Proteome-wide identification of mycobacterial pupylation targets

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Supplement

Results

PUP is a partly intrinsically unstructured protein

To provide insight into the overall structural properties of PUP, we first expressed the *M. tuberculosis* protein (Rv2111c, *mt*PUP) in *Escherichia coli* and purified it to homogeneity (**Figure 1**). *mt*PUP elutes as a single peak on a gel filtration column, with an apparent molecular weight (MW) of about 30 kDa (**Supplement Figure 4A**), considerably exceeding its calculated MW of 6.9 kDa. However, static light scattering data revealed that *mt*PUP is a monomer in solution (**Supplement Figure 4A**). The circular dichroism spectrum of PUP showed a distinct molar ellipticity minimum around 200 nm, indicating that a substantial fraction of the protein exhibits a random coil conformation. In addition, *mt*PUP showed a minimum around 226 nm, indicating limited α-helical content (**Supplement Figure 4B**). The data are supported by secondary structure analysis, which predicts the N-terminal part of *mt*PUP to be unstructured and the C-terminal part to be predominantly $\alpha-$helical (**Supplement Figure 5).** Taken together, the data indicate that *mt*PUP is likely to have an extended, non-globular conformation with a substantial fraction of the protein in an intrinsically unfolded conformation. Our data are in agreement with recent preliminary NMR analyses of PUP (Chen *et al*, 2009; Liao *et al*, 2009). These findings may explain why, in our experience, *mt*PUP could not be crystallized (data not shown). A comparative analysis with ubiquitin reveals that the structural organization of PUP is unrelated (**Supplement Figure 4**).

Materials and Methods

Biophysical characterization of *mt*PUP

The apparent MW and absolute MW were measured by gel filtration and SLS using a Superdex 75-10/300 column (GE Healthcare), connected to a SLS detector (miniDAWN tristar, Wyatt Technology). The system was equilibrated with 50 mM Tris-HCl (pH 8.0) and 300 mM NaCl, before injection of 1 mg *mt*PUP. Due to the low extinction coefficient of *mt*PUP at 280 nm, the SLS calculation was based on the mass of eluted protein.

For circular dichroism measurements, gel filtration-purified *mt*PUP was exchanged into PBS (50 mM phosphate (pH 7.5), 150 mM NaCl), using a PD-10 desalting column (GE Healthcare). Lyophilized bovine ubiquitin (SIGMA) was reconstituted in PBS. All circular dichroism spectra from samples were recorded at a concentration of 5 µM using a Jasco J-810 spectrophotometer. The background spectrum of PBS was subtracted before further data analysis.

Supplement Table Legends

Supplement Table 1: A, complete list of putative pupylation substrates obtained by shotgun sequencing mass spectrometry analysis; B, complete list of pupylated peptides. Column annotation: '% Cov', percent coverage of combined CID spectra that underlies individual protein identifications; 'Uniprot ID', Uniprot database identifier; ' Gene locus, M. smegmatis'*, M. smegmatis* gene identifier (http://cmr.jcvi.org), *mt*PUP is denoted with the gene identifier Rv2111c ; 'Conf', percent value indicating confidence of assignment of given CID spectrum to matched peptide sequence; 'Cleavages', unconventional or missed tryptic cleavages; 'ΔMass', deviation of observed mass from calculated mass; 'Prec MW', inferred mass of observed precursor peptide; 'Prec m/z', experimentally observed mass of precursor peptide depicted as mass over charge; 'Calc. MW', calculated mass of peptide; 'Calc. m/z', inferred calculate mass of peptide depicted as mass over charge; 'Calc. z', inferred charge state of peptide; 'Area 115', peak intensity of 115.11 reporter ion, calculated by integration of area covered by peak.

Supplement Table 2: A, complete peptide list of putative pupylation substrates, detected by 2D gel analyses; B, complete list of pupylated peptides. Column annotation: 'Uniprot ID', Uniprot database identifier; ' Gene locus, M. smegmatis'*, M. smegmatis* gene identifier (http://cmr.jcvi.org); 'pI (seq.)', Isoelectric point of target sequence; 'MW [kDa]', molecular mass; 'MS Cov. [%]', coverage of single mass spectrometry experiment; 'MS/MS Cov. [%]', tandem mass spectrometry experiment; 'MS/MS Mascot Score', as defined in Matrix Science, v.2.2.0; 'z', charge state.

Supplement Table 3. Gene cluster (A) and functional cluster (B) analysis of the complete target list (*cf.* Supplement Tables 1A and 2A)**.** For annotation, see legend Table 1. The total number of *M. tuberculosis* targets analyzed is 217, since 26 *M. smegmatis* targets are without homologues in *M. tuberculosis*.

Supplement Table 4. Identification of the differentially expressed pupylated targets using 2D-DIGE and mass spectroscopy. Tandem mass spectrometry analyses of spots found under all three listed experimental conditions. The intensities under experimental conditions (*cf*. Supplement Figure 3) A (*mt*PUP expression, stationary phase), B (*mt*PUP expression, log phase) and C (*mt*PUP expression under oxidative stress) have been qualitatively estimated and indicated as “+”, “++” and “+++”. The column annotations have been adapted from Table 1 and Supplement Table 3A.

Supplement Figure Legends

Supplement Figure 1. Analysis of proteins expressed in *M. smegmatis*, prior and after NiNTA purification. A, SDS-PAGE analysis of poly-histidine tagged proteins. Lanes 1 and 2, wild-type *mt*PUP (lane 1, crude extract; lane 2, NiNTA-purified sample); lanes 3 and 4: pupylation-incompetent *mt*PUP(Q64A) (lane 3, crude extract; lane 4, NiNTA-purified sample); lanes 5 and 6: control Rv3874 (lane 5, crude extract; lane 6, NiNTA-purified sample). B and C, NiNTA-affinity purified pupylation targets from cultures under different growth conditions, using SDS-PAGE stained with Coomassie blue (panel B) and immunoblots, using an HPR-conjugate anti-His antibody (Qiagen) (panel C). Lane 1, *mt*PUP expression induced at the start of cultivation; lane 2, expression induced at 2.0 OD^{600}; lane 3, expression induced at 4.0 OD^{600}; lane 4, expression induced at the start of cultivation and in presence of 2 mM H_2O_2; lane 5, *mt*PUP(Q64A); lane 6, Rv3874 (control). All protein samples were poly-histidine tagged.

Supplement Figure 2. Analysis of growth phenotypes in the presence / absence of *mt*PUP(wt) under different conditions. Bacterial growth was monitored by measuring the optical densities at 600 nm (OD^{600}), as a function of time. Cultures were prepared in triplicate for each time point, thereby ensuring that the growth of bacteria was not disturbed until the time of measurement. When the cell density exceeded an OD^{600} of 1.5, the culture was diluted to allow density measurements within the linear range of the detector. Specific stress conditions were generated, by adding 2 mM H_2O_2, 3 mM $NaNO_2$ (pH 5.5), or 20 mM epoxomicin (Enzo Life Sciences) to the growth medium prior to inoculation.

Supplement Figure 3. **Differential pupylome pattern analysis by 2D-DIGE.** Approximately 50 µg of CyDye labeled polyhistidine-affinity captured protein samples were analyzed. The images of three spectral channels are shown separately: A, Cy2 labeled sample from culture grown under influence of over-expression of *mt*PUP induced at 2.0 OD^{600}; B, Cy3 labeled sample with *mt*PUP expression induced at the start of culturing; C, Cy5 labeled sample purified from a bacterial culture, supplemented with 2 mM H_2O_2 to the medium. Selected spots with apparent differential expression levels are encircled and numbered. Apparent variations of the level of found pupylated substrates are indicated in Supplement Table 4, suggesting dynamic pupylation of substrates under different growth conditions.

Supplement Figure 4. Biophysical analysis of *mt*PUP. A, *mt*PUP (thick line), monitored at OD280 (left axis), elutes at an apparent molecular weight of 30 kDa from an analytical gel filtration column, which substantially differs from its calculated MW (9.6 kDa). For comparison, ubiquitin (thick dashed line) elutes at an apparent molecular weight of 10 kDa, matching its calculated MW and indicating that it is monomeric and folded. The MW calibration profile of the column is shown as a dashed line. Static light scattering analysis, however, shows PUP to be a monomer (MW, right axis). B, structural analysis of *mt*PUP with CD spectroscopy. The corresponding spectrum (solid line) shows a distinct negative peak at 200 nm, indicating considerable content in random coil conformation. The presence of an additional minimum at 226 nm indicates α-helical content of part of the PUP sequence. For comparison, the CD spectrum for ubiquitin is also shown (dashed line), indicating that the complete protein is folded. Based on this comparison, it can safely be assumed that the 3D structures of ubiquitin and PUP are unrelated.

Supplement Figure 5. Multiple sequence alignment of mycobacterial PUP sequences and secondary structure prediction. A, multiple sequence alignment of PUP homologues, demonstrating little sequence conservation of the N-terminal part of the respective sequences and high sequence similarity for the C-terminal part of the respective sequences. The positions of two lysine residues, which could serve as pupylation sites in *mt*PUP are marked with asterisks (for details see text). B, secondary structure prediction of PUP indicates α-helical content in the C-terminal half of the protein, indicated by high confidence levels (0=low, 9=high). In contrast, the N-terminal part of the protein is predicted to be unstructured. Positive and negatively charged residues are labeled in red and blue respectively, indicating an amphipathic helix topology.

References

Chen X, Solomon WC, Kang Y, Cerda-Maira F, Darwin KH, Walters KJ (2009) Prokaryotic ubiquitin-like protein Pup is intrinsically disordered. *J Mol Biol*. 392: 208-217.

Liao S, Shang Q, Zhang X, Zhang J, Xu C, Tu X (2009) Pup, a prokaryotic ubiquitin-like protein, is an intrinsically disordered protein. *Biochem J*. 422: 207-215.

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
0	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDL	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved L-L@C-term; missed K-L@2	0.07	1479.82	740.92	1479.75	740.88	2	1.864.0
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEI	No iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved I-D@C-term; missed K-L@2	0.00	1805.89	903.95	1805.89	903.95	2	505.4
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEID	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved D-D@C-term; missed K-L@2	-0.02	2065.00	689.34	2065.02	689.35	3	107.4
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDD	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved D-V@C-term; missed K-L@2	0.01	2180.05	727.69	2180.05	727.69	3	46.5
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVL	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved L-E@C-term; missed K-L@2	0.00	2392.20	798.41	2392.20	798.41	3	60.9
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAE	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved E-D@C-term; missed K-L@2	-0.05	2964.35	989.12	2964.41	989.14	3	32.6
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	No iTRAQ4plex@N-term; iTRAQ4plex(K)@2	missed K-L@2	0.03	3337.60	1113.54	3337.57	1113.53	3	144.9
	100.0	B6DAC1	(Rv2111c)	99.0	GGGGGEDDDLPGASAAGQER	iTRAQ4plex@N-term; Glu->Asp@6; Pro->Thr@11		0.02	1948.87	650.63	1948.85	650.62	3	90.7
	100.0	B6DAC1	(Rv2111c)	99.0	LTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term		0.01	3080.44	1027.82	3080.43	1027.82	3	
	100.0	B6DAC1	(Rv2111c)	99.0	MAQEQTK	iTRAQ4plex@N-term; iTRAQ4plex(K)@7		0.02	1122.61	562.31	1122.59	562.30	2	142.2
	100.0	B6DAC1	(Rv2111c)	97.0	GGGGGEDDDLPGASAAGQERR	iTRAQ4plex@N-term; Pro->Ser@11	missed R-R@20	0.07	2105.02	702.68	2104.95	702.66	3	3.262.8
	100.0	B6DAC1	(Rv2111c)	96.0	EKLTEETDDLLD	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved D-E@C-term; missed K-L@2	-0.01	1707.86	854.94	1707.87	854.94	2	1.352.4
	100.0	B6DAC1	(Rv2111c)	95.0	EKLTEETDDLLDE	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved E-I@C-term; missed K-L@2	0.00	1836.91	613.31	1836.91	613.31	3	46.7
	100.0	B6DAC1	(Rv2111c)	91.0	EKLTEETDDLLDEIDDVLEE	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved E-N@C-term; missed K-L@2	0.00	2650.28	884.43	2650.28	884.44	3	42.4
	100.0	B6DAC1	(Rv2111c)	85.0	EKLTEETDDLLDEIDDVLEEN	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved N-A@C-term; missed K-L@2	0.03	2764.36	922.46	2764.33	922.45	3	16.3
	100.0	B6DAC1	(Rv2111c)	81.0	EKLTEETDDLL	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved L-D@C-term; missed K-L@2	-0.03	1592.81	797.41	1592.84	797.43	2	857.8
	100.0	B6DAC1	(Rv2111c)	60.0	EKLTEETDDLLDEIDDVLE	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved E-E@C-term; missed K-L@2	-0.01	2521.23	841.42	2521.24	841.42	3	14.1
	100.0	B6DAC1	(Rv2111c)	78.0	AYVQK	iTRAQ4plex@N-term; iTRAQ4plex(K)@5		0.01	895.55	448.78	895.54	448.78	2	16.3
	100.0	B6DAC1	(Rv2111c)	88.0	EKLTEETDDLLDEIDDVLEENAEDFVRA	No iTRAQ4plex@N-term; iTRAQ4plex(K)@2; Deamidated(N)@21; iTRAQ4plex(Y)@29; iTRAQ4plex(K)@32	missed K-L@2; missed R-A@27; missed K-G	-0.27	4487.92	1122.99	4488.19	1123.06	4	1.675.9
	100.0	B6DAC1	(Rv2111c)	99.0	AEDFVR	iTRAQ4plex@N-term	cleaved N-A@N-term	0.01	879.46	440.74	879.46	440.74	2	747.7
	100.0	B6DAC1	(Rv2111c)	99.0	AQEQTK	iTRAQ4plex@N-term; Lys->Gln@6	cleaved M-A@N-term	0.02	847.44	424.73	847.42	424.72	2	5.4
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDL	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved L-L@C-term; missed K-L@2	0.03	1479.78	740.90	1479.75	740.88	2	2.331.7
	100.0	B6DAC1	(Rv2111c)	75.0	EKLTEETDDL	No iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved L-L@C-term; missed K-L@2	0.01	1335.66	668.84	1335.65	668.83	2	472.2
	100.0	B6DAC1	(Rv2111c)	91.0	EKLTEETDDLLDEID	No iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved D-D@C-term; missed K-L@2	0.03	1920.95	961.48	1920.92	961.47	2	808.2
	100.0	B6DAC1	(Rv2111c)	97.0	EKLTEETDDLLDEIDDVL	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	cleaved L-E@C-term; missed K-L@2	-0.02	2392.18	798.40	2392.20	798.41	3	47.8
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term; iTRAQ4plex(K)@2; Deamidated(N)@21	missed K-L@2	-0.06	3482.59	871.66	3482.66	871.67	4	
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	Glu->pyro-Glu@N-term; iTRAQ4plex(K)@2	missed K-L@2	0.06	3319.62	1107.55	3319.56	1107.53	3	109.9
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term; iTRAQ4plex(K)@2; Leu->His@18	missed K-L@2	-0.01	3505.64	877.42	3505.65	877.42	4	258.7
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	No iTRAQ4plex@N-term; iTRAQ4plex(K)@2	missed K-L@2	-0.13	3337.44	1113.49	3337.57	1113.53	3	339.9
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	No iTRAQ4plex@N-term; iTRAQ4plex(K)@2; Dimethyl(R)@27	missed K-L@2	-0.05	3365.56	842.40	3365.60	842.41	4	10.9
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	No iTRAQ4plex@N-term; Lys->Gln@2	missed K-L@2	0.08	3193.51	1065.51	3193.43	1065.48	3	34.3
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	No iTRAQ4plex@N-term; Lys->Gln@2	missed K-L@2	0.14	3193.57	1065.53	3193.43	1065.48	3	67.6
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	No iTRAQ4plex@N-term; Lys->Gln@2; Glu->Arg@23; Deamidated(R)@27	missed K-L@2	0.04	3221.51	1074.84	3221.47	1074.83	3	23.7
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term; iTRAQ4plex(K)@2; Leu->His@11	missed K-L@2	0.01	3505.66	877.42	3505.65	877.42	4	143.8
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	missed K-L@2	0.08	3481.75	871.44	3481.67	871.43	4	30.4
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term; Lys->Arg@2; iTRAQ4plex(T)@4	missed K-L@2	0.06	3509.74	878.44	3509.68	878.43	4	23.6
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	missed K-L@2	0.04	3481.71	871.44	3481.67	871.43	4	21.6
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	No iTRAQ4plex@N-term; iTRAQ4plex(K)@2	missed K-L@2	-0.02	3337.55	1113.53	3337.57	1113.53	3	196.3
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	No iTRAQ4plex@N-term; iTRAQ4plex(K)@2; Asp->Asn@16; Deamidated(N)@21	missed K-L@2	0.00	3337.57	835.40	3337.57	835.40	4	262.5
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term; iTRAQ4plex(K)@2	missed K-L@2	-0.01	3481.66	871.42	3481.67	871.43	4	143.5
	100.0	B6DAC1	(Rv2111c)	99.0	EKLTEETDDLLDEIDDVLEENAEDFVR	No iTRAQ4plex@N-term; iTRAQ4plex(K)@2	missed K-L@2	0.07	3337.64	835.42	3337.57	835.40	4	112.4
	100.0	B6DAC1	(Rv2111c)	94.0	EKLTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term; iTRAQ4plex(K)@2; Deamidated(N)@21	missed K-L@2	0.07	3482.72	871.69	3482.66	871.67	4	
	100.0	B6DAC1	(Rv2111c)	99.0	GGGGGEDDDLPGASAAGQER	No iTRAQ4plex@N-term; Glu->Asp@6; Oxidation(P)@11; iTRAQ4plex(S)@14		0.05	1960.89	654.64	1960.85	654.62	3	435.0
	100.0	B6DAC1	(Rv2111c)	99.0	GGGGGEDDDLPGASAAGQER	No iTRAQ4plex@N-term; Glu->Asp@6; Oxidation(P)@11; iTRAQ4plex(S)@14		0.05	1960.90	654.64	1960.85	654.62	3	772.6
	100.0	B6DAC1	(Rv2111c)	99.0	GGGGGEDDDLPGASAAGQER	No iTRAQ4plex@N-term; Glu->Asp@6; Oxidation(P)@11; iTRAQ4plex(S)@14		0.01	1960.85	654.63	1960.85	654.62	3	503.4
	100.0	B6DAC1	(Rv2111c)	99.0	GGGGGEDDDLPGASAAGQER	No iTRAQ4plex@N-term; Glu->Asp@6; Oxidation(P)@11; iTRAQ4plex(S)@14		0.04	1960.89	654.64	1960.85	654.62	3	231.1
	100.0	B6DAC1	(Rv2111c)	99.0	GGGGGEDDDLPGASAAGQER	No iTRAQ4plex@N-term; Oxidation(P)@11; iTRAQ4plex(S)@14		0.00	1974.87	659.30	1974.86	659.30	3	33.7
	100.0	B6DAC1	(Rv2111c)	99.0	GGGGGEDDDLPGASAAGQER	iTRAQ4plex@N-term; Glu->Asp@6; Pro->Thr@11		0.01	1948.85	650.63	1948.85	650.62	3	1.246.8
	100.0	B6DAC1	(Rv2111c)	98.0	GGGGGEDDDLPGASAAGQER	iTRAQ4plex@N-term; Glu->Asp@6; Ser->Glu@14		-0.05	1986.81	663.28	1986.86	663.30	3	8.7
	100.0	B6DAC1	(Rv2111c)	96.0	GGGGGEDDDLPGASAAGQER	iTRAQ4plex@N-term; Carboxy(E)@6; Pro->Thr@11		-0.01	2006.84	669.95	2006.85	669.96	3	58.7
	100.0	B6DAC1	(Rv2111c)	91.0	GGGGGEDDDLPGASAAGQER	No iTRAQ4plex@N-term; Carboxy(E)@6; Oxidation(P)@11; iTRAQ4plex(S)@14		0.01	2018.87	673.96	2018.85	673.96	3	81.3
	100.0	B6DAC1	(Rv2111c)	78.0	GGGGGEDDDLPGASAAGQER	iTRAQ4plex@N-term; Pro->Gln@11; Deamidated(Q)@18		0.04	1990.90	664.64	1990.86	664.63	3	42.2
	100.0	B6DAC1	(Rv2111c)	91.0	GGGGGEDDDLPGASAAGQERR	No iTRAQ4plex@N-term; Asp->Ser@9	missed R-R@20	-0.03	1942.85	648.62	1942.87	648.63	3	21.7
	100.0	B6DAC1	(Rv2111c)	99.0	LTEETDDLLDEIDDVLEENAEDFVR	No iTRAQ4plex@N-term		-0.05	2936.28	979.77	2936.33	979.78	3	
	100.0	B6DAC1	(Rv2111c)	99.0	LTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term		-0.04	3080.40	1027.81	3080.43	1027.82	3	33.7
	100.0	B6DAC1	(Rv2111c)	99.0	LTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term; Ala->Val@20		-0.06	3108.40	1037.14	3108.46	1037.16	3	15.0
	100.0	B6DAC1	(Rv2111c)	99.0	LTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term; Dimethyl(R)@25		0.07	3108.53	778.14	3108.46	778.12	4	119.1
	100.0	B6DAC1	(Rv2111c)	99.0	LTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term; Leu->His@16		-0.10	3104.31	777.08	3104.41	777.11	4	53.3
	100.0	B6DAC1	(Rv2111c)	96.0	LTEETDDLLDEIDDVLEENAEDFVR	iTRAQ4plex@N-term; Thr->Glu@5; Dimethyl(R)@25		0.10	3136.56	1046.53	3136.46	1046.49	3	8.6
	100.0	B6DAC1	(Rv2111c)	99.0	REKLTEETDDLLDEIDDVLEENAEDFVR	No iTRAQ4plex@N-term; iTRAQ4plex(K)@3; Oxidation(D)@13	missed R-E@1; missed K-L@3	0.00	3509.66	878.42	3509.67	878.42	4	10.9
	100.0	B6DAC1	(Rv2111c)	99.0	RGGGGGEDDDLPGASAAGQER	No iTRAQ4plex@N-term; Ser->Asp@15	missed R-G@1	-0.03	1998.84	500.72	1998.86	500.72	4	15.2

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
1	98.9	A0R4D0	MSMEG_5790	99.0	ALSSAGNGNVTVAPTGAGIHEVDVK	iTRAQ4plex@N-term; Deamidated(N)@7; iTRAQ4plex(H)@20; User modH on Lys(K)@25	missed K-V@25	-0.04	3065.57	767.40	3065.61	767.41	4	132.1
	98.9	A0R4D0	MSMEG_5790	99.0	DGSGQAVGGAFVR	iTRAQ4plex@N-term	cleaved V-D@N-term	0.04	1363.74	682.88	1363.70	682.86	2	505.8
	98.9	A0R4D0	MSMEG_5790	99.0	FAAPGTWTVR	iTRAQ4plex@N-term	cleaved F-F@N-term	0.01	1248.69	625.35	1248.67	625.34	2	4.376.8
	98.9	A0R4D0	MSMEG_5790	99.0	FFAAPGTWTVR	iTRAQ4plex@N-term		0.03	1395.77	698.89	1395.74	698.88	2	1.642.5
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		0.00	2343.14	782.05	2343.14	782.05	3	26.1
	98.9	A0R4D0	MSMEG_5790	99.0	VDGSGQAVGGAFVR	iTRAQ4plex@N-term	cleaved V-V@N-term	0.02	1462.78	488.60	1462.77	488.60	3	410.9
	98.9	A0R4D0	MSMEG_5790	99.0	FAAPGTWTVR	iTRAQ4plex@N-term; Dimethyl(R)@10	cleaved F-F@N-term	0.00	1276.71	639.36	1276.70	639.36	2	1.892.2
	98.9	A0R4D0	MSMEG_5790	99.0	FAAPGTWTVR	iTRAQ4plex@N-term	cleaved F-F@N-term	0.01	1248.68	625.35	1248.67	625.34	2	7.522.6
	98.9	A0R4D0	MSMEG_5790	99.0	FFAAPGTWTVR	iTRAQ4plex@N-term		0.04	1395.78	698.90	1395.74	698.88	2	4.656.4
	98.9	A0R4D0	MSMEG_5790	99.0	FFAAPGTWTVR	iTRAQ4plex@N-term		-0.01	1395.74	698.88	1395.74	698.88	2	11.648.9
	98.9	A0R4D0	MSMEG_5790	99.0	FFAAPGTWTVR	iTRAQ4plex@N-term		0.03	1395.77	698.89	1395.74	698.88	2	8.399.6
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		0.00	2343.13	782.05	2343.14	782.05	3	22.8
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		0.00	2343.14	782.05	2343.14	782.05	3	35.9
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		-0.01	2343.13	782.05	2343.14	782.05	3	33.7
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		0.00	2343.14	782.05	2343.14	782.05	3	264.4
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		0.02	2343.15	782.06	2343.14	782.05	3	374.1
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term; Dimethyl(R)@21		0.05	2371.21	791.41	2371.17	791.40	3	121.6
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		0.00	2343.13	782.05	2343.14	782.05	3	19.6
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		0.00	2343.14	782.05	2343.14	782.05	3	
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		0.02	2343.16	782.06	2343.14	782.05	3	
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		-0.04	2343.10	782.04	2343.14	782.05	3	
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		0.02	2343.16	782.06	2343.14	782.05	3	
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		0.03	2343.17	782.06	2343.14	782.05	3	177.3
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		-0.05	2343.08	782.03	2343.14	782.05	3	9.8
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term		-0.01	2343.13	782.05	2343.14	782.05	3	30.4
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term; Methyl(E)@11		0.01	2357.16	786.73	2357.15	786.72	3	
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term; Dehydrated(E)@11		0.04	2325.16	776.06	2325.12	776.05	3	17.4
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term; Ala->Val@16		-0.01	2371.16	791.39	2371.17	791.40	3	10.9
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term; Dehydrated(D)@19		0.04	2325.16	776.06	2325.12	776.05	3	28.3
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term; Dimethyl(R)@21		0.04	2371.21	791.41	2371.17	791.40	3	145.3
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term; Dimethyl(R)@21		0.04	2371.20	791.41	2371.17	791.40	3	81.4
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term; Dimethyl(R)@21		-0.06	2371.11	791.38	2371.17	791.40	3	
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term; Dimethyl(R)@21		-0.06	2371.11	791.38	2371.17	791.40	3	
	98.9	A0R4D0	MSMEG_5790	99.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term; Dimethyl(R)@21		-0.06	2371.10	791.38	2371.17	791.40	3	
	98.9	A0R4D0	MSMEG_5790	99.0	VVDGSGQAVGGAFVR	iTRAQ4plex@N-term		-0.02	1561.82	781.92	1561.83	781.92	2	5.891.2
	98.9	A0R4D0	MSMEG_5790	99.0	VVDGSGQAVGGAFVR	iTRAQ4plex@N-term		-0.02	1561.81	781.91	1561.83	781.92	2	5.595.1
	98.9	A0R4D0	MSMEG_5790	99.0	VVDGSGQAVGGAFVR	iTRAQ4plex@N-term		-0.02	1561.82	781.92	1561.83	781.92	2	1.045.9
	98.9	A0R4D0	MSMEG_5790	99.0	VVDGSGQAVGGAFVR	iTRAQ4plex@N-term		-0.01	1561.82	781.92	1561.83	781.92	2	5.760.6
	98.9	A0R4D0	MSMEG_5790	99.0	VVDGSGQAVGGAFVR	iTRAQ4plex@N-term		-0.01	1561.82	781.92	1561.83	781.92	2	58.7
	98.9	A0R4D0	MSMEG_5790	99.0	VVDGSGQAVGGAFVR	iTRAQ4plex@N-term; Dimethyl(R)@15		0.00	1589.86	530.96	1589.86	530.96	3	792.3
	98.9	A0R4D0	MSMEG_5790	99.0	VVDGSGQAVGGAFVR	iTRAQ4plex@N-term; Dimethyl(R)@15		-0.05	1589.82	530.95	1589.86	530.96	3	3.762.7
	98.9	A0R4D0	MSMEG_5790	98.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term; Oxidation(F)@8		0.06	2359.19	787.41	2359.13	787.38	3	33.7
	98.9	A0R4D0	MSMEG_5790	98.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term; Glu->Arg@11		0.01	2370.20	791.07	2370.19	791.07	3	30.3
	98.9	A0R4D0	MSMEG_5790	98.0	LLDGSDEFTAEVVASATGDFR	iTRAQ4plex@N-term; Dehydrated(D)@19		0.01	2325.14	776.05	2325.12	776.05	3	17.4
	98.9	A0R4D0	MSMEG_5790	95.0	ETVITGR	iTRAQ4plex@N-term		0.00	918.53	460.27	918.53	460.27	2	2.096.0
	98.9	A0R4D0	MSMEG_5790	94.0	ETVITGR	iTRAQ4plex@N-term		-0.02	918.51	460.26	918.53	460.27	2	15.924.5
	98.9	A0R4D0	MSMEG_5790	94.0	ETVITGR	iTRAQ4plex@N-term		-0.02	918.51	460.26	918.53	460.27	2	11.984.0
	98.9	A0R4D0	MSMEG_5790	94.0	FFAAPGTWTVR	iTRAQ4plex@N-term; Dimethyl(R)@11		0.00	1423.77	712.89	1423.77	712.89	2	5.405.8
	98.9	A0R4D0	MSMEG_5790	91.0	FFAAPGTWTVR	iTRAQ4plex@N-term; Oxidation(W)@8		-0.01	1411.73	706.87	1411.74	706.88	2	1.042.7
	98.9	A0R4D0	MSMEG_5790	87.0	FFAAPGTWTVR	iTRAQ4plex@N-term; Dehydrated(T)@7		-0.05	1377.68	460.23	1377.73	460.25	3	109.3
	98.9	A0R4D0	MSMEG_5790	82.0	FAAPGTWTVR	iTRAQ4plex@N-term; Dehydrated(T)@6	cleaved F-F@N-term	-0.06	1230.61	411.21	1230.66	411.23	3	47.7
	98.9	A0R4D0	MSMEG_5790	79.0	FFAAPGTWTVR	iTRAQ4plex@N-term; Dimethyl(R)@11		0.00	1423.77	712.89	1423.77	712.89	2	1.024.1
2	84.6	A0R1V9	MSMEG_4891	99.0	ALLTIGDQFPEYDLTAVVGGDLSK	iTRAQ4plex@N-term; Deamidated(Q)@8; iTRAQ4plex(S)@23; Lys->Gln@24	cleaved M-A@N-term	0.05	2810.50	937.84	2810.45	937.82	3	279.4
	84.6	A0R1V9	MSMEG_4891	99.0	DFTFVCPTEIAAFGK	iTRAQ4plex@N-term; Pyridylethyl(C)@6; Lys->Gln@15		0.04	1893.95	632.32	1893.91	632.31	3	180.5
	84.6	A0R1V9	MSMEG_4891	99.0	ELTAACGVLNADGVADR	iTRAQ4plex@N-term; Pyridylethyl(C)@6; Dimethyl(R)@17		0.02	1951.02	651.35	1951.00	651.34	3	166.3
	84.6	A0R1V9	MSMEG_4891	99.0	KGDPTINAGELLAGAV	iTRAQ4plex@N-term; Lys->Trp@1; Dehydrated(D)@3	missed K-G@1	0.08	1708.97	855.49	1708.89	855.45	2	135.3
	84.6	A0R1V9	MSMEG_4891	99.0	LNEDFEDR	iTRAQ4plex@N-term		0.03	1180.57	591.29	1180.55	591.28	2	7.304.6
	84.6	A0R1V9	MSMEG_4891	99.0	NEDFEDR	iTRAQ4plex@N-term	cleaved L-N@N-term	0.00	1067.47	534.74	1067.46	534.74	2	103.1
	84.6	A0R1V9	MSMEG_4891	99.0	TLPFPMVSDLK	iTRAQ4plex@N-term; Lys->Gln@11		0.03	1390.75	696.38	1390.73	696.37	2	688.8

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	84.6	A0R1V9	MSMEG_4891	99.0	ATFIVDPNNEVQFVSVTAGSVGR	iTRAQ4plex@N-term; Val->Asn@11		0.00	2565.29	856.10	2565.29	856.11	3	36.9
	84.6	A0R1V9	MSMEG_4891	99.0	ATFIVDPNNEVQFVSVTAGSVGR	iTRAQ4plex@N-term		0.05	2550.37	851.13	2550.32	851.11	3	10.9
	84.6	A0R1V9	MSMEG_4891	99.0	ATFIVDPNNEVQFVSVTAGSVGR	iTRAQ4plex@N-term		-0.02	2550.30	851.11	2550.32	851.11	3	22.7
	84.6	A0R1V9	MSMEG_4891	99.0	DFTFVCPTEIAAFGK	iTRAQ4plex@N-term; Pyridylethyl(C)@6; Lys->Gln@15		0.05	1893.96	632.33	1893.91	632.31	3	130.9
	84.6	A0R1V9	MSMEG_4891	99	KGDPTINAGELLAGAV	iTRAQ4plex@N-term; User modH on Lys(K)@1	missed K-G@1	0.05	1912.07	638.36	1912.02	638.34	3	
	84.6	A0R1V9	MSMEG_4891	95.0	TLPFPMVSDLK	iTRAQ4plex@N-term; Lys->Arg@11		0.03	1418.80	710.41	1418.77	710.39	2	753.8
	84.6	A0R1V9	MSMEG_4891	93.0	QPDDYFTR	iTRAQ4plex@N-term		0.02	1184.57	593.29	1184.56	593.29	2	6.007.4
	84.6	A0R1V9	MSMEG_4891	93.0	TLPFPMVSDLKR	iTRAQ4plex@N-term; Lys->Gln@11	missed K-R@11	0.01	1546.84	516.62	1546.83	516.62	3	226.0
	84.6	A0R1V9	MSMEG_4891	80.0	TLPFPMVSDLKR	iTRAQ4plex@N-term; Lys->Gln@11	missed K-R@11	0.01	1546.84	516.62	1546.83	516.62	3	47.8
	84.6	A0R1V9	MSMEG_4891	76	TLPFPMVSDLKR	No iTRAQ4plex@N-term; User modH on Lys(K)@11	missed K-R@11	0.03	1645.90	549.64	1645.87	549.63	3	52.1
3	83.7	A0QYW6	MSMEG_3811	99.0	AAGATDIEER	iTRAQ4plex@N-term	cleaved R-P@C-term	0.00	1175.59	588.80	1175.59	588.80	2	184.1
	83.7	A0QYW6	MSMEG_3811	99.0	LIIATAYFPQSEDSR	iTRAQ4plex@N-term		-0.01	1853.96	618.99	1853.96	619.00	3	8.7
	83.7	A0QYW6	MSMEG_3811	99.0	LLGSVPANVAR	iTRAQ4plex@N-term		-0.01	1239.73	620.87	1239.74	620.88	2	10.648.1
	83.7	A0QYW6	MSMEG_3811	99.0	MAGNAPIYAILR	iTRAQ4plex@N-term		-0.01	1432.79	717.40	1432.80	717.41	2	3.074.5
	83.7	A0QYW6	MSMEG_3811	99.0	AAGATDIEER	iTRAQ4plex@N-term	cleaved R-P@C-term	0.01	1175.60	588.81	1175.59	588.80	2	265.9
	83.7	A0QYW6	MSMEG_3811	99.0	ADLLVVGNVGLSTIAGR	iTRAQ4plex@N-term		-0.01	1798.03	600.35	1798.04	600.36	3	13.0
	83.7	A0QYW6	MSMEG_3811	99.0	LLGSVPANVAR	iTRAQ4plex@N-term; Ala->Val@10		0.00	1267.77	634.89	1267.77	634.89	2	1.968.1
	83.7	A0QYW6	MSMEG_3811	99.0	MAGNAPIYAILR	iTRAQ4plex@N-term		-0.01	1432.79	717.40	1432.80	717.41	2	4.132.8
	83.7	A0QYW6	MSMEG_3811	99.0	MAGNAPIYAILR	iTRAQ4plex@N-term; Dimethyl(R)@12		0.03	1460.86	731.44	1460.83	731.42	2	253.7
	83.7	A0QYW6	MSMEG_3811	98.0	IIATAYFPQSEDSR	iTRAQ4plex@N-term	cleaved L-I@N-term	0.00	1740.88	581.30	1740.88	581.30	3	39.1
	83.7	A0QYW6	MSMEG_3811	97.0	AGQIAAASN	iTRAQ4plex@N-term	cleaved N-A@C-term	0.01	945.51	473.76	945.50	473.76	2	19.6
	83.7	A0QYW6	MSMEG_3811	97.0	SKTDVLIVHTS	iTRAQ4plex@N-term; Lys->Gln@2	missed K-T@2	0.05	1342.77	448.60	1342.72	448.58	3	289.2
4	79.1	A0R6E3	MSMEG_6518	99.0	AAVVLSGLR	iTRAQ4plex@N-term		0.00	1028.65	515.33	1028.65	515.33	2	19.250.4
	79.1	A0R6E3	MSMEG_6518	99.0	ATPSVIVALSGVR	iTRAQ4plex@N-term		-0.05	1412.80	707.41	1412.85	707.43	2	3.145.3
	79.1	A0R6E3	MSMEG_6518	99.0	DLIEAVEAEEPATEAETAQIK	iTRAQ4plex@N-term; iTRAQ4plex(T)@17; Lys->Gln@21		-0.01	2544.26	849.09	2544.27	849.10	3	266.3
	79.1	A0R6E3	MSMEG_6518	99.0	LQGSLAEAASR	iTRAQ4plex@N-term; Ser->Asp@10		0.05	1273.72	637.87	1273.67	637.84	2	4.299.1
	79.1	A0R6E3	MSMEG_6518	99.0	LTTAEAANGIGVR	iTRAQ4plex@N-term; Deamidated(N)@8		0.03	1416.80	709.41	1416.77	709.39	2	6.203.2
	79.1	A0R6E3	MSMEG_6518	99.0	TRYDELMTTAAEGPGATLGQR	iTRAQ4plex@N-term; Gln->Arg@20	missed R-Y@2	-0.03	2409.19	804.07	2409.22	804.08	3	122.2
	79.1	A0R6E3	MSMEG_6518	99.0	ATPSVIVALSGVR	iTRAQ4plex@N-term		-0.02	1412.83	707.42	1412.85	707.43	2	533.6
	79.1	A0R6E3	MSMEG_6518	99.0	ATPSVIVALSGVR	iTRAQ4plex@N-term; Dimethyl(R)@13		0.00	1440.88	721.45	1440.88	721.45	2	1.341.3
	79.1	A0R6E3	MSMEG_6518	99.0	LQGSLAEAASR	iTRAQ4plex@N-term		0.04	1245.72	623.87	1245.68	623.85	2	10.732.8
	79.1	A0R6E3	MSMEG_6518	99.0	LTTAEAANGIGVR	iTRAQ4plex@N-term; Deamidated(N)@8		0.03	1416.80	709.41	1416.77	709.39	2	5.261.9
	79.1	A0R6E3	MSMEG_6518	99.0	TRYDELMTTAAEGPGATLGQR	iTRAQ4plex@N-term	missed R-Y@2	0.05	2381.22	794.75	2381.18	794.73	3	87.7
	79.1	A0R6E3	MSMEG_6518	99.0	TRYDELMTTAAEGPGATLGQR	iTRAQ4plex@N-term	missed R-Y@2	0.05	2381.22	794.75	2381.18	794.73	3	590.5
	79.1	A0R6E3	MSMEG_6518	99.0	TRYDELMTTAAEGPGATLGQR	No iTRAQ4plex@N-term	missed R-Y@2	-0.02	2237.06	746.69	2237.07	746.70	3	89.7
	79.1	A0R6E3	MSMEG_6518	97.0	KLQGSLAEAASR	iTRAQ4plex@N-term; Lys->Gln@1	missed K-L@1	0.04	1373.78	458.93	1373.74	458.92	3	384.3
	79.1	A0R6E3	MSMEG_6518	87.0	KLQGSLAEAASR	iTRAQ4plex@N-term; User modH on Lys(K)@1	missed K-L@1	0.04	1616.93	539.98	1616.88	539.97	3	
5	79.0	A0R2W6	MSMEG_5258	99.0	IEPIEVMTFDGDGR	iTRAQ4plex@N-term		0.03	1721.87	861.94	1721.84	861.93	2	3.686.7
	79.0	A0R2W6	MSMEG_5258	99.0	SHDAAALESFVK	iTRAQ4plex@N-term; Lys->Gln@12	cleaved M-S@N-term	0.04	1417.74	473.59	1417.70	473.57	3	317.3
	79.0	A0R2W6	MSMEG_5258	99.0	YLDTVAGGSAADIAALYADDATVEDPVG	iTRAQ4plex@N-term		-0.02	3718.79	930.71	3718.81	930.71	4	158.9
	79.0	A0R2W6	MSMEG_5258	99.0	IEPIEVMTFDGDGR	iTRAQ4plex@N-term; Dimethyl(R)@14		0.00	1749.87	875.94	1749.87	875.94	2	707.9
	79.0	A0R2W6	MSMEG_5258	97.0	AYWSPADIK	iTRAQ4plex@N-term; Lys->Gln@9		0.04	1193.63	597.82	1193.58	597.80	2	270.3
6	79.0	A0R647	MSMEG_6422	99.0	AGSNLFHIEDFVAR	No iTRAQ4plex@N-term; Gly->Pro@2		-0.02	1614.79	539.27	1614.82	539.28	3	54.4
	79.0	A0R647	MSMEG_6422	99.0	DALALALDQER	iTRAQ4plex@N-term; Gln->Arg@9		-0.02	1385.75	693.88	1385.77	693.89	2	1.244.7
	79.0	A0R647	MSMEG_6422	99.0	DEGDHLGEQFMQWF	iTRAQ4plex@N-term	cleaved F-L@C-term	0.02	1881.83	941.92	1881.81	941.91	2	329.2
	79.0	A0R647	MSMEG_6422	99.0	DEGDHLGEQFMQWFLK	iTRAQ4plex@N-term; Lys->Gln@16		0.06	2123.02	708.68	2122.95	708.66	3	78.2
	79.0	A0R647	MSMEG_6422	99.0	DVEVEIPGIDPVCNNFTTPR	iTRAQ4plex@N-term; Pyridylethyl(C)@13		0.04	2463.26	822.09	2463.22	822.08	3	181.8
	79.0	A0R647	MSMEG_6422	99.0	EMSAAGADPTAPR	iTRAQ4plex@N-term		0.03	1416.71	709.36	1416.68	709.35	2	803.2
	79.0	A0R647	MSMEG_6422	99.0	EQVEEVAAMTTLVR	iTRAQ4plex@N-term		0.04	1718.94	860.48	1718.90	860.46	2	628.6
	79.0	A0R647	MSMEG_6422	99.0	MLVQYLLDR	iTRAQ4plex@N-term	cleaved M-M@N-term	0.00	1293.72	647.87	1293.72	647.87	2	1.071.8
	79.0	A0R647	MSMEG_6422	99.0	NHAMMLVQYLLDR	iTRAQ4plex@N-term		0.00	1746.90	583.31	1746.90	583.31	3	882.8
	79.0	A0R647	MSMEG_6422	99.0	AGSNLFHIEDFVAR	iTRAQ4plex@N-term		-0.02	1718.87	573.96	1718.89	573.97	3	254.8
	79.0	A0R647	MSMEG_6422	99.0	AGSNLFHIEDFVAR	iTRAQ4plex@N-term; Deamidated(N)@4; Deamidated(R)@14		0.06	1720.92	574.65	1720.85	574.63	3	830.5
	79.0	A0R647	MSMEG_6422	99.0	AGSNLFHIEDFVAR	iTRAQ4plex@N-term; Ala->Val@13		-0.01	1746.91	583.31	1746.92	583.31	3	242.4
	79.0	A0R647	MSMEG_6422	99.0	AGSNLFHIEDFVAR	iTRAQ4plex@N-term; Deamidated(N)@4		0.01	1719.88	574.30	1719.87	574.30	3	32.6
	79.0	A0R647	MSMEG_6422	99.0	AGSNLFHIEDFVAR	No iTRAQ4plex@N-term		0.01	1574.79	525.94	1574.78	525.94	3	46.5
	79.0	A0R647	MSMEG_6422	99.0	EQVEEVAAMTTLVR	iTRAQ4plex@N-term		0.00	1718.90	573.97	1718.90	573.97	3	

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	79.0	A0R647	MSMEG_6422	99.0	EQVEEVAAMTTLVR	iTRAQ4plex@N-term; Dehydrated(T)@10		0.00	1700.89	567.97	1700.89	567.97	3	
	79.0	A0R647	MSMEG_6422	99.0	EQVEEVAAMTTLVR	iTRAQ4plex@N-term		0.01	1718.91	573.98	1718.90	573.97	3	
	79.0	A0R647	MSMEG_6422	98.0	MLVQYLLDR	iTRAQ4plex@N-term	cleaved M-M@N-term	0.00	1293.72	647.87	1293.72	647.87	2	173.3
	79.0	A0R647	MSMEG_6422	98.0	TVTEQISR	iTRAQ4plex@N-term		-0.01	1076.58	539.30	1076.59	539.30	2	1.265.9
	79.0	A0R647	MSMEG_6422	94.0	EQVEEVAAMTTLVR	iTRAQ4plex@N-term; Ala->Ser@7		0.01	1734.90	579.31	1734.89	579.31	3	32.6
	79.0	A0R647	MSMEG_6422	77.0	LVQYLLDR	iTRAQ4plex@N-term	cleaved M-L@N-term	-0.02	1162.67	582.34	1162.68	582.35	2	410.0
7	74.6	A0QSH8	MSMEG_1484	99.0	LSEKLGIPQISTGDLFR	iTRAQ4plex@N-term; iTRAQ4plex(S)@2; User modH on Lys(K)@4	missed K-L@4	-0.03	2404.31	802.44	2404.34	802.46	3	997.1
	74.6	A0QSH8	MSMEG_1484	99.0	ADDTDEVIR	iTRAQ4plex@N-term		0.03	1176.60	589.31	1176.57	589.29	2	1.081.0
	74.6	A0QSH8	MSMEG_1484	99.0	IDQPDAAEGFILDGYPR	iTRAQ4plex@N-term		-0.01	2020.00	674.34	2020.00	674.34	3	144.0
	74.6	A0QSH8	MSMEG_1484	99.0	LDAVLEFQVSEDELLTR	iTRAQ4plex@N-term		0.01	2120.13	707.72	2120.11	707.71	3	
	74.6	A0QSH8	MSMEG_1484	99.0	LGIPQISTGDLFR	iTRAQ4plex@N-term		0.00	1559.88	780.95	1559.88	780.95	2	382.1
	74.6	A0QSH8	MSMEG_1484	99.0	NIGDGTPLGLEAK	iTRAQ4plex@N-term; Lys->Gln@13		0.04	1427.78	714.90	1427.74	714.88	2	1.245.2
	74.6	A0QSH8	MSMEG_1484	99.0	TVNAVGALDEVFAR	iTRAQ4plex@N-term; Ala->Val@13		-0.01	1632.89	817.45	1632.90	817.46	2	2.570.6
	74.6	A0QSH8	MSMEG_1484	99.0	VVLLGPPGAGK	iTRAQ4plex@N-term; Lys->Gln@11		0.03	1150.71	576.36	1150.68	576.35	2	684.4
	74.6	A0QSH8	MSMEG_1484	99.0	TVNAVGALDEVFAR	iTRAQ4plex@N-term		-0.01	1604.85	803.43	1604.86	803.44	2	2.235.3
	74.6	A0QSH8	MSMEG_1484	99.0	TVNAVGALDEVFAR	iTRAQ4plex@N-term		0.03	1604.89	535.97	1604.86	535.96	3	8.7
	74.6	A0QSH8	MSMEG_1484	98.0	SVEQAGALK	iTRAQ4plex@N-term; Lys->Gln@9		0.03	1045.59	523.80	1045.55	523.78	2	412.5
	74.6	A0QSH8	MSMEG_1484	97.0	ADDTDEVIR	iTRAQ4plex@N-term; Dimethyl(R)@9		0.02	1204.63	603.32	1204.61	603.31	2	1.053.5
	74.6	A0QSH8	MSMEG_1484	97.0	IDQPDAAEGFILDGYPR	iTRAQ4plex@N-term; Dimethyl(R)@17		0.00	2048.03	683.69	2048.03	683.69	3	36.9
	74.6	A0QSH8	MSMEG_1484	96.0	RYLDAGDLVPAELTNR	iTRAQ4plex@N-term	missed R-Y@1	0.00	1946.03	649.68	1946.03	649.69	3	22.8
	74.6	A0QSH8	MSMEG_1484	95.0	SVEQAGALK	iTRAQ4plex@N-term; Lys->Gln@9		0.04	1045.59	523.80	1045.55	523.78	2	532.1
	74.6	A0QSH8	MSMEG_1484	91.0	LGIPQISTGDLFR	iTRAQ4plex@N-term		-0.02	1559.86	780.94	1559.88	780.95	2	738.6
	74.6	A0QSH8	MSMEG_1484	85.0	NIGDGTPLGLEAKR	iTRAQ4plex@N-term; Ala->Val@12; Lys->Ser@13; Deamidated(R)@14	missed K-R@13	0.04	1571.86	524.96	1571.83	524.95	3	636.2
8	74.2	A0QVB9	MSMEG_2520	99.0	NALVEADGDFDKAVELLR	iTRAQ4plex@N-term; User modH on Lys(K)@12	missed K-A@12	-0.06	2361.16	788.06	2361.22	788.08	3	133.1
	74.2	A0QVB9	MSMEG_2520	99.0	AADLPPAVGVLVEYQAGDADK	iTRAQ4plex@N-term; Val->Leu@12; Deamidated(Q)@15; Lys->Gln@21		0.03	2257.16	753.39	2257.12	753.38	3	17.4
	74.2	A0QVB9	MSMEG_2520	99.0	AAYFDGTVEAYLHK	iTRAQ4plex@N-term; iTRAQ4plex(H)@13; Lys->Gln@14		0.02	1871.95	624.99	1871.93	624.98	3	618.4
	74.2	A0QVB9	MSMEG_2520	99.0	ALLDEAGVTVTR	iTRAQ4plex@N-term		-0.01	1387.77	694.89	1387.78	694.90	2	2.959.4
	74.2	A0QVB9	MSMEG_2520	99.0	ANYTAADVK	iTRAQ4plex@N-term; Lys->Gln@9	cleaved M-A@N-term	0.02	1095.56	548.79	1095.53	548.77	2	121.6
	74.2	A0QVB9	MSMEG_2520	99.0	DEAGVTVTR	iTRAQ4plex@N-term	cleaved L-D@N-term	0.02	1090.60	546.30	1090.57	546.29	2	593.7
	74.2	A0QVB9	MSMEG_2520	99.0	DGALIELNSETDFVAK	iTRAQ4plex@N-term; Lys->Gln@16		0.05	1864.97	622.66	1864.92	622.65	3	
	74.2	A0QVB9	MSMEG_2520	99.0	EAAHAVALQIAALK	iTRAQ4plex@N-term; Lys->Gln@14		0.00	1548.88	517.30	1548.87	517.30	3	149.3
	74.2	A0QVB9	MSMEG_2520	99.0	EDVPEDIVANER	iTRAQ4plex@N-term		0.01	1528.76	765.39	1528.75	765.38	2	4.928.2
	74.2	A0QVB9	MSMEG_2520	99.0	ELTGAGMLDSK	iTRAQ4plex@N-term; Lys->Arg@11		0.04	1292.69	647.35	1292.65	647.33	2	488.5
	74.2	A0QVB9	MSMEG_2520	99.0	NAEFQALADQIVAAAVAAK	iTRAQ4plex@N-term; Lys->Gln@19		0.06	2044.13	682.38	2044.07	682.36	3	41.3
	74.2	A0QVB9	MSMEG_2520	99.0	NAEFQALADQIVAAAVAAKAN	iTRAQ4plex@N-term; Lys->Ser@19	cleaved N-D@C-term; missed K-A@19	0.06	2188.18	730.40	2188.12	730.38	3	295.9
	74.2	A0QVB9	MSMEG_2520	99.0	NALVEADGDFDKAVELLR	iTRAQ4plex@N-term; Lys->Gln@12	missed K-A@12	-0.02	2118.06	707.03	2118.07	707.03	3	188.7
	74.2	A0QVB9	MSMEG_2520	99.0	TGDTTVEQAIADLSAK	iTRAQ4plex@N-term; iTRAQ4plex(S)@14; Lys->Gln@16		-0.01	1906.97	636.66	1906.97	636.66	3	115.0
	74.2	A0QVB9	MSMEG_2520	99.0	AADLPPAVGVLVEYQAGDADK	iTRAQ4plex@N-term; Lys->Gln@21		0.03	2242.15	748.39	2242.12	748.38	3	27.2
	74.2	A0QVB9	MSMEG_2520	99.0	ALLDEAGVTVTR	iTRAQ4plex@N-term; Thr->Glu@11		0.05	1415.82	708.92	1415.77	708.89	2	776.7
	74.2	A0QVB9	MSMEG_2520	99.0	DGALIELNSETDFVAK	iTRAQ4plex@N-term; Lys->Gln@16		0.06	1864.98	622.67	1864.92	622.65	3	10.9
	74.2	A0QVB9	MSMEG_2520	99.0	EAAHAVALQIAALK	iTRAQ4plex@N-term; Lys->Gln@14		0.00	1548.88	517.30	1548.87	517.30	3	584.1
	74.2	A0QVB9	MSMEG_2520	99.0	ELTGAGMLDSK	iTRAQ4plex@N-term; Lys->Gln@11		0.04	1264.65	633.33	1264.61	633.31	2	1.301.2
	74.2	A0QVB9	MSMEG_2520	98.0	ANYTAADVK	iTRAQ4plex@N-term; Lys->Gln@9	cleaved M-A@N-term	0.04	1095.57	548.79	1095.53	548.77	2	501.2
	74.2	A0QVB9	MSMEG_2520	98.0	DGALIELNSETDFVAK	iTRAQ4plex@N-term; Lys->Gln@16		0.05	1864.96	622.66	1864.92	622.65	3	6.5
	74.2	A0QVB9	MSMEG_2520	98.0	EDVPEDIVANER	iTRAQ4plex@N-term		-0.02	1528.73	765.37	1528.75	765.38	2	259.5
	74.2	A0QVB9	MSMEG_2520	97.0	AADLPPAVGVLVEYQAGDADK	iTRAQ4plex@N-term; iTRAQ4plex(Y)@14; Lys->Gln@21		-0.04	2386.19	796.40	2386.23	796.42	3	101.5
	74.2	A0QVB9	MSMEG_2520	95.0	NALVEADGDFDKAVELLRI	iTRAQ4plex@N-term; User modH on Lys(K)@12; Glu->Gln@15; Dioxidation(R)@18	cleaved I-K@C-term; missed K-A@12; mi	-0.02	2505.28	627.33	2505.31	627.33	4	101.9
	74.2	A0QVB9	MSMEG_2520	95.0	NALVEADGDFDKAVELLRI	iTRAQ4plex@N-term; Oxidation(D)@11; User modH on Lys(K)@12; Carbamyl(R)@18	cleaved I-K@C-term; missed K-A@12; mi	0.04	2533.34	845.45	2533.30	845.44	3	1.315.0
	74.2	A0QVB9	MSMEG_2520	87	IGEKLELR	iTRAQ4plex@N-term; User modH on Lys(K)@4	missed K-L@4	-0.03	1343.74	448.92	1343.77	448.93	3	453.5
	74.2	A0QVB9	MSMEG_2520	81.0	NAEFQALADQIVAAAVAAK	iTRAQ4plex@N-term; Asp->Asn@9; Lys->Gln@19		0.07	2043.15	682.06	2043.09	682.04	3	82.9
	74.2	A0QVB9	MSMEG_2520	78.0	ATAEGLVAAK	iTRAQ4plex@N-term; Lys->Arg@10		0.02	1101.64	551.83	1101.63	551.82	2	1.667.6
9	71.0	A0QS98	MSMEG_1401	99.0	AFDQIDNAPEER	iTRAQ4plex@N-term		0.01	1547.75	774.88	1547.73	774.87	2	2.318.4
	71.0	A0QS98	MSMEG_1401	99.0	DQIDNAPEER	iTRAQ4plex@N-term	cleaved F-D@N-term	0.03	1329.66	665.84	1329.63	665.82	2	347.7
	71.0	A0QS98	MSMEG_1401	99.0	ELLAAQDFDEEAPVVR	iTRAQ4plex@N-term; Dimethyl(R)@16		0.02	1973.05	658.69	1973.02	658.68	3	206.8
	71.0	A0QS98	MSMEG_1401	99.0	ETDKPFLMPVEDVFTITGR	iTRAQ4plex@N-term; Lys->Gln@4		0.04	2338.20	780.41	2338.16	780.40	3	60.8
	71.0	A0QS98	MSMEG_1401	99.0	FDQIDNAPEER	iTRAQ4plex@N-term	cleaved A-F@N-term	0.03	1476.73	739.37	1476.70	739.36	2	1.485.0
	71.0	A0QS98	MSMEG_1401	99.0	GITINISHVEYQTDKR	iTRAQ4plex@N-term; Lys->Gln@15	missed K-R@15	0.05	2017.08	505.28	2017.04	505.27	4	220.4
	71.0	A0QS98	MSMEG_1401	99.0	GVINVNEEVEIVGIRPETTK	iTRAQ4plex@N-term; iTRAQ4plex(T)@19; Lys->Gln@20		0.00	2483.34	828.79	2483.35	828.79	3	266.3

