

gi | 45550489 | ref | NP_611651.3 | --MTPNPLGDDQEKLLAEATGLARKAFQMNHFLLDK-ERMLDLSLKCASTMLGELRSTVLSLSPKSYVELYMAVTELNCHLELVLSSEKID-KKT--DLYELVQYSHIVPRLYLLITVGVIVIKNDPFLKRSILKDLVEMCRGVQHPRLRGLF 143
gi | 158285212 | ref | XP_308188.4 | MPQTPINSVDEODKLLTEAMTVVRAQSFQMKRFLDK-DRLMEAMRCASTMLGELRSTVLSLSPKSYVELYMAITDELRFHEHYLLDEFQ-KGRKVPDLYEHOYAGNIIPRLLYLLITVGLVVIKNTSALKRSILKDLVEMCRGVQHPRLRGLF 148
gi | 17999541 | ref | NP_060676.2 | MPTTQOSPODEQEKLLDEAIVQAVKVSFQMKRCLDK-NKLMALKKXASNMLGELRSTVLSLSPKSYVELYMAISDELHLVLEVLLTDEFA-KGRKVADLYELVQYAGNIIPRLLYLLITVGVVYVKSFFQSRKDLKDLVEMCRGVQHPRLRGLF 148
gi | 73976907 | ref | XP_532570.2 | MPTTQOSPODEQEKLLDEAIVQAVKVSFQMKRCLDK-NKLMALKKXASNMLGELRSTVLSLSPKSYVELYMAISDELHLVLEVLLTDEFA-KGRKVADLYELVQYAGNIIPRLLYLLITVGVVYVKSFFQSRKDLKDLVEMCRGVQHPRLRGLF 81
gi | 114662311 | ref | XP_001161439.1 | MPTTQOSPODEQEKLLDEAIVQAVKVSFQMKRCLDK-NKLMALKKXASNMLGELRSTVLSLSPKSYVELYMAISDELHLVLEVLLTDEFA-KGRKVADLYELVQYAGNIIPRLLYLLITVGVVYVKSFFQSRKDLKDLVEMCRGVQHPRLRGLF 148
gi | 114053129 | ref | NP_001039723.1 | MPTTQOSPODEQEKLLDEAIVQAVKVSFQMKRCLDK-NKLMALKKXASNMLGELRSTVLSLSPKSYVELYMAISDELHLVLEVLLTDEFA-KGRKVADLYELVQYAGNIIPRLLYLLITVGVVYVKSFFQSRKDLKDLVEMCRGVQHPRLRGLF 148
gi | 109507853 | ref | XP_214646.3 | MPTTQOSPODEQEKLLDEAIVQAVKVSFQMKRCLDK-NKLMALKKXASNMLGELRSTVLSLSPKSYVELYMAISDELHLVLEVLLTDEFA-KGRKVADLYELVQYAGNIIPRLLYLLITVGVVYVKSFFQSRKDLKDLVEMCRGVQHPRLRGLF 148
gi | 13928670 | ref | NP_075373.1 | MPTTQOSPODEQEKLLDEAIVQAVKVSFQMKRCLDK-NKLMALKKXASNMLGELRSTVLSLSPKSYVELYMAISDELHLVLEVLLTDEFA-KGRKVADLYELVQYAGNIIPRLLYLLITVGVVYVKSFFQSRKDLKDLVEMCRGVQHPRLRGLF 148
gi | 57524880 | ref | NP_001005842.1 | MPTTQOSPODEQEKLLDEAIVQAVKVSFQMKRCLDK-NKLMALKKXASNMLGELRSTVLSLSPKSYVELYMAISDELHLVLEVLLTDEFA-KGRKVADLYELVQYAGNIIPRLLYLLITVGVVYVKSFFQSRKDLKDLVEMCRGVQHPRLRGLF 148
gi | 70887665 | ref | NP_001020688.1 | MPTTQOSPODEQEKLLDEAIVQAVKVSFQMKRCLDK-NKLMALKKXASNMLGELRSTVLSLSPKSYVELYMAISDELHLVLEVLLTDEFA-KGRKVADLYELVQYAGNIIPRLLYLLITVGVVYVKSFFQSRKDLKDLVEMCRGVQHPRLRGLF 108
gi | 115533921 | ref | NP_495180.2 | --MYENSGNTTDEKFLDQSRVVKAESFQMKRCLDK-GKTMALKKHALQMLNEMRAELSPKFFYRLVMDMHEFLQCLVNLVQEAQAPAKLGNLVECVQYASAIIPRLLYLLITVGGVFKCGLSRKEITKDLVEMCRGVQHPRLRGLF 148
gi | 145337595 | ref | NP_177713.3 | --MRTLAGEVDEDEKWLAEAGTAGIHNNAFMHRALDA-NNLREVLKYSALMSELRSTKSLSPQKYVDLVMRAFDRQLQLEIFPFDESRHG-LPVVDLYELVQYAGNIPRLLYLLITVGVVYVKSFFQSRKDLKDLVEMCRGVQHPRLRGLF 146
gi | 115455985 | ref | NP_001051593.1 | --MLPDGGADDEERWLAEGTAGVQNAFYMRALDS-NKLDALKKXASNMLGELRSTVLSLSPKSYVELYMAISDELHLVLEVLLTDEFA-KGRKVADLYELVQYAGNIIPRLLYLLITVGVVYVKSFFQSRKDLKDLVEMCRGVQHPRLRGLF 147
