

gi	6753456	ref	NP_034039.1	MGEFKVDKFNIEDFFSGDLD--IFNYSS--GMPSTLDPVAPCHSENLEINSYAVVVIYVVLVLLSLVGNLSLVMVLVILYNRSTCSVTDVYLLNLAIADLFFALILPVAASKVNG-WIFGSLCKVFSFLQBITFYSSVLLLACISMDRYL	145
gi	8393600	ref	NP_058879.1	MGEFRVDNFSLEDFFSGDID--SYNYSS--DPPFTLSDAAPCPANLDINRYAVVVIYVVLVLLSLVGNLSLVMVLVILYNRSTCSVTDVYLLNLAIADLFFALILPVAASKVNG-WIFGSLCKVFSFLQBITFYSSVLLLACISMDRYL	145
gi	4504683	ref	NP_001548.1	MEDFNMSDSFEDFWK-GED--LSNYSSSTLPPFLDAAAPCEPESLEINKYFVVIYALVFLLSLLGNLSLVMVLVILYSRVGRSVTDVYLLNLALADLFFALILPVAASKVNG-WIFGIFLCKVVSLLKEVNFYSGILLLACISVDRYL	146
gi	55616092	ref	XP_526026.1	MEDFNMSDSFEDFWK-GED--LSNYSSSTLPPFLDAAAPCEPESLEINKYFVVIYALVFLLSLLGNLSLVMVLVILYSRVGRSVTDVYLLNLALADLFFALILPVAASKVNG-WIFGIFLCKVVSLLKEVNFYSGILLLACISVDRYL	146
gi	57111005	ref	XP_536064.1	MEYNWWDNYSLEDLFGDIDN-YIYNTEM---PIIPADSAPCRPESLDINKYAVVVIYVVLVFNLLGNLSLVMVLVILYSRVSHSVTDVYLLNLAIADLFFALILPVAASKVNG-WIFGIFLCKVVSLLKEVNFYSGILLLACISMDRYL	144
gi	57111007	ref	XP_536065.1	MTVFMINMWNITDWNESABD-EFGDFEG---TPPEIYSPCKIDETLNKYAVVVIYALVFLLSLLGNLSLVMVLVILYSGIGHSVTDVYLLNLAIADLFFALILPVAASKVNG-WIFGIFLCKVVSLLKEVNFYSGILLLACISMDRYL	144
gi	155372285	ref	NP_001094755.1	MAEIKFTSNIRGFNWNYSDEDFGNYSYNLDLPSILTPSAPCRPEILDINKYAVVVIYALVFLLSLLGNLSLVMVLVILYSRIGRSVTDVYLLNLAMADLFFAMTLPVAASKAKG-WVFGIFLCKVVSLLKEVNFYSGILLLACISMDRYL	149
gi	27805943	ref	NP_776785.1	MTIILKDLNSNSIILWEGFED-EFGNYSG--TPPEIDYDYSPECETSITLNKYAVVVIDALVFLLSLLGNLSLVMVLVILYSRIGRSVTDVYLLNLAMADLFFAMTLPVAASKAKG-WVFGIFLCKVVSLLKEVNFYSGILLLACISMDRYL	146
gi	118112846	ref	XP_001236604.1	-----FTLMTLPCPTVKNLSVTLVVVIYIIVFCLLGLLNTVVIIVFVFMNRRRTSGLDLMLHLAVADLFLSLTLPFFVAVYLAHGHVFPFGITLCKMISGVQVETFYCSVFMLACISIDRYM	124
gi	189523763	ref	XP_001337093.2	-----FTLMTLPCPTVKNLSVTLVVVIYIIVFCLLGLLNTVVIIVFVFMNRRRTSGLDLMLHLAVADLFLSLTLPFFVAVYLAHGHVFPFGITLCKMISGVQVETFYCSVFMLACISIDRYM	124



