SUPPLEMENTARY MATERIAL

Elharar *et al,* 2014

SUPPLEMENTARY FIGURE LEGENDS

Figure S1. Pupylome quantification and purification. (*A*) Aliquots of *M. smegmatis* cultures were collected at the indicated time points, as described in the main text, and prepared together with a purified pupylome for quantification, as described in the Experimental Procedures section. A lysate purified from a Δ*pafA* mutant (designated "B") served as a blank for quantification. Dot blot analysis was carried out with anti-Pup antibodies according to standard protocols. (*B*) Pupylomes were purified from exponentially growing and stationary phase *M. smegmatis* cultures expressing dually polyhistidine- and streptactin-tagged Pup via tandem affinity purification. Shown are fractions of the final purification step, as analyzed by Western analysis using anti-Pup antibodies. (*C*) The same procedure as in (*B*) was carried out for control cultures not expressing the dually-tagged Pup.

Figure S2. Gel loading controls. Shown are the PVDF membranes used in Western blots that are presented throughout this paper. At the end of each Western analysis, the membranes were stained by Coomassie Briliant Blue, de-stained and air-dried. For each membrane presented, the figure number and antibodies used are indicated. Asterisks indicate that the membranes were stripped before a second use with an additional antibody, as indicated. For the membranes presented in Fig. 6C, additional information is provided (P-Z = Pup-Zur; Z=Zur).

Figure S3. The anti-Pup antibodies detect two cross-reacting proteins. (*A*) The *paf* operon was deleted from the Msm chromosome via homologous recombination using a suicide plasmid carrying a hygromycin-resistance cassette. (*B*) Southern analysis of BsrDI-digested DNA from the wild type and Δ*pafA* strains. Probes specific for the hygromycin-resistance gene (left) and for a DNA sequence upstream of the deleted region were used. (*C*, *D*) Western analysis using anti-PafA and anti-Pup antibodies, as indicated. (*E, F*) Following expression of a polyhistidine-streptactin-tagged Pup in the Δ*pafA* mutant, tandem purification was carried out as described (Festa et al., 2010 and Methods). Samples from the purification steps were subjected to Western analysis using anti-Pup antibodies. The final sample was concentrated prior to analysis. Only the dually-tagged Pup was eluted following the final purification step. By contrast, although the two bands in question could be seen in the lysate prior to purification, they were not bound by the affinity columns and as such correspond to antibody-cross-reacting proteins.

Figure S4. *M. smegmatis* growth is limited by the availability of a carbon source under standard growth conditions. A carbon or a nitrogen source, or both, were added to stationary phase *M. smegmatis* cultures previously inoculated in 7H9 supplemented with 0.4% glycerol (v/v). Turbidity was measured before and 24 h after nutrient addition. Whereas carbon source addition allowed growth to resume, nitrogen source addition did not, indicating the carbon source was the limiting factor. The final cell density was, however, higher when both carbon and nitrogen sources were added, indicating that when a carbon source alone was added, a nitrogen source became limiting.

Figure S5. Proteasomal degradation of PPS components. (*A*) Exponentially growing cultures ($O.D._{600}$=0.5) of a Δ*prcSBA* mutant that expresses either *prcS* or the *prcSBA* operon from an integrated plasmid were starved for nitrogen. Aliquots were collected at the indicated time points from the onset of starvation (t=0) for Western analysis. (*B*) As in *A*, except that the cultures were starved for 7 days before the first aliquot (t=0) was collected.

SUPPLEMENTARY TABLE LEGENDS

Table S1 – Exponential phase pupylome, Table S2 – Stationary phase pupylome.

Column annotation: MSMEG – *M. smegmatis* identifier, MH+[Da] – Observed mass of precursor peptide, ΔM[ppm] – deviation of observed peptide mass from calculated mass in parts per million, m – oxidation of methionine, c – Carbamidomethylation of cysteine, k – identified pupylation site.

Colors annotation: Pale blue – depicts *M. smegmatis* proteins that were found to be pupylated in previous studies (Poulsen C, *et al*., 2010, Watrous J, et al., 2010). Yellow – Identified pupylated peptides.

Fig. S1

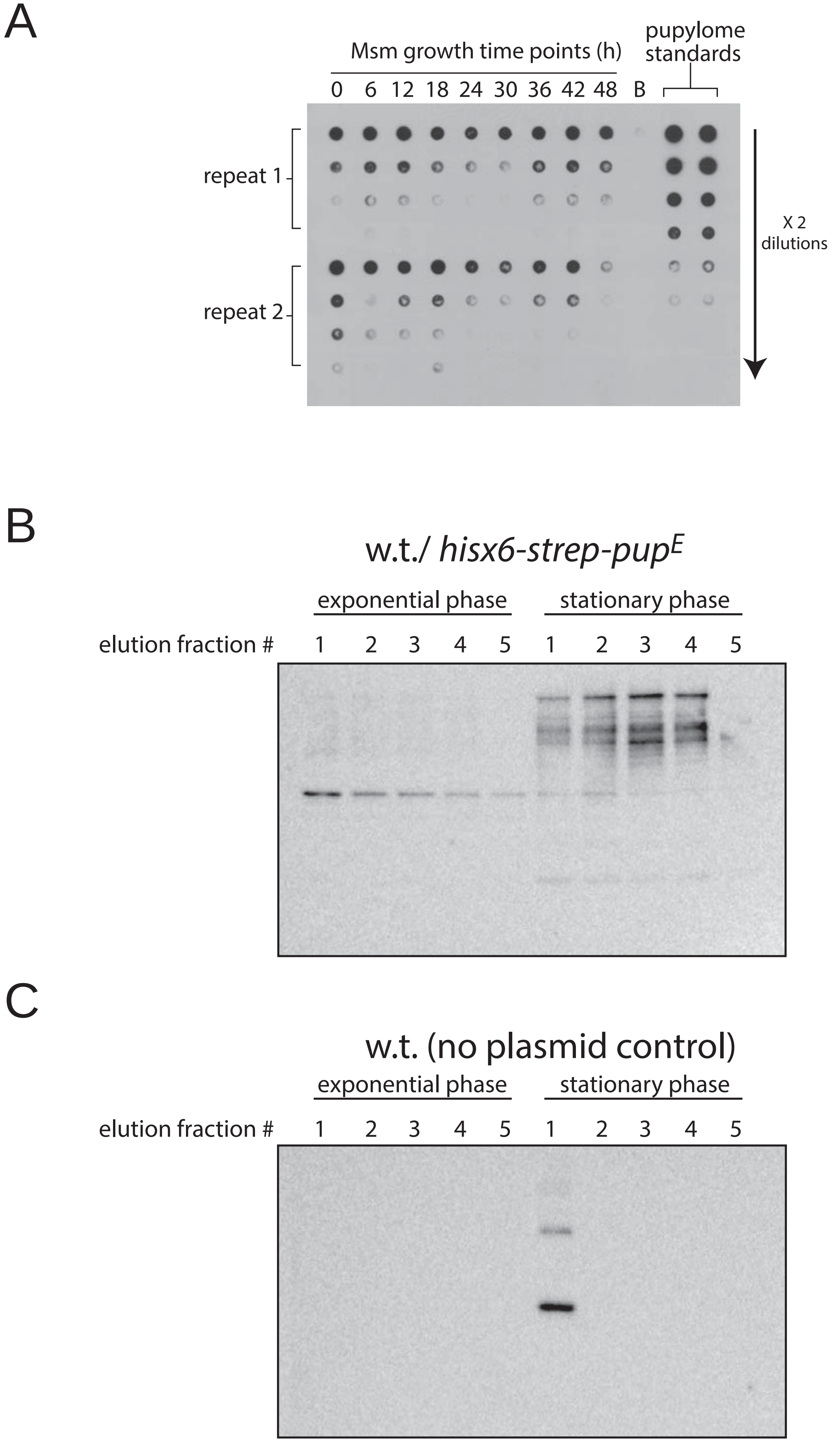

A
Msm growth time points (h)
pupylome standards
0
6
12
18
24
30
36
42
48
B
repeat 1
repeat 2
X 2 dilutions
B
w.t./ *hisx6-strep-pup*^{E}
exponential phase
stationary phase
elution fraction #
1
2
3
4
5
1
2
3
4
5
C
w.t. (no plasmid control)
exponential phase
stationary phase
elution fraction #
1
2
3
4
5
1
2
3
4
5

