

gi|6754714|ref|NP_034939.1| MKMKGLPVLWLCVAVCSYPLHDSARDAGMELLOKYLENYGLAKDVKQFIKKKDSLIVKIKIEMOKFLGLEMTGKLDSTNEMELMHKPRCGVDPVGGFSTFPKPKWRKSHITRYIVNYTPDLPRQSVDSATEKALKVWEEVTPLT 150
gi|19424170|ref|NP_598207.1| --MKGLPVLWLCVAVCSYPLHGSE--EDAGMEVLQKYLENYGLEKDVQFIKKKDSSPVVKIKIEMOKFLGLKMTGKLDSTNEMELMHKPRCGVDPVGGFSTFPKPKWRKSHITRYIVNYTPDLPRQSVDSATEKALKVWEEVTPLT 150
gi|4505217|ref|NP_002413.1| --MKSLPILLLLCVAVCSAYPLDGAARSDTSMNLVQKYLENYDLKDVQFVRRKDSGPVVKIKIEMOKFLGLEVTGKLDSDTLEVMRKPFCGVPDVGHFRITFPKPKWRKSHITRYIVNYTPDLPRQSVDSATEKALKVWEEVTPLT 150
gi|114640107|ref|XP_508723.2| --MKSLPILLLLCVAVCSAYPLDGAARSDTSMNLVQKYLENYDLKDVQFVRRKDSGPVVKIKIEMOKFLGLEVTGKLDSDTLEVMRKPFCGVPDVGHFRITFPKPKWRKSHITRYIVNYTPDLPRQSVDSATEKALKVWEEVTPLT 150
gi|50950195|ref|NP_001002967.1| --MQLNPALLLFCGVVCSAYPVDRAAEDENNNMELFCQKYLENYNLGKDVKQFVRRKDSGPVVKIKIEMOKFLGLEVTGKLDSDTLEVMRKPFCGVPDVGHFRITFPKPKWRKSHITRYIVNYTPDLPRQSVDSATEKALKVWEEVTPLT 150
gi|119906908|ref|XP_586521.2| --MRNLPILLLLCVAVCSAYPLDRAARDKEDTMELVQKYLENYNLAKDKQFVRRKDSGPVVKIKIEMOKFLGLEVTGKLDSDTLEVMRKPFCGVPDVGHFRITFPKPKWRKSHITRYIVNYTPDLPRQSVDSATEKALKVWEEVTPLT 150
gi|50731119|ref|XP_417175.1| MELKMLAFGLLGVVCS--VALFVAPETANEDQFAQKYLENYDFKEDKHSLEKSTNLNEMADKIREMOSFFGLEVTGELNRRKIMDMMKQPRCGIPDVRSYTFPRNPKWKEDVTYRILNYTPDMLQADVDEATAKAFQLWSSVTPLR 150



gi|6754714|ref|NP_034939.1| FSRISGEADIMISFAVGEHGFDFPDPGPTVLAHAYAPGPGINGDAHFDDDERWTDVET--GTLNLFVAAHELGHSLGLYHSAKAEALMYPVYKSTDLRFHLSQDDVDGIQSLYGTPT--ASPV-----LVVPEKSNLEP----- 300
gi|19424170|ref|NP_598207.1| FSRISGEADIMISFAVEEHGDFIPDPGPMVLAHAYAPGPGINGDAHFDDDERWTDVET--GTLNLFVAAHELGHSLGLYHSAKAEALMYPVYKSTDLRFHLSQDDVDGIQSLYGTPT--ESPV-----LVVPEKSNLEP----- 300
gi|4505217|ref|NP_002413.1| FSRLYEGEADIMISFAVREHGDFPDPGPNVLAHAYAPGPGINGDAHFDDDEQWTKDIT--GTLNLFVAAHEIGHSLGLYHSAKAEALMYPVYKSTDLRFHLSQDDVDGIQSLYGTPT--DSPET-----PLVPTPEVPPPEP----- 300
gi|114640107|ref|XP_508723.2| FSRLYEGEADIMISFAVREHGDFPDPGPNVLAHAYAPGPGINGDAHFDDDEQWTKDIT--GTLNLFVAAHEIGHSLGLYHSAKAEALMYPVYKSTDLRFHLSQDDVDGIQSLYGTPT--DSPET-----PLVPTPEVPPPEP----- 300
gi|50950195|ref|NP_001002967.1| FSRIDEGEADIKISFAVRDHGDFNPFDPGNVLGHAYPPGPGIYGAHFDDDEQWTKDIT--GTLNLFVAAHELGHSLGLYHSAKAEALMYPVYKSTDLRFHLSQDDVDGIQSLYGTPT--DSPND-----PVVPTPEVPPPEP----- 300
gi|119906908|ref|XP_586521.2| FSRIVYEGEADIMIIIFAIRREHGDFLFPDPGKVLGHAYPPGPGIYGAHFDDDEQWTKDIT--GTLNLFVAAHELGHSLGLYHSAKAEALMYPVYKSTDLRFHLSQDDVDGIQSLYGTPT--VSPND-----PVVPTPEVPPPEP----- 300
gi|50731119|ref|XP_417175.1| FTRLYSGDADIMISFASGFHGFDFPDPGGTTLAHAYVPTNTIGGDAHFDEENWTKFTIYSGYNLFVAAHELGHSLGLYHSAKAEALMYPVYKSTDLRFHLSQDDVDGIQSLYGTPT--EPPAFPEKAFPPQEPHLEVTTEAPTQMS 300



