```
CLUSTAL 2.1 multiple sequence alignment


humanDPAGT1        ---------------MWAFSELPMPL--LINLIVSLLGFVATVTLIPAFRGHFIAARLCGQDL 46
mouseDPAGT1        ---------------MWAFPELPLPLPLLVNLIGSLLGFVATVTLIPAFRSHFIAARLCGQDL 48
zebrafishDPAGT1    --------------MSPIPVVP-LIINCCMSALGCIATVKLIPAFKEHFISARLYGMDL 44
celegansDPAGT1     -----------------MSLIF-LAINGGLSAVGAVICYQLILTYIPIFIARKMYGNDQ 41
drosophilaDPAGT1   -----------------MSGVA-IAINAAISGAAYCMTVRMIPRFREMFIKANLFGNDL 41
yeastDPAGT1        MLRLFSLALITCLIYYSKNQGPSALVAAVGFGIAGYLATDMLIPRVGKSFIKIGLFGKDL 60
                                      .    .          :*          **    : * *


humanDPAGT1        NKTSRQQIPESQGVISGAVFLIILFCFIPFPF----------------LNCFVKEQCKA 89
mouseDPAGT1        NKLSQQQIPESQGVISGAVFLIILFCFIPFPF----------------LNCFVEEQCKA 91
zebrafishDPAGT1    NKTTKKEVPESQGVISGTVFLIILFLFIPVPF----------------LQCFMGEKCQR 87
celegansDPAGT1     CKVSNAPVPEPMGVICAAVYLIVMFMFIPFPF----------------LEWKGQSE--- 81
drosophilaDPAGT1   CKKDKPQVPESFGVLIGCVFLVSLFLFIPIPFAFDEAA---------ATDAITGGKPDT 91
yeastDPAGT1        SKPGRPVLPETIGAIPAAVYLFVMFIYIPFIFYKYMVITTSGGGHRDVSVVEDNGMNSNI 120
                        *   .   :**. *.:  .  *:*. :* :**. *                     :


humanDPAGT1        FPHHEFVALIGALLAICCMIFLGFADDVLNLRWHKLLLPTAASLPLLMVYFTNFGNTTI 149
mouseDPAGT1        FPHHEFVALIGALLAICCMIFLGFADDVLNLRWHKLLLPTAASLPLLMVYFTNFGNTTI 151
zebrafishDPAGT1    FPHNEFVQLIGALLAICCMIFLGFADDVLNLRWHKLLLPTMASLPLLMVYFTNFGNTVI 147
celegansDPAGT1     FPYEKLLALLSGLISISTAILLGFADDMLDLKWRHKLLFPTLSSLPLLMVYVSGNSTTV 141
drosophilaDPAGT1   FPHDKFVELIAALLSICCMIFLGFADDVLDLRWHKLLLPTIATLPLLMVYYVNYNSTTV 151
yeastDPAGT1        FPHDKLSEYLSAILCLESTVLLGIADDLFDLRWHKFFLPAIAAIPLLMVYYVDFGVTHV 180
                   **:.::   :..:::.:   ::*:*:**::**:***::::*: ::::*****:.. . * :


humanDPAGT1        VVPKPFR------PILGLHLDLGILYYVYMGLLAVFCTNAINILAGINGLEAGQSLVISA 203
mouseDPAGT1        VVPKPFR------WILGLHLDLGILYYVYMGLLAVFCTNAINILAGINGLEAGQSLVISA 205
zebrafishDPAGT1    VVPKPFR------LLLGMHLDLGILYYVYMGMLAVFCTNAINILAGINGIESGQALFISG 201
celegansDPAGT1     IVPTIVRHLVQPIVLLPVTINISFIYYIFMGMVIVFCTNAINILAGINGLESGQSLVISA 201
drosophilaDPAGT1   IMPNFAR------NLIGTSLNIGALYYVFMGMLAVFCTNAINILAGINGLEVGQSFIIAG 205
yeastDPAGT1        LIPGFMER-----WLKKTSVDLGLWYYVYMASMAIFCPNSINILAGVNGLEVGQCIVLAI 235
