

gi | 73962351 | ref | XP\_848757.1 | ... MSAPRPPAGGRLLPLLLALALASLSAQSSE-FSPEAWLQOYGYLPP--GDLRHTHTQRSPQSFSAIAIAMOKFYGLRVTGKADADTKAMRRPRCGVPDKFGAETKANVRRKRYAIQGLKWOH 120  
gi | 27806001 | ref | NP\_776815.1 | ... MSPAPRPPACSLLLPVLTLALALASLSAQSSE-FSPEAWLQOYGYLPP--GDLRHTHTQRSPQSFSAIAIAMOKFYGLRVTGKADADTKAMRRPRCGVPDKFGAETKANVRRKRYAIQGLKWOH 120  
gi | 4826834 | ref | NP\_004986.1 | ... MSPAPRPPRCLLLPLLLALALASLSAQSSE-FSPEAWLQOYGYLPP--GDLRHTHTQRSPQSFSAIAIAMOKFYGLRVTGKADADTKAMRRPRCGVPDKFGAETKANVRRKRYAIQGLKWOH 121  
gi | 114652041 | ref | XP\_001157686.1 | ... MSPAPRPPSRCLLLPLLLALALASLSAQSSE-FSPEAWLQOYGYLPP--GDLRHTHTQRSPQSFSAIAIAMOKFYGLRVTGKADADTKAMRRPRCGVPDKFGAETKANVRRKRYAIQGLKWOH 121  
gi | 31982191 | ref | NP\_032634.2 | ... MSPAPRPPSRSLLLPLLLALALASLGAQSSNFSPPEAWLQOYGYLPP--GDLRHTHTQRSPQSFSAIAIAMOKFYGLRVTGKADADTKAMRRPRCGVPDKFGTEIKANVRRKRYAIQGLKWOH 121  
gi | 13591995 | ref | NP\_112318.1 | ... MSPAPRPPSRSLLLPLLLALALASLGAQSSNFSPPEAWLQOYGYLPP--GDLRHTHTQRSPQSFSAIAIAMOKFYGLRVTGKADADTKAMRRPRCGVPDKFGTEIKANVRRKRYAIQGLKWOH 121  
gi | 35903119 | ref | NP\_919397.1 | ... MLPKIQTLPRLLE--LALASVFAAVQSGSDKEVRRPEAWLQOYGYLPP--GDVRAQATIRSPKINSAISAMOKFYGLRVTGKADADTKAMRRPRCGVPDKFGTEIKANVRRKRYAIQGLKWOH 119  
gi | 24762711 | ref | NP\_726473.1 | ... MNRRRASGATHCKTNNCNISNNSNNSNNTNCSQSVFIVVGGTLFSLIMAAQSAFVITTTQAEIYLSDFGLPASARNPASSLHDPKRWVSAIEEFQSFAGLNVTGELDAEIMKMLSLPRCGVDRVGTG--DTRSKRYALGSSRWK 147  
gi | 158286645 | ref | XP\_001688107.1 | ... MLRNHAHWIRALAIVLVGCAGAGTASPVSTTPOAELYSDFGLSPKRYRNPSTGNLLDQDWEKAIMEFQSFAGLNVTGELDGEIMQLMSLPRCGVKDKVGFGE--DTRSKRYALGSSRWK 120  
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 73962351 | ref | XP\_848757.1 | ... NEITFCIQNYTPKVGEYATFEAIRKAFRVWESATPLRFREVPYAYIREGHEKQADIMIFFAEGFHGSDTPFDGEGGFLAHAYFPGPNIGGDTHFDSAEFPWTVRNEEDLNGNDIFLVAVHELGHALGLEHSDPSAIMAFFYQWMDTENFVL 270  
gi | 27806001 | ref | NP\_776815.1 | ... NEITFCIQNYTPKVGEYATFEAIRKAFRVWESATPLRFREVPYAYIREGHEKQADIMIFFAEGFHGSDTPFDGEGGFLAHAYFPGPNIGGDTHFDSAEFPWTVRNEEDLNGNDIFLVAVHELGHALGLEHSDPSAIMAFFYQWMDTENFVL 270  
