

AAM76341	128	FVTDHELVAFFGIQLIGYHRLPELSMFWEQQPDTGLG.LGI IQ
AAM76342	128	FVTDHELVAFFGIQLIGYHRLPELSMFWEQQPDAGLG.LGI IQ
ABS18391	163	LKDISASYRDINTMEI WALVGILTLTAVMKD.NHLSTDELFDATFSG..TRYV
BAD07480	170	TAA.ENSSAETSFYMQETTLCELKALIALLYLAGLIKS.NRQSLKDLWRTDGTG.VDI FR
BAD11135	170	TAA.ENSSAETSFYMQETTLCELKALIALLYLAGLIKS.NRQSLKDLWRTDGTG.VDI FR
BAD11136	1	
BAF82017	163	RPL.P..EYSQAQEHPTNITHEMKRFLALTITAMGLHT..DGNLASYWDTTTVIS.IPLFS
BAF82019	151	NPL.P..GFSRAQAYPTNINETKRFLALTITAMGLVE..RNSLASYWDNTTVLS.IPLFS
BAF82020	151	HPL.P..GYSRAHAAYPTNVGETKRFLALTITAMGLVE..RNTLASYWDTTTVLS.IPLFS
BAF82021	153	HSL.P..VYSRAQAYPTNVNETKKFLALTITAMGLVE..LNTIASYWDTTTVIS.VPLFS
*BAF82022	145	NPL.P..RYARAHAWHPTDIAEMKRFGVGLTITAMGLIK..ANSLESYWDTTTVLS.IPVFS
BAF82025	145	NPL.P..RYARAHAWHPTDIAEMKRFGVGLTITAMGLIK..ANSLESYWDTTTVLS.IPVFS
CAF99963	194	HQKQRTITRODMYSFLALVLYMGVMP..LKAMTDFWKGSRLYS.LPFPS
CAI18712	172	LSLTAQELKCVLGILILSGYISYPRRRMFWETSP..DSH.HHIVA
NP_689808	135	PPG.PK.GFSRMDKIKDITDNDELKVFVAVMLLOGIVQ..KPELEMFWSTRPLLD.TPYLR
NP_741958	38	FGSDGAVEVTLAEMKAFILGYVISTSVS...HCESVLSIWSGGFYS.NRSLA
*PIGGYBAC-ORF	161	ESMTGATERTDITNEDEIYAFFGILVMTAVRKD.NHMSTDDLDFDRSLs...MVYV
Q8N328	173	LGLTSSEFKCFLGIIIFLSGYVSVPRRRMFWEQR..TDVH.NVLVS
Q8N414	183	FGSDGAVEVTLTETMKAFILGYMISTSTIS...HCESVLSIWSGGFYS.NRSLA
Q96JS3	450	LEVTVQEMRCVFGVLLLSGFMRHPRREMYWEVS...DTD.QNLVR
XP_001030237	159	ALLNLPPDKTLPKEAMDIDSIDLDAYLSILITFMGVQR.....MKS VKA
XP_001541487	85	N.....SAINPREWQPTITSTEIKVFLGQIIMGVHR..SPAIGDYWNRNDVQGPVHSSR
XP_001599370	1	MILMGTHK..LPRVRNYWSSDPFLK.VDCVA
XP_312615	142	YARERDANPTDEMETMALGLVLYIAGTVRDGRENTERLFDTKMGTG.LEAVY
XP_590785	173	LGLTAQELKCVLGILILSGYISYPRRRMFWETSP..DSH.HHIVA
XP_699416	155	AAIKDLWDITDLQAFTIGILILIGVYRSKHESVDSLWDG..VLG.RPIFR
XP_797885	179	LG..VLQQHSRLNKITEITADEMKVETALQISMLVT..KPAITHMYWEENWLIG.TPGFS
consensus	481	y t elk fvgililigvmr m l i

AAM76341	171	QAMTRERERFKFISKHACASPWDDVDPNSSDDPDQEPERPDPIRKIRPLVKRLNESYHVCRK
