

gi|31542017|ref|NP_848756.2|: : : : * . . . : : :
gi|109459467|ref|XP_219372.4|MELFQAKDHYILQOGERALWCSR---DGGLOLRPATDLLLAWNPICLGLVEGVIGKIQLE 150
gi|7662414|ref|NP_055752.1|MVIIVQKVOELWEGEGERPPGGLSDRVLGRVRSPSAEPPCSSVGVWFLGVSSRHGLCGRGGGGRLHRWAGRCGAWVGGPPPPGARGA 150
gi|114633046|ref|XP_508074.2|MELFQAKDHYILQOGERALWCSR---DGGLOLRPATDLLLAWNPICLGLVEGVIGKIQLE 150
gi|73998919|ref|XP_535034.2|MELFQAKDHYILQOGERALWCSR---DGGLOLRPATDLLLAWNPICLGLVEGVIGKIQLE 150
gi|118093078|ref|XP_421792.2|MVPGCFINSNFVFLFRISRAHLVPSKWNIPWFLFRPSTDLLLAWNPICLGLVEGVIGKIQLE 150
gi|187608145|ref|NP_001119904.1|MELFQAKDHYILQSGDNALWCSR---DGSMAVRPATDLLLAWNPICLGLVEGVIGKIQLE 150
gi|17509655|ref|NP_493393.1|MIITYTPTALILEQGERVEFDRR---NGKVLKPEESELLELDQDVPVLCGNVEFLIKISFD 150
gi|116008066|ref|NP_001036740.1|MEVFOQDSHYIFVKRDKSLWVHRR---TSEFSIKAGWDLSSVDDIEICIGVTHGIVGVISLF 150
gi|158288768|ref|XP_310609.3|MEVFOQETHYIFVKRERSLWVHRY---SSEFQLKCGWDLSSVDDIEICIGVTHGIVGVISLF 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|31542017|ref|NP_848756.2|: : : : * * : :
gi|109459467|ref|XP_219372.4|SDLPWWLLILIRKALVQKLPDHEVCVKVTKIAVLSLS EMEPOELELELCKKHHFGINKPEK 300
gi|7662414|ref|NP_055752.1|SDLPWWLLILIRKALVQKLPDHEVCVKVTKIAVLSLS EMEPOELELELCKKHHFGINKPEK 300
gi|114633046|ref|XP_508074.2|SDLPWWLLILIRKALVQKLPDHEVCVKVTKIAVLSLS EMEPOELELELCKKHHFGINKPEK 300
gi|73998919|ref|XP_535034.2|SDLPWWLLILIRKALVQKLPDHEVCVKVTKIAVLSLS EMEPOELELELCKKHHFGINKPEK 300
gi|118093078|ref|XP_421792.2|SDLPWWLLILIRKALVQKLPDHEVCVKVTKIAVLSLS EMEPOELELELCKKHHFGINKPEK 300
gi|187608145|ref|NP_001119904.1|VDFPLGLLILIRKALVQKLPDHEVCVKVTKIAVLSLS EMEPOELELELCKKHHFGINKPEK 300
gi|17509655|ref|NP_493393.1|EQHFLFFVDDSSVACVYRGTSAESSHSIRRIERVITAINVKS D-----G S V I K S ----- 300
gi|116008066|ref|NP_001036740.1|NVYEPHLVVVKEASAVGVLPYPPHLVYKIKSICITL SADDPTDLNCTKTKNSQSPTHSVTSNNNASVPSGGGSSKSTLFE G-----M N K T W G A V K S A G N T I K N T Q Q A A N L A T K V K S V G I R -----P R H I E R R I T E L H K I F D E T 300