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	71.0	A0QS98	MSMEG_1401	99.0	LIQPVAMDEGLR	iTRAQ4plex@N-term; Oxidation(M)@7		0.00	1500.81	751.41	1500.81	751.41	2	1.415.1
	71.0	A0QS98	MSMEG_1401	99.0	LLDQGQAGDNVGLLLR	iTRAQ4plex@N-term; Dimethyl(R)@16		-0.03	1853.02	618.68	1853.05	618.69	3	77.1
	71.0	A0QS98	MSMEG_1401	99.0	LMPVEDVFTITGR	iTRAQ4plex@N-term	cleaved F-L@N-term	0.00	1620.86	811.44	1620.87	811.44	2	2.017.7
	71.0	A0QS98	MSMEG_1401	99.0	NMITGAAQMDGAILVVAATDGPMPQTR	iTRAQ4plex@N-term		0.00	2872.44	958.49	2872.44	958.49	3	19.4
	71.0	A0QS98	MSMEG_1401	99.0	SVEELMEAVDASIPDPVR	iTRAQ4plex@N-term		0.03	2100.08	701.04	2100.05	701.02	3	190.5
	71.0	A0QS98	MSMEG_1401	99.0	TTLTAAITK	iTRAQ4plex@N-term; Lys->Gln@9		0.04	1062.64	532.33	1062.60	532.31	2	1.014.0
	71.0	A0QS98	MSMEG_1401	99.0	TTVTGVEMFR	iTRAQ4plex@N-term		0.01	1283.68	642.85	1283.67	642.84	2	5.025.9
	71.0	A0QS98	MSMEG_1401	99.0	VLHDKFPDLNESR	No iTRAQ4plex@N-term; Lys->Gln@5	missed K-F@5	0.05	1568.80	523.94	1568.76	523.93	3	194.5
	71.0	A0QS98	MSMEG_1401	99.0	AFDQIDNAPEER	iTRAQ4plex@N-term		0.03	1547.76	774.89	1547.73	774.87	2	4.866.2
	71.0	A0QS98	MSMEG_1401	99.0	AFDQIDNAPEER	iTRAQ4plex@N-term; Dimethyl(R)@12		0.02	1575.78	788.90	1575.77	788.89	2	1.307.7
	71.0	A0QS98	MSMEG_1401	99.0	AFDQIDNAPEER	iTRAQ4plex@N-term; Dimethyl(R)@12		0.02	1575.78	788.90	1575.77	788.89	2	4.295.8
	71.0	A0QS98	MSMEG_1401	99.0	ETDKPFLMPVEDVFTITGR	iTRAQ4plex@N-term; iTRAQ4plex(T)@2; Lys->Gln@4; Oxidation(M)@8		0.08	2498.34	833.79	2498.26	833.76	3	239.3
	71.0	A0QS98	MSMEG_1401	99.0	ETDKPFLMPVEDVFTITGR	iTRAQ4plex@N-term; iTRAQ4plex(T)@2; Lys->Gln@4		0.06	2482.32	828.45	2482.27	828.43	3	806.3
	71.0	A0QS98	MSMEG_1401	99.0	ETDKPFLMPVEDVFTITGR	iTRAQ4plex@N-term; Lys->Gln@4		0.00	2338.16	780.39	2338.16	780.40	3	147.4
	71.0	A0QS98	MSMEG_1401	99.0	GITINISHVEYQTDKR	iTRAQ4plex@N-term; Lys->Gln@15	missed K-R@15	0.05	2017.08	505.28	2017.04	505.27	4	348.7
	71.0	A0QS98	MSMEG_1401	99.0	GVINVNEEVEIVGIRPETTK	iTRAQ4plex@N-term; Ile->Asn@11; Lys->Gln@20		0.08	2340.29	781.10	2340.20	781.08	3	426.6
	71.0	A0QS98	MSMEG_1401	99.0	LIQPVAMDEGLR	iTRAQ4plex@N-term		0.00	1484.82	743.42	1484.81	743.41	2	1.437.2
	71.0	A0QS98	MSMEG_1401	99.0	LIQPVAMDEGLR	iTRAQ4plex@N-term; Dimethyl(R)@12		-0.03	1512.82	757.42	1512.85	757.43	2	1.853.1
	71.0	A0QS98	MSMEG_1401	99.0	LLDQGQAGDNVGLLLR	iTRAQ4plex@N-term		0.01	1825.03	913.52	1825.02	913.52	2	4.105.4
	71.0	A0QS98	MSMEG_1401	99.0	LLDQGQAGDNVGLLLR	iTRAQ4plex@N-term; Deamidated(Q)@4; Leu->Asn@13		0.12	1827.08	610.03	1826.96	609.99	3	1.231.6
	71.0	A0QS98	MSMEG_1401	99.0	LLDQGQAGDNVGLLLR	iTRAQ4plex@N-term; Dimethyl(R)@16		-0.01	1853.04	618.69	1853.05	618.69	3	87.7
	71.0	A0QS98	MSMEG_1401	99.0	LLDQGQAGDNVGLLLR	iTRAQ4plex@N-term		-0.01	1825.01	609.34	1825.02	609.35	3	52.9
	71.0	A0QS98	MSMEG_1401	99.0	NMITGAAQMDGAILVVAATDGPMPQTR	iTRAQ4plex@N-term		-0.05	2872.38	958.47	2872.44	958.49	3	32.1
	71.0	A0QS98	MSMEG_1401	99.0	SVEELMEAVDASIPDPVR	iTRAQ4plex@N-term		0.04	2100.09	701.04	2100.05	701.02	3	18.5
	71.0	A0QS98	MSMEG_1401	99.0	TTVTGVEMFR	iTRAQ4plex@N-term; Dimethyl(R)@10		0.00	1311.70	656.86	1311.70	656.86	2	4.030.4
	71.0	A0QS98	MSMEG_1401	99.0	TTVTGVEMFR	iTRAQ4plex@N-term; Dimethyl(R)@10		-0.01	1311.69	656.85	1311.70	656.86	2	575.6
	71.0	A0QS98	MSMEG_1401	97.0	ELLAAQDFDEEAPVVR	iTRAQ4plex@N-term; Asp->Gln@7		-0.07	1957.95	653.66	1958.02	653.68	3	15.2
	71.0	A0QS98	MSMEG_1401	97.0	ELLAAQDFDEEAPVVR	iTRAQ4plex@N-term; Dimethyl(R)@16		0.01	1973.04	658.69	1973.02	658.68	3	14.1
	71.0	A0QS98	MSMEG_1401	95.0	TTLTAAITK	iTRAQ4plex@N-term; iTRAQ4plex(T)@8; Lys->Gln@9		0.03	1206.74	604.38	1206.71	604.36	2	9.540.5
	71.0	A0QS98	MSMEG_1401	94.0	WVKSVEELMEAVDASIPDPVR	iTRAQ4plex@N-term; User modH on Lys(K)@3; iTRAQ4plex(S)@4; Asp->Asn@18	missed K-S@3	-0.07	2899.45	725.87	2899.52	725.89	4	5.4
	71.0	A0QS98	MSMEG_1401	93.0	LIQPVAMDEGLR	iTRAQ4plex@N-term; Dimethyl(R)@12		0.00	1512.85	757.43	1512.85	757.43	2	2.680.5
	71.0	A0QS98	MSMEG_1401	92.0	TTDVTGVVTLPEGTEMVMPGDNTDISV	iTRAQ4plex@N-term; iTRAQ4plex(S)@26; Lys->Gln@28		-0.06	3193.50	1065.51	3193.56	1065.53	3	164.0
	71.0	A0QS98	MSMEG_1401	91.0	TTLTAAITK	iTRAQ4plex@N-term; Lys->Arg@9		0.01	1090.66	546.34	1090.65	546.33	2	391.9
	71.0	A0QS98	MSMEG_1401	89.0	FPDLNESR	iTRAQ4plex@N-term		0.02	1120.58	561.30	1120.56	561.29	2	7.407.6
10	68.7	A0R0B3	MSMEG_4326	99.0	YGVKIPDEDLAGLR	iTRAQ4plex@N-term; iTRAQ4plex(Y)@1; User modH on Lys(K)@4	missed K-I@4	0.01	2076.15	693.06	2076.13	693.05	3	789.5
	68.7	A0R0B3	MSMEG_4326	99.0	TVGDVVAYIQKLEEENPEAAAALR	No iTRAQ4plex@N-term; iTRAQ4plex(Y)@8; User modH on Lys(K)@11	missed K-L@11	-0.02	2972.53	744.14	2972.55	744.14	4	89.6
	68.7	A0R0B3	MSMEG_4326	99.0	TVGDVVAYIQKLEEENPEAAAALR	iTRAQ4plex@N-term; iTRAQ4plex(Y)@8; Deamidated(Q)@10; User modH on Lys(K)@11; Dehydr	missed K-L@11	0.02	3099.64	775.92	3099.62	775.91	4	75.9
	68.7	A0R0B3	MSMEG_4326	99.0	IPDEDLAGLR	iTRAQ4plex@N-term		0.01	1241.68	621.85	1241.67	621.84	2	7.244.4
	68.7	A0R0B3	MSMEG_4326	99.0	LEEENPEAAAALR	iTRAQ4plex@N-term		0.00	1555.79	778.90	1555.80	778.91	2	3.995.2
	68.7	A0R0B3	MSMEG_4326	99.0	IPDEDLAGLR	iTRAQ4plex@N-term		0.00	1241.68	621.85	1241.67	621.84	2	1.246.9
	68.7	A0R0B3	MSMEG_4326	99.0	IPDEDLAGLR	iTRAQ4plex@N-term		0.00	1241.67	621.84	1241.67	621.84	2	2.217.8
	68.7	A0R0B3	MSMEG_4326	99.0	LEEENPEAAAALR	iTRAQ4plex@N-term; Ala->Val@10		0.00	1583.82	792.92	1583.83	792.92	2	1.494.1
	68.7	A0R0B3	MSMEG_4326	84.0	IPDEDLAGLR	iTRAQ4plex@N-term; Dimethyl(R)@10		-0.02	1269.69	635.85	1269.71	635.86	2	1.462.4
11	66.4	A0QYD4	MSMEG_3619	99.0	AALSDWTAGQADFFGTR	iTRAQ4plex@N-term		-0.01	1956.93	653.32	1956.95	653.32	3	131.9
	66.4	A0QYD4	MSMEG_3619	99.0	DAGHNVVIAGAR	iTRAQ4plex@N-term		0.02	1322.74	441.92	1322.72	441.91	3	427.3
	66.4	A0QYD4	MSMEG_3619	99.0	GITINAVAAGR	iTRAQ4plex@N-term		0.00	1185.69	593.85	1185.70	593.85	2	7.916.8
	66.4	A0QYD4	MSMEG_3619	99.0	LALFLSTPAAR	iTRAQ4plex@N-term		-0.03	1302.75	652.38	1302.78	652.40	2	725.9
	66.4	A0QYD4	MSMEG_3619	99.0	SAEQAYDGLTR	iTRAQ4plex@N-term		0.01	1353.67	677.84	1353.66	677.84	2	424.1
	66.4	A0QYD4	MSMEG_3619	99.0	SGGSIVNVLPESAK	iTRAQ4plex@N-term; Lys->Gln@14		0.03	1500.82	751.42	1500.79	751.40	2	1.560.8
	66.4	A0QYD4	MSMEG_3619	99.0	TPPSVADEFTR	iTRAQ4plex@N-term		-0.01	1362.68	682.35	1362.69	682.35	2	1.678.5
	66.4	A0QYD4	MSMEG_3619	99.0	TYTLADLASAWR	iTRAQ4plex@N-term		0.00	1510.79	756.40	1510.79	756.40	2	2.561.5
	66.4	A0QYD4	MSMEG_3619	99.0	TPPSVADEFTR	iTRAQ4plex@N-term		0.00	1362.69	682.35	1362.69	682.35	2	4.094.3
	66.4	A0QYD4	MSMEG_3619	94.0	AIAQGFR	iTRAQ4plex@N-term		0.01	905.53	453.77	905.52	453.77	2	3.651.2
	66.4	A0QYD4	MSMEG_3619	91.0	SGGSIVNVLPESAK	iTRAQ4plex@N-term; iTRAQ4plex(S)@12; Lys->Gln@14		0.03	1644.92	549.32	1644.89	549.30	3	418.9
	66.4	A0QYD4	MSMEG_3619	87.0	RDDLEVAAK	iTRAQ4plex@N-term; Lys->Gln@9	missed R-D@1	0.04	1159.64	387.55	1159.60	387.54	3	18.3
	66.4	A0QYD4	MSMEG_3619	79.0	TPPSVADEFTR	iTRAQ4plex@N-term; Thr->Glu@10		0.05	1390.73	696.37	1390.69	696.35	2	1.329.4
12	65.0	A0QSS4	MSMEG_1583	99.0	AADAVSEALLASATPVDDKK	iTRAQ4plex@N-term; Lys->Gln@19; Lys->Arg@20	missed K-K@19	0.05	2143.14	715.39	2143.09	715.37	3	270.5
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	247.0

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	65.0	A0QSS4	MSMEG_1583	99.0	AFLDDLAIVTGGQVVNPDVGLLLR	iTRAQ4plex@N-term		0.00	2638.48	880.50	2638.48	880.50	3	102.5
	65.0	A0QSS4	MSMEG_1583	99.0	AIAQVATVSSR	iTRAQ4plex@N-term		0.02	1245.74	623.88	1245.72	623.87	2	11.103.3
	65.0	A0QSS4	MSMEG_1583	99.0	AMEAGVDK	iTRAQ4plex@N-term; Lys->Gln@8		0.05	963.50	482.76	963.45	482.73	2	85.7
	65.0	A0QSS4	MSMEG_1583	99.0	DEQVGELVGEAMTK	iTRAQ4plex@N-term; Lys->Gln@14		0.06	1648.83	825.42	1648.77	825.39	2	1.278.8
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		-0.02	1889.92	630.98	1889.95	630.99	3	90.1
	65.0	A0QSS4	MSMEG_1583	99.0	EAVEDAVAAAK	iTRAQ4plex@N-term; Lys->Gln@11		0.04	1216.65	609.33	1216.61	609.31	2	1.145.9
	65.0	A0QSS4	MSMEG_1583	99.0	EVGLEVLGSAR	iTRAQ4plex@N-term		0.01	1272.73	637.37	1272.72	637.37	2	2.282.2
	65.0	A0QSS4	MSMEG_1583	99.0	FVTDFDSQEAVLEDALVLLHR	iTRAQ4plex@N-term	cleaved Y-F@N-term	0.01	2560.34	854.45	2560.33	854.45	3	20.7
	65.0	A0QSS4	MSMEG_1583	99.0	GGGAALVQAR	iTRAQ4plex@N-term	cleaved T-G@N-term	0.03	1042.63	522.32	1042.60	522.31	2	172.1
	65.0	A0QSS4	MSMEG_1583	99.0	GQGFNAATLEFGDLVSAGVVDPAK	iTRAQ4plex@N-term; Oxidation(D)@13; Lys->Arg@24		0.03	2550.31	851.11	2550.28	851.10	3	8.7
	65.0	A0QSS4	MSMEG_1583	99.0	IAQVATVSSR	iTRAQ4plex@N-term	cleaved A-I@N-term	0.03	1174.71	588.36	1174.68	588.35	2	3.472.8
	65.0	A0QSS4	MSMEG_1583	99.0	ISSLPDLLPLLEK	iTRAQ4plex@N-term; Lys->Arg@13		0.03	1608.99	805.50	1608.96	805.49	2	1.498.6
	65.0	A0QSS4	MSMEG_1583	99.0	NVAAGANPIALGSGISK	iTRAQ4plex@N-term; iTRAQ4plex(S)@16; Lys->Gln@17		0.03	1827.04	610.02	1827.01	610.01	3	1.396.4
	65.0	A0QSS4	MSMEG_1583	99.0	QIEFNETAR	iTRAQ4plex@N-term; Deamidated(N)@5		-0.01	1251.61	626.81	1251.62	626.82	2	1.405.4
	65.0	A0QSS4	MSMEG_1583	99.0	SEIETTDSDWDR	iTRAQ4plex@N-term		0.00	1596.70	799.36	1596.70	799.36	2	7.847.1
	65.0	A0QSS4	MSMEG_1583	99.0	SEIETTDSDWDREK	iTRAQ4plex@N-term; Lys->Arg@14	missed R-E@12	0.07	1881.91	628.31	1881.85	628.29	3	532.4
	65.0	A0QSS4	MSMEG_1583	99.0	SFGGPQVTNDGVTIAR	iTRAQ4plex@N-term		0.02	1761.93	881.97	1761.91	881.96	2	606.5
	65.0	A0QSS4	MSMEG_1583	99.0	VGAATETDLK	iTRAQ4plex@N-term; Lys->Arg@10		0.04	1175.66	588.84	1175.63	588.82	2	2.050.6
	65.0	A0QSS4	MSMEG_1583	99.0	VGLEVLGSAR	iTRAQ4plex@N-term	cleaved E-V@N-term	0.01	1143.68	572.85	1143.67	572.84	2	6.028.6
	65.0	A0QSS4	MSMEG_1583	99.0	AADAVSEALLASATPVDDK	iTRAQ4plex@N-term; Lys->Gln@19		0.03	1987.01	663.34	1986.99	663.34	3	
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.03	1912.02	638.35	1912.05	638.36	3	67.2
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		0.04	1912.09	638.37	1912.05	638.36	3	8.7
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	9.2
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.04	1912.01	638.34	1912.05	638.36	3	6.5
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	16.0
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	9.5
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	7.4
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	7.2
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.03	1912.02	638.35	1912.05	638.36	3	17.2
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	28.3
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	12.0
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	10.9
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.03	1912.02	638.35	1912.05	638.36	3	10.9
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	6.3
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.03	1912.02	638.35	1912.05	638.36	3	13.0
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	5.4
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	4.4
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.03	1912.02	638.35	1912.05	638.36	3	6.5
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		0.04	1912.09	638.37	1912.05	638.36	3	21.2
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		0.03	1912.08	638.37	1912.05	638.36	3	784.0
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.01	1912.04	638.35	1912.05	638.36	3	223.8
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.01	1912.04	638.35	1912.05	638.36	3	95.8
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.04	1912.01	638.34	1912.05	638.36	3	505.8
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.01	1912.04	638.35	1912.05	638.36	3	167.2
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term; Dimethyl(R)@19		-0.01	1940.07	647.70	1940.08	647.70	3	208.9
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.05	1912.00	638.34	1912.05	638.36	3	187.4
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term; Gln->Arg@17		-0.03	1940.06	647.69	1940.09	647.70	3	114.4
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.01	1912.04	638.35	1912.05	638.36	3	120.2
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.01	1912.04	638.35	1912.05	638.36	3	64.2
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.04	1912.01	638.34	1912.05	638.36	3	94.8
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.01	1912.04	638.36	1912.05	638.36	3	166.9
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.03	1912.03	638.35	1912.05	638.36	3	411.8
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	31.0
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	16.3
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	17.4
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	37.5
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		0.02	1912.07	957.04	1912.05	957.03	2	924.5
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term; Ile->Gln@7		0.01	1927.03	643.35	1927.02	643.35	3	33.8
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term; Val->Asn@8		0.03	1927.05	643.36	1927.02	643.35	3	10.5
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term; Gly->Ser@10		-0.05	1942.01	648.35	1942.06	648.36	3	17.4
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		0.03	1912.08	638.37	1912.05	638.36	3	

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.02	1912.03	638.35	1912.05	638.36	3	8.7
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.03	1912.02	638.35	1912.05	638.36	3	19.6
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		-0.04	1912.01	638.35	1912.05	638.36	3	
	65.0	A0QSS4	MSMEG_1583	99.0	AAVEEGIVTGGGAALVQAR	iTRAQ4plex@N-term		0.04	1912.09	638.37	1912.05	638.36	3	1.190.0
	65.0	A0QSS4	MSMEG_1583	99.0	AFLDDLAIVTGGQVVNPDVGLLLR	iTRAQ4plex@N-term		0.00	2638.48	880.50	2638.48	880.50	3	154.4
	65.0	A0QSS4	MSMEG_1583	99.0	AFLDDLAIVTGGQVVNPDVGLLLR	iTRAQ4plex@N-term; Deamidated(Q)@13; Dimethyl(R)@24		0.03	2667.53	890.18	2667.50	890.17	3	300.7
	65.0	A0QSS4	MSMEG_1583	99.0	AFLDDLAIVTGGQVVNPDVGLLLR	iTRAQ4plex@N-term; Deamidated(Q)@13; Dimethyl(R)@24		0.00	2667.49	890.17	2667.50	890.17	3	506.5
	65.0	A0QSS4	MSMEG_1583	99.0	AFLDDLAIVTGGQVVNPDVGLLLR	iTRAQ4plex@N-term; Dimethyl(R)@24		-0.01	2666.50	889.84	2666.51	889.84	3	14.1
	65.0	A0QSS4	MSMEG_1583	99.0	AFLDDLAIVTGGQVVNPDVGLLLR	iTRAQ4plex@N-term; Dimethyl(R)@24		0.01	2666.53	889.85	2666.51	889.84	3	15.8
	65.0	A0QSS4	MSMEG_1583	99.0	AFLDDLAIVTGGQVVNPDVGLLLR	iTRAQ4plex@N-term; Methyl(L)@21; Methyl(L)@23		0.00	2666.51	889.84	2666.51	889.84	3	15.8
	65.0	A0QSS4	MSMEG_1583	99.0	AFLDDLAIVTGGQVVNPDVGLLLR	iTRAQ4plex@N-term; Dimethyl(R)@24		0.06	2666.57	889.87	2666.51	889.84	3	68.7
	65.0	A0QSS4	MSMEG_1583	99.0	AFLDDLAIVTGGQVVNPDVGLLLR	iTRAQ4plex@N-term		0.07	2638.55	660.65	2638.48	660.63	4	105.1
	65.0	A0QSS4	MSMEG_1583	99.0	AIAQVATVSSR	iTRAQ4plex@N-term		0.01	1245.73	623.87	1245.72	623.87	2	9.905.4
	65.0	A0QSS4	MSMEG_1583	99.0	AIAQVATVSSR	iTRAQ4plex@N-term; Ser->Asp@10		0.07	1273.78	637.90	1273.71	637.86	2	3.696.1
	65.0	A0QSS4	MSMEG_1583	99.0	DEQVGELVGEAMTK	iTRAQ4plex@N-term; Oxidation(M)@12; iTRAQ4plex(T)@13; Lys->Gln@14		0.05	1808.92	603.98	1808.87	603.96	3	201.9
	65.0	A0QSS4	MSMEG_1583	99.0	DEQVGELVGEAMTK	iTRAQ4plex@N-term; iTRAQ4plex(T)@13; Lys->Gln@14		-0.01	1792.86	598.63	1792.88	598.63	3	491.9
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		0.06	1890.01	631.01	1889.95	630.99	3	5.4
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		-0.02	1889.92	630.98	1889.95	630.99	3	5.2
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		-0.02	1889.93	630.98	1889.95	630.99	3	4.4
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		0.03	1889.98	946.00	1889.95	945.98	2	330.8
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term; Dimethyl(R)@18		-0.01	1917.97	959.99	1917.98	960.00	2	176.3
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		0.02	1889.97	631.00	1889.95	630.99	3	9.6
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		0.01	1889.96	630.99	1889.95	630.99	3	
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		0.01	1889.95	630.99	1889.95	630.99	3	
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		-0.03	1889.91	630.98	1889.95	630.99	3	
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term; Dimethyl(R)@18		-0.02	1917.96	640.33	1917.98	640.33	3	15.9
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		-0.02	1889.92	630.98	1889.95	630.99	3	13.0
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		-0.02	1889.92	630.98	1889.95	630.99	3	
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		0.01	1889.96	630.99	1889.95	630.99	3	24.6
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		0.01	1889.96	630.99	1889.95	630.99	3	7.6
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		0.01	1889.96	630.99	1889.95	630.99	3	
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		-0.02	1889.93	630.98	1889.95	630.99	3	
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		-0.04	1889.91	630.98	1889.95	630.99	3	
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		0.05	1889.99	631.00	1889.95	630.99	3	10.9
	65.0	A0QSS4	MSMEG_1583	99.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		-0.03	1889.92	630.98	1889.95	630.99	3	9.6
	65.0	A0QSS4	MSMEG_1583	99.0	EAVEDAVAAAK	iTRAQ4plex@N-term; Lys->Gln@11		0.05	1216.66	609.34	1216.61	609.31	2	1.646.5
	65.0	A0QSS4	MSMEG_1583	99.0	EAVEDAVAAAK	iTRAQ4plex@N-term; Lys->Arg@11		0.05	1244.69	623.35	1244.65	623.33	2	378.9
	65.0	A0QSS4	MSMEG_1583	99.0	EVGLEVLGSAR	iTRAQ4plex@N-term		0.00	1272.71	637.36	1272.72	637.37	2	2.433.9
	65.0	A0QSS4	MSMEG_1583	99.0	EVGLEVLGSAR	iTRAQ4plex@N-term		0.02	1272.73	637.37	1272.72	637.37	2	628.5
	65.0	A0QSS4	MSMEG_1583	99.0	EVGLEVLGSAR	iTRAQ4plex@N-term; Ser->Asp@9		0.03	1300.74	651.38	1300.71	651.36	2	453.2
	65.0	A0QSS4	MSMEG_1583	99.0	GQGFNAATLEFGDLVSAGVVDPAK	iTRAQ4plex@N-term; Lys->Gln@24		0.01	2506.25	836.42	2506.25	836.42	3	27.1
	65.0	A0QSS4	MSMEG_1583	99.0	GQGFNAATLEFGDLVSAGVVDPAK	iTRAQ4plex@N-term; Methyl(D)@13; Lys->Gln@24		0.01	2520.27	841.10	2520.26	841.09	3	18.5
	65.0	A0QSS4	MSMEG_1583	99.0	GQGFNAATLEFGDLVSAGVVDPAK	iTRAQ4plex@N-term; Lys->Gln@24		0.03	2506.28	836.43	2506.25	836.42	3	20.7
	65.0	A0QSS4	MSMEG_1583	99.0	GQGFNAATLEFGDLVSAGVVDPAK	iTRAQ4plex@N-term; Lys->Arg@24		-0.01	2534.28	845.77	2534.29	845.77	3	
	65.0	A0QSS4	MSMEG_1583	99.0	GQGFNAATLEFGDLVSAGVVDPAK	iTRAQ4plex@N-term; Lys->Gln@24		0.01	2506.25	836.43	2506.25	836.42	3	
	65.0	A0QSS4	MSMEG_1583	99.0	GQGFNAATLEFGDLVSAGVVDPAK	iTRAQ4plex@N-term; Asp->Asn@13; Lys->Gln@24		-0.01	2505.25	836.09	2505.26	836.09	3	8.7
	65.0	A0QSS4	MSMEG_1583	99.0	ISSLPDLLPLLEK	iTRAQ4plex@N-term; Lys->Gln@13		0.02	1580.94	791.48	1580.91	791.46	2	415.3
	65.0	A0QSS4	MSMEG_1583	99.0	NVAAGANPIALGSGISK	iTRAQ4plex@N-term; Lys->Gln@17		0.04	1682.95	842.48	1682.91	842.46	2	1.157.9
	65.0	A0QSS4	MSMEG_1583	99.0	NVAAGANPIALGSGISK	iTRAQ4plex@N-term; Lys->Arg@17		0.05	1711.00	856.51	1710.95	856.48	2	302.4
	65.0	A0QSS4	MSMEG_1583	99.0	NVAAGANPIALGSGISK	iTRAQ4plex@N-term; iTRAQ4plex(S)@16; Lys->Gln@17		0.03	1827.04	610.02	1827.01	610.01	3	645.7
	65.0	A0QSS4	MSMEG_1583	99.0	NVAAGANPIALGSGISK	iTRAQ4plex@N-term; iTRAQ4plex(S)@16; Lys->Gln@17		0.04	1827.05	610.02	1827.01	610.01	3	395.6
	65.0	A0QSS4	MSMEG_1583	99.0	NVAAGANPIALGSGISK	iTRAQ4plex@N-term; Dehydrated(S)@13; iTRAQ4plex(S)@16; Lys->Gln@17		0.05	1809.05	604.02	1809.00	604.01	3	131.0
	65.0	A0QSS4	MSMEG_1583	99.0	NVAAGANPIALGSGISK	iTRAQ4plex@N-term; iTRAQ4plex(S)@16; Lys->Arg@17		0.01	1855.06	619.36	1855.05	619.36	3	462.6
	65.0	A0QSS4	MSMEG_1583	99.0	QIEFNETAR	iTRAQ4plex@N-term		-0.01	1250.62	626.32	1250.64	626.33	2	16.221.1
	65.0	A0QSS4	MSMEG_1583	99.0	QIEFNETAR	iTRAQ4plex@N-term		0.02	1250.66	626.34	1250.64	626.33	2	6.002.4
	65.0	A0QSS4	MSMEG_1583	99.0	QIEFNETAR	iTRAQ4plex@N-term; Deamidated(Q)@1; Deamidated(N)@5		0.05	1252.66	627.34	1252.61	627.31	2	4.913.0
	65.0	A0QSS4	MSMEG_1583	99.0	SAVLNAASVAR	iTRAQ4plex@N-term		0.01	1201.70	601.86	1201.69	601.85	2	6.348.8
	65.0	A0QSS4	MSMEG_1583	99.0	SAVLNAASVAR	iTRAQ4plex@N-term		0.01	1201.70	601.86	1201.69	601.85	2	1.114.9
	65.0	A0QSS4	MSMEG_1583	99.0	SAVLNAASVAR	iTRAQ4plex@N-term		0.01	1201.70	601.86	1201.69	601.85	2	5.564.1
	65.0	A0QSS4	MSMEG_1583	99.0	SAVLNAASVAR	iTRAQ4plex@N-term; Ala->Val@10		0.02	1229.74	615.88	1229.72	615.87	2	4.829.5
	65.0	A0QSS4	MSMEG_1583	99.0	SEIETTDSDWDR	iTRAQ4plex@N-term		0.01	1596.71	799.36	1596.70	799.36	2	1.991.8

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	65.0	A0QSS4	MSMEG_1583	99.0	SEIETTDSDWDR	iTRAQ4plex@N-term; Dioxidation(W)@10		0.02	1628.71	815.36	1628.69	815.35	2	752.7
	65.0	A0QSS4	MSMEG_1583	99.0	SEIETTDSDWDR	iTRAQ4plex@N-term; Dimethyl(R)@12		0.01	1624.75	813.38	1624.73	813.37	2	643.1
	65.0	A0QSS4	MSMEG_1583	99.0	SEIETTDSDWDREK	iTRAQ4plex@N-term; Lys->Gln@14	missed R-E@12	0.10	1853.90	618.98	1853.80	618.94	3	758.2
	65.0	A0QSS4	MSMEG_1583	99.0	SFGGPQVTNDGVTIAR	iTRAQ4plex@N-term; Deamidated(N)@9		0.01	1762.91	882.46	1762.90	882.46	2	1.136.3
	65.0	A0QSS4	MSMEG_1583	99.0	SFGGPQVTNDGVTIAR	iTRAQ4plex@N-term; Ala->Val@15		-0.04	1789.90	597.64	1789.94	597.66	3	178.1
	65.0	A0QSS4	MSMEG_1583	99.0	SFGGPQVTNDGVTIAR	iTRAQ4plex@N-term		0.01	1761.92	588.31	1761.91	588.31	3	654.0
	65.0	A0QSS4	MSMEG_1583	99.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term		-0.01	2217.16	740.06	2217.17	740.06	3	69.6
	65.0	A0QSS4	MSMEG_1583	99.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Dimethyl(R)@21		0.01	2245.21	749.41	2245.20	749.41	3	25.4
	65.0	A0QSS4	MSMEG_1583	99.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Thr->Asn@11		-0.02	2230.15	744.39	2230.17	744.40	3	14.7
	65.0	A0QSS4	MSMEG_1583	99.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Dehydrated(T)@11		-0.06	2199.11	734.04	2199.16	734.06	3	17.2
	65.0	A0QSS4	MSMEG_1583	99.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term		-0.03	2217.14	740.05	2217.17	740.06	3	15.2
	65.0	A0QSS4	MSMEG_1583	99.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term		-0.01	2217.16	740.06	2217.17	740.06	3	20.7
	65.0	A0QSS4	MSMEG_1583	99.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Dimethyl(R)@21		-0.04	2245.16	749.39	2245.20	749.41	3	11.3
	65.0	A0QSS4	MSMEG_1583	99.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term		-0.02	2217.15	740.06	2217.17	740.06	3	
	65.0	A0QSS4	MSMEG_1583	99.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term		-0.01	2217.16	740.06	2217.17	740.06	3	15.2
	65.0	A0QSS4	MSMEG_1583	99.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term		0.00	2217.17	740.06	2217.17	740.06	3	8.7
	65.0	A0QSS4	MSMEG_1583	99.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term		0.00	2217.17	740.06	2217.17	740.06	3	13.0
	65.0	A0QSS4	MSMEG_1583	99.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term		-0.01	2217.16	740.06	2217.17	740.06	3	8.7
	65.0	A0QSS4	MSMEG_1583	99.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Dimethyl(R)@21		-0.02	2245.18	749.40	2245.20	749.41	3	137.0
	65.0	A0QSS4	MSMEG_1583	99.0	VGAATETDLK	iTRAQ4plex@N-term; Lys->Arg@10		0.04	1175.67	588.84	1175.63	588.82	2	1.925.6
	65.0	A0QSS4	MSMEG_1583	98.0	IEFNETAR	iTRAQ4plex@N-term	cleaved Q-I@N-term	0.01	1122.59	562.30	1122.58	562.30	2	6.889.9
	65.0	A0QSS4	MSMEG_1583	98.0	LAGGVAVIK	iTRAQ4plex@N-term; Lys->Gln@9		0.02	970.61	486.31	970.59	486.30	2	6.055.9
	65.0	A0QSS4	MSMEG_1583	98.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term; Ile->Asn@5; Dimethyl(R)@18		0.04	1918.97	640.67	1918.94	640.65	3	74.4
	65.0	A0QSS4	MSMEG_1583	98.0	VGAATETDLK	iTRAQ4plex@N-term; Lys->Gln@10		0.05	1147.64	574.83	1147.58	574.80	2	54.5
	65.0	A0QSS4	MSMEG_1583	97.0	LAGGVAVIK	iTRAQ4plex@N-term; Lys->Gln@9		0.04	970.63	486.32	970.59	486.30	2	1.332.1
	65.0	A0QSS4	MSMEG_1583	97.0	VGAATETDLK	iTRAQ4plex@N-term; Lys->Gln@10		0.04	1147.62	574.82	1147.58	574.80	2	122.7
	65.0	A0QSS4	MSMEG_1583	96.0	AADAVSEALLASATPVDDK	iTRAQ4plex@N-term; iTRAQ4plex(T)@14; Lys->Arg@19		-0.04	2159.09	720.71	2159.13	720.72	3	395.1
	65.0	A0QSS4	MSMEG_1583	96.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term; Dimethyl(R)@18		0.04	1918.02	640.35	1917.98	640.33	3	
	65.0	A0QSS4	MSMEG_1583	96.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		-0.03	1889.91	630.98	1889.95	630.99	3	8.7
	65.0	A0QSS4	MSMEG_1583	96.0	EAVEDAVAAAK	iTRAQ4plex@N-term; Lys->Gln@11		0.05	1216.66	609.34	1216.61	609.31	2	258.5
	65.0	A0QSS4	MSMEG_1583	96.0	NVAAGANPIALGSGISK	iTRAQ4plex@N-term; Deamidated(N)@7; iTRAQ4plex(S)@16; Lys->Glu@17		0.07	1829.05	610.69	1828.98	610.67	3	1.587.7
	65.0	A0QSS4	MSMEG_1583	95.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		0.02	1889.96	630.99	1889.95	630.99	3	45.1
	65.0	A0QSS4	MSMEG_1583	95.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term		-0.04	1889.91	630.98	1889.95	630.99	3	12.8
	65.0	A0QSS4	MSMEG_1583	93.0	APFFGDR	iTRAQ4plex@N-term		0.01	952.49	477.25	952.49	477.25	2	1.416.7
	65.0	A0QSS4	MSMEG_1583	93.0	AIAQVATVSSR	iTRAQ4plex@N-term; Dehydrated(T)@7		0.00	1227.70	410.24	1227.71	410.24	3	16.3
	65.0	A0QSS4	MSMEG_1583	91.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term; Dimethyl(R)@18		0.01	1917.99	640.34	1917.98	640.33	3	
	65.0	A0QSS4	MSMEG_1583	88.0	LAGGVAVIK	iTRAQ4plex@N-term; Lys->Arg@9		0.00	998.63	500.32	998.64	500.33	2	1.471.3
	65.0	A0QSS4	MSMEG_1583	87.0	AMEAGVDK	iTRAQ4plex@N-term; Lys->Arg@8		0.04	991.53	496.77	991.49	496.75	2	233.6
	65.0	A0QSS4	MSMEG_1583	87.0	GQGFNAATLEFGDLVSAGVVDPAK	iTRAQ4plex@N-term; Lys->Arg@24		0.01	2534.30	845.77	2534.29	845.77	3	86.4
	65.0	A0QSS4	MSMEG_1583	85.0	DLLPLLEK	iTRAQ4plex@N-term; Lys->Gln@8	cleaved P-D@N-term	0.03	1083.66	542.84	1083.63	542.82	2	1.273.7
	65.0	A0QSS4	MSMEG_1583	84.0	DEQVGELVGEAMTK	iTRAQ4plex@N-term; Oxidation(M)@12; iTRAQ4plex(T)@13; Lys->Gln@14		-0.01	1808.86	603.96	1808.87	603.96	3	130.8
	65.0	A0QSS4	MSMEG_1583	84.0	DLLPLLEK	iTRAQ4plex@N-term; Lys->Arg@8	cleaved P-D@N-term	0.02	1111.69	556.85	1111.67	556.84	2	502.6
	65.0	A0QSS4	MSMEG_1583	82.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term; Dimethyl(R)@18		-0.01	1917.96	640.33	1917.98	640.33	3	17.4
	65.0	A0QSS4	MSMEG_1583	82.0	VGAATETDLK	No iTRAQ4plex@N-term; iTRAQ4plex(T)@7; Lys->Gln@10		0.05	1147.63	574.82	1147.58	574.80	2	909.9
	65.0	A0QSS4	MSMEG_1583	80.0	AMEAGVDK	iTRAQ4plex@N-term; Lys->Arg@8		0.05	991.54	496.78	991.49	496.75	2	834.9
	65.0	A0QSS4	MSMEG_1583	75.0	DSTVIVDGGGTAEAIADR	iTRAQ4plex@N-term; Dehydrated(S)@2		-0.03	1871.90	624.98	1871.93	624.99	3	
	65.0	A0QSS4	MSMEG_1583	75.0	TNDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Asn->Val@2		-0.07	2202.13	735.05	2202.20	735.07	3	
13	63.8	A0R652	MSMEG_6427	99.0	AEYTLPDLDYDYGALEPHISGQINELHH	iTRAQ4plex@N-term; Lys->Gln@30	cleaved M-A@N-term	0.02	3568.71	714.75	3568.69	714.74	5	106.2
	63.8	A0R652	MSMEG_6427	99.0	AFWNVVNWDDVQNR	iTRAQ4plex@N-term		-0.03	1905.90	636.31	1905.92	636.32	3	17.4
	63.8	A0R652	MSMEG_6427	99.0	ANGDHAAIFLNEK	iTRAQ4plex@N-term; Lys->Gln@13		0.05	1542.81	515.28	1542.75	515.26	3	348.2
	63.8	A0R652	MSMEG_6427	99.0	FQAQFTAAANGLQGSGWAVLGYDSLG	iTRAQ4plex@N-term; Deamidated(N)@10		0.01	2986.48	996.50	2986.47	996.50	3	58.6
	63.8	A0R652	MSMEG_6427	99.0	FQAQFTAAANGLQGSGWAVLGYDSLG	iTRAQ4plex@N-term		-0.06	2985.43	996.15	2985.49	996.17	3	19.6
	63.8	A0R652	MSMEG_6427	99.0	FQAQFTAAANGLQGSGWAVLGYDSLG	iTRAQ4plex@N-term		0.07	2985.55	747.40	2985.49	747.38	4	18.5
	63.8	A0R652	MSMEG_6427	98.0	NLSPNGGDKPTGELAAAIDDQFGSFDK	iTRAQ4plex@N-term; Lys->Gln@9; iTRAQ4plex(T)@11; Lys->Arg@27		0.07	3079.54	770.89	3079.47	770.88	4	29.4
	63.8	A0R652	MSMEG_6427	95.0	FWNVVNWDDVQNR	iTRAQ4plex@N-term	cleaved A-F@N-term	-0.05	1834.84	612.62	1834.89	612.64	3	18.5
	63.8	A0R652	MSMEG_6427	85.0	GVNDAIAK	iTRAQ4plex@N-term; Lys->Gln@8		0.05	930.54	466.28	930.49	466.25	2	104.1
14	63.4	A0R5H1	MSMEG_6189	99.0	AGIFQGVEPTAVAALTK	iTRAQ4plex@N-term; iTRAQ4plex(T)@16; Lys->Gln@17		0.03	1960.11	654.38	1960.09	654.37	3	88.7
	63.4	A0R5H1	MSMEG_6189	99.0	AWIADRPEIAEQLLR	iTRAQ4plex@N-term; Dimethyl(R)@15		-0.02	1952.08	651.70	1952.10	651.71	3	541.7
	63.4	A0R5H1	MSMEG_6189	99.0	FGTQEGGALR	iTRAQ4plex@N-term		0.04	1178.66	590.34	1178.62	590.32	2	7.074.4

