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SUPPLEMENTARY INFORMATION

Table S1: Annotated secreted proteins of *M. abscessus* predicted in silico.

Serial #	Protein ID	Protein name		Locus name	Gene symbol	Molecular function	Biological Function		
1	B1MEL2	Antigen precursor	85-A	MAB_0176	fbpA	Mycolyltransferase	Cell wall biogenesis		
2	B1MEL3	Antigen precursor	85-A/B/C	MAB_0177	fbpA	Mycolyltransferase	Cell wall biogenesis		
3	B1MMV2	Antigen precursor	85-B	MAB_1579	fbpA	Mycolyltransferase	Cell wall biogenesis		
4	B1MEL1	Antigen precursor	85-C	MAB_0175	-	Mycolyltransferase	Cell wall biogenesis		
5	B1MFV7	Probable bifunctional membrane-associated penicillin-binding protein PonA2/glycosyl transferase		MAB_0408c	ponA2	Glycosyltransferase Hydrolase Transferase	Cell wall biogenesis /degradation		
6	B1MP31	Probable penicillin-binding membrane protein PbpB		MAB_2000	pbpB	Hydrolase	Antibiotic resistance/cell wall biogenesis/degradation		
7	B1MEK4	Putative N-acetylmuramoyl-L-alanine amidase		MAB_0168c	-	Protein binding	Peptidoglycan process	catabolic	
8	B1MKI9	Conserved hypothetical protein (lipolytic enzyme G-D-S-L?)		MAB_1193c	-	Hydrolase	Lipid metabolic process		
9	B1MGX0	Probable hemolytic phospholipase C	non-	MAB_0555	-	Hydrolase	Lipid catabolic process		
10	B1MMD5	Phosphate transporter, periplasmic protein	ABC	MAB_4852c	pstS3	Inorganic phosphate transporter activity	Phosphate Stress Transport	transport response	
11	B1MDZ7	Probable FeIII-dicitrate-binding periplasmic lipoprotein		MAB_3390	fecB	Iron ion transmembrane transporter activity	High-affinity transport	iron	ion
12	B1MHE3	Probable low-affinity inorganic phosphate transporter		MAB_3950c	pitA	Transporter activity	Phosphate transport		

13	B1MC95	Probable molybdenum ABC transporter, periplasmic	MAB_2787c	-	Molybdate transmembrane-transporting ATPase activity	Molybdate ion transport
14	B1MLN1	Probable sugar ABC transporter, sugar-binding protein LpqY	MAB_1372	lpqY	Transporter activity	Transport
15	B1MGZ1	Putative ABC transporter solute binding protein	MAB_0577c	-	Transporter activity	Transport
16	B1MBC2	Putative sulfonate ABC transporter, periplasmic protein	MAB_2462	-	Transporter activity	Sulfur metabolic process
17	B1MGZ0	Putative ABC transporter, ATP-binding protein	MAB_0576c		ATPase activity	Transport
18	B1MIT8	Putative amino acid ABC transporter, substrate-binding protein	MAB_4236c	-	Transporter activity	Transport
19	B1MD08	Putative glutamate ABC transporter, periplasmic protein	MAB_3051	-	Transporter activity	Transport
20	B1MJV4	Putative ABC transporter, periplasmic substrate-binding	MAB_4390	-	ATPase activity	Transport
21	B1MH02	Porphyromonas-type peptidyl-arginine deiminase	MAB_0588c	-	Hydrolase	Nitrogen compound metabolic process
22	B1MBK6	Probable amidohydrolase	MAB_2546	-	Hydrolysis	Metabolism
23	B1MG92	Probable cutinase cut2 precursor	MAB_3763	cut2	Hydrolase esterase	Metabolic process
24	B1MG94	Probable cutinase cut3 precursor	MAB_3765	cut3	Cutinase activity	Metabolic process
25	B1MG95	Probable cutinase cut3	MaB_3766	Cut3	Hydrolase activity	Metabolic process
26	B1MG78	Putative phosphodiesterase/alkaline phosphatase	MAB_3749	-	Phosphatase activity	Metabolic process
27	B1MC13	Beta-lactamase precursor (Penicillinase)	MAB_2875	blaC	Hydrolase	Antibiotic resistance
28	B1MBQ0	Putative polysaccharide deacetylase	MAB_2590	-	Hydrolase	Carbohydrate metabolic process
29	B1MDW2	Putative secreted hydrolase	MAB_3355	-	Hydrolase	Carbohydrate metabolic process
30	B1MH82	Putative triacylglycerol lipase precursor	MAB_3889	-	Hydrolase	Lipid degradation
31	B1MHZ7	Putative triacylglycerol lipase precursor	MAB_0723c	-	Hydrolase	Lipid degradation
32	B1MK31	Sulfatase family protein	MAB_4469c	-	Sulfuric ester hydrolase activity	Metabolic process
33	B1MKF7	Conserved hypothetical protein	MAB_1161c	-	Peroxidase activity	Hypothetical

