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gi|6754482|ref|NP_034794.1| MSFTTRSTTFSTNYSRLGSRVTPSQRVRPASP--AASVYAGAGGSGSRI SVSR--SVWGGG-----VGSAG--LAGMG-----G--IQTEKETIMODLNDRLASVLDKVKSLLETENRRRLESKIREHLEKKGPCGVRDWGHY 122
gi|68534953|ref|NP_446428.1| MSFTTRSTTFSTNYSRLGSRVTPSQRVRPASP--AASVYAGAGGSGSRI SVSR--SVWGGG-----VGSAG--LAGMG-----G--VCTEKETIMODLNDRLASVLDKVKNLETENRRRLESKIREYLEKRGPCGVRDWGHY 122
gi|40354195|ref|NP_954657.1| MSFTTRSFSTNYSRLGSRVQAPSYGARPVSS--AASVYAGAGGSGSRI SVSRSTFRGGMGSGGLATGIAGGLAGMG-----G--IQNEKETIMQSLNDRLASVLDKVRSLLETENRRRLESKIREHLEKKGPC--VRDWSHY 129
gi|114644548|ref|XP_509083.2| MSFTTRSFSTNYSRLGSRVQAPSYGARPVSS--AASVYAGAGGSGSRI SVSRSTFRGGMGSGGLATGIAGGLAGMG-----G--IQNEKETIMQSLNDRLASVLDKVRSLLETENRRRLESKIREHLEKKGPC--VRDWSHY 129
gi|57106334|ref|XP_534794.1| MSFTARS--HFSSNYSRLGSRVQAPSHRVRPISSSAASVYAGAGGSGSRI SVSRSTFRGGMGSGGLAAGMAGGLAGIG-----G--IQGEKETIMODLNDRLASVLEKVRSLLEADNRRLLESKIREHLEKKGPC--VRDWSHY 130
gi|76617986|ref|XP_582930.2| MSFPTOS--HFS--NYRSLGSRVQSSGHRVRPVS--AASVYAGAGGSGSRI SVSRSTFRGGMGSGGLAGMAGGLVGVG-----G--IQGEKETIMODLNDRLASVLEKVRSLLEADNRRLLESKIREHLEKKGPC--VRDWHY 128
gi|30410758|ref|NP_848524.1| MSLRISYVRSSTSVVPSQASIKRTNVPVYRAASLYGGAGGQGRISASYSVRSR--LGVPSMSSISIQVS-----AGSGTGETIMGKEMAMNLDRLASVLEKVRILEQANSKLELKIREALEKRGPD--VHDYSRF 133
gi|41055898|ref|NP_956862.1| MSF---YAPQAS-----HISFTRSAFYRAASTYGGAGGQGRISASAMSVRSRPRGGISSSIFPKVSSAGMGSGAGGSLLASGSSGMLNKEKQCMQNLNDRLAAYLDTVRRLEQENGLLEQIIRALEKKGPC--TRDYSKY 137
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi|6754482|ref|NP_034794.1| FKIIEDLRAQILANSVDNARIVLQIDNARLAADDFRVKYE TELAMRQSVESDIHGLRKVVDDTNI TRLOLETEIEALKEELLFMKKNHEEEVQGLEAQIASSGLTVEVDAPKSDLSKIMADIRAOYELAAQNRRELDKYWSQQIEEST 272
gi|68534953|ref|NP_446428.1| FKIIEDLRAQIFANSVDNARIVLQIDNARLAADDFRVKYE TELAMRQSVESDIHGLRKVVDDTNI TRLOLETEIEALKEELLFMKKNHEEEVQGLEAQIASSGLTVEVDAPKSDLSKIMADIRAOYELAAQNRRELDKYWSQQIEEST 272
gi|40354195|ref|NP_954657.1| FKIIEDLRAQIFANTVDNARIVLQIDNARLAADDFRVKYE TELAMRQSVENDIHGLRKVIDDTNI TRLOLETEIEALKEELLFMKKNHEEEVQGLEAQIASSGLTVEVDAPKSDLAKIMADIRAOYDELARKNRRELDKYWSQQIEEST 279
gi|114644548|ref|XP_509083.2| FKIIEDLRAQIFANTVDNARIVLQIDNARLAADDFRVKYE TELAMRQSVENDIHGLRKVIDDTNI TRLOLETEIEALKEELLFMKKNHEEEVQGLEAQIASSGLTVEVDAPKSDLAKIMADIRAOYDELARKNRRELDKYWSQQIEEST 279
gi|57106334|ref|XP_534794.1| FKIIEDLRAQIFASAVDNARIVLQIDNARLAADDFRVKYE TELAMRQSVESDIHGLRKVIDDTNIVRLOLETEIEALKEELLFMKKNHEEEVQGLQNOIANGLTVELDAPKSDLSKIMADIRAOYDELAAQNRRELDKYWSQQIEEST 280
