```
gi|10834994|ref|NP_000632.1|      ------------------------------------------------------------------------------------------------------------------------------------------------------
gi|114679121|ref|XP_001136017.1| MWAPAEFEGLVGQSCSETSWSSRTPTHSRAPALEPECLLRPVEVEGGDANDLTSPSPTTPPFPFSTFPTFPSVPSSERGGVSPARQPLRLNGKGRQGGRPHSLTAAALLLRAHASPPQAAAQLTLGAPPAADREGLKAPGSLPPALGNPW   150
gi|73947466|ref|XP_854055.1|      ------------------------------------------------------------------------------------------------------------------------------------------------------
gi|6680393|ref|NP_032376.1|       ------------------------------------------------------------------------------------------------------------------------------------------------------
gi|19424164|ref|NP_598203.1|      ------------------------------------------------------------------------------------------------------------------------------------------------------
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
```

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                                     **.** ****.****** ..*****.*.**.*.****:***:*****************:**********.************:**:***********.**:**:*********.*.**:*******:*****:************
gi|10834994|ref|NP_000632.1|      ----MNCVCRLVLVVLSLWPDTAVAPGPPPGPPRVSPDPRAELDSTVLLTRSLLADTRQLAAQLRDKFPADGDHNLDSLPTLAMSAGALGALQLPGVLTRLRADLLSYLRHVQWLRRAGGSSLKTLEPELGTLQARLDRLLRRLQLLMSR   146
gi|114679121|ref|XP_001136017.1| PCGDMNCVCRLVLVVLSLWPDTAVAPGPPPGPPRVSPDPRAELDSTVLLTRSLLADTRQLAAQLRDKFPADGDHNLDSLPTLAMSAGALGALQLPGVLTRLRADLLSYLRHVQWLRRAGGSSLKTLEPELGTLQARLDRLLRRLQLLMSR   300
gi|73947466|ref|XP_854055.1|      ----MNSVCCLVLVALSLWPDRAAAPGPPPGPPRASPDPRAELDSAVLLTRSLLADTRQLAAQLRDKFPADGDHNLDSLPTLAMSAGALGALQLPGVLTRLRADLFSYLRHVQWLRRAGGPSLRTLEPELGALQARLDRLLRRLQLLMSR   146
gi|6680393|ref|NP_032376.1|       ----MNCVCRLVLVVLSLWPDRVVAPGPPAGSPRVSSDPRADLDSAVLLTRSLLADTRQLAAQMRDKFPADGDHSLDSLPTLAMSAGTLGSLQLPGVLTRLRVDLMSYLRHVQWLRRAGGPSLKTLEPELGALQARLERLLRRLQLLMSR   146
gi|19424164|ref|NP_598203.1|      ----MNCVCRLVLVVLSLWPDRVVAPGPPAGSPRVSSDPRADLDSAVLLTRSLLADTRQLAAQMRDKFPADGDHNLDSLPTLAMSAGTLGSLQLPGVLTRLRVDLMSYFRHVQWLRRAAGPSLKTLEPELGALQARLERLLRRLQLLMSR   146
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                                  *****..** *. **.**:****.******************************
gi|10834994|ref|NP_000632.1|      LALPQPPPDPPAPPLAPPSSAWGGIRAAHAILGGLHLTLDWAVRGLLLLKTRL   199
gi|114679121|ref|XP_001136017.1| LALPQPPPDPPAPPLAPPSSAWGGIRAAHAILGGLHLTLDWAVRGLLLLKTRL   353
gi|73947466|ref|XP_854055.1|      LALPQAPPDPPAPPLAPPASAWGGIRAAHAILGGLHLTLDWAVRGLLLLKTRL   199
gi|6680393|ref|NP_032376.1|       LALPQAAPDQPVIPLGPPASAWGSIRAAHAILGGLHLTLDWAVRGLLLLKTRL   199
gi|19424164|ref|NP_598203.1|      LALPQAAPDQPAVPLGPPASAWGSIRAAHAILGGLHLTLDWAVRGLLLLKTRL   199
                                  .......310.......320.......330.......340.......350...
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