Table S2: Identification of secretory proteins in the mid-log-phase culture of *M. abscessus* with 2D-GE proteomics.

Spot ID #	Protein ID #	Protein Name	Locus Name	Score	Coverage	Proteins	Unique peptides	Peptides	PSMs	AAs	MW [KDa]	Calc. PI
ML4	B1MCR7	Uncharacterized protein	MAB_2960	14.67	9.53	1	5	5	5	682	73.5	5.03
ML5	B1MIY6	Uncharacterized protein	MAB_4284c	19.52	6.55	1	3	3	5	687	62.9	5.01
ML6	B1MIY6	Uncharacterized protein	MAB_4284c	25.59	9.17	1	4	4	7	687	62.8	5.008
ML7	B1MIY6	Uncharacterized protein	MAB_4284c	34.92	9.17	1	4	4	9	687	62.9	5.01
ML10	B1MMK7	Uncharacterized protein	MAB_4924	20.1	14.02	1	4	4	7	321	32	5.02
ML11	B1MKW1	Uncharacterized protein	MAB_4537c	4.38	4.5	1	2	2	2	333	35.7	5.88
ML13	B1MEL1	Antigen 85-C	MAB_0175	44.88	16.98	1	4	5	12	324	34.7	6.8
ML13	B1MEL2	Antigen 85-A	MAB_0176	17.79	10.21	1	2	3	6	333	35.8	6.57
ML13	B1MEL3	Antigen 85-A/B/C	MAB_0177	10.37	5.85	1	2	2	3	325	34.9	6.13
ML13	B1MDF1	Elongation factor Ts	MAB_3195c	10.77	8.66	1	2	2	3	277	29.1	5.08
ML13	B1MDV5	uncharacterized protein	MAB_3348	6.96	10.10	1	2	2	2	287	29.5	6.34
ML14	B1MEL2	Antigen 85-A	MAB_0176	36.52	16.22	1	3	5	12	333	35.8	6.57
ML14	B1MEL1	Antigen 85-C	MAB_0175	17.34	8.02	1	2	3	5	324	34.7	6.8
ML14	B1MEL3	Antigen 85-A//B/C	MAB_0177	14.31	12	1	2	3	4	325	34.9	6.13
ML15	B1MNL7	Immunogenic protein MPT64	MAB_1835c	15.96	14.55	1	4	4	6	275	29.4	6.19
ML16	B1MEL2	Antigen 85-A	MAB_0176	21.59	12.91	1	4	4	7	333	35.8	6.57
ML16	B1MEL3	Antigen 85-A//B/C	MAB_0177	8.41	8.62	1	3	3	3	325	34.9	6.13
ML17	B1MDW2	Putative secreted hydrolase	MAB_3355	14.2	12.59	1	2	2	4	286	28.9	6.3
ML18	B1MMY7	Uncharacterized protein	MAB_1614	29.25	19.25	1	4	4	8	213	22.3	4.88
ML19	B1MMY7	Uncharacterized protein	MAB_1614	14.6	15.96	1	2	2	3	213	22.3	4.88
ML20	B1MFV4	Uncharacterized protein	MAB_0405c	22.72	13.33	1	3	3	8	195	20.2	5.99
ML21	B1MBL9	Peptidyl-prolyl cis-trans isomerase	MAB_2559c	19	17.86	1	2	2	5	196	19.1	5.06
ML22	B1MCH9	Uncharacterized protein	MAB_2871c	48.17	22.86	1	4	4	15	140	14.8	5.12
ML23	B1MIR3	Uncharacterized protein	MAB_4211c	9.37	22.9	1	2	2	3	131	14	5.14
ML25	B1MBM0	Uncharacterized protein	MAB_2560	30.97	27.36	1	4	4	9	201	20.5	5.88