gi|158288768|ref|XP_310609.3|G V L D P H L I V I K E V V P V G V L Y P H L V Y K I R S I A V L G P D G A D T V L L G C S K H T T S Q T V K V A P A G G T A A P D G H P E P A K G -----R L F E S S A L V N K T W G A V K S A G S T I R N T E K A A A I A T S V K S V I S L V K A D P V I R I E R R I T E L H K I F D E T 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|31542017|ref|NP_848756.2|: : : : * * : :
gi|109459467|ref|XP_219372.4|ESFYYSLYDYLINSVQROS TGERDGRPLWQKVD RFFFNK YMIQALTEIGTPD--VDFWIIPIIIGFVQIEELVNVNYESDDKSSPETPPOESTCVDDIHPRFVALISRRSRHRAGMRYKRRGV D K N G V A N Y V E T Q L I H V H N H T L 450
gi|7662414|ref|NP_055752.1|ESFYYSLYDYLINSVQROS TGERDGRPLWQKVD RFFFNK YMIQDLTEIGTPD--VDFWIIPIIIGFVQIEELVNVNYESDDKSSPETPPOESTCVDDIHPRFVALISRRSRHRAGMRYKRRGV D K N G V A N Y V E T Q L I H V H N H T L 450
gi|114633046|ref|XP_508074.2|ESFYYSLYDYLINSVQROS TGERDGRPLWQKVD RFFFNK YMIQDLTEIGTPD--VDFWIIPIIIGFVQIEELVNVNYESDDKSSPETPPOESTCVDDIHPRFVALISRRSRHRAGMRYKRRGV D K N G V A N Y V E T Q L I H V H N H T L 450
gi|73998919|ref|XP_535034.2|ESFYYSLYDYLINSVQROS AGERDRPLWQKVD RFFFNK YMIQDLTEIGTPE--VDFWILPIIIGFVQIEELVNVNYESDDKSSPETPPOESTCVDDIHPRFVALISRRSRHRAGMRYKRRGV D K N G V A N Y V E T Q L I H V H N H T L 450
gi|118093078|ref|XP_421792.2|DSFYYSLYDYLINSVQROSACERKTDLP LWRKVD RFFFNK YMIQDLTEIGTPE--VDFWILPIIIGFVQIEELVNVNYESDDKSSPETPPOESTCVDDIHPRFVALISRRSRHRAGMRYKRRGV D K N G V A N Y V E T Q L I H V H N H T L 450
gi|187608145|ref|NP_001119904.1|KDFYFCRERDVTIISQKYFEKRE---AHTSEDSFFFNKRMVGNLGEAKIS---DKFTCPIMOGYVAISQLEITD-----QINAYLTIITISRRSTRRAGARVLRGIDEASVNFVETELILNIFEHL 450
gi|17509655|ref|NP_493393.1|DSFYFSFDCDIITNLRHEAKSEES---SOPDRFFFNKHMIRDILNINL---DKTNIWLPPIIIGFMOVENCVIGN-----ECFTLALVSRSRHRAGTRVYKRRGVDEHGN CAN Y V E T Q I L S F R H H Q L 450
gi|158288768|ref|XP_310609.3|DSFYYSFNCDIITNLRGRGAP-----PDRFRVWNRPLAELLRVSEPPGEDVWVPIIIGFVQIEECVIGN-----ECFTLALVSRSRHRAGTRVYKRRGVDEHGN CAN Y V E T Q I L S R Q H Q I 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|31542017|ref|NP_848756.2|: : : : * * : :
