

gi	61098143	ref	NP_598735.2	-----MAHSACGF-----VA	150
gi	27721843	ref	XP_236747.1	-----MARSACGF-----VA	150
gi	30410805	ref	NP_073753.3	-----MAGLNCGV-----TA	150
gi	114586460	ref	XP_001147144.1	-----MAGLNCGV-----TA	150
gi	73986003	ref	XP_541913.2	-----MAGLNCGV-----TA	150
gi	194677155	ref	XP_612363.4	-----MAGLNCGV-----TA	150
gi	118086139	ref	XP_418802.2	-----MAGLNCGV-----TA	150
gi	62122859	ref	NP_001014355.1	MDLWLVLDNKVNIWQSAIQTRKPTVSWAASKETSVTSDQRIKPKPISEAQITPGQPRFEAPQAEEGEAAROSPICGLPGGTAAADPSFPSPSPPCAEAEABAKARRPAPASALGFCGGRWGAHCSRCSLSSSPPRRSISRKGVGMVG	150
				-----MRSWVTCF-----VA	150

1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi	61098143	ref	NP_598735.2	LLGALLLCTAR-----LLRGTSEASIALPQRSGVTVSIKLGPNALPVKICYIVMSRQHITELIIRPGERKSFIFSCSNPEKHVFLKIEKNIDCMSPGCPFGVEVHLPSTSELPIILNRTFIWIDVRAHKSIGLELQFAIPRLRQIGPGESC	300
gi	27721843	ref	XP_236747.1	LLGALLLCTAC-----LLRGTSEASIALPQRSDITVHIKLVSPALPVKFCYIVVSRQHVTELIRPGERKSFIFSCSNPEKHVFLKIEKNIDCMSPGCPFGVEVHLPSTSELPIILNRTFIWIDVRAHKSIGLELQFAIPRLRQIGPGESC	300
gi	30410805	ref	NP_073753.3	LLGVLLLGAAR-----LPRGAFAFIALPRESNITVLIKILGTPLLAKPCYIVISKRHITMLSIKSGERTVVFIFSCQSPENHFVIEIOKNIDCMSPGCPFGVEVLPSTSLPLTLNRTFIWIDVRAHKSIGLELQFAIPRLRQIGPGESC	300
gi	114586460	ref	XP_001147144.1	LLGVLLLGAAR-----LPRGAFAFIALPRESNITVLIKILGTPLLAKPCYIVISKRHITMLSIKSGERTVVFIFSCQSPENHFVIEIOKNIDCMSPGCPFGVEVLPSTSLPLTLNRTFIWIDVRAHKSIGLELQFAIPRLRQIGPGESC	300
gi	73986003	ref	XP_541913.2	LLGVLLLGAAR-----LPRGAFAFIALPRESNITVLIKILGTPLLAKPCYIVISKRHITMLSIKSGERTVVFIFSCQSPENHFVIEIOKNIDCMSPGCPFGVEVLPSTSLPLTLNRTFIWIDVRAHKSIGLELQFAIPRLRQIGPGESC	300
gi	194677155	ref	XP_612363.4	LLGILLLGAAR-----LPR--GVAEIDLPRGSGITVLLKPAIQALPVKCYIIM--SKRNETLTSIKAGEKRVFISFCQDPHNHFVIEIOKNIDCVSGCQPPGVEVLPSTSLPLTLNRTFIWIDVRAHKSIGLELQFAIPRLRQIGPGESC	300
gi	118086139	ref	XP_418802.2	LRGCMKGGGGGGERLALWPGSSFTISLRAADNITVLIKILKPGVLPAA--CLLRVKSGRPELKPGENVHLFSTQNTPEKVLMMIEIOKNIDCVSGCQPPGVEVLPSTSLPLTLNRTFIWIDVRAHKSIGLELQFAIPRLRQIGPGESC	300