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	63.4	A0R5H1	MSMEG_6189	99.0	QLLQLAQR	iTRAQ4plex@N-term		0.01	1112.68	557.35	1112.68	557.35	2	5.245.4
	63.4	A0R5H1	MSMEG_6189	99.0	RTNNNLADLIFTDVPGR	iTRAQ4plex@N-term	missed R-T@1	-0.01	2059.08	687.37	2059.09	687.37	3	31.5
	63.4	A0R5H1	MSMEG_6189	99.0	SVLISDSER	iTRAQ4plex@N-term		0.00	1148.61	575.31	1148.62	575.32	2	7.420.8
	63.4	A0R5H1	MSMEG_6189	99.0	TSSATTITEVR	iTRAQ4plex@N-term		0.00	1308.71	655.36	1308.70	655.36	2	624.9
	63.4	A0R5H1	MSMEG_6189	99.0	VTHDLTQEEIAQLVGASR	iTRAQ4plex@N-term		0.03	2110.14	704.39	2110.11	704.38	3	114.4
	63.4	A0R5H1	MSMEG_6189	99.0	AWIADRPEIAEQLLR	iTRAQ4plex@N-term		0.01	1924.08	642.37	1924.07	642.36	3	206.9
	63.4	A0R5H1	MSMEG_6189	99.0	VTHDLTQEEIAQLVGASR	No iTRAQ4plex@N-term		-0.03	1965.99	656.34	1966.01	656.34	3	83.0
	63.4	A0R5H1	MSMEG_6189	89.0	TNNNLADLIFTDVPGR	iTRAQ4plex@N-term		-0.05	1902.95	635.32	1902.99	635.34	3	100.6
	63.4	A0R5H1	MSMEG_6189	79.0	AWIADRPEIAEQLLR	iTRAQ4plex@N-term		-0.04	1924.03	642.35	1924.07	642.36	3	184.2
	63.4	A0R5H1	MSMEG_6189	76.0	QLQPVDFPR	iTRAQ4plex@N-term		0.02	1242.70	622.36	1242.68	622.35	2	5.075.1
15	62.9	A0QWW2	MSMEG_3084	99.0	VPIPTGSVTDLTAELAKSASVEDINA	iTRAQ4plex@N-term; Glu->Gln@14; User modH on Lys(K)@17; iTRAQ4plex(S)@18; Lys->Gln@2	missed K-S@17	-0.08	3457.73	865.44	3457.81	865.46	4	124.7
	62.9	A0QWW2	MSMEG_3084	99.0	AAAEGPLK	iTRAQ4plex@N-term; Lys->Gln@8		0.04	899.52	450.77	899.48	450.75	2	47.5
	62.9	A0QWW2	MSMEG_3084	99.0	AAALNIVPTSTGAAK	iTRAQ4plex@N-term; Lys->Gln@15		0.06	1527.90	764.96	1527.84	764.93	2	1.511.5
	62.9	A0QWW2	MSMEG_3084	99.0	AIGLVLPELK	iTRAQ4plex@N-term; Lys->Arg@10		0.02	1223.79	612.90	1223.77	612.89	2	389.6
	62.9	A0QWW2	MSMEG_3084	99.0	GLMTTIHAYTQDQNLQDGPHK	iTRAQ4plex@N-term; Lys->Gln@21		0.04	2511.23	628.81	2511.19	628.81	4	204.8
	62.9	A0QWW2	MSMEG_3084	99.0	LADLVALVGK	iTRAQ4plex@N-term; Lys->Gln@10		0.04	1141.72	571.87	1141.68	571.85	2	853.2
	62.9	A0QWW2	MSMEG_3084	99.0	NTDIEIVAVNDLTDNATLAHLLK	iTRAQ4plex@N-term; Lys->Gln@23		-0.01	2636.37	879.80	2636.38	879.80	3	46.7
	62.9	A0QWW2	MSMEG_3084	99.0	SASVEDINAAMK	iTRAQ4plex@N-term; Lys->Gln@12		0.06	1378.71	690.36	1378.65	690.33	2	999.6
	62.9	A0QWW2	MSMEG_3084	99.0	VGVNGFGR	iTRAQ4plex@N-term; Deamidated(N)@4		0.00	949.52	475.76	949.51	475.76	2	9.888.8
	62.9	A0QWW2	MSMEG_3084	99.0	VLNDEFGIVK	iTRAQ4plex@N-term; Lys->Arg@10		0.02	1304.74	653.38	1304.72	653.37	2	833.1
	62.9	A0QWW2	MSMEG_3084	99.0	VPIPTGSVTDLTAELAK	iTRAQ4plex@N-term; Lys->Gln@17		0.07	1855.08	928.55	1855.01	928.51	2	2.346.7
	62.9	A0QWW2	MSMEG_3084	99.0	VVSWYDNEWGYSNR	iTRAQ4plex@N-term		-0.02	1917.86	640.29	1917.88	640.30	3	733.9
	62.9	A0QWW2	MSMEG_3084	99.0	YYDAPIVSSDIVTDPHSSLYDAGLTK	iTRAQ4plex@N-term; iTRAQ4plex(T)@25; Lys->Gln@26		0.01	3114.54	779.64	3114.53	779.64	4	451.5
	62.9	A0QWW2	MSMEG_3084	99.0	LADLVALVGK	iTRAQ4plex@N-term; Lys->Arg@10		0.03	1169.76	585.89	1169.73	585.87	2	33.7
	62.9	A0QWW2	MSMEG_3084	99.0	VLNDEFGIVK	iTRAQ4plex@N-term; Lys->Gln@10		0.04	1276.72	639.37	1276.68	639.35	2	2.972.7
	62.9	A0QWW2	MSMEG_3084	99.0	VPIPTGSVTDLTAELAK	iTRAQ4plex@N-term; Lys->Gln@17		0.00	1855.00	619.34	1855.01	619.34	3	15.2
	62.9	A0QWW2	MSMEG_3084	99.0	VPIPTGSVTDLTAELAK	iTRAQ4plex@N-term; Lys->Arg@17		-0.02	1883.03	628.68	1883.05	628.69	3	32.6
	62.9	A0QWW2	MSMEG_3084	98.0	AIGLVLPELK	iTRAQ4plex@N-term; Lys->Gln@10		0.03	1195.76	598.89	1195.73	598.87	2	332.5
	62.9	A0QWW2	MSMEG_3084	97.0	AAALNIVPTSTGAAK	iTRAQ4plex@N-term; iTRAQ4plex(T)@11; Lys->Gln@15		0.00	1671.94	558.32	1671.94	558.32	3	915.4
	62.9	A0QWW2	MSMEG_3084	97.0	VGVNGFGR	iTRAQ4plex@N-term		0.00	948.52	475.27	948.53	475.27	2	957.1
	62.9	A0QWW2	MSMEG_3084	97.0	VPIPTGSVTDLTAELAK	iTRAQ4plex@N-term; iTRAQ4plex(T)@12; Lys->Gln@17		-0.02	1999.08	667.37	1999.11	667.38	3	343.0
	62.9	A0QWW2	MSMEG_3084	94.0	FDSILGR	iTRAQ4plex@N-term		-0.03	950.50	476.26	950.53	476.27	2	10.231.5
	62.9	A0QWW2	MSMEG_3084	93.0	LDGYALR	iTRAQ4plex@N-term		-0.01	950.52	476.27	950.53	476.27	2	7.938.9
	62.9	A0QWW2	MSMEG_3084	92.0	VPIPTGSVTDLTAELAKSASVEDINA	iTRAQ4plex@N-term; User modH on Lys(K)@17; Ser->Met@20; Deamidated(N)@25; User modH	missed K-S@17	0.10	3602.93	901.74	3602.83	901.71	4	339.3
	62.9	A0QWW2	MSMEG_3084	88.0	VGVNGFGR	iTRAQ4plex@N-term; Deamidated(N)@4		0.01	949.52	475.77	949.51	475.76	2	4.651.7
	62.9	A0QWW2	MSMEG_3084	86.0	YYDAPIVSSDIVTDPHSSLYDAGLTK	iTRAQ4plex@N-term; Asp->Asn@14; iTRAQ4plex(T)@25; Lys->Gln@26		0.11	3113.65	779.42	3113.54	779.39	4	153.5
	62.9	A0QWW2	MSMEG_3084	82.0	LADLVALVGK	iTRAQ4plex@N-term; Lys->Arg@10		0.00	1169.72	585.87	1169.73	585.87	2	168.1
	62.9	A0QWW2	MSMEG_3084	77.0	SASVEDINAAMK	iTRAQ4plex@N-term; Deamidated(N)@8; Lys->Arg@12		0.03	1407.71	704.86	1407.68	704.85	2	599.8
16	61.8	Q9AFI5	MSMEG_6896	99.0	DGEALFLR	iTRAQ4plex@N-term		-0.01	1063.57	532.79	1063.58	532.80	2	1.728.3
	61.8	Q9AFI5	MSMEG_6896	99.0	EAAENVAESLTR	iTRAQ4plex@N-term		0.01	1432.74	717.38	1432.73	717.37	2	2.757.0
	61.8	Q9AFI5	MSMEG_6896	99.0	SGGGGGGFGSGGGGSR	No iTRAQ4plex@N-term; Gly->Pro@2		0.01	1249.55	625.78	1249.54	625.78	2	
	61.8	Q9AFI5	MSMEG_6896	99.0	TVVEVEVDEIGPSLR	iTRAQ4plex@N-term		-0.02	1784.95	595.99	1784.96	596.00	3	
	61.8	Q9AFI5	MSMEG_6896	99.0	SGGGGGGFGSGGGGSR	iTRAQ4plex@N-term		0.01	1353.63	452.22	1353.61	452.21	3	15.2
17	60.9	A0QZA1	MSMEG_3950	99.0	TLIDASKSAQMVVVGNR	iTRAQ4plex@N-term; User modH on Lys(K)@7; iTRAQ4plex(S)@8	missed K-S@7	0.02	2319.29	774.10	2319.27	774.10	3	749.1
	60.9	A0QZA1	MSMEG_3950	99.0	AQPAYWLLEEAK	iTRAQ4plex@N-term; Lys->Gln@12		0.02	1561.81	781.91	1561.79	781.90	2	2.308.0
	60.9	A0QZA1	MSMEG_3950	99.0	LPVLLGIDGSPASEVATSHAFDEASR	iTRAQ4plex@N-term		0.05	2782.47	928.50	2782.43	928.48	3	1.021.0
	60.9	A0QZA1	MSMEG_3950	99.0	MATVLECQEENAR	iTRAQ4plex@N-term; Pyridylethyl(C)@7	cleaved Y-M@N-term	0.02	1741.84	581.62	1741.82	581.62	3	790.4
	60.9	A0QZA1	MSMEG_3950	99.0	QAQLVVVGSHGR	iTRAQ4plex@N-term		0.01	1393.81	465.61	1393.79	465.60	3	530.3
	60.9	A0QZA1	MSMEG_3950	99.0	SAQMVVVGNR	iTRAQ4plex@N-term		0.03	1203.68	602.85	1203.65	602.83	2	2.574.1
	60.9	A0QZA1	MSMEG_3950	99.0	VAQSATTPVMVVR	iTRAQ4plex@N-term	cleaved R-P@C-term	0.00	1501.84	751.93	1501.84	751.93	2	4.931.7
	60.9	A0QZA1	MSMEG_3950	99.0	VAQSATTPVMVVRPR	iTRAQ4plex@N-term		0.03	1755.02	586.01	1754.99	586.01	3	3.593.7
	60.9	A0QZA1	MSMEG_3950	99.0	LPVLLGIDGSPASEVATSHAFDEASR	iTRAQ4plex@N-term		0.00	2782.43	928.48	2782.43	928.48	3	142.2
	60.9	A0QZA1	MSMEG_3950	99.0	LPVLLGIDGSPASEVATSHAFDEASR	iTRAQ4plex@N-term; Dimethyl(R)@26		0.08	2810.54	937.85	2810.46	937.83	3	81.4
	60.9	A0QZA1	MSMEG_3950	99.0	VQSATEYGILVGVDSSAESDAAVR	iTRAQ4plex@N-term	cleaved M-V@N-term	-0.04	2567.24	856.76	2567.28	856.77	3	17.4
	60.9	A0QZA1	MSMEG_3950	99.0	VQSATEYGILVGVDSSAESDAAVR	iTRAQ4plex@N-term	cleaved M-V@N-term	-0.06	2567.23	856.75	2567.28	856.77	3	
	60.9	A0QZA1	MSMEG_3950	91.0	EASLHDAPITLM	iTRAQ4plex@N-term	cleaved M-H@C-term	0.02	1440.76	721.39	1440.74	721.38	2	125.1
	60.9	A0QZA1	MSMEG_3950	75.0	GMGALGR	iTRAQ4plex@N-term		0.01	804.45	403.23	804.44	403.23	2	6.225.7

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
18	59.9	A0R4C9	MSMEG_5789	99.0	DFVDAQQFSKLLSER	iTRAQ4plex@N-term; iTRAQ4plex(S)@9; User modH on Lys(K)@10	missed K-L@10	-0.04	2313.17	772.06	2313.21	772.08	3	771.4
	59.9	A0R4C9	MSMEG_5789	99.0	DFVDAQQFSK	iTRAQ4plex@N-term; Lys->Gln@10		0.04	1327.66	664.83	1327.62	664.82	2	936.7
	59.9	A0R4C9	MSMEG_5789	99.0	ILAPAHLPQEQSQR	iTRAQ4plex@N-term	cleaved R-P@C-term	0.00	1730.95	577.99	1730.95	577.99	3	1.091.5
	59.9	A0R4C9	MSMEG_5789	99.0	SSHTWFVLQELLGHK	No iTRAQ4plex@N-term; Lys->Gln@15		0.02	1780.91	446.24	1780.89	446.23	4	
	59.9	A0R4C9	MSMEG_5789	99.0	TDLQDPIR	iTRAQ4plex@N-term		0.01	1100.61	551.31	1100.59	551.30	2	8.822.7
	59.9	A0R4C9	MSMEG_5789	99.0	TDLQDPIRR	iTRAQ4plex@N-term	missed R-R@8	0.00	1256.69	419.90	1256.70	419.91	3	962.2
	59.9	A0R4C9	MSMEG_5789	98.0	DFVDAQQFSKLLSER	iTRAQ4plex@N-term; iTRAQ4plex(S)@9; User modH on Lys(K)@10	missed K-L@10	-0.02	2313.19	579.30	2313.21	579.31	4	90.2
	59.9	A0R4C9	MSMEG_5789	97.0	NVKNYDGSWTEYGSLVGAPIELGS	iTRAQ4plex@N-term; Lys->Asn@3	missed K-N@3	0.04	2685.31	896.11	2685.27	896.10	3	87.7
	59.9	A0R4C9	MSMEG_5789	96.0	TDLQDPIR	iTRAQ4plex@N-term; Dimethyl(R)@8		-0.01	1128.62	565.32	1128.63	565.32	2	3.608.5
	59.9	A0R4C9	MSMEG_5789	92.0	DFVDAQQFSKLLSER	iTRAQ4plex@N-term; iTRAQ4plex(S)@9; User modH on Lys(K)@10; Dimethyl(R)@15	missed K-L@10	-0.03	2341.21	586.31	2341.24	586.32	4	209.5
19	58.4	A0QVQ3	MSMEG_2654	99.0	GLLLLVGR	iTRAQ4plex@N-term		-0.04	983.62	492.82	983.66	492.84	2	1.062.7
	58.4	A0QVQ3	MSMEG_2654	99.0	YVAQVDVAR	iTRAQ4plex@N-term		0.00	1163.64	582.83	1163.64	582.83	2	2.251.9
	58.4	A0QVQ3	MSMEG_2654	99.0	EILGQYGLHDTDTGSPEAQVALLTK	iTRAQ4plex@N-term; iTRAQ4plex(T)@24; Lys->Gln@25		-0.01	2943.49	736.88	2943.51	736.88	4	208.1
	58.4	A0QVQ3	MSMEG_2654	97.0	IQDLTEHLK	iTRAQ4plex@N-term; Lys->Gln@9		0.03	1239.69	414.24	1239.66	414.23	3	638.1
	58.4	A0QVQ3	MSMEG_2654	84.0	GLLLLVGR	iTRAQ4plex@N-term; Dimethyl(R)@8		0.01	1011.70	506.86	1011.69	506.85	2	107.6
20	56.9	A0QQU5	MSMEG_0880	99.0	AEIENSDSDYDR	iTRAQ4plex@N-term; Deamidated(N)@5		0.00	1557.65	779.83	1557.66	779.83	2	210.2
	56.9	A0QQU5	MSMEG_0880	99.0	AEIENSDSDYDREK	iTRAQ4plex@N-term; Lys->Arg@14	missed R-E@12	0.08	1841.89	614.97	1841.81	614.95	3	429.8
	56.9	A0QQU5	MSMEG_0880	99.0	AGAATEVELK	iTRAQ4plex@N-term; Lys->Gln@10		0.05	1131.64	566.83	1131.59	566.80	2	941.3
	56.9	A0QQU5	MSMEG_0880	99.0	GLNSLADAVK	iTRAQ4plex@N-term; Deamidated(N)@3; Lys->Arg@10		0.01	1159.64	580.83	1159.63	580.82	2	1.420.5
	56.9	A0QQU5	MSMEG_0880	99.0	GYISGYFVTDAER	iTRAQ4plex@N-term		0.01	1620.80	811.41	1620.79	811.40	2	1.535.8
	56.9	A0QQU5	MSMEG_0880	99.0	IAYDEEARR	iTRAQ4plex@N-term	cleaved T-I@N-term; missed R-R@8	0.01	1265.66	422.89	1265.65	422.89	3	476.1
	56.9	A0QQU5	MSMEG_0880	99.0	ISGYFVTDAER	iTRAQ4plex@N-term	cleaved Y-I@N-term	0.00	1400.71	701.36	1400.71	701.36	2	634.8
	56.9	A0QQU5	MSMEG_0880	99.0	KTDDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Lys->Gln@1	missed K-T@1	0.02	2346.24	783.09	2346.21	783.08	3	565.7
	56.9	A0QQU5	MSMEG_0880	99.0	NVAAGANPLGLK	iTRAQ4plex@N-term; Lys->Arg@12		0.04	1295.78	648.90	1295.74	648.88	2	2.602.8
	56.9	A0QQU5	MSMEG_0880	99.0	QEAVLEDPYILLVSSK	iTRAQ4plex@N-term; iTRAQ4plex(S)@15; Lys->Gln@16		0.03	2091.16	698.06	2091.13	698.05	3	1.327.1
	56.9	A0QQU5	MSMEG_0880	99.0	SGYFVTDAER	iTRAQ4plex@N-term	cleaved I-S@N-term	0.02	1287.65	644.83	1287.62	644.82	2	1.986.9
	56.9	A0QQU5	MSMEG_0880	99.0	TIAYDEEAR	iTRAQ4plex@N-term; Ala->Val@8		0.02	1238.65	620.33	1238.63	620.32	2	560.2
	56.9	A0QQU5	MSMEG_0880	99.0	TIAYDEEARR	iTRAQ4plex@N-term	missed R-R@9	0.00	1366.70	456.57	1366.70	456.57	3	4.093.0
	56.9	A0QQU5	MSMEG_0880	99.0	VGNEGVITVEESNTFGLQLELTEGMR	iTRAQ4plex@N-term		-0.08	2965.40	989.47	2965.48	989.50	3	9.8
	56.9	A0QQU5	MSMEG_0880	99.0	VSNLPAGHGLNAATGEYEDLLAAGVADI	iTRAQ4plex@N-term; Lys->Arg@30		0.10	3120.70	781.18	3120.60	781.16	4	28.0
	56.9	A0QQU5	MSMEG_0880	99.0	WGAPTITNDGVSIAK	iTRAQ4plex@N-term; Lys->Arg@15		0.01	1700.91	851.46	1700.90	851.46	2	1.239.2
	56.9	A0QQU5	MSMEG_0880	99.0	AEIENSDSDYDR	iTRAQ4plex@N-term		0.03	1556.70	779.36	1556.67	779.34	2	1.113.1
	56.9	A0QQU5	MSMEG_0880	99.0	AEIENSDSDYDR	iTRAQ4plex@N-term; Dimethyl(R)@12		0.00	1584.70	793.36	1584.70	793.36	2	256.8
	56.9	A0QQU5	MSMEG_0880	99.0	AEIENSDSDYDREK	iTRAQ4plex@N-term; iTRAQ4plex(Y)@10; Lys->Gln@14	missed R-E@12	0.07	1957.94	653.65	1957.87	653.63	3	1.917.0
	56.9	A0QQU5	MSMEG_0880	99.0	AEIENSDSDYDREK	iTRAQ4plex@N-term; Lys->Gln@14	missed R-E@12	0.08	1813.85	605.62	1813.77	605.60	3	609.1
	56.9	A0QQU5	MSMEG_0880	99.0	DETTIVEGAGDAEAIQGR	iTRAQ4plex@N-term		0.01	1974.97	988.49	1974.96	988.49	2	450.1
	56.9	A0QQU5	MSMEG_0880	99.0	DETTIVEGAGDAEAIQGR	iTRAQ4plex@N-term; Gln->Arg@16		-0.02	2002.98	668.67	2003.00	668.68	3	116.7
	56.9	A0QQU5	MSMEG_0880	99.0	DETTIVEGAGDAEAIQGR	iTRAQ4plex@N-term		-0.07	1974.89	659.30	1974.96	659.33	3	15.2
	56.9	A0QQU5	MSMEG_0880	99.0	GLNSLADAVK	iTRAQ4plex@N-term; Lys->Gln@10		0.05	1130.65	566.33	1130.61	566.31	2	3.600.6
	56.9	A0QQU5	MSMEG_0880	99.0	GLNSLADAVK	iTRAQ4plex@N-term; Lys->Arg@10		0.00	1158.65	580.33	1158.65	580.33	2	915.2
	56.9	A0QQU5	MSMEG_0880	99.0	GYISGYFVTDAER	iTRAQ4plex@N-term		-0.01	1620.78	811.40	1620.79	811.40	2	218.8
	56.9	A0QQU5	MSMEG_0880	99.0	GYISGYFVTDAER	iTRAQ4plex@N-term		0.00	1620.80	811.41	1620.79	811.40	2	1.682.6
	56.9	A0QQU5	MSMEG_0880	99.0	GYISGYFVTDAER	iTRAQ4plex@N-term		-0.02	1620.77	811.39	1620.79	811.40	2	965.6
	56.9	A0QQU5	MSMEG_0880	99.0	GYISGYFVTDAER	iTRAQ4plex@N-term		0.01	1620.80	811.41	1620.79	811.40	2	1.017.0
	56.9	A0QQU5	MSMEG_0880	99.0	GYISGYFVTDAER	iTRAQ4plex@N-term		-0.02	1620.77	811.39	1620.79	811.40	2	48.9
	56.9	A0QQU5	MSMEG_0880	99.0	GYISGYFVTDAER	iTRAQ4plex@N-term		0.07	1620.86	811.44	1620.79	811.40	2	47.7
	56.9	A0QQU5	MSMEG_0880	99.0	GYISGYFVTDAER	iTRAQ4plex@N-term; Ala->Val@11		0.04	1648.86	550.63	1648.82	550.61	3	6.5
	56.9	A0QQU5	MSMEG_0880	99.0	GYISGYFVTDAER	iTRAQ4plex@N-term; Dimethyl(R)@13		-0.02	1648.80	825.41	1648.82	825.42	2	2.556.1
	56.9	A0QQU5	MSMEG_0880	99.0	KTDDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Lys->Gln@1; iTRAQ4plex(T)@2	missed K-T@1	0.06	2490.37	831.13	2490.32	831.11	3	226.4
	56.9	A0QQU5	MSMEG_0880	99.0	KTDDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Lys->Gln@1; iTRAQ4plex(T)@2; Ala->Val@19	missed K-T@1	0.00	2518.35	630.60	2518.35	630.59	4	22.7
	56.9	A0QQU5	MSMEG_0880	99.0	KTDDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Lys->Gln@1	missed K-T@1	0.01	2346.23	783.08	2346.21	783.08	3	109.2
	56.9	A0QQU5	MSMEG_0880	99.0	KTDDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Lys->Gln@1; Dimethyl(R)@22	missed K-T@1	0.07	2374.32	792.45	2374.25	792.42	3	175.1
	56.9	A0QQU5	MSMEG_0880	99.0	NVAAGANPLGLK	iTRAQ4plex@N-term; Lys->Gln@12		0.03	1267.73	634.87	1267.70	634.86	2	12.518.6
	56.9	A0QQU5	MSMEG_0880	99.0	QEAVLEDPYILLVSSK	iTRAQ4plex@N-term; iTRAQ4plex(S)@15; Lys->Gln@16		-0.03	2091.10	698.04	2091.13	698.05	3	151.1
	56.9	A0QQU5	MSMEG_0880	99.0	TDDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Asp->Asn@7		0.02	2217.19	740.07	2217.17	740.06	3	17.1
	56.9	A0QQU5	MSMEG_0880	99.0	TDDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Asp->Asn@7; Dimethyl(R)@21		-0.02	2245.18	749.40	2245.20	749.41	3	18.3
	56.9	A0QQU5	MSMEG_0880	99.0	TIAYDEEAR	Carbamyl@N-term		0.05	1109.55	555.78	1109.50	555.76	2	975.1
	56.9	A0QQU5	MSMEG_0880	99.0	TIAYDEEAR	iTRAQ4plex@N-term		0.02	1210.62	606.32	1210.60	606.30	2	376.9
	56.9	A0QQU5	MSMEG_0880	99.0	TIAYDEEAR	iTRAQ4plex@N-term		0.00	1210.59	606.30	1210.60	606.30	2	683.8

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	56.9	A0QQU5	MSMEG_0880	99.0	TIAYDEEAR	iTRAQ4plex@N-term; Ala->Val@8		0.02	1238.64	620.33	1238.63	620.32	2	177.3
	56.9	A0QQU5	MSMEG_0880	99.0	VSNLPAGHGLNAATGEYEDLLAAGVAD	iTRAQ4plex@N-term; Lys->Gln@30		0.02	3092.57	1031.87	3092.55	1031.86	3	912.3
	56.9	A0QQU5	MSMEG_0880	99.0	VSNLPAGHGLNAATGEYEDLLAAGVAD	iTRAQ4plex@N-term; Lys->Gln@30		0.07	3092.63	1031.88	3092.55	1031.86	3	96.6
	56.9	A0QQU5	MSMEG_0880	99.0	VSNLPAGHGLNAATGEYEDLLAAGVAD	No iTRAQ4plex@N-term; Lys->Gln@30		0.00	2948.45	983.82	2948.45	983.82	3	21.7
	56.9	A0QQU5	MSMEG_0880	99.0	WGAPTITNDGVSIAK	iTRAQ4plex@N-term; Lys->Gln@15		0.02	1672.87	837.44	1672.85	837.43	2	1.407.7
	56.9	A0QQU5	MSMEG_0880	99.0	WGAPTITNDGVSIAK	iTRAQ4plex@N-term; iTRAQ4plex(S)@12; Lys->Gln@15		0.04	1817.00	606.67	1816.96	606.66	3	819.9
	56.9	A0QQU5	MSMEG_0880	99.0	WGAPTITNDGVSIAK	iTRAQ4plex@N-term; iTRAQ4plex(S)@12; Lys->Gln@15		0.05	1817.01	606.68	1816.96	606.66	3	1.055.5
	56.9	A0QQU5	MSMEG_0880	99.0	WGAPTITNDGVSIAK	iTRAQ4plex@N-term; iTRAQ4plex(S)@12; Lys->Gln@15		0.05	1817.00	606.68	1816.96	606.66	3	1.282.1
	56.9	A0QQU5	MSMEG_0880	98.0	LAGGVAVIK	iTRAQ4plex@N-term; Lys->Gln@9		0.02	970.61	486.31	970.59	486.30	2	6.055.9
	56.9	A0QQU5	MSMEG_0880	97.0	LAGGVAVIK	iTRAQ4plex@N-term; Lys->Gln@9		0.04	970.63	486.32	970.59	486.30	2	1.332.1
	56.9	A0QQU5	MSMEG_0880	96.0	WGAPTITNDGVSIAK	iTRAQ4plex@N-term; iTRAQ4plex(S)@12; Lys->Gln@15		0.02	1816.97	606.67	1816.96	606.66	3	1.147.2
	56.9	A0QQU5	MSMEG_0880	95.0	GAPTITNDGVSIAK	iTRAQ4plex@N-term; iTRAQ4plex(S)@11; Lys->Gln@14	cleaved W-G@N-term	0.03	1630.90	544.64	1630.88	544.63	3	535.4
	56.9	A0QQU5	MSMEG_0880	94.0	GLNSLADAVK	iTRAQ4plex@N-term; Deamidated(N)@3; Lys->Gln@10		0.05	1131.64	566.83	1131.59	566.80	2	6.042.0
	56.9	A0QQU5	MSMEG_0880	94.0	GLNSLADAVK	iTRAQ4plex@N-term; Lys->Gln@10		0.04	1130.64	566.33	1130.61	566.31	2	1.262.3
	56.9	A0QQU5	MSMEG_0880	94.0	GYISGYFVTDAER	iTRAQ4plex@N-term; Dimethyl(R)@13		0.05	1648.87	550.63	1648.82	550.61	3	
	56.9	A0QQU5	MSMEG_0880	93.0	KWGAPTITNDGVSIAK	iTRAQ4plex@N-term; Lys->Gln@1; Lys->Gln@16	missed K-W@1	0.07	1800.99	601.34	1800.91	601.31	3	196.8
	56.9	A0QQU5	MSMEG_0880	93.0	GYISGYFVTDAER	iTRAQ4plex@N-term; Oxidation(F)@7; Val->Asn@8		0.06	1651.82	551.61	1651.76	551.59	3	
	56.9	A0QQU5	MSMEG_0880	88.0	NVAAGANPLGLKR	iTRAQ4plex@N-term; User modH on Lys(K)@12; Oxidation(R)@13	missed K-R@12	0.00	1682.95	842.48	1682.94	842.48	2	1.157.9
	56.9	A0QQU5	MSMEG_0880	88.0	LAGGVAVIK	iTRAQ4plex@N-term; Lys->Arg@9		0.00	998.63	500.32	998.64	500.33	2	1.471.3
	56.9	A0QQU5	MSMEG_0880	85.0	DLLPLLEK	iTRAQ4plex@N-term; Lys->Gln@8		0.03	1083.66	542.84	1083.63	542.82	2	1.273.7
	56.9	A0QQU5	MSMEG_0880	84.0	DLLPLLEK	iTRAQ4plex@N-term; Lys->Arg@8		0.02	1111.69	556.85	1111.67	556.84	2	502.6
	56.9	A0QQU5	MSMEG_0880	84.0	TIAYDEEAR	Carbamyl@N-term; Ala->Val@8		0.05	1137.58	569.80	1137.53	569.77	2	3.220.9
	56.9	A0QQU5	MSMEG_0880	75.0	TDDVAGDGTTTATVLAQALVR	iTRAQ4plex@N-term; Asp->Val@2		-0.07	2202.13	735.05	2202.20	735.07	3	
21	56.5	A0QVZ3	MSMEG_2750	99.0	DGLLHVAGDR	iTRAQ4plex@N-term		0.00	1195.64	399.55	1195.64	399.55	3	144.7
	56.5	A0QVZ3	MSMEG_2750	99.0	EHVMSEEVER	iTRAQ4plex@N-term	cleaved W-E@N-term	0.03	1387.68	463.57	1387.65	463.56	3	441.6
	56.5	A0QVZ3	MSMEG_2750	99.0	LDQSGPTVSQTVSR	iTRAQ4plex@N-term		0.04	1617.89	809.95	1617.84	809.93	2	377.0
	56.5	A0QVZ3	MSMEG_2750	99.0	LTELPVGMPVAVVVR	iTRAQ4plex@N-term		0.01	1723.03	862.52	1723.02	862.52	2	2.109.4
	56.5	A0QVZ3	MSMEG_2750	99.0	MNDLVDTTEMYLR	iTRAQ4plex@N-term		0.03	1743.86	872.94	1743.83	872.92	2	1.904.5
	56.5	A0QVZ3	MSMEG_2750	99.0	QLTEHVQGDTDLIGR	iTRAQ4plex@N-term		0.04	1824.99	609.34	1824.95	609.32	3	1.004.0
	56.5	A0QVZ3	MSMEG_2750	99.0	WEHVMSEEVER	iTRAQ4plex@N-term		0.02	1573.75	525.59	1573.73	525.58	3	301.6
	56.5	A0QVZ3	MSMEG_2750	99.0	LDQSGPTVSQTVSR	iTRAQ4plex@N-term		0.02	1617.86	809.94	1617.84	809.93	2	680.9
	56.5	A0QVZ3	MSMEG_2750	99.0	MNDLVDTTEMYLR	iTRAQ4plex@N-term; Dimethyl(R)@13		-0.01	1771.85	886.93	1771.86	886.94	2	826.2
	56.5	A0QVZ3	MSMEG_2750	99.0	WEHVMSEEVER	iTRAQ4plex@N-term; Dioxidation(W)@1		0.03	1605.75	536.26	1605.72	536.25	3	663.0
	56.5	A0QVZ3	MSMEG_2750	99.0	WEHVMSEEVER	iTRAQ4plex@N-term; Dimethyl(R)@11		-0.01	1601.75	534.92	1601.76	534.93	3	389.6
	56.5	A0QVZ3	MSMEG_2750	98.0	EAGVVPNAR	iTRAQ4plex@N-term; Deamidated(N)@7		0.01	1056.58	529.30	1056.57	529.29	2	243.3
	56.5	A0QVZ3	MSMEG_2750	97.0	EAGVVPNAR	iTRAQ4plex@N-term		0.02	1055.60	528.81	1055.58	528.80	2	428.5
	56.5	A0QVZ3	MSMEG_2750	94.0	LTELPVGMPVAVVVR	iTRAQ4plex@N-term; Dimethyl(R)@15		-0.03	1751.02	584.68	1751.05	584.69	3	26.1
	56.5	A0QVZ3	MSMEG_2750	92.0	DGLLHVAGDR	No iTRAQ4plex@N-term; Gly->Pro@2		0.02	1091.59	546.80	1091.57	546.79	2	662.6
22	56.4	A0R452	MSMEG_5707	99.0	MSLTALAR	iTRAQ4plex@N-term		-0.02	1005.56	503.79	1005.58	503.80	2	4.337.2
	56.4	A0R452	MSMEG_5707	81.0	MSLTALAR	iTRAQ4plex@N-term; Ala->Val@7		-0.03	1033.58	517.80	1033.61	517.81	2	549.5
	56.4	A0R452	MSMEG_5707	76	VKLANSEASWEGSPGDLLVIPR	iTRAQ4plex@N-term; User modH on Lys(K)@2; iTRAQ4plex(S)@6; Glu->Gln@11	missed K-L@2	-0.01	2867.54	717.89	2867.56	717.89	4	164.47
23	55.3	A0QSX3	MSMEG_1634	99.0	ADIVLSGLR	iTRAQ4plex@N-term		0.00	1086.65	544.33	1086.65	544.33	2	3.395.8
	55.3	A0QSX3	MSMEG_1634	99.0	ETIAALGGLPGADHGEHEGR	iTRAQ4plex@N-term		0.00	2130.06	533.52	2130.06	533.52	4	506.7
	55.3	A0QSX3	MSMEG_1634	99.0	LSAEEVANGAGLRPGLLDELEAGATPT	iTRAQ4plex@N-term; Deamidated(N)@8		-0.02	3452.69	864.18	3452.70	864.18	4	123.5
	55.3	A0QSX3	MSMEG_1634	99.0	SALTEAASAQR	iTRAQ4plex@N-term	cleaved R-P@C-term	0.04	1247.69	624.85	1247.66	624.84	2	3.914.7
	55.3	A0QSX3	MSMEG_1634	99.0	SALTEAASAQRPSPAVAAALSGVR	iTRAQ4plex@N-term		-0.07	2424.25	809.09	2424.32	809.11	3	642.5
	55.3	A0QSX3	MSMEG_1634	99.0	YDSLMAHAAAAPGSSLGQQIYVTR	iTRAQ4plex@N-term		-0.05	2650.28	884.43	2650.33	884.45	3	363.5
	55.3	A0QSX3	MSMEG_1634	99.0	ADIVLSGLR	iTRAQ4plex@N-term		-0.01	1086.64	544.33	1086.65	544.33	2	1.184.0
	55.3	A0QSX3	MSMEG_1634	99.0	LSAEEVANGAGLRPGLLDELEAGATPT	iTRAQ4plex@N-term		0.01	3451.73	863.94	3451.72	863.94	4	346.8
	55.3	A0QSX3	MSMEG_1634	99.0	LSAEEVANGAGLRPGLLDELEAGATPT	iTRAQ4plex@N-term		0.02	3451.74	863.94	3451.72	863.94	4	597.8
	55.3	A0QSX3	MSMEG_1634	99.0	LSAEEVANGAGLRPGLLDELEAGATPT	iTRAQ4plex@N-term; Deamidated(N)@8; Ala->Val@32		-0.01	3480.72	871.19	3480.73	871.19	4	731.1
	55.3	A0QSX3	MSMEG_1634	77.0	ADIVLSGLR	iTRAQ4plex@N-term; Ser->Asp@6		0.00	1114.65	558.33	1114.65	558.33	2	1.180.0
24	53.0	A0R5R7	MSMEG_6286	99.0	DAGIAVTEAGSAFPYR	iTRAQ4plex@N-term		-0.05	1767.84	590.29	1767.89	590.30	3	138.1
	53.0	A0R5R7	MSMEG_6286	99.0	DDLLAQHELQQR	iTRAQ4plex@N-term		0.02	1608.86	537.29	1608.83	537.29	3	873.8
	53.0	A0R5R7	MSMEG_6286	99.0	FALVAEILEDR	iTRAQ4plex@N-term; Dimethyl(R)@11		0.02	1446.84	724.43	1446.82	724.42	2	1.535.9
	53.0	A0R5R7	MSMEG_6286	99.0	FGDADGVR	iTRAQ4plex@N-term	cleaved F-F@N-term	0.03	979.51	490.76	979.48	490.75	2	2.576.9
	53.0	A0R5R7	MSMEG_6286	99.0	GKPSPEQLDLSNGLLSLPGDGADAYR	iTRAQ4plex@N-term; Lys->Gln@2		0.04	2813.43	938.82	2813.40	938.81	3	36.8

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	53.0	A0R5R7	MSMEG_6286	99.0	IAPTFPSLPDVR	iTRAQ4plex@N-term		0.02	1455.85	728.93	1455.82	728.92	2	1.870.2
	53.0	A0R5R7	MSMEG_6286	99.0	ITFAGAGVSFLGASADNIAWYLK	iTRAQ4plex@N-term; Lys->Gln@23		0.04	2515.32	839.45	2515.29	839.44	3	78.3
	53.0	A0R5R7	MSMEG_6286	99.0	DDLLAQHELQQR	iTRAQ4plex@N-term; Dimethyl(R)@12		0.01	1636.88	546.63	1636.87	546.63	3	650.1
	53.0	A0R5R7	MSMEG_6286	99.0	FALVAEILEDR	iTRAQ4plex@N-term		0.01	1418.80	710.41	1418.79	710.40	2	1.178.4
	53.0	A0R5R7	MSMEG_6286	99.0	NYGGVQGLPELR	iTRAQ4plex@N-term; Dimethyl(R)@12		0.01	1473.82	737.92	1473.81	737.91	2	988.0
	53.0	A0R5R7	MSMEG_6286	97.0	NYAELQAK	iTRAQ4plex@N-term; Lys->Gln@8		0.05	1079.59	540.80	1079.54	540.78	2	895.8
	53.0	A0R5R7	MSMEG_6286	92.0	PSLPDVR	No iTRAQ4plex@N-term	cleaved F-P@N-term	-0.03	782.40	392.21	782.43	392.22	2	
	53.0	A0R5R7	MSMEG_6286	88.0	FGDADGVR	No iTRAQ4plex@N-term	cleaved F-F@N-term	0.02	835.40	418.71	835.38	418.70	2	
	53.0	A0R5R7	MSMEG_6286	78.0	GGYFVSLDVWPGTAK	iTRAQ4plex@N-term; iTRAQ4plex(T)@13; Lys->Gln@15		0.00	1883.96	629.00	1883.97	629.00	3	213.6
25	51.0	A0QZ83	MSMEG_3932	99.0	AEVPGIDPAKDIDITVR	iTRAQ4plex@N-term; Lys->Gln@10; iTRAQ4plex(T)@15		0.02	2096.16	699.73	2096.14	699.72	3	412.6
	51.0	A0QZ83	MSMEG_3932	99.0	SLFPEMSDFFAGLPSWASIR	iTRAQ4plex@N-term	cleaved R-P@C-term	0.03	2401.22	801.41	2401.19	801.40	3	85.7
26	50.7	A0QWX9	MSMEG_3102	99.0	EYEASDGVDGR	iTRAQ4plex@N-term		0.01	1340.61	671.31	1340.60	671.31	2	290.1
	50.7	A0QWX9	MSMEG_3102	99.0	GTAYDAQVNELAAR	iTRAQ4plex@N-term		0.04	1621.86	811.94	1621.82	811.92	2	4.005.9
	50.7	A0QWX9	MSMEG_3102	99.0	IGSDEALALR	iTRAQ4plex@N-term		0.02	1187.68	594.85	1187.66	594.84	2	1.474.4
	50.7	A0QWX9	MSMEG_3102	99.0	LAYAAYEEVFGSDR	iTRAQ4plex@N-term		0.00	1733.84	867.93	1733.84	867.93	2	2.917.6
	50.7	A0QWX9	MSMEG_3102	99.0	LQTGNLTELINTR	iTRAQ4plex@N-term		0.02	1615.92	808.97	1615.90	808.96	2	3.786.5
	50.7	A0QWX9	MSMEG_3102	99.0	LVMDAYLEGLEK	iTRAQ4plex@N-term; Lys->Gln@12		0.02	1523.79	762.90	1523.77	762.89	2	57.6
	50.7	A0QWX9	MSMEG_3102	99.0	SVVGVTTNPSIFQAALSK	iTRAQ4plex@N-term; iTRAQ4plex(S)@17; Lys->Gln@18		0.03	2106.18	703.07	2106.16	703.06	3	139.9
	50.7	A0QWX9	MSMEG_3102	99.0	SWQELLDATQGQLDAAK	iTRAQ4plex@N-term; Lys->Arg@17		0.00	2045.03	682.68	2045.03	682.68	3	21.7
	50.7	A0QWX9	MSMEG_3102	99.0	TVTTDDVR	iTRAQ4plex@N-term		0.01	1049.56	525.79	1049.55	525.78	2	140.0
	50.7	A0QWX9	MSMEG_3102	99.0	EYEASDGVDGR	iTRAQ4plex@N-term		0.01	1340.61	671.31	1340.60	671.31	2	178.8
	50.7	A0QWX9	MSMEG_3102	99.0	GADVDATIR	iTRAQ4plex@N-term		0.02	1060.59	531.30	1060.56	531.29	2	6.606.9
	50.7	A0QWX9	MSMEG_3102	99.0	LQTGNLTELINTR	iTRAQ4plex@N-term; Dimethyl(R)@13		0.01	1643.95	822.98	1643.93	822.97	2	831.3
	50.7	A0QWX9	MSMEG_3102	99.0	SWQELLDATQGQLDAAK	iTRAQ4plex@N-term; Lys->Gln@17		0.04	2017.03	673.35	2016.99	673.34	3	206.9
	50.7	A0QWX9	MSMEG_3102	98.0	TVTTDDVR	iTRAQ4plex@N-term		0.01	1049.56	525.79	1049.55	525.78	2	41.2
	50.7	A0QWX9	MSMEG_3102	96.0	GADVDATIR	iTRAQ4plex@N-term		0.01	1060.58	531.30	1060.56	531.29	2	161.4
	50.7	A0QWX9	MSMEG_3102	94.0	TLEAVADHGEITGNTIAGTAASSQETFD	iTRAQ4plex@N-term; iTRAQ4plex(T)@26; Lys->Gln@29		-0.01	3221.55	806.39	3221.56	806.40	4	94.2
	50.7	A0QWX9	MSMEG_3102	93.0	AGVANAR	iTRAQ4plex@N-term		0.00	801.45	401.73	801.46	401.74	2	67.2
	50.7	A0QWX9	MSMEG_3102	91.0	LEKIGSDEALALR	iTRAQ4plex@N-term; User modH on Lys(K)@3; iTRAQ4plex(S)@6	missed K-I@3	-0.04	1945.06	649.36	1945.10	649.37	3	258.8
	50.7	A0QWX9	MSMEG_3102	91.0	GADVDATIR	iTRAQ4plex@N-term; Dimethyl(R)@9		0.01	1088.61	545.31	1088.59	545.30	2	2.596.2
27	50.5	A0QSD0	MSMEG_1435	99.0	AYDHEAIDASAR	iTRAQ4plex@N-term		0.02	1461.72	488.25	1461.70	488.24	3	768.6
	50.5	A0QSD0	MSMEG_1435	99.0	LIDILDPTPK	iTRAQ4plex@N-term; Lys->Gln@10		0.02	1267.73	634.87	1267.71	634.86	2	1.343.6
	50.5	A0QSD0	MSMEG_1435	99.0	TGASVVGPVPLPTEK	iTRAQ4plex@N-term; iTRAQ4plex(T)@13; Lys->Gln@15		0.05	1739.02	580.68	1738.97	580.66	3	604.6
	50.5	A0QSD0	MSMEG_1435	99.0	TVDALMR	iTRAQ4plex@N-term		0.00	948.52	475.27	948.52	475.27	2	80.0
	50.5	A0QSD0	MSMEG_1435	99.0	AYDHEAIDASAR	iTRAQ4plex@N-term; Ala->Val@11		0.02	1489.74	497.59	1489.73	497.58	3	239.7
	50.5	A0QSD0	MSMEG_1435	99.0	AYDHEAIDASAR	No iTRAQ4plex@N-term		0.00	1317.60	440.21	1317.59	440.21	3	26.1
	50.5	A0QSD0	MSMEG_1435	99.0	AYDHEAIDASAR	iTRAQ4plex@N-term		0.06	1461.76	488.26	1461.70	488.24	3	1.893.7
	50.5	A0QSD0	MSMEG_1435	96.0	DHEAIDASAR	iTRAQ4plex@N-term	cleaved Y-D@N-term	0.04	1227.63	410.22	1227.60	410.21	3	70.3
28	49.9	A0QWT3	MSMEG_3055	99.0	AIGEVFDLR	iTRAQ4plex@N-term	cleaved R-P@C-term	-0.01	1162.63	582.32	1162.65	582.33	2	491.0
	49.9	A0QWT3	MSMEG_3055	99.0	AIGEVFDLRPAAIVR	iTRAQ4plex@N-term		-0.04	1769.99	591.00	1770.03	591.02	3	394.2
	49.9	A0QWT3	MSMEG_3055	99.0	DIREKVVNTVLADLGHETLDTSDYR	iTRAQ4plex@N-term; Lys->Met@5	cleaved P-D@N-term; missed R-E@3; misse	0.06	3005.54	752.39	3005.49	752.38	4	667.3
	49.9	A0QWT3	MSMEG_3055	99.0	DLDLLRPIYAPTAAYGHFGR	iTRAQ4plex@N-term		0.06	2389.33	598.34	2389.27	598.32	4	322.7
	49.9	A0QWT3	MSMEG_3055	99.0	FVLGGPMGDAGLTGR	iTRAQ4plex@N-term		0.01	1590.84	796.43	1590.83	796.42	2	931.8
	49.9	A0QWT3	MSMEG_3055	99.0	ICDAISDSVLDALLEQDPK	iTRAQ4plex@N-term; Pyridylethyl(C)@2; Lys->Arg@19		0.03	2321.20	774.74	2321.17	774.73	3	60.9
	49.9	A0QWT3	MSMEG_3055	99.0	IIVDTYGGWAR	iTRAQ4plex@N-term		0.01	1393.76	697.89	1393.75	697.88	2	2.350.2
	49.9	A0QWT3	MSMEG_3055	99.0	LFTSESVTEGHPDK	iTRAQ4plex@N-term; Lys->Gln@14		0.05	1689.85	564.29	1689.80	564.27	3	442.6
	49.9	A0QWT3	MSMEG_3055	99.0	NVVAAGLAER	iTRAQ4plex@N-term		-0.01	1142.64	572.33	1142.65	572.33	2	3.801.6
	49.9	A0QWT3	MSMEG_3055	99.0	TQVTIQYDGTTPVR	iTRAQ4plex@N-term		0.01	1721.92	861.97	1721.91	861.96	2	302.9
	49.9	A0QWT3	MSMEG_3055	99.0	VVNTVLADLGHETLDTSDYR	iTRAQ4plex@N-term		-0.04	2361.16	788.06	2361.19	788.07	3	649.5
	49.9	A0QWT3	MSMEG_3055	99.0	AIGEVFDLRPAAIVR	iTRAQ4plex@N-term		-0.02	1770.01	591.01	1770.03	591.02	3	115.9
	49.9	A0QWT3	MSMEG_3055	99.0	AIGEVFDLRPAAIVR	iTRAQ4plex@N-term; Dimethyl(R)@15		0.02	1798.07	600.37	1798.06	600.36	3	613.9
	49.9	A0QWT3	MSMEG_3055	99.0	FVLGGPMGDAGLTGR	iTRAQ4plex@N-term		0.01	1590.84	796.43	1590.83	796.42	2	1.767.0
	49.9	A0QWT3	MSMEG_3055	99.0	ICDAISDSVLDALLEQDPK	iTRAQ4plex@N-term; Pyridylethyl(C)@2; Lys->Gln@19		0.05	2293.18	765.40	2293.13	765.38	3	80.2
	49.9	A0QWT3	MSMEG_3055	99.0	ICDAISDSVLDALLEQDPK	iTRAQ4plex@N-term; Pyridylethyl(C)@2; Asp->Asn@11; Lys->Gln@19		0.04	2292.18	765.07	2292.14	765.05	3	18.4
	49.9	A0QWT3	MSMEG_3055	99.0	VVNTVLADLGHETLDTSDYR	iTRAQ4plex@N-term		-0.03	2361.16	788.06	2361.19	788.07	3	320.8
	49.9	A0QWT3	MSMEG_3055	99.0	VVNTVLADLGHETLDTSDYR	iTRAQ4plex@N-term; Dimethyl(R)@20		-0.04	2389.19	797.40	2389.22	797.42	3	160.0
	49.9	A0QWT3	MSMEG_3055	97.0	NVVAAGLAER	iTRAQ4plex@N-term		0.03	1142.69	572.35	1142.65	572.33	2	2.755.8

