

gi 31560553 |ref| NP\_035380.2 | MASGGNSPPPPP---AAAASDEEEEDGDAADRAQAGSPHQIQORFEELCSRLNMDAARAEAWSYRSMSESYTLEGNDLHLWLCALYVACRKSVPVTVSKGTAEAGNYVSLTRILRCSEOSLIEFFNKKMKKWEDMANLPPHFRERTE 147  
gi 13592041 |ref| NP\_112356.1 | MASGGNSPPPPP---AAAASDEEEEDGDAADRAQAGSPHQIQORFEELCSRLNMDAARAEAWSYRSMSESYTLEGNDLHLWLCALYVACRKSVPVTVSKGTAEAGNYVSLTRILRCSEOSLIEFFNKKMKKWEDMANLPPHFRERTE 147  
gi 172072597 |ref| NP\_005602.3 | MPSSGGDQSPPPPPPPAAAASDEEEEDDGEAEDAAPPAESPTPIQORFDELCSRLNMDAARAEAWSYRSMSESYTLEGNDLHLWLCALYVACRKSVPVTVSKGTVEGNYVSLTRILRCSEOSLIEFFNKKMKKWEDMANLPPHFRERTE 150  
gi 114662486 |ref| XP\_523371.2 | MPSSGGDQSPPPPPPPAAAASDEEEEDDGEAEDAAPPAESPTPIQORFDELCSRLNMDAARAEAWSYRSMSESYTLEGNDLHLWLCALYVACRKSVPVTVSKGTVEGNYVSLTRILRCSEOSLIEFFNKKMKKWEDMANLPPHFRERTE 150  
gi 73949852 |ref| XP\_535303.2 | MPSSGGDQSPPPPPPPAAAASDEEEEDDGEAEDAAPPAESPTPIQORFDELCSRLNMDAARAEAWSYRSMSESYTLEGNDLHLWLCALYVACRKSVPVTVSKGTVEGNYVSLTRILRCSEOSLIEFFNKKMKKWEDMANLPPHFRERTE 150  
gi 148225699 |ref| NP\_001091542.1 | MPSSGGDQSPPPPPPPAAAASDEEEEDDGEAEDAAPPAESPTPIQORFDELCSRLNMDAARAEAWSYRSMSESYTLEGNDLHLWLCALYVACRKSVPVTVSKGTVEGNYVSLTRILRCSEOSLIEFFNKKMKKWEDMANLPPHFRERTE 150  
gi 118123617 |ref| XP\_414087.2 | -----MLHITLTLCCVDSVLSGIVVSSS-----LIEFFNKKMKKWEDMANLPPHFRERTE 26  
gi 189537876 |ref| XP\_001922168.1 | -----MPKRAADPEPCTSTTDPFHEQSPFDVAVLAGEITDTICEPPAKR---IDLDIKQEFNGGVOGGLIKNESLQMTIKQETEGNIPEARREEDDE 49  
gi 17508261 |ref| NP\_491686.1 | 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150 96



gi 31560553 |ref| NP\_035380.2 | RLERNFVTSAVIFKKEPIFODIFKYVPEEQPROQRGRKRRPCTTVEIFHFQWVLFYAKGNFPMISDDLVSNSYHLLLCALDLVYGNALQCSNRKELVNPVNFKGLSLEDHCPKDKSASSDPPCVIEKLSLHDGLVLEAKGIKEHFWKP 297  
gi 13592041 |ref| NP\_112356.1 | RLERNFVTSAVIFKKEPIFODIFKYVPEEQPROQRGRKRRPCTTVEIFHFQWVLFYAKGNFPMISDDLVSNSYHLLLCALDLVYGNALQCSNRKELVNPVNFKGLSLEDHCPKDKSASSDPPCVIEKLSLHDGLVLEAKGIKEHFWKP 297  
