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                                  : *                 :     .:  :*: :.*  * :  :: *    ::*.::*: *:.:*: :*::  :*  *  . : ::*.: *: . *:: ** ..   .    .*:::* : :...:*. *** .:: :.  ****:*:
gi|118150658|ref|NP_032707.2|     MSRELHDVDLAEVKPLVEKGES-ITGLLQEFDVQEQDIETLHGSLHVTLCGTPKGNRPVILTYHDIGMNHKTCYN-PLFNSEDMQEITQHFAVCHVDAPGQQDGAPSFPVGYMYPSMDQLAEMLPGVLHQFGLKSVIGMGTGAGAYILTR   148
gi|58865550|ref|NP_001011991.1|   MSRELHDVDLAEVKPLVEKGES-ITGLLQEFDVQEQDIETLHGSLHVTLCGTPKGNRPVILTYHDIGMNHKTCYN-PLFNSEDMQEITQHFAVCHVDAPGQQDGAPSFPVGYMYPSMDQLAEMLPGVLHKFGLKSVIGMGTGAGAYILTR   148
gi|207028748|ref|NP_001128714.1|  MSREMQDVDLAEVKPLVEKGET-ITGLLQEFDVQEQDIETLHGSVHVTLCGTPKGNRPVILTYHDIGMNHKTCYN-PLFNYEDMQEITQHFAVCHVDAPGQQDGAASFPAGYMYPSMDQLAEMLPGVLQQFGLKSIIGMGTGAGAYILTR   148
gi|114621833|ref|XP_001140704.1|  MSREMQDVDLAEVKPLVEKGET-ITGLLQEFDVQEQDIETLHGSVHVTLCGTPKGNRPVILTYHDIGMNHKTCYN-PLFNYEDMQEITQHFAVCHVDAPGQQDGAASFPAGYMYPSMDQLAEMLPGVLQQFGLKSIIGMGTGAGAYILTR   148
gi|73974634|ref|XP_539170.2|      MSRELQDVDLAEVKPLVEKGET-ITGLLQEFDVQEQDIETVHGSIHVTLCGTPKGNRPVILTYHDIGMNHKTCYN-PLFNSEDMQEITQHFAVCHVDAPGQQDGAASFPVGYMYPSMDQLAEMLPGVLHQFGLKSIIGMGTGAGAYILTR   148
gi|78042480|ref|NP_001030181.1|   MSRELQDVDLAEVKPLVEKGET-ITGLLQEFDVQEQDIETLHGSIHVTLCGTPKGNRPVILTYHDIGMNHKTCYN-PLFNSEDMQEITQHFAVCHVDAPGQQDGAASFPTGYMYPSMDQLAEMLPGVLQQFGLKSIIGMGTGAGAYILTR   148
gi|118087385|ref|XP_418430.2|     MSTEFQDAHLAEVKPLVEKEEA-ITRLLPDFDVQEQDVETMHGMVHVTMCGTPRGNRPAILTYHDIGLNHKTCFN-PLFNFEDMQEITQHFAVCHVDAPGQQDGAPSFQAGYIYPSMDQLAEMLPGILKQFGLKSIIGMGTGAGAYVLTR   148
gi|125845458|ref|XP_001331750.1|  ----MDDIQVESKPLIVDKDLQGLREAVQKLELKEHDVETPYGKIHCTMKGVPKADRPVILTFHDIGLNHKSCFD-TLFSHEDMQEIMQHFAVCHVDAPGQQEGANTFSTGYEYPSMDQLSETLPSILKHFGLKSVIGMAIGAGAYILSK   145
gi|115462531|ref|NP_001054865.1|  ----MGDSSGSGS----GSGSVSVDVERISFGGKEHQVRTRCGSLSVAIYGDE--DKPALITYPDIALNHMSCFQGLLFCPEVASLLLHNFCIYHINPQGHELGAAPIPSDVPVPSVEDLADQVADVLDFFGLGSVMCLGVTAGAYVLTL   140
gi|115435040|ref|NP_001042278.1|  ----MGDSS----------RSVSIDVERISFGGKEHRVRTRYGSVSVSVFGDE--DKPALITYPDVALNYMSCFQGLFFCPEAASLLLHNFCIYHITPQGHELGAAPISSDVPVPSVDELVDQVADVLDFFGLGSVMCLGVTAGAYILTL   134