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	49.9	A0QWT3	MSMEG_3055	96.0	SAAYAMR	iTRAQ4plex@N-term		0.02	912.48	457.25	912.46	457.24	2	285.6
	49.9	A0QWT3	MSMEG_3055	96.0	ICDAISDSVLDALLEQDPK	No iTRAQ4plex@N-term; Pyridylethyl(C)@2; Lys->Gln@19		0.01	2149.03	717.35	2149.02	717.35	3	138.8
	49.9	A0QWT3	MSMEG_3055	82.0	TDIELPWEQTNK	iTRAQ4plex@N-term; iTRAQ4plex(T)@10; Lys->Gln@12		0.00	1760.88	587.97	1760.88	587.97	3	481.2
29	49.4	A0QXA3	MSMEG_3227	99.0	AASDVTGHAVGIMADLQGPK	iTRAQ4plex@N-term; Lys->Gln@20		0.02	2081.05	694.69	2081.03	694.69	3	127.0
	49.4	A0QXA3	MSMEG_3227	99.0	ALVAFTQSGDTVR	iTRAQ4plex@N-term		0.03	1507.84	754.93	1507.81	754.91	2	1.605.0
	49.4	A0QXA3	MSMEG_3227	99.0	ALVEAGMDVAR	iTRAQ4plex@N-term		0.01	1274.69	638.35	1274.68	638.35	2	2.164.5
	49.4	A0QXA3	MSMEG_3227	99.0	GDLGVELPLEEVPLVQKR	iTRAQ4plex@N-term; Gln->Met@16; Lys->Leu@17	missed K-R@17	-0.01	2122.17	708.40	2122.18	708.40	3	581.1
	49.4	A0QXA3	MSMEG_3227	99.0	GVISYAAR	iTRAQ4plex@N-term		0.00	979.55	490.78	979.56	490.79	2	2.184.9
	49.4	A0QXA3	MSMEG_3227	99.0	IIQAVEDNSVVVPPLTHVPR	iTRAQ4plex@N-term		-0.07	2326.25	776.42	2326.31	776.44	3	47.8
	49.4	A0QXA3	MSMEG_3227	99.0	IVCTLGPATSTDETVR	iTRAQ4plex@N-term; Pyridylethyl(C)@3		0.01	1911.00	638.01	1910.99	638.00	3	884.4
	49.4	A0QXA3	MSMEG_3227	99.0	LHTPLPVLAFTALPEVR	iTRAQ4plex@N-term		0.00	2017.18	673.40	2017.18	673.40	3	103.0
	49.4	A0QXA3	MSMEG_3227	99.0	QLAQDAAR	iTRAQ4plex@N-term		0.02	1015.58	508.80	1015.55	508.78	2	139.4
	49.4	A0QXA3	MSMEG_3227	99.0	SPADIELVHEVMDR	iTRAQ4plex@N-term		-0.08	1753.80	585.61	1753.88	585.63	3	708.2
	49.4	A0QXA3	MSMEG_3227	99.0	GDLGVELPLEEVPLVQKR	iTRAQ4plex@N-term; Gln->Pro@16; Lys->Phe@17	missed K-R@17	-0.03	2122.15	708.39	2122.18	708.40	3	72.7
	49.4	A0QXA3	MSMEG_3227	98.0	AEASDVANAVLDGADAVMLSGETSVGK	iTRAQ4plex@N-term; Asp->Asn@15; iTRAQ4plex(S)@24; Lys->Gln@27		0.06	2863.47	955.50	2863.41	955.48	3	501.8
30	48.9	A0QZ47	MSMEG_3895	99.0	LYAVELEHYEK	iTRAQ4plex@N-term; Lys->Gln@11		-0.01	1536.75	513.26	1536.76	513.26	3	872.4
	48.9	A0QZ47	MSMEG_3895	99.0	LYSQVSDADSALK	iTRAQ4plex@N-term; Ala->Gly@11; Lys->Arg@13		0.03	1553.81	777.91	1553.78	777.90	2	8.868.3
	48.9	A0QZ47	MSMEG_3895	99.0	STQGNMIAGR	iTRAQ4plex@N-term		0.02	1177.62	589.82	1177.60	589.81	2	192.7
	48.9	A0QZ47	MSMEG_3895	99.0	VAVEALYDAADDDSATGGPDLVR	iTRAQ4plex@N-term; Dimethyl(R)@23		-0.02	2491.20	831.41	2491.22	831.41	3	165.8
	48.9	A0QZ47	MSMEG_3895	99.0	YPGGVLIAGDR	iTRAQ4plex@N-term		0.00	1260.70	631.36	1260.69	631.35	2	3.128.2
	48.9	A0QZ47	MSMEG_3895	99.0	LYAVELEHYEK	iTRAQ4plex@N-term; Lys->Arg@11		0.02	1564.82	522.61	1564.80	522.61	3	570.1
	48.9	A0QZ47	MSMEG_3895	99.0	STQGNMIAGR	iTRAQ4plex@N-term; Oxidation(R)@10		0.02	1193.62	597.82	1193.59	597.80	2	359.9
	48.9	A0QZ47	MSMEG_3895	99.0	VAVEALYDAADDDSATGGPDLVR	iTRAQ4plex@N-term; Oxidation(D)@11; Asp->Asn@12		0.03	2478.23	827.08	2478.20	827.07	3	70.5
	48.9	A0QZ47	MSMEG_3895	99.0	VAVEALYDAADDDSATGGPDLVR	iTRAQ4plex@N-term; Dimethyl(R)@23		-0.02	2491.20	831.41	2491.22	831.41	3	
	48.9	A0QZ47	MSMEG_3895	99.0	VAVEALYDAADDDSATGGPDLVR	iTRAQ4plex@N-term; AMP(Y)@7; Asp->Leu@8		0.04	2790.33	698.59	2790.30	698.58	4	197.3
	48.9	A0QZ47	MSMEG_3895	98.0	VAVEALYDAADDDSATGGPDLVR	iTRAQ4plex@N-term		-0.03	2463.16	822.06	2463.19	822.07	3	
	48.9	A0QZ47	MSMEG_3895	97.0	STQGNMIAGR	iTRAQ4plex@N-term; Oxidation(R)@10		0.02	1193.62	597.82	1193.59	597.80	2	507.8
31	48.7	A0QS97	MSMEG_1399	99.0	IVYGALEQAR	iTRAQ4plex@N-term		0.02	1262.73	632.37	1262.71	632.36	2	1.438.2
	48.7	A0QS97	MSMEG_1399	99.0	VGGATYQVPVEVRPDR	iTRAQ4plex@N-term		-0.03	1885.98	629.67	1886.01	629.68	3	1.556.9
	48.7	A0QS97	MSMEG_1399	96.0	STTLALR	iTRAQ4plex@N-term		0.00	904.54	453.28	904.55	453.28	2	1.692.5
	48.7	A0QS97	MSMEG_1399	88.0	RPLVNDPVYGSQLVTQLVNK	iTRAQ4plex@N-term; Lys->Gln@20		0.07	2383.37	795.46	2383.30	795.44	3	27.2
	48.7	A0QS97	MSMEG_1399	83.0	LANEILDASNGLGASVK	iTRAQ4plex@N-term; iTRAQ4plex(S)@15; Lys->Gln@17		0.02	1959.07	654.03	1959.05	654.02	3	70.5
32	46.9	A0QSE0	MSMEG_1445	99.0	AHDENGEAGIGDR	iTRAQ4plex@N-term		0.01	1483.68	495.57	1483.68	495.57	3	25.0
	46.9	A0QSE0	MSMEG_1445	99.0	AHDENGEAGIGDR	iTRAQ4plex@N-term; Deamidated(N)@5		0.02	1484.68	495.90	1484.66	495.89	3	84.7
	46.9	A0QSE0	MSMEG_1445	92.0	VSLMETR	iTRAQ4plex@N-term	cleaved R-P@C-term	0.00	978.53	490.27	978.53	490.27	2	2.420.9
33	46.9	A0QNF6	MSMEG_0024	99.0	HTIFGEVVDEESQKVVDAIASTPTDF	iTRAQ4plex@N-term; Glu->Gln@11; iTRAQ4plex(S)@12; User modH on Lys(K)@14	missed K-V@14	-0.07	3372.66	844.17	3372.73	844.19	4	50.0
	46.9	A0QNF6	MSMEG_0024	99.0	DYSTENASGGTSGPFYDGAVFHR	iTRAQ4plex@N-term		0.03	2578.18	860.40	2578.15	860.39	3	104.9
	46.9	A0QNF6	MSMEG_0024	99.0	TVNNFVGLAQGTK	iTRAQ4plex@N-term; Lys->Gln@13		0.05	1491.83	746.92	1491.78	746.90	2	687.2
	46.9	A0QNF6	MSMEG_0024	99.0	VIDGFMIQGGDPTGTGR	iTRAQ4plex@N-term		-0.04	1863.89	622.30	1863.93	622.32	3	445.3
	46.9	A0QNF6	MSMEG_0024	99.0	VVDAIASTPTDR	iTRAQ4plex@N-term		0.00	1387.75	694.88	1387.74	694.88	2	5.214.4
	46.9	A0QNF6	MSMEG_0024	99.0	TVNNFVGLAQGTK	iTRAQ4plex@N-term; iTRAQ4plex(T)@12; Lys->Gln@13		0.05	1635.94	546.32	1635.88	546.30	3	1.273.9
	46.9	A0QNF6	MSMEG_0024	95.0	HTIFGEVVDEESQKVVDAIASTPTDF	iTRAQ4plex@N-term; iTRAQ4plex(S)@12; User modH on Lys(K)@14	missed K-V@14	-0.05	3373.66	844.42	3373.71	844.44	4	87.8
34	46.7	A0QUZ0	MSMEG_2388	99.0	GSVLVAGPDFGTGSSR	iTRAQ4plex@N-term		0.00	1649.85	825.93	1649.85	825.93	2	215.2
	46.7	A0QUZ0	MSMEG_2388	99.0	LLEGLDDIGLTLR	iTRAQ4plex@N-term		0.02	1570.92	786.47	1570.91	786.46	2	1.467.6
	46.7	A0QUZ0	MSMEG_2388	99.0	MEAFTTHTGIGVPLR	iTRAQ4plex@N-term		0.00	1772.94	591.99	1772.94	591.99	3	147.0
	46.7	A0QUZ0	MSMEG_2388	99.0	LLEGLDDIGLTLR	iTRAQ4plex@N-term		-0.01	1570.90	786.45	1570.91	786.46	2	209.1
	46.7	A0QUZ0	MSMEG_2388	75.0	FADIFR	iTRAQ4plex@N-term		-0.01	911.49	456.75	911.50	456.76	2	431.9
35	46.7	A0R7F9	MSMEG_6897	99.0	AEPATVSELDR	iTRAQ4plex@N-term		0.01	1330.69	666.35	1330.69	666.35	2	2.687.9
	46.7	A0R7F9	MSMEG_6897	99.0	QLNLNESVLR	iTRAQ4plex@N-term		0.00	1328.75	665.38	1328.75	665.38	2	273.8
	46.7	A0R7F9	MSMEG_6897	99.0	TVAPSLETFLNVIR	iTRAQ4plex@N-term		0.01	1702.98	852.50	1702.97	852.49	2	500.6
	46.7	A0R7F9	MSMEG_6897	99.0	QLNLNESVLR	iTRAQ4plex@N-term		-0.01	1328.75	665.38	1328.75	665.38	2	2.800.9
36	45.5	A0QSG1	MSMEG_1467	99.0	LINGAINDLALITGQKPEVR	iTRAQ4plex@N-term; Deamidated(N)@3; iTRAQ4plex(T)@13; Lys->Gln@16		0.03	2423.39	808.80	2423.36	808.79	3	1.110.7
	45.5	A0QSG1	MSMEG_1467	99.0	LINGAINDLALITGQKPEVRR	iTRAQ4plex@N-term; Lys->Gly@16; Pro->Arg@17	missed R-R@20	-0.01	2422.38	606.60	2422.39	606.60	4	71.5

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	45.5	A0QSG1	MSMEG_1467	99.0	VVVNMGVGDAAR	iTRAQ4plex@N-term		-0.01	1330.70	666.36	1330.71	666.36	2	3.338.8
	45.5	A0QSG1	MSMEG_1467	99.0	LINGAINDLALITGQKPEVR	iTRAQ4plex@N-term; Deamidated(N)@3; iTRAQ4plex(T)@13; Lys->Gln@16		0.02	2423.39	606.85	2423.36	606.85	4	64.1
	45.5	A0QSG1	MSMEG_1467	99.0	LINGAINDLALITGQKPEVR	iTRAQ4plex@N-term; Deamidated(N)@3; iTRAQ4plex(T)@13; Lys->Gln@16		0.04	2423.40	606.86	2423.36	606.85	4	597.5
	45.5	A0QSG1	MSMEG_1467	99.0	LINGAINDLALITGQKPEVR	iTRAQ4plex@N-term; Deamidated(N)@3; iTRAQ4plex(T)@13; Lys->Gln@16		0.02	2423.38	606.85	2423.36	606.85	4	18.5
	45.5	A0QSG1	MSMEG_1467	99.0	LINGAINDLALITGQKPEVR	iTRAQ4plex@N-term; Deamidated(N)@3; Lys->Gln@16		0.05	2279.31	760.78	2279.26	760.76	3	47.8
	45.5	A0QSG1	MSMEG_1467	98.0	LISIALPR	iTRAQ4plex@N-term		-0.04	1025.63	513.82	1025.67	513.84	2	1.234.1
37	44.9	A0R5R5	MSMEG_6284	99.0	EQATWAQKAIAQEGLTDLAEVR	iTRAQ4plex@N-term; iTRAQ4plex(T)@4; User modH on Lys(K)@8; Dimethyl(R)@22	missed K-A@8	-0.03	2986.56	747.65	2986.58	747.65	4	68.5
	44.9	A0R5R5	MSMEG_6284	99.0	AIAQEGLTDLAEVR	iTRAQ4plex@N-term		-0.03	1628.86	815.44	1628.89	815.45	2	773.0
	44.9	A0R5R5	MSMEG_6284	99.0	AYVSGDLEPHGVHPGDPYPLLR	iTRAQ4plex@N-term		-0.02	2532.27	634.07	2532.29	634.08	4	366.7
	44.9	A0R5R5	MSMEG_6284	99.0	IITEAQDVGLEVIHEENLR	iTRAQ4plex@N-term		-0.04	2321.20	774.74	2321.23	774.75	3	525.3
	44.9	A0R5R5	MSMEG_6284	99.0	NLVEHWDEAVEEVGLPTAK	iTRAQ4plex@N-term; iTRAQ4plex(T)@17; Lys->Gln@19		0.02	2423.24	606.82	2423.22	606.81	4	19.6
	44.9	A0R5R5	MSMEG_6284	99.0	SAPSAGGFIDR	iTRAQ4plex@N-term		0.01	1220.64	611.33	1220.63	611.32	2	2.726.0
	44.9	A0R5R5	MSMEG_6284	99.0	VWGLYMAGSR	iTRAQ4plex@N-term		-0.03	1282.63	642.32	1282.66	642.34	2	587.4
	44.9	A0R5R5	MSMEG_6284	99.0	YVFPDGELTGSGR	iTRAQ4plex@N-term		0.00	1540.76	771.39	1540.76	771.39	2	2.590.6
	44.9	A0R5R5	MSMEG_6284	99.0	IITEAQDVGLEVIHEENLR	iTRAQ4plex@N-term		-0.03	2321.20	774.74	2321.23	774.75	3	162.8
	44.9	A0R5R5	MSMEG_6284	99.0	IITEAQDVGLEVIHEENLR	iTRAQ4plex@N-term; Glu->Arg@16; Deamidated(N)@17		0.02	2349.29	784.11	2349.28	784.10	3	26.0
	44.9	A0R5R5	MSMEG_6284	98.0	DGGLPLRPWWSA	iTRAQ4plex@N-term		0.01	1497.79	749.90	1497.79	749.90	2	312.0
	44.9	A0R5R5	MSMEG_6284	98.0	GTTYLATAPGDLGLAR	iTRAQ4plex@N-term		-0.03	1719.90	574.31	1719.93	574.32	3	27.2
	44.9	A0R5R5	MSMEG_6284	98.0	TEAQDVGLEVIHEENLR	iTRAQ4plex@N-term; Phospho(T)@1; Deamidated(Q)@4	cleaved I-T@N-term	0.20	2176.22	726.41	2176.02	726.35	3	
	44.9	A0R5R5	MSMEG_6284	92.0	EQATWAQKAIAQEGLTDLAEVR	No iTRAQ4plex@N-term; Deamidated(Q)@2; User modH on Lys(K)@8	missed K-A@8	-0.01	2671.32	1336.67	2671.33	1336.67	2	1.022.9
38	44.8	A0QSG0	MSMEG_1466	99.0	GASSGGIVTQEAPIHVSNVMVVDSDGK	iTRAQ4plex@N-term; Lys->Gln@27; iTRAQ4plex(T)@29		0.10	3295.77	824.95	3295.67	824.93	4	251.3
	44.8	A0QSG0	MSMEG_1466	99.0	VLVEGVNR	iTRAQ4plex@N-term		0.01	1028.62	515.31	1028.61	515.31	2	3.155.6
	44.8	A0QSG0	MSMEG_1466	99.0	GASSGGIVTQEAPIHVSNVMVVDSDGK	iTRAQ4plex@N-term; Lys->Gln@27		0.11	3151.68	788.93	3151.57	788.90	4	70.5
39	44.7	A0R3B8	MSMEG_5415	99.0	AAAESAGLPLFR	iTRAQ4plex@N-term		0.03	1345.77	673.89	1345.75	673.88	2	308.3
	44.7	A0R3B8	MSMEG_5415	99.0	AAVPSGASTGEHEAVELR	iTRAQ4plex@N-term		0.03	1924.01	642.34	1923.98	642.33	3	1.378.0
	44.7	A0R3B8	MSMEG_5415	99.0	GNPTVEVEVALTDGTFAR	iTRAQ4plex@N-term		-0.01	2019.03	674.02	2019.04	674.02	3	10.9
	44.7	A0R3B8	MSMEG_5415	99.0	IQLVGDDLFVTNPER	iTRAQ4plex@N-term		-0.02	1858.97	930.49	1858.99	930.50	2	1.969.5
	44.7	A0R3B8	MSMEG_5415	99.0	VNQIGTLTETLDAVSLAHNSGYR	iTRAQ4plex@N-term		-0.03	2602.31	868.45	2602.35	868.46	3	75.9
	44.7	A0R3B8	MSMEG_5415	99.0	YAGDLAFPR	iTRAQ4plex@N-term		-0.01	1152.60	577.31	1152.60	577.31	2	1.154.2
	44.7	A0R3B8	MSMEG_5415	99.0	AAAESAGLPLFR	iTRAQ4plex@N-term		0.02	1345.77	673.89	1345.75	673.88	2	572.7
	44.7	A0R3B8	MSMEG_5415	99.0	YAGDLAFPR	iTRAQ4plex@N-term		-0.02	1152.59	577.30	1152.60	577.31	2	2.896.5
40	44.5	A0R1Y7	MSMEG_4920	99.0	AGEFDVIVAGGQESMSQAPHLLPKSR	iTRAQ4plex@N-term; Lys->Ala@24; Arg->Orn(R)@26	missed K-S@24	-0.02	2768.37	693.10	2768.39	693.11	4	73.9
	44.5	A0R1Y7	MSMEG_4920	99.0	DFSGTDLGAIAIR	iTRAQ4plex@N-term; Dimethyl(R)@13		0.00	1506.81	754.41	1506.82	754.42	2	2.102.6
	44.5	A0R1Y7	MSMEG_4920	99.0	GDPIEFAEDEGIR	iTRAQ4plex@N-term		0.03	1590.80	796.40	1590.76	796.39	2	1.177.6
	44.5	A0R1Y7	MSMEG_4920	99.0	IALHAALELAR	iTRAQ4plex@N-term		0.00	1320.80	441.27	1320.80	441.27	3	84.7
	44.5	A0R1Y7	MSMEG_4920	99.0	MCLSGIDAIALADQLIR	iTRAQ4plex@N-term; Pyridylethyl(C)@2		-0.01	2051.09	684.70	2051.10	684.71	3	65.1
	44.5	A0R1Y7	MSMEG_4920	99.0	RKGDPIEFAEDEGIR	No iTRAQ4plex@N-term; Lys->Arg@2	cleaved Q-R@N-term; missed R-K@1; misse	0.04	1758.90	587.31	1758.86	587.30	3	129.8
	44.5	A0R1Y7	MSMEG_4920	99.0	TTSVIVAGAR	iTRAQ4plex@N-term	cleaved M-T@N-term	-0.01	1117.65	559.83	1117.66	559.84	2	1.929.7
	44.5	A0R1Y7	MSMEG_4920	99.0	VNVNGGAIAIGHPIGMSGAR	iTRAQ4plex@N-term		-0.01	2034.08	679.03	2034.09	679.04	3	719.2
	44.5	A0R1Y7	MSMEG_4920	99.0	YGDATLVDHLAYDGLHDVFTDQPMGAL	iTRAQ4plex@N-term		0.04	3591.75	898.94	3591.71	898.93	4	209.1
	44.5	A0R1Y7	MSMEG_4920	99.0	DFSGTDLGAIAIR	iTRAQ4plex@N-term		-0.01	1478.77	740.39	1478.79	740.40	2	3.954.3
	44.5	A0R1Y7	MSMEG_4920	99.0	GDPIEFAEDEGIR	iTRAQ4plex@N-term; Dimethyl(R)@13		0.02	1618.82	810.42	1618.80	810.41	2	372.5
	44.5	A0R1Y7	MSMEG_4920	99.0	VNVNGGAIAIGHPIGMSGAR	iTRAQ4plex@N-term; Deamidated(N)@4		0.02	2035.10	679.37	2035.08	679.37	3	1.979.3
	44.5	A0R1Y7	MSMEG_4920	99.0	VNVNGGAIAIGHPIGMSGAR	iTRAQ4plex@N-term; Deamidated(N)@4		0.03	2035.10	679.38	2035.08	679.37	3	322.7
	44.5	A0R1Y7	MSMEG_4920	99.0	YGDATLVDHLAYDGLHDVFTDQPMGAL	iTRAQ4plex@N-term		0.08	3591.79	898.95	3591.71	898.93	4	49.9
	44.5	A0R1Y7	MSMEG_4920	97.0	YGDATLVDHLAYDGLHDVFTDQPMGAL	No iTRAQ4plex@N-term		-0.05	3447.55	862.90	3447.60	862.91	4	44.6
	44.5	A0R1Y7	MSMEG_4920	95.0	AEQDEYAAQSHQK	iTRAQ4plex@N-term; Lys->Gln@13		0.06	1647.78	550.27	1647.72	550.25	3	
	44.5	A0R1Y7	MSMEG_4920	81.0	YGDATLVDHLAYDGLHDVFTDQPMGAL	No iTRAQ4plex@N-term		-0.06	3447.54	862.89	3447.60	862.91	4	34.6
41	44.2	A0R200	MSMEG_4936	99.0	DEQGQDVLLFIDNIFR	iTRAQ4plex@N-term		0.00	2065.06	689.36	2065.06	689.36	3	64.0
	44.2	A0R200	MSMEG_4936	99.0	DTALVFGQMDEPPGTR	iTRAQ4plex@N-term		0.00	1876.91	626.64	1876.91	626.64	3	79.0
	44.2	A0R200	MSMEG_4936	99.0	GIFPAVDPLASSSTILDPAIVGDEHYR	iTRAQ4plex@N-term		-0.03	2983.51	746.89	2983.54	746.89	4	34.8
	44.2	A0R200	MSMEG_4936	99.0	ITGPVVDVEFPR	iTRAQ4plex@N-term		0.01	1471.82	736.92	1471.82	736.92	2	1.747.2
	44.2	A0R200	MSMEG_4936	99.0	NFGGTSVFAGVGER	iTRAQ4plex@N-term		0.00	1540.77	771.39	1540.78	771.40	2	2.553.5
	44.2	A0R200	MSMEG_4936	99.0	TLTLEVAQHLGDSLVR	No iTRAQ4plex@N-term		-0.05	1750.91	584.64	1750.96	584.66	3	34.7
	44.2	A0R200	MSMEG_4936	99.0	TVLIQEMINR	iTRAQ4plex@N-term		-0.01	1359.76	680.89	1359.77	680.89	2	2.237.6
	44.2	A0R200	MSMEG_4936	99.0	VALSALTMAEFFR	iTRAQ4plex@N-term		0.01	1598.88	800.45	1598.86	800.44	2	1.306.6

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	44.2	A0R200	MSMEG_4936	99.0	VVDLLTPYVR	iTRAQ4plex@N-term		0.00	1317.78	659.90	1317.78	659.90	2	3.596.8
	44.2	A0R200	MSMEG_4936	99.0	GIFPAVDPLASSSTILDPAIVGDEHYR	iTRAQ4plex@N-term		0.00	2983.54	746.89	2983.54	746.89	4	
	44.2	A0R200	MSMEG_4936	96.0	GSVPELFNALHAEITFGALAK	iTRAQ4plex@N-term; iTRAQ4plex(T)@15; Lys->Gln@21		0.06	2472.39	825.14	2472.33	825.12	3	252.5
	44.2	A0R200	MSMEG_4936	92.0	VAQEVIR	iTRAQ4plex@N-term		0.02	957.59	479.80	957.57	479.79	2	1.985.1
	44.2	A0R200	MSMEG_4936	83.0	TLTLEVAQHLGDSLVR	iTRAQ4plex@N-term; Ser->Asn@13; Deamidated(R)@16		0.06	1923.11	642.05	1923.05	642.03	3	28.2
42	44.2	A0R566	MSMEG_6082	99.0	ATLSALDEGEVPSGFVR	iTRAQ4plex@N-term		-0.03	1890.95	631.32	1890.98	631.33	3	73.3
	44.2	A0R566	MSMEG_6082	99.0	STAIAQGLAAGTQAIVGTTYHLADGR	iTRAQ4plex@N-term		-0.05	2686.37	896.46	2686.42	896.48	3	95.4
43	44.1	A0QUX7	MSMEG_2373	99.0	EIAQSGVVSVSR	iTRAQ4plex@N-term		0.00	1374.76	688.39	1374.76	688.39	2	339.0
	44.1	A0QUX7	MSMEG_2373	99.0	IVEQEEDNSVSR	iTRAQ4plex@N-term		0.00	1547.76	774.89	1547.75	774.88	2	3.759.4
	44.1	A0QUX7	MSMEG_2373	99.0	VLEPYGIR	iTRAQ4plex@N-term		0.01	1089.64	545.83	1089.63	545.82	2	1.306.2
	44.1	A0QUX7	MSMEG_2373	99.0	EIAQSGVVSVSR	iTRAQ4plex@N-term		0.01	1374.76	688.39	1374.76	688.39	2	680.2
	44.1	A0QUX7	MSMEG_2373	99.0	GQIIEAVNLFR	iTRAQ4plex@N-term		0.02	1402.82	702.42	1402.81	702.41	2	1.304.3
	44.1	A0QUX7	MSMEG_2373	94.0	VSSLFSR	iTRAQ4plex@N-term		0.00	938.53	470.27	938.53	470.27	2	3.301.2
44	43.6	A0QRM0	MSMEG_1165	99.0	ADSSFDVVSK	iTRAQ4plex@N-term; iTRAQ4plex(S)@9; Lys->Gln@10	cleaved M-A@N-term	0.05	1341.72	671.87	1341.67	671.84	2	3.501.7
	43.6	A0QRM0	MSMEG_1165	99.0	AQIQGDEIR	iTRAQ4plex@N-term		0.05	1172.67	587.34	1172.63	587.32	2	1.318.7
	43.6	A0QRM0	MSMEG_1165	99.0	GADLDVALQFVNYR	iTRAQ4plex@N-term		0.02	1723.92	575.65	1723.90	575.64	3	8.7
45	43.5	A0R2V4	MSMEG_5246	99.0	DFPVAPHSSR	iTRAQ4plex@N-term		0.00	1255.65	419.56	1255.64	419.55	3	183.2
	43.5	A0R2V4	MSMEG_5246	99.0	IGLAPALDEVPPPTPR	iTRAQ4plex@N-term		-0.03	1785.98	596.34	1786.01	596.34	3	45.2
	43.5	A0R2V4	MSMEG_5246	99.0	LDVATLANAVQLAAR	iTRAQ4plex@N-term		-0.03	1668.93	835.47	1668.96	835.49	2	695.5
	43.5	A0R2V4	MSMEG_5246	99.0	LIAEDGELK	iTRAQ4plex@N-term; Lys->Gln@9		0.05	1130.65	566.33	1130.59	566.30	2	2.515.9
	43.5	A0R2V4	MSMEG_5246	99.0	LPMSAYVDWDAFETLLR	iTRAQ4plex@N-term; Dimethyl(R)@17		0.05	2198.17	733.73	2198.12	733.71	3	59.4
	43.5	A0R2V4	MSMEG_5246	99.0	RPALNNDAATIVVLSTDGYSR	iTRAQ4plex@N-term		-0.04	2376.21	793.08	2376.25	793.09	3	12.0
	43.5	A0R2V4	MSMEG_5246	99.0	LDVATLANAVQLAAR	iTRAQ4plex@N-term; Dimethyl(R)@15		0.03	1697.02	849.52	1697.00	849.51	2	1.068.9
	43.5	A0R2V4	MSMEG_5246	99.0	LDVATLANAVQLAAR	iTRAQ4plex@N-term		0.01	1668.98	557.33	1668.96	557.33	3	
46	42.4	A0R461	MSMEG_5715	99.0	FGLFIPQGWR	iTRAQ4plex@N-term		0.01	1363.77	682.89	1363.75	682.88	2	98.8
	42.4	A0R461	MSMEG_5715	99.0	LDEGVQIMR	iTRAQ4plex@N-term		0.00	1203.64	602.83	1203.64	602.83	2	1.585.3
	42.4	A0R461	MSMEG_5715	99.0	TVGTDFDAIVR	iTRAQ4plex@N-term		0.01	1336.72	669.37	1336.71	669.36	2	814.8
	42.4	A0R461	MSMEG_5715	99.0	VAATTDVISGGR	iTRAQ4plex@N-term		0.00	1289.70	645.86	1289.71	645.86	2	288.4
	42.4	A0R461	MSMEG_5715	96.0	FGLFIPQGWR	iTRAQ4plex@N-term		0.01	1363.76	682.89	1363.75	682.88	2	176.6
47	42.1	A0QUX8	MSMEG_2374	99.0	ANAEHPIEVTGK	iTRAQ4plex@N-term; Lys->Gln@12		0.04	1408.74	470.59	1408.71	470.58	3	59.8
	42.1	A0QUX8	MSMEG_2374	99.0	APENVTVGMVAPK	iTRAQ4plex@N-term; Lys->Gln@13		0.05	1455.80	728.91	1455.75	728.88	2	1.115.9
	42.1	A0QUX8	MSMEG_2374	99.0	DLMSWVDRPITETA	iTRAQ4plex@N-term		0.00	1776.88	889.45	1776.88	889.45	2	1.216.6
	42.1	A0QUX8	MSMEG_2374	99.0	GEGQALALSYAAAIGGAR	iTRAQ4plex@N-term; Ala->Val@17		0.00	1847.00	616.67	1847.00	616.67	3	20.7
	42.1	A0QUX8	MSMEG_2374	99.0	LIVDLIYEGGIAR	iTRAQ4plex@N-term		-0.01	1574.90	788.46	1574.92	788.46	2	125.7
	42.1	A0QUX8	MSMEG_2374	99.0	LVANVEGGNK	iTRAQ4plex@N-term; Lys->Gln@10		0.05	1143.65	572.83	1143.60	572.81	2	1.088.1
	42.1	A0QUX8	MSMEG_2374	99.0	VAVIGYGSQGHAH	iTRAQ4plex@N-term	cleaved H-S@C-term	0.01	1438.75	480.59	1438.74	480.59	3	198.9
	42.1	A0QUX8	MSMEG_2374	99.0	VAVIGYGSQGHAHSLSLR	No iTRAQ4plex@N-term		-0.02	1850.96	463.75	1850.98	463.75	4	81.9
	42.1	A0QUX8	MSMEG_2374	99.0	AVEMFYDDDADLSIIQGR	iTRAQ4plex@N-term	cleaved M-A@N-term	0.03	2201.07	734.70	2201.04	734.69	3	44.6
	42.1	A0QUX8	MSMEG_2374	99.0	LIVDLIYEGGIAR	iTRAQ4plex@N-term		0.01	1574.92	788.47	1574.92	788.46	2	316.1
48	41.9	A0R0S1	MSMEG_4487	99.0	AAIADLLNETEGFR	iTRAQ4plex@N-term		-0.02	1662.85	832.43	1662.87	832.44	2	1.438.0
	41.9	A0R0S1	MSMEG_4487	99.0	SAQELHDELR	iTRAQ4plex@N-term		0.00	1340.68	447.90	1340.68	447.90	3	319.8
	41.9	A0R0S1	MSMEG_4487	99.0	TDTGESVYR	iTRAQ4plex@N-term		0.01	1170.57	586.29	1170.56	586.29	2	88.3
	41.9	A0R0S1	MSMEG_4487	99.0	AAIADLLNETEGFR	iTRAQ4plex@N-term; Dimethyl(R)@14		-0.03	1690.87	846.44	1690.90	846.46	2	242.3
49	41.9	A0QZ34	MSMEG_3881	99.0	DVLAAEGLAEAFVHR	iTRAQ4plex@N-term		-0.01	1740.92	581.31	1740.93	581.32	3	233.7
	41.9	A0QZ34	MSMEG_3881	99.0	GMAFSVEPGVYFPGQWGAR	iTRAQ4plex@N-term		0.06	2199.13	734.05	2199.07	734.03	3	123.2
	41.9	A0QZ34	MSMEG_3881	99.0	TGHGIGLSVHEEPYIVAGNNLPLER	iTRAQ4plex@N-term		0.02	2815.50	704.88	2815.47	704.88	4	30.4
	41.9	A0QZ34	MSMEG_3881	99.0	YALLQQAQQAAVAAVRPGVTAEQVDAA	iTRAQ4plex@N-term		-0.03	3109.64	778.42	3109.68	778.43	4	251.2
	41.9	A0QZ34	MSMEG_3881	91.0	AQTFER	iTRAQ4plex@N-term		0.00	894.47	448.24	894.47	448.24	2	135.4
50	41.6	A0QQU1	MSMEG_0877	99.0	AGADAVVATPPFYVAPHADEVIR	iTRAQ4plex@N-term		0.04	2509.35	837.46	2509.31	837.44	3	27.0
	41.6	A0QQU1	MSMEG_0877	99.0	AHLAANADTGLR	iTRAQ4plex@N-term		-0.01	1352.72	451.91	1352.73	451.92	3	177.7
	41.6	A0QQU1	MSMEG_0877	99.0	CADPLLPLESSEIDAVR	iTRAQ4plex@N-term; Pyridylethyl(C)@1		0.01	2076.08	693.03	2076.07	693.03	3	248.6
	41.6	A0QQU1	MSMEG_0877	99.0	DSSGDLDGFR	iTRAQ4plex@N-term		-0.01	1211.54	606.78	1211.55	606.78	2	567.0

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	41.6	A0QQU1	MSMEG_0877	99.0	IFAIVDVADR	iTRAQ4plex@N-term		0.02	1261.73	631.87	1261.72	631.86	2	1.530.4
	41.6	A0QQU1	MSMEG_0877	99.0	LIAAAVDVPVVAYDIPSATHSPLTR	iTRAQ4plex@N-term		-0.04	2719.46	680.87	2719.50	680.88	4	91.3
	41.6	A0QQU1	MSMEG_0877	99.0	AIQVAAGAASGQVPVLGGVIDTGTAR	iTRAQ4plex@N-term		0.01	2522.40	841.81	2522.39	841.81	3	172.7
51	40.9	A0QTK6	MSMEG_1878	99.0	DPLAGLDVSR	iTRAQ4plex@N-term		-0.01	1185.63	593.82	1185.65	593.83	2	3.228.5
	40.9	A0QTK6	MSMEG_1878	99.0	GEACADSFYTAFESAVQK	iTRAQ4plex@N-term; Pyridylethyl(C)@4; Lys->Gln@18		-0.01	2171.95	724.99	2171.96	724.99	3	694.7
	40.9	A0QTK6	MSMEG_1878	99.0	NDGVAEHEPGR	iTRAQ4plex@N-term	cleaved Y-N@N-term	0.01	1323.64	442.22	1323.63	442.22	3	
	40.9	A0QTK6	MSMEG_1878	99.0	NVEVPDHFR	iTRAQ4plex@N-term		0.00	1255.64	419.56	1255.64	419.55	3	257.5
	40.9	A0QTK6	MSMEG_1878	99.0	TIYLFDVELDHER	iTRAQ4plex@N-term		-0.04	1792.87	598.63	1792.91	598.64	3	176.8
	40.9	A0QTK6	MSMEG_1878	99.0	TMVVEDDR	iTRAQ4plex@N-term		-0.01	1107.53	554.77	1107.54	554.77	2	380.9
	40.9	A0QTK6	MSMEG_1878	99.0	TPVSLAEATAK	iTRAQ4plex@N-term; Lys->Gln@11		0.03	1230.69	616.35	1230.66	616.34	2	7.200.1
	40.9	A0QTK6	MSMEG_1878	99.0	YNDGVAEHEPGR	iTRAQ4plex@N-term		0.01	1486.70	496.57	1486.69	496.57	3	789.9
	40.9	A0QTK6	MSMEG_1878	99.0	DPLAGLDVSR	iTRAQ4plex@N-term		-0.01	1185.64	593.83	1185.65	593.83	2	1.424.3
	40.9	A0QTK6	MSMEG_1878	99.0	DPLAGLDVSR	iTRAQ4plex@N-term; Ser->Asp@9		0.04	1213.68	607.85	1213.64	607.83	2	539.4
	40.9	A0QTK6	MSMEG_1878	99.0	YNDGVAEHEPGR	iTRAQ4plex@N-term		0.03	1486.72	496.58	1486.69	496.57	3	70.5
	40.9	A0QTK6	MSMEG_1878	99.0	YNDGVAEHEPGR	iTRAQ4plex@N-term		0.01	1486.70	496.57	1486.69	496.57	3	45.7
	40.9	A0QTK6	MSMEG_1878	86.0	TIYLFDVELDHER	iTRAQ4plex@N-term; Dimethyl(R)@13		-0.02	1820.92	607.98	1820.94	607.99	3	39.1
	40.9	A0QTK6	MSMEG_1878	76.0	YNDGVAEHEPGR	No iTRAQ4plex@N-term		0.01	1342.60	448.54	1342.59	448.54	3	10.9
52	40.8	A0QZ58	MSMEG_3906	99.0	AVGPEGSVTSYEVR	iTRAQ4plex@N-term		-0.01	1593.80	797.91	1593.81	797.91	2	1.384.0
	40.8	A0QZ58	MSMEG_3906	99.0	DAAQIVHEGDIFPGAR	iTRAQ4plex@N-term		-0.03	1838.91	613.98	1838.94	613.99	3	879.3
	40.8	A0QZ58	MSMEG_3906	99.0	LAPGAVAPMPLR	iTRAQ4plex@N-term		0.02	1335.80	668.91	1335.78	668.90	2	1.916.3
	40.8	A0QZ58	MSMEG_3906	99.0	NVVTFFGERPANWNLVIGDVSDYDGPE	iTRAQ4plex@N-term		-0.07	3555.62	889.91	3555.69	889.93	4	73.4
	40.8	A0QZ58	MSMEG_3906	99.0	VLEAGAGSGALTCSLLR	iTRAQ4plex@N-term; Pyridylethyl(C)@13		-0.02	1865.99	623.01	1866.02	623.01	3	355.1
	40.8	A0QZ58	MSMEG_3906	98.0	NVVTFFGER	iTRAQ4plex@N-term	cleaved R-P@C-term	-0.01	1211.63	606.82	1211.64	606.83	2	550.9
	40.8	A0QZ58	MSMEG_3906	88.0	NVVTFFGER	iTRAQ4plex@N-term	cleaved R-P@C-term	-0.02	1211.62	606.82	1211.64	606.83	2	1.560.8
53	40.8	A0R6Q7	MSMEG_6636	99.0	AIWNVVNWQDVQVR	iTRAQ4plex@N-term		-0.03	1869.96	624.33	1870.00	624.34	3	100.4
	40.8	A0R6Q7	MSMEG_6636	85.0	GVNDAIAK	iTRAQ4plex@N-term; Lys->Gln@8		0.05	930.54	466.28	930.49	466.25	2	104.1
54	39.7	A0QY23	MSMEG_3507	99.0	IITSPSFGGDR	iTRAQ4plex@N-term		0.01	1292.70	647.36	1292.68	647.35	2	4.128.0
	39.7	A0QY23	MSMEG_3507	99.0	LYGVEESAYSNEDEMFDLIHQMR	iTRAQ4plex@N-term		0.00	2919.32	974.11	2919.32	974.11	3	230.7
	39.7	A0QY23	MSMEG_3507	99.0	MTSGQGFIAALDQSGGSTPK	iTRAQ4plex@N-term; Lys->Gln@20		0.03	2096.03	699.68	2096.00	699.67	3	244.5
	39.7	A0QY23	MSMEG_3507	99.0	VALSGGYSR	iTRAQ4plex@N-term	cleaved V-V@N-term	0.01	1052.58	527.30	1052.57	527.29	2	1.311.0
	39.7	A0QY23	MSMEG_3507	99.0	VLAAILFEQTMDR	iTRAQ4plex@N-term		-0.02	1649.87	825.94	1649.89	825.95	2	192.9
	39.7	A0QY23	MSMEG_3507	99.0	VVALSGGYSR	iTRAQ4plex@N-term		0.03	1151.68	576.85	1151.64	576.83	2	4.659.7
	39.7	A0QY23	MSMEG_3507	99.0	MTSGQGFIAALDQSGGSTPK	iTRAQ4plex@N-term; iTRAQ4plex(T)@18; Lys->Gln@20		0.04	2240.14	747.72	2240.10	747.71	3	217.2
55	39.7	A0QSG6	MSMEG_1472	99.0	ESEALAAAAAR	iTRAQ4plex@N-term		0.01	1202.64	602.33	1202.64	602.33	2	3.420.1
	39.7	A0QSG6	MSMEG_1472	99.0	LLQRPEEVAAR	iTRAQ4plex@N-term		0.03	1424.85	475.96	1424.82	475.95	3	991.5
	39.7	A0QSG6	MSMEG_1472	99.0	SLGSDNAINVVHATVAALK	iTRAQ4plex@N-term; iTRAQ4plex(T)@14; Lys->Gln@19		0.02	2167.20	723.41	2167.18	723.40	3	257.8
	39.7	A0QSG6	MSMEG_1472	99.0	SLGSDNAINVVHATVAALK	iTRAQ4plex@N-term; Lys->Gln@19		-0.01	2023.07	675.37	2023.08	675.37	3	74.8
	39.7	A0QSG6	MSMEG_1472	96.0	GLPIEDVAPAGMLKAR	iTRAQ4plex@N-term; Lys->Ser@14; Arg->Orn(R)@16	missed K-A@14	0.05	1697.96	849.99	1697.91	849.96	2	230.6
56	39.5	A0QSZ1	MSMEG_1652	99.0	DLGSAAAPFNAFLIAQGLETLSLR	iTRAQ4plex@N-term		-0.01	2618.41	873.81	2618.42	873.81	3	227.7
	39.5	A0QSZ1	MSMEG_1652	99.0	LAVGLEGIDDIIADLEQGFAAAR	iTRAQ4plex@N-term	cleaved R-P@C-term	0.04	2500.37	834.47	2500.33	834.45	3	32.6
	39.5	A0QSZ1	MSMEG_1652	99.0	SLVIHPASTTHQQLSPEEQLSTGVTPGL	iTRAQ4plex@N-term		-0.05	3325.73	832.44	3325.78	832.45	4	106.8
57	39.4	A0QSG5	MSMEG_1471	99.0	AAGVETVVFDR	iTRAQ4plex@N-term		0.01	1306.71	654.36	1306.70	654.36	2	1.155.1
58	39.2	A0QQC8	MSMEG_0709	99.0	ALEGTDISAIK	iTRAQ4plex@N-term; Lys->Gln@11		0.04	1260.71	631.36	1260.67	631.34	2	1.363.4
	39.2	A0QQC8	MSMEG_0709	99.0	ATSGDNHLGGDDWDDR	iTRAQ4plex@N-term		0.03	1873.83	625.62	1873.79	625.61	3	394.0
	39.2	A0QQC8	MSMEG_0709	99.0	DAEAHAEEDR	iTRAQ4plex@N-term		0.02	1285.58	429.53	1285.57	429.53	3	71.3
	39.2	A0QQC8	MSMEG_0709	99.0	DAGISVSDIDHVVLVGGSTR	iTRAQ4plex@N-term		0.00	2140.13	714.38	2140.12	714.38	3	130.2
	39.2	A0QQC8	MSMEG_0709	99.0	EAGQIAGLNVLR	iTRAQ4plex@N-term		0.00	1383.79	692.90	1383.80	692.91	2	3.530.1
	39.2	A0QQC8	MSMEG_0709	99.0	GVNPDEVVAVGAALQAGVLK	iTRAQ4plex@N-term; Lys->Gln@20		0.05	2050.17	684.40	2050.12	684.38	3	
	39.2	A0QQC8	MSMEG_0709	99.0	NQAVTNVDR	iTRAQ4plex@N-term		0.05	1159.65	580.83	1159.61	580.81	2	224.1
	39.2	A0QQC8	MSMEG_0709	99.0	YTPQEISAR	iTRAQ4plex@N-term		0.02	1207.65	604.83	1207.63	604.82	2	7.600.2
	39.2	A0QQC8	MSMEG_0709	99.0	DAEAHAEEDR	iTRAQ4plex@N-term; Dimethyl(R)@10		0.02	1313.61	438.88	1313.60	438.87	3	20.7
	39.2	A0QQC8	MSMEG_0709	99.0	DAGISVSDIDHVVLVGGSTR	iTRAQ4plex@N-term		-0.05	2140.08	714.37	2140.12	714.38	3	179.9
	39.2	A0QQC8	MSMEG_0709	99.0	DAGISVSDIDHVVLVGGSTR	No iTRAQ4plex@N-term		0.01	1996.04	666.35	1996.02	666.35	3	

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	39.2	A0QQC8	MSMEG_0709	99.0	DAGISVSDIDHVVLVGGSTR	iTRAQ4plex@N-term		0.06	2140.18	714.40	2140.12	714.38	3	103.0
	39.2	A0QQC8	MSMEG_0709	99.0	GVNPDEVVAVGAALQAGVLK	iTRAQ4plex@N-term; Lys->Arg@20		0.03	2078.19	693.74	2078.16	693.73	3	
	39.2	A0QQC8	MSMEG_0709	98.0	GSSGIDLTK	iTRAQ4plex@N-term; Lys->Gln@9		0.03	1020.55	511.28	1020.52	511.27	2	126.5
	39.2	A0QQC8	MSMEG_0709	98.0	TTPSVVAFAR	iTRAQ4plex@N-term		0.02	1191.69	596.85	1191.67	596.84	2	3.262.6
	39.2	A0QQC8	MSMEG_0709	97.0	ITQDLLDR	iTRAQ4plex@N-term; Dimethyl(R)@8		0.00	1144.66	573.34	1144.66	573.34	2	934.9
	39.2	A0QQC8	MSMEG_0709	82.0	IVNEPTAAALAYGLDK	iTRAQ4plex@N-term; iTRAQ4plex(Y)@12; Lys->Gln@16		0.01	1933.05	645.36	1933.04	645.35	3	144.1
	39.2	A0QQC8	MSMEG_0709	79.0	IVTWLVDK	iTRAQ4plex@N-term; Lys->Gln@8		0.05	1116.68	559.35	1116.63	559.32	2	759.0
59	39.0	A0QTE3	MSMEG_1809	99.0	DTTLDVPTR	iTRAQ4plex@N-term		0.01	1160.62	581.32	1160.62	581.32	2	2.488.9
	39.0	A0QTE3	MSMEG_1809	99.0	LVTADWLASNLGR	iTRAQ4plex@N-term	cleaved R-P@C-term	0.00	1558.86	780.44	1558.86	780.44	2	2.952.3
	39.0	A0QTE3	MSMEG_1809	99.0	NYDGSWTEWGNAVR	iTRAQ4plex@N-term		0.01	1797.82	600.28	1797.82	600.28	3	62.6
	39.0	A0QTE3	MSMEG_1809	99.0	PGLAIVESDEDVLLYDTGHIPGAVK	No iTRAQ4plex@N-term; Lys->Gln@25	cleaved R-P@N-term	0.01	2607.31	870.11	2607.31	870.11	3	8.7
	39.0	A0QTE3	MSMEG_1809	99.0	QSSGYPVVER	iTRAQ4plex@N-term		0.01	1264.67	633.34	1264.65	633.33	2	3.680.4
	39.0	A0QTE3	MSMEG_1809	99.0	SLPADPSPTLAEYAHPER	iTRAQ4plex@N-term	cleaved M-S@N-term	0.06	2094.11	699.04	2094.05	699.02	3	451.3
60	38.5	A0R3E3	MSMEG_5442	99.0	AVNAGGVATSALEMQQNASR	iTRAQ4plex@N-term		0.02	2118.09	707.04	2118.06	707.03	3	210.0
	38.5	A0R3E3	MSMEG_5442	99.0	DSWTFDDTEGR	iTRAQ4plex@N-term		0.02	1471.65	736.83	1471.63	736.82	2	578.1
	38.5	A0R3E3	MSMEG_5442	99.0	HIGEYTDVPAGDIGVGTR	iTRAQ4plex@N-term		0.02	2000.03	667.68	2000.01	667.68	3	332.0
	38.5	A0R3E3	MSMEG_5442	99.0	HPEYADNAIIR	iTRAQ4plex@N-term		0.00	1441.74	481.59	1441.74	481.59	3	393.1
	38.5	A0R3E3	MSMEG_5442	99.0	IDAYAEAR	iTRAQ4plex@N-term		-0.01	1051.53	526.77	1051.54	526.78	2	1.576.6
	38.5	A0R3E3	MSMEG_5442	99.0	LQAVFEEVSHR	iTRAQ4plex@N-term		-0.02	1457.76	486.93	1457.77	486.93	3	313.0
	38.5	A0R3E3	MSMEG_5442	99.0	VPWVDDTGHVQINR	iTRAQ4plex@N-term		0.01	1778.93	593.98	1778.92	593.98	3	500.1
	38.5	A0R3E3	MSMEG_5442	99.0	HIGEYTDVPAGDIGVGTR	iTRAQ4plex@N-term		0.00	2000.01	667.68	2000.01	667.68	3	356.5
	38.5	A0R3E3	MSMEG_5442	86.0	SDAEIMR	iTRAQ4plex@N-term		0.00	964.47	483.24	964.48	483.25	2	98.6
61	38.3	A0QUY2	MSMEG_2378	99.0	ADFISVHLPK	iTRAQ4plex@N-term; Lys->Gln@10		0.02	1269.71	424.24	1269.68	424.24	3	117.7
	38.3	A0QUY2	MSMEG_2378	99.0	AGTDVAASVK	iTRAQ4plex@N-term; Lys->Gln@10		0.03	1061.57	531.79	1061.55	531.78	2	123.3
	38.3	A0QUY2	MSMEG_2378	99.0	GGLIDEQALADAITSGHVR	iTRAQ4plex@N-term		-0.07	2066.02	689.68	2066.09	689.70	3	88.6
	38.3	A0QUY2	MSMEG_2378	99.0	GVLVVNAPTSNIHSAAEHAIALLLATAR	iTRAQ4plex@N-term		-0.06	2952.60	739.16	2952.66	739.17	4	34.4
	38.3	A0QUY2	MSMEG_2378	99.0	GVTAEISTATESPNHR	iTRAQ4plex@N-term		0.03	1812.94	605.32	1812.91	605.31	3	198.4
	38.3	A0QUY2	MSMEG_2378	99.0	IVAYDPYVSQAR	iTRAQ4plex@N-term	cleaved H-I@N-term	0.00	1524.80	763.41	1524.81	763.41	2	426.0
	38.3	A0QUY2	MSMEG_2378	99.0	LAESTVAALGDEVEVR	iTRAQ4plex@N-term		0.01	1801.96	601.66	1801.95	601.66	3	
	38.3	A0QUY2	MSMEG_2378	99.0	LLAAVPEADALLVR	iTRAQ4plex@N-term		0.00	1593.95	797.98	1593.96	797.99	2	1.691.1
	38.3	A0QUY2	MSMEG_2378	99.0	VDTDVPDDVR	iTRAQ4plex@N-term		0.01	1273.64	637.83	1273.63	637.82	2	2.093.1
	38.3	A0QUY2	MSMEG_2378	96.0	GLFSAVVDEQVTFVNAPALAADR	iTRAQ4plex@N-term		0.01	2533.34	845.45	2533.33	845.45	3	13.0
	38.3	A0QUY2	MSMEG_2378	93.0	AGTDVAASVK	iTRAQ4plex@N-term; Lys->Gln@10		0.03	1061.58	531.80	1061.55	531.78	2	152.3
62	38.2	A0QQI6	MSMEG_0768	99.0	FVGVPDLSSLQR	iTRAQ4plex@N-term		0.00	1460.81	731.41	1460.81	731.41	2	994.0
	38.2	A0QQI6	MSMEG_0768	99.0	SIGAAEAATAAGIGPSYNILDGFEGHLDE	iTRAQ4plex@N-term		0.00	3259.58	815.90	3259.59	815.90	4	144.1
	38.2	A0QQI6	MSMEG_0768	99.0	FVGVPDLSSLQR	iTRAQ4plex@N-term		0.02	1460.83	731.42	1460.81	731.41	2	621.9
	38.2	A0QQI6	MSMEG_0768	92.0	DVVYIEWNR	iTRAQ4plex@N-term		-0.01	1336.68	669.35	1336.69	669.35	2	343.0
63	38.0	A0R0B4	MSMEG_4327	99.0	DIDHVNAHATATPIGDTAEANALR	iTRAQ4plex@N-term		0.03	2616.33	655.09	2616.30	655.08	4	1.608.0
	38.0	A0R0B4	MSMEG_4327	99.0	IGGHLVDNIDDHMTR	No iTRAQ4plex@N-term; Gly->Pro@2		0.00	1731.84	578.29	1731.84	578.29	3	118.7
	38.0	A0R0B4	MSMEG_4327	99.0	IVETYDAMNEGGPR	iTRAQ4plex@N-term		0.01	1694.81	848.41	1694.81	848.41	2	2.313.5
	38.0	A0R0B4	MSMEG_4327	99.0	LMGAGITSDAFHMVAPAADGLR	iTRAQ4plex@N-term		0.02	2344.20	782.41	2344.18	782.40	3	173.4
	38.0	A0R0B4	MSMEG_4327	99.0	QLWENAGAPEVDPDR	iTRAQ4plex@N-term; Dimethyl(R)@15		-0.03	1867.89	623.64	1867.92	623.65	3	52.2
	38.0	A0R0B4	MSMEG_4327	99.0	VAGVEHAAVYAPK	iTRAQ4plex@N-term; Lys->Gln@13		0.03	1454.80	485.94	1454.76	485.93	3	1.622.5
	38.0	A0R0B4	MSMEG_4327	99.0	VLEDEFVTK	iTRAQ4plex@N-term; Lys->Gln@9		0.05	1222.67	612.34	1222.62	612.32	2	1.153.7
	38.0	A0R0B4	MSMEG_4327	99.0	YAINNSFGFGGHNVALAFGR	iTRAQ4plex@N-term		0.02	2255.16	752.73	2255.14	752.72	3	721.4
	38.0	A0R0B4	MSMEG_4327	99.0	DIDHVNAHATATPIGDTAEANALR	iTRAQ4plex@N-term		0.04	2616.34	655.09	2616.30	655.08	4	515.2
	38.0	A0R0B4	MSMEG_4327	99.0	DIDHVNAHATATPIGDTAEANALR	iTRAQ4plex@N-term; Dimethyl(R)@24		-0.04	2644.29	662.08	2644.33	662.09	4	236.7
	38.0	A0R0B4	MSMEG_4327	99.0	LMGAGITSDAFHMVAPAADGLR	No iTRAQ4plex@N-term		-0.02	2200.06	734.36	2200.08	734.37	3	109.2
	38.0	A0R0B4	MSMEG_4327	99.0	LMGAGITSDAFHMVAPAADGLR	iTRAQ4plex@N-term; Oxidation(H)@12		0.00	2360.17	787.73	2360.17	787.73	3	122.1
	38.0	A0R0B4	MSMEG_4327	99.0	QLWENAGAPEVDPDR	iTRAQ4plex@N-term		-0.02	1839.87	614.30	1839.89	614.30	3	143.8
	38.0	A0R0B4	MSMEG_4327	99.0	YAINNSFGFGGHNVALAFGR	iTRAQ4plex@N-term		-0.04	2255.10	752.71	2255.14	752.72	3	216.4
	38.0	A0R0B4	MSMEG_4327	96.0	FAVVIGTGLGGGEKI	iTRAQ4plex@N-term; Gly->Ser@12; Lys->Glu@14	cleaved I-V@C-term; missed K-I@14	0.07	1591.93	796.97	1591.86	796.94	2	1.497.3
	38.0	A0R0B4	MSMEG_4327	94.0	VAGVEHAAVYAPK	No iTRAQ4plex@N-term; iTRAQ4plex(Y)@10; Lys->Gln@13		0.03	1454.80	485.94	1454.76	485.93	3	442.4
	38.0	A0R0B4	MSMEG_4327	91.0	VLEDEFVTKWDLPVR	iTRAQ4plex@N-term; iTRAQ4plex(T)@8; User modH on Lys(K)@9	missed K-W@9	-0.07	2376.21	793.08	2376.28	793.10	3	49.9
64	37.9	A0QRA5	MSMEG_1046	99.0	DLVVSAGYAVLGR	iTRAQ4plex@N-term		0.04	1462.86	488.63	1462.83	488.62	3	

