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                          *:   ******** :**::**.*** ********:** *********.: :*******:**:*********** :******* ::* ***:***:*.*:*********:*******:**    .          * ********::*******
gi|18104991|ref|NP_536858.1|      MLSRGWFHRDLSGLDAETLLKGRGVHGSFLARPSRKNQGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKFATLTELVEYYTQQQGVLQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLQAKGEPWTFLVRESLSQPGDFVLS   150
gi|114643118|ref|XP_001163468.1|  MLSHGWFHRDLSGLDAETLLKGRGVHGSFLARPSRKNQGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKFATLTELVEYYTQQQGVLQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQQRRCCSQ-GEPWTFLVRESLTQPGDFVLS   149
gi|118130785|ref|NP_001071173.1|  MLSRGWFHRDLSGPDAETLLKGRGVPGSFLARPSRKNQGDFSLSVRVDDQVTHIRIQNSGDFYDLYGGEKFATLTELVEYYTQQQGILQDRDGTIIHLKYPLNCSDPTSERWYHGHISGGQAESLLQAKGEPWTFLVRESLSQPGDFVLS   150
gi|16758788|ref|NP_446360.1|      MLSRGWFHRDLSGPDAETLLKGRGVPGSFLARPSRKNQGDFSLSVRVDDQVTHIRIQNSGDFYDLYGGEKFATSTELVEYYTQQQGILQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAESLLQAKGEPWTFLVRESLSQPGDFVLS   150
gi|148237209|ref|NP_001091486.1|  MVR--WFHRDLSGLDAETLLKGRGVHGSFLARPSRKNQGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKFATLTELVEYYTQQQGVLQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLQAKGEPWTFLVRESLSQPGDFVLS   148
gi|73997724|ref|XP_543844.2|      MVR--WFHRDLSGLDAETLLKGRGVHGSFLARPSRKNQGDFSLSVRVGDQVTHIRIQNSGDFYDLYGGEKFATLTELVEYYTQQQGVLQDRDGTIIHLKYPLNCSDPTSERWYHGHMSGGQAETLLQAKGEPWTFLVRESLSQPGDFVLS   148
gi|71895573|ref|NP_001026655.1|   MVR--WFHRDLSGLEAEALLKGRGVHGSFLARPSRKNQGDFSLSVRVGDQVTHIRIQNTGDFYDLYGGEKFATLSELVEYYTQQQGSLQDKDGTIIDLRYPLNCSDPTSERWYHGHLSGVAAESLLQAKATPWTFLVRESLSKPGDFVLS   148
gi|41053929|ref|NP_956254.1|      MVR--WFHRDLSGLDAEAVLKSRGVHGSFLARPSKKNVGDFSLSVRVGEIITHIRIQNTGDYYDLYGGEKFATLAELVEYYTGDHGTLQDKDGTVIELKYPLNCSDPTTERWYHGHLSGPNAEKLLRERNEPGTFLVRESLSKPGDFVLS   148
                          1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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                          .*.*:  ...                :*:***:**:..****** : **.*:*******:.**** **::***:****:**:*****:.** :*::..  *      .. *****:**::*** *.*   .* ** *****.*********
gi|18104991|ref|NP_536858.1|      VLSDQPKAGPGSP-----------LRVTHIKVMCEGGRYTVGGLETFDSLTDLVEHFKKTGIEEASGAFVYLRQPYYATRVNAADIENRVLELNKKQESE------DTAKAGFWEEFESLQKQEVKNLHQRLEGQRPENKGKNRYKNILP   283
gi|114643118|ref|XP_001163468.1|  VLSDQPKAGPGSP-----------LRVTHIKVMCEGGRYTVGGLETFDSLTDLVEHFKKTGIEEASGAFVYLRQPYYATRVNAADIENRVLELNKKQESE------DTAKAGFWEEFESLQKQEVKNLHQRLEGQRPENKGKNRYKNILP   282
gi|118130785|ref|NP_001071173.1|  VLNDQPKAGPGSP-----------LRVTHIKVMCEGGRYTVGGSETFDSLTDLVEHFKKTGIEEASGAFVYLRQPYYATRVNAADIENRVLELNKKQESE------DTAKAGFWEEFESLQKQEVKNLHQRLEGQRPENKSKNRYKNILP   283
