

```

      .*:      : * . ** : ***** **.***:*.....**:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*
gi |106507239|ref |NP_110423.3|-----MRRQPAKVAALLG-----LLELCTEAKKHCWYFEGLYPTYYICRSYEDCCGRCCVRALSIQRLWYFWFLLMMGVLFCCGAGFFIRRRMYPPLIEEPAFNVSYTRPPNPAPGAQQPGPPYYTDPGGPGMNPVGNM 150
gi |114613419|ref |XP_001157372.1|-----MRRQPAKVAALLG-----LLELCTEAKKHCWYFEGLYPTYYICRSYEDCCGRCCVRALSIQRLWYFWFLLMMGVLFCCGAGFFIRRRMYPPLIEEPAFNVSYTRPPNPAPGAQQPGPPYYTDPGGPGMNPVGNM 150
gi |22122699|ref |NP_666280.1|-----MGRRLGRVAALLG-----LLVECTEAKKHCWYFEGLYPTYYICRSYEDCCGRCCVRALSIQRLWYFWFLLMMGVLFCCGAGFFIRRRMYPPLIEEPTFNVSYTRPPNPAPGAQQMGPPYYTDPGGPGMNPVGNM 150
gi |109472111|ref |XP_342699.3|-----MARPLGRVAALLG-----LLMECTEAKKHCWYFEGLYPTYYICRSYEDCCGRCCVRALSIQRLWYFWFLLMMGVLFCCGAGFFIRRRMYPPLIEEPTFNVSYTRPPNPAPGAQQMGPPYYTDPGGPGMNPVGNM 150
gi |118086103|ref |XP_001235488.1|-----MRRLQPGAALLS-----LLWECTEAKKHCWYFEGLYPTYYICRSYEDCCGRCCVRALSIQRLW---FLLMMGVLFCCGAGFFIRRRMYPPLVEEPTFNVSYTRPPNPTASGSDQPVPYYTDPGGFVMNP-----M 150
gi |73981878|ref |XP_850711.1|-----MNDGTVKLVKLMVAPEHHLASLIQDARSFHFCSSECTEAKKHCWYFEGLYPTYYICRPYEDCCGRCCVRALSIQRLWYFWFLLMMGVLFCCGAGFFIRRRMYPPLIEEPAFNVSYTRPPNPAPGGQQPLPYTDPGGPGMNPAGNPM 150
gi |116004161|ref |NP_001070440.1|-----MDSLAVRVAALLG-----LLVECTEAKKHCWYFEGLYPTYYICRPYEDCCGRCCVRALSIQRLWYFWFLLMMGVLFCCGAGFFIRRRMYPPLIEEPAFNVSYTRPPNPAPGAQPLGLPYTDPGGSGMNPAGNPM 150
gi |169234886|ref |NP_001108544.1|-----MRGICGLLIT-----LLFAETVAEKKYRWYFEGDYVPVYFICKAYEDCCGTECCVRALAVQRIWYFWLILLIALLCCSTGYFIRRRAPVYPPEDRREFTVAFSRNFIIF-PGLRQPGFHSYGDSETAVIST---V 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

```



```

      * . . . : * * : ***.*****: .
gi |106507239|ref |NP_110423.3|-----AMAFQVPPNSPQGSVACPPPPAYCNI PPPPYEQVVKAK--- 191
gi |114613419|ref |XP_001157372.1|-----AMAFQVPPNSPQGSVACPPPPAYCNI PPPPYEQVVKAK--- 191
gi |22122699|ref |NP_666280.1|-----AMAFQVQPNSPHGGTTVPPPPSYCNI PPPPYEQVVKDK--- 191
gi |109472111|ref |XP_342699.3|-----AMAFQVQPNSPHGGTTVPPPPSYCNI PPPPYEQVVKDK--- 191
gi |118086103|ref |XP_001235488.1|-----AMAFHVQPNSPQGNFVYPPPPSYCNI PPPPYEQVVKSS--- 191
gi |73981878|ref |XP_850711.1|-----AMAFQVQPNSPQGSVACPPPPAYCNI PPPPYEQVVKAK--- 191
gi |116004161|ref |NP_001070440.1|-----AMAFQVQPNSSQGSTGYPPPPSYCNI PPPPYEQVVKTK--- 191
gi |169234886|ref |NP_001108544.1|-----FPAVSALSYSG-----PHF---HHPPPSYEQVMDSQKK 191
.....160.....170.....180.....190.

```

