

sp P02452 CO1A1_HUMAN	RGPPGSAGAPGKDGLNGLPGPIGPPGPRGRTGDAGFVGPPGPPGPPGPPGPPSAGFDFS	1200
sp P11087 CO1A1_MOUSE	RGPPGSAGSPGKDGLNGLPGPIGPPGPRGRTGDSGPAGPPGPPGPPGPPGPPSGGYDFS	1189
	*****:*****:*.*****.*:****	
sp P02452 CO1A1_HUMAN	LPQPPQEKAGHDGGYYRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCR	1260
sp P11087 CO1A1_MOUSE	LPQPPQEKSDGGYYRADDANVVRDRDLEVDTTLKSLSQQIENIRSPEGSRKNPARTCR	1249
	*****.:*****	
sp P02452 CO1A1_HUMAN	DLKMCHSDWKSGEYWIDPNQGCNLDAIKVFCNMETGETCVYPTQPSVAQKNWYISKNP	1320
sp P11087 CO1A1_MOUSE	DLKMCHSDWKSGEYWIDPNQGCNLDAIKVYCNMETGQTCVFPTQPSVPQKNWYISPNP	1309
	*****:*****:*.***** ***** *	
sp P02452 CO1A1_HUMAN	KRHVWFGESMTDGFQFEYGGQGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMD	1380
sp P11087 CO1A1_MOUSE	KKHVWFGESMTDGFPEYGESEGSDPADVAIQLTFLRLMSTEASQNITYHCKNSVAYMD	1369
	*.***** *****.:*****	
sp P02452 CO1A1_HUMAN	TGNLKKALLLQGSNEIEIRAEGNSRFTYSVTVDGCTSHTGAWGKTVIEYKTTKTSRL	1440
sp P11087 CO1A1_MOUSE	TGNLKKALLLQGSNEIELRGEGRFTYSTLVDGCTSHGTGWGKTVIEYKTTKTSRL	1429
	*****.*.*****.*****.*****	
sp P02452 CO1A1_HUMAN	DVAPLDVGAPDQEFQFDVGPVCF	1464
sp P11087 CO1A1_MOUSE	DVAPLDIGAPDQEFGLDIGPACF	1453
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CLUSTAL O(1.2.4) multiple sequence alignment

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sp|P08123|C01A2_HUMAN      MLSFVDTRTLLLLAVTLCLATCQSLQEETVRKGPAGDRGPRGERGPPGPPGRDGEDGPTG 60
sp|Q01149|C01A2_MOUSE      MLSFVDTRTLLLLAVTSLCATCQYLQSGSVRKGPTGDRGPRGQRGPFAGPRGRDGDVDPMG 60
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sp|P08123|C01A2_HUMAN      PPGPPGP-----PGFPGLGGNFAAQYDGKGVGLGPGPMGLMGPRGPPGAAGAPGQGFQ 114
sp|Q01149|C01A2_MOUSE      PPGPPGSPGPPGSPAPPGLTNFAAQYSDKGVSSGPGPMGLMGPRGPPGAVGAPGQGFQ 120
*****
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sp|P08123|C01A2_HUMAN      GPAGEPGEFGQTGPAGARGPAGPPGKAGEDGHPGKPGRPGERGVVGPQGARGFPPTGGLP 174
sp|Q01149|C01A2_MOUSE      GPAGEPGEFGQTGPAGPRGPAGSPGKAGEDGHPGKPGRPGERGVVGPQGARGFPPTGGLP 180
*****
*****

sp|P08123|C01A2_HUMAN      GFKGIRGHNGLDGLKGQPGAPGVKGEPGAENGTPGQGTGARGLPGERGRVGPAGPAGAR 234
sp|Q01149|C01A2_MOUSE      GFKGVKGHSGMDGLKGQPGAQGVKGEPGAENGTPGQAGARGLPGERGRVGPAGPAGAR 240
*****
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sp|P08123|C01A2_HUMAN      GSDGSVGPVGPAGPIGSAGPPGFPAGPGPKGEIGAVGNAGPAGPAGPRGEVGLPGLSGPV 294
sp|Q01149|C01A2_MOUSE      GSDGSVGPVGPAGPIGSAGPPGFPAGPGPKGELGPVGNPGPAGPAGPRGEVGLPGLSGPV 300
*****
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sp|P08123|C01A2_HUMAN      GPPGNPGANGLTGAKGAAGLPVAGAPGLPGPRGIPGPVGAAGATGARGLVGEPGAGSK 354
sp|Q01149|C01A2_MOUSE      GPPGNPGTNGLTGAKGATGLPGVAGAPGLPGPRGIPGPAGAAGATGARGLVGEPGAGSK 360
*****
*****