gi	6753456	ref	NP_034039.1	AIVHATSILIQKRHLVKFVICIAMWLLSVILALPILILRNPKVKNLSLTVCYEDVGNN--TSRLRVVLRILPQTFGFLVPLLLIMLFCYGFILRLTLFKAHMGOKHRAMRVIFAVVLVFLLCWLPYNLVLFDTLMLRKLKIKETCERRDDIDKA	294
gi	8393600	ref	NP_058879.1	AIVHATSILIQKRHLVKFVICITMWFLLSVLVLSPIFILRTTVKANPSTVVCYENIGNN--TSKWRVVRILPQTFGFLVPLLLIMLFCYGFILRLTLFKAHMGOKHRAMRVIFAVVLVFLLCWLPYNLVLFDTLMLRKLKIKETCERRDINKA	294
gi	4504683	ref	NP_001548.1	AIVHATRILTKRHLVKFICLSIWGLSLLALPVLLFRRTVYSSNVSPACYEDMGNN--TANWRMLLRILPQTFGFLVPLLLIMLFCYGFILRLTLFKAHMGOKHRAMRVIFAVVLVFLLCWLPYNLVLLADTLMLRQVIQETCERRNHIDRA	295
gi	55616092	ref	XP_526026.1	AIVHATRILTKRHLVKFICLSIWGLSLLALPVLLFRRTVYSSNVSPACYEDMGNN--TANWRMLLRILPQTFGFLVPLLLIMLFCYGFILRLTLFKAHMGOKHRAMRVIFAVVLVFLLCWLPYNLVLLADTLMLRQVIQETCERRNHIDRA	295
gi	57111005	ref	XP_536064.1	AIVHATRILTKRHWVKFICLGIWALSLLSLPIFVFRRAINPPYSSPVCYEDMGAN--TKLRIVMRALPQTFGFLVPLMIMLFCYGLILRLTLFEAHMGOKHRAMRVIFAVVLVFLLCWLPYNLVLVADTLMLRQAIKETCORRNDIGRA	293
gi	57111007	ref	XP_536065.1	AIVHATRILTKRHWVKFICLGIWALSLLSLPIFVFRRAINPPYSSPVCYEDMGAN--TKLRIVMRALPQTFGFLVPLMIMLFCYGLILRLTLFEAHMGOKHRAMRVIFAVVLVFLLCWLPYNLVLVADTLMLRQAIKETCORRNDIGRA	293
gi	155372285	ref	NP_001094755.1	AIVHATRILTKRHWVKFICLGIWALSLLALPVIFFRRAIHPPYSSAVCYEDMGAN--TTKWRVMVRVLPQTFGFLVPLVLMVFCYGFILRLTLFSAQMGOKHRAMRVIFAVVLVFLLCWLPYNLVLVADTLMLRAHVIAETCORRNDIGRA	298
gi	27805943	ref	NP_776785.1	AIVHATRILTKRHWVKFICLGIWALSLLALPVIFFRRAIHPPYSSAVCYEDMGAN--TTKWRVMVRVLPQTFGFLVPLVLMVFCYGFILRLTLFSAQMGOKHRAMRVIFAVVLVFLLCWLPYNLVLVADTLMLRAHVIAETCORRNDIGRA	295
gi	118112846	ref	XP_001236604.1	-----XNEN--TKWRVVRVLPQTLGFALPLVLMVFCYGVTVHLLQTKNVQKRAMKVILAVVLVFLVCWLPYNIITLVSITLMLRTRAITETCERRKHIDTA	96
gi	189523763	ref	XP_001337093.2	AIVKATQFLNRKLLHLIGFVCAVWLCAALLSLPMVMHREAITVDGVEYICEDNVTAESTDSWRMSLRRIIRHILGFFLPLVMMVFCYGFIMFPLCHTRNSQRQKAMRVILSVLAFIICWLPYNIIEFTDILMRAGQVEETCOLLDNIDVA	274



gi	6753456	ref	NP_034039.1	LNATEILGFLHSCLNPLIYAFIQKFRHGLLKIMATYGLVSKFLAKEGRPSFVSSSSAN-TSTTL	359
gi	8393600	ref	NP_058879.1	LEATEILGFLHSCLNPLIYAFIQKFRHGLLKIMANYGLVSKFLAKEGRPSFVSSSSAN-TSTTL	359
gi	4504683	ref	NP_001548.1	LDATEILGILHSCLNPLIYAFIQKFRHGLLKILAIHGLISKDSLPKDSRPSFVSSSSGH-TSTTL	360
gi	55616092	ref	XP_526026.1	LDATEILGILHSCLNPLIYAFIQKFRHGLLKILAIHGLISKDSLPKDSRPSFVSSSSGH-TSTTL	360
gi	57111005	ref	XP_536064.1	LDATEILGFFHSCLNPLIYAFIQKFRHGLLKIMAFHGLISKEYLPLKDSRPSFVSSSSAN-TSTTF	358
gi	57111007	ref	XP_536065.1	LDATEILGFFHSCLNPLIYAFIQKFRHGLLKIMAFHGLISKEYLPLKDSRPSFVSSSSAN-TSTTF	358
gi	155372285	ref	NP_001094755.1	LDATEILGFLHSCLNPLIYVFIQKFRHGLLKIMAIHGLISKEYLAKDGRPSFVSSSSGN-TSTTL	363
gi	27805943	ref	NP_776785.1	LDATEILGFLHSCLNPLIYVFIQKFRHGLLKIMAIHGLISKEYLAKDGRPSFVSSSSGN-TSTTL	360
gi	118112846	ref	XP_001236604.1	LSITQVLGFAHSCINPLIYAFIQKFRNSFLKILAQRFISKDAVARYGRYSY-TSTGN-TSTTL	160
gi	189523763	ref	XP_001337093.2	LYATQVMFAHSCAINPLIYAFIQKFRNQLLISLFPKGLGRNMLSRYGAGSFGSFGSSTRQMSVTL	340

