23820	<i>purA</i>	Adenylosuccinate synthetase	178 293 415 529 439 308 149 67																																		
c18780	<i>purB</i>	Adenylosuccinate lyase	1.0	1.0	-1.5	-1.2	-1.1	-1.2	-1.1	-1.3	178 377 344 426 449 218 75																										
c01870	<i>adk1</i>	Adenylate kinase	1.0	1.1	-1.2	1.0	1.2	1.5	1.4	1.7	158 336 276 379 353 399 332 294 154																										
c15220	<i>guaB</i>	Inosine-5'-monophosphate dehydrogenase	-1.2	-1.1	-1.7	1.1	1.3	2.1	2.0	1.7	57 391 519 312 519 478 296 153 129																										
c14610	<i>guaA</i>	GMP synthase	122 166 165 208																																		
c15830	<i>gmK</i>	Guanylate kinase	-1.2	-1.0	1.1	-1.1	-1.0	1.3	1.5	1.6	64																										
c06940		Putative adenosylcobalamin (B ₁₂)-dependent ribonucleotide reductases	153																																		
c19750	<i>ndk</i>	Nucleoside diphosphate kinase	212 224 239 206 216 226 187 186 176 40 66 118 77 335 142 230																																		
Pyrimidine nucleotides																																					
c06670	<i>carA</i>	Carbamoyl-phosphate synthase small chain	102 86 152																																		
c24560	<i>carB</i>	Carbamoyl-phosphate synthase large chain	-1.0	-1.2	-1.1	-1.3	-1.8	-4.7	-5.7	-11.5	180 549 394 442 68																										
c03060	<i>pyrB</i>	Aspartate carbamoyltransferase	83																																		
c03020	<i>pyrC1</i>	Dihydroorotase	1.0	1.1	-1.1	-1.2	-1.3	-2.0	-1.8	-2.0	64 148 272 105																										
c10900		Putative orotate phosphoribosyltransferase	141 240 220 196 228 204 89 109																																		
c32450	<i>pyrF</i>	Orotidine 5'-phosphate decarboxylase	113 115 114 160																																		
c14210	<i>pyrH</i>	Uridylate kinase	183 273 315 430 292 330 256 77 118																																		
c04820	<i>cmk</i>	Cytidylate kinase	565 469 447 999 436 456 738 563 664 1103																																		
c23900	<i>pyrG</i>	CTP synthase	1.2	1.1	1.1	-1.6	-1.9	-3.2	-2.2	-3.8	70 74 58 50																										
c11200		Putative deoxycytidine triphosphate deaminase	237 226 195 154 155 93 168 98 135 33																																		
c21180	<i>thyA</i>	Thymidylate synthase	74 72																																		
c08010		Putative thymidylate kinase	95																																		
Glucose catabolism																																					
Glucose activation																																					
c05420	<i>glk</i>	Glucokinase	154 226 271 256 297 281 177 69 52 60 403 339 264 527 73 57																																		
Entner-Doudoroff pathway																																					
c15160	<i>zwf1</i>	Glucose-6-phosphate 1-dehydrogenase	259																																		
c15170	<i>pgl</i>	6-Phosphogluconolactonase	31																																		
c27980	<i>pgi</i>	Glucose-6-phosphate isomerase	-1.2	-1.1	1.1	-1.4	-1.7	-1.6	-1.7	-2.1	235 251 290 451 369 181 125 30 118 566 665 1227 444 231																										
c27990	<i>zwf2</i>	Glucose-6-phosphate 1-dehydrogenase	-1.3	-1.5	1.5	2.0	2.0	1.9	1.8	2.0	212 592 688 956 889 617 346 199 140 115 85 12																										

