

gi | 189458821 | ref | NP_003236.3 | -----MAALGVQSLINWQAFNRQAHHHTDKFSSQELILRRGONFQVLMIMNKGLGNSNERLEFIVSTGPPYFESAMTKAVFPL-NGSSGGWAVLQAENGNTLITISISSPASAPIGRYTALQIFSGGGISSVKLGTIFILL 134
gi | 114680537 | ref | XP_514468.2 | -----MAALGVQSLINWQAFNRQAHHHTDKFSSQELILRRGONFQVLMIMNKGLGNSNERLEFIVSTGPPYFESAMTKAVFPL-NGSSGGWAVLQAENGNTLITISISSPASAPIGRYTALQIFSGGGISSVKLGTIFILL 134
gi | 124001551 | ref | NP_033400.2 | -----MSALQIQNVNWOVPMNRAHHHTDKFSSQDFIVRRGQPEWILLVNRSLSEGDNLNFIVSTGPPQESARTKAVFPLS-GRSTGGWNAALKANSNGLAATAASPVSAPIGLYTLNVEVSSKGRVSSVKLGTIFIML 134
gi | 109468815 | ref | XP_345433.3 | -----MSALEVQININWOMPMMNRAHHHTDKFSSQDFIVRRGQPEWILLVNRSLSEGDNLNFIVSTGPPQESARTKAVFPLS-GRNTSGWNAALKANSNGLAATAASPVSAPIGLYTLNVEVSSKGRVSSVKLGTIFIML 134
gi | 73992006 | ref | XP_534370.2 | -----MVVPLFCLLALPQSLINWQAFNRQAHHHTDKFSSQELILRRGONFQVLMIMNKGLGNSNERLEFIVSTGPPYFESAMTKAVFPLS-GRSTGGWNAELVSNKDNILITISISSPVNAPVQWYTLSTQISSQKDFILKLGIMFILL 142
gi | 156120345 | ref | NP_001095318.1 | -----MSGL--QSVVDQIASNRQAHHHTERFYKDLVRRGOLFQVSLTSLGSLSGGRVTFEASTGPPYFESAMTKAVFPLSNGTSSGGWGAQVLSERNVNLNLSILSPANAPIGRYTALQIFSGGGISSVKLGTIFILL 133
gi | 118100635 | ref | XP_417392.2 | MVFFVSLDIEPQLLQAAQPSIDWHVVENGRDHHHTSKFSSKELIVRRG--AFVITFNGVEQPEQLTPTFIVEIGPKPKQAKTQATFGISTVSKDSWAVLQSSSHSVVSISSPPNAVIGRYKLSVOSTGSSPETLGTIFVLL 148



gi | 189458821 | ref | NP_003236.3 | FNPWLNVDVFMGNHAEREYVQEDAGIIFVGSNTRIGMIGWVFGQFEEDILSICLSILDRSLNFRDDAADVARRNDPKYVGRVLSAMINSDDNGVLAGNWSGTITGGRDPRSNWGSVEILKNWKKSGFSPVRYGCWVFAGTLNLTAL 284
gi | 114680537 | ref | XP_514468.2 | FNPWLNVDVFMGNHAEREYVQEDAGIIFVGSNTRIGMIGWVFGQFEEDILSICLSILDRSLNFRDDAADVARRNDPKYVGRVLSAMINSDDNGVLAGNWSGTITGGRDPRSNWGSVEILKNWKKSGFSPVRYGCWVFAGTLNLTAL 284
gi | 124001551 | ref | NP_033400.2 | FNPWLDQDDVFMNSHAERQYVEEDSGIIVVGSNTRIGMIGWVFGQFEEDILSILSILDRSLNFRDDPVDVARRNDPKYVGRVLSAMINGDDNGVLSGNWGSNVTGGVDPRTWNGSVEILKNWKKSGFSPVRYGCWVFAGTLNLTAL 284
gi | 109468815 | ref | XP_345433.3 | FNPWQGGDDVFMNSHAERQYVEEDSGIIVVGSNTRIGMIGWVFGQFEEDILSILSILDRSLNFRDDPVDVARRNDPKYVGRVLSAMINANDDSSVLSGNWGSNVTGGVDPRTWNGSVEILKNWKKSGFSPVRYGCWVFAGTLNLTAL 284
gi | 73992006 | ref | XP_534370.2 | FNPWLQEDGVFMSNHVEREYVLEDAGIIVVGSNTRIGMIGWVFGQFEEDILSICLSILDRSLNFRDDPVDVARRNDPKYVGRVLSAMVNGDDNGVLSGNWGSNVTGGVDPRTWNGSVEILKNWKKSGFSPVRYGCWVFAGTLNLTAL 292
gi | 156120345 | ref | NP_001095318.1 | FNPWLQADSVFMSNHVEREYVLEDAGIIFVGSNTRISMIGWVYGFEEGILNLSILDRSLNFRDDPVDVARRNDPKYVGRVLSAMINGDDSGVLSGNWGSNVTGGVDPRTWNGSVEILKNWKKSGFSPVRYGCWVFAGTLNLTAL 283
gi | 118100635 | ref | XP_417392.2 | FNPWSSGDNVFMNKAERCEYVLEEFGLIFAGNNYHINSFQWVFGQFEADILNLSILDRSLNFRDDPVDVARRNDPKYVGRVLSAMVANDDQGVVLSGNWGSNVTGGVDPRTWNGSVEILKNWKKSGFSPVRYGCWVFAGTLNLTAL 298



