

Nlec_HY_XP_015511746	MAIPFALPSEDEAE-AQE-RRQLGQLLDVYGILQQVIRARSYNPG-QNHRVNRSSGEVP	57
Nvit_HY_XP_003424554	MAIPFALPSEDEAE-DQSQQQLEQLMLDLYAALQQVLRARNSQHPS-RNHRLPRRSADMS	58
Btre_HY_XP_033214430	MAIPFALPSEDEAE-AQG-QQLEQLMLDLYAALQQVLRNRSLQHPS-RNHRLPRRSGDTS	57
Mdem_HY_XP_008555096	MAIPFNLPSDEAE-AQS-QQLEQLMLDLYAALQQVLRSRSAQHPS-RNHRLPRRVGDTG	57
Ccin_HY_XP_015609297	MARPF ¹ LPSEDEAE-EQG-QQLEQLMLDLYAALQQVLRSRRAEHPS-RNHRLPRRAGDVP	57
Oabi_HY_XP_012277082	MAIPFALPSEDEAE-AQG-QQLEQLMLDLYAALQQVLRIRNAQHPS-RNHRLPRRSGDMP	57
Ccal_HY_XP_017884183	MAIPFALPTEDDAE-AQG-QQLEQLMLDLYAALQQVLRTRTSQHPSRNHRI ¹ PRA----	54
Bimp_HY_XP_024222863	MAIPF ¹ LP ¹ SDDEAE-VQG-QDLEQLMLALYAALQQVLRNRNDQHPS-RNHRLPRM----	53
Bter_HY_XP_012175674	MAIPF ¹ LP ¹ SDDEAE-VQG-QELEQLMLALYAALQQVLRNRNDQHPS-RNHRLPRM----	53
Dnov_HY_XP_015429159	MAIPFSLPSDDDAE-AQG-QQLEQLMLDLYAALQQVLRRTAQHPS-RNHRLPRRAGD--	55
Nmel_HY_XP_031834337	MAIPFSLPSDDDAE-AQG-QQLEQLMLDLYAALQQVLRRTAQHPS-RNHRLPRRAGDGF	57
Mgen_HY_XP_033321541	MAIPFSLPSDDDAE-AQG-QQLEQLMLDLYAALQQVLRRTAQHPS-RNHRLPRRAGDGF	57
Ador_HY_XP_006609937	MAIPFALPSDDEAE-TQT-QQLEQLMLDLYAALQQVLRRTAQHPSRNHRLPRRS----	54
Aflo_HY_XP_012338864	MAIPFALPSDDEAE-TQT-QQLEQLMLDLYAALQQVLRRTAQHPSRNHRLPRRS----	54
Amel_HY_XP_006565903	MAIPFALPSDDEAE-TQT-QQLEQLMLDLYAALQQVLRRTAQHPSRNHRLPRRS----	54
Olig_HY_XP_034171762	MAIPFALPSDDEAE-AQG-QQLEQLMLDLYAALQQVLRRTVQHPS-RNHRI ¹ PRAADGF	57
Obic_HY_XP_029055907	MAIPFALPSDDEAE-AQG-QQLEQLMLDLYAALQQVLRRTVQHPS-RNHRI ¹ PRAADGF	57
Emex_HY_XP_017765203	MAIPFVLPSNDEAE-AQG-QQLEQLMLDLYAALQQVLR ¹ SRNTQHPS-RNHRLPRRV----	53
Pgra_HY_XP_020280259	MAIPFT ¹ SERS-----PEEQVLLD ¹ TYLCIENALRSRSARHP-SRNHRAPRQHVGI-	48
Obir_HY_XP_011342863	MAIPFVQNDNNNERSQLEEQQLKMF ¹ LDYVSLHNVLRSRHAQHTASRNHRVPRQ ¹ PAGTN	60

Nlec_HY_XP_015511746	FPELNP-----SAPVPSRPRPRRRRLVSENSALKKEQPST-----SY	147
Nvit_HY_XP_003424554	FPECSGASAAAMMPVPSRPKPRRRRLTSEGLPEKAQLPQRLDSCGTGGRTCCAHHL--	168
Btre_HY_XP_033214430	FPECS-----APVPSRPRKPRRRRLTSESSIPEKGPSES---NK-CNGTCCPGHLNL	157
Mdem_HY_XP_008555096	FPECSA-----APVPSRPRPRRRRLTSESSVLEKGATSR---SDNINSVCC-RHL--	156
Ccin_HY_XP_015609297	FPECSA-----APVPSRPRPRRRRLTSEGSVLEKER-----VNASC-GQI--	149