Fig. S2

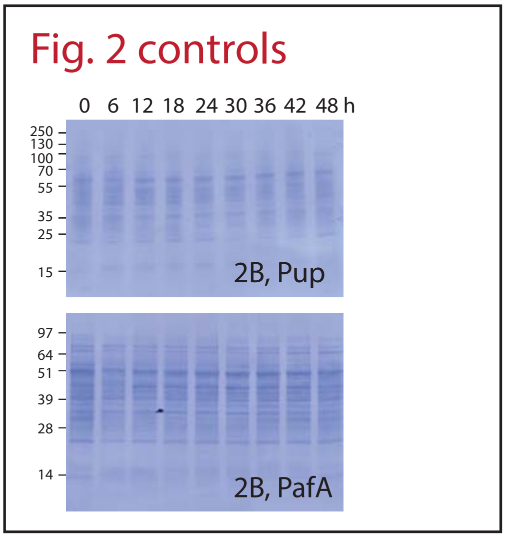


Fig. 2 controls

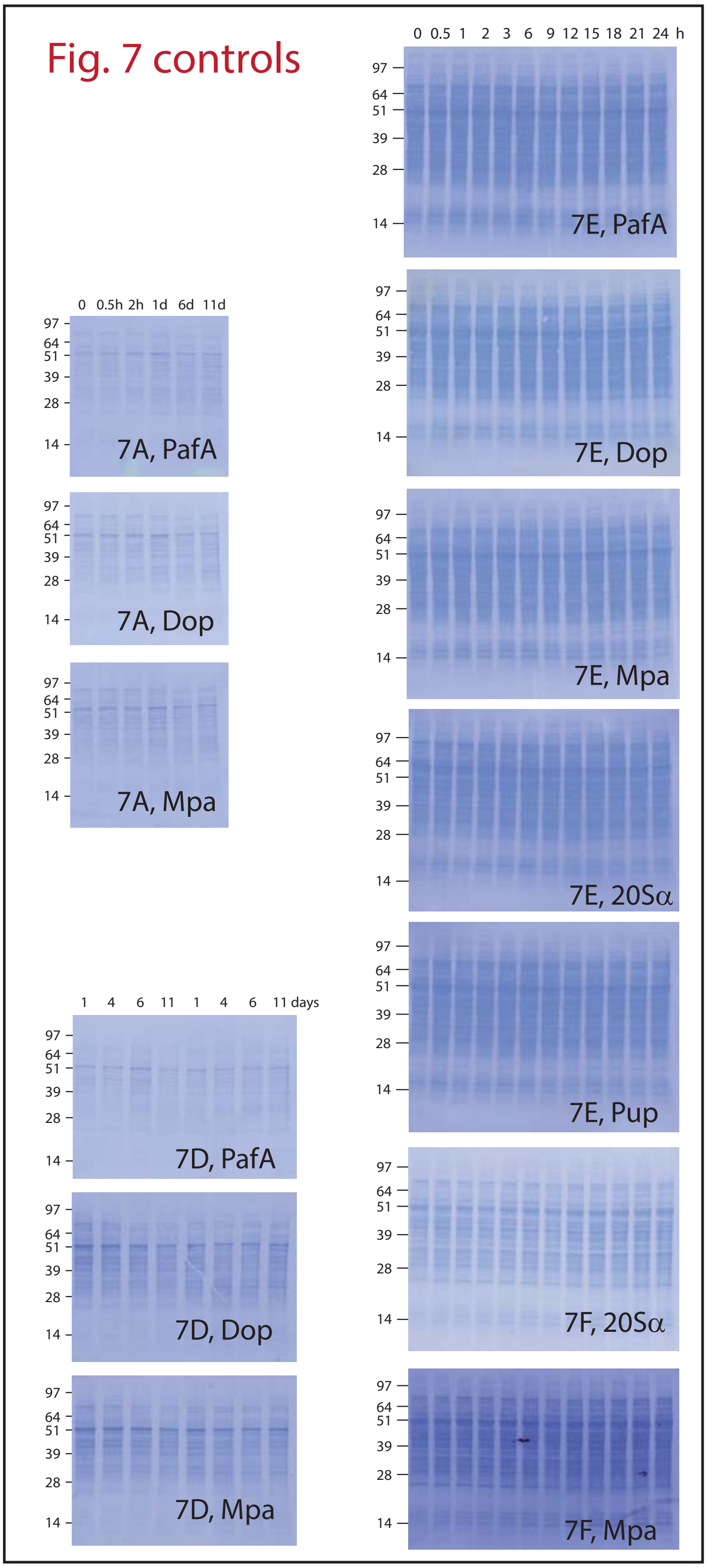


Fig. 7 controls

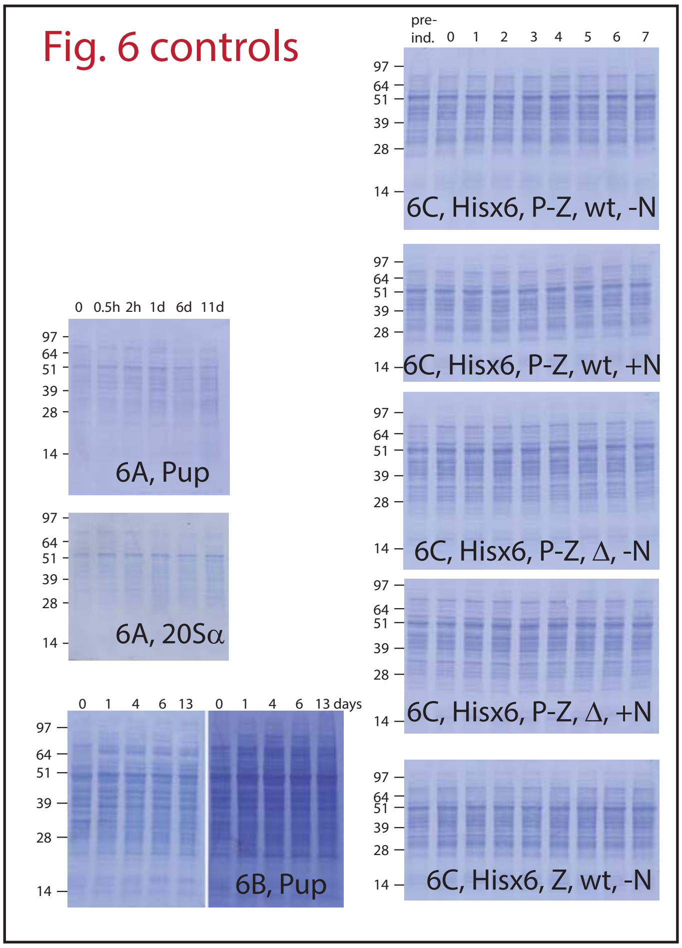


Fig. 6 controls

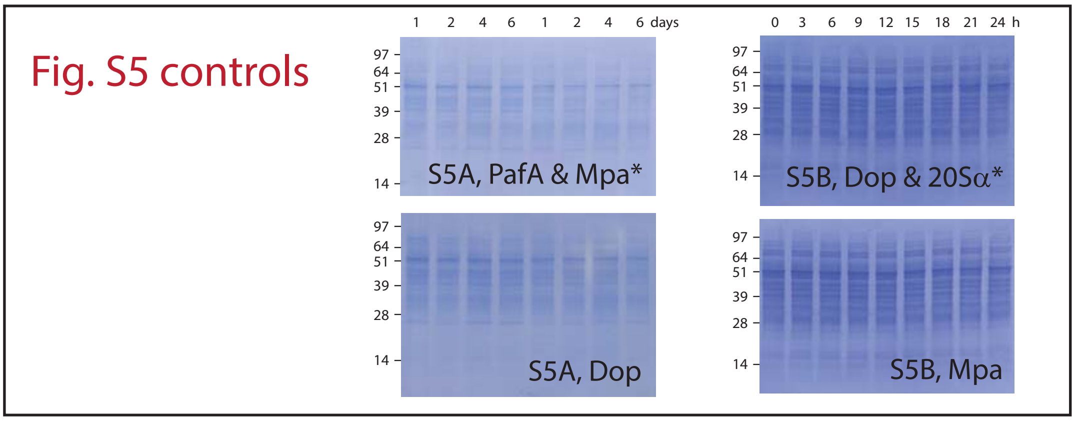


Fig. S5 controls

Fig. S3

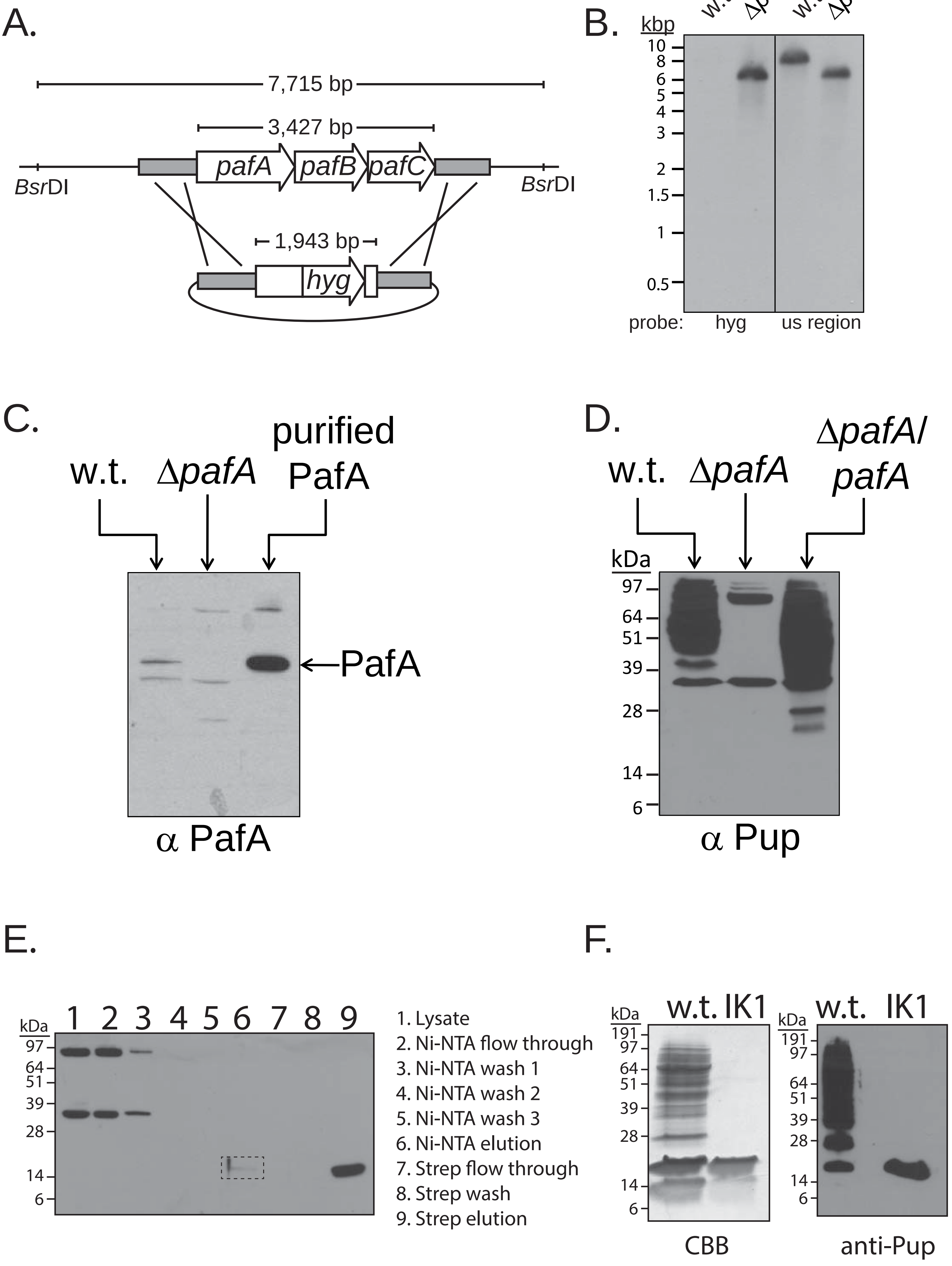
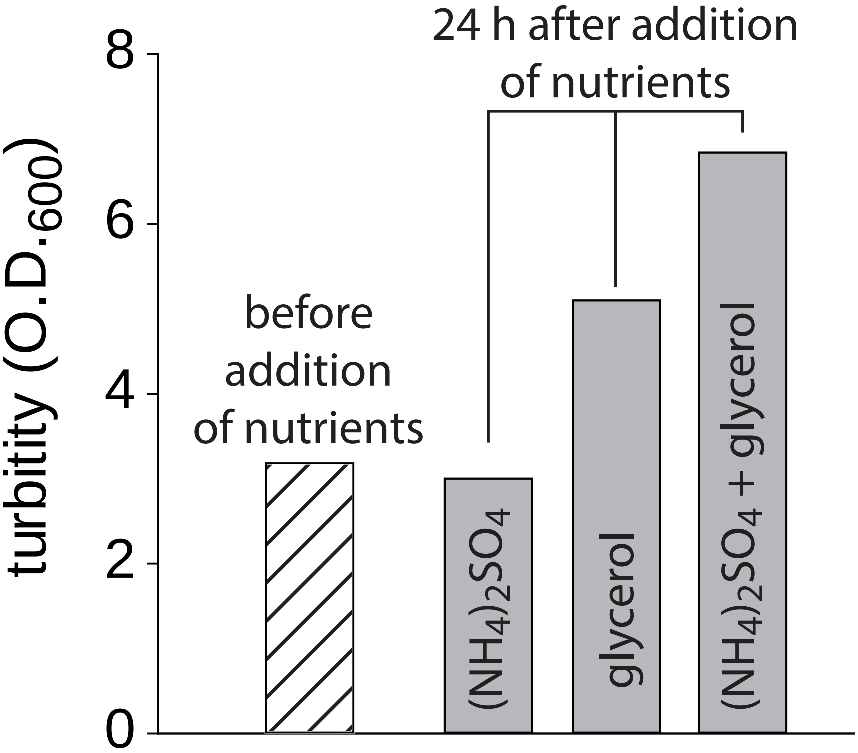

A.
7,715 bp
3,427 bp
pafA
pafB
pafC
BsrDI
BsrDI
1,943 bp
hyg
B.
w.t.
ΔpafA
w.t.
ΔpafA
kbp
10
8
6
5
4
3
2
1.5
1
0.5
probe:
hyg
us region
C.
w.t.
ΔpafA
purified PafA
PafA
α PafA
D.
w.t.
ΔpafA
ΔpafA/ pafA
kDa
97
64
51
39
28
14
6
α Pup
E.
kDa
1 2 3 4 5 6 7 8 9
97
64
51
39
28
14
6
1. Lysate
2. Ni-NTA flow through
3. Ni-NTA wash 1
4. Ni-NTA wash 2
5. Ni-NTA wash 3
6. Ni-NTA elution
7. Strep flow through
8. Strep wash
9. Strep elution
F.
kDa
w.t. IK1
191
97
64
51
39
28
14
6
CBB
kDa
w.t. IK1
191
97
64
51
39
28
14
6
anti-Pup

Fig. S4



24 h after addition of nutrients
before addition of nutrients
turbitity (O.D.$_{600}$)
8
6
4
2
0
$(NH_4)_2SO_4$
glycerol
$(NH_4)_2SO_4$ + glycerol

Fig. S5

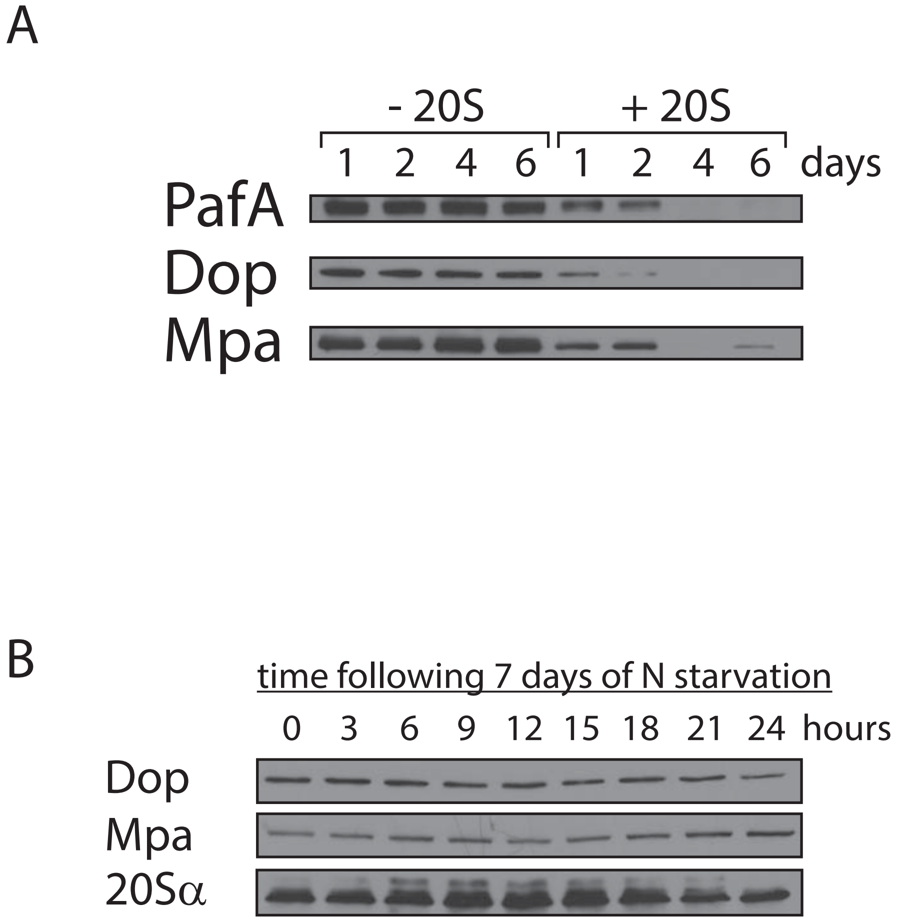

A
- 20S
+ 20S
1 2 4 6 1 2 4 6 days
PafA
Dop
Mpa
B
time following 7 days of N starvation
0 3 6 9 12 15 18 21 24 hours
Dop
Mpa
20Sα

