```
                                                  ..                  *    .    .   :** ***:*.*.*::** **: :::  :: . :**: *:***::**:*:.::*:**: * .   :*  :*: ::*:: :* :.. **::*:*:*
gi|183979982|ref|NP_001116868.1| -------------MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID   150
gi|114586511|ref|XP_001149592.1| -------------MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTID   150
gi|6753466|ref|NP_034045.1|      MEDNNMLPQFIHGILSTSHSLFTRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGNMLVIIILIGCKKLKSMTDIYLLNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKVFTGLYHIGYFGGIFFIILLTID   150
gi|11177914|ref|NP_068638.1|     MEDSNMLPQFIHGILSTSHSLFPRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGNMLVIIILISCKKLKSMTDIYLFNLAISDLLFLLTLPFWAHYAANEWVFGNIMCKLFTGLYHIGYFGGIFFIILLTID   150
gi|57101676|ref|XP_541906.1|     MGDNGTFSQVSHNMLSTSHSLFTTNIQGSDE-PTTIYDYDYSAPCQKSSVRQVAAGLLPPLYSLVFIFGFVGNMLVVLILINCKKLKSMTDIYLLNLAISDLLFLLTIPFWAHYAANGWLLGEVMCKSFTGLYHIGYFGGTFFIILLTID   150
gi|76678466|ref|XP_584158.2|     MDGNDTFS---HNVLPTSHSLFTTNVKGNDEEPTTSYDYDYSEPCRKTSVGQIEAQLLPPLYSLVFIFGFVGNLLVVLILINCKKLKSMTDIYLLNLAISDLLFLLTMPFWAHYAADQWVFGNVMCKFFTGLYHIGYFGGIFFIILLTID   150
gi|113951665|ref|NP_001039300.1| ---------------------MENYTDLGDMPTTTFDYGDTAPCMGTEEKHFAANFLPPLYSLVVIFGFIGNILVVLILVKYKKLKSMTDIYLLNLAISDLLFVFSLPFWAYYAAHDWIFGDALCRILSGVYLLGFYSGIFFIILLTID   150
gi|125838941|ref|XP_001344151.1| --------------------MSATQNSSFDDYYNYNETGHVAPPCNNGNAKAFSEVFLPTLYSIVFIVGFIGNGLVVWVLIRHRQKSNMTDVCLFNLALADLIFLVSLPFWAHNAMDEWILGRFMCHTITGLFMIGLYASIFFMVLMTLD   150
gi|292629253|ref|XP_002667324.1| --------------------MSGAQNRSYDDYYNYNETEHVAPLCNNGNAKAFSEVFLPTLYSIVFIIGFIGNGLVVWVLIRHRQKSNMTDVCLFNLALADLIFLVSLPFWAHNAMDEWIFGKFMCHTITGLFMIGLYASIFFMVLMTLD   150
gi|125838928|ref|XP_001343879.1| --------------------MGMGKKGFNKYYNYNETEHLAPPCNDAKTKAFSEVFLPILYSIVFIIGIIGNGLVVWVFIRCRQKSNMTDVCLLNLALSDLLFLVSLPFWAHNAMNQRTFGKFMCHTITGLFMIGLYASIFFMVLLTLD   150
gi|292621991|ref|XP_001344220.3| -------------MTEEPSTVAATKTDYSDYY--NEEGDFEQPCNNGQTKAFSEVFLPTLYSIVFIIGFIGNGLVVWVLVRYRHKSNMTDVCLFNLALADLLFLVSLPFWAHNAMDEWIFGRFMCHTITGLFMIGLYASIFFMVLMTLD   150
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

                                 **  *:*.   : : *:.. *:    :.* ::::.::* *:* .      .    *   :       *     :  .:*.*::*:::: :*** *: **:  :.:*:  : *::*:.:: .**:*::* :: ::  :*       *
gi|183979982|ref|NP_001116868.1| RYLAIVHAVFAL-KARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKE-DSVYVCGPYFP----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS   300
gi|114586511|ref|XP_001149592.1| RYLAIVHAVFAL-KARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKE-DSVYVCGPYFP----RGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTS   300
