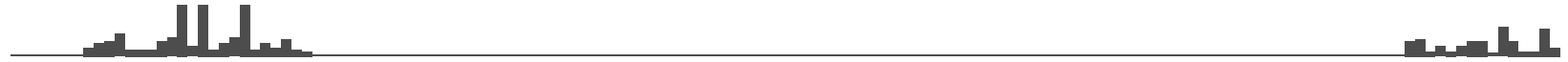


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gi	118082422	ref	XP_425441.2	-----MATSRRADRALLLLLLCLPGLR-----	-----RGALGGGQRPGCLAP	39
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gi	31222076	ref	XP_317111.1	MAIRIINHQTVVKGHVVLVLLVLLFC-----	-----CRHRACGLAPTAQTIGQIKIMLKESELLIPSMDDPEKEAKAMYEKALQOYG-----	93



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gi	119891803	ref	XP_598424.3	CQCEPDGRMLLRVDCSDLGLSELPSNLSVFTSYLDLSMNNISQLPPSPLSLRFLLEELRLAGNALTYIPKGAFTGLYSKLVLMLONNHLRQVTEALONLRSLOSLRLDANHISVPPSCFSGLSLRLHLWDDNALTEIPVQAFRSLSA	187
gi	110624772	ref	NP_034325.2	CHCEPDGRMLLRVDCSDLGLSELPSNLSVFTSYLDLSMNNISQLPASLLHRLCFLEELRLAGNALTYIPKGAFTGLYSKLVLMLONNQLRQVPEEALONLRSLOSLRLDANHISYVPPSCFSGLSLRLHLWDDNALTEIPVQAFRSLSA	187
gi	109480521	ref	XP_235149.4	CHCEPDGRMLLRVDCSDLGLSELPSNLSVFTSYLDLSMNNISQLPASLLHRLCFLEELRLAGNALTYIPKGAFTGLYSKLVLMLONNQLRQVPEEALONLRSLOSLRLDANHISYVPPSCFSGLSLRLHLWDDNALTEIPVQAFRSLSA	187
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gi	110624772	ref	NP_034325.2	LQAMTLALNKIHHIADYAFGNLSSLVVLHLENNRIHSLGKKCFDGLHSLETLDLNYNNLDEFPPTAIRTLNKLKELGFHSNNIRSIPEKAFVGNPSLITTHFYDNPVQVGRSAFQHLPELRTLNLNGASQITEFPDLTGANLESLLTG	337
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gi	19550088	ref	NP_599104.1	LEALNLGSLLLIINDEDFRMPNLIIVLLKRNQIMKISAGALKNLTKLVLELDLNLSSLPGLSKLSQLELSITSNLRWINDTELPSS--MQMLDMRANPLSISPGAFRCMSKLRKLLSDVRTLRSFPELEACHALITLKLDR	448
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gi	19550088	ref	NP_599104.1	AGIQEVPANLCRTPRLKSLKLNLSLKRIPNLSACRDLRLLDLSNQIEKIQCKPFNGLKQLNDLLLSYRIRKALPDAFQGIPLKQLLDLEGNEISYHKCAFSGTALDNLGNLIPPELPSGLRALHLKIFNPKLREFPPDP	598
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gi	19550088	ref	NP_599104.1	TFPRIDTLILSYAHCCAFPLVAMSSGK-KTSQVQEAFLVFPDAEFDMLWNSMMLIWPQMHNSLQLGASMHDPWEIATNFNEBQLQOTQCGIATSYMEEYFEEHDSGAPATGYGFCITGLFSQMSIEDFQGSVGLPMPGFPLPC	747
gi	31222076	ref	XP_317111.1	AFPRIDTLVLSYAHCCSFLPLTALPKVPTNFNIRENVLPDNEFDMSLWNSMMLIWPQMHNSLQLGASMHDPWEIATNFNEBQLQOTQCGIATSYMEEYFEEHDSGAPATGYGFCITGLFSQMSIEDFQGSVGLPMPGFPLPC	672



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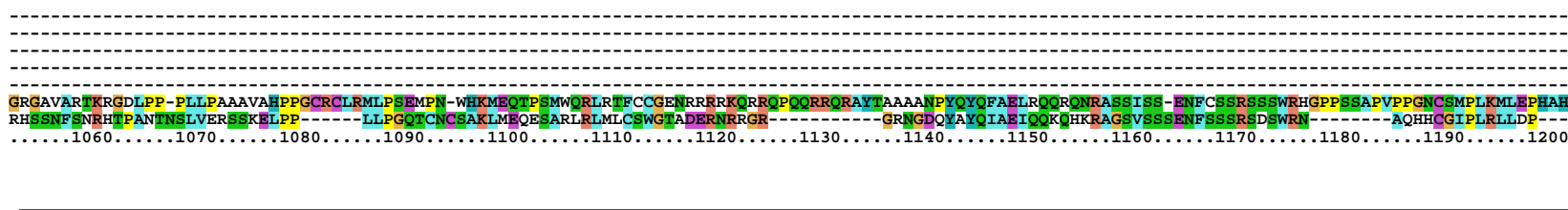
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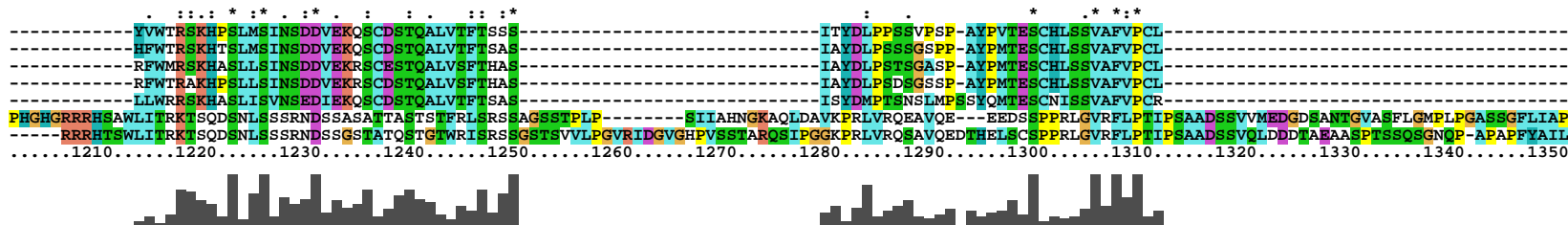
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