                   ::*    .          :    :::.  **::*. :  :**.*:*****:**:* **.:.::


humanDPAGT1        SIIVFNLVELEGDCRDD------HVFSLYFMIPFFFTTLGLLYHNWYPSRVFVGDTFCYF 257
mouseDPAGT1        SIIVFNLVELEGDYRDD------HIFSLYFMIPFFFTTLGLLYHNWYPSRVFVGDTFCYF 259
zebrafishDPAGT1    SIILFNLLELNGDYRDD------HVFSLYFMIPFFFTTLALFYHNWYPSSVFVGDTFCYF 255
celegansDPAGT1     SVCLFNFVQIFRFSAENSTGFWHHTISLYFLLPFTACTAILFYFNKYPSRVFVGDTFCYW 261
drosophilaDPAGT1   SILVFNAIELLLGHQVDS-----HIFSIYFMLPFLATTLALWKFNKYPSQVFVGDTYCYF 260
yeastDPAGT1        LALLNDLLYFSMGPLATRDS---HRFSAVLIIPFLGVSLALWKWNRWPATVFVGDTYCYF 292
                     :  :  :  :           * :*  :::**   :   * * :*: ******:**:


humanDPAGT1        AGMTFAVVGILGHFSKTMLLFFMPQVFNFLYSLPQLLHIIPCPRHRIPRLNIKTGKLEMS 317
mouseDPAGT1        AGMTFAVVGILGHFSKTMLLFFMPQVFNFLYSLPQLFHIIPCPRHRMPRLNAKTGKLEMS 319
zebrafishDPAGT1    AGMTFAVVGILGHFSKTMLLFFIPQVINFIYSLPQLFHIIPCPRHRLPRLQSDTGKLGMS 315
celegansDPAGT1     SGMTLAVVSILGHFSKTLMLFFVPQIINFLYSIPQLFHLVPCPRHRLPKYDPKTDTVSMS 321
drosophilaDPAGT1   AGMTFAVVGILGHFSKTLLLFFLPQILNFLYSTPQLFHFVPCPRHRLPKYDSKTDLLHIS 320
yeastDPAGT1        AGMVFAVVGILGHFSKTMLLLFIPQIVNFIYSCPQLFKLVPCPRHRLPKFNEKDGLMYPS 352
                   :**.:***.*********::*:*:*:.**:*:** ***:::::*****:*: : . . : *


humanDPAGT1        YSKFKTKSLSFLGTFILKVAESLQLVTVHQSETEDGEFTECNNMTLINLLLKVLGPIHER 377
mouseDPAGT1        YSKFKTKNLSFLGTFILKVAENLRLVTVHQGESEDGAFTECNNMTLINLLLKVFGPIHER 379
zebrafishDPAGT1    YSKFKQKDLGKLGQLILKVAEKLWVLDVRRGQEGDDEFIECNNMTLINLVLKILGPTHER 375
celegansDPAGT1     IAEFKKTDLKRLGALFIAVCKSIGMLHVKEVEKDGEIYLQINNLTIINLVLKFAGPLHEK 381
drosophilaDPAGT1   TTEFRLEDLNAPGRLMVTVLRNLRLISWHTKADG---VVRTNNFTLINFVLVVFGPVHER 377
yeastDPAGT1        RANLKEEPPKSIFKPILKLLYCLHLIDLEFDENN--EIISTSNMTLINLTLVWFGPMRED 410
                      ::::          :: :  : ::  .      .*:*:**: *   ** **  :*
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humanDPAGT1          NLTLLLLLLQILGSAITFSIRYQLVRLFYDV------- 408
mouseDPAGT1          NLTLLLLLLQVLSSAATFSIRYQLVRLFYDV------- 410
zebrafishDPAGT1      TLTAIMLLMQVLGSAVAFGIRYHLVRLFYDV------- 406
celegansDPAGT1       TLNDVLMSIQILCSLLAFFIRFYLASLFYDVVE----- 414
drosophilaDPAGT1     VVTQMLMGFQVLCTLIALTIRYPLANYFYAKT------ 409
yeastDPAGT1          KLCNTILKLQFCIGILALLGRHAIGAIIFGHDNLWTVR 448
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