gi|109459467|ref|XP_219372.4|SFIQTRGSPVPFWSQVGYRNP RPRLDKSEKETVDCFAHFEEQLKIYKK-QVIVNLVDQAGREKIIIGDAYLKVLLFNPKLYVVSFD FHEHCRGMKFENVQITLDAIHDIIDMKWCWVDQAGVICK-QEGIFRVN CMDCLDRINNVG 600
gi|7662414|ref|NP_055752.1|SFIQTRGSPVPFWSQVGYRNP RPRLDKSEKETVDCFAHFEEQLKIYKK-QVIVNLVDQAGREKIIIGDAYLKVLLFNPKLYVVSFD FHEHCRGMKFENVQITLDAIHDIIDMKWCWVDQAGVICK-QEGIFRVN CMDCLDRINNVG 600
gi|114633046|ref|XP_508074.2|SFIQTRGSPVPFWSQVGYRNP RPRLDKSEKETVDCFAHFEEQLKIYKK-QVIVNLVDQAGREKIIIGDAYLKVLLFNPKLYVVSFD FHEHCRGMKFENVQITLDAIHDIIDMKWCWVDQAGVICK-QEGIFRVN CMDCLDRINNVG 600
gi|73998919|ref|XP_535034.2|SFIQTRGSPVPFWSQVGYRNP RPRLDKSEKETVDCFAHFEEQLKIYKK-QVIVNLVDQAGREKIIIGDAYLKVLLFNPKLYVVSFD FHEHCRGMKFENVQITLDAIHDIIDMKWCWVDQAGVICK-QEGIFRVN CMDCLDRINNVG 600
gi|118093078|ref|XP_421792.2|SFIQTRGSPVPFWSQVGYRNP RPRLDKSEKETVDCFAHFEEQLKIYKK-QVIVNLVDQAGREKIIIGDAYLKVLLFNPKLYVVSFD FHEHCRGMKFENVQITLDAIHDIIDMKWCWVDQAGVICK-QEGIFRVN CMDCLDRINNVG 600
gi|187608145|ref|NP_001119904.1|SFIQTRGSPVPFWSQVGYRNP RPRLDKSEKETVDCFAHFEEQLKIYKK-QVIVNLVDQAGREKIIIGDAYLKVLLFNPKLYVVSFD FHEHCRGMKFENVQITLDAIHDIIDMKWCWVDQAGVICK-QEGIFRVN CMDCLDRINNVG 600
gi|17509655|ref|NP_493393.1|SFIQTRGSPVPFWSQVGYRNP RPRLDKSEKETVDCFAHFEEQLKIYKK-QVIVNLVDQAGREKIIIGDAYLKVLLFNPKLYVVSFD FHEHCRGMKFENVQITLDAIHDIIDMKWCWVDQAGVICK-QEGIFRVN CMDCLDRINNVG 600
gi|116008066|ref|NP_001036740.1|SFIQTRGSPVPFWSQVGYRNP RPRLDKSEKETVDCFAHFEEQLKIYKK-QVIVNLVDQAGREKIIIGDAYLKVLLFNPKLYVVSFD FHEHCRGMKFENVQITLDAIHDIIDMKWCWVDQAGVICK-QEGIFRVN CMDCLDRINNVG 600
gi|158288768|ref|XP_310609.3|SFIQTRGSPVPFWSQVGYRNP RPRLDKSEKETVDCFAHFEEQLKIYKK-QVIVNLVDQAGREKIIIGDAYLKVLLFNPKLYVVSFD FHEHCRGMKFENVQITLDAIHDIIDMKWCWVDQAGVICK-QEGIFRVN CMDCLDRINNVG 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 31542017 | ref | NP_848756.2 | AAIAARVVMEQQLKLLGVMPPEQPLPVKCNRIYQIMWANNGDSISROYAGTAALKGDFTRTGERKLAGVMKDGVNSANR 750
