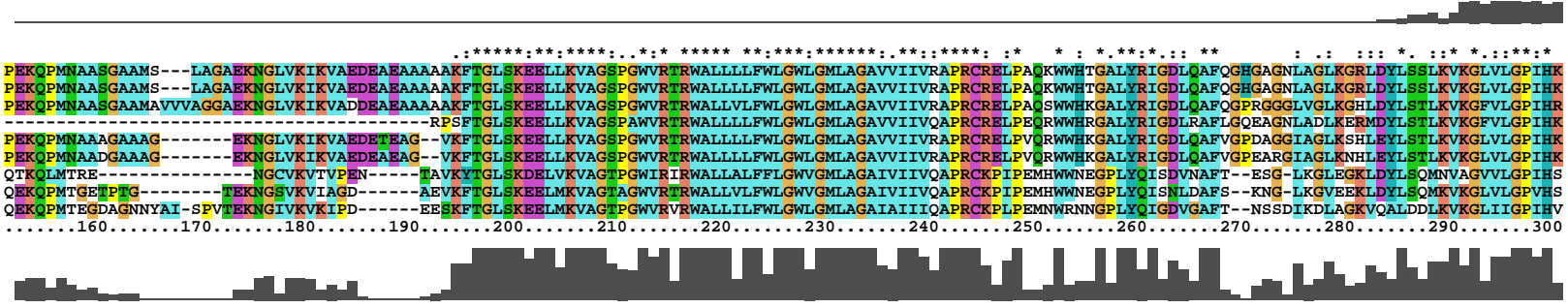


gi | 61744475 | ref | NP_001012679.1 | MELOPPEASIAVAVV... 150
gi | 114638128 | ref | XP_001159413.1 | MELOPPEASIAVAVV... 150
gi | 73983790 | ref | XP_540898.2 | MTAEVVAARGGVRRGRADAER... 150
gi | 66792754 | ref | NP_001019659.1 | MVWLRSRWPTTR... 150
gi | 31560670 | ref | NP_032603.2 | ... 150
gi | 9506891 | ref | NP_062156.1 | ... 150
gi | 121583699 | ref | NP_001073552.1 | ... 150
gi | 18859381 | ref | NP_571676.1 | ... 150
gi | 41393185 | ref | NP_958922.1 | ... 150



gi | 61744475 | ref | NP_001012679.1 | NQKDDVAQTDLLQIDPNFSGKEDFD... 450
gi | 114638128 | ref | XP_001159413.1 | NQKDDVAQTDLLQIDPNFSGKEDFD... 450
gi | 73983790 | ref | XP_540898.2 | NQKDDLSGTNLEQIDPTFSGKEDFD... 450
gi | 66792754 | ref | NP_001019659.1 | HSSLTGNHTNFLVTOYLDAFGNSWCS... 450
gi | 31560670 | ref | NP_032603.2 | NSTFTGERTESLVRFRLNAGSQCWCS... 450
gi | 9506891 | ref | NP_062156.1 | QPVFTGEHAELLVIKYLNAIGSRWCS... 450
gi | 121583699 | ref | NP_001073552.1 | SD--SGERQAQIIFKFNSSITQTS... 450
gi | 18859381 | ref | NP_571676.1 | AG--LSGRQATLMQRLECSGHEASL... 450
gi | 41393185 | ref | NP_958922.1 | SK--VREVAQAVESLSTYNSQRLAW... 450



gi | 61744475 | ref | NP_001012679.1 | RHWDQNERFLVVLNFGDVGLSAGLQ... 679
gi | 114638128 | ref | XP_001159413.1 | RHWDQNERFLVVLNFGDVGLSAGLQ... 679
gi | 73983790 | ref | XP_540898.2 | RQWDQNERFLVVLNFGDVGQLAKL... 679
gi | 66792754 | ref | NP_001019659.1 | RQWDQNERFLVVLNFGDVGQLAKL... 679
gi | 31560670 | ref | NP_032603.2 | RHWDQNERFLVVLNFRDGRSARL... 679
gi | 9506891 | ref | NP_062156.1 | RHWDQNERFLVVLNFGDVGLSAGL... 679
gi | 121583699 | ref | NP_001073552.1 | RVWDQSKRFITALNMG----DKP... 679
gi | 18859381 | ref | NP_571676.1 | RLWDQSERFMVAVNWG----NDS... 679
gi | 41393185 | ref | NP_958922.1 | RLWDQNERFLVLLNHWHS----N... 679

