```
                                 : *                 :     .:  :*: :.*  * :  :: *    ::*.::*: *:.:*: :*::  :*  *  . : ::*.: *: . *:: ** ..   .    .*:::* : :...:*. *** .:: :.  ****:*:
gi|118150658|ref|NP_032707.2|    MSRELHDVDLAEVKPLVEKGES-ITGLLQEFDVQEQDIETLHGSLHVTLCGTPKGNRPVILTYHDIGMNHKTCYN-PLFNSEDMQEITQHFAVCHVDAPGQQDGAPSFPVGYMYPSMDQLAEMLPGVLHQFGLKSVIGMGTGAGAYILTR   150
gi|58865550|ref|NP_001011991.1|  MSRELHDVDLAEVKPLVEKGES-ITGLLQEFDVQEQDIETLHGSLHVTLCGTPKGNRPVILTYHDIGMNHKTCYN-PLFNSEDMQEITQHFAVCHVDAPGQQDGAPSFPVGYMYPSMDQLAEMLPGVLHKFGLKSVIGMGTGAGAYILTR   150
gi|207028748|ref|NP_001128714.1| MSREMQDVDLAEVKPLVEKGET-ITGLLQEFDVQEQDIETLHGSVHVTLCGTPKGNRPVILTYHDIGMNHKTCYN-PLFNYEDMQEITQHFAVCHVDAPGQQDGAASFPAGYMYPSMDQLAEMLPGVLQQFGLKSIIGMGTGAGAYILTR   150
gi|114621833|ref|XP_001140704.1| MSREMQDVDLAEVKPLVEKGET-ITGLLQEFDVQEQDIETLHGSVHVTLCGTPKGNRPVILTYHDIGMNHKTCYN-PLFNYEDMQEITQHFAVCHVDAPGQQDGAASFPAGYMYPSMDQLAEMLPGVLQQFGLKSIIGMGTGAGAYILTR   150
gi|73974634|ref|XP_539170.2|     MSRELQDVDLAEVKPLVEKGET-ITGLLQEFDVQEQDIETVHGSIHVTLCGTPKGNRPVILTYHDIGMNHKTCYN-PLFNSEDMQEITQHFAVCHVDAPGQQDGAASFPVGYMYPSMDQLAEMLPGVLHQFGLKSIIGMGTGAGAYILTR   150
gi|78042480|ref|NP_001030181.1|  MSRELQDVDLAEVKPLVEKGET-ITGLLQEFDVQEQDIETLHGSIHVTLCGTPKGNRPVILTYHDIGMNHKTCYN-PLFNSEDMQEITQHFAVCHVDAPGQQDGAASFPTGYMYPSMDQLAEMLPGVLQQFGLKSIIGMGTGAGAYILTR   150
gi|118087385|ref|XP_418430.2|    MSTEFQDAHLAEVKPLVEKEEA-ITRLLPDFDVQEQDVETMHGMVHVTMCGTPRGNRPAILTYHDIGLNHKTCFN-PLFNFEDMQEITQHFAVCHVDAPGQQDGAPSFQAGYIYPSMDQLAEMLPGILKQFGLKSIIGMGTGAGAYVLTR   150
gi|51226300|ref|NP_998513.2|     ----MDDIQVESKPLIVDKDLQGLREAVQKLELKEHDVETPYGKIHCTMKGVPKADRPVILTFHDIGLNHKSCFD-TLFSHEDMQEIMQHFAVCHVDAPGQQEGANTFSTGYEYPSMDQLSETLPSILKHFGLKSVIGMAIGAGAYILSK   150
gi|115462531|ref|NP_001054865.1| ----MGDSSGSGS----GSGSVSVDVERISFGGKEHQVRTRCGSLSVAIYGDE--DKPALITYPDIALNHMSCFQGLLFCPEVASLLLHNFCIYHINPQGHELGAAPIPSDVPVPSVEDLADQVADVLDFFGLGSVMCLGVTAGAYVLTL   150
gi|115435040|ref|NP_001042278.1| ----MGDSS----------RSVSIDVERISFGGKEHRVRTRYGSVSVSVFGDE--DKPALITYPDVALNYMSCFQGLFFCPEAASLLLHNFCIYHITPQGHELGAAPISSDVPVPSVDELVDQVADVLDFFGLGSVMCLGVTAGAYILTL   150
gi|115445113|ref|NP_001046336.1| ----MGDSGG---------SVVSIDVERISFGGKEHHIHTNHGPVSVAVYGDH--DKPALVTYPDIALNHMSCFQGLLFCPEAASLLLHNFCIYHISPPGHELGAAPISPNAPIPSVDDLADQVADVLDFFGLGSVMCLGVSAGAYILTL   150
