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

humanDDOST mouseDDOST zebrafishDDOST drosophilaDDOST celegansDDOST yeastDDOST	MRWLPGLLLIASIGFHQSLADRVLVLGET-AAVKDT	59 44 44 38 35 39
humanDDOST mouseDDOST zebrafishDDOST drosophilaDDOST celegansDDOST yeastDDOST	HSLFFRSLKDRGFELTFKTADDPSLSLIKYGEFLYDNLIIFSP-SVEDFGGNINVETI HSLFFRSLKDRGFELTFKTADDPSLSLIKYGEFLYDNLIIFSP-SVEDFGGNINVETI HSIFFRSLADRGFDLTFKTADDPGLSLIKYGQFLYDHLILFSP-SVEDFGGNINVETI HSIFFKSLQDRGFKLTYKLADDSSLLLSKYGEYLYKNVIIFAP-SVEEFGGDVSVERL HSVFLNSVKERGHELTVRAADDSQLALFKHGQLIFDHLFILAP-GVQVFGGSLSPSEI YSVYLKDLEQRNYKLEYLDINSTSTTVDLYDKEQRLFDNIIVFPTKGGKNLARQIPVKQL :*:::::::::::::::::::::::::::::::::::	101 101 95 92
humanDDOST mouseDDOST zebrafishDDOST drosophilaDDOST celegansDDOST yeastDDOST	SAFIDGGGSVLVAASS-DIGDPLRELGSECGIEFDEEKTAVIDHHNYDIS-DLGQHTLIV SAFIDGGGSVLVAASS-DIGDPLRELGSECGIEFDEEKTAVIDHHNYDVS-DLGQHTLIV TAFIDGGGNVLVAASS-DIGDPLRELGSECGIEFDEEKTAVIDHHNYDIS-DPGEHTLIV AQFVDDGGNVLVAGSE-KSGDALREFASECGFELDEENAAVIDHLHYDVS-DAGEHTTIL SKFVDAGGNVLVAAGS-NIGDALREIAAEHGFEFEEAGTSVIDHHNYDQTLDSGDHTTLV IKFFENEGNILCMSSPGAVPNTIRLFLNELGIYPSPKGHVIRDYFSPSSEELV *.: *.:* ::* : * :: ::* : :::	159 159 153 151
humanDDOST mouseDDOST zebrafishDDOST drosophilaDDOST celegansDDOST yeastDDOST	ADTENLLKAPTIVGKSSLNPILFRGVGMVADPDNPLVLDILTGSSTSYSFFPDKPI ADTENLLKAPTIVGKSSLNPILFRGVGMVADPDNPLVLDILTGSSTSYSFFPDKPI ADPENLLKAPTIVGKPTDKPVLFKGVGMVADPDNPLVLDILTGSSTSYSYFPDRPI TSAKNLIQADTIVGKANRQADAAPLLYRGTGLIADKENPLVLKLLTAESTAYSYNPEASV VGKDQLISAELIVGNSAKLHPVLFKGIGLVAGKTNNLALSIVRASGTAYSYDPKAVR VSSNHLLNKYVYNARKSEDFVFGESSAALLENREQIVPILNAPRTSFTESKGK:*:. *:::	215 215 213 208
humanDDOST mouseDDOST zebrafishDDOST drosophilaDDOST celegansDDOST yeastDDOST	TQYPHAVGKNTLLIAGLQARNNARVIFSGSLDFFSDSFFNSAVQKAAPGSQRYSQTGNYE TQYPHAVGRNTLLIAGLQARNNARVIFSGSLDFFSDAFFNSAVQKATPGAQRYSQTGNYE TQYPHAVGKNTLLIAGLQARNNARVVFSGSLHFFSDAFFNSAVQKAATGSKRYEQTGNQD SDYPHAVGRGTLLIAALQARNNARVVFSGSLLFFSDESFTTAVQYAQSG-VFHKLAGNRD ATNPSIAGSRTLLVGGLQSRNNARIVFTGSSELFSNTFFSAKTNSVNPS-VQGAQSGNAD -CNSWTSGSQGFLVVGFQNLNNARLVWIGSSDFLKNKNQDSNQE . * :*: .: * ****:: ** :::	290 275 275 272 267 248
humanDDOST mouseDDOST zebrafishDDOST drosophilaDDOST celegansDDOST yeastDDOST	LAVALSRWVFKEEGVLRVGPVSHHRVGETAPPN-AYTVTDLVEYSIVIQQLSNGKWVPFD LAVALSRWVFKEEGVLRVGPVSHHRVGEMAPPN-AYTVTDLVEYSIIIEQLSNGKWVPFD LAEALSRWVFKEAGVLRVGDVTHHPVGESTPPA-AYTVTDLVEYGIVIEMLSGGKWVPFD VAESISKWVFGETGRLRVASVQHHKEGELLPPDQAYTITDPVVYTIGIEELVQGEWRAFK FATAITRWVMKESGVLRVKTVNHHKKGETVPPVEGYFITEDVVYTIEIEELKNGKWVPFQ FAKELLKWTFNEKSVIKSVHAVHSHADGTSYDEEPYKIKDKVIYSVGFSEWNGEEWLPHI .* ::*.: * . :: . : . : . : . : . : . :	334 334 332 327
humanDDOST mouseDDOST zebrafishDDOST drosophilaDDOST celegansDDOST yeastDDOST	GDDIQLEFVRIDPFVRTFLKKKGGKYSVQFKLPDVYGVFQFKVDYNRLGYTHLY GDDIQLEFVRIDPFVRTFLKRKGGKYSVQFKLPDVYGVFQFKVDYNRLGYTHLY GDDIQLEFVRIDPFVRTYLKKNGGKYSVQFKLPDVYGVFQFKVDYNRLGYTHLY ASDIQLEFVRIDPFVRTYLKQTNTGAYQAKFKIPDVYGVYQFKVDYNRVGYTHLY GKDVQLEFVRIDPFVRATLKNSNGRLSVAFKLPDVLGVFKFLVDYRRVGYTHLY ADDIQFELRQVDPYYRLTLSPSGNDSETQYYTTGEFILPDRHGVFTFLTDYRKIGLSFTT*:*::::::::::::::::::::::::::::::::	388 388 387 381

humanDDOST	SSTQVSVRPLQHTQYERFIPSAYPYYASAFSMMLGLFIFSIVFLHMKE 451
mouseDDOST	SSTQVSVRPLQHTQYERFIPSAYPYYASAFSMMAGLFIFSIVFLHMKE 436
zebrafishDDOST	SSTQVSVRPLQHTQYERFIPSAFPYYASAFSMMAGLFVFSVVFLHMRE 436
drosophilaDDOST	STTQVSVRPLEHTQYERFIPSAFPYYTSAFSMMIGVFVFSFVFLHFKDEPVG-RAAKE 444
celegansDDOST	DVQQVSVRPLWHTQYERFIRSAYPYYASSFSMMAGLVLFSIVYLYHKDTPVKGAKVLD 439
yeastDDOST	DKDVKAIRHLANDEYPRSWEISNSWVYISAICGVIVAWIFFVVSFVTTSSVGKKLET 425
	. ::* * : : * * .:: * :: * .::
humanDDOST	KEKSD 456
mouseDDOST	KEKSD 441
zebrafishDDOST	KEKSD 441
drosophilaDDOST	DKKSQ 449
celegansDDOST	SEKKK 444
yeastDDOST	FKKTN 430
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