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gi |17402909|ref|NP_036233.2|
gi |114640802|ref|XP_508817.2|
gi |109483377|ref|XP_236207.4|
gi |150247108|ref|NP_001092849.1|
gi |118101917|ref|XP_417892.2|
MEAADASRSNGSSPEARDARSPGPGSGLNGTKADGKDAKTNGHGGEAAEGKSLG--SALKPGEGRSALFAGNEWRRPIIQFVSGDDKKNYFSDMSMEGKRSPYAGLQLGAAKKPPVTPFAEKGLRKSIFSES----- 135
MEAADASRSNGSSPEARDARSPGPGSGLNGTKADGKDAKTNGHGGEAAEGKSLG--SALKPGEGRSALFAGNEWRRPIIQFVSGDDKKNYFSDMSMEGKRSPYAGLQLGAAKKPPVTPFAEKGLRKSIFSES----- 135
MEAADASRSNGSASPEARDARSPGPGSGLNGTKADGKDAKTNGHGGEVTEGKTLG--SALKSGEGKSGLFSSENEWRRPIIQFVSEVDDKGSYFSDMSAEGRRSPYAGLQLGAAKKPPVTPFAEKGLRKSIFSEP----- 135
MEAADASRSNGSASPEARDARSPGPGSGLNGTKADGKDAKTNGHGGEVTEGKTLG--SALKSGEGKSGLFSSENEWRRPIIQFVSEVDDKGSYFSDMSAEGRRSPYAGLQLGAAKKPPVTPFAEKGLRKSIFSEP----- 135
MEADASRSNGSASPEARDARSPGPGSGLNGTKADGKDAKTNGHGGEVTEGKTLG--SALKSGEGKSGLFSSENEWRRPIIQFVSEVDDKGSYFSDMSAEGRRSPYAGLQLGAAKKPPVTPFAEKGLRKSIFSEP----- 142
METGSAARTNGTAGKPEDVKSPPAP-----KDEEVKKTINPGGGEKEPKIGTGGTSLTETQIKISLFSGSDWKRPPIIQFVSEDEKRSTYFSDMSADSCKMPFASGGIGDMRRTPLSFADKGDRLRKSIFSLDSSKKSFLPNVEGGRK
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |109483377|ref|XP_236207.4|
gi |150247108|ref|NP_001092849.1|
gi |118101917|ref|XP_417892.2|
-----RKPITVSIIMEPGETRRNSYPRADIGLFSRSKSGSEVLDSDSICIGNKQKAVKSCLVCCASFCCELHLKPHLEGAAFRDHQLLEPIRDFEARKCPVHGKIMELFCQTDQTCICVLCMFOEHKNSHTVVEAKAEKETELSL 273
-----RKPITVSIIMEPGETRRNSYTRA-DIGLFSRSKSGSEVLDSDSICIGNKQKAVKSCLVCCASFCCELHLKPHLEGAAFRDHQLLEPIRDFEARKCPVHGKIMELFCQTDQTCICVLCMFOEHKNSHTVVEAKAEKETELSL 273
-----RKPITVSIIMEPGETRRNSYPRADIGLFSRSKSGSEVLDSDSICIGNKQKAVKSCLVCCASFCCELHLKPHLEGAAFRDHQLLEPIRDFEARKCPVHGKIMELFCQTDQTCICVLCMFOEHKNSHTVVEAKAEKETELSL 273
-----RKPITVSIIMEPGETRRNSYPRADIGLFSRSKSGSEVLDSDSICIGNKQKAVKSCLVCCASFCCELHLKPHLEGAAFRDHQLLEPIRDFEARKCPVHGKIMELFCQTDQTCICVLCMFOEHKNSHTVVEAKAEKETELSL 273
-----RKPITVSIIMEPGETRRNSYPRADIGLFSRSKSGSEVLDSDSICIGNKQKAVKSCLVCCASFCCELHLKPHLEGAAFRDHQLLEPIRDFEARKCPVHGKIMELFCQTDQTCICVLCMFOEHKNSHTVVEAKAEKETELSL 292
PLFSSGGIGDMKPKSLPLVETGLRRPTFNKVPDRAAGSRPRVKLEVDVLDSDSICIGNKQKAVKSCLVCCASFCCELHLKPHLEGAAFRDHQLLEPIRDFEARKCPVHGKIMELFCQTDQTCICVLCMFOEHKNSHTVVEAKAEKETELSL
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi |150247108|ref|NP_001092849.1|
gi |118101917|ref|XP_417892.2|
OKEQLDLKIIIEIDEAEKWKQEKDRIKSFTTNEKAILEONFRDLVRDLEKQKEEVRAALEQREODAVDQVKVIMDALDERAKVLHEDKQTREROLHSISDSVLFLOEFGALMSNYSLPPPPTVYHVLLEGEGLGQSLGNFKDLDLNVCMRH 423
OKEQLDLKIIIEIDEAEKWKQEKDRIKSFTTNEKAILEONFRDLVRDLEKQKEEVRAALEQREODAVDQVKVIMDALDERAKVLHEDKQTREROLHSISDSVLFLOEFGALMSNYSLPPPPTVYHVLLEGEGLGQSLGNFKDLDLNVCMRH 423
OKEQLDLKIIIEIDEAEKWKQEKDRIKSFTTNEKAILEONFRDLVRDLEKQKEEVRAALEQREODAVDQVKVIMDALDERAKVLHEDKQTREROLHSISDSVLFLOEFGALMSNYSLPPPPTVYHVLLEGEGLGQSLGNFKDLDLNVCMRH 423
OKEQLDLKIIIEIDEAEKWKQEKDRIKSFTTNEKAILEONFRDLVRDLEKQKEEVRAALEQREODAVDQVKVIMDALDERAKVLHEDKQTREROLHSISDSVLFLOEFGALMSNYSLPPPPTVYHVLLEGEGLGQSLGNFKDLDLNVCMRH 423
OKEQLDLKIIIEIDEAEKWKQEKDRIKSFTTNEKAILEONFRDLVRDLEKQKEEVRAALEQREODAVDQVKVIMDALDERAKVLHEDKQTREROLHSISDSVLFLOEFGALMSNYSLPPPPTVYHVLLEGEGLGQSLGNFKDLDLNVCMRH 442
OKEQLDLKIIIEIDEAEKWKQEKDRIKSFTTNEKAILEONFRDLVRDLEKQKEEVRAALEQREODAVDQVKVIMDALDERAKVLHEDKQTREROLHSISDSVLFLOEFGALMSNYSLPPPPTVYHVLLEGEGLGQSLGNFKDLDLNVCMRH
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi |109483377|ref|XP_236207.4|
gi |150247108|ref|NP_001092849.1|
gi |118101917|ref|XP_417892.2|
VEKMCKADLSRNFIERNHMEGGDHRVNNYNSFGGSEWSPDITMKRYSMYLTPKG----- 479
VEKMCKADLSRNFIERNHMEGGDHRVNNYNSFGGSEWSPDITMKRYSMYLTPKG----- 479
VEKMCKADLSRNFIERNHMEGGDHRVNNYNSFGGSEWSPDITMKRYSMYLTPKG----- 479
VEKMCKADLSRNFIERNHMEGGDHRVNNYNSFGGSEWSPDITMKRYSMYLTPKG----- 479
VEKICAKDLGRNFIERNHMEGGDHRVNNYNSFGGSEWSPDITMKRYSMYLTPKG----- 586
VEKICAKDLGRNFIERNHMEGGDHRVNNYNSFGGSEWSPDITMKRYSMYLTPKG----- 586
YEWNPQDLNKRFSMFLSPKGLQATVLVNDIVSGYIGTDVVLHCSFTNPLPVKIKQVITQKQVINGTKONVAIINPAMGVSIILPPYKERVIFRNPSFKDGIQLSRLLEDEGCV
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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gi |109483377|ref|XP_236207.4|
gi |150247108|ref|NP_001092849.1|
gi |118101917|ref|XP_417892.2|
-----GVRTSYQ-----PSSPGRFTKETTKNFNNLYGKGNYSR-----VWEYSSSIQ-----NS 526
-----GVRTSYQ-----PSSPGRFTKETTKNFNNLYGKGNYSR-----VWEYSSSIQ-----NS 526
-----GGRTSYQ-----PSSPGRFTKETTKNFNNLYGKGNYSR-----VWEYSSSIQ-----NS 526
-----GARTSYQ-----PSSPGRFTKETTKNFNNLYGKGNYSR-----VWEYSSSIQ-----NS 523
YICEFATFPVGNRESQNLNLVLAKPINRMEGLTRPLIAKSGRIEKLIVANCISSNGKPPSTVTDWIKLKGAEFQEIERNNGTFVIISRYRLVPSREAHROQLCVVNYQLDRFTDSIILNVQYBPEVIEGFGCNWFLNRKDKVLLCKE 736
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