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	37.9	A0QRA5	MSMEG_1046	99.0	EQYDDVDYEQAVNMLESVGAEHLAER	iTRAQ4plex@N-term		-0.04	3153.39	789.35	3153.43	789.37	4	50.9
	37.9	A0QRA5	MSMEG_1046	99.0	VVASGLLTDVLTSENLSK	iTRAQ4plex@N-term; iTRAQ4plex(S)@17; Lys->Gln@18		-0.03	2133.15	712.06	2133.18	712.07	3	25.0
	37.9	A0QRA5	MSMEG_1046	80.0	EDLVAR	iTRAQ4plex@N-term		0.00	845.47	423.74	845.47	423.74	2	60.3
65	37.9	A0R7I9	MSMEG_6933	99.0	EGITGPELMDQMR	iTRAQ4plex@N-term		0.01	1619.79	810.90	1619.78	810.90	2	874.2
	37.9	A0R7I9	MSMEG_6933	99.0	ITFLTNTEITQIEGDPK	iTRAQ4plex@N-term; Lys->Gln@17		0.02	2063.07	688.70	2063.05	688.69	3	16.3
	37.9	A0R7I9	MSMEG_6933	99.0	TTYTSLDGVFAAGDLVDHTYR	iTRAQ4plex@N-term; Dimethyl(R)@21		-0.05	2473.18	825.40	2473.22	825.42	3	190.6
	37.9	A0R7I9	MSMEG_6933	99.0	TVVVGDETHQAR	iTRAQ4plex@N-term		0.02	1454.78	485.93	1454.76	485.93	3	389.6
	37.9	A0R7I9	MSMEG_6933	99.0	TTYTSLDGVFAAGDLVDHTYR	iTRAQ4plex@N-term		0.01	2445.20	816.07	2445.19	816.07	3	205.6
	37.9	A0R7I9	MSMEG_6933	98.0	TVVVGDETHQAR	Carbamyl@N-term		0.08	1353.74	452.25	1353.66	452.23	3	80.2
	37.9	A0R7I9	MSMEG_6933	96.0	HLGVPGEEALTGMGVSTCATCDGFFFR	iTRAQ4plex@N-term; No Pyridylethyl(C)@18; Cys->Thr@21		-0.08	2943.32	736.84	2943.40	736.86	4	73.7
	37.9	A0R7I9	MSMEG_6933	88.0	TTYTSLDGVFAAGDLVDHTYR	No iTRAQ4plex@N-term		0.03	2301.12	768.05	2301.09	768.04	3	10.7
66	37.7	A0QSL8	MSMEG_1524	99.0	EGVHTVGELVAR	iTRAQ4plex@N-term		0.01	1409.79	470.94	1409.77	470.93	3	199.2
	37.7	A0QSL8	MSMEG_1524	99.0	ELNADSEHIEIGPSPAEADHIASFALPIDI	iTRAQ4plex@N-term		-0.03	4013.97	1004.50	4014.00	1004.51	4	59.7
	37.7	A0QSL8	MSMEG_1524	99.0	IDGVLHEFTTVPGVK	iTRAQ4plex@N-term; Lys->Gln@15		-0.08	1754.85	585.96	1754.93	585.98	3	92.2
	37.7	A0QSL8	MSMEG_1524	99.0	MLISQRPTLSEETVAENR	iTRAQ4plex@N-term		-0.01	2217.14	740.06	2217.15	740.06	3	1.246.9
	37.7	A0QSL8	MSMEG_1524	99.0	TESDLLDIR	iTRAQ4plex@N-term		-0.02	1204.62	603.32	1204.64	603.33	2	675.7
	37.7	A0QSL8	MSMEG_1524	99.0	TLLSSIPGAAVTSIR	iTRAQ4plex@N-term		0.03	1628.98	815.50	1628.96	815.49	2	1.410.0
	37.7	A0QSL8	MSMEG_1524	99.0	EGVHTVGELVAR	iTRAQ4plex@N-term		-0.03	1409.75	470.92	1409.77	470.93	3	275.5
	37.7	A0QSL8	MSMEG_1524	96.0	ASGAEIGR	iTRAQ4plex@N-term		0.00	903.49	452.75	903.49	452.75	2	71.6
	37.7	A0QSL8	MSMEG_1524	96.0	TESDLLDIR	Carbamyl@N-term		0.04	1103.58	552.80	1103.55	552.78	2	2.162.7
67	37.0	A0QZ46	MSMEG_3894	99.0	FNEFDNLR	iTRAQ4plex@N-term		0.01	1197.60	599.80	1197.59	599.80	2	7.533.8
	37.0	A0QZ46	MSMEG_3894	99.0	GGIQFADTR	iTRAQ4plex@N-term; Dimethyl(R)@9		-0.01	1135.60	568.81	1135.61	568.81	2	805.3
	37.0	A0QZ46	MSMEG_3894	99.0	SFPYFISPEQAMR	iTRAQ4plex@N-term	cleaved M-S@N-term	0.01	1715.86	858.94	1715.85	858.93	2	2.150.3
	37.0	A0QZ46	MSMEG_3894	99.0	GGIQFADTR	iTRAQ4plex@N-term		-0.02	1107.55	554.78	1107.58	554.80	2	10.533.9
	37.0	A0QZ46	MSMEG_3894	99.0	GGIQFADTR	iTRAQ4plex@N-term; Thr->Glu@8		0.05	1135.63	568.82	1135.57	568.79	2	2.775.8
	37.0	A0QZ46	MSMEG_3894	87.0	ITYDGSIADEPHFVVMGGTTEPIIAALN	iTRAQ4plex@N-term; Methyl(N)@28	cleaved N-E@C-term	-0.05	3088.50	1030.51	3088.55	1030.53	3	321.7
68	36.6	A0R079	MSMEG_4290	99.0	DGQPLFHDESGYAGLSDIAR	iTRAQ4plex@N-term		0.04	2291.13	764.72	2291.09	764.71	3	306.9
	36.6	A0R079	MSMEG_4290	99.0	DQMATNLQNAGFTLER	iTRAQ4plex@N-term		-0.02	1951.93	651.65	1951.95	651.66	3	270.1
	36.6	A0R079	MSMEG_4290	99.0	FNTLLAAADDVLLFK	iTRAQ4plex@N-term; Lys->Arg@15		0.06	1822.07	912.04	1822.01	912.01	2	314.4
	36.6	A0R079	MSMEG_4290	99.0	GFQSIHESDMMLLPDPNTAR	iTRAQ4plex@N-term		0.01	2402.16	801.73	2402.15	801.72	3	149.5
	36.6	A0R079	MSMEG_4290	99.0	GGYFPVAPYDHYVDLR	iTRAQ4plex@N-term		-0.03	2011.96	671.66	2011.99	671.67	3	132.1
	36.6	A0R079	MSMEG_4290	99.0	LVPGYEAPINLVYSQR	iTRAQ4plex@N-term		-0.01	1962.06	655.03	1962.07	655.03	3	286.0
	36.6	A0R079	MSMEG_4290	99.0	SIPASAFDESVFEDGLAFDGSSVR	iTRAQ4plex@N-term	cleaved F-S@N-term	-0.04	2646.21	883.08	2646.26	883.09	3	9.8
	36.6	A0R079	MSMEG_4290	97.0	GFQSIHESDMMLLPDPNTAR	iTRAQ4plex@N-term; Dimethyl(R)@20		-0.03	2430.15	811.06	2430.18	811.07	3	20.5
	36.6	A0R079	MSMEG_4290	79.0	TLNMNFFVHDPFTR	iTRAQ4plex@N-term; Deamidated(N)@3		0.00	1882.92	628.65	1882.92	628.65	3	41.3
69	36.6	A0R2E9	MSMEG_5087	99.0	GLVPTGYVSQR	iTRAQ4plex@N-term		0.01	1319.74	660.88	1319.73	660.87	2	1.074.7
	36.6	A0R2E9	MSMEG_5087	99.0	GWTLVSGGGNVSAMGAVAQAAR	iTRAQ4plex@N-term		-0.01	2203.12	735.38	2203.13	735.38	3	133.5
	36.6	A0R2E9	MSMEG_5087	99.0	GLVPTGYVSQR	iTRAQ4plex@N-term		0.01	1319.74	660.88	1319.73	660.87	2	817.1
70	36.4	A0R061	MSMEG_4272	92.0	YNLFFDDR	iTRAQ4plex@N-term		0.02	1232.61	617.31	1232.59	617.30	2	956.0
71	36.4	A0R729	MSMEG_6759	99.0	ATLESICYQSR	iTRAQ4plex@N-term; Pyridylethyl(C)@7		-0.01	1518.75	507.26	1518.76	507.26	3	966.4
	36.4	A0R729	MSMEG_6759	99.0	DQMHVIDSAAESESLAR	iTRAQ4plex@N-term		0.00	2001.95	668.32	2001.95	668.33	3	286.4
	36.4	A0R729	MSMEG_6759	99.0	DVAEAMEADSGVHLDVLK	iTRAQ4plex@N-term; Lys->Gln@18		0.00	2041.98	681.67	2041.97	681.67	3	354.7
	36.4	A0R729	MSMEG_6759	99.0	FMIFDHAGNEVAR	iTRAQ4plex@N-term		-0.01	1649.80	550.94	1649.81	550.94	3	449.4
	36.4	A0R729	MSMEG_6759	99.0	GAIVGLSR	iTRAQ4plex@N-term		-0.01	915.55	458.78	915.56	458.79	2	4.524.5
	36.4	A0R729	MSMEG_6759	99.0	IQWILENVPGVR	iTRAQ4plex@N-term		-0.06	1566.84	523.29	1566.90	523.31	3	54.0
	36.4	A0R729	MSMEG_6759	99.0	LQPSDLAALGVTNQR	iTRAQ4plex@N-term		-0.03	1725.92	576.32	1725.95	576.32	3	67.3
	36.4	A0R729	MSMEG_6759	99.0	NTYGTGNFLLLNTGTTPVR	iTRAQ4plex@N-term		-0.02	2182.13	728.38	2182.15	728.39	3	14.1
	36.4	A0R729	MSMEG_6759	99.0	PGWVEHNPVEIWER	No iTRAQ4plex@N-term	cleaved R-P@N-term	-0.04	1746.80	583.28	1746.85	583.29	3	32.5
	36.4	A0R729	MSMEG_6759	99.0	SSSAVQSALNAAK	iTRAQ4plex@N-term; Lys->Gln@13		0.05	1376.75	689.38	1376.70	689.36	2	1.684.8
	36.4	A0R729	MSMEG_6759	99.0	TDSIAAALDR	iTRAQ4plex@N-term; Dimethyl(R)@10		-0.01	1203.65	602.83	1203.66	602.84	2	457.5
	36.4	A0R729	MSMEG_6759	99.0	YNTNAHLAR	iTRAQ4plex@N-term		0.00	1202.63	401.88	1202.63	401.88	3	108.4
	36.4	A0R729	MSMEG_6759	89.0	YNTNAHLAR	iTRAQ4plex@N-term		0.00	1202.63	401.88	1202.63	401.88	3	327.1
72	36.4	A0QUV7	MSMEG_2352	99.0	GVGSAENFKIVEELADSLGGAVGAS	iTRAQ4plex@N-term; iTRAQ4plex(S)@4; User modH on Lys(K)@9	missed K-I@9	0.01	3063.60	766.91	3063.60	766.91	4	80.4

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	36.4	A0QUV7	MSMEG_2352	99.0	AAVDSGYYPGQFQVGQTGK	iTRAQ4plex@N-term; Lys->Gln@19		0.03	2116.03	706.35	2116.00	706.34	3	83.6
	36.4	A0QUV7	MSMEG_2352	99.0	ALGEPSAVVVGK	iTRAQ4plex@N-term; Lys->Gln@12	cleaved K-P@C-term	0.04	1269.75	635.88	1269.71	635.86	2	927.2
	36.4	A0QUV7	MSMEG_2352	99.0	EPAVAGDRPELTEASVVVAGGR	iTRAQ4plex@N-term		0.02	2323.25	775.42	2323.23	775.42	3	739.7
	36.4	A0QUV7	MSMEG_2352	99.0	IVEELADSLGGAVGASR	iTRAQ4plex@N-term; Ser->Asp@16		0.04	1814.99	606.00	1814.95	605.99	3	82.6
	36.4	A0QUV7	MSMEG_2352	99.0	REPAVAGDRPELTEASVVVAGGR	iTRAQ4plex@N-term	missed R-E@1	0.02	2479.35	620.85	2479.33	620.84	4	79.8
	36.4	A0QUV7	MSMEG_2352	99.0	VSAELLTAAR	iTRAQ4plex@N-term		0.00	1173.69	587.85	1173.68	587.85	2	11.685.5
	36.4	A0QUV7	MSMEG_2352	99.0	AAVDSGYYPGQFQVGQTGK	iTRAQ4plex@N-term; iTRAQ4plex(T)@17; Lys->Gln@19		0.07	2260.17	754.40	2260.10	754.37	3	724.6
	36.4	A0QUV7	MSMEG_2352	99.0	IVEELADSLGGAVGASR	iTRAQ4plex@N-term		0.00	1786.95	894.48	1786.95	894.48	2	1.597.9
	36.4	A0QUV7	MSMEG_2352	98.0	VSAELLTAAR	iTRAQ4plex@N-term; Ala->Val@9		-0.02	1201.70	601.86	1201.72	601.86	2	1.013.8
	36.4	A0QUV7	MSMEG_2352	96.0	GVGSAENFKIVEELADSLGGAVGAS	iTRAQ4plex@N-term; iTRAQ4plex(S)@4; User modH on Lys(K)@9; Glu->Gln@13	missed K-I@9	-0.11	3062.50	766.63	3062.61	766.66	4	8.7
	36.4	A0QUV7	MSMEG_2352	90.0	GVGSAENFK	iTRAQ4plex@N-term; Lys->Gln@9		0.07	1051.58	526.80	1051.51	526.76	2	823.9
	36.4	A0QUV7	MSMEG_2352	81.0	VSPQLTEAVKAR	No iTRAQ4plex@N-term; Lys->Ser@10; Arg->Orn(R)@12	missed K-A@10	0.05	1214.71	608.36	1214.65	608.33	2	440.8
73	36.3	A0QTE1	MSMEG_1807	99.0	AASGDAVTAPMQGTVVK	iTRAQ4plex@N-term; iTRAQ4plex(T)@14; Lys->Gln@17		0.08	1890.05	631.02	1889.98	631.00	3	406.9
	36.3	A0QTE1	MSMEG_1807	99.0	AVVSDPAFIGDGEK	iTRAQ4plex@N-term; Lys->Gln@14		0.05	1547.81	774.91	1547.76	774.89	2	764.4
	36.3	A0QTE1	MSMEG_1807	99.0	AVVSDPAFIGDGEKFDVHTR	iTRAQ4plex@N-term; Lys->Gln@14	missed K-F@14	0.04	2303.17	576.80	2303.13	576.79	4	223.5
	36.3	A0QTE1	MSMEG_1807	99.0	EAIAAFGR	iTRAQ4plex@N-term		-0.02	977.52	489.77	977.54	489.78	2	3.270.3
	36.3	A0QTE1	MSMEG_1807	99.0	FVAPTGPGVR	iTRAQ4plex@N-term		0.00	1143.65	572.83	1143.65	572.83	2	9.342.2
	36.3	A0QTE1	MSMEG_1807	99.0	LIVTGATR	iTRAQ4plex@N-term		-0.02	973.58	487.80	973.60	487.81	2	9.426.7
	36.3	A0QTE1	MSMEG_1807	99.0	LQVEHPVTEETSGIDLVR	iTRAQ4plex@N-term; Dimethyl(R)@18		0.01	2193.19	732.07	2193.18	732.07	3	82.1
	36.3	A0QTE1	MSMEG_1807	99.0	LVEEAPAPFLTDAQR	iTRAQ4plex@N-term		0.01	1799.97	601.00	1799.95	600.99	3	228.1
	36.3	A0QTE1	MSMEG_1807	99.0	MDSGVETGSVIGGQFDSMLAK	iTRAQ4plex@N-term; Lys->Gln@21		-0.01	2272.04	758.35	2272.05	758.36	3	12.0
	36.3	A0QTE1	MSMEG_1807	99.0	QTVVVEVGGR	iTRAQ4plex@N-term		0.00	1186.67	594.34	1186.68	594.35	2	4.256.4
	36.3	A0QTE1	MSMEG_1807	99.0	RLEVSLPGDLAIGGGGGAAAPGVVR	iTRAQ4plex@N-term	missed R-L@1	0.01	2432.37	811.80	2432.36	811.79	3	261.4
	36.3	A0QTE1	MSMEG_1807	99.0	LQVEHPVTEETSGIDLVR	iTRAQ4plex@N-term		-0.02	2165.12	722.71	2165.14	722.72	3	417.1
	36.3	A0QTE1	MSMEG_1807	99.0	LVEEAPAPFLTDAQR	iTRAQ4plex@N-term; Gln->Arg@14		0.00	1827.99	610.34	1828.00	610.34	3	333.4
	36.3	A0QTE1	MSMEG_1807	84.0	GEIAVR	iTRAQ4plex@N-term		-0.01	787.46	394.74	787.47	394.74	2	92.0
74	36.3	A0QZ96	MSMEG_3945	99.0	ALEFAFDAASR	iTRAQ4plex@N-term		-0.02	1340.66	671.34	1340.68	671.35	2	437.5
	36.3	A0QZ96	MSMEG_3945	99.0	ASAIATTAPVVVGVDGSPASEK	iTRAQ4plex@N-term; iTRAQ4plex(S)@20; Lys->Gln@22		0.06	2314.29	772.44	2314.23	772.42	3	1.363.3
	36.3	A0QZ96	MSMEG_3945	99.0	GAPLLAVHAWSDANVAGYPGVR	iTRAQ4plex@N-term		-0.02	2364.23	789.08	2364.25	789.09	3	95.5
	36.3	A0QZ96	MSMEG_3945	99.0	LLGSVTAGLIR	iTRAQ4plex@N-term		-0.02	1242.76	622.39	1242.78	622.40	2	848.9
	36.3	A0QZ96	MSMEG_3945	99.0	SEIAQLTVVGSHGR	iTRAQ4plex@N-term		-0.01	1596.86	533.29	1596.87	533.30	3	609.5
	36.3	A0QZ96	MSMEG_3945	99.0	VQAEESLSER	iTRAQ4plex@N-term		0.00	1290.65	646.33	1290.65	646.33	2	1.113.7
75	36.0	A0QVL0	MSMEG_2611	99.0	DWDDTASLVASDHR	iTRAQ4plex@N-term		0.01	1730.81	577.94	1730.80	577.94	3	699.1
	36.0	A0QVL0	MSMEG_2611	99.0	IDPIAAGGEDYRR	iTRAQ4plex@N-term	missed R-R@12	0.03	1575.84	526.29	1575.81	526.28	3	1.349.5
	36.0	A0QVL0	MSMEG_2611	99.0	SDPNITVYSSHTR	iTRAQ4plex@N-term		0.04	1619.85	540.96	1619.80	540.94	3	1.269.9
	36.0	A0QVL0	MSMEG_2611	99.0	SLGQTAQEIAR	iTRAQ4plex@N-term	cleaved M-S@N-term	0.01	1316.73	659.37	1316.72	659.37	2	2.947.9
	36.0	A0QVL0	MSMEG_2611	99.0	THENVIGSHQDGDR	No iTRAQ4plex@N-term		0.05	1563.75	522.26	1563.70	522.24	3	
	36.0	A0QVL0	MSMEG_2611	99.0	VPNGDLLDAELAGVEVDEDGR	iTRAQ4plex@N-term; Deamidated(N)@3; Glu->Gln@10		0.05	2326.19	776.40	2326.14	776.39	3	10.9
	36.0	A0QVL0	MSMEG_2611	97.0	LLGAHILGHQASSIIQPLIQAM	iTRAQ4plex@N-term	cleaved M-S@C-term	-0.01	2454.38	819.14	2454.39	819.14	3	41.3
	36.0	A0QVL0	MSMEG_2611	94.0	GVFALGDVSSDYQLK	iTRAQ4plex@N-term; Lys->Gln@15		0.06	1741.93	581.65	1741.86	581.63	3	21.7
	36.0	A0QVL0	MSMEG_2611	94.0	VIVDQYQR	iTRAQ4plex@N-term		0.00	1163.64	582.83	1163.64	582.83	2	1.652.9
	36.0	A0QVL0	MSMEG_2611	81.0	GVFALGDVSSDYQLK	iTRAQ4plex@N-term; iTRAQ4plex(Y)@12; Lys->Gln@15		0.00	1885.97	629.66	1885.97	629.66	3	120.3
76	35.0	A0QX83	MSMEG_3207	99.0	FGDAFIPMDESLAHAAVDVSGR	iTRAQ4plex@N-term	cleaved R-P@C-term	0.00	2448.18	817.07	2448.19	817.07	3	567.4
	35.0	A0QX83	MSMEG_3207	99.0	QAVEYDAR	iTRAQ4plex@N-term		0.00	1094.54	548.28	1094.55	548.28	2	692.0
	35.0	A0QX83	MSMEG_3207	99.0	FGDAFIPMDESLAHAAVDVSGR	iTRAQ4plex@N-term	cleaved R-P@C-term	0.05	2448.23	817.09	2448.19	817.07	3	247.0
	35.0	A0QX83	MSMEG_3207	97.0	GDIEIEGHHTVEDTAIVLGQALGQALGDI	iTRAQ4plex@N-term; Lys->Gln@29		0.10	3129.67	783.43	3129.57	783.40	4	7.6
77	34.6	A0R5C5	MSMEG_6142	99.0	FNVGTGVETSTR	iTRAQ4plex@N-term		-0.01	1410.71	706.36	1410.72	706.37	2	2.164.3
	34.6	A0R5C5	MSMEG_6142	99.0	LLADGHGVVGLDDLSSGR	iTRAQ4plex@N-term		-0.02	1923.99	642.34	1924.01	642.35	3	232.5
	34.6	A0R5C5	MSMEG_6142	99.0	SVDDPPFDATVNVVGTVR	iTRAQ4plex@N-term		0.04	2031.08	678.04	2031.04	678.02	3	
	34.6	A0R5C5	MSMEG_6142	97.0	SVDDPPFDATVNVVGTVR	iTRAQ4plex@N-term		0.07	2031.11	678.04	2031.04	678.02	3	
78	34.6	A0QVE0	MSMEG_2541	99.0	NSDLGVNPSNDGNIIR	iTRAQ4plex@N-term		0.04	1827.96	914.99	1827.92	914.97	2	582.8
	34.6	A0QVE0	MSMEG_2541	99.0	VAIPQLTEER	iTRAQ4plex@N-term		0.00	1298.73	650.37	1298.73	650.37	2	1.900.4
	34.6	A0QVE0	MSMEG_2541	80.0	DELGSIR	iTRAQ4plex@N-term		0.01	932.52	467.27	932.50	467.26	2	2.063.5
79	34.5	A0R342	MSMEG_5335	99.0	ALIATDPDR	iTRAQ4plex@N-term		0.01	1114.62	558.32	1114.61	558.31	2	5.219.0

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	34.5	A0R342	MSMEG_5335	99.0	AYMDATMAYR	iTRAQ4plex@N-term	cleaved N-A@N-term	0.01	1335.62	668.82	1335.61	668.81	2	965.3
	34.5	A0R342	MSMEG_5335	99.0	EWTDGQIGNNDSANDVR	iTRAQ4plex@N-term		0.01	2033.92	678.98	2033.92	678.98	3	412.0
	34.5	A0R342	MSMEG_5335	99.0	GGMETYGVTTNPIFMPGR	iTRAQ4plex@N-term; Dimethyl(R)@18		0.05	2099.08	700.70	2099.03	700.68	3	74.5
	34.5	A0R342	MSMEG_5335	99.0	NACLNAIEYLK	iTRAQ4plex@N-term; Pyridylethyl(C)@3; Lys->Gln@11		0.01	1499.77	500.93	1499.76	500.93	3	429.6
	34.5	A0R342	MSMEG_5335	99.0	NAYMDATMAYR	iTRAQ4plex@N-term		0.00	1449.65	725.83	1449.65	725.83	2	9.520.8
	34.5	A0R342	MSMEG_5335	99.0	PEVVFSVDHSK	No iTRAQ4plex@N-term; iTRAQ4plex(S)@10; Lys->Gln@11	cleaved M-P@N-term	0.03	1386.72	463.25	1386.69	463.24	3	456.5
	34.5	A0R342	MSMEG_5335	99.0	VNGGGFLTDYYPDAYK	iTRAQ4plex@N-term; iTRAQ4plex(Y)@15; Lys->Gln@16		0.06	2067.04	690.02	2066.98	690.00	3	222.3
	34.5	A0R342	MSMEG_5335	99.0	WGYTGEQAYLILGTSPIEGR	iTRAQ4plex@N-term		0.01	2354.21	785.74	2354.20	785.74	3	22.8
	34.5	A0R342	MSMEG_5335	99.0	YTGITHPGLFGTAPSPDLLAK	iTRAQ4plex@N-term; iTRAQ4plex(S)@15; Lys->Gln@21		0.05	2443.35	815.46	2443.30	815.44	3	572.0
	34.5	A0R342	MSMEG_5335	99.0	EWTDGQIGNNDSANDVR	iTRAQ4plex@N-term; Dimethyl(R)@17		-0.01	2061.93	688.32	2061.95	688.32	3	493.8
	34.5	A0R342	MSMEG_5335	99.0	GGMETYGVTTNPIFMPGR	iTRAQ4plex@N-term		-0.01	2070.99	691.34	2071.00	691.34	3	204.3
	34.5	A0R342	MSMEG_5335	99.0	NAYMDATMAYR	iTRAQ4plex@N-term		0.00	1449.65	725.83	1449.65	725.83	2	995.2
	34.5	A0R342	MSMEG_5335	99.0	NAYMDATMAYR	iTRAQ4plex@N-term; Dimethyl(R)@11		0.02	1477.70	739.86	1477.68	739.85	2	1.482.5
	34.5	A0R342	MSMEG_5335	99.0	PEVVFSVDHSK	No iTRAQ4plex@N-term; iTRAQ4plex(S)@10; Lys->Gln@11	cleaved M-P@N-term	0.02	1386.71	463.24	1386.69	463.24	3	192.1
	34.5	A0R342	MSMEG_5335	99.0	WGYTGEQAYLILGTSPIEGR	iTRAQ4plex@N-term; Amino(Y)@9		-0.09	2369.13	790.72	2369.21	790.75	3	20.7
	34.5	A0R342	MSMEG_5335	99.0	YTGITHPGLFGTAPSPDLLAK	iTRAQ4plex@N-term; Lys->Gln@21		0.00	2299.19	767.40	2299.20	767.41	3	414.6
	34.5	A0R342	MSMEG_5335	98.0	PEVVFSVDHSK	No iTRAQ4plex@N-term; Lys->Gln@11	cleaved M-P@N-term	0.02	1242.61	415.21	1242.59	415.20	3	52.2
	34.5	A0R342	MSMEG_5335	96.0	VNGGGFLTDYYPDAYK	iTRAQ4plex@N-term; Deamidated(N)@2; iTRAQ4plex(Y)@15; Lys->Gln@16		0.00	2067.97	690.33	2067.97	690.33	3	213.1
	34.5	A0R342	MSMEG_5335	85.0	PEVVFSVDHSK	iTRAQ4plex@N-term; Lys->Gln@11	cleaved M-P@N-term	0.03	1386.72	463.25	1386.69	463.24	3	277.0
80	34.3	A0QVB8	MSMEG_2519	99.0	EHIAVGEAR	iTRAQ4plex@N-term		0.01	1124.62	375.88	1124.61	375.88	3	27.2
	34.3	A0QVB8	MSMEG_2519	99.0	ETVAHGGTVLFVGTK	iTRAQ4plex@N-term; iTRAQ4plex(T)@14; Lys->Gln@15		0.07	1803.04	602.02	1802.98	602.00	3	174.8
	34.3	A0QVB8	MSMEG_2519	99.0	QAQESIAEEATR	iTRAQ4plex@N-term		0.03	1475.76	738.89	1475.73	738.87	2	1.953.7
	34.3	A0QVB8	MSMEG_2519	99.0	VIASAVAEGLQAR	iTRAQ4plex@N-term		0.00	1427.82	714.92	1427.82	714.92	2	3.470.1
	34.3	A0QVB8	MSMEG_2519	99.0	VPSAVWVVDTNK	iTRAQ4plex@N-term; Lys->Gln@12		0.03	1457.79	729.90	1457.76	729.89	2	1.110.7
	34.3	A0QVB8	MSMEG_2519	99.0	WLGGMLTNFSTVHK	iTRAQ4plex@N-term; Lys->Gln@14		0.02	1733.89	578.97	1733.87	578.96	3	75.6
	34.3	A0QVB8	MSMEG_2519	94.0	EILMLTR	iTRAQ4plex@N-term		0.01	1018.60	510.31	1018.60	510.31	2	4.883.7
81	34.3	A0QWS8	MSMEG_3050	99.0	AQEIMTELEIAPTR	iTRAQ4plex@N-term		0.01	1744.92	873.47	1744.92	873.46	2	2.041.1
	34.3	A0QWS8	MSMEG_3050	99.0	AQEIMTELEIAPTR	iTRAQ4plex@N-term; Dimethyl(R)@14		-0.01	1772.93	591.99	1772.95	591.99	3	
82	33.4	A0QYY6	MSMEG_3833	99.0	ATQEDPWR	iTRAQ4plex@N-term		0.01	1145.57	573.79	1145.56	573.79	2	1.861.7
	33.4	A0QYY6	MSMEG_3833	99.0	FAAAEAEAANAPVSNGSSR	iTRAQ4plex@N-term; Deamidated(N)@15		-0.01	1963.93	655.65	1963.94	655.65	3	1.396.0
	33.4	A0QYY6	MSMEG_3833	99.0	GFLPASLVEMR	iTRAQ4plex@N-term		0.00	1362.74	682.38	1362.75	682.38	2	1.007.2
	33.4	A0QYY6	MSMEG_3833	99.0	LVPFGAFVR	iTRAQ4plex@N-term		-0.02	1148.66	575.34	1148.68	575.35	2	4.469.4
	33.4	A0QYY6	MSMEG_3833	99.0	VEEGIEGLVHISELSER	iTRAQ4plex@N-term		-0.05	2039.02	680.68	2039.07	680.70	3	169.8
	33.4	A0QYY6	MSMEG_3833	99.0	FAAAEAEAANAPVSNGSSR	iTRAQ4plex@N-term		0.01	1962.96	655.33	1962.95	655.32	3	1.586.3
	33.4	A0QYY6	MSMEG_3833	99.0	GFLPASLVEMR	iTRAQ4plex@N-term		-0.01	1362.74	682.38	1362.75	682.38	2	448.3
	33.4	A0QYY6	MSMEG_3833	99.0	VEEGIEGLVHISELSER	iTRAQ4plex@N-term; Dimethyl(R)@17		-0.05	2067.05	690.02	2067.10	690.04	3	120.0
	33.4	A0QYY6	MSMEG_3833	98.0	GGLILDIGLR	iTRAQ4plex@N-term		0.01	1169.73	585.87	1169.73	585.87	2	126.7
	33.4	A0QYY6	MSMEG_3833	98.0	GFLPASLVEMR	iTRAQ4plex@N-term; Dimethyl(R)@11		-0.02	1390.76	696.39	1390.78	696.40	2	147.1
	33.4	A0QYY6	MSMEG_3833	98.0	LVPFGAFVR	iTRAQ4plex@N-term		-0.03	1148.65	575.33	1148.68	575.35	2	1.285.1
	33.4	A0QYY6	MSMEG_3833	97.0	DLQPYIGK	iTRAQ4plex@N-term; Lys->Gln@8		0.02	1076.58	539.30	1076.56	539.29	2	1.505.8
	33.4	A0QYY6	MSMEG_3833	93.0	TEGVIPSR	iTRAQ4plex@N-term		0.01	1001.57	501.79	1001.56	501.79	2	2.980.1
	33.4	A0QYY6	MSMEG_3833	91.0	SEESSGGTLASDAQLAALR	iTRAQ4plex@N-term		0.03	2006.03	669.68	2006.00	669.68	3	
	33.4	A0QYY6	MSMEG_3833	88.0	VIDIDLER	iTRAQ4plex@N-term		-0.01	1115.62	558.82	1115.63	558.82	2	1.567.2
	33.4	A0QYY6	MSMEG_3833	84.0	YFNDGDIVEGTIVK	iTRAQ4plex@N-term; iTRAQ4plex(T)@11; Lys->Gln@14		-0.01	1856.93	619.98	1856.94	619.99	3	202.3
83	32.6	A0QSD8	MSMEG_1443	98.0	GIASGGTSVSFGDYGIQALEHAYITNR	iTRAQ4plex@N-term		-0.02	2927.43	732.87	2927.45	732.87	4	91.9
	32.6	A0QSD8	MSMEG_1443	96.0	VWINIFPDRPLTK	iTRAQ4plex@N-term; Lys->Gln@13		0.01	1741.97	581.66	1741.96	581.66	3	33.5
84	31.9	A0QQC1	MSMEG_0702	99.0	LGTMVTSATFR	iTRAQ4plex@N-term		0.00	1326.71	664.36	1326.71	664.36	2	2.996.0
	31.9	A0QQC1	MSMEG_0702	99.0	LGYSAFFR	iTRAQ4plex@N-term		-0.02	1103.56	552.79	1103.59	552.80	2	2.088.5
	31.9	A0QQC1	MSMEG_0702	99.0	MAGDGLPGPTDSWVTLAGIAR	iTRAQ4plex@N-term		-0.02	2228.12	743.71	2228.14	743.72	3	231.3
	31.9	A0QQC1	MSMEG_0702	99.0	VAAAVEGAGR	iTRAQ4plex@N-term		0.03	1043.61	522.81	1043.58	522.80	2	2.360.4
	31.9	A0QQC1	MSMEG_0702	99.0	YPGPLAISVAQVDEMSGGR	iTRAQ4plex@N-term		-0.02	2090.04	697.69	2090.06	697.69	3	164.6
	31.9	A0QQC1	MSMEG_0702	91.0	LGPFIEAGVQR	iTRAQ4plex@N-term		0.01	1329.76	665.89	1329.75	665.88	2	405.6
85	31.8	A0QSG4	MSMEG_1470	99.0	AEDGAIVVTRPDDER	iTRAQ4plex@N-term		0.07	1785.97	596.33	1785.90	596.31	3	1.324.4
	31.8	A0QSG4	MSMEG_1470	99.0	AEDGAIVVTRPDDERR	iTRAQ4plex@N-term	missed R-R@15	0.02	1942.02	486.51	1942.00	486.51	4	135.2
	31.8	A0QSG4	MSMEG_1470	99.0	TLIANLVTGVTEGYTQK	iTRAQ4plex@N-term; Lys->Gln@17		0.03	1951.07	651.36	1951.04	651.35	3	

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	31.8	A0QSG4	MSMEG_1470	98.0	VGQISAVIR	iTRAQ4plex@N-term		0.01	1085.67	543.84	1085.67	543.84	2	1.315.8
	31.8	A0QSG4	MSMEG_1470	96.0	EIFGVGYR	iTRAQ4plex@N-term	cleaved M-E@N-term	-0.02	1083.56	542.79	1083.58	542.80	2	2.555.5
86	31.2	A0R3L1	MSMEG_5512	99.0	AADSGDDLPVEWR	iTRAQ4plex@N-term		0.01	1573.76	787.89	1573.75	787.88	2	132.5
	31.2	A0R3L1	MSMEG_5512	99.0	ALIAGHDVVLLGER	iTRAQ4plex@N-term		0.00	1605.94	536.32	1605.93	536.32	3	554.2
	31.2	A0R3L1	MSMEG_5512	99.0	ENLLAALAER	iTRAQ4plex@N-term		0.00	1242.71	622.36	1242.71	622.36	2	875.6
	31.2	A0R3L1	MSMEG_5512	99.0	EQAVLEHLLR	iTRAQ4plex@N-term; Dimethyl(R)@10		-0.02	1378.78	460.60	1378.81	460.61	3	47.7
	31.2	A0R3L1	MSMEG_5512	99.0	VDLGTVIDVLR	iTRAQ4plex@N-term	cleaved V-V@N-term	-0.01	1342.78	672.40	1342.79	672.40	2	171.2
	31.2	A0R3L1	MSMEG_5512	99.0	VVDLGTVIDVLR	iTRAQ4plex@N-term		-0.02	1441.84	721.93	1441.86	721.94	2	361.6
	31.2	A0R3L1	MSMEG_5512	99.0	EQAVLEHLLR	iTRAQ4plex@N-term		-0.03	1350.74	451.25	1350.77	451.27	3	111.3
	31.2	A0R3L1	MSMEG_5512	87.0	ENLLAALAER	iTRAQ4plex@N-term; Dimethyl(R)@10		-0.01	1270.73	636.37	1270.74	636.38	2	653.1
87	30.9	A0QXX7	MSMEG_3461	99.0	DGAGAGTIPDPFGGPGR	iTRAQ4plex@N-term		-0.04	1684.79	562.60	1684.83	562.62	3	170.6
	30.9	A0QXX7	MSMEG_3461	99.0	NPTMLVTDISMR	iTRAQ4plex@N-term		0.02	1520.80	761.41	1520.78	761.40	2	1.012.8
	30.9	A0QXX7	MSMEG_3461	99.0	TAWASAASYR	iTRAQ4plex@N-term		0.00	1226.61	614.31	1226.62	614.32	2	5.826.7
	30.9	A0QXX7	MSMEG_3461	99.0	WLDHPEELSEAFAK	iTRAQ4plex@N-term; Lys->Gln@14		-0.01	1814.85	605.96	1814.86	605.96	3	239.8
	30.9	A0QXX7	MSMEG_3461	99.0	WTATANDLVFGSHSVLR	iTRAQ4plex@N-term		-0.02	2017.03	673.35	2017.05	673.36	3	336.9
	30.9	A0QXX7	MSMEG_3461	99.0	WLDHPEELSEAFAK	iTRAQ4plex@N-term; Lys->Arg@14		0.00	1842.90	615.31	1842.90	615.31	3	33.7
	30.9	A0QXX7	MSMEG_3461	99.0	WTATANDLVFGSHSVLR	iTRAQ4plex@N-term; Dimethyl(R)@17		0.00	2045.08	682.70	2045.08	682.70	3	183.0
	30.9	A0QXX7	MSMEG_3461	99.0	FAPINSWPDNVSLDKAR	iTRAQ4plex@N-term; Deamidated(N)@10; User modH on Lys(K)@15	missed K-A@15	0.04	2317.21	773.41	2317.17	773.40	3	19.6
	30.9	A0QXX7	MSMEG_3461	98.0	VSLADLIVLAGSAAIEK	iTRAQ4plex@N-term; Lys->Gln@17		0.08	1813.12	605.38	1813.03	605.35	3	69.2
	30.9	A0QXX7	MSMEG_3461	96.0	FAPINSWPDNVSLDKAR	iTRAQ4plex@N-term; Lys->Ser@15; Arg->Orn(R)@17	missed K-A@15	0.04	1990.03	664.35	1989.99	664.34	3	500.7
	30.9	A0QXX7	MSMEG_3461	95.0	TFGFGFGR	iTRAQ4plex@N-term		0.00	1031.53	516.77	1031.53	516.77	2	1.498.0
	30.9	A0QXX7	MSMEG_3461	89.0	ALDVNHGGTK	iTRAQ4plex@N-term; Lys->Gln@10		0.03	1154.61	385.88	1154.58	385.87	3	13.0
88	29.8	A0R4H0	MSMEG_5830	99.0	EIPDVIAQALSELR	iTRAQ4plex@N-term		0.02	1696.97	849.49	1696.95	849.48	2	211.5
	29.8	A0R4H0	MSMEG_5830	99.0	SSSSNPALALPDDAR	iTRAQ4plex@N-term		0.01	1643.83	822.92	1643.82	822.92	2	327.4
	29.8	A0R4H0	MSMEG_5830	99.0	VSETTAHGYPIR	iTRAQ4plex@N-term		0.03	1473.80	492.27	1473.77	492.26	3	211.8
	29.8	A0R4H0	MSMEG_5830	99.0	EIPDVIAQALSELR	iTRAQ4plex@N-term; Dimethyl(R)@14		0.04	1725.02	863.52	1724.98	863.50	2	69.3
	29.8	A0R4H0	MSMEG_5830	99.0	EIPDVIAQALSELR	iTRAQ4plex@N-term; Dimethyl(R)@14		0.00	1724.98	863.50	1724.98	863.50	2	169.3
	29.8	A0R4H0	MSMEG_5830	94.0	LAFVEDR	iTRAQ4plex@N-term		-0.01	992.53	497.27	992.54	497.28	2	306.1
	29.8	A0R4H0	MSMEG_5830	91.0	DIDDVER	iTRAQ4plex@N-term		0.00	1004.49	503.25	1004.49	503.25	2	92.7
89	29.1	A0QV10	MSMEG_2408	99.0	AIANSGVPR	iTRAQ4plex@N-term		0.01	1027.60	514.81	1027.59	514.80	2	1.459.4
	29.1	A0QV10	MSMEG_2408	99.0	AVAAALQAGYR	iTRAQ4plex@N-term		0.00	1233.69	617.85	1233.70	617.85	2	5.254.7
	29.1	A0QV10	MSMEG_2408	99.0	LGIATEAWSPLGQGSLLADPVITGIAEQ	iTRAQ4plex@N-term; iTRAQ4plex(H)@29; Lys->Gln@31		0.05	3416.87	855.23	3416.82	855.21	4	200.8
	29.1	A0QV10	MSMEG_2408	99.0	LWNSDQGYDATLAAFDASVQR	iTRAQ4plex@N-term		-0.02	2471.16	824.73	2471.18	824.74	3	104.1
	29.1	A0QV10	MSMEG_2408	85.0	LWNSDQGYDATLAAFDASVQR	iTRAQ4plex@N-term; Gln->Arg@20		-0.06	2499.17	834.06	2499.23	834.08	3	18.5
	29.1	A0QV10	MSMEG_2408	76.0	TPAQVLIR	iTRAQ4plex@N-term		0.00	1040.64	521.33	1040.65	521.33	2	4.599.3
90	29.0	A0R0B2	MSMEG_4325	99.0	ACAVEPTGMAAVLGGDEAEVLAR	iTRAQ4plex@N-term; Pyridylethyl(C)@2		0.06	2478.29	827.11	2478.24	827.09	3	111.1
	29.0	A0R0B2	MSMEG_4325	99.0	LEALDLVPANR	iTRAQ4plex@N-term		-0.03	1353.74	677.88	1353.77	677.89	2	1.990.3
91	28.9	A0R2Y1	MSMEG_5273	99.0	AEEAINSGFFER	iTRAQ4plex@N-term		0.02	1512.75	757.38	1512.73	757.37	2	2.908.5
	28.9	A0R2Y1	MSMEG_5273	99.0	AVAVQLGYDFLPGTTVNR	iTRAQ4plex@N-term		-0.05	2064.06	689.03	2064.11	689.04	3	26.1
	28.9	A0R2Y1	MSMEG_5273	99.0	ITATLLNNLQTHDK	iTRAQ4plex@N-term; Lys->Gln@14		0.02	1724.94	575.99	1724.92	575.98	3	127.7
	28.9	A0R2Y1	MSMEG_5273	99.0	GSLVEMRPDDLAAQMVK	iTRAQ4plex@N-term; Lys->Gln@17		0.03	2003.02	668.68	2002.99	668.67	3	70.6
	28.9	A0R2Y1	MSMEG_5273	97.0	EDQDHWGVR	iTRAQ4plex@N-term		0.04	1284.64	429.22	1284.60	429.21	3	126.7
	28.9	A0R2Y1	MSMEG_5273	93.0	IVSTGVSGLSPEIMGLGPIEAVKK	iTRAQ4plex@N-term; Oxidation(P)@18; Lys->Gln@23; Lys->Gln@24	missed K-K@23	0.11	2541.45	848.16	2541.35	848.12	3	56.5
92	28.4	A0QT04	MSMEG_1665	99.0	ATAEYSGDHTSSIR	iTRAQ4plex@N-term		0.01	1637.79	546.94	1637.78	546.93	3	894.1
	28.4	A0QT04	MSMEG_1665	99.0	IVVGDPHDPDTDLGPLISYAHR	iTRAQ4plex@N-term		0.03	2530.32	633.59	2530.29	633.58	4	319.1
	28.4	A0QT04	MSMEG_1665	99.0	LASEAGLPDGVFNVVTGSGAEVGTALA	iTRAQ4plex@N-term		0.00	2995.55	749.89	2995.55	749.89	4	67.0
	28.4	A0QT04	MSMEG_1665	99.0	LATEFDVPGSVDNIDFFAGAAR	iTRAQ4plex@N-term		-0.03	2455.19	819.40	2455.21	819.41	3	15.2
	28.4	A0QT04	MSMEG_1665	99.0	SFTDDDDALR	iTRAQ4plex@N-term		0.02	1297.61	649.81	1297.59	649.80	2	3.811.3
	28.4	A0QT04	MSMEG_1665	99.0	SVSEYNLATAADVDTAVAAAR	iTRAQ4plex@N-term; Ala->Val@20		0.04	2266.20	756.41	2266.16	756.39	3	
93	28.4	A0R4B7	MSMEG_5776	99.0	IQEEDDAMDDLHGHLFTVLMDR	iTRAQ4plex@N-term		-0.05	2743.22	686.81	2743.27	686.82	4	31.5
	28.4	A0R4B7	MSMEG_5776	99.0	TVVSAIQIIADVDR	iTRAQ4plex@N-term		0.03	1642.97	548.66	1642.94	548.65	3	
94	27.8	A0QPE8	MSMEG_0373	99.0	LNVNGSSLAAGHPFAATGGR	iTRAQ4plex@N-term		0.04	2040.11	681.04	2040.06	681.03	3	320.0

