```
gi|74003232|ref|XP_545216.2|      MRQ-----HGVTASRCHYA------------------GEARGCS-------------GAGLTVSWRR-----------------------LLRPPLHPHFPWRRGSRHP--R--PADXGSPPRRGRGRA------------------   150
gi|157428050|ref|NP_001098933.1| ------------------------------------------------------------------------------------------------------------------------------------   150
gi|28195386|ref|NP_003097.1|     ------------------------------------------------------------------------------------------------------------------------------------   150
gi|127140986|ref|NP_035573.3|    ------------------------------------------------------------------------------------------------------------------------------------   150
gi|62643333|ref|XP_574919.1|     ------------------------------------------------------------------------------------------------------------------------------------   150
gi|114590606|ref|XP_516895.2|    MGRSIRSCQGREESVCKRGKVVCCLFKTRTERKKRREKERERSLSPRLKPFQKIIITIIGGGRIGQRRREALFLILIPVCLSLFFPQIILRLIFLAEPCAPDTPARLPSSSPPARGPPKVPAGPRVGGRRRAGPAHSARMYNMMETELKP   150
gi|45383968|ref|NP_990519.1|      ------------------------------------------------------------------------------------------------------------------------------------   150
gi|54261783|ref|NP_998283.1|      ------------------------------------------------------------------------------------------------------------------------------------   150
                                  1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

gi|74003232|ref|XP_545216.2|      RGPRGRRGSAGWSG--------------------------LPAGARRPRSRLGPSQLPSNRRGRR----------EGR-----GRRF------PPPDFRS-----------------------GHPALAT-------P----------   300
gi|157428050|ref|NP_001098933.1| ------------------------------------------------------------------------------------------------------------------------------------   300
gi|28195386|ref|NP_003097.1|     ------------------------------------------------------------------------------------------------------------------------------------   300
gi|127140986|ref|NP_035573.3|    ------------------------------------------------------------------------------------------------------------------------------------   300
gi|62643333|ref|XP_574919.1|     ------------------------------------------------------------------------------------------------------------------------------------   300
gi|114590606|ref|XP_516895.2|    PGPQQTSGGGGGGGNSTAAAAGGNQKNSPDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEISKRLGAEWKLLSETEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLMKKDKYTLPGGLLAPGGNSMASGVGVGAGPGRGVNQRMDS   300
gi|45383968|ref|NP_990519.1|      ------------------------------------------------------------------------------------------------------------------------------------   300
gi|54261783|ref|NP_998283.1|      ------------------------------------------------------------------------------------------------------------------------------------   300
                                  .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                                                                                                 ************.**  :**           .: :   ********:********************************
gi|74003232|ref|XP_545216.2|      ----------------------------PPA----SLLLLPRPPARGPPKVPAGPRVGGRRRAGPAHSARMYNMMETELKPPGPQQTSGGGGGGGGGGGNSTAAAAGGNQKNSPDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEIS   450
gi|157428050|ref|NP_001098933.1| ------------------------------------------------------------------MYNMMETELKPPGPQQTSGGGGGGG----GNSTAAAAGGNQKNSPDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEIS   450
gi|28195386|ref|NP_003097.1|     ------------------------------------------------------------------MYNMMETELKPPGPQQTSGGG-------GGNSTAAAAGGNQKNSPDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEIS   450
gi|127140986|ref|NP_035573.3|    ------------------------------------------------------------------MYNMMETELKPPGPQQASGGGGGG-----GNATAAATGGNQKNSPDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEIS   450