gi | 109459467 | ref | XP_219372.4 | AAIAARVVMEQQLKLLGVMPPEQPLPVKCNRIYQIMWANNGDSISROYAGTAALKGDFTRTGERKLAGVMKDGVNSANR 750
gi | 7662414 | ref | NP_055752.1 | AAIAARVVMEQQLKLLGVMPPEQPLPVKCNRIYQIMWANNGDSISROYAGTAALKGDFTRTGERKLAGVMKDGVNSANR 750
gi | 114633046 | ref | XP_508074.2 | AAIAARVVMEQQLKLLGVMPPEQPLPVKCNRIYQIMWANNGDSISROYAGTAALKGDFTRTGERKLAGVMKDGVNSANR 750
gi | 73998919 | ref | XP_535034.2 | AAIAARVVMEQQLKLLGVMPPEQPLPVKCNRIYQIMWANNGDSISROYAGTAALKGDFTRTGERKLAGVMKDGVNSANR 750
gi | 118093078 | ref | XP_421792.2 | AAIAARVVMEQQLKLLGVMPPEQPLPVKCNRIYQIMWANNGDSISROYAGTAALKGDFTRTGERKLAGVMKDGVNSANR 750
gi | 187608145 | ref | NP_001119904.1 | AAIAARVVMEQQLKLLGVMPPEQPLPVKCNRIYQIMWANNGDSISROYAGTAALKGDFTRTGERKLAGVMKDGVNSANR 750
gi | 17509655 | ref | NP_493393.1 | GQISLFLVVLQQAQRLLGIFGFLCEPPEVLLVQIMWANNGDSISROYAGTAALKGDFTRTGERKLAGVMKDGVNSANR 750
gi | 116008066 | ref | NP_001036740.1 | TAIGKAVLESRLVGLGLSPPYTPIPEQLKSPFMVLWANNGDIIISROYAGTALNKGDYTRTGERKISGMMDGMSANRRFIONFADSFRCIIDLMOGQLLRAEDLDEVELSTILGILTPETRPPLHGYINPGVLGPELQLLESIVTTR 750
gi | 158288768 | ref | XP_310609.3 | TAIGKAVLESRLVGLGLSPPYTPIPEQLKSPFMVLWANNGDIIISROYAGTALNKGDYTRTGERKISGMMDGMSANRRFIONFADSFRCIIDLMOGQLLRAEDLDEVELSTILGILTPETRPPLHGYINPGVLGPELQLLESIVTTR 750



gi | 31542017 | ref | NP_848756.2 | YYLSRFKDAYRQAVIDLMOGIPVTEEDLYSIFTRKEKEHEALHKEKSRSHOELISQLLQSYMQLLPGDEKFFHGGWALVDCDPSLTDAHRDVEVLLLLSNA 900
gi | 109459467 | ref | XP_219372.4 | YYLSRFKDAYRQAVIDLMOGIPVTEEDLYSIFTRKEKEHEALHKEKSRSHOELISQLLQSYMQLLPGDEKFFHGGWALVDCDPSLTDAHRDVEVLLLLSNA 900
gi | 7662414 | ref | NP_055752.1 | YYLSRFKDAYRQAVIDLMOGIPVTEEDLYSIFTRKEKEHEALHKEKSRSHOELISQLLQSYMQLLPGDEKFFHGGWALVDCDPSLTDAHRDVEVLLLLSNA 900
gi | 114633046 | ref | XP_508074.2 | YYLSRFKDAYRQAVIDLMOGIPVTEEDLYSIFTRKEKEHEALHKEKSRSHOELISQLLQSYMQLLPGDEKFFHGGWALVDCDPSLTDAHRDVEVLLLLSNA 900
gi | 73998919 | ref | XP_535034.2 | YYLSRFKDAYRQAVIDLMOGIPVTEEDLYSIFTRKEKEHEALHKEKSRSHOELISQLLQSYMQLLPGDEKFFHGGWALVDCDPSLTDAHRDVEVLLLLSNA 900
