

Tcas_C_XP_008194456.1	MAVPFVLPEDINNLIIVAV--IFILS----QTRLQRNEENRELQE-----CMEE	43
Atum_C_XP_019872614.1	MAVPFNPEDHNEVDVIVNQLQSLLT-QLQASVRESQRSTRTRNP-----PGSTRH	50
Rfer_C_KAF7270649	MAVPFIIIPDDQNDQSVILVQLQTLIS-RLQMIHNNQQQQQLSVN-----ASSNSYNNS	53
Sory_C_XP_030755961	MAVPFTMPDDQNEVEVLLIQLQALLT-KLQIAARKHRLRSQQAQSNQSAAVATLTTTAPL	59
Dpon_C_XP_019765467.1	MAVPFNIPEDQSEVEVLLIQLQTLN-KLQATVRQNHQLAQ-QP-----TASIPSGS	50
Dvir_C_XP_028151061.1	MAIPFNLPGEQTEVEVITQLQYLLM-KLQDAIRRSQATNSSYP-----VFSISTR	51
Ldec_C_XP_023021532.1	MAVPFVMPEDENEVEVIIQLQSLLT-KLQAALRRSRGPPPPRT-----SLPT---R	48
Apla_C_XP_018573717.1	MAVPFNPEDQNEVEVIINQLQSLLT-KLQAARRSRGPTIRTN-----QTAV---T	48
Obor_C_KRT86088.1	MAIPFTIPNQEVSQLN-IQELLRELCEILQQLLIICRQQSINQQQ-----QQAT	48
Otau_C_XP_022915163.1	MAIPFAVPGQPPV---SPERLRELYDFLQQLLIVRQQQNHHRQE-----EVVT	45
Nves_C_XP_017785459.1	MAIPFDVLNDEEGDPA-LNELLSQLCDAIICLRVHSH---IQFA-----	41
Aplani_C_XP_018330969.1	MAIPFDVSSDEK----LDQLFTRLYEILQQIYHLTQQTASGQQP-----TI-T	43
Ppyr_C_XP_031336702.1	MAIPFNVENDSDCDEAVLQLLLSLCRTLQQIALFQSRRTQNLN-----RAPS	49
Illum_C_KAF2880729.1	MAIPFLVEDDSEYEEALLQQLYSYDLFHTIQQIELIQRSRRAQHQI-----SPRV	49
Ater_C_KAF5276935.1	MAVPFTVEDESNDYEIVLQQLFSDLRQTLQQIVDMQRLRRTQNLN-----ATTR	49
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Tcas_C_XP_008194456.1	LVRLLAEELQRRSRS-----SEYDNQLKQTL-----LLLRQS-----	75
Atum_C_XP_019872614.1	RVRFASGTRD-RDPERQEET-----DGDGRPSHEHLADLM-----VCRHDVPSAS	94
Rfer_C_KAF7270649	RVRSSSTTRQ-RTRDSSE-----TSSTTPNQNNLSEVISN--LSLFALSAGDQQSSS	102
Sory_C_XP_030755961	RVRGSSINRQ-RSESSET-----AASPAQTNAIPDLISN--LSWLASSHNETQAAS	108
Dpon_C_XP_019765467.1	RVRYPDDRVR-RSREVLQ-----SVERITPVPQNVLPDLLSN--LSWLADSSNEASSSS	101
Dvir_C_XP_028151061.1	RVRTNSSNRA-RGREQSSVSSPSTASPSANANLPELLNN--LAWLAVLTQEAVDNN	108
Ldec_C_XP_023021532.1	NRTSAGSSRS-PTQDQGT-----STSASAPSTQIPDLLNN--LALLAAASQEIQSN	97
Apla_C_XP_018573717.1	RVRSPASSRL-RSRD-ES-----SATTSISSTNFPDLLNN--IAWLAAASQDAASTS	96
Obor_C_KRT86088.1	RNRASTSSVV--NQH-----DPIPEIMTN--LSLLSAA-----	77
Otau_C_XP_022915163.1	TRREDTTSVR--ASG-----RAADG-----RMLSAL-----	69
Nves_C_XP_017785459.1	----SRGSSL-NPQRI-----REAFGPHPNVLERLSRNLLPLPDVVGERTD	82
Aplani_C_XP_018330969.1	RVRCSAGASR----HIQD-----HQIHSSYPVLPPEIVND--LALLPRPSAQYLEGE	89
Ppyr_C_XP_031336702.1	SP--ATTTS----RHSGA-----S---SETERTLLNSTVD--LALSLSQ-----V	83
Illum_C_KAF2880729.1	RTTPSAGTSR-RNREVPG-----DPLDSENLAPEPVVNLA--LALSPAGSQNDL--D	96
Ater_C_KAF5276935.1	AT-----SIR-RPREHGT-----QTEFSEA---LFNSTVN--LALSPAGAQNGL--E	88