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gi |109483377|ref|XP_236207.4|
gi |150247108|ref|NP_001092849.1|
gi |118101917|ref|XP_417892.2|
DNDLPVVQ-----GSSSFSLKQ-----YPSLMRSC-----SPKAQPOTWKSQKOTMLSHYR----- 572
DNDLPVVQ-----GSSSFSLKQTKNTPYQFTLGLQANAEFSKPLGRSGLS-----KNNPGYPSLMRSC-----SPKAQPOTWKSQKOTMLSHYR----- 605
D-DMPITVQ-----GNSSFSKLG-----YPSLLRSC-----VPKAQPOTWKSQKOTMLSHYR----- 571
D-DVPAVG-----GSSSFSLKQ-----YPSLIRSC-----SPKAQPOTWKSQKOTMLSHYR----- 568
DANPPAHTYEWKLPNGILPGSVEIQNNIYIFKGVSYSVAGTYICEASNAIGTRSLGLEVVVTDKPLPQALGGIIGVGGVIAAAILGVAVVFTVYRRQKDRITADHDLDLPPSHKPPPKRKELEKSHLTAEDIQVHLDNMI 866
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900

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gi 17402909 ref NP_036233.2	-----	588
gi 114640802 ref XP_508817.2	-----	621
gi 109483377 ref XP_236207.4	-----	587
gi 150247108 ref NP_001092849.1	-----	584
gi 118101917 ref XP_417892.2	-----	987

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      **      *  *  *
      PFYVKNGN-----GIGSNEAP-----
      PFYVKNGE-----GIGSNEAP-----
      PFYVKNGE-----GIGSNEAP-----
      PFYVKNGN-----GIGSNEAP-----
      HEEELQKLLPQPPYDMAASEPEAYIDKLNFGKCHSEIPNASDYLRRCYSHDGRVLRKIPHVYAPLSDLPDLYPHHSDISFCCPPFGERAPYICPKEQYV
      .....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.

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