ML27	B1MNM5	D-alanyl-D-alanine dipeptidase	MAB_1843	17.51	19.37	1	3	3	5	222	23.8	6.92
ML27	B1MBM0	Uncharacterized protein	MAB_2560	17.1	21.89	1	3	3	5	201	20.5	5.88
ML28	B1MFV1	Uncharacterized protein	MAB_0402	18.92	16.24	1	3	3	6	234	25.2	6.71

Table S3: Identification of secretory proteins in the late-log-phase culture of *M. abscessus* with 2D-GE proteomics.

Spot ID #	Protein ID #	Protein Name	Locus Name	Score	Coverage	Proteins	Unique peptides	Peptides	PSMs	AAs	MW [KDa]	Calc. PI
LL3	B1MJB0	Uncharacterized protein	MAB_0974	9.39	8.09	1	3	3	3	606	61.2	5.39
LL4	B1MCR7	Uncharacterized protein	MAB_2960	8.2	2.49	1	2	2	3	682	73.5	5.03
LL5	B1MJB0	Uncharacterized protein	MAB_0974	12.93	7.1	1	3	3	4	606	61.2	5.39
LL5	B1MCR7	Uncharacterized protein	MAB_2960	8.12	2.49	1	2	2	4	682	73.5	5.03
LL6	B1MIY6	Uncharacterized protein	MAB_4284c	22.85	6.11	1	3	3	7	687	62.9	5.01
LL7	B1MIY6	Uncharacterized protein	MAB_4284c	15.3	3.49	1	2	2	4	687	62.9	5.01
LL8	B1MIY6	Uncharacterized protein	MAB_4284c	36.53	9.17	1	4	4	9	687	62.9	5.01
LL9	B1MIY6	Uncharacterized protein	MAB_4284c	15.73	7.57	1	3	3	4	687	62.9	5.01
LL11	B1MIY6	Uncharacterized protein	MAB_4284c	25.53	9.17	1	4	4	7	687	62.9	5.01
LL12	B1MB96	Uncharacterized protein	MAB_2436	24.95	11.63	1	4	4	8	344	34.8	6.06
LL12	B1MJN7	Aldehyde dehydrogenase family protein	MAB_4322	5.3	4.92	1	2	2	2	447	47.2	4.82
LL13	B1MMK7	Uncharacterized protein	MAB_4924	28.85	23.05	1	5	5	9	321	32	5.02
LL14	B1MMK7	Uncharacterized protein	MAB_4924	36.53	24.92	1	5	5	12	321	32	5.02
LL16	B1MKW1	Uncharacterized protein	MAB_4537c	18.73	13.81	1	3	3	6	333	35.7	5.88
LL17	B1MEL1	Antigen 85-C	MAB_0175	29.86	13.27	1	3	4	8	324	34.7	6.8
LL17	B1MDF1	Elongation factor Ts	tsf	22.48	18.05	1	4	4	6	277	29.1	5.08
LL17	B1MEL2	Antigen 85-A	MAB_0176	19.25	10.21	1	2	3	6	333	35.8	6.57
LL18	B1MEL2	Antigen 85-A	MAB_0176	41.42	16.22	1	4	5	14	333	35.8	6.57
LL18	B1MEL3	Antigen 85-A/B/C	MAB_0177	20.45	12	1	2	3	7	325	34.9	6.13

