

gi	24639634	ref	NP_726910.1	-----MSEVRIIRPQVLLIIVFLVLMVHRNK-----RIGCGPEYLQ-----AMFVGDTLPTIYAVTPIYPRPAQKAELTR	70
gi	158290519	ref	XP_312113.4	-----MNQEVRRFR-RKHVIIIFLSIVGILFIYLSSS-----RDCAGTGGGR-----DAFLPNRRGPTIYAVTPIYARPVQKAELTR	70
gi	62632721	ref	NP_001015059.1	-----MRLKIKTTFVLYFMVSLFGLLYALMQLGRCDCR-----DHEQSKD-----QOISOLKGELOKIQEHIKTSELKKTDPRIYVITPTYSRLVQKAELTR	90
gi	121582394	ref	NP_001073531.1	-----MRMLKIKTTFVLYFMVSLFGLLYALMQLGRCDCR-----DHEQSKD-----QOISOLKGELOKIQEHIKTSELKKTDPRIYVITPTYSRLVQKAELTR	92
gi	73983813	ref	XP_540906.2	-----MKLKLKNVFLAYFLVSIAGLLYALVQLGQPCDCLPPLRAAAEQLROKD-----LRISQLQADLRRPPP--APAQPEPEALPTIYVVTPTIYARLVQKAELVR	95
gi	75832093	ref	NP_991374.2	-----MKLKLKNVFLAYFLVSIAGLLYALVQLGQPCDCLPPLRAAAEQLROKD-----LRISQLQADLRRPPP--APAQPEPEALPTIYVVTPTIYARLVQKAELVR	95
gi	13195672	ref	NP_077218.1	-----MKLKLKNVFLAYFLVSIAGLLYALVQLGQPCDCLPPLRAAAEQLROKD-----LRISQLQADLRRPPP--VPAQPEPEALPTIYVVTPTIYARLVQKAELVR	95
gi	12408654	ref	NP_036332.2	-----MKLKLKNVFLAYFLVSIAGLLYALVQLGQPCDCLPPLRAAAEQLROKD-----LRISQLQADLRRPPP--APAQPEPEALPTIYVVTPTIYARLVQKAELVR	95
gi	114638025	ref	XP_001142393.1	MTGSPVPRRCQPOLGAGRGVGRRRDAGRILCRGGACGQDRGLKLNVFLAYFLVSIAGLLYARVQLGQPCDCLPPLRAAAEQLROKD-----LRISQLQADLRRPPP--APAQPEPEALPTIYVVTPTIYARLVQKAELVR	127
gi	17535739	ref	NP_496076.1	-----MPPSRLLEKWLRAFIALVLIFFVWQLFYAINRQVSLERATLQATIEVLTRKSDGLRITQIFEKERNLVRNLGVVEIDTQIRDHLSLLPRVNRSPPTIYVITPTIYHRAAGRADLIR	117