gi|6753466|ref|NP_034045.1|      RYLAIVHAVFAL-KARTVTFGVITSVVTWVVAVFASLPGIIFTKSKQD-DHHYTCGPYFT----QLWKNFQTIMRNILSLILPLLVMVICYSGILHTLFRCRNEKKRHRAVRLIFAIMIVYFLFWTPYNIVLFLTTFQESLGMSNCVIDK   300
gi|11177914|ref|NP_068638.1|     RYLAIVHAVFAL-KARTVTFGVITSVVTWVVAVFASLPGIIFTKSEQE-DDQHTCGPYFP----TIWKNFQTIMRNILSLILPLLVMVICYSGILHTLFRCRNEKKRHRAVRLIFAIMIVYFLFWTPYNIVLFLTTFQEFLGMSNCVVDM   300
gi|57101676|ref|XP_541906.1|     RYLAIVHAVFAL-KARTVTFGVVTSGVTWMVAVFASLPRIIFTTVQIE-DSFSSCSPQFQ----QAWKNFHTIMRSVLGLVLPLLVMVICYSAILKTLLRCRNEKKRHKAVKLIFVIMIVYFLFWAPNNIVLLLSTFQESFNVSNCKSTS   300
gi|76678466|ref|XP_584158.2|     RYLAIVHAVFAL-KARTVTFGVVTSGVTWVVAVFASLPGIIFIKSLEE-HSGYACAPYFP----LGWKNFHTIMRSILGLVLPLLVMIICYSGIIKTLLRCRNEKKKHKAVRLIFVIMIVYFLFWAPYNIVLLLSTFQEFFGLSNCKSSS   300
gi|113951665|ref|NP_001039300.1| RYLAIVHAVFAL-KARTVTYGILTSIVTWAVALFASVPGIVFHKTQQE-NTQCTCSFHYPSDALINWQHSYILKMNILGLIIPMIIMIFCYSQILRTLFGCRNEKK-QKAVRLIFVIMIFYFIFWTPFHVASFVHTFQTSFFSPDCDSQS   300
gi|125838941|ref|XP_001344151.1| RYAIIVHAHSVFSRNRSTKMGLALASLVWMLSLFASLPNIIFANANNGTNSKSSCRPDFPDN--TSWMSFTYINMNLLSLIFPLIIMSFCYSRIIPTLLSIKSQKR-HKVVRLILAVVAVYFLFWTPYNIVMFLMFLQRMEYMFSCEWHN   300
gi|292629253|ref|XP_002667324.1| RYAIIVHAHSVFSRNRSTKMGLALASLVWIISLFAALPNIIFTNEQMDLNKRKSCQLDFPDN--TSWMSFTYINMNLLSLIFPLIIMIFCYSRIIPTLLSIKSQKR-HKVVRLILAVVAVYFLFWTPYNIVMFLLFLQRRGYMLTCEWHN   300
gi|125838928|ref|XP_001343879.1| RYAIIIHPNCMFFRNRSAKLGLAL--LVWMLSLLASLPNIIFANEKFDLNHIKSCQPDFPDN--TSWMSFTYINMNLLSLIFPLIILIFCYSRIISTLFRMKSEKK-PKLVKLILAVVTVYFLFFTPYNIVIFLLFLQRMEYFFSCEWHI   300
gi|292621991|ref|XP_001344220.3| RYAIIVHAHSVFSRNRSTKMGLALASLVWMLSLLVSLPNIIFAKDKNETNSKISCGSDFPKD--SSWMPFTYLKMNLLSLVFPLIIMIFCYSRIIPTLLSMKSQKK-HKVVRLILAVVAVYFIFWTPYNIVMFLMFLQKMEYMLTCEWHN   300
                                 .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

                                  *.   * .**:.: ***:**:****..::**       .. :..      .                :   *
gi|183979982|ref|NP_001116868.1| QLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRET--------VDGVTSTNTPSTGEQEVSAGL-------------------------------------------------------------   450
gi|114586511|ref|XP_001149592.1| QLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPVFYRET--------ADGVTSTNTPSTGEQEVSAGL-------------------------------------------------------------   450
gi|6753466|ref|NP_034045.1|      HLDQAMQVTETLGMTHCCINPVIYAFVGEKFRRYLSIFFRKHIAKRLCKQCPVFYRET--------ADRVSSTFTPSTGEQEVSVGL-------------------------------------------------------------   450
gi|11177914|ref|NP_068638.1|     HLDQAMQVTETLGMTHCCVNPIIYAFVGEKFRRYLSIFFRKHIAKNLCKQCPVFYRET--------ADRVSSTFTPSTGEQEVSVGL-------------------------------------------------------------   450
