



gi	90186273	ref	NP_034426.2	QHYMLRARYASARGSGTPTAAHSLDRMG	GLSVPPWRSR	TEYPG	YNPNAGVTRRASDPARAADHP	APARVORFKSLGCVHTPP	SVATG-RNFDPHPTSVVSPOPPSITENVAMDRGLQE	706	
gi	62652273	ref	XP_345833.2	QHYMLRARYASARGSGTPTAAHSLDRIG	GLPAPPWRSR	AEYPG	YNPNAGVTRRASDPARAADHP	APARVORFKSLGCVHTPP	SVATG-RNFDPHPTSVVSPOPPSITENVAMDRGLQG	703	
gi	73968515	ref	XP_858885.1	QHYLLRARYASARGGGTPTAAPSLDRMG	SLPAPPWRSR	AEYPG	YNPNAGVTRRASDPARAVDRP	APARVORFKSLGCVHTPP	TVGGGRNFDPQLATGVVSPOPPSITENVAMDRGLRE	713	
gi	149944723	ref	NP_001092470.1	QHYLLRARYASARGGGTPTAAPSLDRIG	ALPAPPWRSR	AEYPG	YNPNAGVTRRASDPARAVDRP	APARVORFKSLGCVHTPP	TVVGGGNFDPQLATGVVSPOPPSITENVAMDRGLRE	705	
gi	4885279	ref	NP_005260.1	QHYLLRARYASARGGGTPTAAHSLDRIG	GLPAPPWRSR	AEYPG	YNPNAGVTRRASDPARAADHP	APARVORFKSLGCVHTPP	TVVGGGNFDPVYLPVTSVYSPOPPSITENAAMDARGLQE	705	
gi	118119480	ref	XP_413682.1							566	
gi	30231244	ref	NP_840081.1	QOYSLKAKYAAATG-GPPPPLNPMNDQAGTPARHVGFLECCGQPLPFLQCGGTRRHSANAEYGTGVLYPHQAPGNNTRRASDPVRSAADPGLPKVORFNSLNSVLSMSRRNALQCCGSDAALSRHMYSPRPPSITENVMMRAMGMG							874



gi	90186273	ref	NP_034426.2	EPVVGTS--VMGNGLNPMDFSS	TDITLG	YGGPEGTAAPFYEARPGSLPLGPGPTNYGPGHCAQOVSYDPDTPENWG	EFPSHAGVYPSNKAPGAAYSQCPRLHYG	QVQVKPEQG	820	
gi	62652273	ref	XP_345833.2	ELVVGTS--MMGNDLNPYDFSS	ADITLG	YGGPEGTAAPESYSGKPGSLPLGPGPTNYGPGHCAQOVSYDPDTPETWG	EFPSHAGVYPTKALGTAYNQCPRLEHYG	QVQVKPEQG	817	
gi	73968515	ref	XP_858885.1	EPVVGTS--MIGSLNPMDFFP	ADITLG	YGGPEGAAAEPYGARGPGLPLGPGPTNYGPNPCQOVVSYPEPPEPWG	EFPSHAGVYPSKAPAGVYSQCPRLHYG	QVQVKPEQG	827	
gi	149944723	ref	NP_001092470.1	EPVVGTS--MMGSLNPMDFFP	ADITLG	YGGPEAAAAEPYGARGPGLPLGPGPTNYGPNPCQOVVSYSEPTPETWS	EFPSHAGVYPSKAPAGVYSQCPRLHYG	QVQVKPEQG	819	
gi	4885279	ref	NP_005260.1	EPVVGTS--MVGSLNPMDFFP	TDITLG	YGGPEGAAAEPYGARGPGLPLGPGPTNYGPNPCQOQASYPDTPQETWG	EFPSHAGVYPSKAPAGVYSQCPRLHYG	QVQVKPEQG	819	
gi	118119480	ref	XP_413682.1						566	
gi	30231244	ref	NP_840081.1	NTVGRQQGNMIPGGDRSYMGYQHNPQASQLSPGQESLGCIDQVYQSQMGGQYCREESCSLGVMGQADIANNLLQQAQAEYGMSTCQLSPGPHYPSGQDGSQGWGQTNQLHSPGMQYQAGMGGQHYTQGGIWDPSNPNLQRTVVKPEQF						1024



