```
                                 *: * *.  *   :    *  : :      **:               *****.********:*:***: ****:: **: *::.**:: .* *.::** **: * ::****::*::::**:.* * .**  *:.*:* *:: **:*.
gi|6679785|ref|NP_032034.1|      MRKWILTRILPTLLYRSCFHLVCLVGTISLACNDMSPEQTATSVNCSSPERHTRSYDYMEGGDIRVRRLFCRTQWYLRIDKRGKVKGTQEMKNSYNIMEIRTVAVG-IVAIKGVESEYYLAMNKEGKLYAKKECNEDCNFKELILENHYN   149
gi|11559943|ref|NP_071518.1|     MRKWILTRILPTPLYRPCFHLVCLVGTISLACNDMSPEQTATSVNCSSPERHTRSYDYMEGGDIRVRRLFCRTQWYLRIDKRGKVKGTQEMRNSYNIMEIMTVAVG-IVAIKGVESEYYLAMNKQGELYAKKECNEDCNFKELILENHYN   149
gi|4503705|ref|NP_002000.1|      MHKWILTWILPTLLYRSCFHIICLVGTISLACNDMTPEQMATNVNCSSPERHTRSYDYMEGGDIRVRRLFCRTQWYLRIDKRGKVKGTQEMKNNYNIMEIRTVAVG-IVAIKGVESEFYLAMNKEGKLYAKKECNEDCNFKELILENHYN   149
gi|114656948|ref|XP_001167290.1| MHKWILTWILPTLLYRSCFHIICLVGTISLACNDMTPEQMATNVNCSSPERHTRSYDYMEGGDIRVRRLFCRTQWYLRIDKRGKVKGTQEMKNNYNIMEIRTVAVG-IVAIKGVESEFYLAMNKEGKLYAKKECNEDCNFKELILENHYN   149
gi|50979022|ref|NP_001003237.1| MRKWILTWILPTLLYRSCFHIICLVGTISLACNDMTPEQMATNVNCSSPERHTRSYDYMEGGDIRVRRLFCRTQWYLRIDKRGKVKGTQEMKNSYNIMEIRTVAVG-IVAIKGVESEYYLAMNKEGKLYAKKECNEDCNFKELILENHYN   149
gi|119902623|ref|XP_874109.2|    MRKWILTWILPSLLYRSCFHIICLVGTISLACNDMTPEQMATNVNCSSPERHTRSYDYMEGGDIRVRRLFCRTQWYLRIDKRGKVKGTQEMKNNYNIMEIRTVAVG-IVAIKGVESEYYLAMNKEGKLYAKKECNEDCNFKELILENHYN   149
gi|60302702|ref|NP_001012543.1| MHKWILTWILPILLYRSYFYIIFLMGTISLACNDMTPEQMATNVNCSSPERHTRSYDYMEGGDVRVRRLFCRTQWYMRIDKRGKVKGTREANNNYSILEIRTVAVG-IVAIKGVESEYFLAMNKSGRLYGKKVCNEDCNFIELIEENHYN   149
gi|56090216|ref|NP_001007762.1| MRLWTLPWKLLQVVL--VFSRVCVC-----ACE---------------GERHTRNYDYMEGGDVRIRRLYNRTQWFLTIDEYGNITGTQDPNNCYSVLEIRTVSEGGVLAIKGLKSQFYISMNRSGMLQGKKDYNDSCDFKEVFLENYYT   128
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                                 : :*.***:.* ***::*.:** *::****:**  ::**:*   :
gi|6679785|ref|NP_032034.1|      TYASAKWTHSGGEMFVALNQKGIPVKGKKTKKEQKTAHFLPMAIT-------   194
gi|11559943|ref|NP_071518.1|     TSASAKWTHSGGEMFVALNQKGLPVKGKKTKKEQKTAHFLPMAIT-------   194
gi|4503705|ref|NP_002000.1|      TYASAKWTHNGGEMFVALNQKGIPVRGKKTKKEQKTAHFLPMAIT-------   194
gi|114656948|ref|XP_001167290.1| TYASAKWTHNGGEMFVALNQKGIPVRGKKTKKEQKTAHFLPMAIT-------   194
gi|50979022|ref|NP_001003237.1| TYASAKWTHSGGEMFVALNQKGVPVRGKKTKKEQKTAHFLPMAIT-------   194
gi|119902623|ref|XP_874109.2|    TYASAKWTHSGGEMFVALNQKGVPVRGKKTKKEQKTAHFLPMAIT-------   194
gi|60302702|ref|NP_001012543.1| TYASAKWTHKGKEMFVTLNHKGVPMKGKKTKKEHRASHFLPLAIS-------   194
gi|56090216|ref|NP_001007762.1| AYSSVKWTKNGREMFISLSQKGRPLKGKKTRKESVASHFIPRKCSEDEKKLA   180
                                 .......160.......170.......180.......190.......200..
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