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	27.8	A0QPE8	MSMEG_0373	99.0	LPASLGVEIPVNSEPR	iTRAQ4plex@N-term		-0.01	1821.00	608.01	1821.01	608.01	3	85.3
	27.8	A0QPE8	MSMEG_0373	99.0	NMAAAYDAGFFDDLVTPFLGVYR	iTRAQ4plex@N-term		0.06	2696.37	899.80	2696.31	899.78	3	116.1
	27.8	A0QPE8	MSMEG_0373	99.0	VAVLGGNR	iTRAQ4plex@N-term		-0.01	928.55	465.28	928.56	465.29	2	1.633.0
	27.8	A0QPE8	MSMEG_0373	99.0	LNVNGSSLAAGHPFAATGGR	iTRAQ4plex@N-term; Deamidated(N)@4		0.00	2041.04	681.35	2041.05	681.36	3	126.0
95	27.8	A0R2V7	MSMEG_5249	99.0	QPAFQQYAQQVADNAQALADGFVK	iTRAQ4plex@N-term; Deamidated(Q)@9; User modH on Lys(K)@24; Arg->Orn(R)@25	cleaved A-G@C-term; missed K-R@24; m	0.06	3295.67	824.93	3295.61	824.91	4	923.9
	27.8	A0R2V7	MSMEG_5249	99.0	HINDLSEADWETLR	iTRAQ4plex@N-term		0.00	1841.90	614.97	1841.90	614.97	3	311.8
	27.8	A0R2V7	MSMEG_5249	99.0	LGTPALTSR	iTRAQ4plex@N-term		0.02	1058.64	530.33	1058.62	530.32	2	3.027.9
	27.8	A0R2V7	MSMEG_5249	99.0	QAESALLDAGIVTNR	iTRAQ4plex@N-term		0.00	1700.92	851.47	1700.92	851.47	2	1.682.3
	27.8	A0R2V7	MSMEG_5249	99.0	VAELIVEVLANTQPEGTSK	iTRAQ4plex@N-term; Lys->Gln@19		0.03	2141.17	714.73	2141.13	714.72	3	29.4
	27.8	A0R2V7	MSMEG_5249	97.0	AVALAEAR	iTRAQ4plex@N-term		0.02	943.58	472.80	943.56	472.79	2	1.789.2
	27.8	A0R2V7	MSMEG_5249	92.0	YAEGTIGHR	iTRAQ4plex@N-term		-0.01	1146.58	383.20	1146.59	383.20	3	100.4
	27.8	A0R2V7	MSMEG_5249	91.0	GADDFDR	iTRAQ4plex@N-term	cleaved F-G@N-term	0.01	938.43	470.22	938.42	470.22	2	53.1
	27.8	A0R2V7	MSMEG_5249	89.0	LADGTAER	iTRAQ4plex@N-term		0.02	975.53	488.77	975.51	488.76	2	149.3
96	27.5	A0R5N7	MSMEG_6256	99.0	FAEAGVIVVDNSSAFR	iTRAQ4plex@N-term		0.00	1824.95	609.32	1824.95	609.32	3	
	27.5	A0R5N7	MSMEG_6256	99.0	ILGIPELLVSGTCVR	iTRAQ4plex@N-term; Pyridylethyl(C)@13		0.00	1818.06	607.03	1818.06	607.03	3	38.1
	27.5	A0R5N7	MSMEG_6256	99.0	VNIGVVGATGQVGQVMR	iTRAQ4plex@N-term	cleaved M-V@N-term	0.02	1828.03	610.35	1828.01	610.34	3	74.8
97	27.4	A0R3V8	MSMEG_5612	99.0	AADDGLSFVVR	iTRAQ4plex@N-term		0.01	1292.70	647.36	1292.68	647.35	2	1.831.0
	27.4	A0R3V8	MSMEG_5612	99.0	LEIGHTWYTAAAR	iTRAQ4plex@N-term		0.02	1631.87	544.96	1631.85	544.96	3	571.7
	27.4	A0R3V8	MSMEG_5612	94.0	GTGVNAEAK	iTRAQ4plex@N-term; Lys->Gln@9		0.04	989.53	495.77	989.49	495.75	2	243.4
	27.4	A0R3V8	MSMEG_5612	84.0	WVQLEPLTR	iTRAQ4plex@N-term		0.00	1284.73	643.37	1284.73	643.37	2	1.443.9
98	27.3	A0QYF5	MSMEG_3640	99.0	FALNAANAR	iTRAQ4plex@N-term		0.03	1090.63	546.32	1090.60	546.31	2	5.183.8
	27.3	A0QYF5	MSMEG_3640	99.0	GFLDEVVPLAEGSWSEATGLK	iTRAQ4plex@N-term; iTRAQ4plex(T)@18; Lys->Gln@21		0.02	2492.29	831.77	2492.27	831.76	3	88.5
	27.3	A0QYF5	MSMEG_3640	99.0	RDELQAQIDK	iTRAQ4plex@N-term; Lys->Gln@10	missed R-D@1	0.05	1358.74	453.92	1358.69	453.90	3	79.8
	27.3	A0QYF5	MSMEG_3640	99.0	TGDEIHTSMEAGPMVR	iTRAQ4plex@N-term		0.05	1873.93	625.65	1873.88	625.63	3	456.3
	27.3	A0QYF5	MSMEG_3640	99.0	TPDGEGELTLPGR	iTRAQ4plex@N-term		0.00	1484.76	743.39	1484.76	743.39	2	707.2
	27.3	A0QYF5	MSMEG_3640	99.0	VPDIHDVALMEDR	iTRAQ4plex@N-term; Dimethyl(R)@13		0.00	1680.86	561.29	1680.86	561.29	3	102.6
	27.3	A0QYF5	MSMEG_3640	99.0	VVFINTGFLDR	iTRAQ4plex@N-term		-0.02	1423.78	712.90	1423.79	712.90	2	920.8
	27.3	A0QYF5	MSMEG_3640	99.0	VPDIHDVALMEDR	iTRAQ4plex@N-term		0.00	1652.83	551.95	1652.83	551.95	3	351.3
	27.3	A0QYF5	MSMEG_3640	99.0	VPDIHDVALMEDR	iTRAQ4plex@N-term		-0.03	1652.80	551.94	1652.83	551.95	3	64.1
	27.3	A0QYF5	MSMEG_3640	92.0	NWLGLNR	iTRAQ4plex@N-term		-0.01	1015.56	508.79	1015.57	508.79	2	2.989.5
	27.3	A0QYF5	MSMEG_3640	91.0	NQELLAR	iTRAQ4plex@N-term		0.02	986.58	494.30	986.56	494.29	2	1.190.2
99	27.3	A0R095	MSMEG_4306	99.0	QASLEEQLLEVMER	iTRAQ4plex@N-term		-0.02	1817.91	606.98	1817.93	606.98	3	10.9
	27.3	A0R095	MSMEG_4306	99.0	QVTEIQHELETLQR	iTRAQ4plex@N-term		-0.05	1866.94	623.32	1866.99	623.34	3	162.3
100	27.2	A0R0W7	MSMEG_4533	99.0	AVVDGKPADIVNFSVEPDVTR	iTRAQ4plex@N-term; Lys->Gln@6		0.00	2371.21	791.41	2371.21	791.41	3	268.5
	27.2	A0R0W7	MSMEG_4533	99.0	GIPFGSVVSLVVR	iTRAQ4plex@N-term		-0.03	1472.86	737.43	1472.88	737.45	2	238.9
	27.2	A0R0W7	MSMEG_4533	99.0	TSFGASGDQSR	iTRAQ4plex@N-term		0.02	1255.61	628.81	1255.59	628.80	2	225.3
	27.2	A0R0W7	MSMEG_4533	96.0	IENPVAVVNTTSHSEAANALK	iTRAQ4plex@N-term; iTRAQ4plex(S)@14; Lys->Gln@21		0.02	2452.30	614.08	2452.28	614.08	4	392.0
	27.2	A0R0W7	MSMEG_4533	95.0	IIPAFTATDEGK	iTRAQ4plex@N-term; Lys->Gln@12		0.02	1405.74	703.88	1405.72	703.87	2	599.3
101	26.4	A0R066	MSMEG_4276	99.0	DSLLQLATDAGFAVEER	iTRAQ4plex@N-term		0.01	1978.02	660.35	1978.01	660.34	3	19.6
	26.4	A0R066	MSMEG_4276	99.0	LVTPELSGSLLPGITR	iTRAQ4plex@N-term		0.00	1796.05	899.03	1796.05	899.03	2	3.177.2
	26.4	A0R066	MSMEG_4276	99.0	VIATEPGLGVRPSNEYR	iTRAQ4plex@N-term	cleaved F-V@N-term	0.02	2001.09	668.04	2001.08	668.03	3	1.896.8
	26.4	A0R066	MSMEG_4276	99.0	WADGSIVSFRPEAN	iTRAQ4plex@N-term	cleaved N-A@C-term	0.01	1691.85	846.93	1691.84	846.93	2	2.490.8
	26.4	A0R066	MSMEG_4276	99.0	WADGSIVSFRPEANAAR	iTRAQ4plex@N-term		0.01	1990.03	664.35	1990.01	664.35	3	771.5
	26.4	A0R066	MSMEG_4276	99.0	DSLLQLATDAGFAVEER	iTRAQ4plex@N-term		0.00	1978.01	660.34	1978.01	660.34	3	
	26.4	A0R066	MSMEG_4276	99.0	DSLLQLATDAGFAVEER	iTRAQ4plex@N-term; Thr->Asn@8		0.02	1991.02	664.68	1991.01	664.68	3	21.7
	26.4	A0R066	MSMEG_4276	99.0	DSLLQLATDAGFAVEER	iTRAQ4plex@N-term		0.04	1978.05	660.36	1978.01	660.34	3	30.4
	26.4	A0R066	MSMEG_4276	99.0	DSLLQLATDAGFAVEER	iTRAQ4plex@N-term; Dimethyl(R)@17		0.03	2006.08	669.70	2006.04	669.69	3	17.2
	26.4	A0R066	MSMEG_4276	99.0	WADGSIVSFRPEANAAR	iTRAQ4plex@N-term		0.00	1990.02	664.35	1990.01	664.35	3	598.1
	26.4	A0R066	MSMEG_4276	97.0	YLLIASPAGAYFK	iTRAQ4plex@N-term; iTRAQ4plex(Y)@11; Lys->Gln@13		0.02	1700.96	567.99	1700.94	567.99	3	95.4
	26.4	A0R066	MSMEG_4276	95.0	DSLLQLATDAGFAVEER	iTRAQ4plex@N-term		0.01	1978.02	660.35	1978.01	660.34	3	6.5
	26.4	A0R066	MSMEG_4276	83.0	DSLLQLATDAGFAVEER	iTRAQ4plex@N-term; Oxidation(D)@9; Oxidation(F)@12		0.05	2010.05	671.02	2010.00	671.01	3	6.5
102	26.3	A0R623	MSMEG_6398	99.0	ANDPTENVATIANNGTR	iTRAQ4plex@N-term; Deamidated(N)@14		0.03	1901.95	951.98	1901.92	951.97	2	895.6
	26.3	A0R623	MSMEG_6398	99.0	VEFQSGGPGAPALYLLDGMR	iTRAQ4plex@N-term		-0.04	2221.09	741.37	2221.13	741.38	3	73.6

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	26.3	A0R623	MSMEG_6398	99.0	WSRPGLPVEYLEVPSAAMGR	iTRAQ4plex@N-term	cleaved A-W@N-term	-0.01	2358.21	787.08	2358.23	787.08	3	165.8
103	25.9	A0R278	MSMEG_5015	99.0	DDLTGYQHLHPALDATGTWSVPLDVPT	iTRAQ4plex@N-term; iTRAQ4plex(T)@27; Lys->Gln@30		0.00	3448.71	863.18	3448.71	863.19	4	122.4
	25.9	A0R278	MSMEG_5015	99.0	DGKPADLQPYLGAYGHLVALR	iTRAQ4plex@N-term; Lys->Gln@3		0.07	2397.33	600.34	2397.26	600.32	4	67.9
	25.9	A0R278	MSMEG_5015	99.0	VFADFVPAGASGVVAEADLR	iTRAQ4plex@N-term		0.00	2134.11	712.38	2134.12	712.38	3	18.5
	25.9	A0R278	MSMEG_5015	99.0	DGKPADLQPYLGAYGHLVALR	iTRAQ4plex@N-term; Asp->Trp@1; Lys->Pro@3		0.00	2437.31	610.33	2437.30	610.33	4	121.7
	25.9	A0R278	MSMEG_5015	99.0	VFADFVPAGASGVVAEADLR	iTRAQ4plex@N-term; Ala->Val@17		-0.02	2162.13	721.72	2162.15	721.72	3	26.8
	25.9	A0R278	MSMEG_5015	98.0	DDLTGYQHLHPALDATGTWSVPLDVPT	iTRAQ4plex@N-term; iTRAQ4plex(T)@27; Lys->Gln@30		0.07	3448.78	863.20	3448.71	863.19	4	211.4
104	25.6	A0QV37	MSMEG_2435	96.0	LDLFNAALAEAESGTTAAATTPK	iTRAQ4plex@N-term; iTRAQ4plex(T)@21; Lys->Gln@23		0.02	2550.33	851.12	2550.31	851.11	3	29.4
	25.6	A0QV37	MSMEG_2435	91.0	IIVADAR	iTRAQ4plex@N-term		0.00	900.55	451.28	900.55	451.28	2	1.282.8
105	25.5	A0R3C8	MSMEG_5427	99.0	DVIIAATHGVLSDPAPQR	iTRAQ4plex@N-term		-0.07	2003.02	668.68	2003.09	668.70	3	370.9
	25.5	A0R3C8	MSMEG_5427	99.0	ITAILPFYPYAR	iTRAQ4plex@N-term		0.03	1567.92	784.97	1567.89	784.95	2	1.867.3
	25.5	A0R3C8	MSMEG_5427	99.0	IVSVDLHTDQIQGFFDGPVDHMR	iTRAQ4plex@N-term		0.01	2769.38	693.35	2769.37	693.35	4	218.2
	25.5	A0R3C8	MSMEG_5427	99.0	NLMLFAGR	iTRAQ4plex@N-term		-0.03	1064.56	533.29	1064.59	533.30	2	2.307.8
	25.5	A0R3C8	MSMEG_5427	94.0	IVSVDLHTDQIQGFFDGPVDHMR	iTRAQ4plex@N-term		0.00	2769.37	693.35	2769.37	693.35	4	78.3
	25.5	A0R3C8	MSMEG_5427	93.0	WADSLGGVPLAFIHK	iTRAQ4plex@N-term; Lys->Gln@15		-0.01	1753.92	585.65	1753.93	585.65	3	192.8
106	25.3	A0R1H2	MSMEG_4752	99.0	AAVVGFIR	iTRAQ4plex@N-term		-0.02	975.58	488.80	975.60	488.81	2	2.066.3
	25.3	A0R1H2	MSMEG_4752	99.0	LALTVDSLAER	iTRAQ4plex@N-term		-0.02	1330.74	666.38	1330.76	666.39	2	828.0
107	25.1	A0R198	MSMEG_4673	99.0	GTGQGLNLVDSVYER	iTRAQ4plex@N-term		-0.01	1750.89	876.45	1750.90	876.46	2	1.390.7
	25.1	A0R198	MSMEG_4673	99.0	IEADSDRDR	iTRAQ4plex@N-term	missed R-D@7	0.00	1219.59	407.54	1219.59	407.54	3	15.2
	25.1	A0R198	MSMEG_4673	99.0	IIFLGSQVDDDIANR	iTRAQ4plex@N-term		-0.04	1818.92	607.31	1818.96	607.33	3	168.7
	25.1	A0R198	MSMEG_4673	99.0	LNAEFTGQPIER	iTRAQ4plex@N-term		0.01	1517.80	759.91	1517.80	759.91	2	2.223.1
108	25.1	A0QXZ4	MSMEG_3478	99.0	APTLADTAMFAR	iTRAQ4plex@N-term		0.01	1407.74	704.88	1407.73	704.87	2	2.103.6
	25.1	A0QXZ4	MSMEG_3478	99.0	EWMFFDAAHR	iTRAQ4plex@N-term	cleaved Y-E@N-term	-0.01	1452.67	485.23	1452.67	485.23	3	110.4
	25.1	A0QXZ4	MSMEG_3478	99.0	LGATLGETEQATAQR	iTRAQ4plex@N-term		0.04	1688.93	845.47	1688.88	845.45	2	2.392.4
	25.1	A0QXZ4	MSMEG_3478	99.0	VGAELMQR	iTRAQ4plex@N-term		-0.01	1046.56	524.29	1046.57	524.29	2	7.273.4
	25.1	A0QXZ4	MSMEG_3478	99.0	APTLADTAMFAR	iTRAQ4plex@N-term		0.01	1407.74	704.88	1407.73	704.87	2	2.288.0
	25.1	A0QXZ4	MSMEG_3478	90.0	YEWMFFDAAHR	iTRAQ4plex@N-term		0.00	1615.74	539.59	1615.74	539.59	3	81.1
	25.1	A0QXZ4	MSMEG_3478	90.0	YEWMFFDAAHR	iTRAQ4plex@N-term		-0.03	1615.70	539.58	1615.74	539.59	3	42.4
109	24.8	A0QSU4	MSMEG_1603	99.0	FEIPVIAHPTDALVSPEFAIEMGR	iTRAQ4plex@N-term		0.00	2782.45	928.49	2782.45	928.49	3	141.0
	24.8	A0QSU4	MSMEG_1603	99.0	TFISELDVPVVAGGVLDHR	iTRAQ4plex@N-term		-0.03	2167.14	723.39	2167.18	723.40	3	376.4
110	24.7	A0R0B5	MSMEG_4328	99.0	IEAVPIAGFAQMR	iTRAQ4plex@N-term		0.00	1545.84	773.93	1545.85	773.93	2	1.023.2
	24.7	A0R0B5	MSMEG_4328	99.0	IGGHLLEEFDSELTR	iTRAQ4plex@N-term		0.02	1858.97	620.67	1858.95	620.66	3	241.2
	24.7	A0R0B5	MSMEG_4328	99.0	LSYLQKMATVLGRR	iTRAQ4plex@N-term; User modH on Lys(K)@6; Deamidated(R)@13	missed K-M@6; missed R-R@13	-0.01	2023.12	675.38	2023.12	675.38	3	95.7
	24.7	A0R0B5	MSMEG_4328	97.0	AGVCTSISACASGSEAIANAWR	iTRAQ4plex@N-term; No Pyridylethyl(C)@4; Cys->Thr@10		-0.08	2266.04	756.35	2266.11	756.38	3	59.4
111	24.5	A0QVY9	MSMEG_2744	99.0	EDEATGAAAVR	iTRAQ4plex@N-term		0.01	1232.62	617.32	1232.61	617.31	2	31.5
	24.5	A0QVY9	MSMEG_2744	99.0	FGNPLGVVDNSTVDPADR	iTRAQ4plex@N-term		0.02	2016.02	673.02	2016.00	673.01	3	436.2
	24.5	A0QVY9	MSMEG_2744	99.0	MFATNLGIR	iTRAQ4plex@N-term		-0.03	1165.61	583.81	1165.64	583.83	2	5.509.9
	24.5	A0QVY9	MSMEG_2744	99.0	EDEATGAAAVR	iTRAQ4plex@N-term		0.02	1232.63	617.32	1232.61	617.31	2	2.539.5
	24.5	A0QVY9	MSMEG_2744	93.0	ITDYLSR	iTRAQ4plex@N-term		-0.01	1010.54	506.28	1010.55	506.28	2	3.469.4
112	24.0	A0QVT1	MSMEG_2684	99.0	DMLTAFNSGDVATAR	iTRAQ4plex@N-term; Ala->Val@14		0.02	1739.88	580.97	1739.86	580.96	3	222.1
	24.0	A0QVT1	MSMEG_2684	99.0	LPQIPATTEEVEALAADMR	iTRAQ4plex@N-term		-0.02	2198.11	733.71	2198.14	733.72	3	
	24.0	A0QVT1	MSMEG_2684	99.0	SVVPIAWDTLR	iTRAQ4plex@N-term		0.01	1399.80	700.91	1399.79	700.90	2	1.653.2
	24.0	A0QVT1	MSMEG_2684	99.0	TVVDAVGDR	iTRAQ4plex@N-term		0.00	1074.58	538.30	1074.58	538.30	2	9.724.5
	24.0	A0QVT1	MSMEG_2684	99.0	VIAGAGSYDTAHSVHLAK	iTRAQ4plex@N-term; Lys->Gln@18		0.05	1940.03	486.02	1939.99	486.00	4	746.5
	24.0	A0QVT1	MSMEG_2684	99.0	LPQIPATTEEVEALAADMR	iTRAQ4plex@N-term		-0.02	2198.12	733.71	2198.14	733.72	3	23.9
113	24.0	A0QZR5	MSMEG_4121	98.0	SSAELATLADIVQR	iTRAQ4plex@N-term		0.04	1616.93	539.98	1616.89	539.97	3	
114	23.8	A0R2V1	MSMEG_5243	99.0	VLPTQITGR	iTRAQ4plex@N-term		0.00	1127.68	564.85	1127.68	564.85	2	4.284.0
115	23.7	A0QVR8	MSMEG_2669	99.0	IPNWGPINLNTVFSDQDER	iTRAQ4plex@N-term		-0.03	2358.14	787.05	2358.17	787.06	3	57.4

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	23.7	A0QVR8	MSMEG_2669	85.0	IAVEDDPDSPHLLADK	iTRAQ4plex@N-term; iTRAQ4plex(H)@11; Lys->Gln@16		0.05	2022.06	675.03	2022.01	675.01	3	943.8
	23.7	A0QVR8	MSMEG_2669	85.0	RLEDALSGASVEHTIEFYPAGHGF	iTRAQ4plex@N-term	cleaved F-A@C-term; missed R-L@1	-0.02	2746.33	687.59	2746.35	687.59	4	
116	23.5	A0R2U8	MSMEG_5240	99.0	ADTDVEYR	iTRAQ4plex@N-term	cleaved M-A@N-term	0.00	1111.52	556.77	1111.53	556.77	2	158.2
	23.5	A0R2U8	MSMEG_5240	99.0	AVENFPISFR	iTRAQ4plex@N-term		0.01	1322.72	662.37	1322.71	662.36	2	732.4
	23.5	A0R2U8	MSMEG_5240	99.0	NLLESFTLLSNVSR	iTRAQ4plex@N-term		0.00	1735.96	868.99	1735.96	868.99	2	514.1
	23.5	A0R2U8	MSMEG_5240	99.0	VVEVLVNETGLAELR	iTRAQ4plex@N-term		0.00	1784.02	595.68	1784.02	595.68	3	
	23.5	A0R2U8	MSMEG_5240	97.0	QIEAGIER	iTRAQ4plex@N-term		0.02	1058.60	530.31	1058.58	530.30	2	1.365.1
117	23.5	A0QQF0	MSMEG_0732	99.0	AIDLVDEAASR	iTRAQ4plex@N-term		0.02	1302.71	652.36	1302.69	652.35	2	1.602.0
	23.5	A0QQF0	MSMEG_0732	99.0	ALAEFLFDDER	iTRAQ4plex@N-term		0.00	1468.73	735.37	1468.73	735.37	2	1.479.0
	23.5	A0QQF0	MSMEG_0732	99.0	ITDSALVAAATLSDR	iTRAQ4plex@N-term		0.02	1646.92	824.47	1646.90	824.46	2	422.4
	23.5	A0QQF0	MSMEG_0732	99.0	IVAGDVPESLR	iTRAQ4plex@N-term		0.00	1298.74	650.38	1298.73	650.37	2	2.009.6
	23.5	A0QQF0	MSMEG_0732	99.0	MEIDSRPVEIDEVER	iTRAQ4plex@N-term		0.07	1960.03	654.35	1959.97	654.33	3	506.6
	23.5	A0QQF0	MSMEG_0732	99.0	TAIVEGLAQR	iTRAQ4plex@N-term		-0.02	1200.68	601.35	1200.69	601.35	2	3.605.9
	23.5	A0QQF0	MSMEG_0732	99.0	ITDSALVAAATLSDR	iTRAQ4plex@N-term		0.03	1646.93	549.98	1646.90	549.97	3	
	23.5	A0QQF0	MSMEG_0732	97.0	TVIALDLGSMVAGAK	iTRAQ4plex@N-term; Lys->Gln@15		0.04	1588.91	530.64	1588.86	530.63	3	
	23.5	A0QQF0	MSMEG_0732	80.0	YSTDLTAR	iTRAQ4plex@N-term		-0.01	1069.54	535.78	1069.55	535.78	2	12.437.7
118	23.5	A0R3Y5	MSMEG_5639	99.0	EAVENAASEDIR	iTRAQ4plex@N-term		-0.01	1446.70	724.35	1446.71	724.36	2	1.802.8
	23.5	A0R3Y5	MSMEG_5639	99.0	LDAETALQTGMANR	iTRAQ4plex@N-term		0.02	1633.84	817.93	1633.82	817.92	2	939.2
	23.5	A0R3Y5	MSMEG_5639	99.0	LTSLVGYGR	iTRAQ4plex@N-term		0.00	1108.64	555.33	1108.64	555.33	2	1.725.1
	23.5	A0R3Y5	MSMEG_5639	99.0	SPDVIEAQVAR	iTRAQ4plex@N-term		0.00	1327.72	664.87	1327.72	664.87	2	2.495.2
	23.5	A0R3Y5	MSMEG_5639	99.0	YGLALDNWSIR	iTRAQ4plex@N-term		-0.01	1450.76	726.39	1450.77	726.39	2	2.670.9
119	23.3	A0R574	MSMEG_6091	99.0	AHQEIYNSLLQVLEDGR	iTRAQ4plex@N-term		-0.01	2128.09	710.37	2128.10	710.38	3	128.8
	23.3	A0R574	MSMEG_6091	99.0	AIDLIDEAGAR	iTRAQ4plex@N-term		0.02	1286.72	644.37	1286.70	644.35	2	705.6
	23.3	A0R574	MSMEG_6091	99.0	EALQLGHNYIGTEHILLGLIR	iTRAQ4plex@N-term		-0.05	2503.36	626.85	2503.40	626.86	4	32.6
	23.3	A0R574	MSMEG_6091	99.0	LTEEETTR	iTRAQ4plex@N-term		0.02	1121.59	561.80	1121.57	561.79	2	440.2
	23.3	A0R574	MSMEG_6091	99.0	SQGGSENNYER	iTRAQ4plex@N-term; Deamidated(Q)@2; Methyl(S)@5	cleaved F-S@N-term	0.05	1398.66	700.34	1398.61	700.31	2	1.832.6
	23.3	A0R574	MSMEG_6091	99.0	VSITDSAMVAAATLADR	iTRAQ4plex@N-term		0.04	1834.99	612.67	1834.96	612.66	3	13.0
120	23.2	A0QWV0	MSMEG_3072	99.0	GEISGPGSDGDDVLVR	iTRAQ4plex@N-term		0.02	1715.86	858.94	1715.84	858.93	2	195.2
	23.2	A0QWV0	MSMEG_3072	99.0	VGLDGYGLHIIER	iTRAQ4plex@N-term		0.00	1584.87	529.30	1584.87	529.30	3	27.1
	23.2	A0QWV0	MSMEG_3072	98.0	HGTAYTVTVDAK	iTRAQ4plex@N-term; Lys->Gln@12		0.04	1405.73	469.58	1405.70	469.57	3	109.0
121	23.0	A0QSD1	MSMEG_1436	99.0	DGYSAVQLAYGEISPR	iTRAQ4plex@N-term		-0.06	1868.88	623.97	1868.94	623.99	3	
	23.0	A0QSD1	MSMEG_1436	98.0	AGPNVVTR	iTRAQ4plex@N-term		0.00	956.55	479.28	956.55	479.28	2	182.9
	23.0	A0QSD1	MSMEG_1436	88.0	AGPNVVTR	No iTRAQ4plex@N-term; Gly->Pro@2		0.02	852.51	427.26	852.48	427.25	2	5.4
122	23.0	A0QSZ3	MSMEG_1654	99.0	GISNFHSPSDVIVDASMPAMIR	iTRAQ4plex@N-term		0.02	2487.26	830.09	2487.24	830.09	3	75.7
	23.0	A0QSZ3	MSMEG_1654	99.0	ILAEFGDHLTEEQR	iTRAQ4plex@N-term		-0.01	1800.90	601.31	1800.91	601.31	3	99.6
	23.0	A0QSZ3	MSMEG_1654	99.0	ILGSAVNPVLR	iTRAQ4plex@N-term		-0.01	1281.78	641.90	1281.79	641.90	2	1.847.1
	23.0	A0QSZ3	MSMEG_1654	98.0	TSDISVAAR	iTRAQ4plex@N-term		0.00	1062.57	532.29	1062.58	532.30	2	273.2
	23.0	A0QSZ3	MSMEG_1654	77.0	VPDNLGELGALTQDPSANIIK	iTRAQ4plex@N-term; iTRAQ4plex(S)@16; Lys->Gln@21		0.00	2452.30	818.44	2452.31	818.44	3	27.1
123	23.0	A0R5L6	MSMEG_6235	99.0	FSTVIDSTLFHSLPVEGR	iTRAQ4plex@N-term		-0.05	2148.09	717.04	2148.13	717.05	3	79.3
	23.0	A0R5L6	MSMEG_6235	99.0	IMFPAFLLEAHRD	iTRAQ4plex@N-term	missed R-D@12	-0.02	1702.87	568.63	1702.90	568.64	3	82.4
	23.0	A0R5L6	MSMEG_6235	99.0	NLATASFVQGDITSFTGYDGR	iTRAQ4plex@N-term		-0.03	2363.12	788.71	2363.15	788.72	3	16.3
124	22.8	A0R597	MSMEG_6114	99.0	WDHIQDVGDISQFELDAIK	iTRAQ4plex@N-term; Lys->Gln@19		0.07	2372.21	791.74	2372.14	791.72	3	51.7
125	22.8	A0QS07	MSMEG_1305	99.0	LAAAVPLTPELAHDLGEFSGR	iTRAQ4plex@N-term		-0.03	2307.21	770.08	2307.23	770.09	3	151.6
	22.8	A0QS07	MSMEG_1305	99.0	LLLWEGLDRNPLDGNPPAAR	iTRAQ4plex@N-term	missed R-N@9	-0.02	2360.25	787.76	2360.27	787.76	3	221.2
126	22.8	A0R4B3	MSMEG_5773	99.0	DVSAAGLDIAPNQAMASLHR	iTRAQ4plex@N-term		-0.08	2180.03	727.69	2180.11	727.71	3	47.8
	22.8	A0R4B3	MSMEG_5773	99.0	EDFTGEGAR	iTRAQ4plex@N-term		0.00	1124.53	563.27	1124.52	563.27	2	143.8
	22.8	A0R4B3	MSMEG_5773	99.0	IHLDDVVMPVLR	iTRAQ4plex@N-term		-0.01	1549.86	517.63	1549.88	517.63	3	171.2
	22.8	A0R4B3	MSMEG_5773	99.0	TAMVQNLLTEDNLPSYHR	iTRAQ4plex@N-term		-0.02	2245.11	749.38	2245.13	749.38	3	115.7
	22.8	A0R4B3	MSMEG_5773	91.0	MPGYTVPDFR	iTRAQ4plex@N-term		0.01	1325.66	663.84	1325.66	663.84	2	929.4

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	∆Mass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
127	22.6	A0QQL0	MSMEG_0793	99.0	ASDPPTMAAAMASAVTAGHLAR	iTRAQ4plex@N-term		0.02	2240.14	747.72	2240.12	747.71	3	85.5
	22.6	A0QQL0	MSMEG_0793	99.0	RFWAQASSPAL	iTRAQ4plex@N-term	missed R-F@1	0.02	1376.75	689.38	1376.73	689.37	2	437.6
	22.6	A0QQL0	MSMEG_0793	99.0	RVDAETGTGVLDLLNR	iTRAQ4plex@N-term	missed R-V@1	-0.02	1872.00	625.01	1872.02	625.01	3	154.9
	22.6	A0QQL0	MSMEG_0793	99.0	RVDAETGTGVLDLLNR	iTRAQ4plex@N-term	missed R-V@1	-0.01	1872.01	625.01	1872.02	625.01	3	110.7
	22.6	A0QQL0	MSMEG_0793	93.0	LEVIADER	iTRAQ4plex@N-term		0.00	1087.60	544.81	1087.60	544.81	2	4.786.3
	22.6	A0QQL0	MSMEG_0793	92.0	RVDAETGTGVLDLLNR	iTRAQ4plex@N-term; Dimethyl(R)@16	missed R-V@1	-0.02	1900.03	634.35	1900.05	634.36	3	28.3
128	22.6	A0QX01	MSMEG_3124	99.0	IAILDETDSGLDVDALR	iTRAQ4plex@N-term		0.02	1959.05	654.02	1959.03	654.02	3	
	22.6	A0QX01	MSMEG_3124	99.0	YIQPQFVHVFVGGR	iTRAQ4plex@N-term		0.00	1789.97	597.66	1789.97	597.67	3	263.3
129	22.4	A0QS81	MSMEG_1383	99.0	AADAPVICETAEAGR	iTRAQ4plex@N-term; Pyridylethyl(C)@8		0.04	1721.90	574.97	1721.85	574.96	3	1.838.1
	22.4	A0QS81	MSMEG_1383	99.0	ALDALDTDVPVYLENTAGGDHAMAR	iTRAQ4plex@N-term		-0.02	2758.31	920.44	2758.34	920.45	3	352.7
	22.4	A0QS81	MSMEG_1383	85.0	DDIAFLR	iTRAQ4plex@N-term		0.00	992.54	497.28	992.54	497.28	2	229.9
130	22.2	A0QWW4	MSMEG_3086	99.0	EAGNHVEFNVNSLR	iTRAQ4plex@N-term		0.00	1728.87	577.30	1728.87	577.30	3	564.6
	22.2	A0QWW4	MSMEG_3086	99.0	GELANLSSSEIAAGVR	iTRAQ4plex@N-term		0.00	1716.91	859.46	1716.91	859.46	2	1.008.7
	22.2	A0QWW4	MSMEG_3086	87.0	LTYGAQDLSQHDSGAYTGEISGAFLAKL	iTRAQ4plex@N-term; Ala->Thr@26; Lys->Glu@27	cleaved L-G@C-term; missed K-L@27	0.10	3087.58	772.90	3087.48	772.88	4	198.2
131	22.1	A0QWV9	MSMEG_3081	99.0	GLPAQVVGGSVGDAEAAWR	iTRAQ4plex@N-term		-0.03	1983.00	662.01	1983.03	662.02	3	62.9
	22.1	A0QWV9	MSMEG_3081	99.0	LGVSAKAR	iTRAQ4plex@N-term; User modH on Lys(K)@6	missed K-A@6	0.05	1187.75	594.88	1187.70	594.86	2	622.9
	22.1	A0QWV9	MSMEG_3081	89.0	AAVAAAAR	iTRAQ4plex@N-term		-0.03	843.48	422.75	843.50	422.76	2	223.6
	22.1	A0QWV9	MSMEG_3081	77.0	LGVSAKAR	iTRAQ4plex@N-term; User modH on Lys(K)@6	missed K-A@6	-0.06	1187.64	396.89	1187.70	396.91	3	41.3
132	22.0	A0QSP9	MSMEG_1557	99.0	EPVIIDRPIQTVGR	iTRAQ4plex@N-term		0.01	1736.01	579.68	1736.01	579.68	3	1.122.6
	22.0	A0QSP9	MSMEG_1557	99.0	LVPGTGQFNLDGR	iTRAQ4plex@N-term		0.02	1516.84	759.43	1516.81	759.41	2	1.011.8
133	22.0	A0R2J4	MSMEG_5136	99.0	LVFTEDALPAVQPVNFR	iTRAQ4plex@N-term		0.03	2059.15	687.39	2059.12	687.38	3	228.1
	22.0	A0R2J4	MSMEG_5136	95.0	NQVVAFEADELDPDLR	iTRAQ4plex@N-term		0.04	1974.02	659.01	1973.98	659.00	3	8.7
134	21.9	A0R3D2	MSMEG_5431	99.0	NIQHADLLVVQR	iTRAQ4plex@N-term		0.00	1548.89	517.30	1548.89	517.30	3	528.4
	21.9	A0R3D2	MSMEG_5431	99.0	VPAVLYGHGTDPQHLELNAR	iTRAQ4plex@N-term		-0.03	2330.20	583.56	2330.23	583.56	4	310.8
	21.9	A0R3D2	MSMEG_5431	82.0	TRTGKGASR	iTRAQ4plex@N-term; User modH on Lys(K)@5	missed R-T@2; missed K-G@5	0.01	1319.74	660.88	1319.73	660.87	2	817.1
135	21.8	A0QSD7	MSMEG_1442	99.0	RSGSAGTTATSTEAGR	iTRAQ4plex@N-term	missed R-S@1	0.01	1652.83	551.95	1652.82	551.95	3	
136	21.8	A0R7G6	MSMEG_6904	99.0	AFGDVPLNLEYK	iTRAQ4plex@N-term; Lys->Gln@12		0.05	1508.82	755.42	1508.76	755.39	2	523.3
	21.8	A0R7G6	MSMEG_6904	99.0	TYQLNVGGNMDFLNMLER	iTRAQ4plex@N-term		-0.02	2258.07	753.70	2258.09	753.71	3	32.6
	21.8	A0R7G6	MSMEG_6904	99.0	SQVGATITHR	iTRAQ4plex@N-term		0.00	1212.67	405.23	1212.67	405.23	3	103.8
	21.8	A0R7G6	MSMEG_6904	95.0	SQVGATITHR	No iTRAQ4plex@N-term		0.00	1068.57	535.29	1068.57	535.29	2	
137	21.6	A0QXH9	MSMEG_3308	99.0	DVAYAAGAR	iTRAQ4plex@N-term		0.01	1036.55	519.28	1036.54	519.28	2	1.135.4
	21.6	A0QXH9	MSMEG_3308	99.0	DVAYAAGAR	iTRAQ4plex@N-term		0.00	1036.54	519.28	1036.54	519.28	2	849.8
138	21.6	A0QP01	MSMEG_0224	99.0	LLSLLAGISGAR	iTRAQ4plex@N-term		0.01	1313.83	657.92	1313.82	657.91	2	182.9
139	21.5	A0QSD5	MSMEG_1440	99.0	STIIPDFIGHTF	iTRAQ4plex@N-term	cleaved F-A@C-term	0.00	1490.79	746.40	1490.79	746.40	2	1.272.7
	21.5	A0QSD5	MSMEG_1440	93.0	LGEFAPTR	iTRAQ4plex@N-term		0.00	1033.57	517.79	1033.57	517.79	2	2.451.8
140	21.5	A0R1Z9	MSMEG_4935	98.0	TTAGEIGILPR	iTRAQ4plex@N-term		-0.05	1270.69	636.35	1270.74	636.38	2	436.3
141	21.4	A0R0W1	MSMEG_4527	99.0	TLGGISTEFAR	iTRAQ4plex@N-term		0.01	1294.71	648.36	1294.70	648.36	2	870.5
	21.4	A0R0W1	MSMEG_4527	99.0	VLSSELGDYIER	iTRAQ4plex@N-term		0.01	1523.80	762.91	1523.80	762.90	2	2.152.2
	21.4	A0R0W1	MSMEG_4527	92.0	FAQWAVR	iTRAQ4plex@N-term		-0.01	1020.55	511.28	1020.56	511.29	2	3.313.1
	21.4	A0R0W1	MSMEG_4527	82.0	RAQVLVPELEKR	iTRAQ4plex@N-term; User modH on Lys(K)@11	missed R-A@1; missed K-R@11	-0.02	1824.04	609.02	1824.06	609.03	3	20.7
	21.4	A0R0W1	MSMEG_4527	77.0	RAQVLVPELEKR	iTRAQ4plex@N-term; User modH on Lys(K)@11	missed R-A@1; missed K-R@11	0.01	1824.07	609.03	1824.06	609.03	3	10.9
142	21.0	A0R1Y8	MSMEG_4921	99.0	GPGLQQLAYR	iTRAQ4plex@N-term		0.03	1245.72	623.87	1245.70	623.85	2	2.265.2
	21.0	A0R1Y8	MSMEG_4921	99.0	TSDIDALSDR	iTRAQ4plex@N-term		0.02	1235.63	618.82	1235.61	618.81	2	1.456.7
143	20.9	A0QZ33	MSMEG_3880	99.0	LTTDALAFLTER	iTRAQ4plex@N-term; Dimethyl(R)@12		-0.01	1521.84	761.93	1521.85	761.93	2	218.8
	20.9	A0QZ33	MSMEG_3880	99.0	LTTDALAFLTER	iTRAQ4plex@N-term		0.02	1493.84	747.93	1493.82	747.92	2	689.9

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
144	20.7	A0R4H2	MSMEG_5832	99.0	AEILDPQGQAIVGALGR	iTRAQ4plex@N-term		-0.02	1851.01	618.01	1851.03	618.02	3	213.6
145	20.5	A0QU93	MSMEG_2123	99.0	DSTFTAGR	iTRAQ4plex@N-term		0.01	997.51	499.76	997.50	499.75	2	97.6
	20.5	A0QU93	MSMEG_2123	99.0	IAGAAAEQGR	iTRAQ4plex@N-term		0.01	1086.61	544.31	1086.59	544.30	2	105.2
	20.5	A0QU93	MSMEG_2123	99.0	LINDPADVIADALR	iTRAQ4plex@N-term		-0.02	1638.89	820.45	1638.91	820.46	2	290.8
	20.5	A0QU93	MSMEG_2123	99.0	SVTEVADVAR	iTRAQ4plex@N-term		0.00	1189.64	595.83	1189.64	595.83	2	411.7
	20.5	A0QU93	MSMEG_2123	78.0	IAGAAAEQGR	No iTRAQ4plex@N-term		0.02	942.51	472.26	942.49	472.25	2	17.3
146	20.2	A0QQF9	MSMEG_0741	99.0	FVLGLGVSHGPLVER	iTRAQ4plex@N-term		0.01	1723.00	575.34	1722.99	575.34	3	397.0
	20.2	A0QQF9	MSMEG_0741	99.0	LVIGTGIANIHVR	iTRAQ4plex@N-term		-0.01	1505.91	502.98	1505.92	502.98	3	210.9
	20.2	A0QQF9	MSMEG_0741	99.0	MIELSGTHADGAHPYLVLPEQTR	iTRAQ4plex@N-term		0.04	2678.40	670.61	2678.36	670.60	4	58.6
147	20.1	A0QX20	MSMEG_3143	99.0	AINDNDLAVTAVLSGNR	iTRAQ4plex@N-term		-0.03	1885.97	629.66	1886.00	629.67	3	132.8
	20.1	A0QX20	MSMEG_3143	99.0	AVITESFER	iTRAQ4plex@N-term		0.02	1194.66	598.34	1194.64	598.33	2	4.383.1
	20.1	A0QX20	MSMEG_3143	99.0	IDTPGEADYYR	iTRAQ4plex@N-term		-0.01	1442.67	722.34	1442.68	722.35	2	2.452.5
	20.1	A0QX20	MSMEG_3143	99.0	NGGILQYVLR	iTRAQ4plex@N-term; Deamidated(N)@1		-0.01	1276.72	639.37	1276.73	639.37	2	274.8
	20.1	A0QX20	MSMEG_3143	99.0	NQLLDDVSGGYTR	iTRAQ4plex@N-term		0.01	1580.80	791.41	1580.79	791.40	2	2.476.0
	20.1	A0QX20	MSMEG_3143	99.0	TNMAPGSQVVTDYYNK	iTRAQ4plex@N-term; iTRAQ4plex(Y)@14; Lys->Gln@16		0.01	2075.00	692.67	2074.99	692.67	3	572.1
	20.1	A0QX20	MSMEG_3143	99.0	VLAENLLR	iTRAQ4plex@N-term		-0.02	1070.63	536.32	1070.66	536.34	2	1.989.8
	20.1	A0QX20	MSMEG_3143	98.0	AGIPLVVLGGK	iTRAQ4plex@N-term; Lys->Gln@11		0.02	1166.73	584.37	1166.71	584.36	2	110.2
	20.1	A0QX20	MSMEG_3143	95.0	GTFANIR	iTRAQ4plex@N-term		0.00	921.51	461.76	921.52	461.76	2	3.297.7
148	20.0	A0QUY3	MSMEG_2379	11.0	VDKAVSEHLATR	iTRAQ4plex@N-term; User modH on Lys(K)@3	missed K-A@3	-0.02	1711.89	428.98	1711.92	428.98	4	30.3
	20.0	A0QUY3	MSMEG_2379	99.0	AVSEHLATR	iTRAQ4plex@N-term		-0.01	1126.61	376.54	1126.62	376.55	3	73.8
	20.0	A0QUY3	MSMEG_2379	99.0	EGTEGPYTGNGGALR	iTRAQ4plex@N-term; Deamidated(N)@10		-0.02	1622.75	812.38	1622.77	812.39	2	344.3
	20.0	A0QUY3	MSMEG_2379	99.0	TNVLAFAGSLWSR	iTRAQ4plex@N-term		-0.02	1564.83	783.42	1564.85	783.43	2	414.8
149	20.0	A0QX81	MSMEG_3205	99.0	ELLSQALENLDADVR	iTRAQ4plex@N-term		-0.04	1828.92	610.65	1828.97	610.66	3	
	20.0	A0QX81	MSMEG_3205	99.0	HSSGLSVQTFLR	iTRAQ4plex@N-term		0.02	1474.82	492.61	1474.80	492.61	3	340.3
	20.0	A0QX81	MSMEG_3205	99.0	GGVDVDAVVPKVRPIVDAVAQR	iTRAQ4plex@N-term; User modH on Lys(K)@11; Deamidated(Q)@21	missed K-V@11	0.01	2647.47	662.88	2647.47	662.87	4	126.8
	20.0	A0QX81	MSMEG_3205	90.0	AALQVSIDR	iTRAQ4plex@N-term		-0.05	1115.59	558.80	1115.64	558.83	2	1.696.3
150	19.9	A0R170	MSMEG_4645	99.0	LINLTHGEPITFGADGEYAVVK	iTRAQ4plex@N-term; iTRAQ4plex(Y)@18; Lys->Gln@22		0.07	2631.45	878.16	2631.38	878.13	3	84.8
	19.9	A0R170	MSMEG_4645	99.0	LSEQNLDHMVMGIFR	iTRAQ4plex@N-term		0.00	1932.97	645.33	1932.97	645.33	3	506.5
	19.9	A0R170	MSMEG_4645	99.0	QQVATAIESRPHDTAALQSLLR	iTRAQ4plex@N-term		-0.02	2548.37	638.10	2548.38	638.10	4	154.7
	19.9	A0R170	MSMEG_4645	99.0	LSEQNLDHMVMGIFR	iTRAQ4plex@N-term; Oxidation(M)@11		-0.03	1948.94	650.65	1948.96	650.66	3	126.7
	19.9	A0R170	MSMEG_4645	99.0	LSEQNLDHMVMGIFR	iTRAQ4plex@N-term; Dimethyl(R)@15		-0.03	1960.97	654.66	1961.00	654.67	3	130.2
	19.9	A0R170	MSMEG_4645	98.0	LSEQNLDHMVMGIFR	iTRAQ4plex@N-term		0.01	1932.97	645.33	1932.97	645.33	3	71.3
	19.9	A0R170	MSMEG_4645	92.0	PHDTAALQSLLR	No iTRAQ4plex@N-term	cleaved R-P@N-term	-0.03	1320.68	441.24	1320.71	441.25	3	83.6
	19.9	A0R170	MSMEG_4645	77.0	DFTSDQEVR	iTRAQ4plex@N-term		-0.01	1239.57	620.79	1239.59	620.80	2	80.3
151	19.6	A0QS46	MSMEG_1347	99.0	LAENYGAALDEVLR	iTRAQ4plex@N-term		0.02	1676.91	839.46	1676.89	839.45	2	1.616.2
	19.6	A0QS46	MSMEG_1347	99.0	LAENYGAALDEVLR	iTRAQ4plex@N-term; Dimethyl(R)@14		-0.01	1704.91	569.31	1704.92	569.31	3	105.3
	19.6	A0QS46	MSMEG_1347	98.0	TGTVTPDVAK	iTRAQ4plex@N-term; Lys->Gln@10		0.04	1131.63	566.82	1131.59	566.80	2	298.6
	19.6	A0QS46	MSMEG_1347	98.0	VAVFAVGEK	iTRAQ4plex@N-term; Lys->Gln@9		0.03	1062.61	532.31	1062.58	532.30	2	364.3
152	19.5	A0R478	MSMEG_5733	99.0	GEHLEPGDGPIVVGIDDSPAAEHALAAA	iTRAQ4plex@N-term; iTRAQ4plex(H)@23; Lys->Gln@34		0.02	3664.87	917.22	3664.85	917.22	4	198.4
	19.5	A0R478	MSMEG_5733	99.0	HAGDAQLLVVGTR	iTRAQ4plex@N-term		-0.01	1479.82	494.28	1479.83	494.28	3	384.6
153	19.2	A0QR08	MSMEG_0943	99.0	ATVTSPAGTTAAGLR	iTRAQ4plex@N-term		0.03	1516.86	759.44	1516.83	759.42	2	324.6
	19.2	A0QR08	MSMEG_0943	99.0	LDQVNAAGGAALDTTPAQLR	iTRAQ4plex@N-term		0.02	2125.14	709.39	2125.12	709.38	3	116.0
154	19.2	A0R012	MSMEG_4222	99.0	GADMVFVTAGEGGGTGTGGAPVVASIA	iTRAQ4plex@N-term		0.00	2648.34	883.79	2648.33	883.79	3	
	19.2	A0R012	MSMEG_4222	99.0	GLGAGADPEVGR	iTRAQ4plex@N-term		0.02	1241.67	621.84	1241.65	621.83	2	797.9
	19.2	A0R012	MSMEG_4222	99.0	GVMSGAGTALMGIGSAR	iTRAQ4plex@N-term		-0.02	1678.84	560.62	1678.86	560.63	3	38.9
155	19.0	A0R072	MSMEG_4283	99.0	AIADIAAR	iTRAQ4plex@N-term		-0.01	943.55	472.78	943.56	472.79	2	6.125.2
	19.0	A0R072	MSMEG_4283	99.0	EGVNLTFLPFIAR	iTRAQ4plex@N-term		0.01	1619.92	810.97	1619.92	810.97	2	301.8
	19.0	A0R072	MSMEG_4283	99.0	IHPNVNASYNEDTK	iTRAQ4plex@N-term; Lys->Gln@14		0.05	1744.86	582.63	1744.81	582.61	3	1.030.8
	19.0	A0R072	MSMEG_4283	99.0	QAPAASPAAAAPAAPAAASATPAPALAH	iTRAQ4plex@N-term		0.03	2803.55	701.89	2803.52	701.89	4	112.6

