

gi | 29570782 | ref | NP_056153.2 | ALPLLSSQTSVAERLVEOP-QLHPDVR-----TECESGTTSWESDDEEGPITPADNGPIPLSLVGDITLEKGTGQALDS--HPTMKDPVNVITPSSITPESSPTD-CLQNRADFDELGLGGSCPPMRESDTROENLKHKALVSNSSLHWIF 900
gi | 114681466 | ref | XP_001155675.1 | ALPLLSSQTSVAERLVEOP-QLHPDVR-----TECESGTTSWESDDEEGPITPADNGPIPLSLVGDITLEKGTGQALDS--HPTMKDPVNVITPSSITPESSPTD-CLQNRADFDELGLGGSCPPMRESDTROENLKHKALVSNSSLHWIF 821
gi | 194672336 | ref | XP_600364.4 | ALPLLPSRIPEPERLVEOL-VSHPEDR-----TECGSGTTAWERGDDEKLAPITPENSPPVRLALAGPTGLEEGGQAPDGGSNPTMKDPVNVITPSSITPESSSLAS-CLQDRPFDDSELDLDDSGPTTRESRSSROENLKHKAEVSPGGAAPWRF 917
gi | 90568303 | ref | NP_001035028.1 | ALPLLSSQTPVAEMLTEOP-KLLLDLR-----TECESGTTIPSESSSGRFLG-DLLGGGDOAFDN-----MKPEVSMTPITFISELSELAN-YLQDRPDDDLGLGATGLLIRE--SRQE-ALTEAPASGSPISWVF 884
gi | 118100785 | ref | XP_425716.2 | ALTVSALDSTALERPESEPELFCADR-----TEASCAVYQQAQSTVEVTVVPPAVGLSCPQAQAGIEGPAGGRVVSSELRDVGIPTVQLDYSADVKNSTSRPALLPELPSGGGKCEHPKVISRFRFNGSETVFEVQCCKVNYSDSKT 868
gi | 189536099 | ref | XP_001341242.2 | KISEQLDTPVPTPSESEFCSHODGRGEAESDSRINLTFVCTSSSNDIAISLVPISIPDLSLPRFAGQVDVIRTLAASQPWEGEKKAVALHPGHTVVICVHGS--DLKLPKETLVFARNGWVENREHEHSMREGMLEHRNGSDANGK 963



gi | 29570782 | ref | NP_056153.2 | LPSNDEVVKQPKPESREHIVSVEPQVGEWEKAAFTPPALPGDLTAEEGLDPLDLSLWTVPSRGGSDNSGYCOQVDIEKLLKINGDSEALSPHGESIDTASDFEGHLEDSSEADTREAAVTKGSSVDKID-EKPNWQNSAPLSKVNGD 1049
gi | 114681466 | ref | XP_001155675.1 | LPSNDEVVKQPKPESREHIVSVEPQVGEWEKAAFTPPALPGDLTAEEGLDPLDLSLWTVPSRGGSDNSGYCOQVDIEKLLKINGDSEALSPHGESIDTASDFEGHLEDSSEADTREAAVTKGSSVDKID-EKPNWQNSAPLSKVNGD 970
gi | 194672336 | ref | XP_600364.4 | GMSNDEAGGQPEPDRREHIVSVEPQVGEWEKAAFTPPALPGDLTAEEGLDPLDLSLWTVPSRGGSDNSGYCOQVDIEKLLKINGDSEALSPHGESIDTASDFEGHLEDSSEADTREAAVTKGSSVDKID-EKPNWQNSAPLSKVNGD 1065
gi | 90568303 | ref | NP_001035028.1 | ILSNDEVVKQPKPESREHIVSVEPQVGEWEKAAFTPPALPGDLTAEEGLDPLDLSLWTVPSRGGSDNSGYCOQVDIEKLLKINGDSEALSPHGESIDTASDFEGHLEDSSEADTREAAVTKGSSVDKID-EKPNWQNSAPLSKVNGD 1024
gi | 118100785 | ref | XP_425716.2 | VITAGAEVGVPLCNFHTLQAGRESDGKPSNEQNAESLLKSSSCDDPISQNRIDTSEKLRERHP--RTESEDDGQTLREAREFKANGDDEVQSTHSESTDTASDFEADVADENMEMCYRNLSCREVARKG--SFCQSSHEEDKISSN 1014
gi | 189536099 | ref | XP_001341242.2 | ESGSLPCLPRCAGEEDTCAHSDSITASDFENESQEDEMVDWHGTQMDGSGMGTQNTKLNRPVITQTSRLTSSIVNPPHQQPVVQAHSINQNHQTOVVIQACFNGVVPVQVHHPKHQAHTHAINHSQDITASAPSAQVQAYLTQT 1113