gi|115468558|ref|NP_001057878.1| ----MGDSGG---------SVVSVDVERISFGGKEHHIQTNHGSVSVAVYGDH--DKPALVTYPDIALNHMSCFQGLLFCPEASSLLLHNFCIYHISPPGHELGAAPVSPSSPVASVDELADQVSDVLDFFGLGPVMCLGVTAGAYILTL   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

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gi|118150658|ref|NP_032707.2|    FALNNPEMVEGLVLMNVNPCAEGWMDWAASKISG---WTQALPDMVVSHLFGKEEIHNNVEVVHTYRQHILNDMNPSNLHLFISAYNSRRDLEIER-------PMPGTHT--VTLQCPALLVVGDNSPAVDAVVECNSKLDPTKTTLLKM   300
gi|58865550|ref|NP_001011991.1|  FALNNPEMVEGLVLMNVNPCAEGWMDWAASKISG---WTQALPDMVVSHLFGKEEIHSNVEVVHTYRQHILNDMNPSNLHLFISAYNSRRDLEIER-------PMPGTHT--VTLQCPALLVVGDNSPAVDAVVECNSKLDPTKTTLLKM   300
gi|207028748|ref|NP_001128714.1| FALNNPEMVEGLVLINVNPCAEGWMDWAASKISG---WTQALPDMVVSHLFGKEEMQSNVEVVHTYRQHIVNDMNPGNLHLFINAYNSRRDLEIER-------PMPGTHT--VTLQCPALLVVGDSSPAVDAVVECNSKLDPTKTTLLKM   300
gi|114621833|ref|XP_001140704.1| FALNNPEMVEGLVLINVNPCAEGWMDWAASKISG---WTQALPDMVVSHLFGKEEMQSNVEVVHTYRQHIVNDMNPGNLHLFINAYNSRRDLEIER-------PMPGTHT--VTLQCPALLVVGDSSPAVDAVVECNSKLDPTKTTLLKM   300
gi|73974634|ref|XP_539170.2|     FALNNPEMVEGLVLINVNPCAEGWMDWAASKISG---WTQALPDMVVSHLFGKEEMQNNVEVVHTYRQHIVNDMNPGNLHLFINAYNSRRDLEIER-------PMPGAHT--VTLQCPALLVVGDSSPAVDAVVECNSKLDPTKTTLLKM   300
gi|78042480|ref|NP_001030181.1|  FALNNPEMVEGLVLINVNPCAEGWMDWAASKISG---WTQALPDMVVSHLFGKEEMQNNVEVVHAYRHHVMNDMNPGNLQLFINAYNGRRDLEIER-------PMPGAHT--VTLQCPALLVVGDSSPAVDAVVECNSKLDPTKTTLLKM   300
gi|118087385|ref|XP_418430.2|    FALNHPDMVEGLVLININPCAEGWMDWAATKISG---WTNALPDLVISHLFGKEEIHSNHDLIHTYRQHIINDMNQTNLHLFVNSYNSRRDLEIER-------PVPGLNV--VTLQCPVLLVVGDSSPAVDAVVECNSKLDPTRTTLLKM   300
gi|51226300|ref|NP_998513.2|     FALDYPAMVEGLVLININPCAEGWMDWAAHKISG---WTHAMPDMIISHLFGKEEIQQNHDLIGRYRHHIVNEMNQYNLQLFVKSYTSRRDLEIER-------PVAGSHINARTLKCPALLVVGDSSPAVDAVVECNTKLDPTKTTLLKM   300
gi|115462531|ref|NP_001054865.1| FATKYRERVIGLMLVSPLCRAPSWSEWLYNKVLLNLIYYYGTRGLVKECLLQRYFSKLLDERQGENIWRFLHSINEYALPPLILFPSQWEYFISWSSYKLHSIRRHDLTDALRKLQCRTLIFVGENSQFHEDAIHMTTKLDKRYCALVEV   300
gi|115435040|ref|NP_001042278.1| FATKYRDRVIGLMLVSPLCKAPSWSEWLYNKVLLNLLYYYGSRGLVKECLLQRYFSTEVRGNGQDPESEIVQAC--RSLLHERQGSNVWRFLQAIN-------ERHDLTEALKKLQCRTLIFVGENSQFHDDAVHMTTKLDRRYCALVEV   300
gi|115445113|ref|NP_001046336.1| FAAKYRDRVLGILVSPLCKPPTWTEWFYNKVASNLLYYYGMCGLVKEGLLQRYFSKEVRGCSDLPESDIVQAC--RSLLDQRQSMNVWRFVQTMN-------MRYDLTEDLKQLQCRTLIFVGEYSQFHTEAVHMTSKLDRRYCALVEV   300