gi 172072597 |ref| NP\_005602.3 | RLERNFVTSAVIFKKEPIFODIFKYVPEEQPROQRGRKRRPCTTVEIFHFQWVLFYAKGNFPMISDDLVSNSYHLLLCALDLVYGNALQCSNRKELVNPVNFKGLSLEDHCPKDKSASSDPPCVIEKLSLHDGLVLEAKGIKEHFWKP 300  
gi 114662486 |ref| XP\_523371.2 | RLERNFVTSAVIFKKEPIFODIFKYVPEEQPROQRGRKRRPCTTVEIFHFQWVLFYAKGNFPMISDDLVSNSYHLLLCALDLVYGNALQCSNRKELVNPVNFKGLSLEDHCPKDKSASSDPPCVIEKLSLHDGLVLEAKGIKEHFWKP 300  
gi 73949852 |ref| XP\_535303.2 | RLERNFVTSAVIFKKEPIFODIFKYVPEEQPROQRGRKRRPCTTVEIFHFQWVLFYAKGNFPMISDDLVSNSYHLLLCALDLVYGNALQCSNRKELVNPVNFKGLSLEDHCPKDKSASSDPPCVIEKLSLHDGLVLEAKGIKEHFWKP 300  
gi 148225699 |ref| NP\_001091542.1 | RLERNFVTSAVIFKKEPIFODIFKYVPEEQPROQRGRKRRPCTTVEIFHFQWVLFYAKGNFPMISDDLVSNSYHLLLCALDLVYGNALQCSNRKELVNPVNFKGLSLEDHCPKDKSASSDPPCVIEKLSLHDGLVLEAKGIKEHFWKP 300  
gi 118123617 |ref| XP\_414087.2 | RLERNFVTSAVIFKKEPIFODIFKYVPEEQPROQRGRKRRPCTTVEIFHFQWVLFYAKGNFPMISDDLVSNSYHLLLCALDLVYGNALQCSNRKELVNPVNFKGLSLEDHCPKDKSASSDPPCVIEKLSLHDGLVLEAKGIKEHFWKP 176  
gi 189537876 |ref| XP\_001922168.1 | KLERNFVTSVIFKKEPIFODIFKYVPEEQPROQRGRKRRPCTTVEIFHFQWVLFYAKGNFPMISDDLVSNSYHLLLCALDLVYGNALQCSNRKELVNPVNFKGLSLEDHCPKDKSASSDPPCVIEKLSLHDGLVLEAKGIKEHFWKP 199  
gi 17508261 |ref| NP\_491686.1 | DSRTSMPPALGEDDDYEDDADSFIDKNTNPPPSFLEGCRANLNDIVGAWETYNHVAQRVLSGSESA-----WQLSAIYYLLSKGTRK---RGKTRILILPPFVSILTIANSTDIWAEMLDKTRARFVEIHSRKRIRRYE 237  
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi 31560553 |ref| NP\_035380.2 | YIRKLFKLLKGGKEENLTFLEPGNFGEFSAKAVNKAYEEVYLAAGNLDERVFLGDEAEEVGLTSLRCLSAAGSTESAERTC---MTDILQOHLDKSKALRVCTPLTGVRYVQENSPCVTPVSTAHSLESLRLHMLTGLRNAPSEKLEQILR 446  
gi 13592041 |ref| NP\_112356.1 | YIRKLFKLLKGGKEENLTFLEPGNFGEFSAKAVNKAYEEVYLAAGNLDERVFLGDEAEEVGLTSLRCLSAAGSTESAERTC---MRDILQOHLDKSKALRVCTPLTGVRYVQENSPCVTPVSTAHSLESLRLHMLTGLRNAPSEKLEQILR 446  
gi 172072597 |ref| NP\_005602.3 | YIRKLYEKKLLKGGKEENLTFLEPGNFGEFSAKAVNKAYEEVYLAAGNLDERVFLGDEAEEVGLTSLRCLSAAGSTESAERTC---MKNILQOHPDQSKALRVCTPLTGVRYVQENSPCVTPVSTAHSLESLRLHMLTGLRNAPSEKLEQILR 449  
