

Table S1: Applied MS/MS search parameters

	1-D SDS-PAGE/ MALDI-MS/MS approach	1-D SDS-PAGE/ CapLC-MS/MS approach	2-DE/ MALDI-MS/MS approach	
Search algorithm	Mascot Version 2.0 (Matrix Science, London, UK)			
Protein database	<i>M. tuberculosis</i> H37Rv protein database of TIGR (Release 1.0; 3915 protein entries)			
MS search parameters	Considered variable modifications Acetylation of N-termini of proteins Modification of cysteines by acrylamide (propionamide) Oxidation of methionines			
	Protein mass restriction	no	no	no
	Mass values	monoisotopic; 1+	monoisotopic; 2+ and 3+	monoisotopic; 1+
	Maximum number of missed cleavages	2	1	2
	Tolerated peptide ion mass error	100 ppm	1 Da	50 ppm
	Tolerated fragment ion mass error	0.4 Da	0.1 Da	0.3 Da