sp|P08123|C01A2_HUMAN      GESGNKGEFGSAGPQGGPPGPSGEEGKRGPNGEAGSAGPPGPPGLRGSPGSRGLPGADGRA 414
sp|Q01149|C01A2_MOUSE      GESGNKGEFGSVGAQQGPPGPSGEEGKRGSPGEAGSAGPAGPPGLRGSPGSRGLPGADGRA 420
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sp|P08123|C01A2_HUMAN      GVMGPPGSRGASGPAGVVRPNGDAGRPGEPLMGPRGLPGSPGNIGPAGKEGPVGLPGID 474
sp|Q01149|C01A2_MOUSE      GVMGPPGNRGSTGPAGIRGPNGDAGRPGEPLMGPRGLPGSPGNVGPSPGKEGPVGLPGID 480
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sp|P08123|C01A2_HUMAN      GRPGPIGPAGARGEPNIGFPGPKGFTGDPGKNGDKHAGLAGARGAPGPDGNNGAQGFP 534
sp|Q01149|C01A2_MOUSE      GRPGPIGPAGPRGEAGNIGFPGPKGPSGDPGKPGERGHPLAGARGAPGPDGNNGAQGFP 540
*****
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sp|P08123|C01A2_HUMAN      GPQGVQGGKGEQGGPPGPFQGLPGSPGAGEVVGKPGERGLHGEFGLPGPAGPRGERGPP 594
sp|Q01149|C01A2_MOUSE      GPQGVQGGKGEQGPAGPPGFQGLPGPSGTTGEVVGKPGERGLPGEFGLPGPAGPRGERGTP 600
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sp|P08123|C01A2_HUMAN      GESGAAGPTGPIGSRGPSGPPGPDGNKGEPGVVGAVGTAGPSGPGSLPGERGAAGIPGGK 654
sp|Q01149|C01A2_MOUSE      GESGAAGPSGPIGSRGPSGAPGPDGNKGEAGAVGAPGSAGASGPGGLPGERGAAGIPGGK 660
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sp|P08123|C01A2_HUMAN      GEKGEPLRGEIGNPGRDGARGAPGAVGAPGAGATGDRGEAGAAGPAGPAGPRGSPGER 714
sp|Q01149|C01A2_MOUSE      GEKGETGLRGDTGNTGRDGARGIPGAVGAPGAGASGDRGEAGAAGPSGAPGPRGSPGER 720
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sp|P08123|C01A2_HUMAN      GEVGPAGPNGFAGPAGAAGQPGAKGERGAKGPKGENGVVGPVGAAGPAGPNPGPPGA 774
sp|Q01149|C01A2_MOUSE      GEVGPAGPNGFAGPAGAAGQPGAKGEKGTGPKGENGIVGPTGSVGAAGPSGPNPGPV 780
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sp|P08123|C01A2_HUMAN      GSRGDGGPPGMTGFPGAAGRTGPPGPSGISGPPGPPGAGKEGLRGRDQGPVGRGTGEV 834
sp|Q01149|C01A2_MOUSE      GSRGDGGPPGMTGFPGAAGRTGPPGPSGIAGPPGPPGAGKEGIRGPRDQGPVGRGTGET 840
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sp|P08123|C01A2_HUMAN      GAVGPPGFAGEKGPSGEAGTAGPPTPGPQGLLGAPGILGLPGSRGERGLPGVAGAVGEP 894
sp|Q01149|C01A2_MOUSE      GASGPPGFVGEKGPSGEPGTAGAPGTAGPQGLLGAPGILGLPGSRGERGLPGIAGALGEP 900
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sp|P08123|C01A2_HUMAN      GPLGIAGPPGARGPPGAVGSPGVNAPGEAGRDGNPGNDGPPGRDGPQGHKGERGYPGNI 954
sp|Q01149|C01A2_MOUSE      GPLGISGPPGARGPPGAVGSPGVNAPGEAGRDGNPGSDGPPGRDGPQGHKGERGYPGSI 960
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sp|P08123|C01A2_HUMAN      GPFVGAAGAPGPHGPVGPAGKHGNRGETGPSGVPVGPAGAVGPRGPSGPPQGIKGDKEPEK 1014
sp|Q01149|C01A2_MOUSE      GPTGAAGAPGPHGVSVPAGKHGNRGEPGAGSVGPVGPAGVGPVGPAGVGPVGPVGPVGP 1020
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sp|P08123|C01A2_HUMAN      GPRGLPGLKGHNGLQGLPGIAGHHGDQAGPSVGPAGPRGPAGPSGPGAKDGRTGHPGTV 1074
sp|Q01149|C01A2_MOUSE      GHRGLPGLKGYSGLQGLPGLAGLHGDQAGPVPVGPAGPRGPAGPSGPGVGDGRSGQPGPV 1080
*****
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sp|P08123|C01A2_HUMAN      GPAGIRGPQGHQGPAGPPGPPGPPGPPGVSGGGYDFGYDGFYRADQPRSAFSLRPKDY 1134
sp|Q01149|C01A2_MOUSE      GPAGVRGSQGSQGPAGPPGPPGPPGPPGVSGGGYDFGEGDFYRADQPRSQPSLRPKDY 1140
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sp|P08123|C01A2_HUMAN      VDATLKSLNNQIETLLTPEGSRKNPARTCRDLRLSHPEWSSGGYYWIDPNQGCTMDAIKVY 1194
sp|Q01149|C01A2_MOUSE      VDATLKSLNNQIETLLTPEGSRKNPARTCRDLRLSHPEWNSDYWIDPNQGCTMDAIKVY 1200

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sp|P08123|CO1A2_HUMAN      CDFSTGETCIRAQPENIPAKNWYRSSKDKKHVWLGETINAGSQFEYNVEGVTSKEMATQL1254
sp|Q01149|CO1A2_MOUSE     CDFSTGETCIIAQPVNTPAKNSYSRAQANKHVWLGETINGGSQFEYNVEGVSSKEMATQL1260
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sp|P08123|CO1A2_HUMAN      AFMRLANYASQNITYHCKNSIAYMDEETGNLKKAVILQGSNDVELVAEGNSRFTYTVLV1314
sp|Q01149|CO1A2_MOUSE     AFMRLANRASQNITYHCKNSIAYLDEETGSLNKAVLLQGSNDVELVAEGNSRFTYSVLV1320
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sp|P08123|CO1A2_HUMAN      DGCSKKTNEWGKTIIEYKTNKPSRLPFLDIAPLDIGGADQEFFVDIGPVCFK      1366
sp|Q01149|CO1A2_MOUSE     DGCSKKTNEWGKTIIEYKTNKPSRLPFLDIAPLDIGGADQEFRVEVGPVCFK      1372
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