```
gi|7305415|ref|NP_038919.1|      ------------------------------------------------------------------------------------------------------------------------------------------------------   150
gi|109509172|ref|XP_001069981.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   150
gi|6912580|ref|NP_036523.1|      ------------------------------------------------------------------------------------------------------------------------------------------------------   150
gi|114606986|ref|XP_001171692.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   150
gi|73972598|ref|XP_538872.2|     MEGMDVDLDPELMQKFSCLGTTDKDVLISEFQRLLGFQLNPAGCAFFLDMTNWNLQAAIGAYYDFESPNISVPSMSFVEDVTIGEGESIPPDTQFIKTWRIQNSGAEAWPPGVCLKYVGGDQFGHVNMVMVRSLEPQEIADVSVQMCSPS   150
gi|125991948|ref|NP_001075047.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   150
gi|118102528|ref|XP_425831.2|    ------------------------------------------------------------------------------------------------------------------------------------------------------   150
gi|125819379|ref|XP_001343077.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
```

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gi|7305415|ref|NP_038919.1|      ------------------------------------------------------------------------------------------------------------------------------------------------------   300
gi|109509172|ref|XP_001069981.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   300
gi|6912580|ref|NP_036523.1|      ------------------------------------------------------------------------------------------------------------------------------------------------------   300
gi|114606986|ref|XP_001171692.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   300
gi|73972598|ref|XP_538872.2|     RAGMYQGQWRMCTATGLYYGDVIWVILSVEVGGLLGVTQQLSSFETEFNTQPHRKVEGNFNPFASPQKNRQSDENNLKDPGGSGFDSISKNTWAPAPDQTEQDENRLSQNSVNLSPSSHANNLSVVTYSKLSMERQKQSKLLPAANVSGH   300
gi|125991948|ref|NP_001075047.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   300
gi|118102528|ref|XP_425831.2|    ------------------------------------------------------------------------------------------------------------------------------------------------------   300
gi|125819379|ref|XP_001343077.1| ------------------------------------------------------------------------------------------------------------------------------------------------------   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
```

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                                                                                                                                                                          *
gi|7305415|ref|NP_038919.1|      ------------------------------------------------------------------------------------------------------------------------------MGSASPGLSNVSPGCLLLFPDVAPRT   450
gi|109509172|ref|XP_001069981.1| ------------------------------------------------------------------------------------------------------------------------------MGSASPGLSNVSPGCLLLSPDVALRT   450
gi|6912580|ref|NP_036523.1|      ------------------------------------------------------------------------------------------------------------------------------MGSASPGLSSVSPSHLLLPPDTVSRT   450
gi|114606986|ref|XP_001171692.1| ------------------------------------------------------------------------------------------------------------------------------MGSASPGLSSVSPSHLLLPPDTVSRT   450
gi|73972598|ref|XP_538872.2|     SHISVLYSQGQQGKYDLHTTEEPRLLPLFLGTDYGNILTKLPATITAKHRALQDEGSKQMLENWGLRYEAVGEQAAAACHPHPRLSELPIVPEHHCTLDLHQARGDTDNTGPTRNTATGPSDSGMGSASPGLSSVSPSRLLLPPDTLLRT   450
gi|125991948|ref|NP_001075047.1| ------------------------------------------------------------------------------------------------------------------------------MGSASPGLSPGPPGRLLLPPDSALRT   450
gi|118102528|ref|XP_425831.2|    ------------------------------------------------------------------------------------------------------------------------------MG------------------------   450
gi|125819379|ref|XP_001343077.1| ------------------------------------------------------------------------------------------------------------------------------MTSP---VRIHSESAVLQPPHS---T   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
```

