

gi	31982262	ref	NP_032343.2	-----MLGLTQHAQKVVWRMKPFS--PEVSPGSSPATAGHLRLRISLFLLELAQVCRGSVVSRRPFIIVWNGDTHWCLTEYGVDDVSVFDDVANKEQSFQG--SNMTIFYREELG	150
gi	46485726	ref	NP_997499.1	-----MKPFS--PEVSPDPCATAAHLRLRITLFLLELAQVCRGSVVSRRPFIIVWNGDTHWCLKHGVDVSVFDDVANKEQNFQG--PNMTIFYREELG	150
gi	6224976	ref	NP_009296.1	-----MAAHLRLPICALFLILLDMAQVGRGRLLPNRPFTIIVWNGDTHWCLERHGVDDVSVFDDVANPGQIFRG--PDMTIFYSSOLG	150
gi	114587044	ref	XP_001168739.1	-----MAAHLRLPICALFLILLDMAQVGRGRLLPNRPFTIIVWNGDTHWCLERHGVDDVSVFDDVANPGQIFRG--PDMTIFYSSOLG	150
gi	62988300	ref	NP_001017941.1	-----MRPFS--LEVSLHLPWAMAHLPLVCLLFLNLLSMTQGSRDVVPVQPFITIIWNNANTQWCMKKHGVDDVSIIFDDVNNPGQIFRG--PNMTIFYSSOLG	150
gi	73985710	ref	XP_850767.1	MTLPALPSAYTEAVAPSVQVCDNIFEDLEDSLMEGAGTAAVAVDGESESESEPALSFASPGQVSLDSSAMAVHLLPIYALFLILLGTAQGSRSSVVPVQPFITIIWNNANTQWCLERHGVDDVSVFDDVANPGQIFRG--PDMTIFYSSOLG	150
gi	50805781	ref	XP_424356.1	-----MAPGNLHLLLLLPVRAAGPGLVLRPFIIVWNGDTHWCLERHGVDDVSVFDDVANPGQIFRG--PDMTIFYSSOLG	150
gi	90652841	ref	NP_001035086.1	-----MDRSRRRCCLMLVFMSCASVLSGLK-LRPIISLWNAFTERRCSRSGVLDLISVFDIVHVNQDFMFG--DNITIFYEDKLG	150
gi	17536397	ref	NP_495830.1	-----MVIWVYHQLLLVLLIFIGAAGKAGYITGSCASQPNRRTDVMVWVPSVCKNEVSIIDVEK--YGIQLQEDQHFVGGKQFAIFVEHSFG	150



gi	31982262	ref	NP_032343.2	YYPYPTTGE--PVFGGLPQNASLVTHLAHAFODIKAAMPEDFSGGLAVLDWEAWRPRWAFNWDKDIYRORSMELVRAEHPDWPETLVEAAAKNFQEAARAWMAGTLQLGQVLRPRGLWGYGFPPDCYN--NDFL--SLNYTGGQCPVF	300
gi	46485726	ref	NP_997499.1	YYPYPTTGE--PVFGGLPQNASLVTHLAHAFODIKAAMPEDFSGGLAVLDWEAWRPRWAFNWDKDIYRORSMELVRAEHPDWPETLVEAAAKNFQEAARAWMAGTLQLGQVLRPRGLWGYGFPPDCYN--NDFL--SLNYTGGQCSLS	300
gi	6224976	ref	NP_009296.1	YYPYPTTGE--PVFGGLPQNASLIAHLARTFODILAAIPAPDFSGGLAVLDWEAWRPRWAFNWDKDIYRORSRALVQAQHPDWPAPQVEAVAQDFQGAARAWMAGTLQGRALRPRGLWGYGFPPDCYN--YDFL--SPNYTGGQCPSG	300