LL18	B1MDV5	Uncharacterized protein	MAB_3348	17.62	10.1	1	2	2	5	287	29.5	6.34
LL19	B1MEL2	Antigen 85-A	MAB_0176	62.34	18.92	1	4	6	19	333	35.8	6.57
LL19	B1MEL3	Antigen 85-A/B/C	MAB_0177	40.29	12	1	2	3	11	325	34.9	6.13
LL19	B1MEL1	Antigen 85-C	MAB_0175	32.15	16.98	1	4	5	9	324	34.7	6.8
LL19	B1MEC9	Uncharacterized protein	MAB_0093	13.39	8.85	1	2	2	4	260	28.4	5.34
LL19	B1MDV5	Uncharacterized protein	MAB_3348	11.23	10.1	1	2	2	3	287	29.5	6.34
LL20	B1MEL1	Antigen 85-C	MAB_0175	19.15	11.42	1	3	3	5	324	34.7	6.8
LL21	B1MNL7	Immunogenic protein MPT64	MAB_1835c	38.19	28.73	1	6	6	12	275	29.4	6.19
LL22	B1MDW2	Putative secreted hydrolase	MAB_3355	20.54	22.03	1	4	4	6	286	28.9	6.3
LL23	B1MMY7	Uncharacterized protein	MAB_1614	36.11	15.96	1	3	3	8	213	22.3	4.88
LL24	B1MMY7	Uncharacterized protein	MAB_1614	20.67	15.96	1	3	3	5	213	22.3	4.88
LL25	B1MBM0	Uncharacterized protein	MAB_2560	25.26	27.36	1	4	4	7	201	20.5	5.88
LL25	B1MG92	Cutinase	MAB_3763	13.46	10.96	1	2	2	4	228	23.5	6.3
LL26	B1MBM0	Uncharacterized protein	MAB_2560	13.87	13.43	1	2	2	4	201	20.5	5.88
LL27	B1MBM0	Uncharacterized protein	MAB_2560	67.28	37.81	1	6	6	18	201	20.5	5.88
LL28	B1MBD4	Uncharacterized protein	MAB_2474	14.46	10.87	1	3	3	4	184	19.1	8.41
LL29	B1MFV4	Uncharacterized protein	MAB_0405c	12.74	12.82	1	2	2	4	195	20.2	5.99
LL29	B1MDB0	Uncharacterized protein	MAB_3154c	6.6	11.79	1	2	2	2	212	21.7	5.06
LL30	B1MBL9	Peptidyl-prolyl cis-trans isomerase	MAB_2559c	13.19	17.86	1	2	2	4	196	19.1	5.06
LL30	B1MFV4	Uncharacterized protein	MAB_0405c	11.75	13.33	1	3	3	4	195	20.2	5.99
LL31	B1MGD1	Uncharacterized protein	MAB_3801c	19.76	25.7	1	3	3	6	179	18.5	6
LL32	B1MGD1	Uncharacterized protein	MAB_3801c	6.1	15.08	1	2	2	2	179	18.5	6
LL36	B1MCH9	Uncharacterized protein	MAB_2871c	60.59	22.86	1	4	4	17	140	14.8	5.12
LL38	B1MDK0	Soluble secreted antigen MPT53	MAB_3243	5.93	11.8	1	2	2	2	178	19.1	9.57
LL39	B1MAH1	Hypothetical low-molecular-weight antigen Mtb12	MAB_2161c	26.23	27.43	1	3	3	7	175	17.3	4.81

LL39	B1MDK6	Uncharacterized protein	MAB_3249	10.43	13.61	1	2	2	4	147	16.2	6.58
LL39	B1MIH2	Probable aldo/keto reductase	MAB_4120c	3.39	4.26	1	2	2	2	329	35.3	5.11
LL42	B1MNM5	D-alanyl-D-alanine dipeptidase	MAB_1843	41.05	35.59	1	6	6	11	222	23.8	6.92
LL45	B1MCS9	Uncharacterized protein	MAB_2972	25.05	24.39	1	3	3	7	164	17.6	7.06
LL47	B1MMY9	Uncharacterized protein	MAB_1616	14.89	19.44	1	3	3	5	180	20.3	7.97

Table S4: N-terminal signal sequences and probable cleavage sites in the secretory proteins of *M. abscessus* predicted with the in silico analysis of the secreted proteins identified with 2D- GE proteomics.

