

AAM76341	54	LEEP.....G.PVLSQFSRFSSPLGVFKTM.....L....GGEDTLYLLREATNDYIA
AAM76342	54	LEEP.....G.PVLSQFNRFSNPLGVFKSM.....L....GGEDTLYLLREATNDYIA
ABS18391	65	IASRESPNLEVTSLTSHRIITLPQRSIRG.....KNNHVWSTTKGRITGR.....T
BAD07480	67	ANESDSDPDDDLPLSLVRQRASASRQVSGPFY...TSKDGTKWYKNCQRPNVR.....L
BAD11135	67	ANESDSDPDDDLPLSLVRQRASASRQVSGPFY...TSKDGTKWYKNCQRPNVR.....L
BAD11136	1	
BAF82017	57	TSCSVSDIIDKAGASFSESLILSEVQIDEKVTEDEVIRSTDAVEAEAAWVPPQN.....YS
BAF82019	52	FSSGGTLTAEAA..EASGSAQDVPMDVEEGE.....GSTDAAVGEPAWGPPCN.....YV
BAF82020	52	ASSGGTLTADES..EAGGSVPDAPMEVEEGE.....GSGDAAVGAPVWGPPCN.....YA
BAF82021	52	ASICSTLTAEAAEAEAGGSLPDVPMEEEEGE.....GSGDAADGAPVWGPPCN.....YA
*BAF82022	43	ESWCSSSTVSALEEPMEVDEDEVDDLLEDQEAG...DRADAAAGGEPAWGPPCN.....FP
BAF82025	43	ESWCSSSTVSALEEPMEVDEDEVDDLLEDQEAG...DRADAAAGGEPAWGPPCN.....FP
CAF99963	74	RRGEPCLCCPSPPRKRMKDASVPQKASSSPRAARVSSSREEQAEKELPGNQPDTERWRDM
CAI18712	70	LPGSVLHASVLCEDSGTG.EDNDDLLELQPAK.....K....RQKAVVKPQRIWTKRDIR
NP_689808	37	...DSDNFSDSALEADKIRPLSHLES DGKS.....STSSDSGRSMKWSARAM.....IP
NP_741958	1	
*PIGGYBAC-ORF	64	LDEQNVIEQPGSSLASNRILTLPQRTIRG.....KNKHCWSTSKSTRRSR.....V
Q8N328	53	LPGSLLHTAAYLIQDGSDAESDSDPSYAPKDDSPDEVPSTFTVQPPPSRRRKMTKILC
Q8N414	78	SCLCGVWCGVGKRTPSLLVSSLQDLELLG.....QRQRQLWMESTPRPPYNPFLVPCT
Q96JS3	353	LLQG.....LSFSGSDSVEKDNEPEIQPAQ.....K....KLKVSCFPEKSWTKRDIK
XP_001030237	46	KRKQFQEGEDAKKPLTEKEVEKRWTEFSKEN.....KMRQQHKEDDLIDDQWRIYSV
XP_001541487	1	MTSTDSTKTGVK.....RKRSVSALLADIPLKSI
XP_001599370	1	
XP_312615	48	GSVAVQNEESTGHVIKIESIDHAFDMLQN.....SVWSIKPPERTGT.....
XP_590785	70	VPGNVLHAFVVPEDSGTGEEEEEDLQLQPAM.....K....KQKAVVEPQRVWTKRDIR
XP_699416	58	GPDYHSSDEPELHMPAETDAAYMSKTG.....HVLWSPTPPPSGHRK.....F
XP_797885	63	SDFEFAPDAAVPEPELDRDIDEDFMHDSSEVEDEVEHQANHNPEPARHEVDDDWISMGE
consensus	361	l v

AAM76341	97	EFWNSRKTPPSRKVGKGP.....EGRLIGPRLPAGG...
AAM76342	97	EFWSSRKTPPSRKVGKGP.....EGRLIGPRLPAGG...
ABS18391	111	SAINIIRTNRGPTRMCRNIV.....DPLLCFQLFITDEIIEIVKWTNVEIIVKRQN
BAD07480	118	RSENIVTEQAQVKNIARDAS.....TEYECWNIFVTSDMLQEILTHTNSSIRHRQTK
BAD11135	118	RSENIVTEQAQVKNIARDAS.....TEYECWNIFVTSDMLQEILTHTNSSIRHRQTK
BAD11136	1	
BAF82017	112	PEIPLFTAVPGIKVNTNNF.....ELVDFFHVFTTEAILQDMVFYTNLYAEQYLSS
BAF82019	100	PEIPPFTAVPGLSVDTTNF.....EIIDFFNLYITEAILQDMVRYTNLYAEQYLAS
BAF82020	100	PEIPPFTAVAGVKVDTTNF.....QIIDFFNQFITEASLQDMVHFTNLYAEQYLAS
BAF82021	102	PEIPPFTAVSGVKVDTTNF.....EIMDFFNLFITEAILQDMVHFTNLYAEQYLAS
*BAF82022	94	PEIPPFTTVPGVKVDTSNF.....EPINFFQLFMTEAILQDMVLYTNVYAEQYLTQ
BAF82025	94	PEIPPFTTVPGVKVDTSNF.....EPINFFQLFMTEAILQDMVLYTNVYAEQYLTQ
CAF99963	134	EEDDSEPPQPRFRPERVPGPQLNRTANYTPELFLQFFSTVIDTLVKHTNANGRKKKQE
CAI18712	119	PDFGSWTASDPHIEDLKSQE.....LSPVGLFELFFDEGTINFIVNETNRYAWQKNVN
NP_689808	83	RQRYDFTGTGPRKVDSDIT.....DPLQYFELFFTEELVSKITRETNAQAALLASK
NP_741958	1	MPPSA.....SAVDFFQLFVPDNVLKMMVVQTNMYARKFQER
*PIGGYBAC-ORF	110	SALNIVRSQRGPTRMCRNIY.....DPLLCFKLFFTDEIIEIVKWTNAEISLKRK.
Q8N328	113	KWKKADLTVQPVAGRVTAPPNDFFTVMRTPTEILELFLDDEVIELIVKYSNLYACSKGVH
Q8N414	131	PVGKLSAEHGGPTRKMPPSA.....SAVDFFQLFVPDNVLKMMVVQTNMYAKKFQER
Q96JS3	397	PNFPSWSALDSGLNLKSEK.....LNPVELFELFFDDETFLNIVNETNNYASQKNVS
XP_001030237	99	DQVPKSFYMKTKFKDKDLNRDFIPYNVPHSPYHLFRMFDDRIVKLIIEETNRYKHQKYQE
XP_001541487	31	RFISMESPHRSPTANLPNIDPR.....NPYTLFSLYISESDIQNIACSTNAYAEIQISR
XP_001599370	1	
XP_312615	90	MGRKVAHPRPAPVGLAKSAK.....SPAECLSLFLDADVIAMITEYTNEQIKAEQPN
XP_590785	120	PDFSSWTATDPHMEDLKSQE.....LSPVGLFELFFDEGTINFIVNETNRYARQKNVN
XP_699416	103	PSHLFENMTPGPTSFACSN.....AQDIKSTFELFFPDEIKEMLMQISNLEGKRVYG.
XP_797885	123	EEWAPSWQNPYNPEEKLLFDAN....HFKPVDFFFYRFFPEDLFTMLAEQTNLYARQTIQR
consensus	421	pl f lfi d ii iv tn ya