gi | 145602221 | ref | XP_359688.2 | -----MLLGSYILKLTAYLLCDR-----S-TLVSELRSTSSLPKQYVELYMSVFDALRYSVHLRENHQ--VNHLDLYELVQYAGNIIPRLLYLLITVGTAYMADAAPVKELMKDMMDSRQVQHPRLRGLF 120
gi | 32411317 | ref | XP_326139.1 | --MSTPAPPEDARLLLDALIAVRQSTLIMRCKLDTGKGLMDALKCCSTLVSELRSTSSLPKQYVELYMSVFDALRYSVHLRENHQ--VNHLDLYELVQYAGNIIPRLLYLLITVGTAYMADAAPVKELMKDMMDSRQVQHPRLRGLF 146
gi | 50303835 | ref | XP_451864.1 | -----MSAYSNDMEGATSHIKQSTILMQRSLTG--KKLDALKKXASNMLGELRSTVLSLSPKSYVELYMAISDELHLVLEVLLTDEFA-KGRKVADLYELVQYAGNIIPRLLYLLITVGTAYMADAAPVKELMKDMMDSRQVQHPRLRGLF 140
gi | 45190500 | ref | NP_984754.1 | -----MSYAEVQAAGVGIKQSTVLQIQRHLAQ--RKLLDALKKXASNMLGELRSTVLSLSPKQYVELYMSVFDALRYSVHLRENHQ--KRHLADLYELVQYAGNIIPRLLYLLITVGTAYMADAAPVKELMKDMMDSRQVQHPRLRGLF 139
gi | 6322307 | ref | NP_012381.1 | -----MAYADSPENATAVIAIKQRALMNRCLSG--HKLMSLQHTSITMLTELRNPNLSPKQYVELYMSVFDALRYSVHLRENHQ--KRHLADLYELVQYAGNIIPRLLYLLITVGTAYMADAAPVKELMKDMMDSRQVQHPRLRGLF 139
gi | 19075760 | ref | NP_588260.1 | -----MRNSALTPKQYVELYMSVFDALRYSVHLRENHQ--KRHLADLYELVQYAGNIIPRLLYLLITVGTAYMADAAPVKELMKDMMDSRQVQHPRLRGLF 97
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 45550489 | ref | NP_611651.3 | LRNVLLQCTRNILPDVME-----E-----NEHEGNVYDAIDFVLINFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 276
gi | 158285212 | ref | XP_308188.4 | LRNVLLQCTRNILPDMHV GAS-----G-----DENEGTVDAIDFVLINFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 284
gi | 17999541 | ref | NP_060676.2 | LRNVLLQCTRNILPDEGEPTD-----EETGDISDSMDFVLLNFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 282
gi | 73976907 | ref | XP_532570.2 | LRNVLLQCTRNILPDEGEPTD-----EETGDISDSMDFVLLNFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 215
gi | 114662311 | ref | XP_001161439.1 | LRNVLLQCTRNILPDEGEPTD-----EETGDISDSMDFVLLNFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 282
gi | 114053129 | ref | NP_001039723.1 | LRNVLLQCTRNILPDEGEPTD-----EETGDISDSMDFVLLNFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 282
gi | 109507853 | ref | XP_214646.3 | LRNVLLQCTRNILPDEGEPTD-----EETGDISDSMDFVLLNFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 287
gi | 13928670 | ref | NP_075373.1 | LRNVLLQCTRNILPDEGEPTD-----EETGDISDSMDFVLLNFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 282
gi | 57524880 | ref | NP_001005842.1 | LRNVLLQCTRNILPDEGEQAD-----EETGDISDSMDFVLLNFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 282
gi | 70887665 | ref | NP_001020688.1 | LRNVLLQCTRNILPDEGEQAD-----EETGDISDSMDFVLLNFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 108