gi|115468558|ref|NP_001057878.1| FATKYRERVLGLILVSPLCRTPSWTEWFHNKVMSNLLYYYGMCNMVKDCLLQRYFSKGVQGCSAVPESDIVQAS--RSFLDQRQSMNVWRFIHTIN-------ERHDLTESLKELQCRTLIFVGQNSQFHAEAVHMTSKLDERYSALVEV   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

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gi|118150658|ref|NP_032707.2|    ADCGGLPQISQPAKLAEAFKYFVQGMGYMPSASMTRLMRSRTASGSSVTSLEGTRSRSHTSEGPRSRSHTSEGSRSRSHTSEDAR--------LNITPNSGATGNNAGPKSMEVSC   416
gi|58865550|ref|NP_001011991.1|  ADCGGLPQISQPAKLAEAFKYFVQGMGYMPSASMTRLMRSRTASGSSVTSLEGTRSRSHTSEGPRSRSHTSEGSRSRSHTSEDAR--------LNITPSSGATGNNAGPKSMEVSC   416
gi|207028748|ref|NP_001128714.1| ADCGGLPQISQPAKLAEAFKYFVQGMGYMPSASMTRLMRSRTASGSSVTSLDGTRSRSHTSEGTRSRSHTSEGTRSRSHTSEGAH--------LDITPNSGAAGNSAGPKSMEVSC   416
gi|114621833|ref|XP_001140704.1| ADCGGLPQISQPAKLAEAFKYFVQGMGYMPSASMTRLMRSRTASGSSVTSLDGTRSRSHTSEGTRSRSHTSEGTRSRSHTSEGAH--------LDITPNSGAAGNNAGPKSMEVSC   416
gi|73974634|ref|XP_539170.2|     ADCGGLPQISQPAKLAEAFKYFVQGMGYMPSASMTRLMRSRTASGSSVTSLEGARSRSHTSEGTRSRSHTSEGAR------------------LDITPNSGATGNNAGPKSMEVSC   416
gi|78042480|ref|NP_001030181.1|  ADCGGLPQISQPAKLAEAFKYFVQGMGYMPSASMTRLMRSRTASGSSVTSLEGARSRSHTSEGTRSRSHTSEGTR------------------LDIIPNSGGPGSSAGPNSTEVSC   416
gi|118087385|ref|XP_418430.2|    ADCGGLPQVSQPAKLAEAFKYFVQGMGYMPSASMTRLMRSRTASGSSVTSLEGQRSRSHTGEGTRSRSHTGEGTRSRSHTGEGSRNRSHTDTRIELTPNSASNAEQSGPKSMEVSC   416
gi|51226300|ref|NP_998513.2|     ADCGGLPQVDQPGKLTEAFKYFIQGMGYMPSASMTRLVRSRTASGSSITSFDGNRSRSHTNEGNRSRSHTNEG-RARAHTSENQRG-------RSHTDNMDSSVDQT-PKSTEVSC   416
gi|115462531|ref|NP_001054865.1| QGCGSLVTEEQPHAMLMPMEYFLMGYGLYRPYQMNSSPRSPLSPCCISPELLSPESMGVKLKPIKTRIAVDY----------------------------------------   416
gi|115435040|ref|NP_001042278.1| QACGSLVTEEQPHAMLIPMEYFLMGYGLYRPSQLDSSPRSTLNPFCISPELLSPESMGVKLKPIKTRISLKV----------------------------------------   416
gi|115445113|ref|NP_001046336.1| QACGSLITEEQPHAMLIPMEYFFMGYGLYRPSQLDCSPRSPLSPFCISPDLLSPESMGVKLKPIKTRVRLEV----------------------------------------   416
gi|115468558|ref|NP_001057878.1| QGCGSVVTEEQPHAMLMPLEYFLMGYGLYRPSQISCSPRSPLNPFCISPELLSPESMGVKLKPIKTRANLEV----------------------------------------   416
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410......
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