Table S1 – Exponential phase pupylome

Accession	MSMEG	Description	Score	%Coverage	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
259546730	3896	RecName: Full=Prokaryotic ubiquitin-like protein Pup; AltName: Full=Bacterial ubiquitin-like modifier	440.35	76.56	EKLTEETDDLLDEIDDVLEENAEDFVR	3194.48069	1.83	6.18
					GGGGGEDDDLPGASAAGQER	1815.77495	0.46	5.18
					LTEETDDLLDEIDDVLEENAEDFVR	2937.34403	2.30	4.95
					RGGGGGEDDDLPGASAAGQERR	2127.97904	1.26	4.01
					RGGGGGEDDDLPGASAAGQER	1971.87700	0.90	3.69
					GGGGGEDDDLPGASAAGQERR	1971.87503	-0.10	3.33
118469767(118472545)	6427	[Mn] superoxide dismutase [Mycobacterium smegmatis str. MC2 155]	125.41	35.75	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					NLSPNGGDKPTGELAAAIDDQFGSFDK	2764.30790	0.62	5.68
					AFWNVVNWDDVQNR	1762.83196	1.30	4.79
					HHATYVkGVNDAIAK	1866.94975	2.15	4.14
					ANGDHAAIFLNEK	1399.69805	1.09	3.88
					GVNDAIAKLEEAR	1385.73796	-0.32	3.83
118470577	4323	pyruvate dehydrogenase subunit E1 [Mycobacterium smegmatis str. MC2 155]	84.16	24.54	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					GLIQVAANEALDNLTFVINcNLQR	2686.40403	2.16	7.42
					LMPDFWEFPTVSMGLGPMNAIYQAR	2871.37534	2.96	4.99
					VPVSDAQLEEDPYLPPYYHPGPEAPEIR	3178.54245	1.75	3.97
					KGSGSQAVATTMATVR	1564.81144	0.12	3.95
					SAQILASGVAMPEALR	1613.86980	1.08	3.39
					KGSGSQAVATTmATVR	1580.80753	0.86	3.35
					SKPLALPGSDTYK	1376.74346	1.01	3.09
					IIQELESFFR	1281.68547	1.29	3.09
					TGDGLWAAADQMAR	1462.67632	1.29	3.05
					GYTLGQHFEGR	1264.60906	1.66	2.91
					TFGMDSWFPSLK	1415.66741	0.66	2.68

					AVPEQIRPWVPGTYVTLGTDGFGFSDTRPAAR	3461.76963	2.71	2.95
					RYFNTDAESVVVAVLQGLAR	2208.17759	0.16	2.23
					LALEDLK	801.47423	3.17	1.49
118470644	6904	myo-inositol-1-phosphate synthase [Mycobacterium smegmatis str. MC2 155]	83.61	41.87	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					TYQLNVGGNMDFLNMLER	2115.00200	1.01	5.22
					VGFDLSEAIFASENNTIK	1954.97539	-0.18	5.06
					KFEDAGVPIVGDDIK	1602.83818	0.45	4.82
					GIGGPIEAASAYLMK	1477.77446	1.66	4.45
					YYADTIEVSDAEPVDVVK	2012.97222	1.11	4.45
					TQAVTSNLSGALAGKVEDK	1889.00640	4.69	4.42
					VAIVGVGNcASSLVQGVQYYR	2240.15141	0.95	4.33
					NADENTTVPGLMHVK	1625.80217	4.25	3.69
					IADVPPTDVIVQR	1422.80058	3.80	2.98
					NADENTTVPGLmHVK	1641.79026	0.05	1.93
118474021	4294	glutamine synthetase [Mycobacterium smegmatis str. MC2 155]	76.71	37.67	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					SPDSAcNPYLTFAVLLAAGLR	2236.14629	1.40	5.42
					LVHGGEAPTAASWGAANR	1764.87847	0.43	4.90
					SVAIAPAELEGAFEEGIGFDGSSIEGFAR	2926.40384	-2.34	4.73
					GYVLGPQAEDNVWSLTQEER	2291.09526	0.57	3.88
					LWFTDVLGYLK	1354.74077	0.12	3.82
					VFESDTVARPDPSTFQVLPWK	2419.23374	1.81	3.58
					SFIAGILEHANEISAVTNQWVNSYK	2791.41245	2.64	3.38
					YADALSMADNVMTFR	1704.77580	2.18	3.23
					SFIAGILEHANEISAVTNQWVNSYKR	2947.51040	1.43	2.09
					SEWENYR	983.42162	-0.15	1.35
300680919	3897	RecName: Full=Pup deamidase/depupylase; AltName: Full=Deamidase of protein Pup	73.18	38.96	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LHVIIGDANLAETSTYLK	1958.06035	0.49	5.10
					IIGTEVEYGISSPSDPTANPILTSTQAVLAYAAAAGIQR	3946.04336	-0.31	4.88
					AHVGALLDSVDSAVELVEQLTN	2280.17681	2.16	4.81

					VGIGPSGDEPGFQLSQR	1743.86687	0.42	4.09
					LVTEQQVLDAVENPPTDTR	2125.07988	1.24	3.76
					TRWDYEVESPLR	1550.76128	0.93	3.68
					LHLVDLQYSDVR	1457.77483	0.05	3.51
					QTPFSAVIAGLTPFMVSR	1922.02117	0.33	3.34
					GASYGSHENYLMSR	1571.69267	1.22	2.95
					LHLVDLQYSDVRLDK	1813.98062	-0.06	2.54
					ELTALALQR	1014.59789	3.56	2.45
					IPTLEPLRGSK	1210.71819	2.25	2.46
					IPTLEPLR	938.56682	-0.18	1.73
118472545(118469767)	6636	[Mn] superoxide dismutase [Mycobacterium smegmatis str. MC2 155]	69.68	49.51	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					NLSPHGGDKPTGDLAAAIDDQFGSFDNFR	3062.42978	1.88	6.83
					AQFTAAANGLQGSGWAVLGYDTLGDR	2639.28838	1.29	5.21
					HHATYVkGVNDAIAK	1866.94975	2.15	4.14
					GVNDAIAKLEEAR	1385.73796	-0.32	3.83
					AIWNVVNWQDVQVR	1726.90372	0.74	3.73
					FAAATGKGPDPIV	1243.67229	3.29	2.18
118470483	6772	hypothetical protein MSMEG_6772 [Mycobacterium smegmatis str. MC2 155]	66.77	45.91	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					TYGELNADKSNAIVYPTWYSGR	2505.20586	0.52	4.54
					MDEFPQDYELFDLGDVTLQHGATLR	2910.36699	1.86	4.52
					MIVAPAEKDLYFPPEDEEFAVK	2538.24980	0.95	4.35
					SALTADAAFKEGWYTEKPTK	2214.10782	0.00	4.07
					YFIIVPNMLGNGLSTSPSNTPPPYNAAR	2991.50859	1.73	3.25
					TSEHNIVFLEGVK	1472.77629	1.26	3.01
					VIPGIYGHFAGGDANPEDNKFIDGLVR	2871.44913	2.29	2.93
118469679	1679	AmiB [Mycobacterium smegmatis str. MC2 155]	63.54	30.13	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					cFEAGALASGAELIVTPESKPYAEFR	2813.38272	0.40	4.90
					RVASTLAEGGFDVTER	1707.87210	3.50	4.36
					GGFDGQHFAAMVHPGPVDVAR	2165.03691	1.05	4.13

					DLYDHPEIAWEEVR	1771.82866	0.00	4.06
					VASTLAEGGFDVTER	1551.77239	4.75	3.26
					AQPFAVSHSHIEYR	1641.81841	3.13	3.13
					AETLGQLAEIERK	1457.80144	3.79	3.00
					AETLGQLAEIER	1329.70000	-0.71	2.84
					QFVSGPDTAMAR	1279.61125	0.96	2.54
118470561	4303	methyltransferase [Mycobacterium smegmatis str. MC2 155]	58.88	35.14	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					APADLYAAGHAELAAYPSVQVR	2270.15923	1.20	6.36
					VASDLPAGHALDLGcGEGGDAVWLAER	2736.30631	0.56	5.70
					HDLSESFPDGEFDLVSAQFLHSTVR	2833.34690	1.42	5.21
					VLLVDAGEQSNLPAHGIGGLLGSDGR	2545.34307	2.37	4.81
					LVAHDGELVAVEFTDGTR	1928.97295	0.84	4.67
					SPLAAQLGAIGAPTPLAGDAVVVDTFGR	2664.44097	1.98	4.36
					VTAVDISHTALSR	1369.74480	0.98	3.54
					SVFHcPFcHGWEVR	1817.79966	-0.17	3.09
					DAPLAVIAR	925.54875	2.33	1.82
118469746	6756	glycerol kinase [Mycobacterium smegmatis str. MC2 155]	57.45	16.24	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					TAGLLPAIAAELDDEILLAR	2065.15605	0.96	6.33
					YIAALDQGTTSTR	1396.70879	1.47	3.97
					IIPQALADADVEPR	1507.81218	0.40	3.06
					GLVVGLTSYVTK	1236.72112	1.02	2.91
					QIMALGITNQR	1244.68230	3.43	2.57
					RIIPQALADADVEPR	1663.92558	7.75	2.51
					AVLEATAWQIR	1257.69536	0.24	2.21
118472263	1439	50S ribosomal protein L2 [Mycobacterium smegmatis str. MC2 155]	47.60	34.89	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					ATVGEVGNAEQSNINWGK	1873.91094	3.72	4.72
					TANIALLHYLDGEKR	1713.92949	0.69	3.83
					RGASVSDFAEITR	1408.72246	3.17	3.60
					QGDVIESGANADIKPGNNLPLR	2278.18814	4.14	3.59
					NIPAGTVIHAVELRPGGGAK	1957.10759	4.96	3.38

					GASVSDFAEITR	1252.62236	4.38	2.90
					YIIAPQGLK	1002.60149	3.20	1.99
118470741	3300	oxidoreductase, Gfo/Idh/MocA family protein [Mycobacterium smegmatis str. MC2 155]	40.36	40.17	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AFAHDQLLGTAAAPTFGDAVALHR	2450.25968	0.83	5.43
					MTPIGVGVIGASPNGGWAALAHVPALR	2612.42264	3.64	4.68
					VPDHYGLITDALTAGK	1670.87578	0.54	4.53
					AVFSEWPLGVALEQAQILHAEAVVAGVPTVVGLQAR	3726.03843	0.13	3.98
					LIAGIEHVNTESHR	1575.82512	0.81	3.20
					VLSTNIVGSGMAWAPGAPAAQAYAFDAR	2792.38547	1.02	2.65
118472266	0255	phosphoenolpyruvate carboxykinase [Mycobacterium smegmatis str. MC2 155]	38.61	21.88	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					IASAMAHDEGWLAEHMLILK	2236.13193	2.91	5.58
					LNPEKQPNSYLALSDPSDVAR	2314.17656	3.93	4.84
					LcAHLVEAGTFQK	1473.75310	0.80	3.91
					TNLAMLQPTIEGWR	1629.84197	0.09	3.46
					TIAAGNTVFTNVAK	1406.77056	4.75	3.17
					VFFVNWFR	1114.58342	0.10	2.33
					TTVPLITEAR	1100.63469	3.31	2.03
					LPTGLKDEFDALK	1446.78467	0.50	2.34
					YITHFPETR	1163.58551	0.95	2.21
					FLWPGFGENSR	1309.63445	1.52	1.60
118468832	4084	acyl-CoA dehydrogenase [Mycobacterium smegmatis str. MC2 155]	38.05	30.39	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					ALADAAETVMADGVGDK	1633.77458	0.42	4.93
					ALGDYLVNGNPLPR	1498.80364	1.54	4.50
					LWLDHIVAGDLFGNANTELTAK	2398.24344	1.33	3.74
					ELNHTSPVDAFAMIQEAR	2028.98271	0.92	3.17
					AKVTIENLVSR	1229.72453	2.65	3.08
					LTASGTAVFDNVR	1350.70952	6.11	2.61
					VTIENLVSR	1030.58769	-1.44	2.58

					VYTHEVFIR	1163.62200	1.03	2.27
					LATVDPNVAHALR	1376.76872	3.04	1.80
118471656	6242	alcohol dehydrogenase, iron-containing [Mycobacterium smegmatis str. MC2 155]	36.19	31.91	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					NMTTVQAADAAVEAAIR	1731.86931	-0.12	5.36
					AISEHIQDDWcTPGNPR	1995.90447	3.32	4.82
					LDFAPSLGNALYSVELVAK	2007.08245	1.31	4.15
					EVTVESMIPVVNHAINESY	2131.04180	1.93	3.80
					ALLGVGAHDIIGVEAK	1562.89018	0.01	3.65
					LAQDVGIPDNFSQVR	1658.85161	1.13	3.19
					YAQLATAMGVDTR	1396.69634	5.26	2.85
					TLLMTTGLR	1005.57543	-0.75	2.60
					NINEFEGFAK	1168.56352	0.13	1.67
118471823	1714	L-ribulose-5-phosphate 4-epimerase [Mycobacterium smegmatis str. MC2 155]	31.18	32.90	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					HMPEVGGVVHTHSTYATAWAAR	2378.14614	0.08	3.83
					LFDRYQNVYGQPQASQEG	2099.98833	4.84	3.27
					AAVMVEDVAR	1060.54668	0.99	3.19
					QLGTPDVIPPADVR	1477.80901	5.42	2.95
					GIVETLQHSNSR	1340.69170	-0.04	2.88
					YQNVYGQPQASQEG	1568.69914	0.98	2.78
118468273	2750	iron-dependent repressor IdeR [Mycobacterium smegmatis str. MC2 155]	29.11	45.65	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LLVDVIGLPWEDVHAEAcR	2192.12114	1.91	3.80
					LDQSGPTVSQTVSR	1474.75224	1.75	3.80
					IAERLDQSGPTVSQTVSR	1944.01517	0.30	3.78
					LTELPVGMPVAVVVR	1579.92571	1.01	3.00
					RLVQVLDNPTTSPFGNPIPGLTELGVTPGVNTEDVSLVR	4102.17588	-1.52	3.51
					TIYDLEEEGVVPLR	1632.84905	0.64	2.23
302595983	6286	RecName: Full=Putative aminotransferase MSMEG_6286	28.66	14.02	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					DAIDGLATcALLAATEALLGDK	2202.13291	0.25	5.77