gi | 118093078 | ref | XP_421792.2 | YYLSRFKDAYRQAVIDLMOGIPVTEEDLYSIFTRKEKEHEALHKEKSRSHOELISQLLQSYMQLLPGDEKFFHGGWALVDCDPSLTDAHRDVEVLLLLSNA 900
gi | 187608145 | ref | NP_001119904.1 | YYLSRFKDAYRQAVIDLMOGIPVTEEDLYSIFTRKEKEHEALHKEKSRSHOELISQLLQSYMQLLPGDEKFFHGGWALVDCDPSLTDAHRDVEVLLLLSNA 900
gi | 17509655 | ref | NP_493393.1 | YYLSRFKDAYRQAVIDLMOGIPVTEEDLYSIFTRKEKEHEALHKEKSRSHOELISQLLQSYMQLLPGDEKFFHGGWALVDCDPSLTDAHRDVEVLLLLSNA 900
gi | 116008066 | ref | NP_001036740.1 | CAARRRYQAGVDGHAIERSHLKFIIVSSIAIYPLIILLQKVLFPPLHLLIILYYLARFKDSYRQATIDLMLGNQVSESLSALGG--DAGPDNDGTEN-ABQAKLLVEDCRRLLLGTAQYFVGAWGLIDADPSGSDINETEVDTLLLLTDD 900
gi | 158288768 | ref | XP_310609.3 | YYLARFKDYRQATIDLMLGNQVSESLSALGG--DAGPDNDGTEN-ABQAKLLVEDCRRLLLGTAQYFVGAWGLIDADPSGSDINETEVDTLLLLTDD 900



gi | 31542017 | ref | NP_848756.2 | AYYVAYYDDEVDKVNQYRSLGLEDLERIEIGPEPT---LFGKPKFSCMRLLHYRCKEAGGYFHTLRAVPRSPBEDGKDTLQCTAEMLOITKQAMGLDVPITTEKLERKSSKPHEDIIGIR---SQNGQS-LAQGKSFLLMSKFSSSLNOKV 1050
gi | 109459467 | ref | XP_219372.4 | AYYVAYYDDEVDKVNQYRSLGLEDLERIEIGPEPT---LFGKPKFSCMRLLHYRCKEAGGYFHTLRAVPRSPBEDGKDTLQCTAEMLOITKQAMGLDVPITTEKLERKSSKPHEDIIGIR---SQNGQS-LAQGKSFLLMSKFSSSLNOKV 1050
gi | 7662414 | ref | NP_055752.1 | AYYVAYYDDEVDKVNQYRSLGLEDLERIEIGPEPT---LFGKPKFSCMRLLHYRCKEAGGYFHTLRAVPRSPBEDGKDTLQCTAEMLOITKQAMGLDVPITTEKLERKSSKPHEDIIGIR---SQNGQS-LAQGKSFLLMSKFSSSLNOKV 1050
gi | 114633046 | ref | XP_508074.2 | AYYVAYYDDEVDKVNQYRSLGLEDLERIEIGPEPT---LFGKPKFSCMRLLHYRCKEAGGYFHTLRAVPRSPBEDGKDTLQCTAEMLOITKQAMGLDVPITTEKLERKSSKPHEDIIGIR---SQNGQS-LAQGKSFLLMSKFSSSLNOKV 1050
gi | 73998919 | ref | XP_535034.2 | AYYVAYYDDEVDKVNQYRSLGLEDLERIEIGPEPT---LFGKPKFSCMRLLHYRCKEAGGYFHTLRAVPRSPBEDGKDTLQCTAEMLOITKQAMGLDVPITTEKLERKSSKPHEDIIGIR---SQNGQS-LAQGKSFLLMSKFSSSLNOKV 1050
gi | 118093078 | ref | XP_421792.2 | AYYVAYYDDEVDKVNQYRSLGLEDLERIEIGPEPT---LFGKPKFSCMRLLHYRCKEAGGYFHTLRAVPRSPBEDGKDTLQCTAEMLOITKQAMGLDVPITTEKLERKSSKPHEDIIGIR---SQNGQS-LAQGKSFLLMSKFSSSLNOKV 1050