gi | 4826834 | ref | NP\_004986.1 | ... NEITFCIQNYTPKVGEYATFEAIRKAFRVWESATPLRFREVPYAYIREGHEKQADIMIFFAEGFHGSDTPFDGEGGFLAHAYFPGPNIGGDTHFDSAEFPWTVRNEEDLNGNDIFLVAVHELGHALGLEHSDPSAIMAFFYQWMDTENFVL 271  
gi | 114652041 | ref | XP\_001157686.1 | ... NEITFCIQNYTPKVGEYATFEAIRKAFRVWESATPLRFREVPYAYIREGHEKQADIMIFFAEGFHGSDTPFDGEGGFLAHAYFPGPNIGGDTHFDSAEFPWTVRNEEDLNGNDIFLVAVHELGHALGLEHSDPSAIMAFFYQWMDTENFVL 271  
gi | 31982191 | ref | NP\_032634.2 | ... NEITFCIQNYTPKVGEYATFEAIRKAFRVWESATPLRFREVPYAYIREGHEKQADIMIFFAEGFHGSDTPFDGEGGFLAHAYFPGPNIGGDTHFDSAEFPWTVRNEEDLNGNDIFLVAVHELGHALGLEHSDPSAIMAFFYQWMDTENFVL 271  
gi | 13591995 | ref | NP\_112318.1 | ... NEITFCIQNYTPKVGEYATFEAIRKAFRVWESATPLRFREVPYAYIREGHEKQADIMIFFAEGFHGSDTPFDGEGGFLAHAYFPGPNIGGDTHFDSAEFPWTVRNEEDLNGNDIFLVAVHELGHALGLEHSDPSAIMAFFYQWMDTENFVL 271  
gi | 35903119 | ref | NP\_919397.1 | ... KNLVTSIQNYTPKVERATFEAIRKAFRVWESATPLRFREVPYAYIREGHEKQADIMIFFAEGFHGSDTPFDGEGGFLAHAYFPGPNIGGDTHFDSAEFPWTVRNEEDLNGNDIFLVAVHELGHALGLEHSDPSAIMAFFYQWMDTENFVL 269  
gi | 24762711 | ref | NP\_726473.1 | ... RMTLYKISKYPKRLKRVDDDAEIKGAFRAVWESDTPDKTRRSTG-----PVHIEIKFVSEHGEGDADPDGEGGFLAHAYFPP--VFGDADHFDAELWIGSF--RGTNLFQVAAEHFCHSLGLSHSDQSSALMAFFYRGFVFPV--FKL 284  
gi | 158286645 | ref | XP\_001688107.1 | ... KDLYRISKYPRRLERLAVDKETAKAFVWSEYDLRFTPKKLG-----AVHIDIRFENEHGGDPPDGGGFLAHAYFP--VYGGDAHFDAAEQWIDKP--RGTNLFQVAAEHFCHSLGLSHSDQSSALMAFFYRGVDPV--FRL 257  
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 73962351 | ref | XP\_848757.1 | ... PDDRRGIQQLYGSSESQSPKMPPOPRITSRPSVDPKPKNPYGNICDGN--FDIVAMLRGEMFVFKERFWVRVRRNNOVMDGYMPPIGQFWRGLPASINTAYERKDGKVFVFKGDK---HWVFDEASLEPGYPKHIKELGRGLPTDKID 418  
gi | 27806001 | ref | NP\_776815.1 | ... PDDRRGIQQLYGSSESQSPKMPPOPRITSRPSVDPKPKNPYGNICDGN--FDIVAMLRGEMFVFKERFWVRVRRNNOVMDGYMPPIGQFWRGLPASINTAYERKDGKVFVFKGDK---HWVFDEASLEPGYPKHIKELGRGLPTDKID 415  