gi 114662486 |ref| XP\_523371.2 | YIRKLYEKKLLKGGKEENLTFLEPGNFGEFSAKAVNKAYEEVYLAAGNLDERVFLGDEAEEVGLTSLRCLSAAGSTESAERTC---MKNILQOHPDQSKALRVCTPLTGVRYVQENSPCVTPVSTAHSLESLRLHMLTGLRNAPSEKLEQILR 449  
gi 73949852 |ref| XP\_535303.2 | YIRKLYEKKLLKGGKEENLTFLEPGNFGEFSAKAVNKAYEEVYLAAGNLDERVFLGDEAEEVGLTSLRCLSAAGSTESAERTC---MKNILQOHPDQSKALRVCTPLTGVRYVQENSPCVTPVSTAHSLESLRLHMLTGLRNAPSEKLEQILR 449  
gi 148225699 |ref| NP\_001091542.1 | YIRKLYEKKLLKGGKEENLTFLEPGNFGEFSAKAVNKAYEEVYLAAGNLDERVFLGDEAEEVGLTSLRCLSAAGSTESAERTC---MKNILQOHPDQSKALRVCTPLTGVRYVQENSPCVTPVSTAHSLESLRLHMLTGLRNAPSEKLEQILR 449  
gi 118123617 |ref| XP\_414087.2 | YIRKLFKLLKGGKEDNLTGFLDPGNFGDFSAKAVNKAYEEVYLAAGNLDERVFLGDEAEEVGLTSLRCLSAAGSTESAERTC---MKNILQOHPDQSKALRVCTPLTGVRYVQENSPCVTPVSTAHSLESLRLHMLTGLRNAPSEKLEQILR 325  
gi 189537876 |ref| XP\_001922168.1 | FTIKLFRKLLKGGKEDLTFLEPGNFGEFSAKAVNKAYEEVYLAAGNLDERVFLGDEAEEVGLTSLRCLSAAGSTESAERTC---MKNILQOHPDQSKALRVCTPLTGVRYVQENSPCVTPVSTAHSLESLRLHMLTGLRNAPSEKLEQILR 348  
gi 17508261 |ref| NP\_491686.1 | YIRRIQEGGLAVS-----CVIFKFKCFRIKCFIEIKVGESECPSS-----SHELFTVLWTFVLMKSRMIVDDLTINYQLLFSILDVYV---EMCSMKEGIVHHLNQKFVEDLLENDCTIRALCQFGGAVLDRHFSDDHIFK 368  
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi 31560553 |ref| NP\_035380.2 | SCNRDPTQAIADRLLKEMEYIYSQHF---PDENFSNCAKEIANKHFRFAEMLYYKLVLESVIEQEKRLGDMDLGVLHDAFHRSLLA---CCLEVVAFSYKPPGNFFPIAEIFDVPVHYHFYKVIIEVIRAEDGLCREVVKHLNNOIEEQILDH 593  
gi 13592041 |ref| NP\_112356.1 | SCNRDPTRAIADRLLREMEYIYSQHF---PDENFSNCAKEMANKHFRFAEMLYYKLVLESVIEQEKRLGDMDLGVLHDAFHRSLLA---CCLEVVAFSYKPPGNFFPIAEIFDVPVHYHFYKVIIEVIRAEDGLCREVVKHLNNOIEEQILDH 593  
gi 172072597 |ref| NP\_005602.3 | TCSRDPDTQAIANRLKEMFEIYSQHF---PDDEFNSNCAKEIASKHFRFAEMLYYKLVLESVIEQEKRLGDMDLGVLHDAFHRSLLA---CCLEVVAFSYKPPGNFFPIAEIFDVPVHYHFYKVIIEVIRAEDGLCREVVKHLNNOIEEQILDH 596  
gi 114662486 |ref| XP\_523371.2 | TCSRDPDTQAIANRLKEMFEIYSQHF---PDDEFNSNCAKEIASKHFRFAEMLYYKLVLESVIEQEKRLGDMDLGVLHDAFHRSLLA---CCLEVVAFSYKPPGNFFPIAEIFDVPVHYHFYKVIIEVIRAEDGLCREVVKHLNNOIEEQILDH 596  