gi | 187608145 | ref | NP_001119904.1 | AYYVAYYDDEVDKVNQYRSLGLEDLERIEIGPEPT---LFGKPKFSCMRLLHYRCKEAGGYFHTLRAVPRSPBEDGKDTLQCTAEMLOITKQAMGLDVPITTEKLERKSSKPHEDIIGIR---SQNGQS-LAQGKSFLLMSKFSSSLNOKV 1050
gi | 17509655 | ref | NP_493393.1 | NLYIVTYEIDGEMTDVQIIVALEIDINTIQTGTSGN---NRQCARLETLEGVFIWRPSTVRLFNNTAIRLKSLEBANEYISSVAEQIVGRNMLTG---AEGSVVVPVAKIHIPQMSV 1050
gi | 116008066 | ref | NP_001036740.1 | CYIVAAYDSDHLDKIVRFKVLQTLQVRLIELGMHQQTIFQGSAPAHLCRLNYSVDQEGYFHMFRSANTLRFNNAAYVTKQEVVAESMTSIVEMFRIALDNAGNTEVRYITGGVLRQ---KSKLPTLDVPRGMPRNLSQSQVLDL 1050
gi | 158288768 | ref | XP_310609.3 | CYIVAAYDSDHLDKIVRFKVLQTLQVRLIELGMHQQTIFQGSAPAHLCRLNYSVDQEGYFHMFRSANTLRFNNAAYVTKQEVVAESMTSIVEMFRIALDNAGNTEVRYITGGVLRQ---KSKLPTLDVPRGMPRNLSQSQVLDL 1050



gi | 31542017 | ref | NP_848756.2 | KQTKSNVNIIGNLR---KLGNFTEKPEMKVNFLLKPNLKVNLWKSDDSSLETME-NPGVMGNKVGESDGDVSSDNDYSYHSDFLNLSKSEEDKOLANSLESVGFIDYVLPSCGIIASAPRLGSRSSQSSSTIDV---SIHAPSEAAAGPSELG 1200
gi | 109459467 | ref | XP_219372.4 | KQTKSNVNIIGNLR---KLGNFTEKPEMKVNFLLKPNLKVNLWKSDDSSLETME-NPGVMGNKVGESDGDVSSDNDYSYHSDFLNLSKSEEDKOLANSLESVGFIDYVLPSCGIIASAPRLGSRSSQSSSTIDV---SIHAPSEATVGHGHELG 1200
gi | 7662414 | ref | NP_055752.1 | KQTKSNVNIIGNLR---KLGNFTEKPEMKVNFLLKPNLKVNLWKSDDSSLETME-NPGVMGNKVGESDGDVSSDNDYSYHSDFLNLSKSEEDKOLANSLESVGFIDYVLPSCGIIASAPRLGSRSSQSSSTIDV---SIHAPSEATVGHGHELG 1200
gi | 114633046 | ref | XP_508074.2 | KQTKSNVNIIGNLR---KLGNFTEKPEMKVNFLLKPNLKVNLWKSDDSSLETME-NPGVMGNKVGESDGDVSSDNDYSYHSDFLNLSKSEEDKOLANSLESVGFIDYVLPSCGIIASAPRLGSRSSQSSSTIDV---SIHAPSEITVAHGSGLG 1200
gi | 73998919 | ref | XP_535034.2 | KQTKSNVNIIGNLR---KLGNFTEKPEMKVNFLLKPNLKVNLWKSDDSSLETME-NPGVMGNKVGESDGDVSSDNDYSYHSDFLNLSKSEEDKOLANSLESVGFIDYVLPSCGIIASAPRLGSRSSQSSSTIDV---SIHAPSEI-VAHGSGLG 1200
gi | 118093078 | ref | XP_421792.2 | KQTKSNVNIIGNLR---KLGNFTEKPEMKVNFLLKPNLKVNLWKSDDSSLETME-NPGVMGNKVGESDGDVSSDNDYSYHSDFLNLSKSEEDKOLANSLESVGFIDYVLPSCGIIASAPRLGSRSSQSSSTIDV---SIHAPSEI-VAHGSGLG 1200