gi | 4826834 | ref | NP\_004986.1 | ... PDDRRGIQQLYGSSESQSPKMPPOPRITSRPSVDPKPKNPYGNICDGN--FDIVAMLRGEMFVFKERFWVRVRRNNOVMDGYMPPIGQFWRGLPASINTAYERKDGKVFVFKGDK---HWVFDEASLEPGYPKHIKELGRGLPTDKID 416  
gi | 114652041 | ref | XP\_001157686.1 | ... PDDRRGIQQLYGSSESQSPKMPPOPRITSRPSVDPKPKNPYGNICDGN--FDIVAMLRGEMFVFKERFWVRVRRNNOVMDGYMPPIGQFWRGLPASINTAYERKDGKVFVFKGDK---HWVFDEASLEPGYPKHIKELGRGLPTDKID 416  
gi | 31982191 | ref | NP\_032634.2 | ... PDDRRGIQQLYGSSESQSPKMPPOPRITSRPSVDPKPKNPYGNICDGN--FDIVAMLRGEMFVFKERFWVRVRRNNOVMDGYMPPIGQFWRGLPASINTAYERKDGKVFVFKGDK---HWVFDEASLEPGYPKHIKELGRGLPTDKID 416  
gi | 13591995 | ref | NP\_112318.1 | ... PDDRRGIQQLYGSSESQSPKMPPOPRITSRPSVDPKPKNPYGNICDGN--FDIVAMLRGEMFVFKERFWVRVRRNNOVMDGYMPPIGQFWRGLPASINTAYERKDGKVFVFKGDK---HWVFDEASLEPGYPKHIKELGRGLPTDKID 416  
gi | 35903119 | ref | NP\_919397.1 | ... PDDRRGIQQLYGSSESQSPKMPPOPRITSRPSVDPKPKNPYGNICDGN--FDIVAMLRGEMFVFKERFWVRVRRNNOVMDGYMPPIGQFWRGLPASINTAYERKDGKVFVFKGDK---HWVFDEASLEPGYPKHIKELGRGLPTDKID 416  
gi | 24762711 | ref | NP\_726473.1 | ... PDDRRGIQQLYGSSESQSPKMPPOPRITSRPSVDPKPKNPYGNICDGN--FDIVAMLRGEMFVFKERFWVRVRRNNOVMDGYMPPIGQFWRGLPASINTAYERKDGKVFVFKGDK---HWVFDEASLEPGYPKHIKELGRGLPTDKID 408  
gi | 158286645 | ref | XP\_001688107.1 | ... DSDDIGIQLYGSSESQSPKMPPOPRITSRPSVDPKPKNPYGNICDGN--FDIVAMLRGEMFVFKERFWVRVRRNNOVMDGYMPPIGQFWRGLPASINTAYERKDGKVFVFKGDK---HWVFDEASLEPGYPKHIKELGRGLPTDKID 399  
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 73962351 | ref | XP\_848757.1 | ... AALFWMPNGKTYFFRGNKYRFFNEELRA--VDSSEYPKNIKVWEGIPESPRGSFMGSDEVFTYFYKGNKYWKFNQKLVKVEPG--YPKSALRDWMCPSGSRPDEGT---EEETEVIIEVDEEGS---GAVS--AAAVVLPVLL 551  
gi | 27806001 | ref | NP\_776815.1 | ... AALFWMPNGKTYFFRGNKYRFFNEELRI--VDSSEYPKNIKVWEGIPESPRGSFMGSDEVFTYFYKGNKYWKFNQKLVKVEPG--YPKSALRDWMCPSGSRPDEGT---EEETEVIIEVDEEGS---GAVS--AAAVVLPVLL 548  
gi | 4826834 | ref | NP\_004986.1 | ... AALFWMPNGKTYFFRGNKYRFFNEELRA--VDSSEYPKNIKVWEGIPESPRGSFMGSDEVFTYFYKGNKYWKFNQKLVKVEPG--YPKSALRDWMCPSGSRPDEGT---EEETEVIIEVDEEGS---GAVS--AAAVVLPVLL 548  