gi	62122859	ref	NP_001014355.1	-LVLLVLSLSS-----VLELTGGAEINVAVEGGTILINISSTQCKVCVRVNRQPLCQAYVVLRSDTLLDFSSQPEKVFIVQIIRDGTGMN-----IEPKDHFALKFNRTFTWNLKPLVSKSLQLNFTGLRQIEPEDSC	300

.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi	61098143	ref	NP_598735.2	ADGVTHSISGHIDA--TEVRIGTFCSNGTVSRIKMQEGVKMALHLPWFHRRNVSGFISIANRSSIKRCLIEISVFEGEGSAILMSANYPGGFPEDELMTWQFVVPAPHLRASVFLNFNLSNCRKKEERVEYIIPGSTTINPEVFLRDKQPGN	450
gi	27721843	ref	XP_236747.1	ADGVTHSISGHIDA--TEVRIGTFCSNGTVSRIKMQEGVKMALHLPWFHRRNIVSGFISIANRSSIKRCLIEISVFEGEGSAILMSANYPGGFPEDELMTWQFVVPAPHLRASVFLNFNLSNCRKKEERVEYIIPGSTTINPEVFLRDKQPGN	450
gi	30410805	ref	NP_073753.3	PDGVTHSISGRIDA--TVVRIGTFCSNGTVSRIKMQEGVKMALHLPWFHRRNVSGFISIANRSSIKRCLIEISVFEGEGSAILMSANYPGGFPEDELMTWQFVVPAPHLRASVFLNFNLSNCRKKEERVEYIIPGSTTINPEVFLRDKQPGN	450
gi	114586460	ref	XP_001147144.1	PDGVTHSISGRIDA--TVVRIGTFCSNGTVSRIKMQEGVKMALHLPWFHRRNVSGFISIANRSSIKRCLIEISVFEGEGSAILMSANYPGGFPEDELMTWQFVVPAPHLRASVFLNFNLSNCRKKEERVEYIIPGSTTINPEVFLRDKQPGN	450
gi	73986003	ref	XP_541913.2	PDGVTHSISGRIDA--TVVRIGTFCSNGTVSRIKMQEGVKMALHLPWFHRRNIVSGFISIANRSSIKRCLIEISVFEGEGSAILMSANYPGGFPEDELMTWQFVVPAPHLRASVFLNFNLSNCRKKEERVEYIIPGSTTINPEVFLRDKQPGN	450
gi	194677155	ref	XP_612363.4	PDGVTHSISGRIDAS--TVVRIGTFCSNGTVSRIKMQEGVKMALHLPWFHRRNVSGFISIANRSSIKRCLIEISVFEGEGSAILMSANYPGGFPEDELMTWQFVVPAPHLRASVFLNFNLSNCRKKEERVEYIIPGSTTINPEVFLRDKQPGN	450
gi	118086139	ref	XP_418802.2	PDLVSYNINSCIDK--ATVNIIGTFCSNGTVSRVKKLGGVIMSLHLPWNLTVAISGFIANRSSIKRCLIEISVFEGEGSAILMSANYPGGFPEDELMTWQFVVPAPHLRASVFLNFNLSNCRKKEERVEYIIPGSTTINPEVFLRDKQPGN	450
gi	62122859	ref	NP_001014355.1	PDNHRVILA--VEN---ISIGTFCSNGTVSRIDVRNAGKLSAEVTTGGQSLSTKVIIVSVGRLLMNSLVNIHAVLPEKSSIQDFI---PNTTPEAETMWFESMPNAYADVRILKYTLPTGLSSESIPMTKLTWQGRDALVKRMNENQPSV	450

.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi	61098143	ref	NP_598735.2	MAGNFNLSLQCGDQDAQS--PGILRLQFVLVQHPQNESNKIYVVDLSENERAMSLTIEPR--PVKHGRRFVPGCFVCLSRICSTNVLTLAGLHKHISFLCDDLRLWVNEKTLSCLDHRYCYRQSKLQVDPDYLLQPLVQLHDFSWKLL	600