gi|57101676|ref|XP_541906.1|     QLDQIMQVTETLGMTHCCVNPIIYAFVGEKFRRYLSLFFRRHIAKHLCKQCPVFYGET--------ADRVSSTYTPSTGEQEVWVGL-------------------------------------------------------------   450
gi|76678466|ref|XP_584158.2|     QLDQAMQVTETLGLTHCCINPIIYAFVGEKFRRYLSTFFRKHIAKHLCKQCPVFYGET--------GDRVSSTYTHSTGEQEVSAAL-------------------------------------------------------------   450
gi|113951665|ref|NP_001039300.1| RLEKTIQVTETISMVHCCINPVIYAFVGEKFRKYLHMFFRKHVATHLCKKCPSLYREK--------LERVSSTFTASTAEHDISTGL-------------------------------------------------------------   450
gi|125838941|ref|XP_001344151.1| GLSLAMQWVETIALSHCCLNPIIYAFAGEKFRRAVLKVLKDQFPMCFKQCASFSQQLS---------ERRSSIFSRSSEISSTQIA-------------------------------------------------------------   450
gi|292629253|ref|XP_002667324.1| GLSLAMQWVETIALSHCCLNPIIYAFAGEKFRRAVLKVLKDQFPMCFKQCASFSQQLS---------ERRSSAFSRASEMSSTQIA-------------------------------------------------------------   450
gi|125838928|ref|XP_001343879.1| DLSLAMQWVETIALSHCCLNPIIYAFASQQFR----GAVKDQFPLCFRRYATVSQQAS---------ERRSSIF----------------------------------------------------------------------   450
gi|292621991|ref|XP_001344220.3| GLSLAMQWVETIALSHCCLNPIIYAFAGEKFRGAVIKVLNDQFPITSPATQAVLQQEVSNLLDHNIIEESQSPWSAPVVLVRKKDGTHRFCVDYRRLNDVTIKDSHPLPRVDDTLDRLSGARVFSTIDLTAGYWQIPLNPSDKEKTAFSY   450
                                 .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

gi|183979982|ref|NP_001116868.1| ------------------------------------------------------------   511
gi|114586511|ref|XP_001149592.1| ------------------------------------------------------------   511
gi|6753466|ref|NP_034045.1|      ------------------------------------------------------------   511
gi|11177914|ref|NP_068638.1|     ------------------------------------------------------------   511
gi|57101676|ref|XP_541906.1|     ------------------------------------------------------------   511
gi|76678466|ref|XP_584158.2|     ------------------------------------------------------------   511
gi|113951665|ref|NP_001039300.1| ------------------------------------------------------------   511
gi|125838941|ref|XP_001344151.1| ------------------------------------------------------------   511
gi|292629253|ref|XP_002667324.1| ------------------------------------------------------------   511
gi|125838928|ref|XP_001343879.1| ------------------------------------------------------------   511
gi|292621991|ref|XP_001344220.3| SIMNVCRLPEKSEQFLACVRVDLNDVTCPFPPSGDAQVLVVGQVHSNNPLSCPGSLLQPYI   511
                                 .......460.......470.......480.......490.......500.......510.
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