

Cpip_D_XP_039434833	MAIPFLQPEDDDAARLQHAAT---QSGPPTLG---PVSP-----	33
Aead_D_XP_029727134	MAIPFLQPEEDSARHHGANG---PNTASAHA---GVGAGAGSSGTGSASASGSGAVVVG	54
Bcop_D_XP_037040268	MAVPFYVPDEE--RENG-----	15
Bcop_D_XP_037050104	MAVPFFVPDGDQRSNG-----	17
Cnas_D_XP_031624166	MAVGFFADDGDDHL-----	14
Dmel_hid	MAVPFYLPEGGADDVASSSSGASGNSSPHNHPLSSASSSVSSSGVSSASASSASSS---	57
Hill_D_XP_037904604	MAVPFYLPNQDEQGA-----	15
Bdor_D_AHX71830	MAVVFMPEGGDDDSASSSSGGHGSAG-----	27
Asus_D_AEF30451	MAVVFMPEAGADDSASSSSGSHGSGG-----	27
Ccap_D_JAB92755	MAVVFMPEGGDDTASSSSGGHSSTG-----	27
Msca_D_APT68153	MAVPFYMPNQEDGD-----	14
Lser_D_AKA64736	MAVPFYLPEGGADDTVSS-GGTTSSDG-----	26
Gfus_D_XP_037879387	MAVPFYLPEGGADDTVAS-AAGLASDG-----	26

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Cpip_D_XP_039434833	GPGSSGGPLLHPPPSPLVSGSIPIPGSPAPIGVPPPPPSGTSTAVQTPLLGPAGLMHGDQ	93
Aead_D_XP_029727134	GAGSSGGAVMLA---GATGMPVPNSPA---APIISSGTSTAVQTPLIGP---MNSDQ	103
Bcop_D_XP_037040268	-----SSSQPQSTTTSATQTPLQSPTN---EH	39
Bcop_D_XP_037050104	-----STPQSQSTISSATQTPLQSPVN---DEH	42
Cnas_D_XP_031624166	-----NSSYHTTVITTN SATQTPLQSPVS---HEY	41
Dmel_hid	SSASSDG-----ASSAASQSPNTTTSSATQTPMQSPLP-T--DQ	93
Hill_D_XP_037904604	---SGS-----SGSSTGSSPN-TTTSATQTPLPSPAP-VNGEQ	48
Bdor_D_AHX71830	---SGS-----AASSTSQSPN-TTTSATQTPMQSPLP---PHF	58
Asus_D_AEF30451	---SGS-----AASSTSQSPN-TTTSATQTPMQSPLM---ASP	58
Ccap_D_JAB92755	---SGS-----AASSTSQSPN-TTTSATQTPMQSPLV---PNP	58
Msca_D_APT68153	-----GSSSSSQSPN-TSTSATQTPLQSPVT---GEY	42
Lser_D_AKA64736	---ASS-----AASSLQSSPN-TTSSATQTPMQSPLL---PGE	57
Gfus_D_XP_037879387	---TGS-----TSSSSQSSPN-TTSSATQTPIQSPLV---PGD	57

