

Clec_HE_XP_014239966.1	MAVPFNVPEEEAEERRVIRIP-----ICEFIRQFIQPE-----ISNLQPENP-----	42
Btac_HE_XP_018898908.1	MAIPFNLPSDEETEDHYKRRLDQLLKDLYDVLRLQILFRPRPIHDDD-----	45
Lstr_HE_RZF36208.1	MAIPFNLPSDEEDTEEYYRRLDQLLADLYDVLRLHILFRPRTQQPAHHNQQA-PVVDAGH	59
Nlug_HE_XP_022189933.1	MAIPFNLPSDEEDTEEYYRRLDQLLADLYDVLRLHILFRPRTQQPAHHNQ-QP-PVIDADG	58
Btac_HE_XP_018895589.1	MAIPFHLPSDEETEENYRRLDQLLADLYDVLRLQILLRPRHMQAPSTRIVENTGFTTESE-	59
Aluc_HE_KAF6204998.1	MAIPFNLPSDEETEDAYRRIDQLLLDLYDLLRQIILRQRPVQNERGVSEARISPTWD-E-	58
Ofas_HE_GCXY01041673.1	MAIPFNWPSDEETEDHYRRLDQLLLDLYDVLRLQILLRRRLHPVPQPE--AQPVPLHEHL-	57
Hhal_HE_XP_014287364.1	MAIPFNLPSDEETADNYRRLDQLLLDLYEVLRLQILLRRRIERVAGPI--ERY-----	50
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Clec_HE_XP_014239966.1	-----RPE--GPVILVLPEAVLRA-----	59
Btac_HE_XP_018898908.1	-----LTGFEARLLALPDLVQSAMSNYPAAATATAHSPWSAIGARD	87
Lstr_HE_RZF36208.1	DNESEDHEPPDHGGEDPSPDALEQRLHPLPDLVANVGSSSAAP-SR-----	104
Nlug_HE_XP_022189933.1	DNESEDQEPDPDHGGEDPSPDALEQRLHPLPDLVANVGSSSAAPSSR-----	104
Btac_HE_XP_018895589.1	-----QDFEPPSDSDLVQERLMALPDLVRSAMSPALNNLSNRLQESNLEC-----	104
Aluc_HE_KAF6204998.1	-----QAASMATQTVETTRLESRLPDLIADTLPSLVANTRQSL-----	96
Ofas_HE_GCXY01041673.1	-----QPQGLQRQQLFRRQARRPDLPLIPSA-----NPIA-----	88
Hhal_HE_XP_014287364.1	-----PQQPQPQPQPGLPDLVP-----	68
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Clec_HE_XP_014239966.1	-----RKAPAAPRRRRRRRQ-----	73
Btac_HE_XP_018898908.1	DAADETNGSRHCRHRHCHTPKRVDLTVAT-VARVDAGGGGHLHLRPPAPPPRPPPGSQS	146
Lstr_HE_RZF36208.1	-----PLGRGHPRRHQDDRRRRRDSTT---TPDDSRSLSP---EDQR-PPPPRKPRESKK	151
Nlug_HE_XP_022189933.1	-----PLGRGHPRRRRRDSTSDSVTINNSRMTSNSRTTDDEEVVDP-PRPLRKLRRESKK	157
Btac_HE_XP_018895589.1	-HCDSSSTVSPSTPVSLPRHQSQSDEVDP--MQRP-----RPATRNL	143
Aluc_HE_KAF6204998.1	-----PLVRKSSSLVPQRRRRRR--AEKP--LRRYAR-----IQT-----	126
Ofas_HE_GCXY01041673.1	-----PLSRKPPVPPPRRRRRR--SDAK--HHSNLQ-----EQQQSHQQ	123
Hhal_HE_XP_014287364.1	-----EGRRPPVPPPRRRRRR--CPKA--QHQLD-----RQ-----	95
Clec_HE_XP_014239966.1	-----EKHPQEMPQQHTLSLGIELRHVEEHTYQS-	102
Btac_HE_XP_018898908.1	GPEPLPRLGPGSATTKFPSKDADSPSSGPAPGKPHTRHKRWTQVGEELRGIAEDFRSNL	206
Lstr_HE_RZF36208.1	RCSSLRR-----KAPCCPASLKFSHSLKTSAENWVMVGEELRKIAEDFRSKT	198
Nlug_HE_XP_022189933.1	RCSSLRR-----KPCCPASLKFSHSLKTSAENWVMVGEELRKIAEDFRTKS	203
Btac_HE_XP_018895589.1	NKRSLSLSP-----K-RYLSKLPHSSMKTLRPQKKWVHVGEELRSIAEDFRSTF	189
Aluc_HE_KAF6204998.1	-----TPYDDLRAAPPQVVAASSWLVNGIELRQIAEEITFIS	162
Ofas_HE_GCXY01041673.1	QHHSLSQH-----RQESAAARADSAIADLQQGPSWLVNGIELRQIAEEFRSAQ	170
Hhal_HE_XP_014287364.1	-DNSVM-----HQDPTPQQGPSWLVNGIELRQIAEEFRSTQ	130
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Clec_HE_XP_014239966.1	-----VGQTKRRRESKTSSFFSLLLPTPLPGSIWTTVIILVGW	141
Btac_HE_XP_018898908.1	S-----VRSSRHLPMEKASHLFSLLIPATM-GPVWTTVILLIFP	245
Lstr_HE_RZF36208.1	TTTTTT---SRSDSSQLKHGAPDLPRTKRVELKASSLLSLLVPAPFCGSVWTTVIIIVGW	255
Nlug_HE_XP_022189933.1	TSTTSTTSRPTTDSHRSKCEAPDLPRTKRVELKASSLLSLLVPAPFCGSVWTTVIIIVGW	263
Btac_HE_XP_018895589.1	QKSPLN-----KTEHSRSPPEMKASSLFSLLVPSPLGKSVWTTIIFIVGW	235
Aluc_HE_KAF6204998.1	RNG-----NSSTAKRRSEIKASSLFSLLVPAPVTGTFWTTVIILVGW	204
Ofas_HE_GCXY01041673.1	I-----DGSEKSRKEIKASSLFSLLVPAPLTGSIWTTVIILVGW	210
Hhal_HE_XP_014287364.1	I-----GDGVEKKRREIKASSLFSLLVPAPLTGSIWTTVIILVGW	170

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Clec_HE_XP_014239966.1	RILTRQR---	148
Btac_HE_XP_018898908.1	VIILSSKNNR	255
Lstr_HE_RZF36208.1	KLLMRHNR--	263
Nlug_HE_XP_022189933.1	KLLMRHNR--	271
Btac_HE_XP_018895589.1	RLITRLQ---	242
Aluc_HE_KAF6204998.1	RILSKQR---	211
Ofas_HE_GCXY01041673.1	RILARNR---	217
Hhal_HE_XP_014287364.1	RILARNR---	177

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