gi|76617986|ref|XP_582930.2| LKIIEDLRAQIFANSVDNARIVLQIDNARLAADDFRVKYE TELAMRQSVESDIHGLRKVIDDTNIVRLOLETEIEALKEELLFMKKNHEEEVQGLQNOIANGLTVELDAPKSDLSKIMADIRAOYDELAAQNRRELDKYWSQQIEEST 278
gi|30410758|ref|NP_848524.1| QPVDLRRKKIFDATTNNARIVLQIDNARLAADDFRVKYESELISIRQGVVADITGLRKVIDDTNINLRNMLESEIEALKEELLIFLKKNHENVEMLRNOISQSGVQVVDVDPKQDLSQIMEEIRAKYKMAKNOBELKAWHESQITEVQ 283
gi|41055898|ref|NP_956862.1| NAILDLRKRKVFDAIVDNARIVLQIDNARLAADDFRVKFEENMAIRQSVEGDIAGLKKVIDETNIGRLNVEGETESLKEELLFLKKNHENEVDLRSQISQSGVQVVDVDPKQDMSQVMEDMRANVEKQALKNAEELKMHETQIADVQ 287
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi|6754482|ref|NP_034794.1| TVVTTKSAEIRDAETLLELRRLQTLLEIDLDSMKNQININLENSLGDVEARYKAOEQLNGVLLHLESELAQTRAEGRQAOEYEALLN IKVKLEAEIATYRRLLEDGEDFSLNDALDSSNSMQTVQKTTTRKIVDGRVSEINDTRVLR 422
gi|68534953|ref|NP_446428.1| TVVTTKSAEIRDAETLLELRRLQTLLEIDLDSMKNQININLENSLGDVEARYRVOMEQLNGVLLHLESELAQTRAEGRQTOEYEALLN IKVKLEAEIATYRRLLEDGEDFSLNDALDSSNSMQTVQKTTTRKIVDGRVSEINDTRVLR 422
gi|40354195|ref|NP_954657.1| TVVTTSQAEVGAETLLELRRTVQSLLEIDLDSMRNLKASLENSLREVEARYALQMEQLNGVLLHLESELAQTRAEGRQAOEYEALLN IKVKLEAEIATYRRLLEDGEDFSLNDALDSSNSMQTIQKTTTRRIVDGVVSEINDTKVLR 429
gi|114644548|ref|XP_509083.2| TVVTTSQAEVGAETLLELRRTVQSLLEIDLDSMRNLKASLENSLREVEARYALQMEQLNGVLLHLESELAQTRAEGRQAOEYEALLN IKVKLEAEIATYRRLLEDGEDFSLNDALDSSNSMQTIQKTTTRRIVDGVVSEINDTKVLR 429
gi|57106334|ref|XP_534794.1| TVVTTSQAEVGAETLLELRRTVQSLLEIDLDSMRNLKASLENSLREVEARYALQMEQLNGVLLHLESELAQTRAEGRQAOEYEALLN IKVKLEAEIATYRRLLEDGEDFSLNDALDSSNSMQTIQKTTTRRIVDGVVSEINDTKVLR 428
gi|76617986|ref|XP_582930.2| TVVTTSQAEVGAETLLELRRTVQSLLEIDLDSMRNLKASLENSLREVEARYALQMEQLNGVLLHLESELAQTRAEGRQAOEYEALLN IKVKLEAEIATYRRLLEDGEDFSLNDALDSSNSMQTIQKTTTRRIVDGVVSEINDTKVLR 428
gi|30410758|ref|NP_848524.1| VQVTQNTAEALQGARBEVNEELRRQIQTLLEIELSKQNLKGSLEGLTRDTEMYNMEIENLNTIILQLEAELTQLRGNIQHTOEYEALLN IKMKLEAEIATYRRLLED--GGDFKLDALBEQKVKVMTVITQI--LVDGKVVSS--TETKERE 430
gi|41055898|ref|NP_956862.1| VQVAQNTAEALQGAQMECNDLRRQIQTLLEIELSKQNLKASLEGLTRDTEMYNMEIENLNTIILQLEAELTQLRGNITOEYEALLN IKMKLEAEIATYRRLLED--GGDFKLDALBEQKVKVMTVITQI--LVDGKVVSS--TETKERE 430
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi|6754482|ref|NP_034794.1| H 423
gi|68534953|ref|NP_446428.1| H 423
gi|40354195|ref|NP_954657.1| H 430
gi|114644548|ref|XP_509083.2| H 430
gi|57106334|ref|XP_534794.1| R 431
gi|76617986|ref|XP_582930.2| H 429
gi|30410758|ref|NP_848524.1| L 431
gi|41055898|ref|NP_956862.1| - 405

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