gi	27721843	ref	XP_236747.1	MAGNFNLSLQCGDQDAQS--PGILRLQFVLVQHPQNESNKIYVVDLSENERAMSLTIEPR--PVKHGRRFVPGCFVCLSRICSTNVLTLAGLHKHISFLCDDLRLWVNEKTLSCLDHRYCYRQSKLQVDPDYLLQPLVQLHDFSWKLL	600
gi	30410805	ref	NP_073753.3	MAGNFNLSLQCGDQDAQS--PGILRLQFVLVQHPQNESNKIYVVDLSENERAMSLTIEPR--PVKHGRRFVPGCFVCLSRICSTNVLTLAGLHKHISFLCDDLRLWVNEKTLSCLDHRYCYRQSKLQVDPDYLLQPLVQLHDFSWKLL	600
gi	114586460	ref	XP_001147144.1	MAGNFNLSLQCGDQDAQS--PGILRLQFVLVQHPQNESNKIYVVDLSENERAMSLTIEPR--PVKHGRRFVPGCFVCLSRICSTNVLTLAGLHKHISFLCDDLRLWVNEKTLSCLDHRYCYRQSKLQVDPDYLLQPLVQLHDFSWKLL	600
gi	73986003	ref	XP_541913.2	MAGNFNLSLQCGDQDAQS--PGILRLQFVLVQHPQNESNKIYVVDLSENERAMSLTIEPR--PVKHGRRFVPGCFVCLSRICSTNVLTLAGLHKHISFLCDDLRLWVNEKTLSCLDHRYCYRQSKLQVDPDYLLQPLVQLHDFSWKLL	600
gi	194677155	ref	XP_612363.4	MAGNFNLSLQCGDQDAQS--PGILRLQFVLVQHPQNESNKIYVVDLSENERAMSLTIEPR--PVKHGRRFVPGCFVCLSRICSTNVLTLAGLHKHISFLCDDLRLWVNEKTLSCLDHRYCYRQSKLQVDPDYLLQPLVQLHDFSWKLL	600
gi	118086139	ref	XP_418802.2	IAGSFNLSLQCGDQDAQS--PGVLRLLQFVIVQHPQIDENIVHLVDLSENERAMSLTIEPR--PVKHGRRFVPGCFVCLSRICSTNVLTLAGLHKHISFLCDDLRLWVNEKTLSCLDHRYCYRQSKLQVDPDYLLQPLVQLHDFSWKLL	600
gi	62122859	ref	NP_001014355.1	EPGNFNISSIKNCKMSTVSSLNRLMVHFQISAIKRKKQCEGDLDPDKQVLRIQVMKDKP-----SVCVLKLSVIMD--VLIASGNHFILNTFDCNCKDELTVIQIEEKKEWRNCTSTLFLPHNYEQCCIPGVLLKMIWYIQ	600

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gi	61098143	ref	NP_598735.2	VPKDKLSLMLVPGQKLOQHTHEKPCNTSFSYLVAIAIPSDLYFGSFCPGGSIKIQIQVKON--SVVLLRFAVAPFQEVSKQGLIVSYTPYFKBEGIFVTPDITKNVYLRSPNWRDGLPALSSVWNISVPSNQAACLTLFKERSGLACQ	750
gi	27721843	ref	XP_236747.1	VPKDKLSLMLVPGQKLOQHTHEKPCNTSFSYLVAIAIPSDLYFGSFCPGGSIKIQIQVKON--SVVLLRFAVAPFQEVSKQGLIVSYTPYFKBEGIFVTPDITKNVYLRSPNWRDGLPALSSVWNISVPSNQAACLTLFKERSGLACQ	750
gi	30410805	ref	NP_073753.3	VPKDKLSLMLVPAQKLOQHTHEKPCNTSFSYLVAIAIPSDLYFGSFCPGGSIKIQIQVKON--ISVTLRFAVAPFQEVSKQGLIVSYTPYFKBEGIFVTPDITKNVYLRSPNWRDGLPALSSVWNISVPSNQAACLTLFKERSGLACQ	750