Oabi_HY_XP_012277082	FPEAS-----VPVPIPRPRRRRLTSECSVQEKER-----MNACC-GQP--	148
Ccal_HY_XP_017884183	FPECSGES--SLAPVPSRPRPRRRRLASESSGAATAKKTTP--PAAKQICNNCF-GDL--	159
Bimp_HY_XP_024222863	FPESNDVN-DVAPVPNPRPRPRRRRLASEGGSSAAVKKT---SAVKSICKCCC-GHI--	158
Bter_HY_XP_012175674	FPESNNDAI-DVAPVPNPRPRPRRRRLASEGGSSAAVKKT---SAVKSICKCCC-GHI--	158
Dnov_HY_XP_015429159	FPECSTDE---APEPSRPRPRRRRLASEG-G--AVKKG---PIGEPTCNSSC-GHF--	153
Nmel_HY_XP_031834337	FPECSSDE---APVPSRPRPRRRRLASEG-G--AVKKG---PVGESACNNCC-GHF--	159
Mgen_HY_XP_033321541	FPECSNDE---APVPSRPRPRRRRLVSESGG--AVKKG---PVGELTCNSCC-GHF--	160
Ador_HY_XP_006609937	FPECSGDEN-GAAPVPSRPRPRRRRLASEGGG-ATMKKG---PATRICKKCC-GHL--	158
Aflo_HY_XP_012338864	FPECSGDEN-GAAPVPSRPRPRRRRLASEGGG-ATTKKG---PATERICKKCC-GHL--	158
Amel_HY_XP_006565903	FPECSGDEN-GAAPVPSRPRPRRRRLASEGGG-ATMKKG---PATERICKKCC-GHL--	158
Olig_HY_XP_034171762	FPECSGDEN-VLAPTNPFRPRRRRLASECGGAAAMKKG---P-AEPTCNNCC-GHF--	161
Obic_HY_XP_029055907	FPECSGDEN-VLAPTNPFRPRRRRLASECGGAAAMKKG---P-AEPTCNNCC-GHF--	161
Emex_HY_XP_017765203	FPECSGDES-GLAPVPSRPRPRRRRLTSEGGSSAAAMKKG---PVAEPICNSCC-GHY--	158
Pgra_HY_XP_020280259	FPECSVNGN--IVPLPSRPLPRR-RLASEGSSLRTLRS-ETRQNEGNTSNTCCC-YP--	155
Obir_HY_XP_011342863	FPECTN-SS--SGPLPSRPRPRR-RFAESSIMESSVMGSPGPIEVSICNGSCC-HL--	170
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Nlec_HY_XP_015511746	YQAPSDENEWANVGANLRNIADDFHASKNTDSGAEKSSLPVIGND-----	192
Nvit_HY_XP_003424554	-AASLDEREWATVGANLRNIADDFHASKTKDAEVEKSRLPFIGSSFSSTSGLGSSGLGS	227
Btre_HY_XP_033214430	SATTLNEREWAVGTNLRNIADDFHASKTKDAEVEKSRLPLLGSTFSSTSS-----	208
Mdem_HY_XP_008555096	-GHSCNETEWASVGANLRNIADDFHASKTKDAEIEKSRLPFFGAGFPSVTTS-----	207
Ccin_HY_XP_015609297	-GTVVNEREWTSVGTNLRNIADDFHAAKTKDAEVEKSRLPFIGSGFSS-----	196
Oabi_HY_XP_012277082	-PTA-IEREWASIGSNLRNIADDFHASHTKGAEVEKSRLPFIGSTS-----	192
Ccal_HY_XP_017884183	HTQAYNQWQWTNMGANLRNIADDFHASKTKAAEIEKSRLAAMNPGYASSGN-----	210
Bimp_HY_XP_024222863	-GQAFNGNYWATVGANLRNIADDFHASKTKAAEIEKSRLSAMNPSFANTNN-----	208
Bter_HY_XP_012175674	-GQAFKGSYWATVGANLRNIADDFHASKTKAAEIEKSRLSAMNPSFANTNN-----	208
Dnov_HY_XP_015429159	-GQAFNESQWASVGANLRNIADDFHASQTKAAEIEKSRLPALSPGFASAQN-----	203
Nmel_HY_XP_031834337	-GQAFNESQWASVGANLRNIADDFHASKTKAAEIEKSRLPALSPGFAGANN-----	209
