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<html><head><style type="text/css"></style></head><body><pre style="word-wrap: break-word;
white-space: pre-wrap;">CLUSTAL 2.1 multiple sequence alignment

humanDHDDS      MS-----WIKEGELSLWERFCANIIKAG-PMPKHIAFIMDGNRRRYAKKCQV-ER  47
mouseDHDDS      MS-----WIKEGELSLWERFCANIIKAG-PVPKHIAFIMDGNRRRYAKKCQV-ER  47
zebrafishDHDDS  MS-----WIREEKLSLLERLTANILKAG-PMPKHVAFIMDGNRRRYAQKEHK-ER  47
drosophilaDHDDS MS-----WVSDYKYTWTERIAMRTLACGYIPHHVAFVMDGNRRRFARSQQI-DK  48
celegansDHDDS   MAANLTADEEDGWFVAQQEQPWWQWLLRRFIASG-PIPRHVAFVMDGNRRRFAKTKHLGNV  59
yeastDHDDS      METDSG-----IPGHSFVLKWTKNIFSRTLRSNCVPRHVGFI MDGNRRRFARKKEM-DV  53
                *               .               : : . : :   :*:*.*:*****:*. .   :

humanDHDDS      QEGHSQGFNKLAE TLRWCLNLGILEVTVYAFS IENFKRSKSEVDGLMDLARQKFSRLMEE 107
mouseDHDDS      QEGHTQGFNKLAE TLRWCLNLGILEVTVYAFS IENFKRSKSEVDGLDLARQKFSCLMEE 107
zebrafishDHDDS  QEGHTQGF EKLAETLRWCLNLGIHEVTVYAFS IENFKRSKEEVDGLMELARQKFSRLLTE 107
drosophilaDHDDS IEGHSRGFEKLADCLRWCLDVG VREVTTFAFS IENFKRSNEEVEGLFNLAREKFARLLEE 108
celegansDHDDS   IKGHEKGFTQLAKILDWCNRF GIREITVYAFS IENFKRSEEEVSGLMRLAEEKFQKLLND 119
yeastDHDDS      KEGHEAGFVSMRILELCYEAGVDTATVFAFS IENFKRSSREVESLMTLARERIRQITER 113
                :**  **  .::  *  *  *:  *.:*****.  **..*:  **.:::  :

humanDHDDS      KEKLQKHGVCIRVLGDLHLLPLDLQELIAQAVQATKNYNKCFLNVCFAYTSRHEISNAVR 167
mouseDHDDS      QEKLQKHGVCIRVLGDLHLLPLDLQEKIAHAIQATKNYNKCFLNVCFAYTSRHEIANAVR 167
zebrafishDHDDS  QENLEKHGVCIRVLGDLTLLPEDLQTLIAKAVVSTRAHNKCFLNVCFAYTSRHEIANAVK 167
drosophilaDHDDS TARLDEHGIRIRVIGNIELLPHDLQKLVASAM LSTERNDKLFLNVAFAYTSRDEITQAVE 168
celegansDHDDS   SEKLDEKRICFRFYGNRSLLSSRLQKLMSDIEHRTENFDGGRLNVCMPYTSRDEIARSFE 179
yeastDHDDS      GELACKYGVRIKIIGDLSLLDKSLLEDVRVAVETTKNNKRATLNICFPYTGREEILHAMK 173
                :  :  ::. *:  **  *  :  * .  **.:..**.*.**  :...

humanDHDDS      EMAWGV EQLLDPSDISESLLDKCLYTNRS-PHPDILIRTSGEVRLSDFLLWQTSHS--C 224
mouseDHDDS      EMAWGV EQLLEPSDVSESLLDKCLYSNHS-PHPDILIRTSGEVRLSDFLLWQTSHS--C 224
zebrafishDHDDS  EMAWGV EQLIKSSDVSEVLLSECLYSSNS-PNPDLLIRTSGEVRLSDFLLWQTSYS--C 224
drosophilaDHDDS TILRHGSQDLAG-EDISERLLEECLYTRHS-PPPDLVFRTSGETRLSDFMMWQLSTS--V 224
celegansDHDDS   TIRKHVKD GKVNVDEINESMIDACLD SGCGGTSPDLFIRTSGEHRLSDFLMWQASET--H 237
yeastDHDDS      ETIVQHKKG----AAIDESTLESHLYTAGV-PPLDLLIRTS GVSRLSDFLIWQASSKGVR 228
                ...      :.*  :.  *  :  .  *.:*****  *****:*** *  .

humanDHDDS      LVFQPV LWPEYTFWNLF EAILQFQMNHSV LQKARDMYAEERKRQQLERDQATVTEQLLRE 284
mouseDHDDS      LVFQPV LWPEYTFWNLC EAILQFQRNHGALQKARDMYAEERKR RQLERDQAAVTEQLLRE 284
zebrafishDHDDS  LVFQSV LWPEYSFWNLC EAILQFQMSHRSIQKARELHREEQVLQOMESDRTCVAEILQHR 284
drosophilaDHDDS LYFSNV LWLPQITFWHFLASILAYQRDRWQLD---DFRRAER----- 262
celegansDHDDS   VYFDDV LWPEFGYFNLCKAILNYQYYRTTVTK----- 269
yeastDHDDS      IELLDCLWPEFGPIRMAWILLKFSFHKSFLNK----- 260
                :  :  ***:  .:  :*  :.  :  :

humanDHDDS      GLQASGDAQLRRLRLHKL SARREERVQGFLQALELKRADWLARLGTASA-- 333
mouseDHDDS      GLQASGDAQLRRLRLHKL STKREERVQGFLKALELKRANWLALWGTASA-- 333
zebrafishDHDDS  GNGKPM DGQSQQONALLNYS SREERVGFLNTLQHKRDAFFDDLSSQAVVA 335
drosophilaDHDDS -----MQSCQLAKATDFYSERVQNFLT TIDEDRRKLLVRLAAN---- 300
celegansDHDDS   -----MTSSKVSDDNATSWKMNFSGNDRDLISVKS----- 299
yeastDHDDS      -----EYRLEEGDYDEETNGDPIDLKEKKLN----- 286
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