gi	114586460	ref	XP_001147144.1	VPKDKLSLMLVPAQKLOQHTHEKPCNTSFSYLVAIAIPSDLYFGSFCPGGSIKIQIQVKON--ISVTLRFAVAPFQEVSKQGLIVSYTPYFKBEGIFVTPDITKNVYLRSPNWRDGLPALSSVWNISVPSNQAACLTLFKERSGLACQ	750
gi	73986003	ref	XP_541913.2	VPKDKLSLMLVPAQKLOQHTHEKPCNTSFSYLVAIAIPSDLYFGSFCPGGSIKIQIQVKON--ISVTLRFAVAPFQEVSKQGLIVSYTPYFKBEGIFVTPDITKNVYLRSPNWRDGLPALSSVWNISVPSNQAACLTLFKERSGLACQ	750
gi	194677155	ref	XP_612363.4	VPKDKLSLMLVPAQKLOQHTHEKPCNTSFSYLVAIAIPSDLYFGSFCPGGSIKIQIQVKON--ISVTLRFAVAPFQEVSKQGLIVSYTPYFKBEGIFVTPDITKNVYLRSPNWRDGLPALSSVWNISVPSNQAACLTLFKERSGLACQ	750
gi	118086139	ref	XP_418802.2	APETINTEIISPSLKLRLHLPQNCNTSFSYLVAIAIPSDLYFGSFCPGGSIKIQIQVKON--ISVTLRFAVAPFQEVSKQGLIVSYTPYFKBEGIFVTPDITKNVYLRSPNWRDGLPALSSVWNISVPSNQAACLTLFKERSGLACQ	750
gi	62122859	ref	NP_001014355.1	GPVNSAVELQSPDTGLRYCLPEDNCSNILLNVSQVMN--PGITVVGQFCPKGVSQKIQIRESKIAVTSVFSFSDRSVAAPFLSYLSYFTQGISENYIFSVTPKMDNPTLALPGVPSAMKASSVTEWVNMFEQYTSVLTFRN--VSQPKCK	750

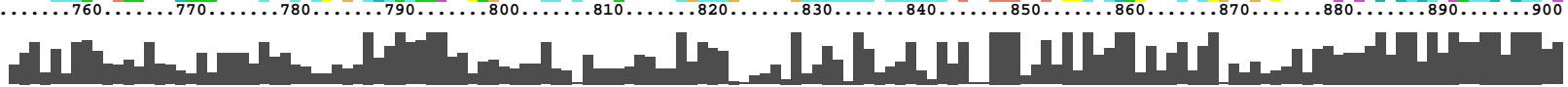
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gi | 61098143 | ref | NP_598735.2 | SGRAPFMIIQEQQSRABEIFSLDEEVLKPKSFHHHSFWVNI S NCS PMNGKQLDLLFWVTLTPRTVDLAVVIG--AAGGGALLLFALGLIICLVK--KKKVDKGPVAVGIYNGVNTQMP--TQKFPKGRKNDSDSHVYAVIEDTMVYGHLLQD 900
gi | 27721843 | ref | XP_236747.1 | SGRAPFMIIQEQQTRABEIFSLDEEVLKPKSFHHHSFWVNI S NCS PMNGKQLDLLFWVTLTPRTVDLAVVIG--AAGGGALLLFALGLIICLVK--KKKVDKGPVAVGIYNGVNTQMP--TQKFKRRKNDSDSHVYAVIEDTMVYGHLLQD 900
gi | 30410805 | ref | NP_073753.3 | TGRAFMIIQEQRTRABEIFSLDEDVLPKPSFHHHSFWVNI S NCS P TSGKQLDLLFSVTLTPRTVDLTVILIAAVGGGVLSSALGLIICCVK--KKKKTNRKGPVAVGIYNDNINTEMPRPKKFKRGRKNDSDSHVYAVIEDTMVYGHLLQD 900
gi | 114586460 | ref | XP_001147144.1 | TGRAFMIIQEQRTRABEIFSLDEDVLPKPSFHHHSFWVNI S NCS P TSGKQLDLLFSVTLTPRTVDLTVILIAAVGGGVLSSALGLIICCVK--KKKKTNRKGPVAVGIYNGVNTQMP--PKKFKRGRKNDSDSHVYAVIEDTMVYGHLLQD 900
gi | 73986003 | ref | XP_541913.2 | TGRAFMIIQEQRSAKAEIFSLDEEVLKPKSFHHHSFWVNI S NCS P VSGKQLDLLFFVLLTPRTVDLTVVILIAVGGGALLLFALGFIIICVVK--KKKKTNRKGPVAVGIYNGVNTQMP--SKKFKRGRKNDSDSHVYAVIEDTMVYGHLLQD 900