					GGYFVSLDVWPGTAK	1596.80754	1.13	2.63
					FALVAEILEDR	1275.69438	-0.01	2.36
					IAPTFPSLPDVR	1312.72746	1.09	1.77
118469099	3532	serine/threonine dehydratase [Mycobacterium smegmatis str. MC2 155]	27.70	17.41	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					IFAVEPELAADTAESLALGSIVEWPVAK	2926.54483	-0.05	5.99
					LVAEPSGAVSLAGYR	1489.80596	3.33	3.67
					TPLLAADWGDPR	1311.66997	0.55	1.92
118473637	3061	primosome assembly protein PriA [Mycobacterium smegmatis str. MC2 155]	27.45	14.56	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					DVDALHAAVTAHVPESR	1787.90764	2.28	4.50
					ADGGVVAVVAESVLPTVQALIR	2164.24101	3.37	3.32
					TALDADRPVLIQVPR	1663.95169	1.58	3.22
					VVALSAGLGPSAR	1197.69890	3.20	2.53
					LPSMALQAAR	1057.58599	3.45	2.49
					LVDAFILER	1075.61370	-0.92	2.31
					LGPVDLPFGAR	1141.63689	0.35	2.58
118473746	4668	oxidoreductase alpha (molybdopterin) subunit [Mycobacterium smegmatis str. MC2 155]	27.06	10.38	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					APDAFLDALDAHFGITSPR	2014.00981	3.40	5.56
					GMIGKPGAGVcPVR	1398.73432	-0.16	3.11
					SEVAIVcQLAR	1245.66130	-0.60	2.79
					VVFVNPTDIAR	1230.68437	0.17	2.27
					GmIGKPGAGVcPVR	1414.72986	0.29	2.19
					ScNLTVQVSTK	1236.62517	-0.11	1.98
					VIAINPLPEAGLIR	1475.89067	-2.60	2.25
118469193	3396	IclR family transcriptional regulator [Mycobacterium smegmatis str. MC2 155]	24.95	43.41	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					FLNTLETIQETGVcAAPHISDVADGVAVAVR	3253.65818	1.80	5.11
					RDELVDLLTSHR	1453.77555	-0.20	3.75
					LGGAPYLLNLMAGR	1445.79460	0.82	3.01

					VAGILELAAR	1012.61528	0.26	2.56
					TVAAVSVVGPHEEIHSR	1787.93937	-0.33	2.86
					LLDAPLSSLQGLVNGLVAAGYLDEHDRR	2992.59243	2.41	2.87
118469097	5469	acetyltransferase, GNAT family protein [Mycobacterium smegmatis str. MC2 155]	23.76	24.40	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					TGGGIATAALAMGLDHcFTAVQLHR	2568.28543	1.69	3.85
					VPAGVVGLRPVR	1219.76323	-0.16	3.17
					HAVTSWPSIcSGLR	1570.78032	0.50	2.33
118471394	3517	HAD-superfamily protein subfamily protein IB hydrolase [Mycobacterium smegmatis str. MC2 155]	23.72	22.42	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					GHTVVLSSSALTIHAEPVAR	2045.12444	5.15	6.11
					QAAFGEVLGIIEASVR	1659.90837	1.10	3.53
					LTGDIVKPVIWGAR	1524.89006	0.20	3.38
302595980	5435	RecName: Full=Putative ligase MSMEG_5435	21.87	11.19	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AVIISEPFLVATPVLEEK	1955.11247	1.23	3.95
					LASLGPLLNDLEAR	1481.83220	-0.07	3.92
					TVTTGMVTGEPHEPVR	1710.85027	1.31	3.34
					GASLTMLHQPTPR	1408.73882	1.57	3.08
					TVTTGmVTGEPHEPVR	1726.84311	0.10	2.26
118469401	1028	geranylgeranyl reductase [Mycobacterium smegmatis str. MC2 155]	17.57	11.14	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VYGDAVIAADGAYSPIKR	1865.98638	5.74	4.67
					VTVFSPSEWELSFPR	1780.89287	1.31	3.83
					VVVLDKAEFPR	1272.73540	3.36	3.08
118468008	0402	linear gramicidin synthetase subunit D [Mycobacterium smegmatis str. MC2 155]	17.06	2.74	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LVGYITGTADPAAAR	1475.79045	3.46	3.37
					APDAVALVSGDR	1170.61638	4.25	2.96
					LVGYITGTADPAQLR	1574.85454	0.50	2.87
					GGGGGLTPSDVAPAR	1311.66570	0.35	2.33

					SGEAILSILSVLK	1329.80046	1.20	2.54
118473001	3200	L-aspartate oxidase [Mycobacterium smegmatis str. MC2 155]	16.10	9.42	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LAATGDPcVYLDAR	1521.74260	3.89	3.80
					TDVVVIGTGVAGLVAALAAHR	1990.14548	0.49	3.27
					LASNSLLEGLVVGSR	1514.85588	1.40	2.95
118473338	5181	IS1549, transposase [Mycobacterium smegmatis str. MC2 155]	14.76	10.86	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					NIEHVGSAHDEAELAALK	1903.95549	2.40	4.10
					VLTEVGVEPASYATVK	1662.90288	4.77	3.01
					LPIYAQPQWR	1271.68022	-7.34	2.76
					IPFLPDVVR	1055.62505	0.19	2.02
118472674	6519	pyridoxamine 5'-phosphate oxidase [Mycobacterium smegmatis str. MC2 155]	14.51	14.29	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					ASIAIVAPSAESDPLASAR	1825.96611	0.32	4.23
					VTLAGVAERPEGDELAAAR	1925.01641	3.95	4.10
118472433	6284	cyclopropane-fatty-acyl-phospholipid synthase [Mycobacterium smegmatis str. MC2 155]	14.20	21.51	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AYVSGDLEPHGVHPGDPYPLLR	2389.19803	1.85	3.66
					IITEAQDVGLEVIHEENLR	2178.14005	-0.07	2.99
					SIGIEHLKPIAPPPQEALPR	2163.22807	-0.22	2.94
					LGFETNVVQLHQVLAVK	1895.07584	0.45	2.46
					GTTYLATAPGDLGLAR	1576.83330	0.18	2.14
118470142	2293	hypothetical protein MSMEG_2293 [Mycobacterium smegmatis str. MC2 155]	12.47	14.72	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					TPVLSDDGSDLAAAVQTIIEAGLDDLQR	2883.47715	6.52	3.98
					TPSAFTLDPEIKR	1474.79551	3.67	2.18
					EAVFAGPVLRPSSTLVR	1799.01982	1.30	2.37
118472727	4029	hypothetical protein MSMEG_4029 [Mycobacterium smegmatis str. MC2 155]	12.34	20.40	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VDEPAPLALANTLWIDR	1894.00749	0.27	4.34
					LDVRPAPGSTDGLR	1453.77582	-0.02	2.42

					QAIELATSPR	1085.59538	0.35	2.21
118468233	3132	DNA-binding protein [Mycobacterium smegmatis str. MC2 155]	11.31	9.74	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					ERPSDQVLDALAR	1469.77239	1.11	2.49
					LSPSFAHGGNPLR	1352.71074	2.75	2.34
118471885	4042	GntR family transcriptional regulator [Mycobacterium smegmatis str. MC2 155]	7.55	13.49	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LQSEGLVQLVR	1241.72234	0.86	2.42
					EDEVTAEAGVSR	1262.58635	0.30	2.32
					LELEQAFAHHR	1350.69682	4.05	2.82
118469328	4124	hypothetical protein MSMEG_4124 [Mycobacterium smegmatis str. MC2 155]	7.49	15.19	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LQPALAVQSGVSATLAAAAGLR	2065.17844	0.92	3.96
					VAAHPGLAVIPVAVAITEDTWNDSRPSEDR	3186.62912	3.50	3.53
					SIAVAAFR	834.48546	2.64	1.58
118467565	2271	hydrogenase accessory protein HypB [Mycobacterium smegmatis str. MC2 155]	6.53	6.18	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VREVNPTTEILPVSAR	1781.00090	5.19	4.33
					EVNPTTEILPVSAR	1525.82353	0.93	2.20
118472927	3773	acetylornithine aminotransferase [Mycobacterium smegmatis str. MC2 155]	6.47	7.95	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					DAGFLVNAAAPEVVR	1528.81291	0.66	3.50
					VFFcNSGTEANEVAFK	1819.83257	0.29	2.97
118471393	0022	L-ornithine 5-monooxygenase [Mycobacterium smegmatis str. MC2 155]	5.82	7.05	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VFDPDAVDDFFVADPAVR	1994.95415	2.30	3.46
					SGEILESVITHTR	1441.77729	8.81	2.37
302595893	1843	RecName: Full=Adenosylhomocysteinase; AltName: Full=S-adenosyl-L-homocysteine hydrolase; Short=AdoHcyase	4.62	7.22	Sequence	MH+ [Da]	ΔM [ppm]	XCorr

					GVTEETTTGVLR	1262.65837	-0.28	2.95
					AGVVPPAEDDDPAEWK	1695.79228	3.61	1.67
					VFLGVLR	803.51293	-1.13	1.52
302595855	2621	RecName: Full=Prolyl-tRNA synthetase; AltName: Full=Proline--tRNA ligase; Short=ProRS	2.69	5.13	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					APEAQPTEGLPEAK	1437.72258	0.35	2.69
					LVAVIAEQQHDQLGLR	1790.00113	5.11	1.60

Table S2 – stationary phase pupylome

Accession	MSMEG	Description	Score	Coverage	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
259546730	3896	RecName: Full=Prokaryotic ubiquitin-like protein Pup; AltName: Full=Bacterial ubiquitin-like modifier	500.85	76.56	EKLTEETDDLLDEIDDVLEENAEDFVR	3194.48362	2.74	6.00
					LTEETDDLLDEIDDVLEENAEDFVR	2937.34220	1.67	5.26
					RGGGGGEDDDLPGASAAGQERR	2127.97556	-0.37	4.55
					GGGGGEDDDLPGASAAGQER	1815.77287	-0.68	4.28
					RGGGGGEDDDLPGASAAGQER	1971.87590	0.34	4.24
					GGGGGEDDDLPGASAAGQERR	1971.87577	0.27	3.01
300680919	3897	RecName: Full=Pup deamidase/depupylase; AltName: Full=Deamidase of protein Pup	271.96191	70.28	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LYVDHAHPEYSAPEcTDPMDAVIWDK	3059.37119	5.26	6.47
					LHVIIGDANLAETSTYLK	1958.06987	5.35	6.07
					LGTTSLVLDLIEEGVDLSDLALARPVHAVHVISR	3609.00234	0.32	5.58
					ASHVIETWANVLDLLERDPMEcAEILDWPAK	3621.77268	0.24	5.42
					QTPFSAVIAGLTPFMVSR	1922.02373	1.66	5.09
					VGIGPSGDEPGFQLSQR	1743.87419	4.62	4.70
					AHVGALLDSVDSAVELVEQLTN	2280.17070	-0.52	4.52
					LHLVDLQYSDVRLDK	1813.98857	4.32	4.21
					RLVTEQQVLDAVENPPTDTR	2281.18869	4.53	3.87
					LVTEQQVLDAVENPPTDTR	2125.08183	2.16	3.77
					LHLVDLQYSDVR	1457.78105	4.32	3.50
					LGTTSLVLDLIEEGVDLSDLALARPVHAVHVISRDPSLR	4177.30309	1.19	3.28
					TRWDYEVESPLR	1550.76653	4.31	3.26
					GASYGSHENYLMSR	1571.69316	1.53	3.25
					QRENLTWQAPR	1398.72498	0.89	3.07
					GIINTRDEPHADADKYR	1970.96866	0.36	2.78
					ELTALALQR	1014.59850	4.17	2.68
					IPTLEPLRGSK	1210.71831	2.35	2.61