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Cpip_D_XP_039434833	LVQLFYEALYRYSRGDTP-STPISQ--SPQSSSCSPFTTGYNTTPP-----GGQ	139
Aead_D_XP_029727134	LVQLFYEALYRYSRGDTP-STPISQ--SPQSSSCSPFTTGYNSGGGSAGYANATTTGQ	160
Bcop_D_XP_037040268	LVQVFYEALSLYSASLVL-RSPCS-TSPSSPSCCHPHINN-----YRGN	82
Bcop_D_XP_037050104	LVQAFYEALSLYSANLLQ-ATPAC-LSPPSSPSCCHRH-NN-----YRGD	84
Cnas_D_XP_031624166	LVQAFCEALHRCS----IAGSPGIQSVPP-SPSCSHP-----NGHGE	78
Dmel_hid	VLYALYEWVRM--YQSQQSAPQIFQYPPP-SPSCNFT-----GGD	130
Hill_D_XP_037904604	LVQAFMEVLRYCSSSTSNGGSPGFQFPPP-SPSCNLNSPGGF-----YSDE	93
Bdor_D_AHX71830	MMA-----FYQ-----YMNATAFQYPPASPCCQVHSPSPYTGSGGGGGGGGAGVGNGE	107
Asus_D_AEF30451	HIVMALCEAVYQS----LNNTPAFQYPPASPCCVHSPSPYTGSG--GG-----GGE	104
Ccap_D_JAB92755	YMVALCEALLYQS----MNNPPAFQYPPASPCCPVHSPSPFTGGSVGGA-----NGE	107
MscA_D_APT68153	LVQAICEALHRCS-----GSYPSPSCSVHSPCYN-----GGD	75
Lser_D_AKA64736	VIMAIYEL---IRY---NSGAPVFQYPTPPSPSCSIHGPSYT-----GGE	96
Gfus_D_XP_037879387	LVMAFCEAFYRYSI---NSGAPVFQYPTPQSPSCSVHSPSYV-----GGD	99
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Cpip_D_XP_039434833	VFFPQT---PSGVLPPRTPNATGGGGRGGARIFFGQP--TPSPSGSSSYSSSQHSANSPD	194
Aead_D_XP_029727134	VFFPQT---PNGVFRPGGGGGIGSYGATTGVFFGQPP-TPSPSGSS--SHSQHSANSPD	214
Bcop_D_XP_037040268	VFFPRP-----HVAPQTPVSFG---R-----	100
Bcop_D_XP_037050104	VFFPQT-----NSSPRTPSASD---T-----	102
Cnas_D_XP_031624166	VFFPRGSNSSNGSGSSSTPS-----	98
Dmel_hid	VFFPHGHPNPNNSNPHRTPRTSVSFSSGEEYNFFRQQQPQPHPSY---PA--PSTPQPM	184
Hill_D_XP_037904604	VFFPRN-----RSTPRSPRNSFH---DEGAFFRHPIPTPSRSM-----	128
Bdor_D_AHX71830	VFFPLS-----LSTPRTPTRTSVSYAAGEENTFFRHHNISGGC-----SNASHLQ	151
Asus_D_AEF30451	VFFPPS-----RSTPRTPTRTSVSFAAGEENTFFRQHNISSGGYS-----STQHLQ	149
Ccap_D_JAB92755	VFFPIS-----RSTPRTPTRTSVSFAAGEENTFFRHHNISGGGG--GCSS--SSATHLQ	157
MscA_D_APT68153	IFFPRD-----RSTPLSFSRQQ-----Q-----	93
Lser_D_AKA64736	VFFPRS-----RSTPRIPTRTSVSFAPGDEVNFFHQSAAPAASSGNAQTQT-----TQ	142
Gfus_D_XP_037879387	VFFPRS-----RSTPRTPTRTSVSFAAGDEVNFFHQSSPAASSSNLQPEPN--NSNSSNQ	151
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Cpip_D_XP_039434833	ASHTTTPASCSSAA-----PIFHQFPS-----SFSGPTADGGSTTSPAMAG	235
Aead_D_XP_029727134	-----TAACSSAP-----PIIHQFPS-----SYQLPSTSNAST-----	242
Bcop_D_XP_037040268	-----	100
Bcop_D_XP_037050104	-----	102
Cnas_D_XP_031624166	PFS-TP---SSN-----STVIRMHDDYRS-----	118
Dmel_hid	PPQSAPPMHCSHSYPQSAHMMPHSA----PFGMGTTYAGYTPPPTPNTASAGTSSSS	240
Hill_D_XP_037904604	-----	128
Bdor_D_AHX71830	PPQSAPPMPPSSSHNGAHSQPA-----PQQYQQYTYPTYQYTPPPTPLTANASTCTGN	204
Asus_D_AEF30451	PPQSAPPMPPSSHTSAHSQTT-----PQ-QYQQYSYPHYQYTPPPTPLTANASTCTGN	201
Ccap_D_JAB92755	PPQSAPAMQQSSSHNNAHSQTA-----PQ-QYQQYTYPTYQYTPPPTPLTANASTCTGG	209
MscA_D_APT68153	-----	93
Lser_D_AKA64736	APQSAPPVPNSHH--HNQHQLYGHHPHFA---YQHS GPNYYQYTPPPTPNAATATTSTGT	197
Gfus_D_XP_037879387	PPQSAPPTVNNSSHQHYYHSFFPLHPRVAAYHHPNTASGYCQYTPPPTPTTATTST----	207

Cpip_D_XP_039434833	QPTSWP----DDGSESSES DSSSQPSSSSEAAPTGSSPTGCSSSHCLGLGQLHQHRLHHHQ	291
Aead_D_XP_029727134	-ATNWT HVSSGDGDDSESSES DSSSQPSSASDGDSITAPIAGCSPHCLGLLGPPHHHLHQLLD	301
Bcop_D_XP_037040268	-----SHQWSTPR	108
Bcop_D_XP_037050104	-----SQCWR SRA	110
Cnas_D_XP_031624166	-----AQWSARRS	126
Dmel_hid	AAFGWHGHP---HSPFTST-----ST-----PLSAPVAPKMRLQRSQS	275
Hill_D_XP_037904604	-----RNGPPE	134
Bdor_D_AHX71830	I--FGATEATHQRCGVATASTST-----S-----TTSCGMGGHSRLHRSLS	244
Asus_D_AEF30451	V--FGSTEATHQRTC VASTST-----S-----TQSCMAKG HARLHRSFS	239
Ccap_D_JAB92755	NLFNGSTEATHQRTC VASTSTAT---ASTSTAAS-----TSSCGAKG HARLHRSLS	258
MscA_D_APT68153	-----SLRSPR	99
Lser_D_AKA64736	S-----TSGAGGMAHRS LHRSL S	215
Gfus_D_XP_037879387	-----GTSTGAVHRLHRSLS	223