gi | 115533921 | ref | NP_495180.2 | LRNVLMQCTRSVLPDFPETEEMLVAHNDNLSKGTLPKLPKPRDGTVDITDFVLINFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 298
gi | 145337595 | ref | NP_177713.3 | LRSYLAQVSRDKLPEIGSDYEG-----DANTVMDAVEFVLQNFTEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 279
gi | 115455985 | ref | NP_001051593.1 | LRSYLSQISRDKLPDISEYEG-----DADSNVAVEFVLQNFTEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 280
gi | 145602221 | ref | XP_359688.2 | LRYVLSGQARDFLPQEGEGDF-----EGNLQDSINFLINFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 249
gi | 32411317 | ref | XP_326139.1 | LRYVLSGQARDFLPQEGEGDF-----EGNLQDSINFLINFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 275
gi | 50303835 | ref | XP_451864.1 | LRYVLSQRTEKQSLT-----DISLSD--KKFPIQFIIITNFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 267
gi | 45190500 | ref | NP_984754.1 | LRYVLSQRTEKQSLT-----DISLSD--KKFPIQFIIITNFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 282
gi | 6322307 | ref | NP_012381.1 | LRYVLSQRTEKQSLT-----DISLSD--KKFPIQFIIITNFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 263
gi | 19075760 | ref | NP_588260.1 | LRHYLLTQIRKGLPLGSEDEED-----EDDPS-----FNSQFIMNFAEMNKLWVRMHOQHGSSEKTRREKEREELKILVGTNLVRLSLESATLEIYQRLILPGILEQVVS CRDIAOAEYLMCEIIOVFPDEFHLQTLNDFP 231
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 45550489 | ref | NP_611651.3 | LKSCAQLQPGVNVKNIISLIERLAAVNRQSRGKTSGN-----AIDAIIPAEVELFEVFSVQV 333
gi | 158285212 | ref | XP_308188.4 | LKSCAQLQPGVNVKNIISLIERLAAVNRQSRGKTSGN-----AIDAIIPAEVELFEVFSVQV 346
gi | 17999541 | ref | NP_060676.2 | LRACAEHLQNVNVKNIISLIERLAAVNRQSRGKTSGN-----AIDAIIPAEVELFEVFSVQV 332
gi | 73976907 | ref | XP_532570.2 | LRACAEHLQNVNVKNIISLIERLAAVNRQSRGKTSGN-----AIDAIIPAEVELFEVFSVQV 265
gi | 114662311 | ref | XP_001161439.1 | LRACAEHLQNVNVKNIISLIERLAAVNRQSRGKTSGN-----AIDAIIPAEVELFEVFSVQV 332
gi | 114053129 | ref | NP_001039723.1 | LRACAEHLQNVNVKNIISLIERLAAVNRQSRGKTSGN-----AIDAIIPAEVELFEVFSVQV 332
gi | 109507853 | ref | XP_214646.3 | LRACAEHLQNVNVKNIISLIERLAAVNRQSRGKTSGN-----AIDAIIPAEVELFEVFSVQV 337
gi | 13928670 | ref | NP_075373.1 | LRACAEHLQNVNVKNIISLIERLAAVNRQSRGKTSGN-----AIDAIIPAEVELFEVFSVQV 332
gi | 57524880 | ref | NP_001005842.1 | LRACAEHLQNVNVKNIISLIERLAAVNRQSRGKTSGN-----AIDAIIPAEVELFEVFSVQV 332
gi | 70887665 | ref | NP_001020688.1 | LRACAEHLQNVNVKNIISLIERLAAVNRQSRGKTSGN-----AIDAIIPAEVELFEVFSVQV 332