gi	114587044	ref	XP_001168739.1	YYPYPTTGE--PVFGGLPQNASLIAHLARTFODILAAIPAPDFSGGLAVLDWEAWRPRWAFNWDKDIYRORSRALVQAQHPDWPAPQVEAVAQDFQGAARAWMAGTLQGRALRPRGLWGYGFPPDCYN--YDFL--SPNYTGGQCPSG	300
gi	62988300	ref	NP_001017941.1	YYPYTSAGE--PVFGGLPQNASLNAHLARTFODILAAAMPEDFSGGLAVLDWEAWRPRWAFNWDKDIYRORSRALVQKQHPDWPAPQVEAVAQDFQGAARAWMAGTLKLGQALRPRGLWGYGFPPDCYN--YDFK--SPNYTGGQCPGN	300
gi	73985710	ref	XP_850767.1	YYPYTSAGE--PVFGGLPQNASLDTHLVHSEFDIQAAPESDFSGGLAVLDWEAWRPRWAFNWDKDIYRORSRALVQKQHPDWPAPQVEAVAQDFQGAARAWMAGTLKLGQALRPRGLWGYGFPPDCYN--YDFL--SPNYTGGQCPGN	300
gi	50805781	ref	XP_424356.1	LPFYTAQGG--PVGGGLPQNASLVLAHLQARRRDIQAALPSTRDGLAVDWEAWRPRWAFNWDKDIYRORSRALVQKQHPDWPAPQVEAVAQDFQGAARAWMAGTLKLGQALRPRGLWGYGFPPDCYN--NNFS--DELNNGSPVW	300
gi	90652841	ref	NP_001035086.1	LPFYHGFNDE--PIYGGVQNASLNEHLKKADEDIRKNIPEPFQGLAIIIDWEKWRPLNERWDSKVEVYWKASRAIVKAKHPWSDQILETEAVKLFKFAASMAFMVNEHLKLRRESRSGGLWGYGFPPDCYN--VQKKNETITGECPLG	300
gi	17536397	ref	NP_495830.1	KIPVFKAQNE--DDPKNGGLPQMGDLEAHLIQAQKIDINEITPDENFNGIAVDIEEFRPMWELSWGPFVYKTESIRLTRODHPYWSIKQIEWQAEERDYKACQKFFIEHLRLKRLRPNKAWGYLFPKNGDVGQ--KSDTDGCSL	300



gi	31982262	ref	NP_032343.2	VRDQNDQLGWLWNQSYALYPSIYLPAAALMGTEK--SQMVVRRVQVQALRVAIVSRDHPVVPVYVQIFVE--MDYLLPLELEHSLGESAAQGVAGAVLWLSDKKSTKESCOAIKAYMDSITLGPFFILNVTSAAALLCSEALCSGHGRVC	450
gi	46485726	ref	NP_997499.1	IHDQNDQLGWLWNQSYALYPSIYLPAAALMGTEK--SQMVVRRVQVQAEFRRLALVSRDHPVIMPVYVQIFVE--KDYLLPLELEHSLGESAAQGAAGAVLWISSEKSTKESCOAIKAYMDSITLGPFFILNVTSAAALLCSEALCSGHGRVC	450
gi	6224976	ref	NP_009296.1	IRAQNDQLGWLWQSRALYPSIYMPAVLEGTGK--SQMVVQHRVAEAFRVAVAAGDPNLPVLPVYVQIFVD--TNNHFLPLDELEHSLGESAAQGAAGVVLWVSWENIRTKESCOAIKEYMDITLGPFFILNVTSGALLCSQALCSGHGRVC	450
gi	114587044	ref	XP_001168739.1	IRAQNDQLGWLWQSRALYPSIYMPAVLEGTGK--SQMVVQHRVAEAFRVAVAAGDPNLPVLPVYVQIFVD--TNNHFLPLDELEHSLGESAAQGAAGVVLWVSWENIRTKESCOAIKEYMDITLGPFFILNVTSGALLCSQALCSGHGRVC	450