Mgen_HY_XP_033321541	-GQAFNESQWASVGANLRNIADDFHASKTKAAEIEKSRLPTLSPGFVGSNP-----AA	212
Ador_HY_XP_006609937	-GQAFNESQWASVGANLRNIADDFHASQTKAAEIEKSRLPAMNPSFADSNN-----	208
Aflo_HY_XP_012338864	-GQAFNESQWASVGANLRNIADDFHASQTKAAEIEKSRLPAMNPSFADSNN-----	208
Amel_HY_XP_006565903	-GQAFNESQWASVGANLRNIADDFHASQTKAAEIEKSRLPAMDPSFADSNN-----	208
Olig_HY_XP_034171762	-GQAFNESQWANVGANLRNIADDFHASKTKAAEIEKSRLPAMNPGFANSNGN-----	211
Obic_HY_XP_029055907	-GQAFNESQWANVGANLRNIADDFHASKTKAAEIEKSRLPAMNPGFANSNGN-----	211
Emex_HY_XP_017765203	-GQAFNESQWASVGANLRNIADDFHASKTKAAEIEKSRLPAMNSGFANSNN-----	208
Pgra_HY_XP_020280259	-S-QNERQSWTNMGTNLRNIAGDFHACKTKDAESEKSRLSVNGRRLTNG-----	202
Obir_HY_XP_011342863	-G-QNERQSWANVGNTNLRSIAGDFHACRTKDAEGEKSRLPVIGPLPNARN-----	219
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Nlec_HY_XP_015511746	--ESSPDSFLLIPAPLRETLWTTVALYLGWRLVSHLR	229
Nvit_HY_XP_003424554	SPSGSTDSILSLLMPAPLRETLWTTVALYLGWRLVSRLR	266
Btre_HY_XP_033214430	--NSSTDSILSLLIPAPLRETLWTTVALYLGWRLVSRLR	245
Mdem_HY_XP_008555096	--IPSSDGFLSMLIPAPLRETLWTTVALYLGWRLVSRLR	244
Ccin_HY_XP_015609297	--SPSTDSLLSLLIPAPLRETLWTTVALYLGWRLVSRLR	233
Oabi_HY_XP_012277082	---SAADSFLLIPAPLRETLWTTVALYLGWRLVSRLR	228
Ccal_HY_XP_017884183	---SSTDSYMSLLIPAPLRETLWTTVALYLGWRLVSHLR	246
Bimp_HY_XP_024222863	-SSESTDSFLLIPAPLRETLWTTVALYLGWRLVSRLR	246
Bter_HY_XP_012175674	-TSGSTDSFLLIPAPLRETLWTTVALYLGWRLVSRLR	246
Dnov_HY_XP_015429159	-TNGSTDSLLSLLIPAPLRETLWTTVALYLGWRLVSRLR	241
Nmel_HY_XP_031834337	-TNGSTDSILSLLIPAPLRETLWTTVALYLGWRLVSRLR	247
Mgen_HY_XP_033321541	SNAGSTDSLLSLLIPAPLRETLWTTVALYLGWRLVSRLR	251
Ador_HY_XP_006609937	-TSGSTDSILSLLIPAPLRETLWTTVALYLGWRLVSRLR	246
Aflo_HY_XP_012338864	-TSGSTDSILSLLIPAPLRETLWTTVALYLGWRLVSRLR	246
Amel_HY_XP_006565903	-TSGSTDSILSLLIPAPLRETLWTTVALYLGWRLVSRLR	246
Olig_HY_XP_034171762	-ATGSTDSLLSLLIPAPLRETLWTTVALYLGWRLVSRLR	249
Obic_HY_XP_029055907	-AAGSTDSLLSLLIPAPLRETLWTTVALYLGWRLVSRLR	249
Emex_HY_XP_017765203	-ANGSTDSILSLLIPAPLRETLWTTVALYLGWRLVSRLR	246
Pgra_HY_XP_020280259	-NSNSTDMLSLLIPTPLRETLWATVALYVGWKLVSRLR	240
Obir_HY_XP_011342863	RNSSFTDNLSLLIPTPLRETLWATMALYLGWRLVSRLR	258
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