					ENLTWQAPR	1114.56694	2.61	2.38
					WDYEVESPLR	1293.61699	4.60	2.30
					IPTLEPLR	938.57054	3.78	1.70
					GASYGSHENYLmSR	1587.68589	0.13	1.59
					LLEGFR	734.42241	3.84	1.43
					SSGPPPIVDADEVGAANMILTNGAR	2452.21611	0.94	1.30
					IIGTEVEYGISSPSDPTANPILTSTQAVLAYAAAAGIQR		2.46	2.06
118471656	6242	alcohol dehydrogenase, iron-containing [Mycobacterium smegmatis str. MC2 155]	247.35	47.99	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LDFAPSLGNALYSVELVAK	2007.08054	0.36	6.01
					NMTTVQAADAAVEAAIR	1731.86992	0.24	5.49
					EGMMNAQYIAGQAFNSGGLGIVHSISHAVSAFFDSHHGLNNAIALPR	4907.39545	1.21	5.07
					AISEHIQDDWcTPGNPR	1995.90679	4.48	4.66
					EVTVESMIPVVNHAINESY	2131.04009	1.13	4.48
					ALLGVGAHDIIGVEAK	1562.89690	4.31	4.14
					EGmMNAQYIAGQAFNSGGLGIVHSISHAVSAFFDSHHGLNNAIALPR	4923.39918	2.99	3.87
					LAQDVGIPDNFSQVR	1658.85723	4.51	3.37
					YAQLATAmGVDTR	1412.68608	1.54	3.13
					RTLLMTTGLR	1161.68132	3.46	2.92
					YAQLATAMGVDTR	1396.69487	4.21	2.81
					GSGIIEELTGK	1103.59502	0.61	2.51
					TLLMTTGLR	1005.57964	3.44	2.42
					VWEYNLPAR	1147.59453	4.37	2.24
					TLLmTTGLR	1021.57506	3.88	2.04
					NINEFEGFAK	1168.56767	3.68	1.87
118470577	4323	pyruvate dehydrogenase subunit E1 [Mycobacterium smegmatis str. MC2 155]	195.53	45.96	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					GLIQVAANEALDNLTFVINcNLQR	2686.40036	0.79	6.39
					YFNTDAESVVVAVLQGLAR	2052.07988	1.83	5.23
					VPVSDAQLEEDPYLPPYYHPGPEAPEIR	3178.54831	3.59	5.14
					LRHPDEPAGTPHVTSALADAAGPVIAVSDWMR	3337.67683	0.61	4.84
					RYFNTDAESVVVAVLQGLAR	2208.18047	1.46	4.32
					TkALVADMSDQEIWNLKR	2361.19754	4.54	4.20

					LMPDFWEFPTVSMGLGPMNAIYQAR	2871.37090	1.42	4.15
					TFGMDSWFPSLK	1415.66826	1.26	4.10
					TTLTGEGLQHADGHSLLLASTNPAAVTYDPAFAYEIAHIIESGLQR	4849.45327	2.05	3.77
					KGSGSQAVATTMATVR	1564.81290	1.05	3.76
					TGDGLWAAADQMAR	1462.68132	4.71	3.44
					KGSGSQAVATTmATVR	1580.80588	-0.18	3.42
					AVPEQIRPWVPGTYVTLGTDGFGFSDTRPAAR	3461.76230	0.60	3.38
					WNAAIMVHR	1097.56951	1.96	3.33
					IIQELESFFR	1281.68523	1.10	3.18
					TIKGYTLGQHFEGR	1606.83542	1.09	3.17
					GFVLGATAGR	948.52825	2.16	3.00
					SAQILASGVAMPEALR	1613.87688	5.47	2.98
					LTTDQLDGFRQEHSHSGGGLPSYPHPR	2989.44155	3.84	2.67
					SKPLALPGSDTYK	1376.74419	1.54	2.54
					EGVASYLPDIDTEETAEWLESFDELLER	3256.51030	1.40	2.28
					GYTLGQHFEGR	1264.60784	0.70	2.23
					DVTRVPVSDAQLEEDPYLPPYYHPGPEAPEIR	3649.79995	5.17	1.95
					GLYLYRPAPEKR	1462.81903	1.69	1.85
					LALEDLK	801.47533	4.54	1.35
					IVPIIPDEAR	1122.65679	4.44	1.53
118467956	4290	glutamine synthetase [Mycobacterium smegmatis str. MC2 155]	176.36	49.58	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					cPDSSGNPYLAFAAMLMAGIDGIKK	2627.27048	1.41	6.78
					cPDSSGNPYLAFAAMLMAGIDGIK	2499.17485	1.22	5.87
					FNTLLAAADDVLLFK	1650.90836	-1.13	5.69
					FcDLPGVVQHFSIPASAFDESVFEDGLAFDGSSVR	3802.78159	3.16	5.39
					HYIGGILHHAPSLLAFTNPTVNSYK	2750.44461	1.18	5.01
					DGQPLFHDESGYAGLSDIAR	2148.00957	4.77	4.40
					LIKDENVEYVDIR	1605.85398	3.52	4.26
					GGYFPVAPYDHYVDLRDQMATNLQNAGFTLER	3658.74424	1.57	4.24
					GGYFPVAPYDHYVDLR	1868.90764	5.87	4.16
					DQMATNLQNAGFTLER	1808.86858	4.93	3.85

					GFQSIHESDMMLLPDPNTAR	2259.05718	1.68	3.63
					TLNMNFFVHDPFTR	1738.83818	0.64	3.47
					LVPGYEAPINLVYSQR	1818.97666	0.95	2.96
					ENEIMPIQIRPHPYEFSLYYDV	2753.33159	1.29	2.74
302595855	2621	RecName: Full=Prolyl-tRNA synthetase; AltName: Full=Proline--tRNA ligase; Short=ProRS	153.35	50.43	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LGAALEPAEFALLDDADFAANPFLVK	2718.40434	0.62	4.98
					LVAVIAEQQHDQLGLR	1790.00127	5.18	4.71
					FKDAELLGMPWIVVVGR	1930.06243	0.21	4.54
					VVHGSSWITGADAPNR	1666.83158	1.14	4.44
					AGAAELVADLDRLGHEVLFDDRQASPGVK	3049.57046	0.05	4.41
					AVGPGIYSWLPLGLR	1598.90434	-0.66	4.24
					AGAAELVADLDRLGHEVLFDDR	2382.20670	0.73	3.86
					VYDTPDTPTIATLVEWANSASLPQFEGR	3078.50932	1.21	3.76
					WPSSVAPFDVHVVVANK	1851.97593	0.35	3.69
					APEAQPTEGLPEAK	1437.72270	0.43	3.67
					DGDPSPDGAGVLTSAR	1514.70989	1.09	3.65
					NNDYLLGPTHEELFTLTVK	2204.12473	0.58	3.63
					AGAAELVADLDR	1200.62724	4.39	3.51
					RLGAALEPAEFALLDDADFAANPFLVK	2874.51836	5.07	3.17
					GIEIGHIFQLGR	1339.75054	1.77	3.13
					SEMNAIGAQEILLPALLPR	2036.12546	2.20	3.12
					GWADGVVELR	1101.57329	4.07	2.45
					WTEYGDTLFR	1287.60430	2.97	2.44
					DFTPDGTIEAAEVR	1520.72856	3.78	2.34
					MSELFLR	895.47368	3.38	2.28
					HVVGLVAGR	907.54698	-0.31	1.75
302595983	6286	RecName: Full=Putative aminotransferase MSMEG_6286	141.06	50.23	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LMWDNAYAVHTLTDEFVEPVDVLGLAAAAGNPNRPLVFASTSK	4600.31357	-1.03	7.17
					HFAITESFGIENVPVPIREDGPDVDVIEQLVASDPTIK	4147.12387	0.07	6.11
					DAIDGLATcALLAATEALLGDK	2202.13346	0.50	6.03

					IAPTFPSLPDVRDAIDGLATcALLAATEALLGDK	3495.84775	2.06	5.60
					ITFAGAGVSFLGASADNIAWYLK	2372.23369	2.14	4.74
					GIWcVPVYSNPTGATYSTDVIR	2456.19414	1.05	4.54
					DAGIAVTEAGSAFPYRK	1752.90056	5.11	3.87
					GGYFVSLDVWPGTAK	1596.80657	0.52	3.39
					NYGGVQGLPELR	1302.68572	4.29	2.90
					FALVAEILEDR	1275.69560	0.94	2.87
					DAGIAVTEAGSAFPYR	1624.80388	4.46	2.79
					IAPTFPSLPDVR	1312.72612	0.07	1.93
118468273	2750	iron-dependent repressor IdeR [Mycobacterium smegmatis str. MC2 155]	126.68	76.52	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					RLVQVLDNPTTSPFGNPIPGLTELGVTPGVNTEDVSLVR	4102.18613	0.98	6.63
					MNDLVDTTEMYLR	1600.73955	3.07	4.33
					LVQVLDNPTTSPFGNPIPGLTELGVTPGVNTEDVSLVR	3946.09047	2.41	4.17
					IAERLDQSGPTVSQTVSR	1944.01627	0.87	3.79
					mNDLVDTTEMYLR	1616.73210	1.58	3.46
					LDQSGPTVSQTVSR	1474.75005	0.26	3.38
					WEHVMSEEVER	1430.63898	1.41	3.29
					LLVDVIGLPWEDVHAEAcR	2192.11943	1.13	3.18
					LTELPVGMPVAVVVR	1579.92313	-0.62	3.14
					LLVDVIGLPWEDVHAEAcRWEHVMSEEVER	3603.74494	2.46	3.03
					WEHVMSEEVERR	1586.73931	0.77	2.79
					LTELPVGmPVAVVVR	1595.92583	4.26	2.68
					QLTEHVQGDTDLIGR	1681.85392	2.05	2.67
					LKEAGVVPNAR	1153.66863	-0.19	2.61
					TIYDLEEEGVVPLR	1632.85039	1.46	2.28
					MERDGLLHVAGDR	1468.73638	2.56	2.24
					ALAVAVMR	830.49486	3.77	1.95
					DGLLHVAGDR	1052.55036	1.87	1.50
118468231	0817	LysR family transcriptional regulator [Mycobacterium smegmatis str. MC2 155]	76.80	61.56	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AEREELVGDLVVGIFSPIAPFHAPNILTAVEK	3431.86008	0.75	8.31
					AAALDLNVTQSTLSAAIHQLER	2322.24224	0.40	4.94

					IRHFVSGYETVR	1463.77457	-0.58	4.84
					IVALELADDVPPIEVVLVR	2060.20244	1.04	4.50
					AAHPEQPVHLRDFEDEPFVLLDLK	2815.44546	1.41	3.56
					SYVGLGQGYSVLNR	1512.78728	4.44	3.49
					TVLEDADQLYQSVR	1636.82134	2.19	3.41
					LTFLEGDQETLMR	1552.76921	1.01	2.63
					DFEDEPFVLLDLK	1579.78996	0.55	2.50
					IPPHVLVSADHPR	1437.79641	0.16	2.38
					EVGAELFQR	1048.54595	3.53	2.13
					SFTLVQLR	963.56633	4.26	1.88
					EYYLDIFKR	1246.64824	1.25	1.64
118471676	3143	aconitate hydratase 1 [Mycobacterium smegmatis str. MC2 155]	76.60	30.01	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					EAVAALGGDPNKVNPLAPAELVIDHSVILDVFGNASAFER	4116.14902	2.13	6.84
					LSGEIKPGVTATDVVLTVTDMLR	2415.32207	2.32	5.46
					KAPYFDGMPAEPEPVSDIK	2091.02178	5.43	4.72
					AINDNDLAVTAVLSGNR	1742.90532	1.19	3.99
					TNMAPGSQVVTDYYNK	1787.83440	4.18	3.91
					VIMQDFTGVPcIVDLATMR	2166.07915	1.59	3.66
					TDEQLALVEAYAK	1450.74932	4.72	3.37
					SLPTPEGDTFEWDPASTYVR	2268.05351	3.48	3.32
					NQLLDDVSGGYTR	1437.70256	3.94	3.21
					NGGILQYVLR	1132.64885	1.32	2.93
					DIHNYVEQNHPTPETK	1921.90354	-0.20	2.83
					GVAEVPLANR	1025.57549	1.57	2.74
					LNAVPGTEKLPYSLK	1629.92803	4.25	2.58
					IDTPGEADYYR	1299.58513	-0.06	2.37
					LSGEIKPGVTATDVVLTVTDMLRR	2571.41800	0.16	2.36
					AGIPLVVLGGK	1023.65666	0.49	2.07
					VLAENLLR	927.56603	4.08	1.92
					EMFTESYADVFK	1466.65361	1.87	1.43
					AGLWPYLEK	1076.57854	0.92	1.31