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	19.0	A0R072	MSMEG_4283	99.0	RLEEGAFEADLGL	iTRAQ4plex@N-term	missed R-L@1	-0.01	1562.80	782.41	1562.81	782.41	2	26.1
	19.0	A0R072	MSMEG_4283	91.0	AEFAER	iTRAQ4plex@N-term		0.02	865.46	433.74	865.44	433.73	2	85.4
156	19.0	A0QVB1	MSMEG_2511	99.0	ADLVPEDR	iTRAQ4plex@N-term		0.01	1057.57	529.79	1057.55	529.78	2	983.9
	19.0	A0QVB1	MSMEG_2511	95.0	LVIVPEGVDVSSLPQPLTLDSFQGLPEA	iTRAQ4plex@N-term		-0.03	3801.05	951.27	3801.08	951.28	4	15.2
157	18.8	A0R716	MSMEG_6746	99.0	ATARPTFDDDLVTDQVR	iTRAQ4plex@N-term		0.00	2063.04	688.69	2063.04	688.69	3	286.3
	18.8	A0R716	MSMEG_6746	99.0	DSGIDLWR	iTRAQ4plex@N-term		-0.01	1104.56	553.29	1104.57	553.29	2	1.056.3
	18.8	A0R716	MSMEG_6746	99.0	LGTPLVIHQPSYSLLNR	iTRAQ4plex@N-term		-0.04	2051.13	684.72	2051.16	684.73	3	259.6
158	18.8	A0QWG8	MSMEG_2937	99.0	ATTFYDDPDVLAKVSR	iTRAQ4plex@N-term; User modH on Lys(K)@13; iTRAQ4plex(S)@15	missed K-V@13	0.02	2328.23	777.08	2328.21	777.08	3	343.5
	18.8	A0QWG8	MSMEG_2937	99.0	FTVPFVCGATNLGEALR	iTRAQ4plex@N-term; Pyridylethyl(C)@7		-0.01	2043.06	682.03	2043.07	682.03	3	328.1
	18.8	A0QWG8	MSMEG_2937	99.0	ITEGAAMIR	iTRAQ4plex@N-term		0.01	1104.62	553.32	1104.61	553.31	2	2.909.7
159	18.6	A0QR00	MSMEG_0935	99.0	TVLIAAHGNSLR	iTRAQ4plex@N-term		-0.01	1394.80	465.94	1394.81	465.94	3	365.3
	18.6	A0QR00	MSMEG_0935	98.0	TVLIAAHGN	iTRAQ4plex@N-term	cleaved N-S@C-term	0.01	1038.61	520.31	1038.59	520.30	2	237.1
160	18.6	P42829	MSMEG_3151	99.0	AVLPIMNPGGGIVGMDFDPTR	iTRAQ4plex@N-term		-0.01	2300.17	767.73	2300.18	767.73	3	80.4
	18.6	P42829	MSMEG_3151	99.0	SALESVNR	iTRAQ4plex@N-term		0.01	1018.56	510.29	1018.55	510.28	2	596.7
	18.6	P42829	MSMEG_3151	97.0	PAPLLELDVQNEEHLSTLADR	No iTRAQ4plex@N-term	cleaved K-P@N-term	-0.02	2359.18	787.40	2359.20	787.41	3	
161	18.5	A0R2G5	MSMEG_5104	99.0	AIELSGASNLLFR	iTRAQ4plex@N-term		0.00	1533.87	767.94	1533.86	767.94	2	717.3
	18.5	A0R2G5	MSMEG_5104	99.0	MVDYVTPSGVR	iTRAQ4plex@N-term		0.02	1366.72	684.37	1366.70	684.36	2	1.597.8
	18.5	A0R2G5	MSMEG_5104	99.0	NSLSGAVEVVKRDGTGITLNEALHAI	iTRAQ4plex@N-term; User modH on Lys(K)@11; Deamidated(N)@20	missed K-R@11; missed R-D@12	-0.09	3052.49	764.13	3052.58	764.15	4	83.7
162	18.3	A0QRA6	MSMEG_1047	99.0	AALANHSLSFADFLR	iTRAQ4plex@N-term		-0.05	1775.90	592.97	1775.94	592.99	3	217.6
	18.3	A0QRA6	MSMEG_1047	99.0	LGVDEGLAEALVCAAAR	No iTRAQ4plex@N-term; Gly->Pro@2; Pyridylethyl(C)@13		-0.02	1801.92	601.65	1801.94	601.65	3	15.2
163	18.0	A0QS36	MSMEG_1334	99.0	DFAGADPIAQQMR	iTRAQ4plex@N-term		0.06	1562.82	782.42	1562.76	782.39	2	287.5
	18.0	A0QS36	MSMEG_1334	99.0	GVAELLEHR	iTRAQ4plex@N-term		-0.03	1166.63	389.88	1166.65	389.89	3	112.6
	18.0	A0QS36	MSMEG_1334	99.0	SVPVHVNSHEADWVSQVTGIAR	iTRAQ4plex@N-term		-0.01	2531.29	633.83	2531.30	633.83	4	64.4
164	17.9	A0R0R1	MSMEG_4476	99.0	QALAQAANPLVEALAQAAR	iTRAQ4plex@N-term		-0.02	2049.13	684.05	2049.15	684.06	3	16.3
	17.9	A0R0R1	MSMEG_4476	99.0	QALAQAANPLVEALAQAAR	iTRAQ4plex@N-term; Ala->Val@18		-0.05	2077.12	693.38	2077.18	693.40	3	
165	17.9	A0R7G8	MSMEG_6907	99.0	LDDLAAALPR	iTRAQ4plex@N-term		0.00	1197.68	599.85	1197.68	599.85	2	701.7
	17.9	A0R7G8	MSMEG_6907	92.0	TVDHISDGR	iTRAQ4plex@N-term		0.00	1142.58	381.87	1142.58	381.87	3	54.7
166	17.8	A0QQ65	MSMEG_0643	99.0	ASDFTYAIQR	iTRAQ4plex@N-term		0.01	1314.67	658.34	1314.67	658.34	2	1.528.5
	17.8	A0QQ65	MSMEG_0643	99.0	DAGADEVADAHVDK	iTRAQ4plex@N-term; iTRAQ4plex(H)@11; Lys->Gln@14		0.04	1699.83	567.62	1699.79	567.60	3	840.8
	17.8	A0QQ65	MSMEG_0643	99.0	QAVNYAIDPEALNR	iTRAQ4plex@N-term		0.04	1716.93	573.32	1716.89	573.30	3	326.9
	17.8	A0QQ65	MSMEG_0643	99.0	QLIAEANPADR	iTRAQ4plex@N-term		0.01	1340.72	671.37	1340.72	671.37	2	204.0
	17.8	A0QQ65	MSMEG_0643	82.0	YADGTPIKASDFTYAIQR	iTRAQ4plex@N-term; User modH on Lys(K)@8	missed K-A@8	-0.01	2403.20	802.07	2403.21	802.08	3	400.4
	17.8	A0QQ65	MSMEG_0643	76.0	YADGTPIKASDFTYAIQR	iTRAQ4plex@N-term; User modH on Lys(K)@8; iTRAQ4plex(Y)@14	missed K-A@8	0.04	2547.35	850.12	2547.31	850.11	3	56.4
167	17.8	A0R203	MSMEG_4939	99.0	ADEAVIDLAELAVSR	iTRAQ4plex@N-term		0.02	1714.94	572.66	1714.92	572.65	3	
	17.8	A0R203	MSMEG_4939	99.0	VSATTLDLLR	iTRAQ4plex@N-term		0.01	1231.73	616.87	1231.73	616.87	2	526.1
	17.8	A0R203	MSMEG_4939	99.0	WSTESNLIDAVEHTAR	iTRAQ4plex@N-term		-0.04	1971.94	658.32	1971.98	658.33	3	80.2
168	17.7	A0R3M3	MSMEG_5524	99.0	AGTQIVGGVNAR	iTRAQ4plex@N-term		0.03	1285.75	643.88	1285.72	643.87	2	2.341.2
	17.7	A0R3M3	MSMEG_5524	99.0	ANVTKPVVGYVAGFTAPEGK	iTRAQ4plex@N-term; iTRAQ4plex(T)@4; Lys->Gln@5; Lys->Gln@20		0.10	2292.30	765.11	2292.20	765.07	3	534.0
	17.7	A0R3M3	MSMEG_5524	99.0	VIVMIGEIGGDAEER	iTRAQ4plex@N-term		0.02	1730.92	577.98	1730.90	577.97	3	
169	17.5	A0QQJ4	MSMEG_0777	99.0	ASAEQFAPR	iTRAQ4plex@N-term		0.03	1119.61	560.81	1119.58	560.80	2	1.835.6
	17.5	A0QQJ4	MSMEG_0777	99.0	NLVLGTSVLTPTFR	iTRAQ4plex@N-term		-0.01	1660.95	831.48	1660.96	831.49	2	1.254.8
170	17.5	A0R0Q9	MSMEG_4474	99.0	AANTWHASTAIQEAR	iTRAQ4plex@N-term		0.04	1769.94	590.99	1769.89	590.97	3	219.3
	17.5	A0R0Q9	MSMEG_4474	99.0	ENLSNEVFRPHYTPNTAIAR	iTRAQ4plex@N-term		0.00	2472.26	619.07	2472.26	619.07	4	159.0
	17.5	A0R0Q9	MSMEG_4474	99.0	GMSPVEWVR	iTRAQ4plex@N-term		-0.01	1203.61	602.81	1203.62	602.82	2	1.036.2
	17.5	A0R0Q9	MSMEG_4474	99.0	IMAAAGAAEDGFR	iTRAQ4plex@N-term		-0.02	1422.68	712.35	1422.70	712.36	2	1.077.1
	17.5	A0R0Q9	MSMEG_4474	99.0	TAAQTIIQTILDTR	iTRAQ4plex@N-term		0.01	1687.96	844.99	1687.96	844.99	2	769.9

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
	17.5	A0R0Q9	MSMEG_4474	99.0	ENLSNEVFRPHYTPNTAIAR	iTRAQ4plex@N-term		-0.10	2472.16	619.05	2472.26	619.07	4	561.3
171	17.3	A0QPE7	MSMEG_0372	99.0	ELYTFFTPLLR	iTRAQ4plex@N-term		0.00	1542.86	772.44	1542.86	772.44	2	655.9
	17.3	A0QPE7	MSMEG_0372	99.0	GIGATIAEVFAR	iTRAQ4plex@N-term		-0.01	1347.75	674.88	1347.76	674.89	2	813.6
	17.3	A0QPE7	MSMEG_0372	99.0	SAYVDGQVFR	iTRAQ4plex@N-term		0.01	1284.67	643.34	1284.66	643.34	2	2.324.4
	17.3	A0QPE7	MSMEG_0372	99.0	VDILVNNAGITR	iTRAQ4plex@N-term		-0.01	1427.81	714.91	1427.82	714.92	2	639.7
	17.3	A0QPE7	MSMEG_0372	99.0	GIGATIAEVFAR	iTRAQ4plex@N-term		0.00	1347.76	674.89	1347.76	674.89	2	293.2
	17.3	A0QPE7	MSMEG_0372	97.0	MTEAIPLATR	iTRAQ4plex@N-term		0.00	1245.69	623.85	1245.69	623.85	2	1.439.1
172	17.1	A0QNZ7	MSMEG_0220	99.0	DLSEFVEDFR	iTRAQ4plex@N-term		0.03	1399.71	700.86	1399.67	700.84	2	261.6
	17.1	A0QNZ7	MSMEG_0220	99.0	FGAAGLLVYALDHR	iTRAQ4plex@N-term		0.00	1645.91	549.64	1645.91	549.64	3	52.2
173	17.1	A0QT08	MSMEG_1670	99.0	YAPTIVDLAPR	iTRAQ4plex@N-term		0.01	1358.78	680.40	1358.77	680.39	2	386.3
	17.1	A0QT08	MSMEG_1670	98.0	SMVLEVLEGR	iTRAQ4plex@N-term		-0.01	1275.69	638.85	1275.70	638.86	2	932.4
	17.1	A0QT08	MSMEG_1670	97.0	AAVEAGPR	iTRAQ4plex@N-term		0.00	913.51	457.76	913.51	457.76	2	42.3
174	17.0	A0R3N8	MSMEG_5538	99.0	GEVAYGAEFFR	iTRAQ4plex@N-term		0.01	1388.69	695.35	1388.68	695.35	2	1.315.4
	17.0	A0R3N8	MSMEG_5538	99.0	VAETIQSGMVGINR	iTRAQ4plex@N-term		0.00	1617.86	809.94	1617.86	809.94	2	463.2
	17.0	A0R3N8	MSMEG_5538	97.0	GLDPSSTLGPLINSK	iTRAQ4plex@N-term; iTRAQ4plex(S)@14; Lys->Gln@15		0.03	1786.00	596.34	1785.97	596.33	3	142.6
175	17.0	A0QR89	MSMEG_1028	99.0	HAESAGAEVR	iTRAQ4plex@N-term		0.00	1169.59	390.87	1169.59	390.87	3	51.1
	17.0	A0QR89	MSMEG_1028	99.0	MGLADEVATYHR	iTRAQ4plex@N-term		0.00	1505.74	502.92	1505.74	502.92	3	341.5
	17.0	A0QR89	MSMEG_1028	99.0	VTVFSPSEWELSFPR	iTRAQ4plex@N-term		-0.01	1923.98	642.33	1923.99	642.34	3	27.2
	17.0	A0QR89	MSMEG_1028	91.0	AESAGAEVR	iTRAQ4plex@N-term	cleaved H-A@N-term	0.02	1032.55	517.28	1032.53	517.27	2	46.7
176	16.8	A0R609	MSMEG_6384	99.0	ANLLGLSAPEMTTLVGGLR	iTRAQ4plex@N-term		-0.01	2056.13	686.39	2056.15	686.39	3	
	16.8	A0R609	MSMEG_6384	99.0	LQPQLGWEANEPDELAQVVR	iTRAQ4plex@N-term		-0.06	2435.20	812.74	2435.26	812.76	3	147.3
	16.8	A0R609	MSMEG_6384	99.0	THPSMLTSDLALR	iTRAQ4plex@N-term		-0.01	1584.83	529.28	1584.84	529.29	3	484.0
	16.8	A0R609	MSMEG_6384	99.0	VDPIYEQITR	iTRAQ4plex@N-term		0.00	1376.74	689.38	1376.74	689.38	2	805.9
	16.8	A0R609	MSMEG_6384	80.0	DMGPVTR	iTRAQ4plex@N-term		-0.01	918.46	460.24	918.47	460.24	2	116.8
177	16.7	A0QSL6	MSMEG_1522	99.0	STPFAAQLAAENAAR	iTRAQ4plex@N-term		0.00	1660.86	831.44	1660.87	831.44	2	1.141.9
	16.7	A0QSL6	MSMEG_1522	99.0	STPFAAQLAAENAAR	iTRAQ4plex@N-term		0.00	1660.87	554.63	1660.87	554.63	3	418.9
	16.7	A0QSL6	MSMEG_1522	99.0	GSRKSTPFAAQLAAENAAR	No iTRAQ4plex@N-term; User modH on Lys(K)@4	missed R-K@3; missed K-S@4	0.06	2188.18	730.40	2188.12	730.38	3	295.9
178	16.7	A0QTD7	MSMEG_1803	99.0	SAVPDATLVLR	iTRAQ4plex@N-term		0.01	1284.76	643.39	1284.75	643.38	2	1.678.0
	16.7	A0QTD7	MSMEG_1803	99.0	VAAMLENLAVVR	iTRAQ4plex@N-term		-0.01	1428.82	715.42	1428.82	715.42	2	831.0
179	16.7	A0R0A1	MSMEG_4313	99.0	LDELGIAHGGIVDAPYGSGLSFR	iTRAQ4plex@N-term		0.05	2487.34	830.12	2487.29	830.10	3	134.0
180	16.5	A0QXC8	MSMEG_3255	99.0	GAELAETAR	iTRAQ4plex@N-term		-0.01	1060.55	531.28	1060.56	531.29	2	121.9
181	16.3	A0QU45	MSMEG_2072	99.0	AVGHDLPSALLR	iTRAQ4plex@N-term		-0.01	1391.79	464.94	1391.80	464.94	3	81.3
	16.3	A0QU45	MSMEG_2072	99.0	MDLPTHVDIR	iTRAQ4plex@N-term		0.00	1339.70	447.57	1339.70	447.58	3	187.1
	16.3	A0QU45	MSMEG_2072	99.0	VLDIVSAAVEYGADR	iTRAQ4plex@N-term		0.01	1720.92	574.65	1720.91	574.64	3	
182	16.3	A0QYS6	MSMEG_3770	99.0	ALESFVAHTQEHVSGEIR	iTRAQ4plex@N-term		0.00	2153.10	539.28	2153.10	539.28	4	108.1
	16.3	A0QYS6	MSMEG_3770	99.0	GVPVSIDGRPVSVLQAIEELNR	iTRAQ4plex@N-term		-0.03	2491.36	831.46	2491.39	831.47	3	139.6
	16.3	A0QYS6	MSMEG_3770	99.0	GVPVSIDGRPVSVLQAIEELNRR	iTRAQ4plex@N-term	missed R-R@22	-0.02	2647.47	662.88	2647.49	662.88	4	126.8
	16.3	A0QYS6	MSMEG_3770	96.0	AIAFAEENAIPINVTK	iTRAQ4plex@N-term; iTRAQ4plex(T)@15; Lys->Gln@16		0.02	1988.10	663.71	1988.08	663.70	3	93.5
183	16.3	A0QSD2	MSMEG_1437	99.0	IHAVTELVEGQTPSTK	iTRAQ4plex@N-term; Lys->Gln@16		0.04	1853.01	618.68	1852.97	618.66	3	808.9
	16.3	A0QSD2	MSMEG_1437	99.0	IHAVTELVEGQTPSTK	No iTRAQ4plex@N-term; iTRAQ4plex(T)@15; Lys->Gln@16		0.05	1853.02	618.68	1852.97	618.66	3	337.5
	16.3	A0QSD2	MSMEG_1437	95.0	GALSDR	iTRAQ4plex@N-term		0.00	761.42	381.72	761.42	381.71	2	44.3
184	16.2	A0R0I8	MSMEG_4401	99.0	AAYAEHPPVPLPGVPDAIR	iTRAQ4plex@N-term		-0.02	2113.13	705.38	2113.14	705.39	3	310.0
	16.2	A0R0I8	MSMEG_4401	99.0	AMEHSGVQDISR	iTRAQ4plex@N-term		-0.02	1472.70	491.91	1472.72	491.91	3	200.9
185	16.1	A0QUY9	MSMEG_2387	99.0	AQAESEGLDQIFTAAGAQWR	iTRAQ4plex@N-term		-0.05	2292.07	765.03	2292.13	765.05	3	272.7
	16.1	A0QUY9	MSMEG_2387	76.0	VVADVLRGRKVADGVR	iTRAQ4plex@N-term; User modH on Lys(K)@10; Oxidation(D)@13	missed R-G@7; missed R-K@9; missed	0.12	2112.33	705.12	2112.21	705.08	3	67.7
	16.1	A0QUY9	MSMEG_2387	76.0	VVADVLRGRKVADGVR	iTRAQ4plex@N-term; Deamidated(R)@9; User modH on Lys(K)@10	missed R-G@7; missed R-K@9; missed	0.02	2097.22	525.31	2097.20	525.31	4	2.108.0

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
186	16.1	A0R2U7	MSMEG_5239	99.0	GAMFDPSAVFYMNK	iTRAQ4plex@N-term; iTRAQ4plex(Y)@11; Lys->Gln@14		0.01	1864.89	622.64	1864.87	622.63	3	194.8
	16.1	A0R2U7	MSMEG_5239	98.0	NLALELVR	iTRAQ4plex@N-term		0.01	1070.67	536.34	1070.66	536.34	2	567.2
187	16.0	A0QS62	MSMEG_1364	99.0	ASTATVVTEYR	iTRAQ4plex@N-term		0.02	1340.73	671.37	1340.71	671.36	2	1.880.6
188	15.8	A0QUY6	MSMEG_2382	99.0	EIAEHPFGNPNFTGR	iTRAQ4plex@N-term		0.06	1828.95	610.66	1828.90	610.64	3	372.2
	15.8	A0QUY6	MSMEG_2382	99.0	TEVNGQVR	iTRAQ4plex@N-term		0.01	1045.58	523.80	1045.56	523.79	2	71.6
	15.8	A0QUY6	MSMEG_2382	99.0	TSLLLHDIGR	iTRAQ4plex@N-term		-0.01	1267.73	423.58	1267.74	423.59	3	476.5
189	15.8	A0QU58	MSMEG_2086	99.0	LREDIEAMEVR	iTRAQ4plex@N-term	missed R-E@2	0.02	1503.80	502.28	1503.78	502.27	3	176.1
	15.8	A0QU58	MSMEG_2086	99.0	SGAGGVDAADWAEMLMR	iTRAQ4plex@N-term		-0.01	1879.86	627.63	1879.87	627.63	3	23.9
	15.8	A0QU58	MSMEG_2086	96.0	EAVVTIR	iTRAQ4plex@N-term		0.00	930.56	466.29	930.56	466.29	2	193.6
190	15.6	A0QW25	MSMEG_2782	99.0	GLYDVAGLR	iTRAQ4plex@N-term		-0.01	1106.61	554.31	1106.62	554.32	2	1.365.4
	15.6	A0QW25	MSMEG_2782	99.0	LDFDALNSTIR	iTRAQ4plex@N-term		-0.01	1407.74	704.88	1407.75	704.88	2	1.040.1
	15.6	A0QW25	MSMEG_2782	98.0	EETPFFTGPR	iTRAQ4plex@N-term		0.01	1323.66	662.84	1323.66	662.84	2	2.667.0
191	15.6	A0R199	MSMEG_4674	99.0	GAVLEQVVNDALPSR	iTRAQ4plex@N-term		0.01	1710.95	856.48	1710.94	856.48	2	520.0
	15.6	A0R199	MSMEG_4674	93.0	EEFDAETR	iTRAQ4plex@N-term		0.01	1139.53	570.77	1139.52	570.77	2	3.124.2
192	15.5	A0QNZ3	MSMEG_0216	99.0	ALVNSAGIGWAQR	iTRAQ4plex@N-term		0.05	1485.86	743.94	1485.82	743.92	2	1.456.8
	15.5	A0QNZ3	MSMEG_0216	99.0	DLSAVGIR	iTRAQ4plex@N-term		-0.01	973.56	487.79	973.57	487.79	2	1.427.4
	15.5	A0QNZ3	MSMEG_0216	99.0	GGVVGLTLPVAR	iTRAQ4plex@N-term		-0.01	1281.78	641.90	1281.79	641.90	2	988.3
	15.5	A0QNZ3	MSMEG_0216	98.0	AAELGPLR	iTRAQ4plex@N-term		0.01	969.59	485.80	969.57	485.79	2	1.497.8
193	15.4	A0R2V3	MSMEG_5245	99.0	DAPLSVMTTWQHR	iTRAQ4plex@N-term		-0.03	1684.82	562.61	1684.85	562.62	3	730.2
	15.4	A0R2V3	MSMEG_5245	99.0	GGIGSVASAVLR	iTRAQ4plex@N-term		0.01	1229.74	615.88	1229.72	615.87	2	1.186.0
	15.4	A0R2V3	MSMEG_5245	95.0	LAQSQLDR	iTRAQ4plex@N-term		0.02	1073.61	537.81	1073.60	537.80	2	900.9
194	15.3	A0QSL5	MSMEG_1521	99.0	SNEILAATGIDK	iTRAQ4plex@N-term; Lys->Gln@12		0.05	1374.76	688.39	1374.71	688.36	2	338.2
195	15.3	A0R2W9	MSMEG_5261	99.0	GDFFHAPIEWQQR	iTRAQ4plex@N-term		0.01	1773.88	592.30	1773.87	592.30	3	48.9
	15.3	A0R2W9	MSMEG_5261	99.0	WLEHWDPDNDVFANR	iTRAQ4plex@N-term		-0.02	2056.93	686.65	2056.95	686.66	3	108.1
196	15.1	A0R202	MSMEG_4938	99.0	ALELQAPSVVQR	iTRAQ4plex@N-term		-0.01	1453.83	727.92	1453.84	727.93	2	398.2
	15.1	A0R202	MSMEG_4938	99.0	FESELLEHVK	iTRAQ4plex@N-term; Lys->Gln@10		0.02	1373.71	458.91	1373.69	458.91	3	91.2
	15.1	A0R202	MSMEG_4938	97.0	LVSVINEFK	iTRAQ4plex@N-term; Lys->Gln@9		0.03	1191.70	596.86	1191.66	596.84	2	825.7
	15.1	A0R202	MSMEG_4938	95.0	AISLLLR	iTRAQ4plex@N-term		-0.03	928.59	465.30	928.62	465.32	2	494.4
197	15.1	A0QT22	MSMEG_1684	99.0	FFNGNPVLSTVGGGIEAFSGR	iTRAQ4plex@N-term		-0.07	2269.09	757.37	2269.16	757.39	3	67.9
	15.1	A0QT22	MSMEG_1684	99.0	GDLYTLWAPR	iTRAQ4plex@N-term		0.00	1334.71	668.36	1334.71	668.36	2	552.4
198	14.3	A0QVQ8	MSMEG_2659	99.0	LSAQVGAYHLMR	iTRAQ4plex@N-term		-0.03	1488.77	497.26	1488.80	497.27	3	441.5
199	14.2	A0R067	MSMEG_4278	99.0	TEMGYPLHGHELSLDISPLQAR	iTRAQ4plex@N-term		0.04	2607.36	652.85	2607.32	652.84	4	101.9
	14.2	A0R067	MSMEG_4278	98.0	GPGAAAYVNSALTNDLGK	iTRAQ4plex@N-term; iTRAQ4plex(T)@13; Lys->Gln@18		0.05	2006.08	669.70	2006.03	669.68	3	137.5
200	14.1	A0QUV6	MSMEG_2351	99.0	DDGLHGSDLIQTAWTLAR	iTRAQ4plex@N-term		0.03	2112.10	705.04	2112.07	705.03	3	62.7
	14.1	A0QUV6	MSMEG_2351	99.0	EAADAVLDEINER	iTRAQ4plex@N-term		0.01	1587.80	794.91	1587.79	794.90	2	595.9
201	14.0	A0QWY3	MSMEG_3106	99.0	ADAIGVNFIDTYFR	iTRAQ4plex@N-term		0.01	1744.90	873.46	1744.89	873.45	2	420.1
	14.0	A0QWY3	MSMEG_3106	99.0	GTLALFGASSGPVPPFDPQR	iTRAQ4plex@N-term		-0.06	2157.07	720.03	2157.13	720.05	3	45.7
	14.0	A0QWY3	MSMEG_3106	99.0	ITVGGTYPLAEASR	iTRAQ4plex@N-term		0.00	1577.85	789.93	1577.85	789.93	2	1.430.3
202	14.0	A0R5M8	MSMEG_6247	99.0	FRPENVVAELAEAGLR	iTRAQ4plex@N-term		0.02	1914.06	639.03	1914.04	639.02	3	19.6
	14.0	A0R5M8	MSMEG_6247	98.0	ELSADFDLDAFEHVAKWNSDEERIE	iTRAQ4plex@N-term; User modH on Lys(K)@16	missed K-W@16; missed R-I@23	-0.24	3937.61	788.53	3937.86	788.58	5	
203	14.0	A0QS85	MSMEG_1387	99.0	EGGEWGLDEVHALGALSGSR	iTRAQ4plex@N-term		0.00	2183.07	728.70	2183.07	728.70	3	128.7
	14.0	A0QS85	MSMEG_1387	99.0	GVPTIIEMVNLTR	iTRAQ4plex@N-term		0.03	1585.93	793.97	1585.90	793.96	2	277.1

Supplement Table 1A

Index	% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence	Modifications	Cleavages	ΔMass	Prec MW	Prec m/z	Calc. MW	Calc. m/z	Theor z	Area 115
204	13.9	A0R0B0	MSMEG_4323	99.0	ANDGAYVR	iTRAQ4plex@N-term		0.00	1008.51	505.26	1008.51	505.26	2	113.9
	13.9	A0R0B0	MSMEG_4323	99.0	EWDVLLHADR	iTRAQ4plex@N-term		-0.02	1396.70	466.57	1396.72	466.58	3	186.9
	13.9	A0R0B0	MSMEG_4323	99.0	GYTLGQHFEGR	iTRAQ4plex@N-term		0.01	1407.71	470.24	1407.70	470.24	3	271.3
	13.9	A0R0B0	MSMEG_4323	99.0	IIQELESFFR	iTRAQ4plex@N-term		-0.01	1424.77	713.39	1424.78	713.40	2	168.3
	13.9	A0R0B0	MSMEG_4323	99.0	LTTDQLDGFR	iTRAQ4plex@N-term		0.03	1308.71	655.36	1308.68	655.35	2	768.9
	13.9	A0R0B0	MSMEG_4323	99.0	QDLAQNSSTAAEPDR	iTRAQ4plex@N-term		0.00	1745.83	582.95	1745.83	582.95	3	26.1
205	13.9	A0QV45	MSMEG_2443	99.0	DIVGQFSYVVETER	iTRAQ4plex@N-term		0.02	1784.92	595.98	1784.91	595.98	3	19.6
206	13.8	A0R2X8	MSMEG_5270	99.0	ELLSAVFEGR	iTRAQ4plex@N-term		0.01	1263.70	632.86	1263.69	632.85	2	767.6
	13.8	A0R2X8	MSMEG_5270	99.0	ITHFVAGVGTGGTITGTGR	iTRAQ4plex@N-term		0.04	1945.09	649.37	1945.05	649.36	3	205.4
207	13.8	A0R472	MSMEG_5727	99.0	NNFEVHSEDR	iTRAQ4plex@N-term		0.01	1389.65	464.23	1389.64	464.22	3	51.8
	13.8	A0R472	MSMEG_5727	87.0	EAGHDSAIVR	iTRAQ4plex@N-term		0.00	1197.62	400.21	1197.62	400.21	3	15.2
208	13.2	A0R0E9	MSMEG_4362	99.0	AAAIVVGSR	iTRAQ4plex@N-term		0.01	986.61	494.31	986.60	494.31	2	1.077.8
209	13.2	A0R4G4	MSMEG_5824	99.0	LLAEVLTAASR	iTRAQ4plex@N-term		-0.01	1286.76	644.39	1286.77	644.39	2	157.2
	13.2	A0R4G4	MSMEG_5824	99.0	VESHNHPSYVEPYQGAATGVGGIVR	iTRAQ4plex@N-term		0.02	2767.40	692.86	2767.38	692.85	4	123.8
	13.2	A0R4G4	MSMEG_5824	82.0	IILFGAR	iTRAQ4plex@N-term		-0.03	932.56	467.29	932.59	467.30	2	742.6
210	13.2	A0R3M4	MSMEG_5525	99.0	GVDLAFAR	iTRAQ4plex@N-term		-0.02	991.54	496.78	991.56	496.79	2	4.338.8
	13.2	A0R3M4	MSMEG_5525	99.0	YAATPDDAFTHANNILGLDIK	iTRAQ4plex@N-term; Lys->Gln@21		0.01	2403.20	802.07	2403.18	802.07	3	400.4
211	13.2	A0R1G3	MSMEG_4742	99.0	AALDEILHSWR	iTRAQ4plex@N-term		-0.03	1453.75	485.59	1453.78	485.60	3	173.6
	13.2	A0R1G3	MSMEG_4742	99.0	VGVGPTEDTEILR	iTRAQ4plex@N-term		0.00	1528.82	765.42	1528.82	765.42	2	415.6
212	13.2	A0QX96	MSMEG_3220	99.0	GDQTFLDELDR	iTRAQ4plex@N-term		-0.01	1451.69	726.85	1451.70	726.86	2	1.075.4
	13.2	A0QX96	MSMEG_3220	99.0	TEGIIPAIESAHAVAGALKL	iTRAQ4plex@N-term; Ala->Thr@17; Lys->Glu@19	cleaved L-G@C-term; missed K-L@19	0.06	2135.22	712.75	2135.16	712.73	3	358.1
	13.2	A0QX96	MSMEG_3220	99.0	VQVQDQAGR	iTRAQ4plex@N-term		0.00	1143.61	572.81	1143.61	572.81	2	118.2
213	13.0	A0QU00	MSMEG_2026	99.0	AAVEEGDDADVR	iTRAQ4plex@N-term		0.00	1389.65	695.83	1389.65	695.83	2	345.4
	13.0	A0QU00	MSMEG_2026	99.0	TLAEAVAAAGHNLVVTAR	No iTRAQ4plex@N-term		0.00	1762.97	588.66	1762.97	588.66	3	105.2
214	12.9	A0R069	MSMEG_4281	99.0	ALGATGGEGQTHR	iTRAQ4plex@N-term		0.02	1397.73	466.92	1397.71	466.91	3	16.3
	12.9	A0R069	MSMEG_4281	99.0	STVADLANVSGSR	iTRAQ4plex@N-term		0.02	1419.77	710.89	1419.74	710.88	2	833.4
215	12.7	A0QWW3	MSMEG_3085	99.0	AEGLTDGDVLLLENIR	iTRAQ4plex@N-term		-0.02	1870.99	624.67	1871.01	624.68	3	
	12.7	A0QWW3	MSMEG_3085	99.0	TLDDLLAEGVQGR	iTRAQ4plex@N-term		-0.01	1529.81	765.91	1529.82	765.92	2	1.669.8
	12.7	A0QWW3	MSMEG_3085	91.0	LAVIENLATK	iTRAQ4plex@N-term; iTRAQ4plex(T)@9; Lys->Gln@10		0.02	1358.82	680.42	1358.80	680.41	2	493.6
216	12.6	A0QU53	MSMEG_2080	98.0	ASDTAVIR	iTRAQ4plex@N-term		-0.01	975.54	488.78	975.55	488.78	2	119.9
	12.6	A0QU53	MSMEG_2080	98.0	EHPGVTVER	iTRAQ4plex@N-term		0.00	1166.62	389.88	1166.62	389.88	3	197.8
217	12.5	A0QP11	MSMEG_0234	99.0	MDELVANLR	iTRAQ4plex@N-term		0.00	1203.64	602.83	1203.64	602.83	2	661.1
	12.5	A0QP11	MSMEG_0234	98.0	GYIVNSDR	iTRAQ4plex@N-term		0.00	1066.55	534.28	1066.55	534.28	2	139.6
	12.5	A0QP11	MSMEG_0234	95.0	ATDGAFR	iTRAQ4plex@N-term		0.00	880.46	441.24	880.45	441.23	2	79.2
	12.5	A0QP11	MSMEG_0234	88.0	SGIDLTHVDPR	iTRAQ4plex@N-term		-0.01	1352.71	451.91	1352.72	451.91	3	487.1
218	12.4	A0QR33	MSMEG_0969	99.0	LAGLLTGALTEAGVAHQVQR	iTRAQ4plex@N-term		-0.06	2148.16	717.06	2148.21	717.08	3	64.0
	12.4	A0QR33	MSMEG_0969	95.0	AEALPAAAR	iTRAQ4plex@N-term; Pro->Ser@5	cleaved I-A@N-term	0.00	1002.56	502.28	1002.56	502.29	2	123.3
219	12.4	A0QQX4	MSMEG_0909	99.0	IADDFLAGLR	iTRAQ4plex@N-term		-0.03	1233.65	617.83	1233.68	617.85	2	614.8
	12.4	A0QQX4	MSMEG_0909	99.0	QLGFEDTHPAWIVR	iTRAQ4plex@N-term		0.01	1811.96	604.99	1811.94	604.99	3	634.6
220	12.3	A0R0T8	MSMEG_4504	99.0	LENSDIELLR	iTRAQ4plex@N-term; Dimethyl(R)@10		-0.01	1372.75	687.38	1372.77	687.39	2	955.2
	12.3	A0R0T8	MSMEG_4504	99.0	SLLGQVMTSR	iTRAQ4plex@N-term	cleaved R-P@C-term	0.01	1234.70	618.36	1234.68	618.35	2	1.328.7
	12.3	A0R0T8	MSMEG_4504	98.0	GEIQTVQR	iTRAQ4plex@N-term		0.01	1073.60	537.81	1073.60	537.80	2	151.9
	12.3	A0R0T8	MSMEG_4504	96.0	DYYGLLGVSK	iTRAQ4plex@N-term; iTRAQ4plex(S)@9; Lys->Gln@10		0.01	1401.75	701.88	1401.74	701.88	2	93.3
221	12.2	A0R220	MSMEG_4956	99.0	AAVHQPWPGLIEAYR	iTRAQ4plex@N-term		0.01	1851.00	618.01	1850.99	618.00	3	193.5

Supplement Table 1A

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	12.2	A0R220	MSMEG_4956	99.0	MLGTQAAGAAPLVTGAPVKDPETIATAI	iTRAQ4plex@N-term; Lys->Gln@19		0.04	2963.62	741.91	2963.59	741.90	4	88.9
222	12.0	A0QSK7	MSMEG_1513	99.0	KPYDALVEYLDVLDAAK	iTRAQ4plex@N-term; Lys->Gln@1; iTRAQ4plex(Y)@3; Lys->Gln@17		0.07	2210.20	737.74	2210.14	737.72	3	116.1
	12.0	A0QSK7	MSMEG_1513	99.0	LIDAVVAHGTAGDIAAR	iTRAQ4plex@N-term		-0.01	1792.98	598.67	1792.99	598.67	3	794.6
223	12.0	A0R2T0	MSMEG_5222	99.0	VFNDDDVVHVDGR	iTRAQ4plex@N-term		0.00	1629.79	544.27	1629.79	544.27	3	307.4
	12.0	A0R2T0	MSMEG_5222	88.0	ESIGQTERGLDALAR	iTRAQ4plex@N-term; Deamidated(Q)@5; Deamidated(R)@8; Leu->Val@13	cleaved L-E@N-term; missed R-G@8	0.05	1746.94	583.32	1746.89	583.30	3	1.573.5
224	11.7	A0QVX6	MSMEG_2731	99.0	LSSILEQADEAAQNER	iTRAQ4plex@N-term		-0.01	1916.95	639.99	1916.96	639.99	3	122.7
	11.7	A0QVX6	MSMEG_2731	99.0	VIGAWQAGDTESAFAHFGR	iTRAQ4plex@N-term		-0.01	2163.05	722.02	2163.06	722.03	3	93.5
225	11.7	A0QSY5	MSMEG_1647	99.0	HLDENAALER	iTRAQ4plex@N-term		0.00	1310.67	437.90	1310.67	437.90	3	182.3
	11.7	A0QSY5	MSMEG_1647	94.0	VAALTAAGR	iTRAQ4plex@N-term		0.01	972.59	487.30	972.58	487.30	2	2.395.5
	11.7	A0QSY5	MSMEG_1647	79.0	AFLLTNVVEAEESK	iTRAQ4plex@N-term; iTRAQ4plex(S)@13; Lys->Gln@14		-0.04	1836.93	613.32	1836.97	613.33	3	85.4
226	11.4	A0R1H5	MSMEG_4755	99.0	AATAEALLLDALGR	iTRAQ4plex@N-term		-0.01	1527.86	764.94	1527.87	764.94	2	247.4
	11.4	A0R1H5	MSMEG_4755	99.0	ADLEDLVR	iTRAQ4plex@N-term		-0.01	1073.58	537.80	1073.58	537.80	2	191.6
227	11.3	A0QYD5	MSMEG_3620	99.0	TENALANPR	iTRAQ4plex@N-term		0.03	1128.63	565.32	1128.60	565.31	2	88.9
	11.3	A0QYD5	MSMEG_3620	99.0	VQLGTLVTGNTYR	iTRAQ4plex@N-term		-0.02	1564.85	783.43	1564.87	783.44	2	1.824.7
228	11.3	A0QV09	MSMEG_2407	99.0	EVNAGYNIVTEAYGPLGVGR	iTRAQ4plex@N-term		-0.02	2222.13	741.72	2222.15	741.72	3	18.5
229	11.0	A0R218	MSMEG_4954	99.0	TTILQDIANAITR	iTRAQ4plex@N-term		0.00	1572.90	787.46	1572.90	787.46	2	1.145.1
	11.0	A0R218	MSMEG_4954	93.0	KNGLRRGDAVTGAVR	iTRAQ4plex@N-term; User modH on Lys(K)@1	missed K-N@1; missed R-R@5; missed	-0.01	1956.09	653.04	1956.10	653.04	3	
230	10.9	A0QSG8	MSMEG_1474	99.0	NVPVMFEGGQMPIHMR	iTRAQ4plex@N-term		-0.02	1985.95	662.99	1985.98	663.00	3	147.3
231	10.1	A0QSD4	MSMEG_1439	99.0	GASVSDFAEITR	iTRAQ4plex@N-term		0.00	1395.71	698.86	1395.71	698.86	2	1.046.5
	10.1	A0QSD4	MSMEG_1439	99.0	VAHIEYDPNR	iTRAQ4plex@N-term		0.01	1356.70	453.24	1356.69	453.24	3	399.0
232	10.0	A0R0W4	MSMEG_4530	99.0	IAVLNKGR	iTRAQ4plex@N-term; User modH on Lys(K)@6	missed K-G@6	-0.02	1256.74	419.92	1256.76	419.93	3	223.6
	10.0	A0R0W4	MSMEG_4530	95.0	YPNQLSGGQR	iTRAQ4plex@N-term; Deamidated(Q)@4; Deamidated(Q)@9		0.03	1264.65	633.33	1264.62	633.32	2	10.169.2
233	9.6	A0QVL2	MSMEG_2613	99.0	DFSEPVALNWSQHGTDVDFGSLSR	iTRAQ4plex@N-term		-0.01	2807.32	936.78	2807.33	936.78	3	215.4
	9.6	A0QVL2	MSMEG_2613	99.0	GFGGFPVGGAFLR	iTRAQ4plex@N-term		-0.02	1424.75	713.38	1424.77	713.39	2	118.3
234	9.5	A0R618	MSMEG_6393	99.0	DVLLTAAGAIPR	iTRAQ4plex@N-term		0.01	1339.81	670.91	1339.79	670.90	2	555.4
	9.5	A0R618	MSMEG_6393	99.0	IAVPLFDPSEPGHVGR	iTRAQ4plex@N-term		0.01	1834.00	612.34	1833.99	612.34	3	179.3
	9.5	A0R618	MSMEG_6393	99.0	LDIGPITDDIR	iTRAQ4plex@N-term		0.01	1370.76	686.39	1370.75	686.38	2	2.127.8
235	9.5	A0QQW8	MSMEG_0903	99.0	WDLTVNELAR	iTRAQ4plex@N-term		0.02	1359.75	680.88	1359.73	680.87	2	2.671.2
	9.5	A0QQW8	MSMEG_0903	80.0	DLTVNELAR	iTRAQ4plex@N-term	cleaved W-D@N-term	0.01	1173.66	587.84	1173.65	587.83	2	1.561.6
236	9.4	A0R417	MSMEG_5672	99.0	SAITYIDGDAGILR	iTRAQ4plex@N-term		0.01	1607.88	804.95	1607.86	804.94	2	1.877.1
	9.4	A0R417	MSMEG_5672	99.0	SQGGDVSDFVR	iTRAQ4plex@N-term		0.02	1309.66	655.83	1309.64	655.83	2	996.5
	9.4	A0R417	MSMEG_5672	96.0	GYTDIAGR	iTRAQ4plex@N-term		0.01	995.53	498.77	995.52	498.77	2	1.006.3
	9.4	A0R417	MSMEG_5672	78.0	QVELSTIR	iTRAQ4plex@N-term		0.01	1088.64	545.33	1088.63	545.32	2	2.988.7
237	9.1	A0QZ54	MSMEG_3902	99.0	ALVVGHADEER	iTRAQ4plex@N-term		0.04	1338.74	447.26	1338.70	447.24	3	172.9
	9.1	A0QZ54	MSMEG_3902	99.0	EDMIDPAILRPGR	iTRAQ4plex@N-term		0.01	1625.87	542.97	1625.87	542.96	3	357.4
	9.1	A0QZ54	MSMEG_3902	99.0	YLTEDLPVHADDLTEFNGDR	iTRAQ4plex@N-term		-0.06	2463.11	822.04	2463.17	822.06	3	633.8
238	8.9	A0QUX1	MSMEG_2367	99.0	DLVNAGAVELVAATVDHGVSSEAAR	iTRAQ4plex@N-term		-0.03	2594.32	865.78	2594.34	865.79	3	58.7
	8.9	A0QUX1	MSMEG_2367	78.0	SVEVAVR	iTRAQ4plex@N-term		0.01	902.54	452.28	902.53	452.27	2	732.6
239	8.9	A0R059	MSMEG_4270	99.0	SAGLSLER	iTRAQ4plex@N-term		0.02	975.57	488.79	975.55	488.78	2	2.596.5
	8.9	A0R059	MSMEG_4270	99.0	VSLSFLVDDLVIHR	iTRAQ4plex@N-term		-0.01	1755.99	586.34	1756.00	586.34	3	
240	8.9	A0R343	MSMEG_5336	99.0	LAAPSVTNPPPAALAATTR	iTRAQ4plex@N-term		-0.03	1962.07	655.03	1962.10	655.04	3	366.7
	8.9	A0R343	MSMEG_5336	99.0	LAAPSVTNPPPAALAATTR	iTRAQ4plex@N-term		-0.04	1962.07	655.03	1962.10	655.04	3	424.4

Supplement Table 1A

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241	8.9	A0R4Z5	MSMEG_6008	99.0	LFATMLNTLER	iTRAQ4plex@N-term		0.02	1451.81	726.91	1451.79	726.90	2	157.3
	8.9	A0R4Z5	MSMEG_6008	99.0	ETTLEKMAAL	No iTRAQ4plex@N-term; User modH on Lys(K)@6	cleaved L-Q@C-term; missed K-M@6	-0.02	1348.66	675.34	1348.68	675.35	2	96.6
242	8.9	A0QT01	MSMEG_1662	99.0	ETFNDEESER	iTRAQ4plex@N-term		0.00	1398.60	700.31	1398.60	700.31	2	457.6
	8.9	A0QT01	MSMEG_1662	99.0	GFLTPALWEAGLYCR	iTRAQ4plex@N-term; Pyridylethyl(C)@14		0.01	1945.02	649.35	1945.00	649.34	3	
	8.9	A0QT01	MSMEG_1662	98.0	APFEPLTPGGFR	iTRAQ4plex@N-term		0.00	1431.76	716.89	1431.76	716.89	2	739.0
243	8.9	A0QS66	MSMEG_1368	99.0	GHDLGDPAIDALLAAGITTVK	iTRAQ4plex@N-term; iTRAQ4plex(T)@19; Lys->Gln@21		0.01	2335.27	584.83	2335.26	584.82	4	46.7
	8.9	A0QS66	MSMEG_1368	99.0	MLDVNFFDELR	iTRAQ4plex@N-term		-0.01	1541.75	771.88	1541.77	771.89	2	225.3
	8.9	A0QS66	MSMEG_1368	99.0	TFHQGGVTGGADIVGGLPR	iTRAQ4plex@N-term		0.00	1982.04	661.69	1982.05	661.69	3	531.2
	8.9	A0QS66	MSMEG_1368	98.0	FATSDLNDLYR	iTRAQ4plex@N-term		0.01	1457.74	729.88	1457.73	729.87	2	1.238.5
	8.9	A0QS66	MSMEG_1368	97.0	HEAEADAIER	iTRAQ4plex@N-term		0.01	1283.64	428.89	1283.62	428.88	3	76.9

Supplement Table 1B

% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence		Cleavages	Δmass	Prec MW	Prec m/z	Theor MW	Theor m/z	Theor z	Area 115
98.9	A0R4D0	MSMEG_5790	99.0	ALSSAGNGNVTVAPTGAGIHEVDVKVA	iTRAQ4plex@N-term; Deamidated(N)@7; iTRAQ4plex(H)@20; User modH on Lys(K)@25	missed K-V@25	-0.04	3065.57	767.40	3065.61	767.41	4	132.1
79.1	A0R6E3	MSMEG_6518	87.0	KLQGSLAEAASR	iTRAQ4plex@N-term; User modH on Lys(K)@1	missed K-L@1	0.04	1616.93	539.98	1616.88	539.97	3	
74.6	A0QSH8	MSMEG_1484	99.0	LSEKLGIPQISTGDLFR	iTRAQ4plex@N-term; iTRAQ4plex(S)@2; User modH on Lys(K)@4	missed K-L@4	-0.03	2404.31	802.44	2404.34	802.46	3	997.1
74.2	A0QVB9	MSMEG_2520	95.0	NALVEADGDFDKAVELLRI	iTRAQ4plex@N-term; User modH on Lys(K)@12; Glu->Gln@15; Dioxidation(R)@18	cleaved I-K@C-term; missed K-A@12; missed R-I@18	-0.02	2505.28	627.33	2505.31	627.33	4	101.9
74.2	A0QVB9	MSMEG_2520	95.0	NALVEADGDFDKAVELLRI	iTRAQ4plex@N-term; Oxidation(D)@11; User modH on Lys(K)@12; Carbamyl(R)@18	cleaved I-K@C-term; missed K-A@12; missed R-I@18	0.04	2533.34	845.45	2533.30	845.44	3	1315.0
74.2	A0QVB9	MSMEG_2520	99.0	NALVEADGDFDKAVELLR	iTRAQ4plex@N-term; User modH on Lys(K)@12	missed K-A@12	-0.06	2361.16	788.06	2361.22	788.08	3	133.1
71.0	A0QS98	MSMEG_2520	94.0	WVKSVEELMEAVDASIPDPVR	iTRAQ4plex@N-term; User modH on Lys(K)@3; iTRAQ4plex(S)@4; Asp->Asn@18	missed K-S@3	-0.07	2899.45	725.87	2899.52	725.89	4	5.4
71.0	A0QS98	MSMEG_1401	94.0	WVKSVEELMEAVDASIPDPVR	iTRAQ4plex@N-term; User modH on Lys(K)@3; iTRAQ4plex(S)@4; Asp->Asn@18	missed K-S@3	-0.07	2899.45	725.87	2899.52	725.89	4	5.4
68.7	A0R0B3	MSMEG_4326	99.0	YGVKIPDEDLAGLR	iTRAQ4plex@N-term; iTRAQ4plex(Y)@1; User modH on Lys(K)@4	missed K-I@4	0.01	2076.15	693.06	2076.13	693.05	3	789.5
68.7	A0R0B3	MSMEG_4326	99.0	TVGDVVAYIQKLEEENPEAAAALR	No iTRAQ4plex@N-term; iTRAQ4plex(Y)@8; User modH on Lys(K)@11	missed K-L@11	-0.02	2972.53	744.14	2972.55	744.14	4	89.6
68.7	A0R0B3	MSMEG_4326	99.0	TVGDVVAYIQKLEEENPEAAAALR	iTRAQ4plex@N-term; iTRAQ4plex(Y)@8; Deamidated(Q)@10; User modH on Lys(K)@11; De	missed K-L@11	0.02	3099.64	775.92	3099.62	775.91	4	75.9
62.9	A0QWW2	MSMEG_3084	99.0	VPIPTGSVTDLTAELAKSASVEDINAAMK	iTRAQ4plex@N-term; Glu->Gln@14; User modH on Lys(K)@17; iTRAQ4plex(S)@18; Lys->G	missed K-S@17	-0.08	3457.73	865.44	3457.81	865.46	4	124.7
62.9	A0QWW2	MSMEG_3084	92.0	VPIPTGSVTDLTAELAKSASVEDINAAMK	iTRAQ4plex@N-term; User modH on Lys(K)@17; Ser->Met@20; Deamidated(N)@25; User m	missed K-S@17	0.10	3602.93	901.74	3602.83	901.71	4	339.3
60.9	A0QZA1	MSMEG_3950	99.0	TLIDASKSAQMVVVGNR	iTRAQ4plex@N-term; User modH on Lys(K)@7; iTRAQ4plex(S)@8	missed K-S@7	0.02	2319.29	774.10	2319.27	774.10	3	749.1
59.9	A0R4C9	MSMEG_5789	99.0	DFVDAQQFSKLLSER	iTRAQ4plex@N-term; iTRAQ4plex(S)@9; User modH on Lys(K)@10	missed K-L@10	-0.04	2313.17	772.06	2313.21	772.08	3	771.4
59.9	A0R4C9	MSMEG_5789	98.0	DFVDAQQFSKLLSER	iTRAQ4plex@N-term; iTRAQ4plex(S)@9; User modH on Lys(K)@10	missed K-L@10	-0.02	2313.19	579.30	2313.21	579.31	4	90.2
59.9	A0R4C9	MSMEG_5789	92.0	DFVDAQQFSKLLSER	iTRAQ4plex@N-term; iTRAQ4plex(S)@9; User modH on Lys(K)@10; Dimethyl(R)@15	missed K-L@10	-0.03	2341.21	586.31	2341.24	586.32	4	209.5
56.9	A0QQU5	MSMEG_0880	88.0	NVAAGANPLGLKR	iTRAQ4plex@N-term; User modH on Lys(K)@12; Oxidation(R)@13	missed K-R@12	0.00	1682.95	842.48	1682.94	842.48	2	1157.9
50.7	A0QWX9	MSMEG_3102	91.0	LEKIGSDEALALR	iTRAQ4plex@N-term; User modH on Lys(K)@3; iTRAQ4plex(S)@6	missed K-I@3	-0.04	1945.06	649.36	1945.10	649.37	3	258.8
46.9	A0QNF6	MSMEG_0024	99.0	HTIFGEVVDEESQKVVDAIASTPTDR	iTRAQ4plex@N-term; Glu->Gln@11; iTRAQ4plex(S)@12; User modH on Lys(K)@14	missed K-V@14	-0.07	3372.66	844.17	3372.73	844.19	4	50.0
46.9	A0QNF6	MSMEG_0024	95.0	HTIFGEVVDEESQKVVDAIASTPTDR	iTRAQ4plex@N-term; iTRAQ4plex(S)@12; User modH on Lys(K)@14	missed K-V@14	-0.05	3373.66	844.42	3373.71	844.44	4	87.8
46.9	A0QNF6	MSMEG_0024	28.0	HTIFGEVVDEESQKVVDAIASTPTDR	iTRAQ4plex@N-term; iTRAQ4plex(S)@12; User modH on Lys(K)@14	missed K-V@14	-0.08	3373.63	675.73	3373.71	675.75	5	70.4
44.9	A0R5R5	MSMEG_6284	99.0	EQATWAQKAIAQEGLTDLAEVR	iTRAQ4plex@N-term; iTRAQ4plex(T)@4; User modH on Lys(K)@8; Dimethyl(R)@22	missed K-A@8	-0.03	2986.56	747.65	2986.58	747.65	4	68.5
44.9	A0R5R5	MSMEG_6284	92.0	EQATWAQKAIAQEGLTDLAEVR	No iTRAQ4plex@N-term; Deamidated(Q)@2; User modH on Lys(K)@8	missed K-A@8	-0.01	2671.32	1336.67	2671.33	1336.67	2	1022.9
38.0	A0R0B4	MSMEG_4327	91.0	VLEDEFVTKWDLPVR	iTRAQ4plex@N-term; iTRAQ4plex(T)@8; User modH on Lys(K)@9	missed K-W@9	-0.07	2376.21	793.08	2376.28	793.10	3	49.9
36.4	A0QUV7	MSMEG_2352	99.0	GVGSAENFKIVEELADSLGGAVGASR	iTRAQ4plex@N-term; iTRAQ4plex(S)@4; User modH on Lys(K)@9	missed K-I@9	0.01	3063.60	766.91	3063.60	766.91	4	80.4
36.4	A0QUV7	MSMEG_2352	96.0	GVGSAENFKIVEELADSLGGAVGASR	iTRAQ4plex@N-term; iTRAQ4plex(S)@4; User modH on Lys(K)@9; Glu->Gln@13	missed K-I@9	-0.11	3062.50	766.63	3062.61	766.66	4	8.7
30.9	A0QXX7	MSMEG_3461	99.0	FAPINSWPDNVSLDKAR	iTRAQ4plex@N-term; Deamidated(N)@10; User modH on Lys(K)@15	missed K-A@15	0.04	2317.21	773.41	2317.17	773.40	3	19.6
27.8	A0R2V7	MSMEG_5249	99.0	QPAFQQYAQQVADNAQALADGFVKRDA	iTRAQ4plex@N-term; Deamidated(Q)@9; User modH on Lys(K)@24; Arg->Orn(R)@25	cleaved A-G@C-term; missed K-R@24; missed R-D@25	0.06	3295.67	824.93	3295.61	824.91	4	923.9
24.7	A0R0B5	MSMEG_4328	99.0	LSYLQKMATVLGRR	iTRAQ4plex@N-term; User modH on Lys(K)@6; Deamidated(R)@13	missed K-M@6; missed R-R@13	-0.01	2023.12	675.38	2023.12	675.38	3	95.7
22.1	A0QWV9	MSMEG_3081	77.0	LGVSAKAR	iTRAQ4plex@N-term; User modH on Lys(K)@6	missed K-A@6	-0.06	1187.64	396.89	1187.70	396.91	3	41.3
22.1	A0QWV9	MSMEG_3081	99.0	LGVSAKAR	iTRAQ4plex@N-term; User modH on Lys(K)@6	missed K-A@6	0.05	1187.75	594.88	1187.70	594.86	2	622.9
21.9	A0R3D2	MSMEG_5431	82.0	TRTGKGASR	iTRAQ4plex@N-term; User modH on Lys(K)@5	missed R-T@2; missed K-G@5	0.01	1319.74	660.88	1319.73	660.87	2	817.1
21.4	A0R0W1	MSMEG_4527	82.0	RAQVLVPELEKR	iTRAQ4plex@N-term; User modH on Lys(K)@11	missed R-A@1; missed K-R@11	-0.02	1824.04	609.02	1824.06	609.03	3	20.7
21.4	A0R0W1	MSMEG_4527	77.0	RAQVLVPELEKR	iTRAQ4plex@N-term; User modH on Lys(K)@11	missed R-A@1; missed K-R@11	0.01	1824.07	609.03	1824.06	609.03	3	10.9
20.0	A0QUY3	MSMEG_2379	11.0	VDKAVSEHLATR	iTRAQ4plex@N-term; User modH on Lys(K)@3	missed K-A@3	-0.02	1711.90	428.98	1711.92	428.99	4	30.3
20.0	A0QX81	MSMEG_3205	99.0	GGVDVDAVVPKVRPIVDAVAQR	iTRAQ4plex@N-term; User modH on Lys(K)@11; Deamidated(Q)@21	missed K-V@11	0.01	2647.47	662.88	2647.47	662.87	4	126.8

