>Ppa\_SYP-4

MPLWEIDFSDIDSETEVPDDIDGDEDLPEGYNEEFEKVDDFIHDNLVRAKEGNDVDMIKFVVEQGILRYTRLGLKKEVLDKQIWITKQLGKGNVQEMIADQKKKELELKNRVASLRAERDFKKARLEAYEEEKARREDLRQTFIGYSEDLDRQLENAPWLLEKQKKAARRKELEDEIKSLQSDLAKIDLIEERNRIAGKFLAQKLAELYIKREKLFKQLSEEKTSVKKLEEEKRSRRFMEESSQMDCTQAILDGDLDDEETLMKMAKHYKIDTQNLNVPISQMTQESQPTQSICRKRAQSPAESTASSEANDSMSESGEPTAAVFPPPTKKVSIVEPIHNPDESVDERAAQIGANNETNLDESCMEEDDQNGDKSQPEQLETDEREEDDEGREEEEEYREEEEEHAEQHEQEESPTSQESHATGASQESVAYAPDEMVEEETDNNDGFRRPSNPAKVDFEENEDNLEAETSFNPEMILNISANSNDPGGDFFDMMNNQATHKRAVADANGSSPSVGARDNDFMSMFGGGGGGDTGAPVDDATSFSFNFGGADANETNGGGGGGGGEFNFFGF

>Celeg\_SYP-4

MSFPTLQVRPNEKNPKVLRCHEFLRQSNQLVERNMINTEGRKMLAKLLTKMVSEAKGIYALDERRAELAKSGKLQEKLKSAYQTSLTVMEDRLHIAELSRQVQEKKLTVQQKYYECDDLRKSVQETNTEARRVQEINEQRLVDTTRATEELIVKSASILKNLENSSDVHKLRAMEEEKRILEEVVEGLRDQKKCLADDIRTKKATLKAESKKSFEKTVIECAKHYKLHQSLMPKLDKSKRSLETLKDEEENRRICGSLSLDETMQFDRSFILASMDKTNKPEKAVQQLTSKSSEVSITPQISETAKSSFSKEPIPTQHPMEVGEEPVIEHSAEESVHIEPPNVTEIREVVPQITIQPTRQDSVVQRDAEELDTSAVPSPQPESILDEPEEEEEELSNHENHADQSMDVMEVDQEVPEESPMEVGEQEEIEQPSVFKDILATEQAALSQEQEPEIVEKQADNDVQFVDDQQVGAQLDVEDEEEVMSENGSNKSNNFSFNFFGNSKGTSAGEGGGEGNFDFNFDGIGAGDDGSNNGGSTGDLDFLNYDGEDEGKGSGNTQSDPFGFASNGNAAGGGGDGSFNFNFDGDGEGGATSGAGGNSTSFFNF

>Cbrig\_SYP-4

MSLPSLKKRPNETNSKILRSHEFLRQSTQLIDRSLINAEGSQMLEKMLTKMIAEAQGKYALDEEGAKIAQSGKLLEDLKTTYQTSITVMEERFLLTELARHVQKKLDVNRNYTQCDLLRKATQSSNAEIRRERNVYEKRLQNAKKSALELSTKHACILRLLENSTDVGQLRTIEEDKSILEKEVDLSRSEKIYLAEDIRTKTSTLKAESKKTFQKTIIECAKHYTLFQTLSPKLMSCKTNLERLKNEEESRRACGSLDEMQFDRSFVLASMEKEKSPEKNDLSPPVNLNTSQKVSSRSTSFNESIQQPDQMEVEEFEGDGERNHSKNESAEKINTSRSLLEDITVFPTAPIPRIVDQAPKRRESVVETQRVVPRDPSPEPVDQGEEIEKQTDQSIDVMELDNQEEVEPMEEESQEQTKQGDVKSQKISEKLNSSVTSSFEFPKLNKPAVEVQKSNALKILDKSVDEDDILSENGSNRSTNFSFNFFGNTKSGAGSDVNGVENDTDGNFDFNFGSIGAGDDGLYNGSGGAFDFLGCGGDEEGSTSSTNASDPFGFGASAAGSGGGDTSFNLNFDGDNEGGGASDAGGNSTSFFNF