Cpip_D_XP_039434833	PLDVGGGG-----GPS-GF--IPPH	308
Aead_D_XP_029727134	AAAAAGSGSSTGV-----SSSFNNGSSS-----SSSSNSAGGSSAMVPMS-GC--IPPH	347
Bcop_D_XP_037040268	NEMPRRLNSTGEEEDDEDIDSDIGIDECPSATSSSSNSSNSTPASPLPVDFNFEE---H	165
Bcop_D_XP_037050104	NGLR-RLHSTGDDTHDDAESSD-----EFSMANGCNVPRQSVVPDYDLEE---H	156
Cnas_D_XP_031624166	VFRRRYRLTSAS-----DEEDYE-----D--EQP-----LSDYEE---H	155
Dmel_hid	DAARRKRLTSTG---EDEREYQ-----SDHEAT-----WDEFGD--RY	308
Hill_D_XP_037904604	AVSRRSRLTSTG---DDDNEGH-----SEHETS-----WDELDE--RY	167
Bdor_D_AHX71830	DAQKRSRRTST---TNDDEREYH-----SEHETS-----WDEFDD--RY	278
Asus_D_AEF30451	DAQKRSRRTST---TNDDERECH-----SEHETS-----WDEFDD--RY	273
Ccap_D_JAB92755	DAQKRSRRSSTN--ANDDERECH-----SEHETS-----WDEFDD--RY	293
MscA_D_APT68153	TSTRRSRLTSTGDYDDDDHECH-----SEHETS-----WDELEHHRL	138
Lser_D_AKA64736	DSARRSRLTSTG---EDEREYQ-----SEHETS-----WDEFED--RY	248
Gfus_D_XP_037879387	DTARRSRLTSTG---EDEREYQ-----SEHETS-----WDEYDD--RY	256

Cpip_D_XP_039434833	LDFMAGREQLQEFAGKIPQRKKKSK-----	333
Aead_D_XP_029727134	LDYMAGREQLQEFAGKIPQRKKKSSSSK-----	375
Bcop_D_XP_037040268	YTYLAARERLQEFPGQVPQKKKKVVSEKAEA-----	197
Bcop_D_XP_037050104	YTYLAAREHLQPFSGQVPPKKKKRVVEHTEAD-----	188
Cnas_D_XP_031624166	MQYMAERERLQVFPGRVPPPKKRDTTNTQ-----	184
Dmel_hid	DNFTAGRERLQEFNGRIPPRKKKSSNSHSSSSNPNVCHTDSQPGGTSQAESGAIHGHSQ	368
Hill_D_XP_037904604	EQYMAARERLQEFPGRIPNRKKRKEGKK-----	195
Bdor_D_AHX71830	DNFTAGRERLQEFNGRIPPRKKKKDVPK-----	306
Asus_D_AEF30451	DNFTAGRERLQEFNGRIPPRKKKKDVPK-----	301
Ccap_D_JAB92755	ENFTAGRERLQEFNGRIPPRKKKKDVPK-----	321
MscA_D_APT68153	ENFTAGRERLQEFKGRIPPRKKKKEAPK-----	166
Lser_D_AKA64736	DNFTAGRERLQEFNGRIPPRKKKKDVPK-----	276
Gfus_D_XP_037879387	DNFTAGRERLQEFNGRIPPRKKKKDLPK-----	284

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Cpip_D_XP_039434833	-----AGGKSKKAGFLEQTLVWPTLAVTATLIALGCGLLAAR	370
Aead_D_XP_029727134	-----SSSKSKKSKFLEQTLVWPTLAVTATLIALGCGLLAAR	412
Bcop_D_XP_037040268	-----VAVKTQKKPKSKEQRFVWTTV-VTAAVLAVGYISSR--	232
Bcop_D_XP_037050104	-----SPVAAKSKEQNFVWPTV-VTAVVLAVGCGFLVT-	220
Cnas_D_XP_031624166	-----PRKSTDPKMWPAV-AAVVVLAVGCGFLVSR	213
Dmel_hid	QRQVERERQKAKAEKKKPSFTWPTV-VTVFVLAMGCGFFAAR	410
Hill_D_XP_037904604	-----TK-----EQSFTWPTV-VTVFVFAVGCGLVAR	222
Bdor_D_AHX71830	-----SKYEKKVRERPFKGFIWPTV-VTVIVVAIGCGFLVTR	342
Asus_D_AEF30451	-----SKSEK----KQFKAFIWPTV-VTVIVVAMGCGFLVAR	333
Ccap_D_JAB92755	-----SRAER---KQFKAFIWPTV-VTVIVVAMGCGFLVAR	353
MscA_D_APT68153	-----TKPKAK----DPCFTWPTV-VTVFVFAMGCGYLVAR	197
Lser_D_AKA64736	-----TKPEKK----EQSFTWPAV-VTVFVFAMGCGFLVAR	307
Gfus_D_XP_037879387	-----PKSEKK----EQSFTWPAV-VTVFVAMGCGFLVAR	315

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