118472725	0759	adenylosuccinate synthetase [Mycobacterium smegmatis str. MC2 155]	62.95	38.05	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					ALEPAEVLENLLEQAEGFK	2100.08574	-0.14	5.52
					VADVLDEQVLAEKIEAALEFK	2330.25298	1.66	5.16
					AEPVYEELPGWWEDISGAR	2204.03374	1.89	4.43
					RVDEMPMTQSDIAR	1648.78105	1.70	4.29
					KALEPAEVLENLLEQAEGFK	2228.18364	1.18	4.15
					VNGITDYFLTK	1270.66887	0.83	2.82
					LDVLSSLETVPVcVGYTVDGK	2251.15727	2.02	2.09
					ITTVLGILK	957.63555	1.26	1.92
					VGSGPFPTELFDEHGAYLAK	2135.05021	2.68	1.57
					GVDTSNLLISADAHLLMPYHVAIDKVVER	3176.68348	1.92	1.37
118467565	2271	hydrogenase accessory protein HypB [Mycobacterium smegmatis str. MC2 155]	59.49	41.70	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					ALQGLDLTRLDLVIIENVGNLVcPAEFDVGEHAK	3718.94858	0.30	6.83
					VREVNPTTEILPVSAR	1780.99980	4.57	4.82
					LDLVIIENVGNLVcPAEFDVGEHAK	2751.40262	0.10	3.45
					IEVLESIFAENDIR	1647.86199	1.87	3.10
					VMVYSVTEGEDKPLKYPVMFR	2488.27365	4.85	2.95
					EVNPTTEILPVSAR	1525.83013	5.25	2.89
					TGEGMEAWYDWLR	1613.70659	0.75	2.85
					AVDVVLLNK	970.59673	3.62	2.59
					ALQGLDLTR	986.56688	3.96	2.27
					TGEGMEAWYDWLRR	1769.80808	0.89	2.00
118468832	4084	acyl-CoA dehydrogenase [Mycobacterium smegmatis str. MC2 155]	54.84	46.23	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					ALADAAETVMADGVGDK	1633.78093	4.31	4.97
					TFAHGVGSSAKDDPLLQHVVGQLASDAFAGR	3151.59707	1.58	4.31
					QAGHVDGYGSPMAQLYLTAVTAGILEAINR	3116.58652	0.98	4.27
					ALGDYLVNGNPLPR	1498.80937	5.37	4.19
					LTASGTAVFDNVR	1350.70867	5.47	3.07
					VTIENLVSR	1030.59197	2.70	2.71
					LATVDPNVAHALR	1376.76848	2.86	2.67

					AKVTIENLVSR	1229.72612	3.94	2.57
					LWLDHIVAGDLFGNANTELTAK	2398.25333	5.45	2.47
					VYTHEVFIR	1163.62212	1.13	2.42
					ELNHTSPVDAFAMIQEAR	2028.98453	1.81	2.11
118467594	1543	eptc-inducible aldehyde dehydrogenase [Mycobacterium smegmatis str. MC2 155]	53.29	34.82	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					SPNIFFNNVLAQADDYQDK	2199.03569	0.15	5.66
					SLIQSDIFDEFLELAAIR	2080.09551	-0.33	5.59
					VWTNcYHQYPAHAAFGGYK	2270.03325	4.22	5.30
					SSEADIDKALDAAHAAAPAWGK	2195.08481	5.44	4.46
					YFENPTPVTGQVFcEVAR	2114.00420	1.40	4.06
					LIMQYASQNLIPVTLELGGK	2188.20952	2.20	4.02
					ALDAAHAAAPAWGK	1349.69780	1.23	3.88
					ILSYIEIGKSEGAK	1507.84258	3.90	3.36
					YDNYIGGEWVAPVEGR	1824.86479	5.25	3.13
					ETLNADIPLAIDHFR	1724.89775	0.62	2.72
					IAFTGETTTGR	1153.58586	0.89	2.66
					YFAGVLR	825.46514	4.06	1.59
118470741	3300	oxidoreductase, Gfo/Idh/MocA family protein [Mycobacterium smegmatis str. MC2 155]	49.40	47.09	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AFAHDQLLGTAAAPTFGDAVALHR	2450.26773	4.12	6.03
					MTPIGVGVIGASPNGGWAALAHVPALR	2612.42099	3.01	4.43
					VLSTNIVGSGMAWAPGAPAAQAYAFDAR	2792.38994	2.62	4.37
					VPDHYGLITDALTAGK	1670.88224	4.40	3.69
					AVFSEWPLGVALEQAQILHAEAVVAGVPTVVGLQAR	3726.04209	1.11	3.26
					VAWGVDAYHDPR	1385.66216	1.75	2.42
					MRELVDAGYVGK	1337.69109	2.11	1.74
					LIAGIEHVNTESHR	1575.82436	0.33	1.62
					VAWGVDAYHDPRR	1541.76445	2.34	1.48
118472727	4029	hypothetical protein MSMEG_4029 [Mycobacterium smegmatis str. MC2 155]	49.09	54.73	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VDEPAPLALANTLWIDR	1894.00760	0.32	5.35
					DLVASPVPDVATAVSLINAASAAETVWPELR	3162.67119	0.92	4.85

					AcEAPAcAYFFIK	1547.70366	0.94	4.15
					HGVHDALADKDYVQAWIR	2094.05947	3.74	3.16
					LDVRPAPGSTDGLR	1453.77683	0.67	2.65
					QAIELATSPR	1085.59697	1.81	2.21
					RLDVRPAPGSTDGLRLEAVGR	2235.23940	3.41	1.52
					RLDVRPAPGSTDGLR	1609.87749	0.32	1.53
118469328	4124	hypothetical protein MSMEG_4124 [Mycobacterium smegmatis str. MC2 155]	44.71	30.63	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LHLHPFAVQYGNQSQNSAGSISDVR	2725.35642	4.49	5.87
					LQPALAVQSGVSATLAAAAGLR	2065.17827	0.84	5.30
					VAAHPGLAVIPVAVAITEDTWNDSRPSEDRFLR	3602.88540	3.83	4.59
					VAAHPGLAVIPVAVAITEDTWNDSRPSEDR	3186.62143	1.08	3.45
					AVVAGYEcAGILADQLLPNVSNR	2430.24863	1.62	2.99
					cFHPGVSLPR	1169.58989	1.21	2.31
					SIAVAAFR	834.48668	4.10	2.20
118469921	6759	glycerol kinase [Mycobacterium smegmatis str. MC2 155]	43.73	31.09	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					NTYGTGNFLLLNTGTTPVR	2039.06084	2.52	5.34
					DQMHVIDSAAESESLAR	1858.86955	5.11	4.96
					TGRPYYNAIVWQDTR	1839.92217	4.60	3.82
					LVDDNGGVYFVPAFSGLFAPYWR	2590.28349	2.65	3.72
					LGDDAPVYALEGSIAVTGSAVQWLR	2588.33841	1.08	3.56
					LQPSDLAALGVTNQR	1582.86174	4.37	2.52
					IQWILENVPGVR	1423.80669	0.71	2.42
					AGLPPATYFAGGK	1249.66301	4.32	1.59
					TDSIAAALDRDGRGDVIR	1900.99308	4.96	1.64
118469637	5119	1-pyrroline-5-carboxylate dehydrogenase [Mycobacterium smegmatis str. MC2 155]	42.57	30.07	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LAGIHFTGSTATFQHLWR	2043.05674	0.37	5.36
					LVGETGGKDFVLAHSSAHPDVLR	2405.26810	4.49	5.01
					YGLTGAVIADDRTAVQQALDGLR	2403.26694	1.73	4.23
					SAYQAEIDAPcELIDFWR	2184.00981	1.41	3.41
					QILAQQPISSPGVWNR	1793.97417	4.68	2.98

					MGDDFLSATEALR	1425.66985	1.34	2.63
					AADLLSGPWR	1085.57842	4.18	2.28
					QDWAALPFDQR	1346.65093	1.55	2.21
					IIDVVDTGAK	1030.57842	0.44	2.05
					EVGANIDRYHTYPR	1690.83159	1.15	2.57
					FNVAFAR	824.44481	4.15	1.86
118471263	6489	hypothetical protein MSMEG_6489 [Mycobacterium smegmatis str. MC2 155]	41.74	47.73	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					TAAADLVVFADGITSAAR	1748.92095	1.78	4.23
					AAADAWTLAGALAASDGDIAAALR	2242.15044	1.81	3.87
					GFGGSVSVHPGQVQDR	1626.80022	1.14	3.27
					AVVVGGSIGGLTTALLLR	1697.03349	0.83	3.15
					KWEPAQLQLSDSLLR	1783.97295	1.55	3.12
					SSQDLGDLQTATR	1391.67949	2.39	3.02
					GTVALSALSEPTR	1301.71013	3.16	2.98
					ADAAELFAPAVAETVVR	1729.91472	1.55	2.49
					NVPAGPELTEMLIDKR	1782.94402	1.16	2.44
					ERFDPDATLR	1219.60649	-0.12	2.41
					LMNYVWYR	1144.56597	4.48	2.27
					VALIGDAAcASRPHAAAGTAK	2008.03928	-0.05	2.01
118468818	5249	serine hydroxymethyltransferase [Mycobacterium smegmatis str. MC2 155]	40.27	35.51	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					EIADEVGATLMVDMAHFAGLVAGK	2445.21538	-0.01	5.31
					SYGTNPETGFLDYDAVAAAAR	2189.01860	1.81	4.58
					QAESALLDAGIVTNR	1557.82988	4.29	3.95
					QPAFQQYAQQVADNAQALADGFVKR	2764.38297	0.98	3.67
					LIASENYASPAVLLTMGTWFSDKYAEGTIGHR	3498.75014	3.94	3.57
					EFKPLVLVAGYSAYPR	1809.99455	2.60	3.37
					VHAASSELLSANPLYPGLTL	2053.09819	0.82	2.78
					VFTGDEDPVPHAHVTTTTTHK	2290.11216	0.97	2.38
302595980	5435	RecName: Full=Putative ligase MSMEG_5435	36.78	23.12	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LASLGPLLNDLEAR	1481.83269	0.26	4.17

					AVIISEPFLVATPVLEEK	1955.11101	0.48	3.92
					TVTTGMVTGEPHEPVR	1710.84990	1.09	3.61
					GASLTMLHQPTPR	1408.73918	1.83	3.46
					VTPMDFLRDTLLWAK	1805.96391	1.09	3.12
					NIHSNAEAMFVGAK	1488.73064	2.81	2.90
					NVVVLGPGSIPK	1179.71501	4.55	2.63
					GTMTAAPNFAYALLAK	1639.85332	1.22	2.56
					TVTTGmVTGEPHEPVR	1726.84165	-0.75	2.30
					VTPMDFLR	978.50914	1.40	1.15
					GVGVIELR	842.51348	4.74	1.94
118472055	5049	alpha-ketoglutarate decarboxylase [Mycobacterium smegmatis str. MC2 155]	36.62	15.73	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					FSLEGAETVIPMMDAVIDQcAEHGLDEVVIAMPHR	3880.83657	-0.34	4.05
					ISFTHLLGYAIVQAVK	1760.01194	0.77	3.79
					HVGVEYTHILEPEQQR	1934.98149	4.93	3.49
					IGDAHLALPEGFTVHPR	1829.97353	4.24	3.27
					IDWAFAELLALGSLIAEGK	2017.10491	2.15	3.20
					AAVSDIRDFTESK	1438.71977	1.70	2.76
					TTTAAPVTPPTPAPAPAPEPK	2012.07500	2.49	2.67
					LITLTSTYDHR	1319.69890	2.64	2.66
					LAETLDRYPNVK	1418.76238	-1.05	2.45
					VIELIAAYR	1047.62407	4.12	2.30
					IIQGAESGDFLR	1305.68523	4.15	2.25
					LATAVDkAmLQR	1576.82279	4.00	1.61
118469401	1028	geranylgeranyl reductase [Mycobacterium smegmatis str. MC2 155]	34.47	35.19	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VYGDAVIAADGAYSPIKR	1865.98467	4.82	4.50
					VTVFSPSEWELSFPR	1780.89202	0.83	4.45
					NWQSINATQFLGEFLR	1923.97380	1.33	4.40
					QGAEVAGPEFDANGR	1517.69853	0.35	3.90
					LPMGFTAWPPWRPGVLFTGDSLGAGKPASGAGISK	3526.82900	-0.45	3.69
					MGLADEVATYHR	1362.65064	2.58	3.56
					VVVLDKAEFPR	1272.73662	4.32	2.81

					THLDTVLLK	1039.61626	1.54	2.05
					LIDNAAFR	919.49968	0.04	1.65
302595893	1801	RecName: Full=Adenosylhomocysteinase; AltName: Full=S-adenosyl-L-homocysteine hydrolase; Short=AdoHcyase	29.57	18.56	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VSVTEIDPINALQALMDGFDVR	2403.22807	2.29	5.43
					AGVVPPAEDDDPAEWK	1695.79436	4.83	3.48
					LAEHEMPGLMALR	1467.75006	3.61	3.23
					IHVEALGGTLTK	1238.71391	2.86	2.83
					VADLSLADFGR	1163.60661	0.89	2.45
					SIIVLSEGR	973.57176	4.15	2.11
					VFLGVLR	803.51641	3.20	1.74
118468558	4497	PhoH family protein [Mycobacterium smegmatis str. MC2 155]	29.26	50.00	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LMSAGVIEVAPLAYMR	1720.91582	1.89	4.24
					TLNDAFIILDEAQNTTAEQMK	2366.15776	1.37	3.90
					IVVTGDVTQVDLPGGATSGLR	2055.11846	5.00	3.88
					HSVAILTGAGDESPAEVLTLDILSR	2564.35874	0.77	2.88
					IILTRPAVEAGER	1424.82207	0.00	2.69
					HYVDAIDAHTIVFGIGPAGTGK	2239.14548	-2.33	2.59
					IDPYLRPLYDALHDMMDTELIPK	2759.38218	1.36	2.55
					SSITVPPDIIVGLLGSADENLR	2266.23198	1.31	1.87
					LGFLPGTLSEK	1161.65764	5.32	1.51
118468959	6422	ferritin family protein [Mycobacterium smegmatis str. MC2 155]	27.76	44.75	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LASVARDEGDHLGEQFMQWFLK	2577.25650	0.35	5.05
					DALALALDQER	1214.64311	4.53	3.66
					AGSNLFHIEDFVAR	1575.79302	0.97	3.30
					HFYAQALEER	1263.61211	0.32	2.53
					EQVEEVAAMTTLVR	1575.81377	5.71	2.41
					FHALIQDQIR	1240.68437	3.74	2.26
118470644	6904	myo-inositol-1-phosphate synthase [Mycobacterium smegmatis str. MC2 155]	26.00	25.90	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VAIVGVGNcASSLVQGVQYYR	2240.15264	1.49	4.39