>Crem\_SYP-4

MFPLNKTQIPLHIPVKFQLLFNKSASLHVALGGNMSFPTLLVRPNEKNPKVLRAHEFLRQSNQLVERNLINAEGRKMLAKMLATMVAEVKGIYALDEKRAELTKSGILFEKLKLAHQTSRDVMEDRYSLAELGRQVQEKKLDVQRNYYECDHLRKSVQTTNAEVRRERESNEKRLNKTKTSTETLIAKSASILKLLENSTDVCKLRTMEEEKRILLEEVDELRDEKKALADDIHTKKATLKAESKKPFKKMVIECAKHYALCETLTPKLIKSKKNLQLLKEEEESRRACGSLDETMQFDRSFVLASMDKDTTAENTSRNAAAHNESVQKSSSRSTSFNESIQQNQTMEVEEEQDASHHSENSRDGSTEMPPVPVETTPTPVVVPKPTPAVSKVAPVVAKPAPVVAKPTPVVTKPAPITAKPAPVVTKSYSVATKPAPVAANPPEATPKRRESMVETQRVIPREPSPEPEEEPEEEDANRSVDVMDQGEDQEEDVEPMETEEQPDVVIPPSPAPHENVDIKPSAPEVLDISHQEDSQNDVEMRIDDDEVLSENGSSRSASFNFNFFGNTKGGAGEVVANDTDGNFDFNFGGGDDVSTNGSGGAFDFLNCGGGDEGQSNNNDADPFGFGANTGGTGGGDMSFNFNFDGDNEGGTSLGAGGNSTSFFNF

>Hcon\_SYP-4

MSFRTREKGVWRSRDKTTDFLRKRKELEEECRRLSAQVEQNNAVWISRLQTARNQQTRFDELISCSVRIAKQNNEKKAVEALTERLAKLKMECCQFEKERAKLKKELEFQTITPLRVFMVNFAKIALRTYEMQEKLHEARRTEEHLKIEEAERRARVGASEYDVFDITFASQDLALNKTQERAVPTEPPRASLHVLPETAEEETASGGTLNSCESLCSTSPAQPPPASEQDVVLARTNAVKSYVTQQSEAVARETVQSDDNDSGELTRDEDERVSFCSRDFKQAQGMDVEVASNADEECVPLHKDNDRNGTLEERDTMIRDQDVGVGDFSDDDSAIDPEAEDDEMNNSMENGNEKVMEQTEYIEKQDAHSNSFFLPKKSSDKDSNNYSTPISSSQSFVEGQTSAPSSQQSQQNSMNNCAAIPNRKGPSSMMPNSKNPTSMDPSQEADAILNTLLKAPPSPIQEEMAFDFNCSLDNDEFDPTAALNISAHSNDPGADFLSLMESTNEKREKQRQNSSSPAKDFSFSIFGLGGDAASDQGSDKGFAFDFGGTLNGDEDRDGGGFQFDFNASSANDGSGEKTDKGFNLFDF

>Dviv\_SYP-4

MELPFVYIDPHEENEDIANVAAFLGQARRIIVNNAVSEEMKRAIFDLASEYIVDVRKYYQlAKEKEALLVKRDADIDEKLHQVERELAEKERINNALRASIEEKKRNIKLSEITIKKSRNKTSDLFRQRKELEEDCKKLDAKVKESNSTLASSLQTAHKQRDRLQMLMEKSPRLAKQITERDAVNALEVRLEQLKSEQSDLKAEEERLRKELELQTATPLRVFIVNFAKITLRTLEMQEKLGEARKVYEQLKAEETERLKSGVCDHEFDASFLSTDYSFKKVNDHGNILRTELMRPAVVSKPVTPVDDGFSTPETLTSGSSSKSSVEPPQTTEEDIIKARTNAVKSYVTQQSETVARNVESSKNGYKDTIYDENERESIYCLENADKSLGVMRTADKETVPSTLENNNIVEIADDDMDVNVSQGVIPEDFSDEDGEEQEVEDDGTIAVENENDDVAINTNYILINWGVNSAERILSQESEDSTAVEGISRMKIDPINTLKIAQMSETSQSILGSDNREKSPISQKFHENSAGRRASMSHRQGCSSQTSENVFNGGSPSPCVDASQEAGAFFSNLLDQPPSPIQDGIPFNFGSGGITEEIDPSVVLNISTHSNDPGGDFLLLMENEKRERDRRSEGSSSAAEFSFSMFGTAADPATSGLGGEFAFDFDAPSQCNERIDSTTFQFNFSEGSNDQEQNNNDGGFNFFDF