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                                                  ..*           : *  *: ::.:* :* .:     :             :*****:*** . .            ::*:****:**:******************:.** :*. .*****:***** ***
gi|7305415|ref|NP_038919.1|      GTEKAASGAMGPEKQEWSPSPPATPEQGLSAFYLSYFN-MYPDDSSWVAKVPEARAGEDHP-------EEPEQCPVIDSQASGS----------TLDEHSLEQVQSMVVGEVLKDIETACKLLNITADPGDWSPGNVQKWLLWTEHQYRL   600
gi|109509172|ref|XP_001069981.1| GVEKAASGAMGLEKQEWSPSPPATPEQGLSAFYLSYFN-MYPEDGSWVAKVPEASAREDHP-------EEPEQCPVIDSQASGN----------TLDEHSLEQVQSMVVGEVLKDIETACKLLNITADPGDWSPGNVQKWLLWTEHQYRL   600
gi|6912580|ref|NP_036523.1|      GLEKAAAGAVGLERRDWSPSPPATPEQGLSAFYLSYFDMLYPEDSSWAAKAPGASSREEPP-------EEPEQCPVIDSQAPAGSLD-LVPGGLTLEEHSLEQVQSMVVGEVLKDIETACKLLNITADPMDWSPSNVQKWLLWTEHQYRL   600
gi|114606986|ref|XP_001171692.1| GLEKAAAGAVGLERRDWSPSPPATPEQGLSAFYLSYFDMLYPEDSSWAVKAPGASSREEPP-------EEPEQCPVIDSQAPGGSLD-LVPGGLTLEEHSLEQVQSMVVGEVLKDIETACKLLNITADPMDWSSSNVQKWLLWTEHQYRL   600
gi|73972598|ref|XP_538872.2|     GLEKAAVGAVAPERRDWSPSPPATPEQGLSTFYLSYFDMLYPEDSSWAAKGPGASAREEPS-------EDPEQCPVIDSQAPGGSLD-LAPGGLTLEEHSLEQVQSMVVGEVLKDIETACKLLNITADPVDWSPGNVQKWLLWTEHQYRL   600
gi|125991948|ref|NP_001075047.1| GLEKAAAAGTGPERRDWSPSPPATPEQGLPTFYLSYFDMLYPEDSSWVAKGPGASTRVEPP-------DEPEQCPVIDSQAPGGSLD-LAPGGLTLEEHSLEQVQSMVVGEVLKDIETACKLLNITADPVDWSPGNVQKWLLWTEHQYRL   600
gi|118102528|ref|XP_425831.2|    -----------------SPSPPGTP------FCLHYFDMLYSEDVAWAAKGMGETSQSGTPGGRGEVKKEPEQCPIIDSQGLGLGGDGELQGGLPLEEHSLEQMQSMVVGEVLKDIETACKLLNIAADPADWSPGNVQKWILWTEHQYRL   600
gi|125819379|ref|XP_001343077.1| GFTESSLALLKREDGIVQSSEMLEHKASDRGLYLSCFDMLFTEDAAWLVRVTDAPAAAGAR-------LEPEQCPVIDSPGLGASPL-SPTLEEQVEERSLEQVQSLVVGEVLKDIETACKLLNITPDPMEWNCGNVQKWLLWTEHLYRL   600
                                 .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
```

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                                 *  **:**:* **:**:****:* **:*  .:.****************: : *  :   . .      .*.****:**********:*******.*** *****************:******:*************************
gi|7305415|ref|NP_038919.1|      PPAGKAFQELGGKELCAMSEEQFRQRAPLGGDVLHAHLDIWKSAAWMKERTSPGTLHYCASTSEEGWTDGEVDSSCSGQPIHLWQFLKELLLKPHSYGRFIRWLNKEKGIFKIEDSAQVARLWGVRKNRPAMNYDKLSRSIRQYYKKGII   750
gi|109509172|ref|XP_001069981.1| PPAGKAFQELGGKELCAMSEEQFRQRAPLGGDVLHAHLDIWKSAAWMKERTSPGALHYCASTSEEGWTDGEVDSSCSGQPIHLWQFLKELLLKPHSYGRFIRWLNKEKGIFKIEDSAQVARLWGVRKNRPAMNYDKLSRSIRQYYKKGII   750
gi|6912580|ref|NP_036523.1|      PPMGKAFQELAGKELCAMSEEQFRQRSPLGGDVLHAHLDIWKSAAWMKERTSPGAIHYCASTSEESWTDSEVDSSCSGQPIHLWQFLKELLLKPHSYGRFIRWLNKEKGIFKIEDSAQVARLWGIRKNRPAMNYDKLSRSIRQYYKKGII   750
gi|114606986|ref|XP_001171692.1| PPVGKAFQELAGKELCAMSEEQFRQRSPLGGDVLHAHLDIWKSAAWMKERTSPGAIHYCASTSEESWTDSEVDSSCSGQPIHLWQFLKELLLKPHSYGRFIRWLNKEKGIFKIEDSAQVARLWGIRKNRPAMNYDKLSRSIRQYYKKGII   750
gi|73972598|ref|XP_538872.2|     PPVGKAFQELGGKELCAMSEEQFRQRSPLGGDVLHAHLDIWKSAAWMKERTSPGTVHYCASTSEDSWTDSEVDSSCSGQPIHLWQFLKELLLKPHSYGRFIRWLNKEKGIFKIEDSAQVARLWGIRKNRPAMNYDKLSRSIRQYYKKGII   750
gi|125991948|ref|NP_001075047.1| PPVGKAFQELGGKELCAMSEEQFRQRSPLGGDVLHAHLDIWKSAAWMKERTSPGAIHFCASTSEESWTDSEVDSSCSGQPIHLWQFLKELLLKPHSYGRFIRWLNKEKGIFKIEDSAQVARLWGIRKNRPAMNYDKLSRSIRQYYKKGII   750
gi|118102528|ref|XP_425831.2|    PQLGKSFQELSGKELCAMSEEQFCQRSPLCGDVLHAHLDIWKSAAWMKEKAAPGDVRYCGGDS--GWADSEVDSSCAGQPIHLWQFLKELLLKPHNYGRFIRWLNKEKGIFKIEDSAQVARLWGIRKNRPAMNYDKLSRSIRQYYKKGII   750
gi|125819379|ref|XP_001343077.1| PQVGKAFQDLDGKDLCSMSEEDFRQRSPQCSETLHAHLDIWKSAAWMKERCSGGETRMREGEE----LWSEADSSCSGQPIHLWQFLRELLLKPHSYGRCIRWLNKEKGIFKIEDSAHVARLWGLRKNRPAMNYDKLSRSIRQYYKKGII   750
                                 .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750
```

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                                   ****:***********:
gi|7305415|ref|NP_038919.1|        RKPDISQRLVYQFVHPV   767
gi|109509172|ref|XP_001069981.1|   RKPDISQRLVYQFVHPV   767
gi|6912580|ref|NP_036523.1|        RKPDISQRLVYQFVHPI   767
gi|114606986|ref|XP_001171692.1|   RKPDISQRLVYQFVHPI   767
gi|73972598|ref|XP_538872.2|       RKPDISQRLVYQFVHPI   767
gi|125991948|ref|NP_001075047.1|   RKPDISQRLVYQFVHPI   767
gi|118102528|ref|XP_425831.2|      RKPDISQRLVYQFVHPL   767
gi|125819379|ref|XP_001343077.1|   RKPDVSQRLVYQFVHPV   767
                                   .......760.......
```