gi|115445113|ref|NP_001046336.1|  ----MGDSGG---------SVVSIDVERISFGGKEHHIHTNHGPVSVAVYGDH--DKPALVTYPDIALNHMSCFQGLLFCPEAASLLLHNFCIYHISPPGHELGAAPISPNAPIPSVDDLADQVADVLDFFGLGSVMCLGVSAGAYILTL   135
gi|115468558|ref|NP_001057878.1|  ----MGDSGG---------SVVSVDVERISFGGKEHHIQTNHGSVSVAVYGDH--DKPALVTYPDIALNHMSCFQGLLFCPEASSLLLHNFCIYHISPPGHELGAAPVSPSSPVASVDELADQVSDVLDFFGLGPVMCLGVTAGAYILTL   135
                                  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   286
gi|58865550|ref|NP_001011991.1|   FALNNPEMVEGLVLMNVNPCAEGWMDWAASKISG---WTQALPDMVVSHLFGKEEIHSNVEVVHTYRQHILNDMNPSNLHLFISAYNSRRDLEIER-------PMPGTHT--VTLQCPALLVVGDNSPAVDAVVECNSKLDPTKTTLLKM   286
gi|207028748|ref|NP_001128714.1|  FALNNPEMVEGLVLINVNPCAEGWMDWAASKISG---WTQALPDMVVSHLFGKEEMQSNVEVVHTYRQHIVNDMNPGNLHLFINAYNSRRDLEIER-------PMPGTHT--VTLQCPALLVVGDSSPAVDAVVECNSKLDPTKTTLLKM   286
gi|114621833|ref|XP_001140704.1|  FALNNPEMVEGLVLINVNPCAEGWMDWAASKISG---WTQALPDMVVSHLFGKEEMQSNVEVVHTYRQHIVNDMNPGNLHLFINAYNSRRDLEIER-------PMPGTHT--VTLQCPALLVVGDSSPAVDAVVECNSKLDPTKTTLLKM   286
gi|73974634|ref|XP_539170.2|      FALNNPEMVEGLVLINVNPCAEGWMDWAASKISG---WTQALPDMVVSHLFGKEEMQNNVEVVHTYRQHIVNDMNPGNLHLFINAYNSRRDLEIER-------PMPGAHT--VTLQCPALLVVGDSSPAVDAVVECNSKLDPTKTTLLKM   286
gi|78042480|ref|NP_001030181.1|   FALNNPEMVEGLVLINVNPCAEGWMDWAASKISG---WTQALPDMVVSHLFGKEEMQNNVEVVHAYRHHVMNDMNPGNLQLFINAYNGRRDLEIER-------PMPGAHT--VTLQCPALLVVGDSSPAVDAVVECNSKLDPTKTTLLKM   286
gi|118087385|ref|XP_418430.2|     FALNHPDMVEGLVLININPCAEGWMDWAATKISG---WTNALPDLVISHLFGKEEIHSNHDLIHTYRQHIINDMNQTNLHLFVNSYNSRRDLEIER-------PVPGLNV--VTLQCPVLLVVGDSSPAVDAVVECNSKLDPTRTTLLKM   286
gi|125845458|ref|XP_001331750.1|  FALDYPAMVEGLVLININPCAEGWMDWAAHKISG---WTHAMPDMIISHLFGKEEIQQNHDLIGRYRHHIVNEMNQYNLQLFVKSYTSRRDLEIER-------PVAGSHINARTLKCPALLVVGDSSPAVDAVVECNTKLDPTKTTLLKM   285
gi|115462531|ref|NP_001054865.1|  FATKYRERVIGLMLVSPLCRAPSWSEWLYNKVLLNLIYYYGTRGLVKECLLQRYFSKLLDERQGENIWRFLHSINEYALPPLILFPSQWEYFISWSSYKLHSIRRHDLTDALRKLQCRTLIFVGENSQFHEDAIHMTTKLDKRYCALVEV   290
gi|115435040|ref|NP_001042278.1|  FATKYRDRVIGLMLVSPLCKAPSWSEWLYNKVLLNLLYYYGSRGLVKECLLQRYFSTEVRGNGQDPESEIVQAC--RSLLHERQGSNVWRFLQAIN-------ERHDLTEALKKLQCRTLIFVGENSQFHDDAVHMTTKLDRRYCALVEV   275
gi|115445113|ref|NP_001046336.1|  FAAKYRDRVLGLILVSPLCKPPTWTEWFYNKVASNLLYYYGMCGLVKEGLLQRYFSKEVRGCSDLPESDIVQAC--RSLLDQRQSMNVWRFVQTMN-------MRYDLTEDLKQLQCRTLIFVGEYSQFHTEAVHMTSKLDRRYCALVEV   276