Tcas_C_XP_008194456.1	-----LSHFTPTLSR-IQRRSNFESCCDDCKISLH-----EDCATKDCSQVGL	117
Atum_C_XP_019872614.1	-----TQLTASPIRRRTTRFQTDCEDETKINIT-----TIVDT-GSQQDWAQIGI	137
Rfer_C_KAF7270649	-----TYTAIPVRSRPRTRG-CSESSNCDVTKTATK-----T-----TFDQDWNKMNC	143
Sory_C_XP_030755961	-----ALTAMPVRSRPRRRTNSESSNCDKTTKTTT-----T-----DLSQDWNKVNC	150
Dpon_C_XP_019765467.1	SPL-----T-AMSARSRRRTASESSNPDETKISVT-----AIVTTDFCAQDWEKNC	148
Dvir_C_XP_028151061.1	SQ-----QTTAMAVPRPTRNRRTSSESSCCQETKSDET-----TASNS-GSVQAWNQETD	156
Ldec_C_XP_023021532.1	QPEGAPQVAASATFRSTRRRRTNSESSCCEESKVSIT-----TA-NR-NGVQDWNQVNE	148
Agla_C_XP_018573717.1	S-----SLTANSVTRSPRRRTSSESSNCKETKISIT-----AI--V-NHAQDWNQADG	141
Obor_C_KRT86088.1	--FNSIQTTPARALRRPRRYRLSESSCDETKNFDHQTSTTTSPTTSAQISPEWMEVDM	135
Otau_C_XP_022915163.1	--SDA-----LHTSRRPRRRWPKSPTHH-----DDSSNSNSAAKEAQNQRWKRVT	113
Nves_C_XP_017785459.1	-VSL--QTIEASAIIPGRQRRTSESSCKVPKIANM-----QTPIDQPQ-DYSEDD	130
Aplani_C_XP_018330969.1	-AVLQPQ--AMPTPRRRKRRRTSSKSCCDANKSVEA-----ATVEDDGHQVWTQVGM	138
Ppyr_C_XP_031336702.1	-EALQQQNASVSTRRRHPRRSRSEPSCKEKPVI-----SVAVEVTNKDWIQKEH	134
Illum_C_KAF2880729.1	-AILRPQNLSTPTRRRRRRTRRSEPSCEENKPKVKV-----SVSVEVTNKEWNQQEK	147
Ater_C_KAF5276935.1	-MLLQLESFLPVRRLHRRRSQSEPPFCKEVKPKVKV-----SVSVEVGKNDWIIQQEQ	139

Tcas_C_XP_008194456.1	ILRKIDDETSIAIFKEGVEEE-----KEGFVEESLLSRLVPRVR---	156
Atum_C_XP_019872614.1	TLRNIADDINPVTFREVV-----LFPTTKRGLLSKL-PDALT-C	174
Rfer_C_KAF7270649	NNGDDDDDDDDDE-----NKEASSVGLLSKLTPASVSSC	177
Sory_C_XP_030755961	DDDGDD-----EGGSSDGLLSKIMPATVSSC	176
Dpon_C_XP_019765467.1	VD-----SGT-----SNVIPADGLFSKLIPGPVSSC	174
Dvir_C_XP_028151061.1	NEQSSE----DGS-----DKSYSRQGILSRLIPGPVS-A	185
Ldec_C_XP_023021532.1	PE-----ISS-----AKTLSSSESIFSKFVPGPVS-A	173
Agla_C_XP_018573717.1	SP-----DSE-----PEQASGDGILSKFVPGPVS-A	166
Obor_C_KRT86088.1	DLRKISEDFAAGFHKDDDAEEEDTTALQSSSKSSSSPSTSTKRDSIFSKEVPAPF-TG	194
Otau_C_XP_022915163.1	ELRKIADEFESAAFEVDDVDVDSLLP-----CCSRLSTSKERKGTFSKILSMPVMVS	167
Nves_C_XP_017785459.1	-----P-----SSQRPKTRTACDGDGLSTLVPSPi-KT	158
Aplani_C_XP_018330969.1	PLLKMAKDFDPSEQQFTCKEK-ND-----DEVTGAKEDSCQSESIFSKLVPDLS-SK	188
Ppyr_C_XP_031336702.1	-----HISPTTKKPWYRSDGLLSKLIPAPL-SG	161
Illum_C_KAF2880729.1	-----SSQSSPDKQSCGSESLLSKLVPAPF-SG	174
Ater_C_KAF5276935.1	-----STETSTKKKWCSENLLSKLVPAPF-SG	166

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Tcas_C_XP_008194456.1	TFWKAVPLICVVGHLHLFQISYSM 179
Atum_C_XP_019872614.1	TIWTA--MLGCVGWHLFRSR--- 192
Rfer_C_KAF7270649	SLMTA--VICFVGWHIFRGR--- 195
Sory_C_XP_030755961	SFMTA--MICFVGWHIFCGR--- 194
Dpon_C_XP_019765467.1	SLMTA--MICFVGWHIFRAR--- 192
Dvir_C_XP_028151061.1	PLFTA--MICFVGWHIFRAR--- 203
Ldec_C_XP_023021532.1	PLWTA--MICFVGWHLFGTR--- 191
Agla_C_XP_018573717.1	PLWTA--MICFVGWHLFRAR--- 184
Obor_C_KRT86088.1	SICTA--VICVVGWHLRLNR--- 212
Otau_C_XP_022915163.1	SICTA--VLC-VGWHLRLNR--- 184
Nves_C_XP_017785459.1	SIWTA--VICA VGWYMFAR--- 176
Aplani_C_XP_018330969.1	SIWTA--VICVVGWHLRLRTR--- 206
Ppyr_C_XP_031336702.1	PLWTA--VICMVGWHLRLRTR--- 179
Ilum_C_KAF2880729.1	PLWTA--VICVVGWHLRLRTR--- 192
Ater_C_KAF5276935.1	PLWTA--VICVVGWHLRLRTR--- 184
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