gi 73949852 |ref| XP\_535303.2 | TCSRDPDTQAIANRLKEMEYIYSQHF---PDDEFNSN---SKEIASKHFRFAEMLYYKLVLESVIEQEKRLGDMDLGVLHDAFHRSLLA---CCLEVVAFSYKPPGNFFPIAEIFDVPVHYHFYKVIIEVIRAEDGLCREVVKHLNNOIEEQILDH 595  
gi 148225699 |ref| NP\_001091542.1 | TCSRDPDTQAIANRLKEMEYIYSQHF---SEEDGSNCAKDIAASKHFRFAEMLYYKLVLESVIEQEKRLGDMDLGVLHDAFHRSLLA---CCLEVVAFSYKPPGNFFPIAEIFDVPVHYHFYKVIIEVIRAEDGLCREVVKHLNNOIEEQILDH 596  
gi 118123617 |ref| XP\_414087.2 | ACSRDPSQSIASRVKEMEYIYSQHF---ABEEDFSNLSKDVASKHFRFAEMLYYKLVLESVIEQEKRLGDMDLGVLHDAFHRSLLA---CCLEVVAFSYKPPGNFFPIAEIFDVPVHYHFYKVIIEVIRAEDGLCREVVKHLNNOIEEQILDH 472  
gi 189537876 |ref| XP\_001922168.1 | SCVRDPTESVAARLLKEMEYIYSQHF---SEEDGSNCAKDIAASKHFRFAEMLYYKLVLESVIEQEKRLGDMDLGVLHDAFHRSLLA---CCLEVVAFSYKPPGNFFPIAEIFDVPVHYHFYKVIIEVIRAEDGLCREVVKHLNNOIEEQILDH 485  
gi 17508261 |ref| NP\_491686.1 | KMEKGTIPSTWVNFQERDILMNVKRAYENKLLQGRSISDRIFIPVSEDFSKIFQSDPTYSVADILKVSYSGRRRFRAEFLKISNNHCLKELKALGGKVAS-EKLVTC-SKEQPRVPCVEYNLELGNIPDPLESNNOQLNRLTKITIG-- 514  
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi 31560553 |ref| NP\_035380.2 | LAWKTKSPLWDRIRDNRVPTCEEVMPNQLERTDEIYIAGSPLTPTRRVGEVR-ADAGGLGRSITS---PTLLYDRYSSPVSITRRRLFE-NDSPSEGSISGRIPPOPLVNAVPPVQVPEVTVSVTPVPGQTLVIMATAIVTANNQGTVI 740  
gi 13592041 |ref| NP\_112356.1 | LAWKTKSPLWDRIRDNRVPTCEEVTPPHNLERTDEIYIAGSPLTPTRRVGEVR-ADAGGLGRSITS---PTLLYDRYSSPVSITRRRLFE-SDSPSEGSISGRIPPOPLVNAVPPVQVPEVTVSVTPVPGQTLVIMATAIVTANNQGTVI 740  
gi 172072597 |ref| NP\_005602.3 | LAWKPESSLWEKIRDNRVPTCEEVMPNQLERADEICIASGSLTPTRRVTEVR-ADTGGGLRSITS---PTLLYDRYSSPPASITRRRLFEVNDSPSDGGTGRMPPPOPLVNAVPPVQVPEVTVSVTPVPGQTLVIMATAIVTANNQGTVI 744  
gi 114662486 |ref| XP\_523371.2 | LAWKPESSLWEKIRDNRVPTCEEVMPNQLERADEICIASGSLTPTRRVTEVR-ADTGGGLRSITS---PTLLYDRYSSPPASITRRRLFEVNDSPSDGGTGRMPPPOPLVNAVPPVQVPEVTVSVTPVPGQTLVIMATAIVTANNQGTVI 744  
gi 73949852 |ref| XP\_535303.2 | LAWKPESSLWDRIRDNRVPTCEEVMPNQLERADEICIASGSLTPTRRVTEVR-ADTGGGLRSITS---PALLYDRYSSPPASITRRRLFEVNDSPSDGGTGRMPPPOPLVNAVPPVQVPEVTVSVTPVPGQTLVIMATAIVTANNQGTVI 743  