gi | 29570782 | ref | NP_056153.2 | MRLVTRTDGMVAPQSWVSRVCAVRQKIPDS-----LLLASTEYOPRAVCLMPGSSVEATNPLVMOLLOGSLPLEKVLPPAADDMSSESPVPLTKDQSHG--SLRMGSLHGLGKNSG-----MVDGSSPSSLRALKEPLLDS--CET 1184
gi | 114681466 | ref | XP_001155675.1 | MRLVTRTDGMVAPQSWVSRVCAVRQKIPDS-----LLLASTEYOPRAVCLMPGSSVEATNPLVMOLLOGSLPLEKVLPPAADDMSSESPVPLTKDQSHG--SLRMGSLHGLGKNSG-----MVDGSSPSSLRALKEPLLDS--CET 1105
gi | 194672336 | ref | XP_600364.4 | LSLVTRTDGMVAPQSWVSRVCAVPPKIPDS-----LLLASTEYOPRAVCLMPGSSVEATNPLVMOLLOGSLPLEKVLPPAADDMSSESPVPLTKDQSHG--SLRMGSLHGLGKNSG-----MVDGSSPSSLRALKEPLLDS--CET 1194
gi | 90568303 | ref | NP_001035028.1 | LSLVTRTDGMVAPQSWVSRVCAVPPKIPDS-----LLLASTEYOPRAVCLMPGSSVEATNPLVMOLLOGSLPLEKVLPPAADDMSSESPVPLTKDQSHG--SLRMGSLHGLGKNSG-----MVDGSSPSSLRALKEPLLDS--CET 1155
gi | 118100785 | ref | XP_425716.2 | LSLVTRTDGMVAPQSWVSRVCAVPPKIPDS-----LLLASTEYOPRAVCLMPGSSVEATNPLVMOLLOGSLPLEKVLPPAADDMSSESPVPLTKDQSHG--SLRMGSLHGLGKNSG-----MVDGSSPSSLRALKEPLLDS--CET 1157
gi | 189536099 | ref | XP_001341242.2 | EMDQERNLRLNDNGVVKLLLEDDTKFLGREDDLKLNKAGPPVGRVQVSSRPVIVTEANPLVQLLOGSLPLEKVLPPAADDMSSESPVPLTKDQSHG--SLRMGSLHGLGKNSG-----MVDGSSPSSLRALKEPLLDS--CET 1238



gi | 29570782 | ref | NP_056153.2 | GTGLARIEATQAPGAPQKNCKAVPSFDSLHPVTNPTITSSRKLSEMDSKE--QFSSFCEDQKEV---RAMSQDENSNAAPGKSPGDLTTSRTRPFSSPNV-ISFGPEQTRALGDSNVTGQCKKLFSGNVAALFLRPRPADPMLPAE 1328
gi | 114681466 | ref | XP_001155675.1 | GTGLARIEATQAPGAPQKNCKAVPSFDSLHPVTNPTITSSRKLSEMDSKE--QFSSFCEDQKEV---RAMSQDENSNAAPGKSPGDLTTSRTRPFSSPNV-ISFGPEQTRALGDSNVTGQCKKLFSGNVAALFLRPRPADPMLPAE 1249
gi | 194672336 | ref | XP_600364.4 | SNGCFARLEASQAPGAPQKNCKAVPSFDSLHPVTNPTITSSRKLSEMDSKE--QFSSFCEDQKEV---RAMSQDENSNAAPGKSPGDLTTSRTRPFSSPNV-ISFGPEQTRALGDSNVTGQCKKLFSGNVAALFLRPRPADPMLPAE 1337
gi | 90568303 | ref | NP_001035028.1 | SAGLVRAMASKAPAMSKIAKMTSLDQPETELTPSSGNLEBIDSKHLSLDFLCEBQKEG---HSLSQGDGPAAGPQCLGDHTTTSKVPFCSSTNVSLSFGSBOITDGTLDONNAGGHEKLFSGNVAALFLRPRPADPMLPAE 1300
gi | 118100785 | ref | XP_425716.2 | GAALPRAEDMENQVPEKHSKIGLTLSCQDQLANVASASQKPEDTSPRETFSSCFEBQKESKXVHRVQHNPLNVTTSQSEKPNPTPEPPLSPNV-GSLGPNQMGNTSVNQNVTGQCKKLFSGNVAALFLRPRPADPMLPAE 1306
gi | 189536099 | ref | XP_001341242.2 | PDDTVSDFQHKTPPARVSPGGRNFGSPPGSAPSRMAQCFEASPRS-ANQFSSQPGGVVPPGAVFVITLPLNSTRSMDMNQNAPVSEAVIKEHPGPLSRSETPERPSEFQHPNPNVQSVCVRNIPDAPSPPHGDLCPSE 1387