gi | 187608145 | ref | NP_001119904.1 | KQTKSNVNIIGNLR---KLGNFTEKPEMKVNFLLKPNLKVNLWKSDDSSLETME-NPGVMGNKVGESDGDVSSDNDYSYHSDFLNLSKSEEDKOLANSLESVGFIDYVLPSCGIIASAPRLGSRSSQSSSTIDV---SIHAPSEI-VAHGSGLG 1200
gi | 17509655 | ref | NP_493393.1 | HRKSMAMGALFG---KIKRVGKP 1200
gi | 116008066 | ref | NP_001036740.1 | SSKALSNMAGQFS---KLGQTFKPKQAHPSLLAATMNPQVMRQRDSEIESQEAEEKAVFTLGRKHNSNSASSTIDEDHNSLYEPEVSDSDEIAMDKNYNENAFPLPSVGVIMGN---QKEDSPSSSDEIR---HLEQKDSMCKITEDVL 1200
gi | 158288768 | ref | XP_310609.3 | GSKAFSNMAGQFS---KIGQSLNASKIGRSGGSKGKPKGG-ADDAVAGD--GAAARSRRDSSGSRSSSEEE-GACMYEPED---ELVEQNPLYNENVFLPVGIVMGCGGAGEGEGVGSASS---VLEERDSIAKMSDLS 1200



gi|31542017|ref|NP_848756.2| KGLESP^LLK^KSP^SAD^SI^HTR^LGF^TK^PMD^VY^CQ^RFV^DA^NK^MN^DL^SE^IR^SV^AK^S-EEG^SH^KT^N-R^VS^NEE^TQ^SE^PM^GT^PPP^RPS^QL^NV^SC^SV^AG^PPP^LS^VE^PV^HS^VL^SO^KT^PSS^GSS^LL^LE^AG^LC^VT^PS-SESS^SRAV^SPF^AK^IR^SSM 1350
 gi|109459467|ref|XP_219372.4| KGLESP^LLK^KSP^SAD^NI^HT^LGF^AK^PM^DV^YC^QR^FV^DA^NK^MN^AL^SE^VR^AV^AQ^NS-EEG^NH^KT^N-P^VS^NEE^TQ^SE^VE^OM^PS^RPS^QL^NV^SC^SV^TG^POLL^SV^EP^AH^PA^VS^OK^TP^GS^GSS^LL^DL^EA^GL^CV^TP^S-SESS^S-RAV^SPF^AK^IR^SSM 1350
 gi|7662414|ref|NP_055752.1| KQ^ES^PL^KK^SPS^AG^DV^HI^LTG^FA^KP^MD^IY^CH^RF^VO^DA^NK^VT^HL^SE^TR^SV^SO^QA^SO^ER^NO^MT^N-Q^VS^N-E^TO^SE^ST^EQ^TP^SR^PS^QL^DV^SL^SA^TG^PO^FL^SV^EP^AH^SV^AS^OK^TP^TS^ASS^ML^EL^TG^LH^VT^PS^PSESS^SRAV^SPF^AK^IR^SSM 1350
 gi|114633046|ref|XP_508074.2| KQ^ES^PL^KK^SPS^AG^NV^HI^LTG^FA^KP^MD^IY^CH^RF^VO^DA^NK^VT^HL^SE^TR^SV^SO^QA^SO^ER^NO^MT^N-Q^VS^NEE^TQ^SE^ST^EQ^TP^SR^PS^QL^DV^SL^SA^TG^PO^FL^SV^EP^AH^SV^AS^OK^TP^TS^ASS^ML^EL^TG^LH^VT^PS^PSESS^SRAV^SPF^AK^IR^SSM 1350
 gi|73998919|ref|XP_535034.2| KG^HE^SP^LK^KSP^SAD^NI^VL^LTG^FA^KP^VD^IY^CH^RF^VO^DA^NK^MT^QL^SE^TG^SV^SO^QA^SEE^GN^OM^TH-Q^VS^NEE^TQ^SE^ST^EQ^TP^SR^PS^QL^DV^SF^PA^TG^PO^YL^SV^EP^VH^PV^VG^OK^TP^GS^ASS^ML^EL^TG^LQ^VT^PS^PSESS^SRAV^SPF^AK^IR^SSM 1350