gi|62643333|ref|XP_574919.1|     ------------------------------------------------------------------MYNMMETELKPPGPQQASGGGGGG-----GNATAAATGGNQKNSPDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEIS   450
gi|114590606|ref|XP_516895.2|    YAHMNCWXHGSYSMIWIHCESHELTRFRIKPARDTRKSLLSSSPPARGPPKVPAGPRVGGRRRAGPAHSARMYNMMETELKPPGPQQTSGGGGGG-----GNSTAAAAGGNQKNSPDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEIS   450
gi|45383968|ref|NP_990519.1|      ------------------------------------------------------------------MYNMMETELKPPAPQQTSGGGT-------GNSNSAAN--NQKNSPDRVKRPMNAFMVWSRGQRRKMAQENPKMHNSEIS   450
gi|54261783|ref|NP_998283.1|      ------------------------------------------------------------------MYNMMETELKPPAPQPNTGGTG----------NTNSSGNNQKNSPDRIKRPMNAFMVWSRGQRRKMAQENPKMHNSEIS   450
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                                  ************:*************************************************** * * :****** *******************:**.*.***:********.****.:***********:*********.***********
gi|74003232|ref|XP_545216.2|      KRLGAEWKLLSETEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLMKKDKYTLPGGLLAPGGNSMASGVGVGAGLGAGVNQRMDSYAHMNGWSNGSYSMMQDQLGYPQHPGLNAHGAAQMQPMHRYDVSALQYNSMTSSQTYMNGSPT   600
gi|157428050|ref|NP_001098933.1| KRLGAEWKLLSETEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLMKKDKYTLPGGLLAPGGNSMASGVGVGAGLGAGVNQRMDSYAHMNGWSNGSYSMMQDQLGYPQHPGLNAHGAAQMQPMHRYDVSALQYNSMTSSQTYMNGSPT   600
gi|28195386|ref|NP_003097.1|     KRLGAEWKLLSETEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLMKKDKYTLPGGLLAPGGNSMASGVGVGAGLGAGVNQRMDSYAHMNGWSNGSYSMMQDQLGYPQHPGLNAHGAAQMQPMHRYDVSALQYNSMTSSQTYMNGSPT   600
gi|127140986|ref|NP_035573.3|    KRLGAEWKLLSETEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLMKKDKYTLPGGLLAPGGNSMASGVGVGAGLGAGVNQRMDSYAHMNGWSNGSYSMMQEQLGYPQHPGLNAHGAAQMQPMHRYDVSALQYNSMTSSQTYMNGSPT   600
gi|62643333|ref|XP_574919.1|     KRLGAEWKLLSETEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLMKKDKYTLPGGLLAPGGNSMASGVGVGAGLGAGVNQRMDSYAHMNGWSNGSYSMMQEQLGYPQHPGLNAHGAAQMQPMHRYDVSALQYNSMTSSQTYMNGSPT   600
gi|114590606|ref|XP_516895.2|    KRLGAEWKLLSETEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLMKKDKYTLPGGLLAPGGNSMASGVGVGAGLGAGVNQRMDSYAHMNGWSNGSYSMMQDQLGYPQHPGLNAHGAAQMQPMHRYDVSALQYNSMTSSQTYMNGSPT   600
gi|45383968|ref|NP_990519.1|      KRLGAEWKLLSEAEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLMKKDKYTLPGGLLAPGTNTMTTGVGVGATLGAGVNQRMDSYAHMNGWTNGGYGMMQEQLGYPQHPGLNAHNAAQMQPMHRYDVSALQYNSMTSSQTYMNGSPT   600
gi|54261783|ref|NP_998283.1|      KRLGAEWKLLSESEKRPFIDEAKRLRALHMKEHPDYKYRPRRKTKTLMKKDKYTLPGGLLAPGGNGMGAGVGVGAGLGAGVNQRMDSYAHMNGWTNGGYGMMQEQLGYPQHPSLNAHNTAQMQPMHRYDMSALQYNSMTNSQTYMNGSPT   600
                                  .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

                                  ********.****:*********:*:***************  **:**************** :  ..   * **:*****.*****:****:*****
gi|74003232|ref|XP_545216.2|      YSMSYSQQGTPGMALGSMGSVVKSEASSSPPVVTSSSHSRA-PCQAGDLRDMISMYLPGAEVPEPAAPSRLHMSQHYQSGPVPGTAINGTLPLSHM   696
gi|157428050|ref|NP_001098933.1| YSMSYSQQGTPGMALGSMGSVVKSEASSSPPVVTSSSHSRA-PCQAGDLRDMISMYLPGAEVPEPAAPSRLHMSQHYQSGPVPGTAINGTLPLSHM   696
gi|28195386|ref|NP_003097.1|     YSMSYSQQGTPGMALGSMGSVVKSEASSSPPVVTSSSHSRA-PCQAGDLRDMISMYLPGAEVPEPAAPSRLHMSQHYQSGPVPGTAINGTLPLSHM   696
gi|127140986|ref|NP_035573.3|    YSMSYSQQGTPGMALGSMGSVVKSEASSSPPVVTSSSHSRA-PCQAGDLRDMISMYLPGAEVPEPAAPSRLHMAQHYQSGPVPGTAINGTLPLSHM   696
gi|62643333|ref|XP_574919.1|     YSMSYSQQGTPGMALGSMGSVVKSEASSSPPVVTSSSHSRA-PCQAGDLRDMISMYLPGAEVPEPAAPSRLHMAQHYQSGPVPGTAINGTLPLSHM   696
gi|114590606|ref|XP_516895.2|    YSMSYSQQGTPGMALGSMGSVVKSEASSSPPVVTSSSHSRA-PCQAGDLRDMISMYLPGAEVPEPGGPRRDHMSQHYQSGPVPGTAINGTLPLSHM   696
gi|45383968|ref|NP_990519.1|     YSMSYSQQGTPGMALGSMGSVVKTESSSSPPVVTSSSHSRA-PCQAGDLRDMISMYLPGAEVPEPAAPSRLHMSQHYQSAPVPGTAINGTLPLSHM   696
gi|54261783|ref|NP_998283.1|     YSMSYSQQSTPGMTLGSMGSVVKSESSSSPPVVTSSSHSRAGQCQTGDLRDMISMYLPGAEVQDQSAQSRLHMSQHYQSAPVPGTTINGTIPLSHM   696
                                  .......610.......620.......630.......640.......650.......660.......670.......680.......690.....
```