AAM76342	171	QAMTRERERFKFISKHACASPWDDVDPNSSDDPDQEPERPDPIRKIRPLVKRLNERYHACRK
ABS18391	213	SVMSREREFELIRCLRMDDK.....TLRPTLRSDDAFLPVRKIWEIFINQCRQNHV
BAD07480	227	TTMSLQRFQFLQNNIRFDDK.....STRDERKQTDNMAAFRSIFDQFVQCCQNAYS
BAD11135	227	TTMSLQRFQFLQNNIRFDDK.....STRDERKQTDNMAAFRSIFDQFVQCCQNAYS
BAD11136	1	
BAF82017	217	AVMPNRNYQILRLFLHFNDNAT.....AAPPNEPGHDLRLHKLRLPLIESLCKCFAEVYT
BAF82019	205	AVMARNRYQILRLFLHFNDNTT.....AVAPNEPGYDRLYKLRPLIDSLSQRFAEVYT
BAF82020	205	AVMPNRNYQILRLFLHFNDNAA.....AVPPNEPGHDLRLYKLRPLIDSLSQRFAEVYT
BAF82021	207	AVMPNRNYQILRLFLHFNDNAA.....AVPPNEPGHDLRLYKLRPLIDSLSQRFAEVYT
*BAF82022	199	ATMSRNRYQLRLRLHFNNNAT.....AVPPDQPGHDLRLHKLRLPLIDSLSERFAAVYT
BAF82025	199	ATMSRNRYQLRLRLHFNNNAT.....AVPPDQPGHDLRLHKLRLPLIDSLSERFAAVYT
CAF99963	241	SVMPNTRFLATSRSLHMNDLAVEAAN...DLKKGTPGYDKLCRIKPLYEQILAACYTFH
CAI18712	214	DATRRDRFELIFSYLHFADNN.....ELDASDRFAKVRPLIIRMNCFQKHAP
NP_689808	190	QIMTGERFLLFRCLHFVNSS.....ISAGQSKAQISLQKIKPVDFL VNKFSTVYT
NP_741958	86	LVMSQARFEKILKYFHVVAFR.....SSQTTHGLYKVQPFDSLQSGFDAAFRPSQT
*PIGGYBAC-ORF	210	SVMSRDRFDFELIRCLRMDDK.....SIRPTLRENDVFTPVRKIWDLFIHQCIQNYT
Q8N328	215	AAMRRDRFETIFSNLHFADN.....ANLDPVDKFSKLRLPLISKINERCMKFVP
Q8N414	231	LVMSQARFEKILKYFHVVAFR.....SSQTTHGLYKVQPFDSLQNSFDSA FRPSQT
Q96JS3	491	DATRRDRFELIFSNLHFADNG.....HLDQDKDKFTKLRLPLIKQMNKNFLLYAP
XP_001030237	202	CIMKYSRFEQIDKHLHLADN.....EDPKIRSDPIGKVRQYMDYL NENFKKYYY
XP_001541487	137	LHMGQKRFEQIKRYIHISNPRR.....PESS.SFIQKLEPLYSNFHAACRKYYN
XP_001599370	30	NIMPYTRFSKITEMHFNDNDS.....MLPRTDPNYDKLHKLRLPLIDHINQTSNKSYN
XP_312615	193	LTMTSLRYHFLIRSRIFDDP.....TAAPDEIEGDKLAPIRPIYERIVSNQCQKYL R
XP_590785	215	DATRRDRFELIFSYLHFADNN.....ELDESDRFAKVRPLIVRMNYNFQKHAP
XP_699416	200	ATMALYTFKSWSRVTCFRKRDP.....EPGQKSGDKLAPILNVWDKWVERLPLMYN
XP_797885	234	KVMSRNRYQLINSLHFVDNEDR.....VPRGQPGHNVLFKVQPIIDRV RPTYQEAF A
consensus	541	m r rf i k lhf dn dri kirplve l y y