Serial #	Protein ID	Protein Name	Signal peptide sequence	Cleavage position
1	B1MCR7	Uncharacterized protein	Non-classically secreted protein that lacks SP	-
2	B1MIY6	Uncharacterized protein	Non-classically secreted protein that lacks SP	-
3	B1MMK7	Uncharacterized protein	MTTTRYSVRF AA ATASVAALLAGTAAVAMA-DPQP	30
4	B1MEL2	Antigen 85-A	MKLFSKMRGALARQSARRI AV A-ATAV	22
5	B1MEL1	Antigen 85-C	MSVRVKARRVLSALLA AF VMPSMAAA-MTIN	27
6	B1MEL3	Antigen 85-A//B/C	MKLFSQLRGKTARRLATVAAA-AAVL	21
7	B1MNL7	Immunogenic protein MPT64	MPYLSLR SIS ASVLVTAASIFGFSGVAGA-APHD	29
8	B1MDW2	Putative secreted hydrolase	MRALRTLSTMIGLAAVVAATAAVPPIASA-EPAA	29
9	B1MMY7	Uncharacterized protein	MTGRITGIVSALVGAVALVLGLFGSMAVATA-SPDT	31
10	B1MFV4	Uncharacterized protein	MKKRLVSAGVIALAAALSGPAALA-AAAP	24
11	B1MBL9	Peptidyl-prolyl cis-trans isomerase	MNLFRVSPSATLAACTASFVMALAACGSDTEANSAPA-DPPS	37
12	B1MCH9	Uncharacterized protein	MTGMGRITAALLATASTATLTLALAPAAEA-APHQ	30
13	B1MIR3	Uncharacterized protein	MLVTLASGVVIGAAAAPMTA-ADPG	20

14	B1MBM0	Uncharacterized protein	MRTIAIRHRAVIGLSAVALITVGCSNG-TSVD	27
15	B1MNM5	D-alanyl-D-alanine dipeptidase	MMKRLILGFGYAALGIGCALGQVAPASA-DPDI	28
16	B1MFV1	Uncharacterized protein	Non-classically secreted protein that lacks SP	-
17	B1MJB0	Uncharacterized protein	MHVGIRTVAVAAVCGLCVGAGVDARA-VRPN	26
18	B1MB96	Uncharacterized protein	MQQPRATSAAKRTHRARVIAATIAVTSLSGAGA-YTLA	33
19	B1MJN7	Aldehyde dehydrogenase family protein	Not predictable as secretory protein	-
20	B1MKW1	Uncharacterized protein	MLVLTRWFRRALVSGVCVAGLLGAGVVPALA-DPGD	31
21	B1MDF1	Elongation factor Ts	Not predictable as secretory protein	-
22	B1MDV5	Uncharacterized protein	MTSVGDKGRRRTGPWGRLTAYAAAVAALSGIGLANPI AAHA-DPLI	40
23	B1MEC9	Uncharacterized protein	MRIAASVLAAALCGWAGTAPVVRA-EPSS	24
24	B1MG92	Cutinase	MTLQPNPRPASKLLTAAARAAVVSVAAIMLTTGLAV VIPATASA-ACPN	44
25	B1MBD4	Uncharacterized protein	MKSTYAVLLGIALLLVTPGLASA-DVPR	23
26	B1MDB0	Uncharacterized protein	MIARLITTTGLLMAALGLTEAAAAIA-EPID	25
27	B1MGD1	Uncharacterized protein	MDTPMQVSQGRRGISKARVRATGVAALTALALVALPGVA GA-DPEV	41
28	B1MDK0	Soluble secreted antigen MPT53	MNIQFGGRKKFRAQQVRGLTRTVAVVVAVLLVSAGLVRAP SARA-DGLL	44
29	B1MAH1	Hypothetical low-molecular-weight antigen Mtb12	MTGVAMLGLLAAVAVGSAVPTGEPTASS-ASPT	28
30	B1MDK6	Uncharacterized protein	MTSRPQCYVIAAITAAATFCASFFWAQTAAA-EPIV	31
31	B1MIH2	Probable aldo/keto reductase	Not predictable as secretory protein	-
32	B1MCS9	Uncharacterized protein	MRLRPALSLIAALTAVITALAPTASA-LPDR	26
33	B1MMY9	Uncharacterized protein	MKRMLAATALTAALTALGTPAVHA-APNR	24