gi | 29570782 | ref | NP_056153.2 | IPPVFPSGKLGPSINMSG-GVQTPREDWAPK-HAFVGSVKNKETFVGG-PLKANAENRKAATGHSPLLELVGHLEGMFVMDLFFWKLPRE-----PGKGLSEPLEPSSLSQSLIKQAFYGKLSKLLS-----STSFNYSS-----S 1459
gi | 114681466 | ref | XP_001155675.1 | IPPVFPSGKLGPSINMSG-GVQTPREDWAPK-HAFVGSVKNKETFVGG-PLKANAENRKAATGHSPLLELVGHLEGMFVMDLFFWKLPRE-----PGKGLSEPLEPSSLSQSLIKQAFYGKLSKLLS-----STSFNYSS-----S 1380
gi | 194672336 | ref | XP_600364.4 | APPAFPNRKSFGPKTSLSG-GVQTPREDWAPK-HAFVGSVKNKETFVGG-PLKANAENRKAATGHSPLLELVGHLEGMFVMDLFFWKLPRE-----PGKGLSEPLEPSSLSQSLIKQAFYGKLSKLLS-----STSFNYSS-----S 1469
gi | 90568303 | ref | NP_001035028.1 | VPPVFPKRIEPSKNSVSG-GVQTPRENRMKPPPVASDSIKTQTLFRD-PIKADAENRKAAGYSLELVGHLEGMFVMDLFFWKLPRE-----PGKGLSEPLEPSSLSQSLIKQAFYGKLSKLLS-----STSFNYSS-----S 1432
gi | 118100785 | ref | XP_425716.2 | VGALAPKQIPLTKSCASAEQMPAAREEWTSKQHGNSLGGTKNENVLACGSPAKSSEGSQKDAANPAELREHQSQVPLVMDLFFWKLPRE-----AGKRNHPLEPSSLSQSLIKQAFYGKLSKLLS-----STSFNYSS-----S 1440
gi | 189536099 | ref | XP_001341242.2 | VVPTVKIN-WRPNKQOQPIIPVAVTQNEVSLRPSQQALTKNSPAPISGNTISVVTITKKEPLDGFHGGGGAMEGLLNMEMSLVLRMARKEQVKNPVRQADTASPVSSPSSASSLPPFQYGLPKLQSGGNGSSSSSYANVSVVD 1536



gi | 29570782 | ref | NP_056153.2 | SPPTFPKGLAGSVVQLSHKANFGAS--HSASLSLQMFDTSSIVESISLQACSLKAMIMCGCGAFCHDDCIGPSKLCVLCVVR 1541
gi | 114681466 | ref | XP_001155675.1 | SPPTFPKGLAGSVVQLSHKANFGAS--HSASLSLQMFDTSSIVESISLQACSLKAMIMCGCGAFCHDDCIGPSKLCVLCVVR 1462
gi | 194672336 | ref | XP_600364.4 | SPPTFPKGLAGSVVQLSHKANFGAS--HSASLSLQMFDTSSIVESISLQACSLKAMIMCGCGAFCHDDCIGPSKLCVLCVVR 1551
gi | 90568303 | ref | NP_001035028.1 | SATFPKGLAGSVVQLSHKANFGAS--HTASLSLQMFDTSSIVESISLQACSLKAMIMCGCGAFCHDDCIGPSKLCVLCVVR 1514
gi | 118100785 | ref | XP_425716.2 | APAFPRSLAGSMMLQTHKANFAAN--HNISLQVQMFADSSNVEIISFKCSSLKAMIMCKGCGAFCHDDCIGPSKLCVLCVVR 1522
gi | 189536099 | ref | XP_001341242.2 | GSGFTRTLADSVLQLRPRVSVSGGGQSATLGIQAFITDS-AAEVALKCSCKLKAMIMCGCGAFCHDDCIGPSKLCVLCVVR 1619

