CLUSTAL 2.1 multiple sequence alignment

```
humanALG1        --MAAS--CLVLLALCLLLPLLLLGG---WK----------------RWRRGRAARHVV 36
mouseALG1        --MAAS--CVALLVLALLLLVLLLGL---WK----------------RGRQTGRARHMV 36
zebrafishALG1    --MADANAAVAVVTVSLVLLGLLSGLSVLWSLLPVAVVVLIFVLASGLKGRDELAHLNVC 58
drosophilaALG1   --MA-----------------------------------------------EVLPKKRNAC 12
celegansALG1     --MAKE----------------------------------------DDESPDERSEAA 16
yeastALG1        MFLEIPRWLLALIILYLSIPLVVYYVIP----------------YLFYGNKSTKKRII 42
                   :                                                     .

humanALG1        AVVLGDVGRSPRMQYHALSLAMHGFSVTLLGFCNSKPHDELLQNNRIQIVGLTELQS-LA 95
mouseALG1        VVVLGDVGRSPRMQYHALSLAQSGFSVTLLGFYNSKPRDELLQNDRIRIVKLTDLRG-LG 95
zebrafishALG1    VLVLGDIGRSPRMQYHALSLSKHGYNVTIIGFLGTKPHQDILEDDRIDILPISELKG-LT 117
drosophilaALG1   VIVLGDIGRSPRMQYHAQSLLEENYHVDMIGYLETRPLEELTQHPRCRIHELTAVP--VT 70
celegansALG1     VVVLGDVGRSPRMCNHAKMLADEGFDVKLIGFFDSIPGEQIMNHPRIKIVGIPPPPDFMD 76
yeastALG1        IFVLGDVGHSPRICYHAISFSKLGWQVELCGYVEDTLPKIISSDPNITVHHMSNLKR-KG 101
                   .****:*:***:   **   :    .: * : *:       . : .. . :   :.

humanALG1        VGPRVFQYGVKVVLQAMYLLWKLMWREPGA---YIFLQNPPGLPSIAVCWFVGCLCGSKL 152
mouseALG1        AGPRILQYGVKVVFQAVYLLWKMMRMDPAA---YIFLQNPPGLPAIAVCWFVGCICGSKL 152
zebrafishALG1    VGPRIFRYISKVTLQSFQLLYVLMTIEDQG---YILMQNPPGLPAIAVTWMASRIRGNQF 174
drosophilaALG1   NLTPKLRLLFKAFWQTLSLLMALISIGRPS---FLLVQNPPGIPTLIVCYLYCAVTRTKL 127
celegansALG1     SLPAFVQLPLKLFWNFITLFLALAFQTSAFNLRIILMQNPPALPTMIVCFMFSIFKFAKF 136
yeastALG1        GGTSVIFMVKKVLFQVLSIFKLLWELRGSD---YILVQNPPSIPILPIAVLY-KLTGCKL 157
                    .  .     *   :. .:: :          :::****.:* : : :   .   ::

humanALG1        VIDWHNYGYSIMG------------LVHGPNHPLVLLAKWYEKFFGRLSHLNLCVTNAM 199
mouseALG1        VIDWHNYGYSIMG------------LVHGPRHPIVLLAKWYEKFFGRLSHLNLCVTNAM 199
zebrafishALG1    IIDWHNYGYTIMA------------LSHGENHLIVRLAKWYEKIFGCLSDHNLCVTSAM 221
drosophilaALG1   AIDWHNYTYTVLA---------LGMSK-GEQSPLIRLVRRLERYFGSKAHTHFCVTRAM 176
celegansALG1     SIDWHNYMYSILQNKYQLTDDQVFGNDKKTKKAQIVRCVGFLEGLCGKLSDYNLCVTNAM 196
yeastALG1        IIDWHNLAYSILQLK----------FKGNFYHPLVLISYMVEMIFSKFADYNLTVTEAM 206
                   ***** *:::                  ::       *    .   :. :: ** **

humanALG1        REDLADNWHIR---AVTVYDKPA-SFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPVT 255
mouseALG1        REDLAENWCVR---AVTLYDKPA-SFFKETPLDLQHELFMKLSHTYSPFQSCSDPSHPDT 255
zebrafishALG1    REDLCKNWNIE---ATTLYDKPP-SIFRETPLKLQHELFVRMGSAYLPFRPSSAVTKEYM 277
drosophilaALG1   QEDLQQNWGIGP--VKVLYDRAP-AQFHPIDLTHKHELYLKLAKDYPQFQAKDAEQSDVL 233
celegansALG1     RRDLMDRWGIR---ASTFYDRPPTWKFRDTTIQEIHDLYLRLSQKERILQGKDED----- 248
