```
                                 **:                      * ::****************************************:***  :**********************:*.*******:**  *: *: *:.*************:******:**: **
gi|6677819|ref|NP_033127.1|      MSSGAASGTGRGRPRGGGPGPRDPPPGETHKLVVVGGGGVGKSALTIQFIQSYFVSDYDPTIEDSYTKICTVDGIPARLDILDTAGQEEFGAMREQYMRAGNGFLLVFAINDRQSFNEVGKLFTQILRVKDRDDFPIVLVGNKADLENQR   150
gi|34856057|ref|XP_341852.1|     MSSGAASGTGRGRPRGGGPGPRDPPPGETHKLVVVGGGGVGKSALTIQFIQSYFVSDYDPTIEDSYTKICTVDGIPARLDILDTAGQEEFGAMREQYMRAGNGFLLVFAINDRQSFIEVSKLFTQILRVKDRDDFPIVLVGNKADLETQR   150
gi|5454028|ref|NP_006261.1|      MSSGAASGTGRGRPRGGGPGPGDPPPSETHKLVVVGGGGVGKSALTIQFIQSYFVSDYDPTIEDSYTKICSVDGIPARLDILDTAGQEEFGAMREQYMRAGHGFLLVFAINDRQSFNEVGKLFTQILRVKDRDDFPVVLVGNKADLESQR   150
gi|55649695|ref|XP_524339.1|     MSSGAASGTGRGRPRGGGPGPGDPPPSETHNLVVVGGGGVGKSALTIQFIQSYFVSDYDPTIEDSYTKICSVDGIPARLDILDTAGQEEFGAMREQYMRAGHGFLLVFAINDRQSFNEVGKLFTQILRVKDRDDFPVVLVGNKADLESQR   150
gi|57036335|ref|XP_533617.1|     MSSGAASGTGRGRPRGGGPGPGDPPPSETHKLVVVGGGGVGKSALTIQFIQSYFVSDYDPTIEDSYTKICTVDGVPARLDILDTAGQEEFGAMREQYMRAGHGFLLVFAINDRQSFNEVGKLFTQILRVKDRDDFPIVLVGNKADLETQR   150
gi|84579874|ref|NP_001033777.1|  MSSGAASGTGRGRPRGGVPGPGDPPPSETHKLVVVGGGGVGKSALTIQFIQSYFVSDYDPTIEDSYTKICTVDGVPARLDILDTAGQEEFGAMREQYMRAGHGFLLVFAINDRQSFNEVGKLFTQILRVKDRDDFPVVLVGNKADLETQR   150
gi|67514545|ref|NP_001005931.2|  MST-----------------------EERYKLVVVGGGGVGKSALTIQFIQSYFVSDYDPTIEDSYTKICTVDGKETRLDILDTAGQEEFGAMREQYMRSGEGFLLVFALNDSGSYNEIQKFHTQILRVKDRDDFPMVLVGNKSDLDQQR   127
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
```

```
                                 : :.** :*. .::: *:*:*** * ****** ::**::**:** * ** *.. . ::* * ***.**
gi|6677819|ref|NP_033127.1|      QVLRSEASSFSASHHMTYFEASAKLRLNVDEAFEQLVRAVRKYQEQELPPSPPSAP-RKKDGGCPCVLL   218
gi|34856057|ref|XP_341852.1|     QVLRSEASSFSASHHMTYFEASAKLRLNVDEAFEQLVRTVRKYQEQELPPSPPSAP-RKKDGRCPCVLL   218
gi|5454028|ref|NP_006261.1|      QVPRSEASAFGASHHVAYFEASAKLRLNVDEAFEQLVRAVRKYQEQELPPSPPSAP-RKKGGGCPCVLL   218
gi|55649695|ref|XP_524339.1|     QVPRSEASAFGASHHVAYFEASAKLRLNVDEAFEQLVRAVRKYQEQELPPSPPSAP-RKKGGGCPCVLL   218
gi|57036335|ref|XP_533617.1|     QVPRSEASAFGASHHVAYFEASAKLRLNVDEAFEQLVRAVRKYQEQELPPSPPSAP-RKKDGGCPCVLL   218
gi|84579874|ref|NP_001033777.1|  QVPRSEASTFSASHHVAYFEASAKLRLNVDEAFEQLVRAVRKYQEQELPPSPPSAP-RKKAGGCPCVLL   218
gi|67514545|ref|NP_001005931.2|  VISKEEAMTFARENRIHYMESSAKNRHNVDEAFMEVVRAIRKFQETESPPLPANHTGKQKSGGCPCTLL   196
                                 .......160.......170.......180.......190.......200.......210........
```