Potential cleavage sites are indicated by hyphens in amino acid sequences.

Table S5: N-terminal signal sequences and probable cleavage sites in the secreted proteins of *M. abscessus* predicted in silico.

Gene ID	Signal sequences	Amino acid residues
MAB_0046	MNLNVVPEGLTATSAAVEALTARLAAAHAAA-APVI	31
MAB_0063c	MKFSHHLTRRTAGAACVLGAAAVITAPAASA-APDC	31
MAB_0093	MRIAASVLAAALCGWAGTAPVVRA-EPSS	24
MAB_0168c	MRVSKMPVRRQLALAVAATATVMTVSVVDHIKSGQ-AEETA	35
MAB_0169c	MPNRRRRRLSTALSSVAALAVASPFALATNMTQAA-APAP	37
MAB_0353	MRTARTVLTSVAAAFLGTATPAAGA-VPSD	26
MAB_0360	MRSVMGALSVALGVMTPATATA-DPSS	22
MAB_036	MDINGVSAIVTGGASGLGAATARLLAAQGAKVVIA-DVQD	35
MAB_0424	MRYGLPVLIALFGLFAAAIPAAA-APAA	23
MAB_0463c	MAVSRSQWGRRGFLQLGAATAAGVLA-ACGT	27
MAB_0521	MTEVAVALSGGADSLALAAAVARA-WSVT	25
MAB_0555	MSPLTRRRLLTSAAGTAAFSAAVSLMPANLQRVLAQP-APRS	37
MAB_0560	MSRDTGRRRPKHALPKSNKRWSVSKTAAA-RTIF	29
MAB_0565c	MKRTLAAATAATAVMSLVLPATAQA-APPK	25
MAB_0576c	MSAATLRDASLNRGGRTLWQGLDLTVEPGEFIAVLGPNGSGK-TSLL	46
MAB_0588c	MHRRHLFKLGAATAGAVMLTACA-DPPD	23
MAB_0620c	MTRWTGLMVAAITLTGGIAASTAVAPNVACA-CSCV	32
MAB_0684c	MRDLSRRSLLKLGAATGAGAALLGAGAFPAGA-DGAI	32
MAB_0723c	MPTASHRARGALRDPAPQHPRAGKLRIILLATALVASLVTTEGA-PTTL	43
MAB_0734	MAGTFIRCIRSACFAAVVVGVAVLQAPPVFA-EPVT	31
MAB_0743c	MRKPLIATIAAVCALALAATGTDFGFA-IFAE	27
MAB_0848c	MLRRLCTATATLALAAAAYPPVAQA-EPEQ	25
MAB_0869c	MSGRHSPSKASAKAAKVAVAGAGLVGGGLMMAATANA-ATDG	38
MAB_0884c	MKRVWAAVVGGAMLAATQSSCA-ASTQ	22
MAB_0957	MCAALGVGLLSGGAAVAHA-DPAF	19
MAB_1003c	MRISKLFAGRVARGVAGTVVAAAMAGTALVGAPLAGA-SAQS	37
MAB_1026c	MKINVPITAAVAAAAAAGLALMPTAGA-DTTL	28
MAB_1042c	MYLVTCFAFFMVGGLMALLIRA-ELTT	22
MAB_1161c	MSTGLNRRKLLGAAGVTAAVAGAAGAGVLGGRASA-ASTG	35
MAB_1164	MSSVAVRSLPARFGRIMLVVSISVFLLA-AGCS	28
MAB_1193c	MSILATRRRTIWAALSTGAAGA-AMGT	22
MAB_1261	MTKSGYFATALDAMVVVLPVAAVALA-AVAH	26
MAB_1271c	MNTGMSPRLDRRELLRLGMTAAAAGFLASCTKNTSGA-ATSP	37
MAB_1322	MNKFLCATAVLLSMAGWAPAAAA-EPGN	23
MAB_1323	MATVVMGLAVGLAVPATA-APPP	18
MAB_1363	MVDSGSFRRASFSSFSRLPSPFA-SQSG	25
MAB_1372	MLESSARWFRKGVGVALGSSLLTCLTLASLTGCA-RSDD	33
MAB_1543	MKGLSLTAMIAMGAGAAIAMASPAYA-DDVS	27
MAB_1553c	MDKLRTRVVIGIAAVGMSVGSFSAAGIAQA-NDHT	30
MAB_1616	MKRMLAATALTAALTALGTPAVHA-APNR	24
MAB_1843	MMKRLILGFGYAALGIGCALGQVAPASA-DPDI	28
MAB_1974	MSVGRLLRNHSDRLTPSPLRRAMLAVTAAALVGGVFTGAQTATA-DPNN	44
MAB_2000	MNRQDRSRPVGARRTRPAAAVSRTAGFA-FRHR	29
MAB_2113	MITNFRRFSAAGILAASAVALAAPAHA-DGEV	27