gi	62988300	ref	NP_001017941.1	ICAQNDQLGWLWQSRALYPSIYLPAAALMGTEK--SQMVVQHRVAEAFRVAVAAGDPKLPVLPVYVQIFVD--MNNHFLPLDELEHSLGESAAQGAAGVVLWVSWLSSTKESCOAIKEYVDTITLGPFFILNVTSGARLCSQVLCSSGHGRCA	450
gi	73985710	ref	XP_850767.1	IGAQNDQLGWLWQSRALYPSIYLPAAALMGTEK--SQMVVQHRVAEAFRVAEADGDPYLPVLPYVQIFVD--NNNRVLPLDELEHSLGESAAQGAAGVVLWVSWENIRTKESCOAIKEYVDTITLGPFFILNVTSQVLLCSQALCSGHGRVC	450
gi	50805781	ref	XP_424356.1	EQQRNQLGWLWNCQSRALYPSIYLPQQLQGTDK--VLRVYRVAEAFRVAQKGLISNAVPLVYVTEIIVA--NNSDFLSEEDLVNIIGESAAQGAAGIIVGRSADTASKSKKCLKLRDYLGDALGHYIVNVTSQALCSQSLCSGHGRVC	450
gi	90652841	ref	NP_001035086.1	EMKRNQKLAWMNVSSALYPDIVLDLGLRGRGODILLVSRVRIIEAMRVREKTHOMVSVFPYVARIAPT--YEMFPLSQDDLVNIIGESVVALGASGVVWLDGQNFTRKRAEAVRDYLDVILGRYIVNVTEAFLCRKVCSSQGRVC	450
gi	17536397	ref	NP_495830.1	FQKFNQDLHLWLGESTALFPSIYLYPSQKQNEPYNFVNSGALITETKRIRKN--YCPSCIEHVFVRIKIEINPYVTPDDFYSKQNLASLDDLAIKMNNANSVWIVSISGISGR--CGSLQTVVDNLDLGRYVQLTDRNLDKCRMERCEGRGECY	450



gi	31982262	ref	NP_032343.2	RHPSYPEALLILNPASFSIEL--THDGRPPSLKGLLSLK--DRAQMAKFKRCRCYRGRWKWQDKRGM--	539
gi	46485726	ref	NP_997499.1	RHPSYPEALLILNPASFSIEP--THDGRPLSLKGLLSLK--DRAQMAKFKRCRCYRGSWGEWCKKQDM--	539
gi	6224976	ref	NP_009296.1	RRTSHPKALLLLNPASFSIQL--TPGGGPLSLQGALSLE--DQAQMAVEFKRCRCYPGWQAPWCEQKSMW--	539
gi	114587044	ref	XP_001168739.1	RRTSHPKALLLLNPASFSIQL--TPGGGPLSLQGALSLE--DQAQMAVEFKRCRCYPGWQAPWCEQKSMW--	539
gi	62988300	ref	NP_001017941.1	RRPSYPKARLLILNPSTFSIKP--TPGGGPLTLQGALSLE--DRLRMVAEVEFKRCRCYRGRWTRCEQWGMW--	539
gi	73985710	ref	XP_850767.1	RRPSYPEALLFLNPSTFSIQL--PPGGRPLTLQGALSRE--DRMRMAVEFKRCRCYRGRWGVRCQEQGMR--	539
gi	50805781	ref	XP_424356.1	RKEGK--VAFLQLDNNRFAINL--KAK--KPQPMVWILLNADSDMS--LAEFGTCCYSGWRGEHDSHGSSNK--	539
gi	90652841	ref	NP_001035086.1	RRDPSASVYLHLNPEMWSIIPRAQLPGPI--TGGPSVVAHRRLLWTCQETSRFADSFRCQCFPGWEGEQCKPVPVETVF--	539
gi	17536397	ref	NP_495830.1	LPRPKTNPAIYNFACRCERPFYFG--KSCYRGRMRMGVSMPKASQTPQVIVPDVTAIFYSTSSNGTKKYNAPNQFYERGGDIKLRKLI--	539