gi | 115533921 | ref | NP_495180.2 | LNACGGLQDDVNIKILLIALVDRALALVTSYNE-----GQFAPLTKMQLFEIFSEDA 148
gi | 145337595 | ref | NP_177713.3 | LAACPOLMPTVDTRIVLTQLMDRLSNYAASSPD-----VLHEFLQVEAFAKLSNAI 330
gi | 115455985 | ref | NP_001051593.1 | LSAPFQLQPNVDITVLSQLMDRLSNYAASSPD-----VLHEFLQVEAFAKLSNAI 331
gi | 145602221 | ref | XP_359688.2 | LAAVSRLLNPHVNVKAIIVGLMDRLSDYAEERAEQNEEGEDRGLEEEALANLLEKRVKLSAAETEEASAPTP-----EAPENGEHAETLVGSTDDEPLNAP-SVAETAETVING--DEVEPAKCHKRGIPENVPLVEIFFGQV 399
gi | 32411317 | ref | XP_326139.1 | LDITLKLNPDPVINKVVISLIARLNGFDWRQDDPNAIQNLN-----HLKLDNSNIDEEHSAADDGESLAEKLDSEPVSRNKDFLDFVFWKYL 409
gi | 50303835 | ref | XP_451864.1 | LETTLKFNPDVSNKVVSNLVERFNGYVERQSG-----DIDSVQNTFRKLCIQGQPTASAGDTISSSGG---LFFVFWRYL 355
gi | 45190500 | ref | NP_984754.1 | LQTLHLNPDVSNKVVSNLVERFNGYVERQSG-----DIDSVQNTFRKLCIQGQPTASAGDTISSSGG---LFFVFWRYL 320
gi | 6322307 | ref | NP_012381.1 | LQTLHLNPDVSNKVVSNLVERFNGYVERQSG-----DIDSVQNTFRKLCIQGQPTASAGDTISSSGG---LFFVFWRYL 320
gi | 19075760 | ref | NP_588260.1 | FGVVILKLSVSNVTVQLVVMNLRLTDVYQREYESDSSNEDE-----ETVTEKLDIKINEVQKDEECPGDKVIPPETAIQEVLWSHV 317
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi|45550489|ref|NP_611651.3| R-----LKGPA^{CSHN}-----AHVHF-----
gi|158285212|ref|XP_308188.4| RDEKRTLECLKKAAKIAS^{CLDVGVLQLVYELLNHYIFYFTRNTQ}---ITVSMNLNOLIAKIN^{ELP}-NLEPTE-----ETKQIEMHYQNI 785
gi|17999541|ref|NP_060676.2| HGGKRVMECLKALKKIANQ^{CMDPSLQVOLFIEILNRYIYFYEKENDA}---VTIQVLNQLIQKIRE^{DLP}-NLESSE-----ETEQINKHFHNT 773
gi|73976907|ref|XP_532570.2| HGGKRVMECLKALKKIANQ^{CMDPSLQVOLFIEILNRYIYFYEKENDA}---VTIQVLNQLIQKIRE^{DLP}-NLESSE-----ETEQINKHFHNT 706
gi|114662311|ref|XP_001161439.1| HGGKRVMECLKALKKIANQ^{CMDPSLQVOLFIEILNRYIYFYEKENDA}---VTIQVLNQLIQKIRE^{DLP}-NLESSE-----ETEQINKHFHNT 773
gi|114053129|ref|NP_001039723.1| HGGKRVMECLKALKKIANQ^{CMDPSLQVOLFIEILNRYIYFYEKENDA}---VTIQVLNQLIQKIRE^{DLP}-NLESSE-----ETEQINKHFHNT 773
gi|109507853|ref|XP_214646.3| HGGKRVMECLKALKKIANQ^{CMDPSLQVOLFIEILNRYIYFYEKENDA}---VTIQVLNQLIQKIRE^{DLP}-NLESSE-----ETEQINKHFHNT 778
gi|13928670|ref|NP_075373.1| HGGKRVMECLKALKKIANQ^{CMDPSLQVOLFIEILNRYIYFYEKENDA}---VTIQVLNQLIQKIRE^{DLP}-NLESSE-----ETEQINKHFHNT 773
gi|57524880|ref|NP_001005842.1| HGGKRVMECLKALKKIANQ^{CMDPSLQVOLFIEILNRYIYFYEKENEA}---VTIQVLNQLIQKIRE^{DLP}-NLESSE-----ETEQINKHFHNT 773
gi|70887665|ref|NP_001020688.1| -----
gi|115533921|ref|NP_495180.2| KNGKRVVDILRKAAKIAR^{ECL}ELPLV^{QQLFIQLLSAVTYYYEDNCSE}---VNV^{DHIEELIARTQDNAV}-QLDVEA-----EADSLKQLGEA 791
gi|145337595|ref|NP_177713.3| LCLRRALRIANAAQ^{OMASATRGSSG}PVTLFVEILNKYIYFFKGNPH---ITP^{SDIQSLIELINNEM}-QSDNGN-----TILHSDPFFTSI 767