gi | 189458821 | ref | NP_003236.3 | RSLGIPSRVITNFNSAHDIDRNLSVDVYDPMGNPLDKGSDSVNHFVWNEGFVRSDLGSPYGGWQVLDATPQERSQGVFCGPPASVIGVREGDVQLNDFDMPFIFAENVADRITWLYDNTTGKQWKNVSNVSHIIGRYISTKAVGNSARM 434
gi | 114680537 | ref | XP_514468.2 | RSLGIPSRVITNFNSAHDIDRNLSVDVYDPMGNPLDKGSDSVNHFVWNEGFVRSDLGSPYGGWQVLDATPQERSQGVFCGPPASVIGVREGDVQLNDFDMPFIFAENVADRITWLYDNTTGKQWKNVSNVSHIIGRYISTKAVGNSARM 434
gi | 124001551 | ref | NP_033400.2 | RCLGVPSRVITNFNSAHDIDRNLSVDVYDPMGNPLDKGSDSVNHFVWNEGFVRSDLGSPYGGWQVLDATPQERSQGVFCGPPASVIAIKAGVDVDFMDFIFAENVADRITWLYDNTTGKQWKNVSNVSHIIGRYISTKAVGNSARM 434
gi | 109468815 | ref | XP_345433.3 | RCLGVPSRVITNFNSAHDIDRNLSVDVYDPMGNPLDKGSDSVNHFVWNEGFVRSDLGSPYGGWQVLDATPQERSQGVFCGPPASVIAIKAGVDVDFMDFIFAENVADRITWLYDNTTGKQWKNVSNVSHIIGRYISTKAVGNSARM 434
gi | 73992006 | ref | XP_534370.2 | RSFGIPSRVITNFNSAHDIDRNLSVDVYDPMGNPLDKGSDSVNHFVWNEGFVRSDLGSPYGGWQVLDATPQERSQGVFCGPPASVIAIKAGVDVDFMDFIFAENVADRITWLYDNTTGKQWKNVSNVSHIIGRYISTKAVGNSARM 442
gi | 156120345 | ref | NP_001095318.1 | RCLGIPSRVITNFNSAHDIDRNLSVDVYDPMGNPLDKGSDSVNHFVWNEGFVRSDLGSPYGGWQVLDATPQERSQGVFCGPPASVIAIKAGVDVDFMDFIFAENVADRITWLYDNTTGKQWKNVSNVSHIIGRYISTKAVGNSARM 432
gi | 118100635 | ref | XP_417392.2 | RCLGIPTRPTNFNSAHDIDRNLSVDVYDPMGNPLDKGSDSVNHFVWNEGFVRSDLGSPYGGWQVLDATPQERSQGVFCGPPASVIAIKAGVDVDFMDFIFAENVADRITWLYDNTTGKQWKNVSNVSHIIGRYISTKAVGNSARM 448