gi|16758788|ref|NP_446360.1|      VLNDQPKAAPGSP-----------LRVTHIKVMCEGGRYTVGGSETFDSLTDLVEHFKKTGIEEASGAFVYLRQPYYATRVNAADIENRVLELNKKQESE------DTAKAGFWEEFESLQKQEAKNLHQRLEGQRPENKSKNRYKNILP   283
gi|148237209|ref|NP_001091486.1|  VLSDQPKAGPGSP-----------LRVTHIKVMCEGGRYTVGGSETFDSLTDLVEHFKRTGIEEASGAFVYLRQPYYATRVNAADIENRVLELNKKQESE------ETAKAGFWEEFESLQKQEVKNLHQRLEGQRPENKSKNRYKNILP   281
gi|73997724|ref|XP_543844.2|      VLSDQPKAGLGSP-----------LRVTHIKVMCEGGRYTVGGAETFDSLTDLVEHFKKTGIEEASGAFVYLRQPYYATRVNAADIENRVLELNKKQESE------DTAKAGFWEEFESLQKQEVKNLHQRLEGQRPENKSKNRYKNILP   281
gi|71895573|ref|NP_001026655.1|   VLTDQPKPGSDAPPAGATSASGARLKVTHIKIMCENGRYTVGGSEKFDSLADLVEHFKKTGIEEVSGSFVYLKQPYYATRVNAADIENRVHELNKKSLSE------ETSKAGFWKEFDSLQKQEAKQLFDRHEGQRPENKSKNRYKNILP   292
gi|41053929|ref|NP_956254.1|      ALTDDQTSSG--------------RRVSHIKIMCNNDRYTVGGKDQFDNLTDLVEHFKRVGIEELSGTMVYLKQPYYSTRLNAADIQSRVNQLDQTSEREKMDGADKKIKAGFWEEFDALQKLETKVTKSRDEGMRPENKSKNRYKNILP   284
                          .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300
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                          **.:**:*:. *.*: *********: *.*: .:   *****.**** :**:***** ***:: :********************   *  :  * * *    * *: :**:* : : .  :  *:**::***********.******
gi|18104991|ref|NP_536858.1|      FDHSRVILQGRDSNIPGSDYINANYIKNQLLGPDENAKTYIASQGCLEATVNDFWQMAWQENSRVIVMTTREVEKGRNKCVPYWP-EVGMQRAYGPYSVTNCGEHDTTEYKLRTLQVSPLDNGDLIREIWHYQYLSWPDHGVPSEPGGVL   432
gi|114643118|ref|XP_001163468.1|  FDHSRVILQGRDSNIPGSDYINANYIKNQLLGPDENAKTYIASQGCLEATVNDFWQMAWQENSRVIVMTTREVEKGRNKCVPYWP-EVGMQRAYGPYSVTNCGEHDTTEYKLRTLQVSPLDNGDLIREIWHYQYLSWPDHGVPSEPGGVL   431
gi|118130785|ref|NP_001071173.1|  FDHSRVILQGRDSNIPGSDYINANYVKNQLLGPDENSKTYIASQGCLDATVNDFWQMAWQENTRVIVMTTREVEKGRNKCVPYWP-EVGTQRVYGLYSVTNSREHDTAEYKLRTLQISPLDNGDLVREIWHYQYLSWPDHGVPSEPGGVL   432
gi|16758788|ref|NP_446360.1|      FDHSRVILQGRDSNIPGSDYINANYVKNQLLGPDENSKTYIASQGCLDATVNDFWQMAWQENTRVIVMTTREVEKGRNKCVPYWP-EVGTQRVYGLYSVTNCKEHDTAEYKLRTLQISPLDNGDLVREIWHYQYLSWPDHGVPSEPGGVL   432
gi|148237209|ref|NP_001091486.1|  FDHSRVVLQGRDSNIPGSDYINANYVKNQLLGPDENAKTYIASQGCLEATVNDFWQMVWQENTCVIVMTTREVEKGRNKCVPYWP-EVGSQRVYGPYTVTNCGEHDTTEYKLRNLQVSPLENENLIREIWHYQYLSWPDHGVPSEPGGVL   430
gi|73997724|ref|XP_543844.2|      FDHTRVILQGRDSNIPGSDYINANYVKNELLGPDENTKTYIASQGCLEATVNDFWQMAWQENTRVIVMTTREVEKGRNKCVPYWP-EVGTQRAYGPYVVTNCREHDAAEYKLRTLQVSPLENEDLVREIWHYQYLSWPDHGVPSEPGGVL   430
gi|71895573|ref|NP_001026655.1|   FDHSRVILQGRDPNIPGSDYINANYVKNNLISPDECPKTYIASQGCLDTTVNDFWQMVWQENTHIIVMTTREVEKGRNKCVPYWP-EAGSTKEYGPYLVENVGEHDALEYKLRHLCVCPINDSEAVREIWQYQYLSWPDHGVPSEPGGVL   441