			Harvesting times (see Fig. 1) and applied proteomic approaches																																	
			2D DIGE										Shotgun										Membrane proteins										Exoproteins			
			Fold change in protein abundance (as compared to 30 h)										Identification metascors										Identification metascors										Identification metascors			
			15 h	20 h	40 h	60 h	70 h	80 h	90 h	100 h	15 h	20 h	30 h	40 h	60 h	70 h	80 h	90 h	100 h	13 h	18 h	25 h	30 h	40 h	51 h	60 h	70 h	80 h	95 h	13 h	30 h	50 h	80 h			
Accession (PGA1_)	Gene	Functional prediction																																		
Pyruvate dehydrogenase complex																																				
c17550	<i>pdhA</i>	Pyruvate dehydrogenase E1 component alpha subunit	-1.6	-1.4	-1.1	1.5	1.3	-1.0	-1.0	-1.1	79	215	245	188	422	341																				
c17560	<i>pdhB</i>	Pyruvate dehydrogenase E1 component beta subunit	-1.6	-1.4	-1.2	1.4	1.6	1.9	1.7	1.8	381	518	606	654	816	735	731	480	477		279	204	200	262	379	438	631	692	980	1604						
c17570	<i>pdhC</i>	Dihydrolipoylysine-residue acetyltransferase component of pyruvate dehydrogenase complex									311	509	591	750	707	694	766	425	537			77	112	30				109	292	559						
c17390	<i>lpdA2</i>	Dihydrolipoyl dehydrogenase	-2.5	-2.0	-1.0	2.6	2.5	2.2	2.2	2.3	181	533	586	801	1010	752	541	356	170		922	918	961	784	632	699	763	1014	1046	1669	180	82	336	393		
TCA cycle																																				
c16970	<i>glitA1</i>	Citrate synthase	1.1	1.1	1.1	-1.6	-1.7	-2.7	-3.4	-4.8	284	308	210	205	331	139																				
c18830	<i>acnA</i>	Aconitate hydratase	1.0	-1.1	-1.1	-1.3	-1.8	-3.6	-2.8	-4.6	369	616	781	1031	813	602	258	311	168		48					59	230	213	502	677		707		420		
c28340	<i>icd</i>	Isocitrate dehydrogenase [NADP] complex	1.3	1.3	-1.1	-1.8	-2.0	-4.5	-3.5	-5.2	710	1005	1030	1184	1037	775	405	204	165													593		188		
c03590	<i>sucB</i>	2-Oxoglutarate dehydrogenase E1 component									340	420	620	781	934	829	592	375	229		885	630	545	584	555	606	640	803	700	1494						
c03600	<i>sucA</i>	Dihydrolipoyl dehydrogenase 2									82	184	179	179	482	170					336	270	434	553	759	634	431	744	539	1707						
c03550	<i>lpd2</i>	Succinyl-CoA ligase [ADP-forming] alpha subunit	-2.9	-2.1	-1.8	2.0	2.0	1.4	1.3	1.5											38															
c03610	<i>sucD</i>	Succinyl-CoA ligase [ADP-forming] beta subunit	-1.6	-1.3	-1.4	-1.1	1.0	1.1	-1.0	1.0											108	83	68	74	78	94	168	146	265	618		207	79	182		
c03630	<i>sucC</i>	Succinate dehydrogenase cytochrome <i>b</i> ₅₅₈ subunit	-1.0	1.0	-1.2	-1.4	-1.6	-2.5	-2.2	-3.5	477	610	831	812	842	800	551	231	144		214	126	133	114	206	194	233	327	440	1113		226	108	433		
c03740	<i>sdhC</i>	Succinate dehydrogenase hydrophobic membrane anchor subunit																			59	30	89	59	63											
c03750	<i>sdhD</i>	Succinate dehydrogenase flavoprotein subunit																																		
c03760	<i>sdhA</i>	Succinate dehydrogenase iron-sulfur subunit	1.1	-1.0	1.1	-1.8	-2.6	-3.6	-4.8	-5.1											65	29	476	857	834	965										

Table S3 continued

			Harvesting times (see Fig. 1) and applied proteomic approaches																																			
Accession (PGA1_)	Gene	Functional prediction	2D DIGE								Shotgun										Membrane proteins										Exoproteins							
			Fold change in protein abundance (as compared to 30 h)								Identification metascores										Identification metascores										Identification metascores							
			15 h	20 h	40 h	60 h	70 h	80 h	90 h	100 h	15 h	20 h	30 h	40 h	60 h	70 h	80 h	90 h	100 h	13 h	18 h	25 h	30 h	40 h	51 h	60 h	70 h	80 h	95 h	13 h	30 h	50 h	80 h					
c26770	trpS	Tryptophanyl-tRNA synthetase	-1.0	-1.0	-1.4	-1.5	-1.6	-1.9	-1.6	-2.1	114	168	267	332	108	179	163											47	76	215								
c01510	fusA	Elongation factor G	1.1	-1.0	-1.0	-1.1	-1.7	-4.8	-3.7	-5.3	1031	1415	1430	1378	1589	1075	493	484	299		2967	2560	2009	2504	2035	1867	1662	1884	1602	2065		1338		773				
c01320	tuf1	Elongation factor Tu	-1.1	-1.0	-1.0	-1.4	-1.8	-3.4	-3.0	-3.4	1311	1614	1685	1797	1724	1557	1202	927	803		1275	991	985	1131	1358	1413	1720	1865	1740	2285		874	293	928	239			
Stringent response																																						
c01010	spoT	Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase																					571 724 862 619 407 295 344 275 225															
Clp-dependent protein degradation																																						
c12520	clpP	ATP-dependent Clp protease	-1.6	-1.4	-1.1	1.4	1.8	2.4	2.4	2.7	141	264	295	454	319	307	241	141	203		215	214					76		71	191								
c12530	clpX	ATP-dependent Clp protease ATP-binding subunit											377	456	263	317	61					474	276	164	159	141	119	151	155	195								
General stress response																																						
262p00250		Ferritin-like protein (DSP-like)	-4.3	-2.8	-1.2	2.3	3.4	4.2	3.9	4.5				205	166	288	393	326	235	203				58			52											
c19110	sodB	Superoxide dismutase	-1.7	-1.5	-1.2	1.5	1.7	2.1	1.7	2.1		131	215	222	201	264	236	100	130										37				57	143				
c24920	groL	60 kDa Chaperonin	-1.6	-1.6	-1.9	2.5	2.9	4.1	4.2	4.8	1940	2549	2675	2539	3022	3291	2960	2360	2320		1336	777	984	1037	978	1151	1214	1306	1283	2317		991	509	605	198			
c29670	ibpA2	Small heat shock protein	1.4	1.4	-1.8	1.0	1.7	2.2	2.3	2.1	125	224	134	172	269	382	255	230	225		136	116					32	50	122									
c07120		Putative universal stress protein	-1.4	-1.0	1.1	1.2	1.7	3.0	2.3	3.3	196	281	294	451	299	346	320	329	146				100	112			112		134									
													Fold change: < -5.0 < -1.5 > 1.5 > 1.5										Metascore: < 200 < 500 > 500 > 1000															