gi | 194677155 | ref | XP_612363.4 | TGRAFMIIQEQRSAKAEIFSLDEEVLKPKSFHHHSFWVNI S NCS P M S G K Q L D L L F W V L T P R T V D L T V I L I A V V G G G A L L L F A L G F I I C F V K K K K K K I T R G P A V G I Y N G V N T Q M P M R K K F O R G R K N D S D S H V Y A V I D D T M V Y G H L L Q D 900
gi | 118086139 | ref | XP_418802.2 | TGRAVYNIKEQMPGAEITVRRDELPLPRNMHYNFVNI S NCS K P V D P M Q L S L K F V T V E K Q I D L A V I V G V L A G F G --V L A A I G L T V C I K K --K K K K S N P M V G V Y N T N V N T Q M P G K O R L F K K D R K T N E S H V Y A V I D D A M V Y G H L L K E 900
gi | 62122859 | ref | NP_001014355.1 | QVHTNIAVQTIIRSGTVLYTITKDDKMKDLLLPEG-FYLNMTNCKSPKGAFRAMMEVTVQSN TNKLLGIILG--VVGVLAIAVAVVIVFVLR--KKKRNKAPPVSVYVNSEHAFLLPGLHGIFKTEEBEENHTVAVIDDILVSHLLND 900

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gi | 61098143 | ref | NP_598735.2 | SGGSFIQPEVDIYRPFQGPMDGCPPPPPLFRTPTAKFTAELAPSPPPESESEPYTFSHPNKGEI-----GVRDIDIPLLHIGQPVETEE 996
gi | 27721843 | ref | XP_236747.1 | SGGSFIQAEVDIYRPFQGPMDGCPPPPPIFRTPTAKFTAADKLAPSPPPESESEPYTFSHPNKGEV-----GVRDTGIPLLNIQPMETEE 996
gi | 30410805 | ref | NP_073753.3 | SSGSFLOPEVDIYRPFQGTMGVCPSPPTICSRAPTAKLATEEPPRSPPPESESEPYTFSHPNNGDV-----SKDIDIPLLNTOEPMPEAE 996
gi | 114586460 | ref | XP_001147144.1 | SGGSFLOPEVDIYRPFQGTMGVCPSPPTICSRAPTAKLATEEPPRCSPPESESEPYTFSHPNNGDV-----SKDIDIPLLNTOEPMPEAE 996
gi | 73986003 | ref | XP_541913.2 | SNGSFLOPEVDIYRPFQGTGDCPPSPPAICSRAPTAKLATEEPLGIPAESESESEPYTFSHPNN-----RDTIDIPLLDHEPEEPT 996
gi | 194677155 | ref | XP_612363.4 | ASGPFIQAEVDIYRPFQGTGDFPPSPPPIKSKAPTAKLATEEPPGSPSESESEPYTFSHPKDGKV-----NRSIDIPLLDAHEPTPEGE 996
gi | 118086139 | ref | XP_418802.2 | SNGS-VTPEVDVYQPFDPMGSLPPSPPPF SFRKDVKHSPTNEEPP-LLAETDHDAYTFAHQKSGELEDN GEGNAKNNGDTSM S L L E N K E R D S L E E 996
gi | 62122859 | ref | NP_001014355.1 | DADN----KQHYEDTSGPHLNKPLPDRPDRNVDSHALDKALLPNELYGVVGGSTTSGPTRTAGK-----SSEHTYETRLCV--- 996

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