gi|115455985|ref|NP_001051593.1| LCLKRALRIANAAQ^{OMANVIRGSSG}SVALFVEILNKYIYFFKGIPE---ITNT^{VIQDLIELIRTEK}--QSENIV-----ADPSTEAFFAST 769
gi|145602221|ref|XP_359688.2| RDGKRVLECLQRALRVADS^{CMTATATSIELFVEILDRIYVYFDQRNES}---VTIK^{YLNGLIELIHSNFAGNQD}EA-----SVEACKKHFOHI 854
gi|32411317|ref|XP_326139.1| RDGKRVLECLQRALRVADS^{CMTATATSIELFVEILDRIYVYFDQRNES}---VTIK^{YLNGLIELIHSNLAGNQD}EA-----SVEASRKHFMQI 864
gi|50303835|ref|XP_451864.1| REGKRVLECLQRSIRVADS^{IMDNVQSCQLMVEILGSCCYFFIHGDESE}THVGVKYIAGLVELIQANLKG^{LQLEE}-----EGEVQDF^{WAP}---QTIVIG^{CDGSIYICKTLE}---ESTCM---V^{SKT}PNVRIED 848
gi|45190500|ref|NP_984754.1| REGKRVLECLQRSIRVADS^{IMDNVQSCQLMVEILNRC^{CCYFFVHGDESE}ATHVGVK^{YINGLIELIETNLKSLKIEE}}-----SVEFAS^{KLPKPYANFVVGVDGSIYQVETSEPTAVAA}---VMSK^{PPNITIS} 858
gi|6322307|ref|NP_012381.1| RDGKRVLECLQRSIRVADS^{IMDNEQSCQLMVEILNRCLYFFIHGDESE}THISIKYINGLIELIK^{TNLKSLKLEDNSASMITNSISDLHTIGENNVKAS}SNADD^{GSVINDKES}NVAIG^{DGTIQLNLNLNGSSLLIRGVVATASGSKLLHQ} 913
gi|19075760|ref|NP_588260.1| QD^{PKRVLECLQKSLKIADA}CMD^{QLTSLKLFINILERYFYVYDQHCS}---ITAK^{HISGLIDLTEENMRSILIS}EP-----ADLIAS^{DPRAWASIWEVANVSV} 756
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



gi|45550489|ref|NP_611651.3| ----- 612
gi|158285212|ref|XP_308188.4| LAH^{IRSRMESTDAGIEASFAGITLN}----- 810
gi|17999541|ref|NP_060676.2| LEHLRLRRES^{PES}-EGPIYEG^{LIL}----- 796
gi|73976907|ref|XP_532570.2| LEHLRLRRES^{PES}-EGPIYEG^{LVL}----- 729
gi|114662311|ref|XP_001161439.1| LEHLRLRRES^{PES}-EGPIYEG^{LIL}----- 796
gi|114053129|ref|NP_001039723.1| LEHLRLRRES^{PES}-EGPIYEG^{LIL}----- 796
gi|109507853|ref|XP_214646.3| LEHL^{SRRES}PES-EGPIYEG^{LIL}----- 801
gi|13928670|ref|NP_075373.1| LEHL^{SRRES}PES-EGPIYEG^{LIL}----- 796
gi|57524880|ref|NP_001005842.1| LEHLRLRRES^{PES}-EGPIYEG^{LVL}----- 796
gi|70887665|ref|NP_001020688.1| ----- 108
gi|115533921|ref|NP_495180.2| IRR^{LQANLDVAAAGATTIRSEPELP}PPS----- 821
gi|145337595|ref|NP_177713.3| LRYIK^{FKKGGGL}-MGEK^{YDPKIL}----- 790
gi|115455985|ref|NP_001051593.1| LRYIEF^{KKGGG}-IGEK^{YQIKIT}----- 793
gi|145602221|ref|XP_359688.2| L^{DLIR}-----SKEV^{EGIVLDPK}----- 871
gi|32411317|ref|XP_326139.1| LEI^{IR}-----SKEV^{EGIVLTPK}----- 881
gi|50303835|ref|XP_451864.1| LIAV^{PVSFYFERTLEYIENQKQVDRFN}AITI 879
gi|45190500|ref|NP_984754.1| LV^{PVITGYLQRTLNYIEDQKVVD}DRFRAIIV 889
gi|6322307|ref|NP_012381.1| LKYI^{PIHHFRRTCEYIESQREVDDR}FKVIYV 944
gi|19075760|ref|NP_588260.1| L^{DSLK^{NHLE}ERATAYAEKRS}EDERWSIFQ-- 785
.....1060.....1070.....1080.