gi	24639634	ref	NP_726910.1	LSHLFMLLPHLHWIIVEDINATPLVNRLLDRAGLEKRSLLNLIKTPSEFKLKGKDPNWKPRGVEQRNLALAWLRN-----HVDVDRHSIVFFMDDDNYSYTELFAEMSKIERGRVGVVPGVLVGGMLVERPLLTEDGTVKVTGF	210
gi	158290519	ref	XP_312113.4	LSQVIRLVPNVFWVIVEDASQSTLVTNLLRRSGLQERSVQLFAKTPNFKLQCKDPNWLKPRGVEQRNEALKWIRNRKHNAL--GEPESPSSHSIVFFMDDDNYSYTELFEEMSTIERGKVGWVPGVLVGGMLVERPVLNRDGLVLGTF	217
gi	62632721	ref	NP_001015059.1	LAHTFLHVPQLHWIIVVEDAQOQLVSDFLSASGLT--YTHLNKLTPKERKLEGGDPNWLKPRGAEQRNEGLRWLRWMSGTVHG--KEAAALEEAVVVFADDNNTYSLQLFEEEMRYTYR--VSVVPGVLVGGMKFERFVVEDGK--VVRFF	232
gi	121582394	ref	NP_001073531.1	LAHTFLHVPQLHWIIVVEDAQOQLVSDFLSASGLT--YTHLNKLTPKERKLEGGDPNWLKPRGAEQRNEGLRWLRWMSGTVHG--KEAAALEEAVVVFADDNNTYSLQLFEEEMRYTYR--VSVVPGVLVGGRRYERFLVEKGGK--VVGW	234
gi	73983813	ref	XP_540906.2	LSQTLSELVPRLHWLLVEDAEGPTPLVSGLLAASGLL--FTHLAVLTPKAQRLREGEFGVWRPRGVEQRNRALDNLRSGGGAVGGEKDPPTGQGVVVFADDNNTYSRELFEEMRWTRG--VSVVPGVLVGGMLRFEFGPQVODGR--VVG	239
gi	75832093	ref	NP_991374.2	LSQTLSELVPRLHWLLVEDAEGPTPLVSGLLAASGLL--FTHLAVLTPKAQRLREGEFGVWRPRGVEQRNRALDNLRSGGGAVGGEKDPPTGQGVVVFADDNNTYSRELFEEMRWTRG--VSVVPGVLVGGMLRFEFGPQVODGR--VVG	239
gi	13195672	ref	NP_077218.1	LSQTLSELVPRLHWLLVEDAEGPTPLVSGLLAASGLL--FTHLAVLTPKAQRLREGEFGVWRPRGVEQRNKALDNLRSGGGAVGGEKDPPTGQGVVVFADDNNTYSRELFEEMRWTRG--VSVVPGVLVGGMLRFEFGPQVODGR--VVG	239
gi	12408654	ref	NP_036332.2	LSQTLSELVPRLHWLLVEDAEGPTPLVSGLLAASGLL--FTHLAVLTPKAQRLREGEFGVWRPRGVEQRNKALDNLRSGGGAVGGEKDPPTGQGVVVFADDNNTYSRELFEEMRWTRG--VSVVPGVLVGGMLRFEFGPQVODGR--VVG	239
gi	114638025	ref	XP_001142393.1	-----DPE-----ANLQ-----QLSGVKVEGVVVFADDNNTYDLKIFGEMRRVKN--AGVVPVGVVGGMVFETPILKNG-SISHE	134
gi	17535739	ref	NP_496076.1	LSYTLSEVPLNHWIIVVEDDELTPSITAGILKRSKIP--NTHLNARTPSDQKMRYYDPPNWTLPKRGVEQRNRALLWN--QLSGVKVEGVVVFADDNNTYDLKIFGEMRRVKN--AGVVPVGVVGGMVFETPILKNG-SISHE	252



gi	24639634	ref	NP_726910.1	NAAWRPERPPFIDMAFAISMDLFRNPOATFSY-EVQRGYQESSEILRHL--TRDQLOPLANRCQDVLVWHTRETKKLAABEALLKKGQRSDGGMEV-----	306
gi	158290519	ref	XP_312113.4	NFAWKPERPPFLDMAGFAISSDLEENPOAQFSY-EVERGYQESSEILRHL--IVHDMQPLANRCQDVLVWHTRETETPKLDAEKALQKSGKKENDGMEV-----	313
gi	62632721	ref	NP_001015059.1	HTGWRPNRPPFIDMAGFAVSLRLVLTNKEALFDG-DAQMGFLESSFLQHL--VTMDLPEKADLCQKVLVWHTRETKPKMKREBALLKQGMGSDPDEV-----	328
gi	121582394	ref	NP_001073531.1	YTGWKADRPPFAIDMAGFAVSLQVILSNPRALFKRRGAKPGMESDFLQI--EKVEDLEPKAKNCQVLVWHTRETKVNLGNE--PKRQDS-VFIEV-----	327
gi	73983813	ref	XP_540906.2	HTAWEPNRPFPVDMAGFAVALSLLAKPNAQFDA-TAPRGHLESSLSHL--VDPKDLPEPRAANCQVLVWHTRETKPKMKQEBEQLORQGSDPAVEV-----	335
gi	75832093	ref	NP_991374.2	HTAWEPNRPFPVDMAGFAIALSLLAKPNAQFDA-TAPRGHLESSLSHL--VDPKDLPEPRAANCQVLVWHTRETKPKMKQEBEQLORQGSDPAVEV-----	335
gi	13195672	ref	NP_077218.1	HTAWEPNRPFPVDMAGFAVALPPLLAKPNAQFDA-TAPRGHLESSLSHL--VDPKDLPEPRAANCQVLVWHTRETKPKMKQEBEQLORQGSDPAIEV-----	335
gi	12408654	ref	NP_036332.2	HTAWEPNRPFPVDMAGFAVALPPLLAKPNAQFDS-TAPRGHLESSLSHL--VDPKDLPEPRAANCQVLVWHTRETKPKMKQEBEQLORQGSDPAIEV-----	335
gi	114638025	ref	XP_001142393.1	-----LGLALTASLLA-----QVLVWHTRETKPKMKQEBEQLORQGSDPAIEV-----	178
gi	17535739	ref	NP_496076.1	NAVWKPERPPFIDMAFAVNISLVLSNANALFSF-DVPRGYQESTPLENIGIHRYNMEPLAEMCKVYVWHTRETKPKLSKESIDRLTKKTFNLSLEAHLGVDN-----	356