gi	90186273	ref	NP_034426.2	CP--VGS DSTGLAPCLNAHPSSESGPQPLF	HHPLPQPQYPOS GPYPQPPHG	YLSLEPRPGLNFPSSSHSTGOLKAQLVCNVVSOQELLWEGRRNGLPNC	ELPYQSPKFLGGGQ	937	
gi	62652273	ref	XP_345833.2	CP--VGS DSTGLAPCLNAHPSSESGPQPLF	HHSQLPPPOYLQSGPYQPPHD	CLSLESRRPGLNFPSS--HSTGOLKAQLVCNVVSOQELLWEGRRSRGGIPNC	ELPYQSPKFLGGGQ	933	
gi	73968515	ref	XP_858885.1	CP--VGS DSTGLAPCLNAHPSDGPHPQPLF	HYQPPPPQYPOS GAYTQPPPD	YLPSEPRPALDFDST--HSTGOLKAQLVCNVVSOQELLWEGRRGDPVVC	ELPYQSPKFLGGGQ	943	
gi	149944723	ref	NP_001092470.1	CP--VGS DSTGLAPCLNAHPSSESGPQPLF	HYQPPPPQYPOS GSYTQPPPD	YLPSEPRPALDFDSEPT--HSTGOLKAQLVCNVVSOQELLWEGRRGDPVVC	ELPYQSPKFLGGGQ	935	
gi	4885279	ref	NP_005260.1	CP--VGS DSTGLAPCLNAHPSSESGPQPLF	HYQPPSPPOYLQSGPYTQPPPD	YLPSEPRPALDFDSEPT--HSTGOLKAQLVCNVVSOQELLWEGRRGDPVVC	ELPYQSPKFLGGGQ	935	
gi	118119480	ref	XP_413682.1					566	
gi	30231244	ref	NP_840081.1	HPSPGGSSSCONTKALHQRNRHANNMOTYPLQCGIMNRRSSASDFHHSQMGTOPNQQGSGFSGTGINLALAESRRRQTPMHMKMMVVRNVVSOQALLWQEQEQSVSEKPDGMDMGOTQMMQHSPOHQANONLYVPGNTYCYGPNQN					1174



gi	90186273	ref	NP_034426.2	-VSSPAKTPAAAAA-YSGGFA-PASANKHSGSYAPAPSPCHETFTVG	VNRPSHRPAAPPR	LLPPLSPCYGPKLVGDINPSCG	HPEVGRLGAGPALYF	PPEGOVCNPLDSL	1045	
gi	62652273	ref	XP_345833.2	-VSSPAKTPAAAAA-YSGGFA-PASANKHSGSYAPAPSPCHETFTVG	VNRPPHRPAAPPR	LLPPLSPCYGPKLVGDANPSCG	HPEVGRLGAGPALYF	PPEGOVCNPLDSL	1043	
gi	73968515	ref	XP_858885.1	-VSSPAKGP---VAITYGPFPA-PNLPHKSGSYAPAPPCHENFTVG	ANKTSHRAAAPPR	LLPPLPTCYGTLKAGGTNPSCG	HPEVGRLGAGPALYA	PPEGOVCNPLDSL	1048	
gi	149944723	ref	NP_001092470.1	-VSSPAKAP---VAITYGPFPA-PNMPNHKSGSYAPAPPCHENFTVG	ANKASHRAAAPPR	LLPPLPACYGPKLVGDINPSCG	HPEVGRLGAGPALYF	PPEGOVCNPLDSL	1039	
gi	4885279	ref	NP_005260.1	-VSSPAKAP---VNTYGGPFG-PNLPHKSGSYAPAPPCHENFTVG	ANKASHRAAAPPR	LLPPLPTCYGPKLVGGTNPSCG	HPEVGRLGAGPALYF	PPEGOVCNPLDSL	1040	
gi	118119480	ref	XP_413682.1						566	
gi	30231244	ref	NP_840081.1	LMS PQQRNVPGSVKEQMGS CYGPDMPRPPQVRKSLSRQNSLQQAGGAYLGGPPHLSFVHSASPRRGVRLPPVQQQQQQQHQSENFNNNNNPNMYYSGQMMHMDLEKTPGGPCLAQOHLTSSDPITKPTISISYDPPAPMSNALEHL						1324



gi	90186273	ref	NP_034426.2	DLNLTQLDFVAILDEAG	LSPLSHEQGD	SSKNTPS	PSGPPNMAVGNMVSLLGSLPGETQFLNSSA	1111
gi	62652273	ref	XP_345833.2	DLNLTQLDFVAILDEAG	LSPPPHEQGD	SSKNTPP	PSGPPNMAVGNMVSLLGSLPGETQFLNSSA	1109
gi	73968515	ref	XP_858885.1	DLNLTQLDFVAILDEAG	LSPPPHEQGD	SSEHTPP	PSGPPNMAVGNMVSLLGSLPGETQFLNSSA	1114
gi	149944723	ref	NP_001092470.1	DLNLTQLDFVAILDEAG	LSPPPHEQGD	SSEHTPP	PSGPPNMAVGNMVSLLGSLPGETQFLNSSA	1105
gi	4885279	ref	NP_005260.1	DLNLTQLDFVAILDEAG	LSPPPHEQGD	SSEHTPP	PSGPPNMAVGNMVSLLGSLPGETQFLNSSA	1106
gi	118119480	ref	XP_413682.1					566
gi	30231244	ref	NP_840081.1	DLENAGIDFTSIIDQEPSSYSPIINAPIGHNCSEOTSRRLLTPONSITLPSGLSNMAIGDMSMLTLAGENKVLNTLE				1404

