

gi	6679120	ref	NP_032756.1	MLAGRAARTCALLAL-CLLGSQ-AQDFGPTRFICTSVPPVDADMCASVAAGG-AEELRSNVLQRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGPGEARSGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	147
gi	24308510	ref	NP_714957.1	MLAGRAARTCALLAL-CLLGER-AQDFGPTRFICTSVPPVDADMCASVAAGG-AEELRSNVLQRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGPGEARSGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	147
gi	55770878	ref	NP_002513.2	MPAGRAARTCALLAL-CLLGSQ-AQDFGPTRFICTSVPPVDADMCASVAAGG-AEELRSNVLQRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGPGEARSGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	147
gi	114670889	ref	XP_523739.2	MPAGRAARTCALLAL-CLLGSQ-AQDFGPTRFICTSVPPVDADMCASVAAGG-AEELRSNVLQRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGPGEARSGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	147
gi	73964857	ref	XP_540475.2	MPAGRAARTCALLAL-CLLGSQ-AQDFGPTRFICTSVPPVDADMCASVAAGG-AEELRSNVLQRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGPGEARSGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	147
gi	76669694	ref	XP_591233.2	MPAGRAARTCALLAL-CLLGSQ-AQDFGPTRFICTSVPPVDADMCASVAAGG-AEELRSNVLQRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGPGEARSGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	147
gi	47086163	ref	NP_998101.1	MEAGARGMHKLLLSCLLADGMSQDFGQTFICTSVPKDMDCAALQNSVPGDLKSTVMQLRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGPGEARSGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	147



gi	6679120	ref	NP_032756.1	EQYSRLNSSQTSNLKDLLQSKIDDLERQVLSRVNLTLEEGKGGPKNDTEERAKIESALTSLHQRISLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPFSYAVPGQANLVLEWGNPMEILIN	297
gi	24308510	ref	NP_714957.1	EQYSRLNSSQTSNLKDLLQSKIDDLERQVLSRVNLTLEEGKGGPKNDTEERAKIESALTSLHQRISLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPFSYAVPGQANLVLEWGNPMEILIN	297
gi	55770878	ref	NP_002513.2	EQYSRLNSSQTSNLKDLLQSKIDDLERQVLSRVNLTLEEGKGGPRNDTEERVKIEALTSLHQRISLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPFSYAVPGQANLVLEWGNPMEILIN	297
gi	114670889	ref	XP_523739.2	EQYSRLNSSQTSNLKDLLQSKIDDLERQVLSRVNLTLEEGKGGPRNDTEERVKIEALTSLHQRISLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPFSYAVPGQANLVLEWGNPMEILIN	297
gi	73964857	ref	XP_540475.2	EQYSRLNSSQTSNLKDLLQSKIDDLERQVLSRVNLTLEEGKGGPKNDTEERVKIESALTSLHQRISLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPFSYAVPGQANLVLEWGNPMEILIN	297
gi	76669694	ref	XP_591233.2	EQYSRLNSSQTSNLKDLLQSKIDDLERQVLSRVNLTLEEGKGGPKNDTEERVKIESALTSLHQRISLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPFSYAVPGQANLVLEWGNPMEILIN	297
gi	47086163	ref	NP_998101.1	EQFSRNNNSVQANSKDLLQSKIDDLERQVLSRVNLTLEEGKGGPRNESEQRGRVETLTSLHQRITDLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPFSYAVPGQANLVLEWGNPMEILIN	297



gi	6679120	ref	NP_032756.1	DKVAKLPFVINDGKWHHCIVTWTTRDGVWEAYQDGTGGNGENLAPYHPKPKGVLVLGQEQDITLGGGFDAQAFVGLAHFNIDWRKLTPEVYNLATCSSKALSGNVIWAESQIEIFGGATKWTFEACROIN	432
gi	24308510	ref	NP_714957.1	DKVAKLPFVINDGKWHHCIVTWTTRDGVWEAYQDGTGGNGENLAPYHPKPKGVLVLGQEQDITLGGGFDAQAFVGLAHFNIDWRKLTPEVYNLATCSSKALSGNVIWAESQIEIFGGATKWTFEACROIN	432
gi	55770878	ref	NP_002513.2	DKVAKLPFVINDGKWHHCIVTWTTRDGVWEAYQDGTGGSGENLAPYHPKPKGVLVLGQEQDITLGGGFDAQAFVGLAHFNIDWRKLTPEVYNLATCSTKALSGNVIWAESSHIEIYGGATKWTFEACROIN	432
gi	114670889	ref	XP_523739.2	DKVAKLPFVINDGKWHHCIVTWTTRDGVWEAYQDGTGGSGENLAPYHPKPKGVLVLGQEQDITLGGGFDAQAFVGLAHFNIDWRKLTPEVYNLATCSTKALSGNVIWAESSHIEIYGGATKWTFEACROIN	432
gi	73964857	ref	XP_540475.2	DKVAKLPFVINDGKWHHCIVTWTTRDGVWEAYQDGTGGNGENLAPYHPKPKGVLVLGQEQDITLGGGFDAQAFVGLAHFNIDWRKLTPEVYNLATCSSKALAGNVIWAESSHIEIYGGATKWTFEACROIN	432
gi	76669694	ref	XP_591233.2	DKVAKLPFVINDGKWHHCIVTWTTRDGVWEAYQDGTGGNGENLAPYHPKPKGVLVLGQEQDITLGGGFDAQAFVGLAHFNIDWRKLTPEVYNLATCSTKALSGNVIWAESSHIEIYGGATKWTFEACROIN	432
gi	47086163	ref	NP_998101.1	DKVAKLPFLINDGKWHHCIVTWTTRDGVWEAYQDGVMRNGDSLAPYHPKPKGVLVLGQEQDITLGGGFDAQAFVGLAHFNIDWRKLTPEVYNLATCSSKAQVGNVFSWLESHIEIYGGATKWTFEACROIN	432