MAB_2329c	MAVRKRVGAVMALVTAICTFATAPAHA-DPVA	27
MAB_2456	MDPQSRPALMTRRTVLSAGAMLALG-STSL	25
MAB_2462	MNGRAPRRAVLTGAAGIAATAGLFGATGLVRA-AMFD	32
MAB_2546	MCTACEWAPHFAALSAKSTRRTALRAAVALTLAAGAAA-CSAG	38
MAB_2590	MFDRRRFLTLLAGAAAAGASFIEYVSA-AADP	27
MAB_2594	MVPISRRDVLKYAAAI PAAALAGAVSAAAPRANA-ASLG	34
MAB_1511	MVPISRRDVLKYAAAI PAAALAGAVSAAAPRANA-ASLG	34
MAB_2697c	MILGAAVVVATLSGCASSGGQQDAEA-SIAV	26
MAB_2699c	MTSRSLPVPDGLSGMRVDAGLARLLGLSRTAAA-ALAE	30
MAB_2750c	MKFGPGTSAGTAATAAPSLNAAPA-ASTE	24
MAB_2787c	MFGGAPQTAGLFGPRRSASLVVALA-AFLA	25
MAB_2798c	MRLLNIRRYLAVPAVTAFa-AGLA	19
MAB_2799	MLKSLVSLTTVCALALTAPLAFA-DPED	23
MAB_2800	MNDTHSNSSHLSTRGATPMLKSLAAATAVCALAVTAPFALA-DPGD	41
MAB_2805c	MSAVAAGVGLVASPALSADPAAET-APKI	26
MAB_2871c	MTGMGRITAALLATASTATLTLALAPAAEA-APHQ	30
MAB_2875	MISRRALLVGVSAGVVAAGCSRNGNRRPA-PDEL	31
MAB_2878c	MDSRSPARTGARRIARIGAIVTTVLLAAGLLTSCWTSAA-KTLD	39
MAB_3031c	MTASRLVATMVVAGCCAAIAPA-CTRA	22
MAB_3051	MSRLRDEDARVMRRRHTALVAALALLATLVSA-CGST	32
MAB_3154c	MIARLITTGLLMAALGLTEAAAAIA-EPID	25
MAB_3165c	MLVVTGLVSLLMNAAVTAPATLGHALA-ASPS	27
MAB_3215c	MTVPVVVVALPMGSPGATVSG-SPVH	21
MAB_3264c	MVAVASGAVSLAAAGVALA-DDGD	19
MAB_3305c	MAVMISRRGWLVASAVALSGQAIPA-CSAP	25
MAB_3348	MTSVGDKGRRTGPWGRLTAYAAVAALSGIGLANPIAHA-DPLI	40
MAB_3355	MRALRTLSTMIGLAAVVAATAAVPPIASA-EPAA	29
MAB_3390	MQTARLWGAAAI SAALVTATVSG-CTEK	23
MAB_3454	MSTRRRISVVLMTSAVIGSSVAVDVAPVAYA-DPCA	31
MAB_3472	MRMLLITCVAVAAGATTTFAGQAAA-DPPP	24
