

```

gi | 83415134 | ref | NP_001032784.1 | -----MKAGIVFLPLLLPLVSA--QVFRWGPCPTPMVQPNFELDKYLKWKYIEIKLPAEFKGG-KCIETANYMLRPPDKTVQVLIQITYK-GKIRKAGGTAIQDIKEPAKLGVSFS--YFPPYAPYWILSDYNSISLV 128
gi | 115495287 | ref | NP_001070050.1 | -----MKVFLVFLA-LFLPLMSA--QVPHWGPCPEPATQPAFNLQKFMGRWFEIAKLPQAFERG-RCIETNFTLKLIDGTAHVVSSEILK-GELKTI DGTAVVEDKRNPAKLGISFS--YVLPYTPYWILSDYENSALV 127
gi | 75677437 | ref | NP_031496.2 | -----MVTMLMFLAFLAGLFTTAKGONFHLGKCPSPVVOENFDVKKYLGRWYIEIKIPASFEKGG-NCIQANYSLMENGNIEVLNKLKSLPDTMNOVKGEAKQSNVSEPAKLEVOFF--PLMPPAPYWILATDYENYALV 131
gi | 6978523 | ref | NP_036909.1 | -----MATMLLLAFLAGLFTTTEGOSFHLGKCPSPVVOENFDVKKYLGRWYIEIKIPVSEFEKGG-NCIQANYSLMENGNIKVNLKELRPPDGTLNQVGEAKQSNMSEPAKLEVOFF--SLMPPAPYWILATDYESVALV 131
gi | 4502163 | ref | NP_001638.1 | -----MVMLLLLSALAGLFGAAEGQAFHLGKCPNPVVOENFDVKNKYLGRWYIEIKIPTTFENG-RCIQANYSLMENGGIKVNLQELRADGTVNOIEGEATPVNLTPEAKLEVKFS--WFMPSPAPYWILATDYENYALV 131
gi | 55621758 | ref | XP_516965.1 | -----MVMLLLLSALAGLFGAAEGQAFHLGKCPKPPVVOENFDVKNKYLGRWYIEIKIPTTFENG-RCIQANYSLMENGGIKVNLQELRADGTVNOIEGEATPVNLTPEAKLEVKFS--WFMPSPAPYWILATDYENYALV 131
gi | 57109608 | ref | XP_535780.1 | MSLHVEAFILTKKPRMLTALLLLPALAGLLPAADGQAFHLGRCPTPPVVOENFDVHKYLGRWYIEIKIPVSEFEKGG-SCIQANYSLMENGNIKVINQELRSDGTVNOIEGEATQGNLTPEAKLVKFF--WLMPSAPYWILATDYENYALV 147
gi | 115494984 | ref | NP_001069769.1 | -----MVFVLLLLPALAGLFGAAEGQAFHLGKCPHPVVOENFDVKNKYLKWKYIEIKIPVSEFEKGG-SCIQANYSLKENGKVEVINKELRADGTVNOIEGEATPENITPEAKLVKFF--WFMPSPAPYWILATDYENYALV 131
gi | 58696426 | ref | NP_001011692.1 | -----MLGTAALQSLVLLSLLGLGNAQMFHMGCPDPPVQDFDINKYLKWKYIEIKLPSNFEKGG-SCVQANYSLKENGKFKVINKEMLSSGKINALEGEIMHTDVKEPAKLGVRFN--WFMPSPAPYWVISTDYENYSLV 131
gi | 28574799 | ref | NP_787960.1 | -----MNHSSSHLLLLISVVFQAVVVA--HAQVPPFGKCPDVKLLDTFDAEAYMGVWYIEYAAVPAFEBGKCKIYANYSLLIDNSTVSVVNAANR--FTGQPSNVHGGQAKVLGPGQLAVAFYPTQPLTKANLVLTIDYESVAVV 137
gi | 158300081 | ref | XP_320076.4 | -----MATTRIPRWAGIGVGLLAVLLLVGEAQVPGFGKCPKVPVVENFDIYAYLGRWYIEQEKYPPFFELGGKCTITADYSLNPDGTIGVLTQKNS--ITGNENSIVGSARIVGSARLAVRFPAPENVEAPYVWVGTIDYKTFAVV 139
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

```



```

gi | 83415134 | ref | NP_001032784.1 | YSCTDVLRLFHVDYAWILSRSRFLPAGAIYHAKEIFSRDNDVSKMFAIDQGCNDNPI----- 186
gi | 115495287 | ref | NP_001070050.1 | YSCSDVLRFLFHVDFAWILGRTRSLPAAITIEHGKEVFTSNNDVSRMILSRQGCQDKL----- 185
gi | 75677437 | ref | NP_031496.2 | YSCTIFFWFLFHVDFVWILGRNRYLPPETITVYKLDILTNGIDIEKMTITDOANCPDFL----- 189
gi | 6978523 | ref | NP_036909.1 | YSCTIFFWFLFHVDFVWILGRNRYLPPETITVYKYLILTSNDIDIAKILTKDOANCPDFL----- 189
gi | 4502163 | ref | NP_001638.1 | YSCTCIIQLFHVDFAWILARNPNLPPETVDSLKNILTSNNIDVKKMIVTDQVNCPKLS----- 189
gi | 55621758 | ref | XP_516965.1 | YSCTSIIQLFHVDFAWILARNPNLPPETVDSLKNILTSNNIDVKKMIVTDQVNCPKLS----- 189
gi | 57109608 | ref | XP_535780.1 | YSCTIIVWLFHMDHVWILGRNRYLPPETITVYKLDILTNDIDIEKMTITDOVNCPESL----- 205
gi | 115494984 | ref | NP_001069769.1 | YSCTIIVWLFHMDHVWILGRNRYLPPETITVYKLDILTNDIDIEKMTITDOVNCPESM----- 189
gi | 58696426 | ref | NP_001011692.1 | YSCTINILWLFHFDYAWIMSRSPDMHPDITVEHLKSMRLTYKIDITDKMPTDOLNCPAEM----- 189
gi | 28574799 | ref | NP_787960.1 | YSCTSITPLANFKIIVWILTRQREPSAEAVDAARKILENDVSAFLIDITVCKNCPRLDNGCTGLAGEDGLVDVDFVSTVFNAIKA----- 224
gi | 158300081 | ref | XP_320076.4 | YACSDLRGFINAKVAVILTRKRHPDIEIMKKAYSVLDAKISRAYLRTDQKNC----- 193
.....160.....170.....180.....190.....200.....210.....220.....230.....

```

