

```

gi | 98986447 | ref | NP_001035744.1 | -----
gi | 13928746 | ref | NP_113738.1 | -----
gi | 4502749 | ref | NP_000068.1 | -----
gi | 55633063 | ref | XP_520513.1 | -----
MGGIFSRKEKCEKCEGDRKKKPYFPYDTHKHPDSIWQLGRLYRGGRRKGGGFLFNRVNALKHAFAGRRGSAAGSREAGGRCGGVGRSPVLLPCORWLWRGLLPAGAPGGDPTWGDFRGATFAKCSLELIAPPSTRSRRPLAWKDTAVPP
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

```

```

*****
gi | 98986447 | ref | NP_001035744.1 | -----MESAADRLARAAAQGRVHDVRLLEAGVSPNAPNSFGRTPIQVMMMGNVHVAALLLNYGADSNCEDPITFSRPVHDAAREGFLDLVLVHG 300
gi | 13928746 | ref | NP_113738.1 | -----MESAADRLARAAALGREHEVRALLEAGASPNAPNTFGRTPIQVMMMGNVKVAALLLSYGADSNCEDPITFSRPVHDAAREGFLDLVLVHQ 300
gi | 4502749 | ref | NP_000068.1 | -----MEPAAGSSMEPSADWLAIAAARGRVEEVRALLEAGALPNAPNSYGRRPVQVMMMG SARVAE LLLLHGAEPN CADPAILTRPVHDAAREGFLDLVLVLR 300
gi | 55633063 | ref | XP_520513.1 | -----EDLRDRVGGGSSASTGGRKRGWLVTIRGWGPPRALGGCEGESRQRAAGSSMEPAAGSSMEPSADWLAIAAARGRVEEVRALLEAGALPNAPNSYGRRPVQVMMMG SARVAE LLLLHGAEPN CADPAILTRPVHDAAREGFLDLVLVLR 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

```



```

*****
gi | 98986447 | ref | NP_001035744.1 | SGARLDVRDAWGRLPLDLAQERGHQDIVRVYLRAGCSLCSAGWSLCTAGNVA-QTDGHSFSSTPRALELRGQEQES 378
gi | 13928746 | ref | NP_113738.1 | AGARLDVRDAWGRLPLDLALERGHHDVVRVYLR-----YLLSSAGNVSRTDRHNFCSSTPRCLGLRGQPPKQR 378
gi | 4502749 | ref | NP_000068.1 | AGARLDVRDAWGRLPVDLAEELGHRDVARYLVR-----AAAGGTR-----GSNHARIDAAEGPSDIPD 378
gi | 55633063 | ref | XP_520513.1 | AGARLDVRDAWGRLPVDLAEELGHRDVARYLVR-----AAAGGTR-----GSNHARIDAAEGPLDIPD 378
.....310.....320.....330.....340.....350.....360.....370.....

```

