

```

** . : :*****: * * . * . : * * : * * :
gi |82906344|ref|XP_894909.1|-----MAV-VLTFRWLLT-----LPRAA--RGFRVRLPFGSEKITHTGQVYDEKDYRRIRFVDRQKEVNFNFAIDLIAQG 67
gi |109504524|ref|XP_001053017.1|-----MAA-ALTFRRLLA-----LPRAA--RGFGVVRVRSSEKITHTGQVYDEKDYRRIRFVDRQKEVNFNFAIDLIAQG 67
gi |56711244|ref|NP_035018.1|-----MAA-VLTFRRLLT-----LPRAA--RGFGVQVSPSSEKITHTGQVYDEKDYRRIRFVDRQKEVNFNFAIDLIAQG 75
gi |4758792|ref|NP_004544.1|-----MAA-AMTFCRLLNRCGEAARSLPLGA--RCFGVVRVSPTEKIVTHTGQVYDDKDYRRIRFVGRQKEVNFNFAIDLIAQG 75
gi |114598870|ref|XP_001142587.1|-----MAA-AMTFCRLLNRCGEAARSLPLGA--RCFGVVRVSPTEKIVTHTGQVYDDKDYRRIRFVGRQKEVNFNFAIDLIAQG 75
gi |74003113|ref|XP_535802.2|MEPPMIINNYHMRRLHLRFPPSPAPPAGITQOHCRLVRLDLPLPADRARAPLHLLAAPAERTARFSPKMAA-AVTFCRLLGRSGSAAALRPPRGA--RCLGVRSPTSEKITHTGQVYDDQDYRKVRFVGRQKEVNFNFAIDLIAQG 146
gi |28461239|ref|NP_787004.1|-----MAA-VLTFRLRFLGRGGAVIRGLPGGA--RCFGVRTSPTSEKIVTHTGQVYDDQDYRKVRFVGRQKEVNFNFAIDLIAQG 75
gi |50736146|ref|XP_419061.1|-----MAAFCATFRCLLFPWRLLALLRQAAAGSLRFYGVRAAANGELVTHTGQVYDEKDYRRIRFVGRQKEVNFNFAIDLIAQG 79
gi |52219138|ref|NP_001004651.1|-----MAAILPRILSFGKNTKVLNCLRLSAVPEVQVSVVPEVNHGEIITHTGQVYDENDVRRARFVGRHKEVNFNFAINLVABE 79
gi |20129243|ref|NP_608909.1|-----MAA-KQLVNNLSKLGPRQNWMSPLA--SVRHSSCRGDIEKIVTHTGQVDFKEDYRNARFVNAKRYVNFNFWGIKLIEV 75
gi |118791575|ref|XP_319821.3|-----MAA-RMILSPARRLAS-VVSTRSITT--VLAATCCATIKDEIITHTGQVYFYEANDYRNARFVNATKVVNPNWAIKLLIDEL 74
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

```



```

* . *:: ***** . * . : :*** ***** :* . **
gi |82906344|ref|XP_894909.1|PVNEVDHRIIACDGGGGA-LGHPKVYINLDKETKTGT CGYCGLOFK--QH-- 116
gi |109504524|ref|XP_001053017.1|PVNEVDHRIIACDGGGGA-LGHPKVYINLDKETKTGT CGYCGLOFK--QH-- 116
gi |56711244|ref|NP_035018.1|PVNEVEHRIIACDGGGGA-LGHPKVYINLDKETKTGT CGYCGLOFK--QH-- 116
gi |4758792|ref|NP_004544.1|PVSEVEIRVIA CDGGGGA-LGHPKVYINLDKETKTGT CGYCGLOFR--QH-- 124
gi |114598870|ref|XP_001142587.1|PVSEVEIRVIA CDGGGGA-LATQKRLGLDKEKTKTGT CGYCGLOFR--QH-- 124
gi |74003113|ref|XP_535802.2|PVSEVESRVISCDGGGGA-LGHPKVYINLDKETKTGT CGYCGLOFK--HH-- 195
gi |28461239|ref|NP_787004.1|PVSVVGSRVISCDGGGGA-LGHPRVYINLDKETKTGT CGYCGLOFR--QH-- 124
gi |50736146|ref|XP_419061.1|PVSEVESRIISCDGGGGA-LGHPKVYINLDKETKTGT CGYCGLOFK--QH-- 128
gi |52219138|ref|NP_001004651.1|PVTHVESRVVSCDGGGGA-LGHPKVYINLDKDTRVGT CGYCGLOFK--QH-- 129
gi |20129243|ref|NP_608909.1|PKKTECTERVVFCDDGGDGP-LGHPKVYINLDKPGNH-ICGYCGLRFVKKDDHHE 126
gi |118791575|ref|XP_319821.3|PIVKSEQRVVCCDGGTDPALGHPKVYINLDKPGAH-ACGYCGRFVKIDHHE 125
.....160.....170.....180.....190.....200...

```