 gi|118093078|ref|XP_421792.2| DG^ED^VP^V---P^SAD^N--A^EM^EF^AK^PI^DV^YC^QR^FV^DA^NK^MS^DA^LE^AE^TC^SE^EP^RH^VI^NE^TS^NN^VC^KA^EN^KE^TI^GG^IP^SR^PS^KL^DV^QS^EP^N-P^OL^LA^VH^GI^DF^IK^SH^RS^PG^SA^SG--I^LE^TG^LH^TT^PS^AD^SSS^SRAV^SPF^AK^IR^SSM 1350
 gi|187608145|ref|NP_001119904.1| VA^AD^QS^PG-AA^SE^AE^AE^AI^LI^DF^GT^PI^DV^YC^HQ^FV^DA^KT^KP^IE^VF^EV^AP^AK^PQ^GP^VL^AP---D^AK^LG^SS^HS^QN^OL^RP^RS^OL^EV^SN^VH^GA^NL^LV^QP^VG----S^AL^SC^GS^QK^SL^EG--I^TG^PS^AD^SSS^SRAV^SPF^AK^IR^SSM 1350
 gi|17509655|ref|NP_493393.1| -----S^LL^KA^SI^SI^SA^QL^PE^DG^NE----- 1350
 gi|116008066|ref|NP_001036740.1| T^IS^II^SV^TD^HV^GL^PT^GL^LE^NA^PA^IR^PI^TP^NP^LI^CV^EA^HE^AF^DD^RE^GV^KP^VS^ST^SA^RD^LS^LP^G-----L^PT^HP^EA^NK^LK^LL^SP^LS^KL^AK^NI 1350
 gi|158288768|ref|XP_310609.3| T^MS^IS^VT^DH^IN^MP^VG^ML^EC^AS^PI^RV^SS^PA^PE^IF^VD^G----- 1350
1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



gi|31542017|ref|NP_848756.2| VQ^VA^NI^TQ^AG^LT^HG^IN^LA^VA^KV^QK^SP^AE^PE^AV^NE^IQ^ON^EL^KN^MF^TQ^CO^TR^II^QI 1404
 gi|109459467|ref|XP_219372.4| VQ^VA^NI^TQ^AG^LT^HG^IN^LA^VA^KV^QK^SP^AE^PE^VV^NE^IQ^ON^EL^KN^MF^TQ^CO^TR^II^QI 1404
 gi|7662414|ref|NP_055752.1| VQ^VA^SI^TQ^AG^LT^HG^IN^FA^VS^KV^QK^SP^PE^PE^II^NO^VQ^ON^EL^KK^MF^IQ^CO^TR^II^QI 1404
 gi|114633046|ref|XP_508074.2| VQ^VA^SI^TQ^AG^LT^HG^IN^FA^VS^KV^QK^SP^PE^PE^II^NO^VQ^ON^EL^KK^MF^IQ^CO^TR^II^QI 1404
 gi|73998919|ref|XP_535034.2| VQ^VA^SI^TQ^AG^LT^QG^IN^FA^VA^KV^QK^SP^AE^PE^VV^NO^VQ^ON^EL^KN^MF^TQ^CO^TR^II^QI 1404
 gi|118093078|ref|XP_421792.2| VQ^VA^NI^TQ^AG^LT^QG^IN^FA^VA^KV^QK^SP^AE^SE^AL^NE^IK^QE^LK^EM^FT^QC^OT^RI^IQ^I 1404
 gi|187608145|ref|NP_001119904.1| VQ^VA^SL^TQ^AG^LT^QG^IN^FA^VA^KV^QK^SP-EP^DA^VN^ET^OE^NE^LR^AM^FT^QC^OT^RI^IQ^I 1404
 gi|17509655|ref|NP_493393.1| S^DA^SQ^KS^DH^LM^TK^IL^KM^SQ^FK^SD^SP^OP^EP^FS-----L^LP^AI^SE^CO^TR^IS^LL 1404
 gi|116008066|ref|NP_001036740.1| G^LN^LD^PR^KI^AK^TG^VL^EP^II^LS^AE^NS^PP^ER^DP^SS^RD^HL^LE^LL^WE^AE^KC^KT^KL^IA^L 1404
 gi|158288768|ref|XP_310609.3| ----- 1404
1360.....1370.....1380.....1390.....1400....