					KFEDAGVPIVGDDIK	1602.84429	4.26	4.27
					NADENTTVPGLMHVK	1625.80144	3.80	3.80
					GIGGPIEAASAYLMK	1477.77287	0.58	3.00
					TQAVTSNLSGALAGK	1417.77056	4.20	2.70
					IADVPPTDVIVQR	1422.80181	4.66	1.74
118472266	0255	phosphoenolpyruvate carboxykinase [Mycobacterium smegmatis str. MC2 155]	25.79	19.24	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					IASAMAHDEGWLAEHMLILK	2236.12735	0.86	4.70
					TIAAGNTVFTNVAK	1406.77043	4.66	3.76
					LcAHLVEAGTFQK	1473.75566	2.54	3.37
					TNLAMLQPTIEGWR	1629.84575	2.41	3.00
					ALHSIGAPLEPGQK	1417.78386	2.82	2.59
					VFFVNWFR	1114.58245	-0.78	2.57
					AALDKLGDDGFFVK	1495.78415	3.30	1.91
					YITHFPETR	1163.58769	2.82	1.79
					FLWPGFGENSR	1309.63347	0.77	1.88
118468100	2748	soluble pyridine nucleotide transhydrogenase [Mycobacterium smegmatis str. MC2 155]	25.48	22.93	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					DNMLEFcDPEIVEALK	1922.88762	0.04	4.61
					LAAYHAFGEPAK	1274.65581	2.32	3.07
					QGQTEHLDLANAGLGVDGR	1950.97173	4.53	2.58
					QIPADTVMYSAGR	1408.69451	3.91	2.57
					EAVVYLTGMNQR	1380.70146	5.35	2.24
					GQMLGGVcVNTGTIPSK	1718.86540	5.18	2.16
					ITVDSNFQTK	1152.59258	2.61	1.91
					LLVSTEDLR	1045.59368	4.61	1.81
118470278	4932	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium smegmatis str. MC2 155]	25.43	26.79	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AGAGLVLAGLVADGETEVHDVFHIDR	2661.36728	1.51	4.32
					GYPLFVENLVSLGAEIER	2006.07256	6.55	4.19
					LHDAGATVTQNDNGFR	1715.81046	0.46	3.57
					ITSPDEPKYDADFAAVR	1894.92522	3.69	3.08

					GIPQLSSAPVWSSDIR	1712.89849	1.05	2.59
					GDITVTGVDPQHLQLVLHK	2070.14371	4.55	1.68
118470200	3102	transaldolase [Mycobacterium smegmatis str. MC2 155]	23.89	23.72	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					GTAYDAQVNELAAR	1478.72771	2.87	4.58
					LAAIGIDLPDVFR	1399.79534	0.62	3.49
					VQRPLWASTGVK	1341.76641	1.93	2.91
					VLEDEGVEKFEK	1421.71697	0.73	2.71
					VSIEVDPR	914.49492	0.76	2.09
					SWQELLDATQGQLDAAKK	2002.03031	3.10	1.84
					IHSVASFFVSR	1249.67632	5.99	2.15
118468007	3055	S-adenosylmethionine synthetase [Mycobacterium smegmatis str. MC2 155]	23.56	23.56	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					DLDLLRPIYAPTAAYGHFGR	2246.17362	0.83	4.97
					AAPVGLFVETFGSETVDPAKIEK	2405.26738	3.07	4.29
					FVLGGPMGDAGLTGR	1447.74407	5.36	3.33
					NVVAAGLAER	999.55901	0.78	2.88
					AIGEVFDLRPAAIVR	1626.93437	1.03	2.75
					IIVDTYGGWAR	1250.65752	3.73	2.50
302425159	3890	RecName: Full=Pup--protein ligase; AltName: Full=Proteasome accessory factor A; AltName: Full=Pup-conjugating enzyme	22.49	18.58	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					ISQLDLAYHDIKR	1571.86040	4.03	3.71
					VGTASLVLEMIEAGVPFRDFSLDNPIR	2946.54068	0.39	3.42
					ISDVLLPFLVTR	1372.81975	-0.13	2.91
					GVFDLLQR	947.53325	2.44	2.03
					EPNTQIEQVVDLWGR	1783.90080	1.90	1.93
					TVLcKDPFR	1135.59473	1.62	1.60
118473811	2089	cell division ATP-binding protein FtsE [Mycobacterium smegmatis str. MC2 155]	21.71	43.23	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AFVNRPLVLIADEPTGNLDPETSKDIMDLLER	3581.85422	0.57	5.67
					LLLGADTPTSGDVR	1414.75908	3.80	3.03
					ANRLPSELSGGEQQR	1641.82999	-0.25	2.89
					QVIGcVFQDFR	1368.67473	1.30	2.56

					VVELELGR	914.53386	3.55	2.35
					TGTTVVMATHDHHIVDSMR	2108.00380	1.21	1.09
118468392	5933	hypothetical protein MSMEG_5933 [Mycobacterium smegmatis str. MC2 155]	21.69	29.80	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VGQSYPFAPPVGLMYVLWDDDALR	2709.34355	1.95	4.15
					GVVAAADAVTAQLGGVKPTR	1881.06333	4.24	3.59
					LGPALIALGHMAQESMR	1794.93619	0.42	3.23
					LPDELQALLR	1167.67388	0.53	3.10
					VVAILDFLAR	1116.67815	0.47	2.86
					ELVSDIGER	1017.52336	2.15	2.16
118473843	1678	LysR family transcriptional regulator [Mycobacterium smegmatis str. MC2 155]	21.57	35.69	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					GLALTAAGEEMLHDTR	1684.84050	4.81	4.26
					GTYDGGEVSVVPIRDELPGLPIVLAR	2722.48386	2.32	4.18
					AADELHIAQSAVSAAISQLEQQIGTQLFIR	3208.69829	0.65	3.96
					RRPDVTLAQLR	1324.78122	0.27	2.67
					GHGFSILNQIPAHR	1546.82993	3.97	2.44
					LAcFVTLTPFVLPR	1633.91753	2.45	1.93
118472062	1443	50S ribosomal protein L16 [Mycobacterium smegmatis str. MC2 155]	20.81	47.10	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VWINIFPDRPLTK	1598.90593	0.33	3.86
					GIASGGTSVSFGDYGIQALEHAYITNR	2784.36380	1.78	3.69
					GSPEWWVANVKPGR	1582.81975	4.54	3.56
					VLFELSYPDEK	1339.67900	0.70	3.51
118473275	3054	bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate synthase [Mycobacterium smegmatis str. MC2 155]	20.16	28.02	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LTGADSGPGRLPEAEEITTLAQLLLER	2850.52494	1.42	4.08
					IGQQADLVVIAPATADLLAR	2035.15776	1.49	3.08
					ADDLLTATLLTAR	1373.76604	1.82	2.46
					IVDSIAAFLK	1076.63616	1.00	2.23
					FVGAATFEALSGNPVHTGVFTDVHEVQHVR	3221.61977	2.16	1.52
					ALVTAGGTREPLDPVR	1651.91631	2.19	2.40

118470801	3902	ATPase AAA [Mycobacterium smegmatis str. MC2 155]	20.13	8.97	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					ASEGTPVIVFFDEMDSIFR	2160.03398	0.96	4.31
					EQLENAVGPQSGLR	1497.76738	1.14	3.12
					IVWLAEPLVAAK	1309.78826	0.26	2.60
					LTcSPNIEVK	1160.59868	0.56	1.77
118469413	3953	hypothetical protein MSMEG_3953 [Mycobacterium smegmatis str. MC2 155]	19.90	20.90	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					FHGGLTQYLEPTMSSDVAHAIGAR	2558.24997	1.65	5.78
					ELASLTLGDAGAALLLER	1813.00908	1.33	4.23
					VPAGGSGITLAGFTTIADYSR	2054.05864	1.58	3.67
					AAITNTPVLLR	1168.70952	3.96	2.49
118469767	6427	[Mn] superoxide dismutase [Mycobacterium smegmatis str. MC2 155]	19.86	19.32	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AFWNVVNWDDVQNR	1762.83245	1.57	4.35
					ANGDHAAIFLNEK	1399.69817	1.18	2.88
					GVNDAIAKLEEAR	1385.74463	4.50	2.74
118470831	6271	2-isopropylmalate synthase [Mycobacterium smegmatis str. MC2 155]	18.20	16.45	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					TITPPSGAPHPGQPAWNTQR	2113.06474	3.45	4.43
					TGNVcLVTLGLNMFSR	1781.90691	1.76	3.54
					RMFDLLVR	1049.59636	3.67	2.53
					QKVDAAEEDGGTDKITAVVK	2074.07096	2.21	2.22
					EMWDAFSEEYLAPITPLER	2297.08501	2.37	2.06
					GVDPQIDFSNIDEIRR	1873.94620	3.12	1.54
118472070	1662	hypothetical protein MSMEG_1662 [Mycobacterium smegmatis str. MC2 155]	17.08	29.72	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LSFFPLWSYATPPAIELAER	2308.22051	8.31	4.51
					GFLTPALWEAGLYcR	1753.87493	1.03	4.12
					GLTSGYSPLGAMVASDR	1681.82231	0.49	3.55
					HGDGITPPIITR	1276.70391	2.38	2.90
					ADDRGDPVVQLAPPLISGQAEFDAIYDILHNVLTEAGNRL	4303.20327	0.86	1.75
					APFEPLTPGGFR	1288.67412	4.34	2.01
					SIAYHGTPQGALAITGIPAFK	2113.14731	1.50	1.12

118468233	3132	DNA-binding protein [Mycobacterium smegmatis str. MC2 155]	14.89	23.22	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					GLLLVNHPEVGPLDLHFQHLSLR	2604.44565	1.78	5.27
					LSPSFAHGGNPLR	1352.70964	1.94	2.70
					ERPSDQVLDALAR	1469.77788	4.84	2.47
					ALLLSPDATVYMR	1449.77837	0.89	1.83
118468644	0906	DNA-binding protein [Mycobacterium smegmatis str. MC2 155]	14.03	12.76	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					MAAELAYLEFGDLIDKLVDEGR	2468.24082	1.19	6.48
					RIDMGETVLHR	1326.69477	0.01	3.15
					LGLANYFAAATVLPYR	1739.95036	1.37	2.45
					ILVQIAQMPDGR	1340.74138	4.34	1.95
118472028	6423	glycerophosphoryl diester phosphodiesterase [Mycobacterium smegmatis str. MC2 155]	13.95	26.69	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					TSTGTGLVSEMTLAELR	1765.90605	3.35	3.59
					KLNFGSWHPSWR	1514.77137	4.07	3.21
					AAPMLPTVLLGETSR	1555.85295	1.04	2.75
					LLALLHR	835.55486	4.29	2.09
					DVGVAWIATNHPGR	1492.77188	4.20	1.78
					MALDWNRPVK	1229.65129	4.30	2.31
118473840	3906	tRNA (adenine-N(1)-)-methyltransferase [Mycobacterium smegmatis str. MC2 155]	13.68	39.36	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					STNGDQFLVLRPLLVDYVMSMPR	2651.37082	0.87	4.11
					DAAQIVHEGDIFPGAR	1695.85295	4.69	3.67
					VLEAGAGSGALTcSLLR	1674.89336	5.33	3.43
					GIIAFDDVIGLPEGSVVK	1829.00725	0.90	2.46
					KLAPGAVAPMPLRR	1476.88300	-0.17	1.61
					AVGPEGSVTSYEVRDDHAVHAER	2481.17983	1.78	1.07
118467605	6059	hypothetical protein MSMEG_6059 [Mycobacterium smegmatis str. MC2 155]	13.42	54.26	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					EAAVATTALALR	1186.68352	3.74	3.35
					LKVADVMAEAR	1202.66118	4.10	3.34
					IGEEVPPPAAGDAGHDHDH	1920.84830	0.58	2.19
					mVWHGLLVK	1098.61772	4.38	1.16