gi 148225699 |ref| NP\_001091542.1 | LAWKPESSLWDRIRDNRVPTCEEVMPNQLERADEICIASGSLTPTRRVTEVR-ADTGGGLRSITS---PTLLYDRYSSPPASITRRRLFEVNDSPSDGGTGRMPPPOPLVNAVPPVQVPEVTVSVTPVPGQTLVIMATAIVTANNQGTVI 744  
gi 118123617 |ref| XP\_414087.2 | MAWKQESLLWDRIRDNRVPTCEEVMPNQLERADEICIASGSLTPTRRVTEVR-ADTGGGLRSITS---PALLYDRYSSPPASITRRRLFEVNDSPSDGGTGRMPPPOPLVNAVPPVQVPEVTVSVTPVPGQTLVIMATAIVTANNQGTVI 621  
gi 189537876 |ref| XP\_001922168.1 | LAWKQESPLWERIREAKVCPVCEVMPNQLERADEICIASGSLTPTRRVTEVR-ADTGGGLRSITS---PTLLYDRYSSPPASITRRRLFEVNDSPSDGGTGRMPPPOPLVNAVPPVQVPEVTVSVTPVPGQTLVIMATAIVTANNQGTVI 617  
gi 17508261 |ref| NP\_491686.1 | -SWKLENSKLEVEVCGTMSDSPMATILLQSDENMTNFKERLSS-----AELGEMINENIPKHYNNRKELELVFLIEMKTIIVAELEKVKVREDLNLN-----VIRREBEFLDSVFCVLELILVSNYDRFPFSAELCGVHPMFHKVLD 651  
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



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gi|31560553|ref|NP_035380.2|IPVCGIANENGGIIFFPVQVNVGGQAQAVTGSIQPLSAQALAGSLSSQOVTGII--TLOVPGPVAIQIISPGGQOONPGOPLTSSSIRPKRTSSSLFFFRKVVYLAGVRLRDLCAKLDISDELRRKIWTCFEFSIIQCPPELMMDRHLDOLL 888
gi|13592041|ref|NP_112356.1|IPVCGIANENGGIIFFPVQVNVGGQAQAVTGSIQPLSAQALAGSLSSQOVTGII--TLOVPGPVAIQIISPGGQOONPGOPLTSSSIRPKRTSSSLFFFRKVVYLAGVRLRDLCAKLDISDELRRKIWTCFEFSIIQCPPELMMDRHLDOLL 888
gi|172072597|ref|NP_005602.3|IPVCGIANENGGIIFFPVQVNVGGQAQAVTGSIQPLSAQALAGSLSSQOVTGII--TLOVPGPVAIQIISPGGQOONPGOPLTSSSIRPKRTSSSLFFFRKVVYLAGVRLRDLCAKLDISDELRRKIWTCFEFSIIQCPPELMMDRHLDOLL 892
gi|114662486|ref|XP_523371.2|IPVCGIANENGGIIFFPVQVNVGGQAQAVTGSIQPLSAQALAGSLSSQOVTGII--TLOVPGPVAIQIISPGGQOONPGOPLTSSSIRPKRTSSSLFFFRKVVYLAGVRLRDLCAKLDISDELRRKIWTCFEFSIIQCPPELMMDRHLDOLL 892
gi|73949852|ref|XP_535303.2|IPVCGIANENGGIIFFPVQVNVGGQAQAVTGSIQPLSAQALAGSLSSQOVTGII--TLOVPGPVAIQIISPGGQOONPGOPLTSSSIRPKRTSSSLFFFRKVVYLAGVRLRDLCAKLDISDELRRKIWTCFEFSIIQCPPELMMDRHLDOLL 891
