

Cced_HEA_VVC35986	MAVPFDFDEIHPE--GNHFTVIQNLLREMLTLLRWLPWTASGNPLPNSTLDNPFVPPYLI	58
Sfla_HEA_XP_025413012	MAVPFRVEG---DSEDHSHYLRIENLLKELLTLLRWMPWTVTGMPTATA--VIDNS----	51
Apis_HEA_XP_001950202	MAVPFRM-EPDPEVMRRHYLRIQDLIIQLMVQLRQLPSVMIGNSARPSVINYHDL-----	55
Agos_XP_027846023	MAVPFRPPSHNSDTARDHYLRIENLLRELLTLLSRMPSWMSGDLSSYSNNGINISP----	56
Acra_HEA_KAF0773171	MAIPFRPPSHNSDTARDHYLRIENLLRELLTLLSRMPSWMNGDLSSYSNNGINVSP----	56
Agly_HEA_KAE9536444	MAVPFRPPSHNSDTARDHYLRIENLLRELLTLLSRMPSWMNGDLSSYSNNGINISP----	56
Mper_HEA_XP_022175586	MAIPFVMPEPDPDTPMAHYLRIQNLLRELLTLLSRMPSRMIGDPTNYPYTNISIFS----	56
Dnox_HEA_XP_015379466	MAIPFVMPEPDPDTPMAHYLRIQNLLRELLTLLRRMPSRIIGDPSNYPYTNISLFS----	56
Rmai_HEA_XP_026810777	MAIPFNPPSSNPDATRDHYLRIQNLLKELLTLLRRMPSWMIGDQ---YANINMAS----	52
Msac_HEA_XP_025190335	MAIPFDPPSPNPDTARDHYLQIQNLLKELLTLLRRMPSWMIGDQHNYPYTNINIST----	56
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Cced_HEA_VVC35986	QDFPVIQRLMEGVERVRQQVEREDLREQHQIHLERLRLRQRAH--QIRQQERQQEREQ	116
Sfla_HEA_XP_025413012	QA----TF-ML---QRRQTAGNRQQSARGLVHHHRLATAT-----AET-HNR	90
Apis_HEA_XP_001950202	---PQPDPLEE---RRRPWIQQRSSE----HRRRMREEQ-----	85
Agos_XP_027846023	QTVPPAQSLLE---RDRLWVQQQHSIR--MFHRRRLRERQQERREQQQVVEEQ-ESQ	110
Acra_HEA_KAF0773171	QTVPPAQSLLE---RDRLWVQQQHSIR--MFHRRRLRERQQERREQQQVVEEQ-ESQ	110
Agly_HEA_KAE9536444	QTVPPAQSLLE---RDRLWVQQQHSIR--MFHRRRLRERQQERREQQQVVEEQ-ESQ	110
Mper_HEA_XP_022175586	SGPPPYSE-EV---RDRLWAQQQASAR--AFNRRCVRERLQQR-----Q----	95
Dnox_HEA_XP_015379466	SDPPPYSE-EV---RDRLWVQQQSSAR--AFHRRRLRE---R-----Q----	91
Rmai_HEA_XP_026810777	QTPLTYLQEEE---NNRLWVQQQQRSMR--AFHRRRLRERQHQERRAQQQELERQQ----	103
Msac_HEA_XP_025190335	QTPSPYSA-EE---SNRLWVQQQHSMR--LFHRRRLRERQQE-RREQQQELERQQ----	105
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Cced_HEA_VVC35986	RRQQQQPGFLPDLVASSVAIPGPAPRLEPDLIRPERQPAPEPQPEPEPAP-----	167
Sfla_HEA_XP_025413012	SEGQQQLPLPDLITSTMSSAPPPPP-----	117
Apis_HEA_XP_001950202	QRSEEQPPLLPDLVASCQSAGPSHSAGPSHSGVPSHSAGPSHLAGPSHSAGPSHSAGPS	145
Agos_XP_027846023	QHAEQQQVLLPDLVTSCGPTVRQQPPP-----	137
Acra_HEA_KAF0773171	QHGEQQQVLLPDLVSSCGPTVRQQPPP-----	137
Agly_HEA_KAE9536444	QHVEQQQVLLPDLVTSCGPTVRQQPPP-----	137
Mper_HEA_XP_022175586	QQRQQQSLLPDLVTSCQQSANPPPPP-----	122
Dnox_HEA_XP_015379466	QREQQQPPLPDLVTSCGQAANPPPPP-----	118
Rmai_HEA_XP_026810777	QSE-QQRPLLPDLVSSCGPSRQLPPP-----	129
Msac_HEA_XP_025190335	QSDQQQLLLPDLVSSCGPTSRQPPPP-----	132
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Cced_HEA_VVC35986	-----APAPADPVPRSPQPR--	184
Sfla_HEA_XP_025413012	-----PPPPQP--	124
Apis_HEA_XP_001950202	HSAGPSHLAGPSHSAGPSQSAGPLQSAGPSQSASPPQSDSSLQSDSPQSDNPPQQQLQ	205
Agos_XP_027846023	-----PPPPSSQ---QRP	148
Acra_HEA_KAF0773171	-----PPPPSSQ---QRS	148
Agly_HEA_KAE9536444	-----PPPPSSQ---QRP	148
Mper_HEA_XP_022175586	-----PPPPPPSPQQQLQ	136
Dnox_HEA_XP_015379466	-----PPPPPPSPQQQLQ	132
Rmai_HEA_XP_026810777	-----PPPPPSAPLQQQQQ	143
Msac_HEA_XP_025190335	-----PPPPQ-----Q	138