MAB_3493	MALTATLMTACTAAVGATAFG-ASLA	21
MAB_3532	MIAPERTRADI IAAAVIAVVAVTGTTIWWTSDARA-TVSR	37
MAB_3681	MTTWT PAPDRRPSRTAVTRLAAATAAGLIVAVLPLCAPPLASA-EPGF 44	
MAB_3749	MTAFPRRTVLRAALLGLAAVPVAA-CGPA	24
MAB_3763	MTLQPNPRPASKLLTAAARA VVSVAAIMLTTGLAVVIPATASA-ACPN	44
MAB_3765	MTTHSAVL PATSYVRRPGYLLAALLMFASLVAMSQVPVAAA-DPCA	41
MAB_3889	MIKRGLALAAVTALT VAGLNSSQVVA-GYGD	26
MAB_3910	MSDPAPRGPKRPSVISPMVLAPAGTTEA-KALA	28
MAB_3950c	MDATMIILVLLIATALA-FDFT	17
MAB_4037	MSHRLRGLRAGIAATALLASAQVIHPVATARA-ALPP	32
MAB_4061c	MKYPRPHLGDALTRRRALTILGLTVPAVAAA-CTTV	31
MAB_4062c	MRI AIVTLVMWLGLTAAPPATA-DPGP	22
MAB_4185c	MNERVPDSHGLPLRAMVMVLLFLGVIFLLVGFNALG-SDKS	36
MAB_4192	MRRGHV I IAMQTIACLLLLAGSAYL-YTIV	25
MAB_4211c	MLVTLASGVVIGAAAAPMTA-ADPG	20
MAB_4212c	MALFSARGLARGCSLLAIAAVASCCAHPSTPGA-AAPT	33
MAB_4236c	MRFLT VLVCTALT VLAGCAEGA-APGS	22
MAB_4280c	MRGWLRTISALVVIAGLGAAVPAAA-EPKS	25

MAB_4281c	MMMLRFVATLALVAGFSTATATAAA-EPTP	23
MAB_4390	MPPGMITRRGLLAAGAALAASTALA-SCAK	25
MAB_4469c	MAELNRRTVLTTGAIAAGA-AAVG	19
MAB_4576c	MRGLLGAFVAGAALLTPVATA-EPHD	21
MAB_4782	MHHSSAPGRHSGSSLVSRRDALRYVLTAPLLAGLPVFAAPQAAA-DGLR	44
MAB_4852c	MKLNRFGAVLTLVASGALVLSACGSDNNASG-SSGS	31
MAB_4903	MTSRRLSTALAGFAIITGAAA-GCGT	21
MAB_4914c	MRGAPVILLSVTVLLSSCTQAIA-GDAT	23
MAB_4915c	MRRGMAAVCIVLSLAGCSRISGGE-PTAP	24
MAB_4924	MTTTRYSVRFAAATASVAALLAGTAAVAMA-DPQP	30

Potential cleavage sites are indicated by hyphens in the amino acid sequences.