

gi	21704108	ref	NP_663537.1	-MVCKVLLIALCIFAAGLRVQGSPT-VPLPVSLMTKSSAPVAIWTTSAPHTARATTPVAEATHNAEVLRTAAASLTSQLP---DHRREEAVTSPPLKRDVNSIDSSPAGFPSTSDGHLAPTPEEHSLSPEATVPAATGSSQ-----F	137
gi	27465557	ref	NP_775137.1	-MVCKALITLFCIFAAGLMVQGSPTPLLVSLLTKSTAPMATWTTSAOHTAMATTPVAEATHNAEVLRTAAASLTSQLP---DHRREEAVTSPPLKRDVNSIDSSPAGFPSTSDGHLAPTPEEHSLSPEATVPAATGSSQ-----F	138
gi	54400758	ref	NP_056208.2	-MVYKTLFALCILTAGWRVQSLPTSAPLSVSLPTNIVPPTTIWTSPPONIDADTASPNGTNNNSVLPVTASAPTSLLPKNIEESREEEITSPGNSWEGINTDPPSPGFSSTSGGVHLTTLEEHSSGTPEAGVAATLSQSAE---PP	146
gi	114594244	ref	XP_001155067.1	-MVYKTLFALCILTAGWRVQSLPTSAPLSVSLPTNIVPPTTIWTSPPONIDADTASPNGTNNNSVLPVTASAPTSLLPKNIEESREEEITSPGNSWEGINTDPPSPGFSSTSGGVHLTTLEEHSSGTPEAGVAATLSQSAE---PP	146
gi	115494988	ref	NP_001069239.1	-MVCKTLFALCIFTAGLRVQSVSASIPSTDSLLAEITPTAIWTSPPQ---SPPASPTSGFSNSVLLDPTVPVPTSLPTKNISTEPREEQSTSPASNWEG---TDPSP---TSGGVHLTPTPEEHSSTPEAGVPTTGSQPPAE---SP	136
gi	118089990	ref	XP_429964.2	MHPDLAVRPAALVPCRNYQKLDSSWPAALPALQDSYEFAPDFQADHGGAAGLKDQTPGLGDDPVAPSLAPFPVVGTSAGPGSGGTPVPLAAPHQSTPLAVGPTNNGVSPVGDNRGSTTAMLSRASTLTNTVTAADSPSVAPSSVPP	150



gi	21704108	ref	NP_663537.1	MLLSQCAPTSATTSPANLSE-----LSASVTSSHNSIVANIQPTA--APMAPASPTPEEHSSSHPTSHVIAEPVPEKESQDPEPKVIC-----ESETTTPFLIMQEVENALSSGIAAIVTVIAVLLVFGAAAYLKIRH	270
gi	27465557	ref	NP_775137.1	MLLSQCAPTSATTSPANLSE-----LSASVTSSHNSIVANIQPTA--APMAPASPTPEEHSSSHPTSHVIAEPVPEKESQDPEPKVIC-----ESETTTPFLIMQEVENALSSGIAAIVTVIAVLLVFGAAAYLKIRH	270
gi	54400758	ref	NP_056208.2	LLISPOAPASSPSSLSLTPPEV-----FSASVTNHSSIVTSTQPTG--APTAPESPTPEEHSSDHTPTSHAVIAEPVPEKESQDPEPKVIC-----ESETTTPFLIMQEVENALSSGIAAIVTVIAVLLVFGAAAYLKIRH	284
gi	114594244	ref	XP_001155067.1	LLISPOAPASSPSSLSLTPPEV-----FSASVTNHSSIVTSTQPTG--APTAPESPTPEEHSSDHTPTSHAVIAEPVPEKESQDPEPKVIC-----ESETTTPFLIMQEVENALSSGIAAIVTVIAVLLVFGAAAYLKIRH	284
gi	115494988	ref	NP_001069239.1	LLISPOAPASSPSSLSLTPPEV-----FSASVTNHSSIVTSTQPTG--APTAPESPTPEEHSSDHTPTSHAVIAEPVPEKESQDPEPKVIC-----ESETTTPFLIMQEVENALSSGIAAIVTVIAVLLVFGAAAYLKIRH	274
gi	118089990	ref	XP_429964.2	MLETVLSPWTAHSSVARGTIDLCTNPSPVDPTSFSSSSPHNSTLHSSPGTALLSPAIPATQPPGLTKDVPPEPGLAVAPSLAMEPHSPEVTAASPTKGMABEGRKTPSTGVITIEVPHALSAGSIVAVTVIVVVVLLVFGAAAYLKIRH	300



gi	21704108	ref	NP_663537.1	SSYGRLLDDHDYG--SWGNYNNPLYDSS	296
gi	27465557	ref	NP_775137.1	SSYGRLLDDHDYGSWGNYNNPLYDSS	298
gi	54400758	ref	NP_056208.2	SSYGRLLDDHDYG--SWGNYNNPLYDSS	310
gi	114594244	ref	XP_001155067.1	SSYGRLLDDHDYG--SWGNYNNPLYDSS	310
gi	115494988	ref	NP_001069239.1	SSYGRLLDDHDYG--SWGNYNNPLYDSS	300
gi	118089990	ref	XP_429964.2	SSYGRLLDDHDYG--SWGNYNNPLYDSS	326

