

gi	6679120	ref	NP_032756.1	MLAGRAARTCALLAL-CLLGSQ-AQDFGPTRFICTSVPPVDADMCAASVAAGG-AEELRNVQLRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGAGEARAGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	150
gi	24308510	ref	NP_714957.1	MLAGRAARTCALLAL-CLLGER-AQDFGPTRFICTSVPPVDADMCAASVAAGG-AEELRNVQLRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGAGEARAGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	150
gi	55770878	ref	NP_002513.2	MPAGRAARTCALLAL-CLLGSQ-AQDFGPTRFICTSVPPVDADMCAASVAAGG-AEELRNVQLRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGAGEARAGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	150
gi	114670889	ref	XP_523739.2	MPAGRAARTCALLAL-CLLGSQ-AQDFGPTRFICTSVPPVDADMCAASVAAGG-AEELRNVQLRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGAGEARAGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	150
gi	73964857	ref	XP_540475.2	MPAGRAARTCALLAL-CLLGSQ-AQDFGPTRFICTSVPPVDADMCAASVAAGG-AEELRNVQLRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGAGEARAGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	150
gi	76669694	ref	XP_591233.2	MPAGRAARTCALLAL-CLLGSQ-AQDFGPTRFICTSVPPVDADMCAASVAAGG-AEELRNVQLRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGAGEARAGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	150
gi	47086163	ref	NP_998101.1	MEAGARGMHWKLLLSCLLADGMSQDFGQTFICTSVPKDMDCAALQNSVPGDELKSTVMQLRETVLQOKETILSQKETIRELTAKLGRCESQSTLDAGAGEARAGGGRKOPGSGKNTMGDLRTPAETLSOLGOTLQSLKTRLENL	150



gi	6679120	ref	NP_032756.1	EQYSRLNSSSQTNLSKDLLQSKIDDLERQVLSRVNTLEEGKGGPKNDTEERAKIESALTSLHQRISLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPPFSYAVPGQANLVLEWGNPMEILIN	300
gi	24308510	ref	NP_714957.1	EQYSRLNSSSQTNLSKDLLQSKIDDLERQVLSRVNTLEEGKGGPKNDTEERAKIESALTSLHQRISLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPPFSYAVPGQANLVLEWGNPMEILIN	300
gi	55770878	ref	NP_002513.2	EQYSRLNSSSQTNLSKDLLQSKIDDLERQVLSRVNTLEEGKGGPKNDTEERAKIESALTSLHQRISLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPPFSYAVPGQANLVLEWGNPMEILIN	300
gi	114670889	ref	XP_523739.2	EQYSRLNSSSQTNLSKDLLQSKIDDLERQVLSRVNTLEEGKGGPKNDTEERAKIESALTSLHQRISLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPPFSYAVPGQANLVLEWGNPMEILIN	300
gi	73964857	ref	XP_540475.2	EQYSRLNSSSQTNLSKDLLQSKIDDLERQVLSRVNTLEEGKGGPKNDTEERAKIESALTSLHQRISLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPPFSYAVPGQANLVLEWGNPMEILIN	300
gi	76669694	ref	XP_591233.2	EQYSRLNSSSQTNLSKDLLQSKIDDLERQVLSRVNTLEEGKGGPKNDTEERAKIESALTSLHQRISLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPPFSYAVPGQANLVLEWGNPMEILIN	300
gi	47086163	ref	NP_998101.1	EQFSRNNNSVQANSKDLLQSKIDDLERQVLSRVNTLEEGKGGPKNDTEERAKIESALTSLHQRISLEKGGKDNRPDGFOLFPLRLTNYMYAKVKKSLPEMYAFTVCMWLKSSAAPGVGTPPFSYAVPGQANLVLEWGNPMEILIN	300



gi	6679120	ref	NP_032756.1	DKVAKLPFVINDGKWHHCIVTWTTRDGVWEAYQDGTGGNGENLAPYHPKPKGVVLVGGQEDTLGGGFDAQAFVGLAHFNIDWRKLTPEVYVNLATCSSKALSGNVIWAESQIEIFGGATKWTFEACROIN	435
gi	24308510	ref	NP_714957.1	DKVAKLPFVINDGKWHHCIVTWTTRDGVWEAYQDGTGGNGENLAPYHPKPKGVVLVGGQEDTLGGGFDAQAFVGLAHFNIDWRKLTPEVYVNLATCSSKALSGNVIWAESQIEIFGGATKWTFEACROIN	435
gi	55770878	ref	NP_002513.2	DKVAKLPFVINDGKWHHCIVTWTTRDGVWEAYQDGTGGNGENLAPYHPKPKGVVLVGGQEDTLGGGFDAQAFVGLAHFNIDWRKLTPEVYVNLATCSSKALSGNVIWAESQIEIFGGATKWTFEACROIN	435
gi	114670889	ref	XP_523739.2	DKVAKLPFVINDGKWHHCIVTWTTRDGVWEAYQDGTGGNGENLAPYHPKPKGVVLVGGQEDTLGGGFDAQAFVGLAHFNIDWRKLTPEVYVNLATCSSKALSGNVIWAESQIEIFGGATKWTFEACROIN	435
gi	73964857	ref	XP_540475.2	DKVAKLPFVINDGKWHHCIVTWTTRDGVWEAYQDGTGGNGENLAPYHPKPKGVVLVGGQEDTLGGGFDAQAFVGLAHFNIDWRKLTPEVYVNLATCSSKALSGNVIWAESQIEIFGGATKWTFEACROIN	435
gi	76669694	ref	XP_591233.2	DKVAKLPFVINDGKWHHCIVTWTTRDGVWEAYQDGTGGNGENLAPYHPKPKGVVLVGGQEDTLGGGFDAQAFVGLAHFNIDWRKLTPEVYVNLATCSSKALSGNVIWAESQIEIFGGATKWTFEACROIN	435
gi	47086163	ref	NP_998101.1	DKVAKLPFLINDGKWHHCIVTWTTRDGVWEAYQDGVMRNGDSLAPYHPKPKGVVLVGGQEDTLGGGFDAQAFVGLAHFNIDWRKLTPEVYVNLATCSSKALSGNVIWAESQIEIFGGATKWTFEACROIN	435