yeastALG1        RKYLIQSFHLNPKRCAVLYDRPA-SQFQPLAGDISRQKALTT---------------- 247
                   :.  *  . : :        ..**:..    *:           :      :

humanALG1        ERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAALEKFEQLTLDGHN-LPS 314
mouseALG1        ERSAFTERDCQSGVVRRLHGRPALLVSSTSWTEDEDFSILLRALEKFEQQALTGDS-LPS 314
zebrafishALG1    ELTAFTERNTQTGAVTRSAGRPALLISSTSWTEDEDFSVLLQALEEYEKFVETENR-LPS 336
drosophilaALG1   EATALTQK-LASGVVQYRPQRQAVLVSSTSWTPDEDFGILLKALQAYEETAQAEPLVYPS 292
celegansALG1     -STILTHK-SSNGVVQLLTTRPIVFLSSTSWTPDERFEILLDALVAYDKTIG-----LPR 301
yeastALG1        --KAFIKNYIRDDFDTEKGDK--IIVTSTSFTPDEDIGILLGALKIYENSYVKFDSSLPK 303
                     . : ..    .        :  ::::***:* ** : :** **   :::         *

humanALG1        LVCVITGKGPLREYYSRLIHQKHFQHIQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLD 374
mouseALG1        LVCVITGKGPLREHYRHLISQKHLQHVRFCTPWLEAEDYPLLLGSADLGVCLHMSSSGLD 374
zebrafishALG1    LVCVITGKGPQKEYYKKLIDSREFHHVKICTPWLEAEDYPVLLGSADLGVCLHKSSSGLD 396
drosophilaALG1   LLCIITGKGPQKEHYVAEIEKLQWQKVSVITPWLEIEDYPTVLASADLGVCLHWSTSGLD 352
celegansALG1     VLMIITGKGPLKAKYLQEIHEKNLKNVDVLTPWLEAEDYPKILASADLGISLHTSTSGLD 361
yeastALG1        ILCFITGKGPLKEKYMKQVEEYDWKRCQIEFVWLSAEDYPKLLQLCDYGVSLHTSSSGLD 363
                   :: .*******  :   *    : . . :.   **. **** :*  .*  *:.** *:****
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```
humanALG1       LPMKVVDMFGCCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFPDPAGKL 434
mouseALG1       LPMKVVDMFGCHLPVCAVNFKCLHELVRHGENGLVFKDAEELAAQLQMLFSKFPDPAGKL 434
zebrafishALG1   LPMKVVDMFGCCLPVCAIHFECLHELVKHEENGLIFKDSSELAEQLKLLFLDFPGDQGKL 456
drosophilaALG1  LPMKVVDMFGSGLPVCAYDFKCLDELVKHGENGFVFGDHVQLAEQLRIWFENFPKNP-SI 411
celegansALG1    LPMKVVDMFGAKVPALALKFKCIDELVEEKTNGYLFDDSEQLSRQIIELSRGFPNNCNEL 421
yeastALG1       LPMKILDMFGSGLPVIAMNYPVLDELVQHNVNGLKFVDRRELHESLIFAMK----DADLY 419
                ****::****. :*. * .:  :.***..  **  * *  :*  .:

humanALG1       NQFRKNLRESQQLRWDESWVQTVLP----------------LVMDT-------------- 464
mouseALG1       SQFRKKLQESGQQRWDESWQHTVLP--------------LLAHSQMTPRPHPPCGHPS 478
zebrafishALG1   GIFRKNLQESRQQRWDENWDQNVLP---------------LIKEHCD----------- 488
drosophilaALG1  LETRAGFQRKIQEFQELRWRESWR--------------LIAAPVLEAFL-------- 446
celegansALG1    IRLKKNTQEQKFDSWEVMWKRSATSGADFRVPDNGFAKLRAIIQFSFFAILLIMPIHLFM 481
yeastALG1       QKLKKNVTQEAENRWQSNWERTMRD--------------LKLIH------------- 449
                  :     ..     : * ..                       :

humanALG1       ----------
mouseALG1       CRGF------ 482
zebrafishALG1   ----------
drosophilaALG1  ----------
celegansALG1    GTFSGAFRSL 491
yeastALG1       ----------
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