gi|6754714|ref|NP_034939.1| -----EISPMCSSLFFDAVSLRGEVLFKDRHFWRKSLRTPPEFYLISSFWPSLPSNMDAAAYEVNTRDVFIFKGNQFWAIRGHEELAGYPKSIHTLGLPETVQKIDAAISLKDQKKTYFFVEDKFWRFDEKKQSMDFPFPRKIA 450
gi|19424170|ref|NP_598207.1| -----EILPMCSSALSFDVAVSLRGEVLFKDRHFWRKSLRTPPEFYLISSFWPSLPSNMDAAAYEVNTRDVFIFKGNQFWAIRGHEELAGYPKSIHTLGLPETVQKIDAAISLKDQKKTYFFVEDKFWRFDEKKQSMDFPFPRKIA 450
gi|4505217|ref|NP_002413.1| -----GTPANCDPALSFDAVSLRGEILLIFKDRHFWRKSLRLEPELHLLISSFWPSLPSGVDAAYEVTSKDLVFIKGNQFWAIRGNEVQAGYPRGIHTLGFPPTRVKIDAAISDKKKNKYFFVEDKFWRFDEKRNSEMPGFPKRIA 450
gi|114640107|ref|XP_508723.2| -----GTPAKCDPALSFDAVSLRGEILLIFKDRHFWRKSLRLEPELHLLISSFWPSLPSGVDAAYEVTSKDLVFIKGNQFWAIRGNEVQAGYPRGIHTLGFPPTRVKIDAAISDKKKNKYFFVEDKFWRFDEKRNSEMPGFPKRIA 450
gi|50950195|ref|NP_001002967.1| -----GTPAACDPLSFDVAISLIRGEVLFKDRHFWRKSLRLEPEFYLISSFWPSLPSGLDAAAYEVTSKDVIFIFKGNQFWAMRGTEVQAGYPKGIHTLGFPPTRVKIDAAVFDKPKKTYFFVEDKFWRFDEKRNSEMPGFPKRIA 450
gi|119906908|ref|XP_586521.2| -----GTPAACDPALSFDAVSLRGEILLIFKDRHFWRKSLRLEPEFYLISSFWPSLPSGIDAAAYEVTSKDVIFIFKGNQFWAIRGNEVQAGYPRGIHTLGFPPTRVKIDAAVFDKPKKTYFFVEDKFWRFDEKRNSEMPGFPKQIV 450
gi|50731119|ref|XP_417175.1| PTEMAPTERPEDCDPHLIFDAITLIRGEILLIFKGSVWRKSPYFQIIEHDTISTFWPSLVAGDAAYEIDKDRVIFFKDNOYVAVSGYRIEPPGPKPQNLGFPFRVRRKIDAAVHDQNTKKTIFVGNKYWSDENTQSMERGVPRKIA 450



gi|6754714|ref|NP_034939.1| EDPPGVDSRVDVAFVFAFGFLYFFSGSSQLEFDPNAKKVTHILKSNSWFC 500
gi|19424170|ref|NP_598207.1| ENPPGIGTKVDVAFVFAFGFLYFFSGSSQLEFDPNAKKVTHILKSNSWFC 500
gi|4505217|ref|NP_002413.1| EDPPGIDSKIDAVFEFEGFFVFFSGSSQLEFDPNAKKVTHILKSNSWFC 500
gi|114640107|ref|XP_508723.2| EDPPGIDSKIDAVFEFEGFFVFFSGSSQLEFDPNAKKVTHILKSNSWFC 500
gi|50950195|ref|NP_001002967.1| EDPPGVDSKVDAAVFAFGFYFFNGSSQLEFDPNAKKVTHVLSNSWFC 500
gi|119906908|ref|XP_586521.2| EDPPGVSEVDAVFEVFGFYFFSGSSQLEFDPNAKKVTHVLSNSWFC 500
gi|50731119|ref|XP_417175.1| ADPQIGHFVDAALQKNGHFYFFHGSNOYEVDIKNKKLVKMKNSWFC 500