Cced_HEA_VVC35986	-----GA---YRRKKHVKVESVRIQMCPSCSLNGGTFTAINTLSTDQQR--E-----	227
Sfla_HEA_XP_025413012	-----SADKKPTKKILLELCEPCYYDHQ-KFKVVAANRRDKSNDGLPLSRRHR	173
Apis_HEA_XP_001950202	AQQQTAV---EGEDKIAGAVKLQVAVCPTCYYGKERKLVIAIAKLDENG--NPI-----	255
Agos_XP_027846023	EQQHQSABD---DDKFVDAVKLQVAVCPTCYYGKERKLVIGVAKLDGNG--KPI-----	198
Acra_HEA_KAF0773171	E-QHQSABD---DDKFVDAVKLQVAVCPTCYYGKERKLVIGVAKLDGNG--KPI-----	197
Agly_HEA_KAE9536444	E-QHQSABD---DDKFVDAVKLQVAVCPTCYYGKERKLVIGVAKLDGNG--KPI-----	197
Mper_HEA_XP_022175586	AQQ-QSAEEEDIEDKIARAVKLQVAVCPTCYYSEERKLVIAIAKLDENG--NPI-----	188
Dnox_HEA_XP_015379466	AQQ-LSABD---EDKIGRAVMLQVAVCPTCYYSKEGKLVIAIAKLDENG--KPI-----	181
Rmai_HEA_XP_026810777	PEQQQSTVD---DDKFVDAVKLQVAVCPTCYYGKERKLVIAIAKLDENG--KPI-----	193
Msac_HEA_XP_025190335	SVQRQSABD---DDKFLGAVKLQVALCPTCYYGKERKLVIAIAKLDENG--KPI-----	188

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Cced_HEA_VVC35986	-----PTFDDDEED-----GYCWEIKRRLKSLFQPSNIDSSILTAAMVIIGWKMF	275
Sfla_HEA_XP_025413012	STGIADRRSFDNDAEESVTVVKS--NVKQRLMSLLTPSKIDSSILTAVFVIIGWKMF	231
Apis_HEA_XP_001950202	-----RWTN-RDDEEPVVFENKSSK-VKRRIMSLQPSHIESSVLTAMFVIIGWKMF	307
Agos_XP_027846023	-----RWSTHREVSTYIYFYTTCSFSAQPRVSSNLYQLRXTKRYLLSFYFI-----	244
Acra_HEA_KAF0773171	-----RWNTHRDDEELLVIEDKSTK-VKRRIMSLQPSKIESSVLTAMFVIIGWKMF	250
Agly_HEA_KAE9536444	-----RWSTHREDEELLVIEDKSTK-VKRRIMSLQPSKIESSVLTAMFVIIGWKMF	250
Mper_HEA_XP_022175586	-----RWTNNRDDEEPMVVENKISK-VKRRIMSLQPSKIESSVLTAMFVIIGWKMF	241
Dnox_HEA_XP_015379466	-----RWTNHRDDEEPVVENKSSK-VKRRIMSLQPSKIESSVLTAMFVIIGWKMF	234
Rmai_HEA_XP_026810777	-----RWNANRDDEELLVFENKSTK-VKRRIMSLQPSKIESSVLTAMFVIIGWKMF	246
Msac_HEA_XP_025190335	-----RWTNTRDDEELLIVENQSTK-VKRRIMSLHPSKIESSVLTAMFVIIGWKMF	241

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Cced_HEA_VVC35986	Q	276
Sfla_HEA_XP_025413012	Q	232
Apis_HEA_XP_001950202	Q	308
Agos_XP_027846023	-	244
Acra_HEA_KAF0773171	Q	251
Agly_HEA_KAE9536444	Q	251
Mper_HEA_XP_022175586	Q	242
Dnox_HEA_XP_015379466	Q	235
Rmai_HEA_XP_026810777	Q	247
Msac_HEA_XP_025190335	Q	242