gi|148225699|ref|NP_001091542.1|IPVCGIANENGGIIFFPVQVNVGGQAQAVTGSIQPLSAQALAGSLSSQOVTGII--TLOVPGPVAIQIISPGGQOONPGOPLTSSSIRPKRTSSSLFFFRKVVYLAGVRLRDLCAKLDISDELRRKIWTCFEFSIIQCPPELMMDRHLDOLL 892
gi|118123617|ref|XP_414087.2|IPVCGIANENGGIIFFPVQVNVGQAQAVTGSIQPLSAQALAGSLSSQOVTGII--TLOVPGPVAIQIISPGGQOONPGOPLTSSSIRPKRTSSSLFFFRKVVYLAGVRLRDLCAKLDISDELRRKIWTCFEFSIIQCPPELMMDRHLDOLL 767
gi|189537876|ref|XP_001922168.1|IPVCGIANENGGIIFFPVQVNVGQAQAVTGSIQPLSAQALAGSLSSQOVTGII--TLOVPGPVAIQIISPGGQOONPGOPLTSSSIRPKRTSSSLFFFRKVVYLAGVRLRDLCAKLDISDELRRKIWTCFEFSIIQCPPELMMDRHLDOLL 757
gi|17508261|ref|NP_491686.1|LMTITHEKQLSRQMVQHSRLEETVIEYFSWKDSDPLWPMVVRCPFAHFQEFQEDWADKLNYSYPIKFPPIKPPDLDRLGRPIVQNTSRRLRIFLKRVTFTARRLODLDRVSMGARAKSCWLSFDVYLLRNDTLIFMDRHLQDIL 801
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900

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gi|31560553|ref|NP_035380.2|MCAIYVMKAVTKEDKSFONIMRCYRTPQARSQVYRSVLIKGRK--RNSGSCENRSHQNSPTELNDRASRDSPPV-MRNSSTLPVPOPSSAPPTPTRLTGASDVEEEERGDLIQFYNNIYRQIQTAFAMKYSQANS---MDTPPLSP 1032
gi|13592041|ref|NP_112356.1|MCAIYVMKAVTKEDKSFONIMRCYRTPQARSQVYRSVLIKGRK--RNSGSCENRSHQNSPTELNDRASRDSPPV-MRNSSTLPVPOPSSAPPTPTRLTGASDVEEEERGDLIQFYNNIYRQIQTAFAMKYSQANS---MDTPPLSP 1032
gi|172072597|ref|NP_005602.3|MCAIYVMKAVTKEDKSFONIMRCYRTPQARSQVYRSVLIKGRKRRRNSGSSDRSHQNSPTELNDRASRDSPPV-MRNSSTLPVPOPSSAPPTPTRLTGASDVEEEERGDLIQFYNNIYRQIQTAFAMKYSQANS---MDAPPLSP 1036
gi|114662486|ref|XP_523371.2|MCAIYVMKAVTKEDKSFONIMRCYRTPQARSQVYRSVLIKGRKRRRNSGSSDRSHQNSPTELNDRASRDSPPV-MRNSSTLPVPOPSSAPPTPTRLTGASDVEEEERGDLIQFYNNIYRQIQTAFAMKYSQANS---MDAPPLSP 1036
gi|73949852|ref|XP_535303.2|MCAIYVMKAVTKEDKSFONIMRCYRTPQARSQVYRSVLIKGRKRRRNSGSSDRSHQNSPTELNDRASRDSPPV-MRNSSTLPVPOPSSAPPTPTRLTGASDVEEEERGDLIQFYNNIYRQIQTAFAMKYSQANS---MDAPPLSP 1036
gi|148225699|ref|NP_001091542.1|MCAIYVMKAVTKEDKSFONIMRCYRTPQARSQVYRSVLIKGRKRRRNSGSSDRSHQNSPTELNDRASRDSPPV-MRNSSTLPVPOPSSAPPTPTRLTGASDVEEEERGDLIQFYNNIYRQIQTAFAMKYSQANS---MDAPPLSP 1037
