<html><head><style type="text/css"></style></head><body>CLUSTAL 2.1 multiple sequence alignment

humanDPAGT1	PWAFSELPMPLLINLIVSLLGFVATVTLI <mark>P</mark> AFRG <mark>H</mark> FIAARLCGQDL	46
mouseDPAGT1	PWAFPELPLPLPLLVNLIGSLLGFVATVTLI <mark>P</mark> AFRS <mark>H</mark> FIAARLCGQDL	48
zebrafishDPAGT1	PSPIPVVP-LIINCCMSALGCIATVKLI <mark>P</mark> AFKE <mark>H</mark> FISARLYGMDL	44
celegansDPAGT1	<mark>LTYIPIFIARKMYGNDQ</mark>	41
drosophilaDPAGT1	<mark>PRFREMFIKANLFGNDLBSGVA-IAINAAISGAAYCMTVRMI</mark>	41
yeastDPAGT1	MLRLFSLALITCLIYYSKNQGPSALVAAVGFGIAGYLATDMLI <mark>P</mark> RVGK <mark>S</mark> FIKIGLFGKDL	60
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humanDPAGT1	NKTSRQQIPESQGVISGAVFLIILFCFIPFPFLNCFVKEQCKA	89
mouseDPAGT1	NKLSQQQIPESQGVISGAVFLIILFCFIPFPFLNCFVEEQCKA	91
zebrafishDPAGT1	NKTTKKEVPESQGVISGTVFLIILFLFIPVPFLQCFMGEKCQR	
celegansDPAGT1	CKVSNAPVPEPMGVICAAVYLIVMFMFIPFPFLEWKGQSE	
drosophilaDPAGT1	CKKDKPQVPESFGVLIGCVFLVSLFLFIPIPFAFDEAAATDAITGGKPDT	91
yeastDPAGT1	SKPGRPVLPETIGAIPAAVYLFVMFIYIPFIFYKYMVITTSGGGHRDVSVVEDNGMNSNI	
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humanDPAGT1	FPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLPTAASLPLLMVYFTNFGNTTI	149
mouseDPAGT1	FPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLPTAASLPLLMVYFTNFGNTTI	151
zebrafishDPAGT1	FPHNEFVQLIGALLAICCMIFLGFADDVLNLRWRHKLLLPTMASLPLLMVYFTNFGNTVI	147
celegansDPAGT1	FPYEKLLALLSGLISISTAILLGFADDMLDLKWRHKLLFPTLSSLPLLMVYYVSGNSTTV	
drosophilaDPAGT1	FPHDKFVELIAALLSICCMIFLGFADDVLDLRWRHKLLLPTIATLPLLMVYYVNYNSTTV	
yeastDPAGT1	FPHDKLSEYLSAILCLESTVLLGIADDLFDLRWRHKFFLPAIAAIPLLMVYYVDFGVTHV	
yeasesineri	**:.:: ::::::::::::::::::::::::::::::::	100
humanDPAGT1	VVPKPFRPILGLHLDLGILYYVYMGLLAVFCTNAINILAGINGLEAGQSLVISA	203
mouseDPAGT1	VVPKPFRWILGLHLDLGILYYVYMGLLAVFCTNAINILAGINGLEAGQSLVISA	
zebrafishDPAGT1	VVPKPFRLLLGMHLDLGILYYVYMGMLAVFCTNAINILAGINGIESGOALFISG	
celegansDPAGT1	IVPTIVRHLVQPIVLLPVTINISFIYYIFMGMVIVFCTNAINILAGINGLESGQSLVISA	
drosophilaDPAGT1	IMPNFARNLIGTSLNIGALYYVFMGMLAVFCTNAINILAGINGLEVGQSFIIAG	
-	LIPGFMERWLKKTSVDLGLWYYVYMASMAIFCPNSINILAGVNGLEVGQCIVLAI	
yeastDPAGT1	::* . :::: **::* : :** **:** **:** **::::	233
humanDPAGT1	SIIVFNLVELEGDCRDDHVFSLYFMIPFFFTTLGLLYHNWYPSRVFVGDTFCYF	257
mouseDPAGT1	SIIVFNLVELEGDYRDDHIFSLYFMIPFFFTTLGLLYHNWYPSRVFVGDTFCYF	259
zebrafishDPAGT1		255
celegansDPAGT1	SVCLFNFVQIFRFSAENSTGFWHHTISLYFLLPFTACTAILFYFNKYPSRVFVGDTFCYW	261
drosophilaDPAGT1	-	260
yeastDPAGT1		292
yeastDPAGTI		292
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humanDPAGT1	AGMTFAVVGILGHFSKTMLLFFMPQVFNFLYSLPQLLHIIPCPRHRIPRLNIKTGKLEMS	317
mouseDPAGT1	AGMTFAVVGILGHFSKTMLLFFMPQVFNFLYSLPQLFHIIPCPRHRMPRLNAKTGKLEMS AGMTFAVVGILGHFSKTMLLFFMPQVFNFLYSLPQLFHIIPCPRHRMPRLNAKTGKLEMS	317
zebrafishDPAGT1		315
		321
celegansDPAGT1	SGMTLAVVSILGHFSKTLMLFFVPQIINFLYSIPQLFHLVPCPRHRLPKYDPKTDTVSMS	321
drosophilaDPAGT1		
yeastDPAGT1	2	352
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humanDPAGT1	VCVEVEVCI CEL CELL VIA ECI OI VEVILOCEMENCEEMECNIMMI INI I I VVI CELLED	277
	YSKFKTKSLSFLGTFILKVAESLQLVTVHQSETEDGEFTECNNMTLINLLLKVLGPIHER	
mouseDPAGT1	YSKFKTKNLSFLGTFILKVAENLRLVTVHQGESEDGAFTECNNMTLINLLLKVFGPIHER	
zebrafishDPAGT1	YSKFKQKDLGKLGQLILKVAEKLWVLDVRRGQEGDDEFIECNNMTLINLVLKILGPTHER	
celegansDPAGT1	IAEFKKTDLKRLGALFIAVCKSIGMLHVKEVEKDGEIYLQINNLTIINLVLKFAGPLHEK	
drosophilaDPAGT1	TTEFRLEDLNAPGRLMVTVLRNLRLISWHTKADGVVRTNNFTLINFVLVVFGPVHER	
yeastDPAGT1		410
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NLTLLLLLQILGSAITFSIRYQLVRLFYDV 408
NLTLLLLLQVLSSAATFSIRYQLVRLFYDV 410
TLTAIMLLMQVLGSAVAFGIRYHLVRLFYDV 406
TLNDVLMSIQILCSLLAFFIRFYLASLFYDVVE 414
VVTQMLMGFQVLCTLIALTIRYPLANYFYAKT 409
KLCNTILKLQFCIGILALLGRHAIGAIIFGHDNLWTVR 448
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