gi | 114652041 | ref | XP\_001157686.1 | ... AALFWMPNGKTYFFRGNKYRFFNEELRA--VDSSEYPKNIKVWEGIPESPRGSFMGSDEVFTYFYKGNKYWKFNQKLVKVEPG--YPKSALRDWMCPSGSRPDEGT---EEETEVIIEVDEEGS---GAVS--AAAVVLPVLL 548  
gi | 31982191 | ref | NP\_032634.2 | ... AALFWMPNGKTYFFRGNKYRFFNEEFRA--VDSSEYPKNIKVWEGIPESPRGSFMGSDEVFTYFYKGNKYWKFNQKLVKVEPG--YPKSALRDWMCPSGSRPDEGT---EEETEVIIEVDEEGS---GAVS--AAAVVLPVLL 548  
gi | 13591995 | ref | NP\_112318.1 | ... AALFWMPNGKTYFFRGNKYRFFNEEFRA--VDSSEYPKNIKVWEGIPESPRGSFMGSDEVFTYFYKGNKYWKFNQKLVKVEPG--YPKSALRDWMCPSGSRPDEGT---EEETEVIIEVDEEGS---GAVS--AAAVVLPVLL 548  
gi | 35903119 | ref | NP\_919397.1 | ... AAFYVPTGNLYFFRGNKYRFFNEESRS--VDSSEYPKNIKVWEGIPESPRGSFMGSDEVFTYFYKGNKYWKFNQKLVKVEPG--YPKSALRDWMCPSGSRPDEGT---EEETEVIIEVDEEGS---GAVS--AAAVVLPVLL 540  
gi | 24762711 | ref | NP\_726473.1 | ... AAMVWGGNCKIYFFFKGKWRFDPAKRPVVKASYPKPISNWEGVPPNLDAAALQYIN--GYTYFFKDKYRFDHARFAVDSAPPPFPAHWWYVCKNIPSTQNVIGESDNEFQGHADDGNDGDDAAGVDQNDQFIVPEVA 576  
gi | 158286645 | ref | XP\_001688107.1 | ... AAMVWGGNCKIYFFFKGKWRFDPLRPPVVK--TYPKPISNWEGVPPNLDAAALQYIN--GYTYFFKDKYRFDHARFAVDSAPPPFPAHWWYVCKNIPSTQNVIGESDNEFQGHADDGNDGDDAAGVDQNDQFIVPEVA 576  
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 73962351 | ref | XP\_848757.1 | ... LLLVLAVGLAVFFFRHGTPKRLLYCORSLLDKV--- 585  
gi | 27806001 | ref | NP\_776815.1 | ... LLLVLAVGLAVFFFRHGTTPKRLLYCORSLLDKV--- 582  
gi | 4826834 | ref | NP\_004986.1 | ... LLLVLAVGLAVFFFRHGTTPRRLLYCORSLLDKV--- 582  
gi | 114652041 | ref | XP\_001157686.1 | ... LLLVLAVGLAVFFFRHGTTPRRLLYCORSLLDKV--- 582  
gi | 31982191 | ref | NP\_032634.2 | ... LLLVLAVGLAVFFFRHGTTPKRLLYCORSLLDKV--- 582  
gi | 13591995 | ref | NP\_112318.1 | ... LLLVLAVGLAVFFFRHGTTPKRLLYCORSLLDKV--- 582  
gi | 35903119 | ref | NP\_919397.1 | ... LACVLVTLGALLFFRRYGTTPRRLLYCHRSLLDKV--- 574  
gi | 24762711 | ref | NP\_726473.1 | ... ERVNGAMSQSKLSSAVSTVITILMCLVSKLIVS 613  
gi | 158286645 | ref | XP\_001688107.1 | ... GYSGNGASITIGSVSITIALAGFLLYGAYLVSR--- 570  
.....610.....620.....630.....