					MVWHGLLVK	1082.62287	4.50	2.27
118473835	3265	arabitol-phosphate dehydrogenase [Mycobacterium smegmatis str. MC2 155]	12.67	17.96	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VSPDIPAQHAAFAEPLScSLHAVER	2702.34995	5.30	3.81
					TPGAMASYMVYPAEALVHK	2036.00296	2.40	3.57
					VIALDMAPDKLK	1313.75542	4.26	3.27
					LEEVAVPQR	1040.57378	0.23	2.01
118469514	1568	glucosamine--fructose-6-phosphate aminotransferase [Mycobacterium smegmatis str. MC2 155]	12.59	10.67	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					TFLAQIAANYLVGLALAQAR	2104.19756	2.91	4.23
					VLAGMDSVAALAER	1402.74272	4.81	3.13
					HVGYPVALEGALK	1353.75859	4.45	2.65
					FAPSSTVLFLGR	1294.71562	0.13	2.58
					YAIEHWTR	1075.53293	0.88	1.80
118472788	5789	thiosulfate sulfurtransferase [Mycobacterium smegmatis str. MC2 155]	12.35	17.69	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AANEDGTFKSDEELAK	1724.79875	0.76	3.51
					SSHTWFVLQELLGHK	1781.93497	0.89	3.16
					VERPQTSYTAKEPDNSIR	2091.04629	-0.15	2.91
118473775	5247	PhoH family protein [Mycobacterium smegmatis str. MC2 155]	12.00	6.64	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					SPIAALVTEMLEEISPGALP	2038.07792	0.06	3.58
					NVLLTVLSR	1014.63109	0.43	2.50
118473519	6266	thiocyanate hydrolase subunit beta [Mycobacterium smegmatis str. MC2 155]	11.96	21.80	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					FSVGEAVVVR	1062.59819	3.68	2.87
					AVGIGDPQIYAGK	1288.69548	4.53	2.72
					DLPALLYTR	1061.59929	0.26	2.38
					AIYQGIPYYGR	1300.67412	4.34	2.08
					WLWAVAR	901.50530	1.07	1.91
					GIWLSEER	989.50878	3.69	1.29
118472240	0220	monoglyceride lipase [Mycobacterium smegmatis str. MC2 155]	11.84	15.36	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					FGAAGLLVYALDHR	1502.81183	0.23	4.07

					TLVGIAANDHPTLPR	1574.87358	5.46	3.98
					LVLDDVTSWIVSHL	1596.86601	1.73	3.79
118470580	5727	allantoicase [Mycobacterium smegmatis str. MC2 155]	11.44	17.81	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					FYSSPHNLIFPGLAQVMGDGWETAR	2793.35227	2.43	4.68
					FLVDVADVVSEVR	1447.78154	1.62	3.11
					LGVPGVIR	810.52239	3.37	1.63
					LNIFPDGGVAR	1158.63127	3.99	2.02
118473102	3103	transketolase [Mycobacterium smegmatis str. MC2 155]	10.77	14.66	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LASLMDIDPIYVWTHDSIGLGEDGPTHQPIEHLAALR	4081.06306	3.45	3.76
					MNTGGVHGSALGADEVAATKK	2014.00339	0.53	2.92
					AASGAVLSAVGPK	1127.64324	1.12	2.20
					TIIGYPAPNK	1073.59917	0.15	1.89
					AIPNLSVVRPGDPNETAYAWK	2298.19974	5.19	1.37
118473351	4474	acyl-CoA oxidase [Mycobacterium smegmatis str. MC2 155]	10.67	5.94	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					SYALQFAQNELVAK	1581.83513	5.02	4.09
					TAAQTIIQTILDTR	1544.86650	1.42	3.76
					FFTMLGTLIR	1198.66692	1.32	2.83
118471237	6263	glutamate synthase [Mycobacterium smegmatis str. MC2 155]	10.29	15.70	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					GASEVGTSTTTGDGGMTPEER	2039.88371	0.68	4.33
					ALALGADAVAIGTAALIALGDNHPR	2371.31211	1.16	3.57
					HPLHLDIPVTIAGmSFGALSAGAk	2663.38749	7.93	2.39
118467533	3951	hypothetical protein MSMEG_3951 [Mycobacterium smegmatis str. MC2 155]	10.17	14.70	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AALIVASDANPGFGMSK	1648.84368	4.40	3.70
					LGVPPAHLVVAADPR	1511.87326	2.58	2.67
					HFPYSPVGSALLcR	1603.81059	3.48	1.74
118467777	4298	3-methyl-2-oxobutanoate hydroxymethyltransferase [Mycobacterium smegmatis str. MC2 155]	10.02	13.59	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					GAPHALVIGDLPFGSYEDGPSQALATATR	2911.46225	1.25	7.22
					VADQIATLSR	1073.59709	1.95	2.81

118470813	6267	thiocyanate hydrolase subunit gamma [Mycobacterium smegmatis str. MC2 155]	9.95	20.76	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AVGVDWLEPTGFGTPSDFTAFK	2342.13725	1.36	4.35
					FTEFAEQIGPTPAAR	1634.82646	5.56	3.36
					QLALTDALAASK	1201.68291	3.47	2.23
118469884	1424	FMN-dependent dehydrogenase [Mycobacterium smegmatis str. MC2 155]	9.78	12.28	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					TMVTMMPEALTKPR	1605.82488	5.39	3.44
					ALPVIAEAVGDQVEVLLDGGIRR	2390.34299	1.11	3.27
					GGIDSALMGLGR	1146.59844	4.17	3.07
118472340	1091	urease accessory protein UreE [Mycobacterium smegmatis str. MC2 155]	9.54	30.92	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					ILDTIVGWSTDQPIAGR	1841.97820	1.37	3.44
					AGAPQTLTLR	1027.59209	2.50	2.19
					LGFLAGHLHWK	1278.71610	4.27	2.00
					IADLLASGR	915.52910	3.54	1.90
118469672	5252	pantothenate kinase [Mycobacterium smegmatis str. MC2 155]	9.05	17.95	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VDLVTTDGFLYPNAELAR	1994.02690	1.95	4.05
					LIHLQVAAR	1020.63315	1.79	2.76
					VLQALLAR	883.57652	4.66	2.24
					DIWHSINRPNLIENILPTRPR	2554.40395	1.46	1.99
118471384	0688	aminotransferase AlaT [Mycobacterium smegmatis str. MC2 155]	8.63	9.43	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LNIGNPAPFGFEAPDVIMR	2058.05229	2.17	3.78
					LNEIPGVScVKPR	1468.79802	2.65	2.92
					IVTLPWAR	955.57323	0.86	1.93
118467799	3084	glyceraldehyde-3-phosphate dehydrogenase [Mycobacterium smegmatis str. MC2 155]	8.43	12.35	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VPIPTGSVTDLTAELAK	1711.95195	2.47	3.41
					LADLVALVGK	998.62505	0.53	2.81
					AAALNIVPTSTGAAK	1384.78398	3.21	2.21
118470673	4694	HNH endonuclease [Mycobacterium smegmatis str. MC2 155]	7.00	18.75	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					ADVVHDDPTSPVIHSASR	1902.93033	-0.09	4.54

					VLLLNATYEPLTALPLRR	2053.21946	1.24	1.96
118470943	3535	agmatinase [Mycobacterium smegmatis str. MC2 155]	6.90	8.93	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LIESGAVPGSHFVQVGLR	1866.03130	4.29	4.69
					AVMDDAVGEALAK	1289.64690	4.83	2.21
118468699	5790	SseC protein [Mycobacterium smegmatis str. MC2 155]	6.74	28.89	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VVDGSGQAVGGAFVR	1418.74053	1.26	3.14
					FFAAPGTWTVR	1252.64861	0.98	1.95
118472927	3773	acetylornithine aminotransferase [Mycobacterium smegmatis str. MC2 155]	6.38	11.54	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					DAGFLVNAAAPEVVR	1528.81877	4.49	3.96
					GLLQGIVLTVPSAK	1395.85893	1.35	2.42
					HGALLVLDEVQTGVGR	1663.92130	5.18	1.58
118471704	3461	catalase/peroxidase HPI [Mycobacterium smegmatis str. MC2 155]	6.23	4.81	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AYFLGVTAPQLTALVGGLR	1947.10808	0.91	3.53
					VSLADLIVLAGSAAIEK	1669.97502	0.88	2.70
118471043	6142	nucleoside-diphosphate-sugar epimerase [Mycobacterium smegmatis str. MC2 155]	6.02	13.65	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LLADGHGVVGLDDLSSGR	1780.92752	4.84	3.38
					NLYDLDcSHIAPANVYGPR	2175.03897	4.66	2.64
					TVEFFR	798.41765	3.94	0.91
118472335	2447	regulatory protein [Mycobacterium smegmatis str. MC2 155]	6.01	8.74	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AAADMINESVVLEDLSHQVLAISPR	2678.39408	4.53	3.61
					LIIPHTPAAPAR	1256.74956	1.69	2.41
					ILDAVTHSVR	1110.62885	2.00	1.25
118473788	2211	DNA-binding protein [Mycobacterium smegmatis str. MC2 155]	5.99	10.39	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					IFDRLDDTPAEIVTELGETLR	2403.24076	0.18	3.40
					TGLAEFLR	906.50780	3.76	2.59
118473160	1442	30S ribosomal protein S3 [Mycobacterium smegmatis str. MC2 155]	5.80	20.36	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					QVQLNILEVKNPESQAQLVAQGVAEQLSNR	3303.77085	1.56	3.19
					AGIADVEIER	1072.56706	3.43	2.61

					LGITTEWK	947.52410	4.64	1.43
					LLATGLER	872.51970	-0.39	1.36
118468954	2600	regulatory protein [Mycobacterium smegmatis str. MC2 155]	5.73	10.57	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LIWQAGLLAPVEGPLR	1733.01164	0.40	2.98
					LIQALQGAAR	1040.62261	1.39	2.74
118470281	0314	glucose-6-phosphate 1-dehydrogenase [Mycobacterium smegmatis str. MC2 155]	5.43	5.25	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VLEALEPLTAEQTQR	1697.91496	4.74	3.22
					GDYYDQSGALR	1244.55461	0.30	2.21
118468890	4956	threonine synthase [Mycobacterium smegmatis str. MC2 155]	5.32	10.28	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					FLAATDEEILAAYHLVAR	2003.06211	1.18	2.84
					TEGVFVEPASAASIAGLLK	1860.01286	0.78	2.49
118472834	1456	hypothetical protein MSMEG_1456 [Mycobacterium smegmatis str. MC2 155]	5.31	4.46	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					FGVFVAPGVLPR	1258.73467	3.13	3.15
					LDLLDEVHSAVER	1495.77674	1.05	2.16
118473872	5438	dimethyladenosine transferase [Mycobacterium smegmatis str. MC2 155]	5.13	10.77	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					QVARPSASAPSVSAEA	1527.77580	-0.29	2.60
					LAAEPGGKDYGVPSAK	1559.80606	-0.27	2.53
118468571	1682	flavin-containing monooxygenase FMO [Mycobacterium smegmatis str. MC2 155]	4.91	6.18	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					YVVAATGAFQKPVIPR	1716.98674	4.14	4.91
					YIADHIAIQR	1199.65317	0.00	1.70
190358683	4936	RecName: Full=ATP synthase subunit beta; AltName: Full=ATP synthase F1 sector subunit beta; AltName: Full=F-ATPase subunit beta	4.70	4.63	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					ITGPVVDVEFPR	1328.72759	4.99	2.37
					VVDLLTPYVR	1174.68437	1.10	2.33
118472797	2310	monooxygenase [Mycobacterium smegmatis str. MC2 155]	4.70	8.02	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VAVIGTGASAIQIVPEIVKDVAELHLYQR	3089.73672	0.27	2.74
					YVGQAIAAVDK	1134.61614	0.65	1.95

118467862	4367	formamidase [Mycobacterium smegmatis str. MC2 155]	4.19	5.50	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					YLDSHLSYQR	1281.62336	0.87	2.17
					IDPGMGAPHSSFN	1329.59050	0.92	2.02
118469867	5937	4-hydroxy-2-ketovalerate aldolase [Mycobacterium smegmatis str. MC2 155]	4.09	8.60	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					FGAGAGNAPVEALIGVFDK	1832.95879	2.48	4.09
					YGVPAHQLLHR	1290.70815	1.20	1.95
118472253	6720	epoxide hydrolase [Mycobacterium smegmatis str. MC2 155]	4.02	10.10	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AGAGEPVVLLHGWPQTWYAWR	2394.21805	1.57	2.05
					LLIEYWMR	1123.59795	0.92	1.97
116266976	1395	putative elongation factor G [Mycobacterium smegmatis str. MC2 155]	3.53	4.28	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					AQVPLSEMFGYVGDLR	1781.89238	1.80	3.53
					LFQMHANKENPVER	1712.85573	1.14	1.33
118472859	3847	tyramine oxidase [Mycobacterium smegmatis str. MC2 155]	3.14	4.75	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					LVPTGAIPPMLDPESPVLQR	2130.16460	0.82	3.14
					SHPDVIAALAR	1149.64177	3.68	1.23
118471203	1119	glutamine amidotransferase, class I [Mycobacterium smegmatis str. MC2 155]	2.91	15.55	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					ISTVVGPGPVVTTYHHQGIGR	2175.17143	2.04	2.91
					AGGEPLLLPTALGHAR	1572.89261	4.37	1.78
118467676	0695	isoniazid inductible protein IniA [Mycobacterium smegmatis str. MC2 155]	2.80	4.32	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					SQLLNSLLNIPVAR	1537.90752	0.91	2.80
					QIVDANIAHLQR	1377.76055	0.55	1.55
118470190	2260	transcriptional regulator [Mycobacterium smegmatis str. MC2 155]	2.47	6.52	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					IEEEAMNAHLTR	1413.67920	0.03	2.47
					WGETPSETLRR	1331.67221	1.44	1.62
118472108	2594	asparagine synthase (glutamine-hydrolyzing) [Mycobacterium smegmatis str. MC2 155]	2.30	4.99	Sequence	MH+ [Da]	ΔM [ppm]	XCorr
					VPFLDHELVELAATcPPELK	2278.18320	1.89	2.30
					GLFRPEAVER	1173.64002	2.10	1.90