gi|115468558|ref|NP_001057878.1|  FATKYRERVLGLILVSPLCRTPSWTEWFHNKVMSNLLYYYGMCNMVKDCLLQRYFSKGVQGCSAVPESDIVQAS--RSFLDQRQSMNVWRFIHTIN-------ERHDLTESLKELQCRTLIFVGQNSQFHAEAVHMTSKLDERYSALVEV   276
                                  .......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   394
gi|58865550|ref|NP_001011991.1|   ADCGGLPQISQPAKLAEAFKYFVQGMGYMPSASMTRLMRSRTASGSSVTSLEGTRSRSHTSEGPRSRSHTSEGSRSRSHTSEDAR--------LNITPSSGATGNNAGPKSMEVSC   394
gi|207028748|ref|NP_001128714.1|  ADCGGLPQISQPAKLAEAFKYFVQGMGYMPSASMTRLMRSRTASGSSVTSLDGTRSRSHTSEGTRSRSHTSEGTRSRSHTSEGAH--------LDITPNSGAAGNSAGPKSMEVSC   394
gi|114621833|ref|XP_001140704.1|  ADCGGLPQISQPAKLAEAFKYFVQGMGYMPSASMTRLMRSRTASGSSVTSLDGTRSRSHTSEGTRSRSHTSEGTRSRSHTSEGAH--------LDITPNSGAAGNNAGPKSMEVSC   394
gi|73974634|ref|XP_539170.2|      ADCGGLPQISQPAKLAEAFKYFVQGMGYMPSASMTRLMRSRTASGSSVTSLEGARSRSHTSEGTRSRSHTSEGAR----------------LDITPNSGATGNNAGPKSMEVSC   384
gi|78042480|ref|NP_001030181.1|   ADCGGLPQISQPAKLAEAFKYFVQGMGYMPSASMTRLMRSRTASGSSVTSLEGARSRSHTSEGTRSRSHTSEGTR----------------LDIIPNSGGPGSSAGPNSTEVSC   384
gi|118087385|ref|XP_418430.2|     ADCGGLPQVSQPAKLAEAFKYFVQGMGYMPSASMTRLMRSRTASGSSVTSLEGQRSRSHTGEGTRSRSHTGEGTRSRSHTGEGSRNRSHTDTRIELTPNSASNAEQSGPKSMEVSC   402
gi|125845458|ref|XP_001331750.1|  ADCGGLPQVDQPGKLTEAFKYFIQGMGYMPSASMTRLVRSRTASGSSITSFDGNRSRSHTNEGNRSRSHTNEG-RARAHTSENQRG-------RSHTDNMDSSVDQT-PKSTEVSC   392
gi|115462531|ref|NP_001054865.1|  QGCGSLVTEEQPHAMLMPMEYFLMGYGLYRPYQMNSSPRSPLSPCCISPELLSPESMGVKLKPIKTRIAVDY-------------------------------------------   362
gi|115435040|ref|NP_001042278.1|  QACGSLVTEEQPHAMLIPMEYFLMGYGLYRPSQLDSSPRSTLNPFCISPELLSPESMGVKLKPIKTRISLKV-------------------------------------------   347
gi|115445113|ref|NP_001046336.1|  QACGSLITEEQPHAMLIPMEYFFMGYGLYRPSQLDCSPRSPLSPFCISPDLLSPESMGVKLKPIKTRVRLEV-------------------------------------------   348
gi|115468558|ref|NP_001057878.1|  QGCGSVVTEEQPHAMLMPLEYFLMGYGLYRPSQISCSPRSPLNPFCISPELLSPESMGVKLKPIKTRANLEV-------------------------------------------   348
                                  .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410......
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