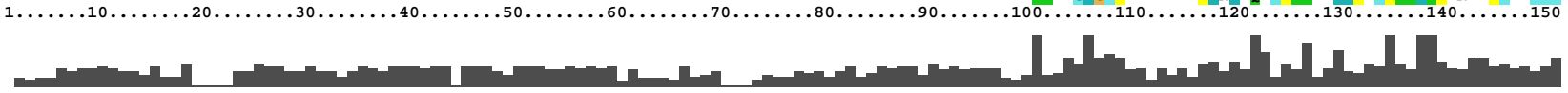


gi	73976148	ref	XP_539484.2	MDNARMSFLEYPIILSGG---DSGTC SARAYPSDHGITTFOQ-CAVSANS CGGDDRFLVGRGVQISPP---HHHHHHHPQAATYQTPGNLGVSYSHSSCGPSYGAONFGAPYSPYALNQEAEVSGGYPCAPAAYSGNLSSPMVQH	142
gi	76615431	ref	XP_618076.2	MDNARMSFLEYPIILSGG---DSGTC SARAYPSDHGITTFOQ-CAVSANS CGSDDRFLVGRGVQISPP---HHHHHHHPQPTTYQTSGNLGVSYSHSSCGPSYSAONFGAPYSPYALNQEAEVSGGYPCAPAVYSGNLS	142
gi	5031761	ref	NP_005513.1	MDNARMSFLEYPIILSGG---DSGTC SARAYPSDHGITTFOQ-CAVSANS CGGDDRFLVGRGVQISPP---HHHHHHHPQPAATYQTSGNLGVSYSHSSCGPSYSONFSAFYSPYALNQEADVSGGYPCAPAVYSGNLS	144
gi	55628252	ref	XP_519009.1	MDNARMSFLEYPIILSGG---DSGTC PARAYPSDHGITTFOQ-CAVSANS CGGDDRFLMGRGVQIGSP---HHHHHHHPQPAATYQTSGNLGVSYSHSSCGPSYSONFSAFYSPYALNQEADVSGGYPCAPAVYSGNLS	144
gi	84000011	ref	NP_034579.2	MDNARMSFLEYPIILSGG---DSGTC SARAYPSDHGITTFOQ-CAVSANS CGGDDRFLVGRGVQISPPHHHHHHHPQATYQTSGNLGVSYSHSSCGPSYGAONFSAFYSPYALNQEADVSGGYPCAPAVYSGNLS	145
gi	6981040	ref	NP_037207.1	MDNARMSFLEYPIILSGG---DSGTC SARAVYSSDHGITTFOQ-CAVSANS CGGDDRFLGGRGVQISPP---HHHHHHHPQPAATYQTSGNLGVSYSHSSCGPSYGAONFSAFYSPYALNQEADVSGGYPCAPAVYSGNLS	143
gi	18858823	ref	NP_571611.1	---MSFLDFSSISGGGDSGSCSVRAFPHDGLSTFOSSCAVRLNSCSGDERFMSN---ISSQ---DVINSQPQAGSYQSPGTLSTIY---SAHPSYGTQSFCTGYNHYALNQDVESVSPFCGGLVYSGNISSTVQHRH	134
gi	17552734	ref	NP_498655.1	-----MSSTECYGAPE-----PHNYQDWPITHSYVPSVPSYSPLNHHHPADIWAA	45



gi	73976148	ref	XP_539484.2	HHQGYAGGAVGSP---QYIHHSYGO--EHOSLALAT-YNNSLSPHASHQEACRSPASETSSPAQTFDWMKVKRNPPKTKGVGEYGVVGPNAVRTNFTTKQLTELEKEFHFNKYLTRARRVEIAASLQLNETQVKIWFQRRMKQKKRE	286
gi	76615431	ref	XP_618076.2	HHQGYAGGAVGSP---QYIHHSYGO--EHOSLALAT-YNNSLSPHASHQEACRSPASETSSPAQTFDWMKVKRNPPKTKGIGEYGVVGPNAVRTNFTTKQLTELEKEFHFNKYLTRARRVEIAASLQLNETQVKIWFQRRMKQKKRE	286
gi	5031761	ref	NP_005513.1	HHQGYAGGAVGSP---QYIHHSYGO--EHOSLALAT-YNNSLSPHASHQEACRSPASETSSPAQTFDWMKVKRNPPKTKGVGEYGVVGPNAVRTNFTTKQLTELEKEFHFNKYLTRARRVEIAASLQLNETQVKIWFQRRMKQKKRE	288
gi	55628252	ref	XP_519009.1	HHQGYAGGAVGSP---QYIHHSYGO--EHOSLALAT-YNNSLSPHASHQEACRSPASETSSPAQTFDWMKVKRNPPKTKGVGEYGVVGPNAVRTNFTTKQLTELEKEFHFNKYLTRARRVEIAASLQLNETQVKIWFQRRMKQKKRE	288
gi	84000011	ref	NP_034579.2	HHQGYAGGAVGSP---QYIHHSYGO--EHOSLALAT-YNNSLSPHASHQEACRSPASETSSPAQTFDWMKVKRNPPKTKGVGEYGVVGPNAVRTNFTTKQLTELEKEFHFNKYLTRARRVEIAASLQLNETQVKIWFQRRMKQKKRE	289
gi	6981040	ref	NP_037207.1	HHQGYAGGAVGSP---QYIHHSYGO--EHOSLALAT-YNNSLSPHASHQEACRSPASETSSPAQTFDWMKVKRNPPKTKGVGEYGVVGPNAVRTNFTTKQLTELEKEFHFNKYLTRARRVEIAASLQLNETQVKIWFQRRMKQKKRE	286
gi	18858823	ref	NP_571611.1	HRHGYSGNVHLHGQFYGSATYGNSSDQANLTFVAGCSNPLSPLVPHHDACCSPLSDGVPTGQTFDWMKVKRNPPKTKGAGEYGFVGPNTVTRNFTTKQLTELEKEFHFNKYLTRARRVEIAASLQLNETQVKIWFQRRMKQKKRE	284
gi	17552734	ref	NP_498655.1	HPSNYIMG---NGHVSPPATASGLSPASRSNSSAELPPTGVNASQHNLYKWMHTKRS--QRPAPKKKVIDENGINRNTFTTQHLTELEKEFHFNKYLTRARRVEIASNLKQEAQVKIWFQRRMKQKKRE	173



gi	73976148	ref	XP_539484.2	KEGLLPISPATPPGSEKAEESSEKSSSSPCIPSPGSSTSDILTTSH	333
gi	76615431	ref	XP_618076.2	KEGLLPISPATPPGSEKAEESSEKSSSSPCVPSPGSSTSDILPTSH	333
gi	5031761	ref	NP_005513.1	KEGLLPISPATPPGNDEKAEESSEKSSSSPCVPSPGSSTSDILTTSH	335
gi	55628252	ref	XP_519009.1	KEGLLPISPATPPGNDEKAEESSEKSSSSPCVPSPGSSTSDILTTSH	335
gi	84000011	ref	NP_034579.2	KEGLLPISPATPPGSEKAEESSEKSSSPSPASPASSTSDILTTSH	336
gi	6981040	ref	NP_037207.1	KEGLLPISPATPPGSEKAEESSEKSSSPSPASPASSTSDILTTSH	333
gi	18858823	ref	NP_571611.1	KEGLLPKLSSEQDGLKTDAAEKSPAPSIPSP-SPVVAYSN-	329
gi	17552734	ref	NP_498655.1	KE-----KAFIARNWESNSPISSCGEGDVKNFK-	202