gi|41053929|ref|NP_956254.1|      FDETRVILENADPNVVGSDYINANYVINKLMVTNP-QKTYIACQGCLATTVDDFWQMMWQEDSRVIVMTTREVEKGRNKCVPYWPTTEGESKEVGRYVVKLLSEMDAADYKVRVVELTAPHRNEAPRKIWHFQYLSWPDHGVPQEPGGVL   433
                          .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450
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gi|18104991|ref|NP_536858.1|      SFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKLEVLQSQKGQ--ESEYGNITYPPAMKNAHAKASR-TSSKHKEDVYENLHTKNKREEKV   579
gi|114643118|ref|XP_001163468.1|  SFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKLEVLQSQKGQ--ESEYGNITYPPAMKNAHAKASR-TSSKHKEDVYENLHTKNKREEKV   578
gi|118130785|ref|NP_001071173.1|  SFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVIDMLMESISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKLEIIQSQKGQ--ESEYGNITYPPAVRSAHAKASR-TSSKHKEEVYENVHSKSKKEEKV   579
gi|16758788|ref|NP_446360.1|      SFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVIDMLMESVSTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKLEIIQSQRGQ--ESEYGNITYPPALRSAHAKASR-TSSKHKEEVYENVHSKNKKEEKV   579
gi|148237209|ref|NP_001091486.1|  SFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVIDMLMESISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKLEVMQSQKGR--ESEYGNITYPPAMKNAHAKASR-TSS--KEDVYENVHSKNKKEEKV   575
gi|73997724|ref|XP_543844.2|      SFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVIDMLMESISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKLEVMQSQKGR--ESEYGNITYPLAMKNAHAKASR-TSSKHKEDVYENLQSKNKKEEKV   577
gi|71895573|ref|NP_001026655.1|   SFLDQINQKQESIPNAGPILVHCSAGIGRTGTIIVIDMIVETISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYMAICQFIETTKRKLEVIQSQKSKQNESEYGNITYPPAVKNMHAKVSR-KSSKQKETIYENLG---KKEEKV   587
gi|41053929|ref|NP_956254.1|      SFLDQVNRKQEELRSSAPIVIHCSAGIGRTGTIVVIDMLIDSIDAKGLDCDIDIQKCIMMVRDQRSGMVQTEAQYKFIYLAVLQYVESTKVTRRAIMET-----ETEYGNLS----IQSKHPKASRKASSKKNEDVYENLGAKGKKD--V   572
                          .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600
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                          :** * :* *  .*:::.
gi|18104991|ref|NP_536858.1|      KKQRSADKEKSKGSLKRK----------------   597
gi|114643118|ref|XP_001163468.1|  KKQRSADKEKSKGSLKRK----------------   596
gi|118130785|ref|NP_001071173.1|  KKQRSADKEKNKGSLKRK----------------   597
gi|16758788|ref|NP_446360.1|      KKQRSADKEKNKGSLKRNISLTPCRGLRWADRDL   613
gi|148237209|ref|NP_001091486.1|  KKQRSADKEKNKGSLKRK----------------   593
gi|73997724|ref|XP_543844.2|      KKQRSADKEKSKGSLKRK----------------   595
gi|71895573|ref|NP_001026655.1|   RKQLSSEK-KLKSSLKKK----------------   604
gi|41053929|ref|NP_956254.1|      KKQKSEEK-KGGGSVRKR----------------   589
                          .......610.......620.......630....
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