gi|118123617|ref|XP_414087.2|MCAIYVMKAVTKEDKSFONIMRCYRTPQAKSHVYRSVLIKGRRRRNSGSSDRSHQNSPTGRSKERTSRDSPPV-MRNSSTLPVPOPSSAPPTPTRLTGASDVEEEERGDLIQFYNNIYRQIQTAFAMKYSQANS---MDTPPLSP 911
gi|189537876|ref|XP_001922168.1|MCAIYVMKAVTKEDKSFONIMRCYRTPQARSQVYRSVLIKGRK--RRHSNTEHTHRCSPTREGAQAQSGSSPVMRNSSTLPVPOPSSAPPTPTRAPGG-POEVEEERGDLIQFYNNIYRQIQTAFAMKYSQANS---PKNGAETPPLCP 905
gi|17508261|ref|NP_491686.1|LCCVFMKINNESSMLTEIMAYRRDSANSLLVYRSVTVFQEG---LNPNPQAVNTKEIILERLEGPKKKTVDIIRKYYNIEFRDRKIYIIGQIDSASD---EDLMEMP 907
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050

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gi|31560553|ref|NP_035380.2|YPFVRTGSPRRVQLSOSHPIYIISPHNNEAMPSPREKIFYFYSNSPSKRLREINSMIRTGETPTKKRGILLDDGESPAKRICPENHSALLRRLQDVANDRGSH- 1135
gi|13592041|ref|NP_112356.1|YPFVRTGSPRRVQLSOSHPIYIISPHNNEAMPSPREKIFYFYSNSPSKRLREINSMIRTGETPTKKRGILLDDGESPAKRICPENHSALLRRLQDVANDRGSH- 1135
gi|172072597|ref|NP_005602.3|YPFVRTGSPRRVQLSOSHPIYIISPHNNEAMPSPREKIFYFYSNSPSKRLREINSMIRTGETPTKKRGILLDDGESPAKRICPENHSALLRRLQDVANDRGSH- 1139
gi|114662486|ref|XP_523371.2|YPFVRTGSPRRVQLSOSHPIYIISPHNNEAMPSPREKIFYFYSNSPSKRLREINSMIRTGETPTKKRGILLDDGESPAKRICPENHSALLRRLQDVANDRGSH- 1139
gi|73949852|ref|XP_535303.2|YPFVRTGSPRRVQLSOSHPIYIISPHNNEAMPSPREKIFYFYSNSPSKRLREINSMIRTGETPTKKRGILLDDGESPAKRICPENHSALLRRLQDVANDRGSH- 1139
gi|148225699|ref|NP_001091542.1|YPFVRTGSPRRVQLSOSHPIYIISPHNNEAMPSPREKIFYFYSNSPSKRLREINSMIRTGETPTKKRGILLDDGESPAKRICPENHSALLRRLQDVANDRGSH- 1140
gi|118123617|ref|XP_414087.2|YPSVRISSPRLVQLSOSHPIYIISPHNNEAMPSPREKIFYFYSNSPSKRLREINSMIRTGETPTKKRGILLDDGESPAKRICPENHSALLRRLQDVANDRGSH- 979
gi|189537876|ref|XP_001922168.1|YPSLRIGSPRRVQLSOSHPIYIISPHNNEAMPSPREKIFYFYSNSPSKRLREINSMIRTGETPTKKRSIALEEQSPAKRLCQENQALLRRLQDVANDRGSH- 1009
gi|17508261|ref|NP_491686.1|VATESGLMPVRYVYLTHKLSIQTLPKTKHGESQERAIAIAN---LEKSGIITAMERSGD- 961
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150....

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