

gi	6754956 ref NP_035149.1	HMLLQIILPMLCVLLSIIVCYWKSCQWVKEKCYPDIPNPKSSILSLIKSKKNP-HLIMNVKDCIPDVLEVINKAEGSKTQCVGSGKLEHIEDVPTKP---PIVPTKDSGQVPCIFFENFTYDQSAFDSGSHGLIPGLKDTAHLGLL	900
gi	52851389 ref NP_001005384.1	HMLLQIILPMLGVFLSIIVCYWKSCQWVKEKCYPDIPNPKSSILSLIKSKKNP-HLIMNVKDCIPDVLEVINKAEGSKTQCVGSGKLEHIEDVPTKP---PLVPTKDSGPMFVFLFNFTYDQSAFDSGSHGFIPGLKNTPHQLGLL	900
gi	4557040 ref NP_003990.1	SMLIHILLPMVFCVLLIMVMCYLKSQWIKETCYPDIPDPYKSSILSLIKFKENPHLIIMNVSDCIPDAIEVVSKEGPKTIQFLGTRKSLTETELTKPNLYLLPTEKNHSGPGPCICFENLTYNQAAASDSGSCGHVPVSPK-APSMLGLM	900
gi	114600500 ref XP_001141406.1	SMLIHILLPMVFCVLLIMVMCYLKSQWIKETCYPDIPDPYKSSILSLIKFKENPHLIIMNVSDCIPDAIEVVSKEGPKTIQFLGTRKSLTETELTKPNLYLLPTEKNHSGPGPCICFENLTYNQAAASDSGSCGHVPVSPK-APSMLGLM	900
gi	73954301 ref XP_546341.2	PMLIRIILPMIFCILLIMLICYLKSQWVKEKCYPDIPDPYKSSVLSLIKSKENPRLTIMNIRKDCVPTIEVVNKHEG-----TGKSPTEPEAAKPTVLYLLPAEESYSGPGPCICFENLTYNQAAASDSGSCGHVPVPTK-APSQLGLL	900
gi	122692559 ref NP_001073741.1	-----	900
gi	118103710 ref XP_425020.2	-----	900
	760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900	



gi	6754956 ref NP_035149.1	APPNKFQNVLKNDYMKPLVESPTFEETSLIYVSQLASPMCGDKDNLAEPPVPVHGSEYKRMVVPGLASPLKEDNSLSTVLLGQGEQ--	992
gi	52851389 ref NP_001005384.1	APPNKLQNVLENDYMKPLVESPTFEETSLIYVSQLASPMCGDKDSLVTNPPMPVHGSEYKRMALPGSLTSASLKENN-LTS-----	992
gi	4557040 ref NP_003990.1	TSPENVLKALEKNYINSLGEIPAGESSLNYVSQLASPMFGDKDSLPTNPVEAPHCSEYKRMMAVSLRLALPPPTESSLSSTILLDPGEHYC	992
gi	114600500 ref XP_001141406.1	TSPENVLKALEKNYINSLGEIPAGESSLNYVSQLASPMFGDKDSLPTNPVEAPHCSEYKRMMAVSLRLALPPPTESSLSSTILLDPGEHYC	992
gi	73954301 ref XP_546341.2	TSPENLLTALAKNCMNSLEEIPAGESSLNYVSQLASPMVSGDKDSLPTNPPOPELCSSEYKRMMAIPLGLAAPSSSGSSLSSTILLDEGEHYH	992
gi	122692559 ref NP_001073741.1	-----	992
gi	118103710 ref XP_425020.2	-----	992
	910.....920.....930.....940.....950.....960.....970.....980.....990..	

