

```

      : : : * : * : * * : * * * * : * * * * * * * : : : * : * : : * * * : : : * * * * : * * * * : * :
gi | 31542359 | ref | NP_031668.2 | -----MILRLLFLALNFPSVQVTENKILVKQSPLLVVDSEVSLSCRYSYNLLAKEFRASLYKGVNSDVEVCVGNNGFTYQPFNSNAEFNCDGDFDNETVIFRLWNLVNHDIYFCKIEVMYPPPYLDNEKSNGTIIHVK 137
gi | 6978625 | ref | NP_037253.1 | -----MILRLLFLALSFPFSVQVTENKILVKQSPLLVVDNEVSLSCRYSYNLLAKEFRASLYKGVNSDVEVCVGNNGFTYQPFNPVGFNCDGNFDNETVIFRLWNLVDVNHDIYFCKIEVMYPPPYLDNEKSNGTIIHVK 137
gi | 5453611 | ref | NP_006130.1 | -----MLRLLALALNFPSIQVTGNKILVKQSPMLVAYDNVAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQLQVYKTFGNCDGKLGNESVTFYLLQNLVNVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVK 136
gi | 55614916 | ref | XP_525998.1 | MPCGLSALIMCPKGMVAVVVAVDDGDSQALAGNKILVKOSPMLVAYDNVAVNLSCKYSYNLFSREFRASLHKGLDSAVEVCVVYGNYSQQLQVYKTFGNCDGKLGNESVTFYLLQNLVNQTDIYFCKIEVMYPPPYLDNEKSNGTIIHVK 150
gi | 74004979 | ref | XP_855561.1 | -----MILRLLALNFPSIQVTENKILVKQSPRLVYDNEVSLSCRYSYNLLAKEFRASLYKGVNSDVEVCVGNNGFTYQPFNSNAEFNCDGDFDNETVIFRLWNLVNHDIYFCKIEVMYPPPYLDNEKSNGTIIHVK 137
gi | 30794304 | ref | NP_851347.1 | -----MLRLLALALNFPSIQVAENKILVKQSPMLVVDNEVSLSCRYSYNLLAKEFRASLYKGVNSDVEVCVGNNGFTYQPFNSNAEFNCDGDFDNETVIFRLWNLVNHDIYFCKIEVMYPPPYLDNEKSNGTIIHVK 135
gi | 46048702 | ref | NP_990642.1 | -----MLGILVVLCLIPAADVTENKILVAQRPLLIVANRTALVCNYTYNGTGKEFRASLHKGLDSAVEVCFISWNMT-KINSNKEFNCRGIHDKVIFNLWNSASDTIYFCKIEAMYPPPYVYNEKSNGTIVHVR 135
      1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

```



```

      . : * : * * * * * : * * * * * * : : * * * * * * :
gi | 31542359 | ref | NP_031668.2 | EKHLCHTQSSP---ELFWALVVVAGVLFCYGLLVIVALCVIWTSRRRNRLLOSDYMNMTPRRPGLTR-KPYQPYAPARDFAARP--- 218
gi | 6978625 | ref | NP_037253.1 | EKHLCHAQTSP---KLFWPLVVVAGVLLCYGLLVIVTLCIIWTSRRRNRLLOSDYMNMTPRRLGPTR-KHYQPYAPARDFAARP--- 218
gi | 5453611 | ref | NP_006130.1 | GKHLCPSPLFFGPSKPFWLVVVGVGLACYSLLVVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTR-KHYQPYAPPRDFAARS--- 220
gi | 55614916 | ref | XP_525998.1 | GKHLCPSPLFFGPSKPFWLVVVGVGLACYSLLVVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTR-KHYQPYAPPRDFAARS--- 234
gi | 74004979 | ref | XP_855561.1 | EKHLCPDELFPDSSKPFWALVVVGAVLVFYSLLVTVALCAYWIKSSRILOSDYMNMTPRRPGPTR-RHYQPYAPARDFAARS--- 221
gi | 30794304 | ref | NP_851347.1 | EKHLCPSPRSPESSKPFWALVVVGVLVFYSLLVIVALSNCWMKNKRNRMLOSDYMNMTPRRPGPTR-RHYQPYAPARDFAARS--- 219
gi | 46048702 | ref | NP_990642.1 | ETPIQTQ---EPESATSYWVMVAVTGLLGFYSMLIIAVFIIYRQKRRRYROSDYMNMTPRHPHQKNGVPSYAPTRDYTARSWQE 221
      .....160.....170.....180.....190.....200.....210.....220.....230.....

```