gi | 189458821 | ref | NP_003236.3 | DVTDKYYPEGSDQERQVFKALGKLPNTPFAATSSMGLTEBEQEPSIIGKLVAGMLAVGKEVNLVLLKLNLSRDTKVTVMNTAWTIIYNGILVHEVWKDSATMSLDPPEEAHPIKISYAYEKYKSDNMIRITAVCKVPEDESEV 584
gi | 114680537 | ref | XP_514468.2 | DVTDKYYPEGSDQERQVFKALGKLPNTPFAATSSMGLTEBEQEPSIIGKLVAGMLAVGKEVNLVLLKLNLSRDTKVTVMNTAWTIIYNGILVHEVWKDSATMSLDPPEEAHPIKISYAYEKYKSDNMIRITAVCKVPEDESEV 584
gi | 124001551 | ref | NP_033400.2 | DVTDKYYPEGSEERQVFKALGKLPNTPFAATSSMGLTEBEQEPSIIGKLVAGMLAVGKEVNLVLLKLNLSRDTKVTVMNTAWTIIYNGILVHEVWKDSATMSLDPPEEAHPIKISYAYEKYKSDNMIRITAVCKVPEDESEV 584
gi | 109468815 | ref | XP_345433.3 | DVTDKYYPEGSEERQVFKALGKLPNTPFAATSSMGLTEBEQEPSIIGKLVAGMLAVGKEVNLVLLKLNLSRDTKVTVMNTAWTIIYNGILVHEVWKDSATMSLDPPEEAHPIKISYAYEKYKSDNMIRITAVCKVPEDESEV 584
gi | 73992006 | ref | XP_534370.2 | DITEKYKHPGESSQERQVFEKALGKLPNTPFAATSSMGLTEBEQEPSIIGKLVAGMLAVGKEVNLVLLKLNLSRDTKVTVMNTAWTIIYNGILVHEVWKDSATMSLDPPEEAHPIKISYAYEKYKSDNMIRITAVCKVPEDESEV 592
gi | 156120345 | ref | NP_001095318.1 | DVTEKYKHPGESSQERQVFEKALGKLPNTPFAATSSMGLTEBEQEPSIIGKLVAGMLAVGKEVNLVLLKLNLSRDTKVTVMNTAWTIIYNGILVHEVWKDSATMSLDPPEEAHPIKISYAYEKYKSDNMIRITAVCKVPEDESEV 582
gi | 118100635 | ref | XP_417392.2 | DVTSYKVEGSKKERDIFKARKKLGLEDKDPNAP-TPKEIEQKFDISGKFKMAGPLEVQKDLNLLVLLKLNLSRDTKVTVMNTAWTIIYNGILVHEVWKDSATMSLDPPEEAHPIKISYAYEKYKSDNMIRITAVCKVPEDESEV 597



gi | 189458821 | ref | NP_003236.3 | VVERDIILDNPTLLEVLNENARVRKPVVQMLFNSPLDEPVRDCVLMVEGSGLLLNKLDVPLIGPKERSRVRFDILPFRSGTKQLLADFFCNKFFPAIKAMLSIDVAE 693
gi | 114680537 | ref | XP_514468.2 | VVERDVILDNPTLLEVLNENARVRKPVVQMLFNSPLDEPVRDCVLMVEGSGLLLNKLDVPLIGPKERSRVRFDILPFRSGTKQLLADFFCNKFFPAIKAMLSIDVAE 693
gi | 124001551 | ref | NP_033400.2 | VVERDVILDNPTLLEVLNENARVRKPVVQMLFNSPLDEPVRDCVLMVEGSGLLLNKLDVPLIGPKERSRVRFDILPFRSGTKQLLADFFCNKFFPAIKAMLSIDVAE 693
gi | 109468815 | ref | XP_345433.3 | VVERDVILDNPTLLEVLNENARVRKPVVQMLFNSPLDEPVRDCVLMVEGSGLLLNKLDVPLIGPKERSRVRFDILPFRSGTKQLLADFFCNKFFPAIKAMLSIDVAE 693
gi | 73992006 | ref | XP_534370.2 | VVERDIILDNPTLLEVLNENARVRKPVVQMLFNSPLDEPVRDCVLMVEGSGLLLNKLDVPLIGPKERSRVRFDILPFRSGTKQLLADFFCNKFFPAIKAMLSIDVAE 701
gi | 156120345 | ref | NP_001095318.1 | VVERDIILDNPTLLEVLNENARVRKPVVQMLFNSPLDEPVRDCVLMVEGSGLLLNKLDVPLIGPKERSRVRFDILPFRSGTKQLLADFFCNKFFPAIKAMLSIDVAE 691
gi | 118100635 | ref | XP_417392.2 | LVORHIALDNPTLLEVLNENARVRKPVVQMLFNSPLDEPVRDCVLMVEGSGLLLNKLDVPLIGPKERSRVRFDILPFRSGTKQLLADFFCNKFFPAIKAMLSIDVAE 706