Supplement Table 1B

% Cov	Uniprot ID	Gene locus (M. smegmatis)	Conf	Peptide Sequence		Cleavages	Δmass	Prec MW	Prec m/z	Theor MW	Theor m/z	Theor z	Area 115
18.8	A0QWG8	MSMEG_2937	99.0	ATTFYDDPDVLAKVSR	iTRAQ4plex@N-term; User modH on Lys(K)@13; iTRAQ4plex(S)@15	missed K-V@13	0.02	2328.23	777.08	2328.21	777.08	3	343.5
18.5	A0R2G5	MSMEG_5104	99.0	NSLSGAVEVVKRDGTGITLNEALHAN	iTRAQ4plex@N-term; User modH on Lys(K)@11; Deamidated(N)@20	missed K-R@11; missed R-D@12	-0.09	3052.49	764.13	3052.58	764.15	4	83.7
17.8	A0QQ65	MSMEG_0643	76.0	YADGTPIKASDFTYAIQR	iTRAQ4plex@N-term; User modH on Lys(K)@8; iTRAQ4plex(Y)@14	missed K-A@8	0.04	2547.35	850.12	2547.31	850.11	3	56.4
17.8	A0QQ65	MSMEG_0643	82.0	YADGTPIKASDFTYAIQR	iTRAQ4plex@N-term; User modH on Lys(K)@8	missed K-A@8	-0.01	2403.20	802.07	2403.21	802.08	3	400.4
16.7	A0QSL6	MSMEG_1522	99.0	GSRKSTPFAAQLAAENAAR	No iTRAQ4plex@N-term; User modH on Lys(K)@4	missed R-K@3; missed K-S@4	0.06	2188.18	730.40	2188.12	730.38	3	295.9
16.1	A0QUY9	MSMEG_2387	76.0	VVADVLRGRKVADGVR	iTRAQ4plex@N-term; User modH on Lys(K)@10; Oxidation(D)@13	missed R-G@7; missed R-K@9; missed K-V@10	0.12	2112.33	705.12	2112.21	705.08	3	67.7
16.1	A0QUY9	MSMEG_2387	76.0	VVADVLRGRKVADGVR	iTRAQ4plex@N-term; Deamidated(R)@9; User modH on Lys(K)@10	missed R-G@7; missed R-K@9; missed K-V@10	0.02	2097.22	525.31	2097.20	525.31	4	2108.0
14.0	A0R5M8	MSMEG_6247	98.0	ELSADFDLDAFEHVAKWNSDEERIEMWLR	iTRAQ4plex@N-term; User modH on Lys(K)@16	missed K-W@16; missed R-I@23	-0.24	3937.61	788.53	3937.86	788.58	5	
11.0	A0R218	MSMEG_4954	93.0	KNGLRRGDAVTGAVR	iTRAQ4plex@N-term; User modH on Lys(K)@1	missed K-N@1; missed R-R@5; missed R-G@6	-0.01	1956.09	653.04	1956.10	653.04	3	
10.0	A0R0W4	MSMEG_4530	99.0	IAVLNKGR	iTRAQ4plex@N-term; User modH on Lys(K)@6	missed K-G@6	-0.02	1256.74	419.92	1256.76	419.93	3	223.6
8.9	A0R4Z5	MSMEG_6008	99.0	ETTLEKMAAL	No iTRAQ4plex@N-term; User modH on Lys(K)@6	cleaved L-Q@C-term; missed K-M@6	-0.02	1348.66	675.34	1348.68	675.35	2	96.6

Supplement Table 2A

Spot number	Uniprot ID	Gene locus (M. smegmatis)	pI (seq.)	MW [kDa]	Sequence Cov. [%]	MS/MS Mascot Score
1	B6DAC1	(Rv2111c)	3.8	6.9	42.2	119.3
2	B6DAC1	(Rv2111c)	3.8	6.9	42.2	105.6
4	A0QYF5	MSMEG_3640	4.6	78.2	10.5	288.6
4	B6DAC1	(Rv2111c)	3.8	6.9	75.0	256.9
5	A0QVB9	MSMEG_2520	5.0	29.4	18.9	213.1
5	A0QWT3	MSMEG_3055	4.8	42.6	29.1	173.3
5	A0QWX9	MSMEG_3102	4.6	39.9	14.6	76.2
5	B6DAC1	(Rv2111c)	3.8	6.9	81.3	248.6
6	A0QWT3	MSMEG_3055	4.8	42.6	37.8	491.3
6	A0R0B5	MSMEG_4328	4.9	43.8	20.7	250.7
6	A0R4Z5	MSMEG_6008	4.8	42.6	4.9	77.6
6	A0R7G6	MSMEG_6904	4.7	39.3	10.5	224.2
6	B6DAC1	(Rv2111c)	3.8	6.9	84.4	388.9
7	A0QUX8	MSMEG_2374	4.7	36.4	6.5	107.0
7	A0R0B5	MSMEG_4328	4.9	43.8	8.4	104.9
7	A0QQU5	MSMEG_0880	4.7	56.5	12.2	99.4
7	B6DAC1	(Rv2111c)	3.8	6.9	84.4	409.2
8	A0QVB9	MSMEG_2520	5.0	29.4	92.0	1665.4
8	B6DAC1	(Rv2111c)	3.8	6.9	84.4	345.7
9	A0R087	MSMEG_4298	5.3	30.0	45.3	430.6
9	B6DAC1	(Rv2111c)	3.8	6.9	76.6	215.0
10	A0QZA1	MSMEG_3950	5.4	29.8	35.6	395.6
10	B6DAC1	(Rv2111c)	3.8	6.9	76.6	350.4
11	A0R220	MSMEG_4956	5.6	37.4	30.0	218.9
11	B6DAC1	(Rv2111c)	3.8	6.9	75.0	234.6
12	A0QVQ8	MSMEG_2659	5.5	38.9	41.8	537.7
12	B6DAC1	(Rv2111c)	3.8	6.9	73.4	142.6
13	A0QX96	MSMEG_3220	5.2	45.0	41.9	842.6
13	B6DAC1	(Rv2111c)	3.8	6.9	75.0	118.7
14	A0R5R7	MSMEG_6286	5.2	46.4	27.1	429.5
14	B6DAC1	(Rv2111c)	3.8	6.9	75.0	220.6
15	A0R342	MSMEG_5335	4.7	44.8	48.9	666.3
15	A0R4C9	MSMEG_5789	4.8	31.0	13.7	61.7
15	B6DAC1	(Rv2111c)	3.8	6.9	82.8	304.0
16	A0R1V9	MSMEG_4891	4.3	21.6	78.5	603.6
16	B6DAC1	(Rv2111c)	3.8	6.9	84.4	362.5
17	A0QUZ0	MSMEG_2388	5.1	21.9	49.2	438.3
17	A0R066	MSMEG_4276	4.8	39.8	21.5	316.8
17	B6DAC1	(Rv2111c)	3.8	6.9	82.8	317.3
18	A0R7I9	MSMEG_6933	4.6	33.5	76.8	1272.1
18	B6DAC1	(Rv2111c)	3.8	6.9	84.4	408.8
19	A0R1Y7	MSMEG_4920	5.2	42.6	52.8	513.5
19	B6DAC1	(Rv2111c)	3.8	6.9	75.0	182.2
20	A0R0B3	MSMEG_4326	3.7	10.7	56.6	157.8
20	B6DAC1	(Rv2111c)	3.8	6.9	76.6	429.7
21	B6DAC1	(Rv2111c)	3.8	6.9	75.0	108.8
22	A0QUX8	MSMEG_2374	4.7	36.4	8.6	122.7
22	A0QVZ3	MSMEG_2750	5.1	25.4	54.8	425.9
22	B6DAC1	(Rv2111c)	3.8	6.9	75.0	213.3
23	A0QU00	MSMEG_2026	5.0	23.5	16.1	113.7
23	B6DAC1	(Rv2111c)	3.8	6.9	76.6	98.8
24	A0R652	MSMEG_6427	5.4	22.9	53.6	280.6
24	B6DAC1	(Rv2111c)	3.8	6.9	34.4	225.2
25	B6DAC1	(Rv2111c)	3.8	6.9	89.1	790.0
26	B6DAC1	(Rv2111c)	3.8	6.9	84.4	538.5
27	A0R4D0	MSMEG_5790	4.3	9.0	70.0	184.1
27	B6DAC1	(Rv2111c)	3.8	6.9	84.4	298.1
28	A0R2W6	MSMEG_5258	4.4	13.2	65.3	215.0
28	A0R4D0	MSMEG_5790	4.3	9.0	58.9	168.3
28	B6DAC1	(Rv2111c)	3.8	6.9	84.4	415.9
29	A0R4D0	MSMEG_5790	4.3	9.0	40.0	73.7
29	B6DAC1	(Rv2111c)	3.8	6.9	84.4	385.7
30	B6DAC1	(Rv2111c)	3.8	6.9	84.4	651.7
31	B6DAC1	(Rv2111c)	3.8	6.9	89.1	665.6
32	B6DAC1	(Rv2111c)	3.8	6.9	76.6	410.0

Supplement Table 2A

Spot number	Uniprot ID	Gene locus (M. smegmatis)	pI (seq.)	MW [kDa]	Sequence Cov. [%]	MS/MS Mascot Score
33	B6DAC1	(Rv2111c)	3.8	6.9	95.3	627.4
34	B6DAC1	(Rv2111c)	3.8	6.9	84.4	535.4
35	B6DAC1	(Rv2111c)	3.8	6.9	76.6	435.3
36	B6DAC1	(Rv2111c)	3.8	6.9	100.0	653.6
37	B6DAC1	(Rv2111c)	3.8	6.9	76.6	397.6
38	B6DAC1	(Rv2111c)	3.8	6.9	82.8	422.5
39	B6DAC1	(Rv2111c)	3.8	6.9	84.4	620.6
40	B6DAC1	(Rv2111c)	3.8	6.9	76.6	430.1

Supplement Table 2B

Spot Number	Uniprot ID	Gene locus (M. smegmatis)	Peptid sequence	Sequence range	z	Mascot score
5	A0QWT3	MSMEG_3055	GFDGASC$^{\text{PAm}}$GVNVAIGAQSPDIAQGVDTAHETR	85 - 115	3	78.8
			LDTVVLSTQHADGIDLEGTLTPDIR	192 - 216	3	15.6
			VVNTVLADLGHETLDTSDYR	219 - 238	3	12.2
			DLDLLRPIYAPTAAYGHFGR	360 - 379	3	58.4
			TDIELPWEQTNKVDDLK$^{\text{PupylGGE}}$SAI	380 - 399	3	14.9
8	A0QVB9	MSMEG_2520	ANYTAADVKR	2-11	2	63.1
			LRELTGAGMLDSK	12-24	2	41.7
			LRELTGAGM$^{\text{Ox}}$LDSK	12-24	3	19.0
			NALVEADGDFDK$^{\text{PupylGGE}}$AVELLR	25 - 42	3	60.0
			ATAEGLVAAK	56 - 65	1	10.6
			ATAEGLVAAK	56 - 65	2	67.2
			DGALIELNSETDFVAK	66 - 81	2	124.9
			NAEFQALADQIVAAAVAAK	82 - 100	3	109.7
			ANDIETLK	101 - 108	2	54.1
			AAK$^{\text{PupylGGE}}$TGDTTVEQAIADLSAK	109 - 127	3	59.0
			TGDTTVEQAIADLSAK	112 - 127	2	118.9
			TGDTTVEQAIADLSAK	112 - 127	3	57.7
			IGEK$^{\text{PupylGGE}}$LELR	128 - 135	2	53.6
			RAAYFDGTVEAYLHK	136 - 150	3	23.8
			AAYFDGTVEAYLHKR	137 - 151	3	34.9
			AADLPPAVGVLVEYQAGDADK	152 - 172	3	85.2
			GKEAAHAVALQIAALK	173 - 188	3	42.1
			EAAHAVALQIAALK	175 - 188	2	81.1
			EAAHAVALQIAALK	175 - 188	3	51.5
			YLTREDVPEDIVANER	191 - 206	3	50.6
			YLTREDVPEDIVANERR	191 - 207	3	33.8
			EDVPEDIVANER	195 - 206	2	74.2
			EDVPEDIVANERR	195 - 207	2	19.9
			EDVPEDIVANERR	195 - 207	3	35.6
			RIAEETAR	207 - 214	2	31.4
			IAEETAR	208 - 214	1	16.2
			IAEETAR	208 - 214	2	61.1
			NEGKPEQALPK	215 - 225	2	50.2
			IVEGR	226 - 230	1	10.3
			VTGFYKDVVLLDQPSVSDNKK	231 - 251	3	42.4
			DVVLLDQPSVSDNK	237 - 250	2	92.5
			DVVLLDQPSVSDNKK	237 - 251	2	81.4
			DVVLLDQPSVSDNKK	237 - 251	3	38.3
			ALLDEAGVTVTR	255 - 266	2	101.8
			FEVGQA	270 - 275	1	19.3
11	A0R220	MSMEG_4956	GQQAVLC$^{\text{PAm}}$ASTGNTSASAAAYAAR	84 - 106	3	62.4
			K$^{\text{PupylGGE}}$LTADFPTIALVNSVNPYR	151 - 169	3	11.8
			MLGTQAAGAAPLVTGAPVKDPETIATAIR	223 - 251	3	21.5
			M$^{\text{Ox}}$LGTQAAGAAPLVTGAPVKDPETIATAIR	223 - 251	3	19.0
			FLAATDEEILAAYHLVAR	272 - 289	3	55.8
			TEGVFVEPASAASIAGLLK	290 - 308	2	73.8
14	A0R5R7	MSMEG_6286	SFQSLGRDDLLAQHELQQR	2-20	3	32.0
			GKPSPEQLDLSNGLLSLPGDGADAYR	37 - 62	3	29.0
			NYGGVQGLPELR	71 - 82	2	72.1
			LVQMPTAAK	205 - 213	2	23.6
			FFGDADGVR	302 - 310	2	51.3
			FALVAEILEDR	324 - 334	2	87.6
			LGESK$^{\text{PupylGGE}}$IASWTDPK	335 - 347	3	17.0
			DAGIAVTEAGSAFPYR	370 - 385	2	85.6
			DAGIAVTEAGSAFPYRK	370 - 386	2	43.0
			DAGIAVTEAGSAFPYRK	370 - 386	3	33.7
15	A0R342	MSMEG_5335	DQAVPGHNR	16 - 24	2	36.8
			WHPDIPAAATVK$^{\text{PupylGGQ}}$PGSEFR	25 - 42	3	21.6
			WHPDIPAAATVK$^{\text{PupylGGE}}$PGSEFR	25 - 42	3	39.5
			EWTDGQIGNNDSANDVR	47 - 63	2	73.0

Supplement Table 2B

Spot Number	Uniprot ID	Gene locus (M. smegmatis)	Peptid sequence	Sequence range	z	Mascot score
			EWTDGQIGNNDSANDVR	47 - 63	3	68.5
			DVDLAPC^{PAm}HMLSGPIK	64 - 78	2	67.4
			DVDLAPC^{PAm}HM^{Ox}LSGPIK	64 - 78	3	18.9
			VNGGGFLTDYYPDAYK	119 - 134	2	95.0
			HVPGVR	148 - 153	2	20.0
			YTGITHPGLFGTAPSPDLLAK	154 - 174	3	35.1
			ALIATDPDR	181 - 189	2	44.6
			AR	181 - 221	3	75.9
			AR	181 - 221	4	22.7
			VPPLALPPLVDGTLGGTASGDLLQAIANDGAR	190 - 221	3	53.4
			VEPLYSEWLTFIGISVDHAENR	307 - 328	3	36.6
			NAYM^{Ox}DATM^{Ox}AYR	329 - 339	2	24.8
			NAYMDATMAYR	329 - 339	2	10.3
			WGYTGEQAYLILGTSPIEGR	352 - 371	3	55.3
			GQVAVTS	409 - 415	1	16.0
15	A0R4C9	MSMEG_5789	TVFVEVDEDTSAYDTGHIEGAVK	22 - 44	3	47.9
			DFVDAQQFSK^{PupylGGE}LLSER	58 - 72	3	17.1
16	A0R1V9	MSMEG_4891	ALLTIGDQFPEYDLTAVVGGDLSK	2-25	3	55.2
			ALLTIGDQFPEYDLTAVVGGDLSK^{PupylGGE}VDAK	2-29	3	43.5
			VDAK^{PupylGGE}QPDDYFTR	26 - 37	3	53.1
			VTSK^{PupylGGE}DYEGK	38 - 46	2	41.5
			LNEDFEDRDAK	71 - 81	2	53.0
			LNEDFEDRDAK	71 - 81	3	12.5
			VLGVSVDNEFVHFQWR	82 - 97	3	36.2
			AQHEDLKTLPFPMVSDLKR	98 - 116	3	23.9
			TLPFPMVSDLKR	105 - 116	2	40.2
			TLPFPM^{Ox}VSDLKR	105 - 116	2	44.6
			ELTAAC^{PAm}GVLNADGVADR	117 - 133	2	118.2
			ATFIVDPNNEVQFVSVTAGSVGR	134 - 156	3	61.7
			NVDEVLR	157 - 163	1	36.4
			NVDEVLR	157 - 163	2	35.6
			GDPTINAGELLAGAV	181 - 195	2	42.8
17	A0QUZ0	MSMEG_2388	M^{Ox}EAFTTHTGIGVPLR	1-15	3	38.5
			SNVDTDQIIPAVYLK	17 - 31	2	105.2
			NDPSFILNLSPFDK^{PupylGGE}GSVLVAGPDFGTGSSR	48 - 77	3	60.6
			NDPSFILNLSPFDK^{PupylGGE}GSVLVAGPDFGTGSSR	48 - 77	4	17.2
			FADIFR	97 - 102	1	19.6
			FADIFR	97 - 102	2	37.0
			TVTAGTVVVPFR	143 - 154	2	78.6
			IDDYTR	155 - 160	1	21.8
			IDDYTR	155 - 160	2	31.7
			LLEGLDDIGLTLR	163 - 175	2	88.0
19	A0R1Y7	MSMEG_4920	DFSGTDLGAIAIR	42 - 54	2	87.1
			ANVPASM^{Ox}VEYVIMGQVLTAGAGQMPAR	60 - 86	3	52.9
			ANVPASM^{Ox}VEYVIM^{Ox}GQVLTAGAGQMPAR	60 - 86	3	48.3
			ANVPASM^{Ox}VEYVIMGQVLTAGAGQM^{Ox}PAR	60 - 86	3	65.5
			ANVPASM^{Ox}VEYVIM^{Ox}GQVLTAGAGQM^{Ox}PAR	60 - 86	3	31.0
			AGEFDVIVAGGQESMSQAPHLLPK	123 - 146	3	47.5
			AGEFDVIVAGGQESM^{Ox}SQAPHLLPK	123 - 146	3	41.7
			YGDATLVDHLAYDGLHDVFTDQPM^{Ox}GALTEQR	153 - 183	3	17.9
			YGDATLVDHLAYDGLHDVFTDQPM^{Ox}GALTEQR	153 - 183	4	28.4
			AEQDEYAAQSHQK	192 - 204	3	16.0
			AAAAWK^{PupylGGE}DGVFADEVVPVSIPQR	205 - 226	3	46.9
			KGDPIEFAEDEGIR	227 - 240	3	49.7
			ANTTAESLAGLKPAFR	241 - 256	3	14.9
			EGITVDQLDVIEINEAFAAVALASTK	323 - 348	3	57.7
			VNVNGGAIAIGHPIGMSGAR	357 - 376	2	41.4
			VNVNGGAIAIGHPIGMSGAR	357 - 376	3	39.8
			VNVNGGAIAIGHPIGM^{Ox}SGAR	357 - 376	2	29.0
			IALHAALELAR	377 - 387	2	69.0

Supplement Table 2B

Spot Number	Uniprot ID	Gene locus (M. smegmatis)	Peptid sequence	Sequence range	z	Mascot score
			IALHAALELAR	377 - 387	3	43.3
20	A0R0B3	MSMEG_4326	AATQEEIIAGLAEIIEEVTGIEPSEVTPEK	2-31	3	44.6
			TVGDVVAYIQK$^{\text{PupylGGE}}$LEEENPEAAAALR	69 - 92	3	70.9
			TVGDVVAYIQK$^{\text{PupylGGE}}$LEEENPEAAAALREK	69 - 94	3	46.0
			TVGDVVAYIQK$^{\text{PupylGGE}}$LEEENPEAAAALREK	69 - 94	4	14.9
24	A0R652	MSMEG_6427	HHATYVK$^{\text{PupylGGE}}$GVNDAIAK	32 - 46	3	27.1
			ANGDHAAIFLNEK	52 - 64	3	26.2
			NLSPNGGDKPTGELAAAIDDQFGSFDK	82 - 108	3	47.1
			FQAQFTAAANGLQGSGWAVLGYDSLGGR	109 - 136	3	72.6
			AFWNVVNWDDVQNR	180 - 193	2	68.0
			FAAATSK	194 - 200	1	24.2
			TSGLIFG	201 - 207	1	21.0
25	B6DAC1	(Rv2111c)	RGGGGGDDDDIAGSTAAGQER	8-28	2	86.1
			RGGGGGDDDDIAGSTAAGQER	8-28	3	29.5
			RGGGGGDDDDIAGSTAAGQERR	8-29	2	55.7
			RGGGGGDDDDIAGSTAAGQERR	9-28	3	109.8
			GGGGGDDDDIAGSTAAGQER	9-28	2	99.4
			GGGGGDDDDIAGSTAAGQER	9-29	3	55.8
			GGGGGDDDDIAGSTAAGQERR	9-29	2	27.9
			GGGGGDDDDIAGSTAAGQERR	8 - 29	3	79.9
			REKLTEETDDLLDEIDDVLEENAEDFVR	29 - 56	3	154.6
			REKLTEETDDLLDEIDDVLEENAEDFVR	29 - 56	4	30.0
			EKLTEETDDLLDEIDDVLEENAEDFVR	30 - 56	3	56.1
			EKLTEETDDLLDEIDDVLEENAEDFVR	30 - 56	4	27.3
			LTEETDDLLDEIDDVLEENAEDFVR	32 - 56	2	151.9
			LTEETDDLLDEIDDVLEENAEDFVR	32 - 56	3	95.8
			AYVQK	57 - 61	1	27.5
			AYVQK$^{\text{PupylGGE}}$GGQ	57 - 64	2	30.0
26	B6DAC1	(Rv2111c)	RGGGGGDDDDIAGSTAAGQER	8-28	2	82.1
			RGGGGGDDDDIAGSTAAGQER	8-28	3	32.5
			RGGGGGDDDDIAGSTAAGQERR	8-29	2	64.1
			RGGGGGDDDDIAGSTAAGQERR	8-29	3	79.8
			GGGGGDDDDIAGSTAAGQER	9-28	2	112.9
			GGGGGDDDDIAGSTAAGQER	9-28	3	57.5
			GGGGGDDDDIAGSTAAGQERR	9-29	2	32.3
			GGGGGDDDDIAGSTAAGQERR	9-29	3	59.4
			REK$^{\text{PupylGGE}}$LTEETDDLLDEIDDVLEENAEDFVR	29 - 56	4	28.3
			EKLTEETDDLLDEIDDVLEENAEDFVR	30 - 56	3	61.4
			EK$^{\text{PupylGGE}}$LTEETDDLLDEIDDVLEENAEDFVR	30 - 56	3	73.6
			LTEETDDLLDEIDDVLEENAEDFVR	32 - 56	3	79.8
			AYVQK	57 - 61	1	26.9
27	B6DAC1	(Rv2111c)	RGGGGGDDDDIAGSTAAGQER	8-28	2	10.3
			RGGGGGDDDDIAGSTAAGQERR	8-29	3	42.4
			GGGGGDDDDIAGSTAAGQER	9-28	3	58.1
			GGGGGDDDDIAGSTAAGQERR	9-29	3	40.2
			EKLTEETDDLLDEIDDVLEENAEDFVR	30 - 56	3	61.4
			EK$^{\text{PupylGGE}}$LTEETDDLLDEIDDVLEENAEDFVR	30 - 56	3	5.8
			LTEETDDLLDEIDDVLEENAEDFVR	32 - 56	3	64.1
			AYVQK	57 - 61	1	24.5
27	A0R4D0	MSMEG_5790	VVDGSGGQAVGGAFVR	17 - 31	2	109.7
			LLDGSDEFTAEVVASATGDFR	32 - 52	3	59.9
			ALSSAGNGNVTVAPTGAGIHEVDVK$^{\text{PupylGGE}}$VA	64 - 90	3	14.5
28	A0R2W6	MSMEG_5258	SHDAAALESFVKR	2-14	3	62.3
			YLDTVAGGSAADIAALYADDATVEDPVGSGEVHIGR	15 - 50	3	89.0
			YLDTVAGGSAADIAALYADDATVEDPVGSGEVHIGR	15 - 50	4	57.5
			QAIEGFYK$^{\text{PupylGGE}}$NM$^{\text{Ox}}$TAATTDIK	51 - 68	3	10.8
			IEPIEVM$^{\text{Ox}}$TFDGDGR	95 - 108	2	54.4

Supplement Table 2B

Spot Number	Uniprot ID	Gene locus (M. smegmatis)	Peptid sequence	Sequence range	z	Mascot score
28	A0R4D0	MSMEG_5790	VVDGSGQAVGGAFVR	17 - 31	2	105.2
			FFAAPGTWTVR	53 - 63	2	46.8
			ALSSAGNGNVTVAPTGAGIHEVDVK$^{\text{PupylGGE}}$VA	64 - 90	3	17.7

Supplement Table 3A

Target number	Target ID in Table 1	Gene locus (M. smegmatis)	Functional Annotation	Gene locus (M. tuberculosis)	Functional categorization	Gene clusters
1	1	MSMEG_0024	Peptidyl-prolyl cis-trans isomerase	Rv0009	2	
2		MSMEG_0216	3-hydroxyacyl-CoA dehydrogenase	Rv1144	7	
3		MSMEG_0220	Monoglyceride lipase	Rv0183	7	
4		MSMEG_0224	O-methyltransferase MdmC	Rv0187	7	
5		MSMEG_0234	Metallopeptidase	Rv0198c	7	
6		MSMEG_0372	Oxidoreductase, short chain dehydrogenase/reductase family protein	Rv0242c	1	1
7		MSMEG_0373	3-ketoacyl-CoA thiolase	Rv0243	1	
8	2	MSMEG_0643	Extracellular solute-binding protein, family protein 5			
9		MSMEG_0702	Monooxygenase	Rv0044c	7	
10		MSMEG_0709	Chaperone protein dnaK	Rv0350	0	
11		MSMEG_0732	Chaperone ClpB	Rv0384c	0	
12		MSMEG_0741	Putative uncharacterized protein	Rv3463	10	
13		MSMEG_0768	Putative uncharacterized protein			
14		MSMEG_0777	F420-dependent gluce-6-Phosphate dehydrogenase	Rv0407	7	
15		MSMEG_0793	Thiazole biynthesis protein thiG	Rv0417	7	
16		MSMEG_0877	Dihydrodipicolinate synthase	Rv0439c	7	
17	3	MSMEG_0880	60 kDa chaperonin 1	Rv0440	0	
18		MSMEG_0903	Dihydrolipoyl dehydrogenase	Rv0462	7	
19		MSMEG_0909	Acyl-ACP thioesterase superfamily protein	Rv0466	10	
20		MSMEG_0935	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	Rv0489	7	
21		MSMEG_0943	Pyrroline-5-carboxylate reductase	Rv0500	7	
22		MSMEG_0969	Glutamate-1-semialdehyde-2,1-aminomutase	Rv0524	7	
23		MSMEG_1028	Geranylgeranyl reductase	Rv0561c	7	
24		MSMEG_1046	ABC-type molybdenum transport system, ATPase component	Rv3041c	3	2
25		MSMEG_1047	Nudix hydrolase	Rv3040c	10	
26		MSMEG_1165	UPF0234 protein	Rv0566c	10	
27		MSMEG_1305	TetR family protein regulatory protein	Rv0238	9	
28		MSMEG_1334	Metallo-beta-lactamase family protein	Rv0634c	0	
29		MSMEG_1347	50S ribomal protein L1	Rv0640	2	

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30		MSMEG_1364	50S ribomal protein L10	Rv0651	2	
31		MSMEG_1368	DNA-directed RNA polymerase subunit beta'	Rv0668	2	
32		MSMEG_1383	Endonuclease IV	Rv0670	2	
33		MSMEG_1387	Putative acyl-CoA dehydrogenase	Rv0673	1	
34		MSMEG_1399	30S ribomal protein S7	Rv0683	2	
35	4	MSMEG_1401	Elongation factor Tu	Rv0685	2	
36		MSMEG_1435	30S ribomal protein S10	Rv0700	2	3
37		MSMEG_1436	50S ribomal protein L3	Rv0701	2	
38		MSMEG_1437	50S ribomal protein L4	Rv0702	2	
39		MSMEG_1439	50S ribomal protein L2	Rv0704	2	
40		MSMEG_1440	30S ribomal protein S19	Rv0705	2	
41		MSMEG_1442	30S ribomal protein S3	Rv0707	2	
42		MSMEG_1443	50S ribomal protein L16	Rv0708	2	
43		MSMEG_1445	30S ribomal protein S17	Rv0709	2	
44		MSMEG_1466	50S ribomal protein L24	Rv0715	2	
45		MSMEG_1467	50S ribomal protein L5	Rv0716	2	
46		MSMEG_1470	50S ribomal protein L6	Rv0719	2	
47		MSMEG_1471	Ribomal protein L18	Rv0720	2	
48		MSMEG_1472	30S ribomal protein S5	Rv0721	2	
49		MSMEG_1474	50S ribomal protein L15	Rv0723	2	
50	5	MSMEG_1484	Adenylate kinase	Rv0733	7	
51		MSMEG_1513	Putative uncharacterized protein	Rv3463	10	
52		MSMEG_1521	30S ribomal protein S13	Rv3460c	2	4
53	6	MSMEG_1522	30S ribomal protein S11	Rv3459c	2	
54		MSMEG_1524	DNA-directed RNA polymerase subunit alpha	Rv3457c	2	
55		MSMEG_1557	30S ribomal protein S9	Rv3455c	2	
56		MSMEG_1583	60 kDa chaperonin 2	Rv3417c	0	
57		MSMEG_1603	IMP dehydrogenase family protein	Rv3410c	7	
58		MSMEG_1634	Probable forkhead-associated protein			
59		MSMEG_1647	Bifunctional protein folD	Rv3356c	7	
60		MSMEG_1652	O-acetylhomerine sulfhydrylase	Rv3340	7	
61		MSMEG_1654	Isocitrate dehydrogenase, NADP-dependent	Rv0066c	7	
62		MSMEG_1662	Taurine-pyruvate aminotransferase	Rv3329	7	

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63		MSMEG_1665	Aldehyde dehydrogenase (NAD) family protein			
64		MSMEG_1670	Succinate dehydrogenase, flavoprotein subunit	Rv3318	7	
65		MSMEG_1684	Putative uncharacterized protein	Rv3311	10	
66		MSMEG_1803	RsbW protein			
67		MSMEG_1807	Acetyl-/propionyl-coenzyme A carboxylase alpha chain	Rv3285	1	
68		MSMEG_1809	Putative thiulfate sulfurtransferase	Rv3283	7	
69		MSMEG_1878	S30AE family protein	Rv3241c	2	
70		MSMEG_2026	Short chain dehydrogenase	Rv1245c	7	
71		MSMEG_2072	3-hydroxy-3-methylglutaryl-CoA lyase			
72		MSMEG_2080	Putative acyl-CoA dehydrogenase	Rv3140	1	
73		MSMEG_2086	Peptide chain release factor 2	Rv3105c	2	
74		MSMEG_2123	Dihydroxyacetone kinase, DhaK subunit			
75		MSMEG_2351	Electron transfer flavoprotein, beta subunit	Rv3029c	7	5
76	7	MSMEG_2352	Electron transfer flavoprotein, alpha subunit	Rv3028c	7	
77		MSMEG_2367	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	Rv3009c	2	
78		MSMEG_2373	Acetolactate synthase, small subunit	Rv3002c	7	6
79		MSMEG_2374	Ketol-acid reductoisomerase	Rv3001c	7	
80		MSMEG_2378	D-3-phosphoglycerate dehydrogenase	Rv2996c	7	7
81	8	MSMEG_2379	3-isopropylmalate dehydrogenase	Rv2995c	7	
82		MSMEG_2382	5-carboxymethyl-2-hydroxymuconate delta-isomerase	Rv2993c	2	
83	9	MSMEG_2387	3-isopropylmalate dehydratase, large subunit	Rv2988c	7	8 (I)
84	10	MSMEG_2388	3-isopropylmalate dehydratase, small subunit	Rv2987c	7	
85		MSMEG_2407	Morphine 6-dehydrogenase	Rv2971	2	9
86		MSMEG_2408	2,5-diketo-D-gluconic acid reductase A	Rv2971	2	
87		MSMEG_2435	30S ribomal protein S16	Rv2909c	2	
88		MSMEG_2443	Putative uncharacterized protein	Rv2901c	10	
89		MSMEG_2511	Siderophore utilization protein	Rv2895c	7	
90		MSMEG_2519	30S ribomal protein S2	Rv2890c	2	10
91	11	MSMEG_2520	Elongation factor Ts	Rv2889c	2	
92		MSMEG_2541	Ribome-recycling factor	Rv2882c	2	
93		MSMEG_2611	Pyridine nucleotide-disulphide oxidoreductase family protein	Rv2855	7	
94		MSMEG_2613	Probable malate:quinone oxidoreductase	Rv2852c	7	
95		MSMEG_2654	30S ribomal protein S15	Rv2785c	2	

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96		MSMEG_2659	Alanine dehydrogenase	Rv2780	7	
97		MSMEG_2669	Hydrolase	Rv2765	7	
98		MSMEG_2684	Dihydrodipicolinate synthase	Rv2753c	7	
99		MSMEG_2731	ATPase involved in DNA repair	Rv2731	10	
100		MSMEG_2744	Thymidylate synthase	Rv2716	10	
101		MSMEG_2750	Iron-dependent repressor IdeR	Rv2711	9	
102		MSMEG_2782	Putative uncharacterized protein	Rv2676c	10	
103	12	MSMEG_2937	Pyridoxal biynthesis lyase pdxS	Rv2606c	7	
104		MSMEG_3050	Integration ht factor	Rv1388	2	
105	13	MSMEG_3055	S-adenylmethionine synthetase	Rv1392	7	
106		MSMEG_3072	Riboflavin biynthesis protein ribAB	Rv1415	7	
107	14	MSMEG_3081	Putative uncharacterized protein	Rv1423	9	11 (II)
108	15	MSMEG_3084	Glyceraldehyde-3-phosphate dehydrogenase, type I	Rv1436	7	
109		MSMEG_3085	Phosphoglycerate kinase	Rv1437	7	12
110		MSMEG_3086	Triephosphate isomerase	Rv1438	7	
111	16	MSMEG_3102	Transaldolase	Rv1448c	7	
112		MSMEG_3106	Quinone oxidoreductase	Rv1454c	7	
113		MSMEG_3124	FeS assembly ATPase SufC	Rv1463	3	
114		MSMEG_3143	Aconitate hydratase 1 (Putatice aconitate hydratase)	Rv1475c	7	
115		MSMEG_3151	Enoyl-[acyl-carrier-protein] reductase [NADH]	Rv1484	1	
116	17	MSMEG_3205	Histidinol dehydrogenase	Rv1599	7	
117		MSMEG_3207	Imidazoleglycerol-phosphate dehydratase	Rv1601	7	
118		MSMEG_3220	Tryptophan synthase, beta subunit	Rv1612	7	
119		MSMEG_3227	Pyruvate kinase	Rv1617	7	
120		MSMEG_3255	DoxX subfamily protein, putative			
121		MSMEG_3308	Universal stress protein family protein, putative	Rv1636	10	
120	18	MSMEG_3461	Catalase-peroxidase 2	Rv1908c	0	
123		MSMEG_3478	Tena/thi-4 family protein			
124		MSMEG_3507	Fructose-bisphosphate aldolase class-I			
125		MSMEG_3619	Short chain dehydrogenase	Rv1856c	7	13
126		MSMEG_3620	Putative uncharacterized protein	Rv1855c	7	
127		MSMEG_3640	Malate synthase G	Rv1837c	7	
128		MSMEG_3770	Argininuccinate synthase	Rv1658	7	

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129		MSMEG_3811	Universal stress protein family protein, putative	Rv1636	10	
130		MSMEG_3833	30S ribomal protein S1	Rv1630	2	
131		MSMEG_3880	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase	Rv2074	7	14
132		MSMEG_3881	Proline dipeptidase	Rv2075c	3	
133		MSMEG_3894	Proteasome alpha subunit	Rv2109c	7	15
134		MSMEG_3895	Proteasome beta subunit	Rv2110c	7	
135		MSMEG_3902	ATPase, AAA family protein	Rv2115c	3	
136		MSMEG_3906	TRNA (Adenine-N(1)-)-methyltransferase	Rv2118c	7	
137		MSMEG_3932	14 kDa antigen	Rv2031c	0	
138		MSMEG_3945	Universal stress protein family protein	Rv2028c	10	
139	19	MSMEG_3950	Universal stress protein family protein	Rv2026c	10	
140		MSMEG_4121	GntR-family protein transcriptional regulator			
141		MSMEG_4222	Cell division protein ftsZ	Rv2150c	3	
142		MSMEG_4270	Adenine kinase	Rv2202c	7	16
143		MSMEG_4272	HesB/YadR/YfhF family protein	Rv2204c	10	
144		MSMEG_4276	Branched-chain amino acid aminotransferase	Rv2210c	7	
145		MSMEG_4278	Aminomethyltransferase	Rv2211c	7	
146		MSMEG_4281	Cytol aminopeptidase	Rv2213	7	17
147		MSMEG_4283	2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide succ	Rv2215	7	
148		MSMEG_4290	Glutamine synthetase	Rv2220	7	
149		MSMEG_4306	Putative uncharacterized protein	Rv2229c	10	
150		MSMEG_4313	Glyoxalase/bleomycin resistance protein/dioxygenase			
151		MSMEG_4323	Pyruvate dehydrogenase E1 component	Rv2241	7	18 (III)
152		MSMEG_4325	Malonyl CoA-acyl carrier protein transacylase	Rv2243	1	
153	20	MSMEG_4326	Acyl carrier protein	Rv2244	1	
154	21	MSMEG_4327	3-oxoacyl-[acyl-carrier-protein] synthase 1	Rv2245	1	
155	22	MSMEG_4328	3-oxoacyl-[acyl-carrier-protein] synthase 2	Rv2246	1	
156		MSMEG_4362	Universal stress protein family protein			
157		MSMEG_4401	Phosphonoacetaldehyde hydrolase			
158		MSMEG_4474	Acyl-CoA oxidase			
159		MSMEG_4476				
160		MSMEG_4487	Ferric uptake regulation protein	Rv2359	9	
161		MSMEG_4504	Chaperone protein DnaJ	Rv2373c	0	

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160	23	MSMEG_4527	Ferredoxin sulfite reductase	Rv2391	7	
161	24	MSMEG_4530	Sulfate ABC transporter, ATP-binding protein	Rv2397c	3	
164		MSMEG_4533	Sulfate-binding protein	Rv2400c	3	
165		MSMEG_4645	Alpha oxoglutarate ferredoxin oxidoreductase, beta subunit	Rv2454c	7	
166		MSMEG_4673	ATP-dependent Clp protease proteolytic subunit	Rv2461c	7	19
167		MSMEG_4674	Trigger factor	Rv2462c	3	
168		MSMEG_4742	Clavaldehyde dehydrogenase	Rv0484c	7	
169		MSMEG_4752	Putative uncharacterized protein	Rv2520c	3	
170		MSMEG_4755	Peptidase M20	Rv2522c	10	
171	25	MSMEG_4891	Alkylhydroperoxide reductase	Rv2428	0	
172	26	MSMEG_4920	Acetyl-CoA acetyltransferase	Rv1323	1	
173		MSMEG_4921				
174		MSMEG_4935	ATP synthase epsilon chain	Rv1311	7	20
175		MSMEG_4936	ATP synthase subunit beta	Rv1312	3	
176		MSMEG_4938	ATP synthase subunit alpha	Rv1308	7	
177		MSMEG_4939	ATP synthase delta chain	Rv1307	7	
178	27	MSMEG_4954	Transcription termination factor Rho	Rv1297	2	21 (IV)
179	28	MSMEG_4956	Threonine synthase	Rv1295	7	
180		MSMEG_5015	Secreted protein			
181		MSMEG_5087	Putative uncharacterized protein	Rv1205	10	
182	29	MSMEG_5104	Tetrahydropicolinate succinylase	Rv1201c	7	
183		MSMEG_5136	Helix-turn-helix motif	Rv0080	10	
184		MSMEG_5222	GTP-binding protein YchF	Rv1112	10	
185		MSMEG_5239	Fructe-1,6-bisphosphatase, class II	Rv1099c	7	22
186		MSMEG_5240	Fumarate hydratase class II	Rv1098c	7	
187		MSMEG_5243	Helix-turn-helix motif	Rv3129	10	23
188		MSMEG_5245	Universal stress protein family protein	Rv3134c	10	
189		MSMEG_5246	Putative uncharacterized protein	Rv3131	10	
190	30	MSMEG_5249	Serine hydroxymethyltransferase	Rv1093	7	
191	31	MSMEG_5258	Steroid delta-isomerase			
192		MSMEG_5261	Mycothiol conjugate amidase Mca	Rv1082	0	
193		MSMEG_5270	Cystathionine beta-synthase	Rv1077	7	
194		MSMEG_5273	Beta-ketoadipyl CoA thiolase	Rv1074	1	

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195	32	MSMEG_5335	Formamidase			24
196		MSMEG_5336	Amidate substrates transporter protein			
197		MSMEG_5415	Enolase	Rv1023	7	
198		MSMEG_5427	Ribe-phosphate pyrophosphokinase	Rv1017c	7	
199	33	MSMEG_5431	Ribomal protein L25, Ctc-form	Rv1015c	2	
200		MSMEG_5442	Glutamate dehydrogenase			
201		MSMEG_5512	Magnesium chelatase	Rv0958	7	
202		MSMEG_5524	Succinyl-CoA ligase [ADP-forming] subunit alpha	Rv0952	7	25
203		MSMEG_5525	Succinyl-CoA ligase [ADP-forming] subunit beta	Rv0951	7	
204		MSMEG_5538	[NADP+] succinate-semialdehyde dehydrogenase			
205		MSMEG_5612	Amino-acid acetyltransferase	Rv0995	2	
206		MSMEG_5639	Enoyl-CoA hydratase	Rv0905	1	
207		MSMEG_5672	Citrate synthase	Rv0896	7	
208		MSMEG_5707	Cupin domain protein	Rv2619c	10	
209		MSMEG_5715	Putative uncharacterized protein	Rv0791c	10	
210		MSMEG_5727	Allantoicase			
211		MSMEG_5733	Universal stress protein family protein	Rv2624c	10	
212		MSMEG_5773	Fatty acid desaturase	Rv0824c	1	
213		MSMEG_5776	Phosphate transport system regulatory protein PhoU	Rv0821c	3	
214	34	MSMEG_5789	Putative thiulfate sulfurtransferase	Rv0815c	7	26 (V)
215	35	MSMEG_5790	SseC protein	Rv0814c	7	
216		MSMEG_5824	Phosphoribylformylglycinamidine synthase II	Rv0803	7	
217		MSMEG_5830	29 kDa antigen Cfp29	Rv0798c	0	27
218		MSMEG_5832	Phosphoribylformylglycinamidine synthase, PurS protein			
219	36	MSMEG_6008	Acetyl-CoA acetyltransferase	Rv3556c	1	
220		MSMEG_6082	Carbonic anhydrase	Rv3588c	7	
221		MSMEG_6091	Negative regulator of genetic competence ClpC/mecB	Rv3596c	7	
222		MSMEG_6114	Inorganic pyrophosphatase	Rv3628	7	
223		MSMEG_6142	Nucleide-diphosphate-sugar epimerase	Rv3634c	7	
224		MSMEG_6189	Transcriptional regulator, Crp/Fnr family protein	Rv3676	9	
225		MSMEG_6235	Thiopurine S-methyltransferase (Tpmt) superfamily protein	Rv3699	10	
226	37	MSMEG_6247	Putative uncharacterized protein	Rv3701c	10	
227		MSMEG_6256	Aspartate-semialdehyde dehydrogenase	Rv3708c	7	

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228	38	MSMEG_6284	Cyclopropane-fatty-acyl-phospholipid synthase	Rv3720	1	28 (VI)
229	39	MSMEG_6286	Aspartate transaminase	Rv3722c	10	
230		MSMEG_6384	Catalase-peroxidase 1	Rv1908c	0	
231		MSMEG_6393	Acyl-CoA synthase	Rv3801c	1	
232		MSMEG_6398	Antigen 85-A	Rv3803c	1	
233		MSMEG_6422	Ferritin family protein	Rv3841	7	
234	40	MSMEG_6427	Superoxide dismutase	Rv3846	0	
235	41	MSMEG_6518	Putative uncharacterized protein	Rv3863	10	
236		MSMEG_6636	Superoxide dismutase	Rv3846	0	
237		MSMEG_6746	Oxidoreductase, aldo/keto reductase family protein			
238		MSMEG_6759	Glycerol kinase	Rv3696c	7	
239		MSMEG_6896	Single-stranded DNA-binding protein	Rv0054	2	29
240		MSMEG_6897	Ribomal protein S6	Rv0053	2	
241		MSMEG_6904	Myo-initol-1-phosphate synthase	Rv0046c	7	
242		MSMEG_6907	MmcI protein	Rv0044c	7	
243		MSMEG_6933	Thioredoxin reductase	Rv3913	7	

Supplement Table 3B

Category	Functional Categorization	Number of genes (proteome)	Relative distribution (proteome)	Number of confirmed PUP targets	Relative distribution confirmed PUP targets	Number of pup candidate targets	Relative distribution of pup candidate targets
0	Virulence, detoxification, adaptation	99	2.4	14	6.5	14	6.5
1	Lipid metabolism	233	5.8	18	8.3	18	8.3
2	Information pathways	229	5.7	43	19.8	43	19.8
3	Cell wall and cell processes	708	17.5	11	5.1	11	5.1
4	Stable RNAs	50	1.2	0	0	0	0.0
5	Insertion seqs and phages	149	3.7	0	0	0	0.0
6	PE/PPE	170	4.2	0	0	0	0.0
7	Intermediary metabolism and respiration	894	22.1	96	44.2	96	44.2
8	Proteins of unknown function	272	6.7	0	0	0	0.0
9	Regulatory proteins	189	4.7	5	2.3	5	2.3
10	Conserved hypotheticals	1051	26	30	13.8	30	13.8
Total		4044	100	217	100	217	100

Supplement Table 4

2D Gel spots No. (Supplement Figure 3)	**Taget No. (Supplement Table 3A)**	**Target ID (Table 1)**	**Gene locus (*M. smegmatis*)**	**Detected Pupylation Sequences**	**Pupylated lysines**	**Spot intensity (stationary phase, panel A)**	**Spot intensity (log phase, panel B)**	**Spot intensity (oxidative stress, panel C)**
9	108	15	MSMEG_3084	AAAEGPLK$^{\text{PupylGGE}}$GILK	K277	+	+	++
16	139	19	MSMEG_3950	YPDVK$^{\text{PupylGGE}}$VHR	K234	+++	++	+++
50	81	8	MSMEG_2379	VDK$^{\text{PupylGGE}}$AVSEHLATR	K313	++	+++	+++
10	91	11	MSMEG_2520	IGEK$^{\text{PupylGGE}}$LELR	K36	++	+	+++
6	120	18	MSMEG_3461	NYVRPGEK$^{\text{PupylGGE}}$VQLEK	K401	+	++	+
56	125	n.d.	MSMEG_3619	RDDLEVAAK$^{\text{PupylGGE}}$ELDIESIVFDNTDAASLEAVR	K43	+	+++	+++