TABLE S1 The 85 proteins identified by MTB proteome microarray that bound POA

Name	SNR	Function
Rv3248c	10.65	SAHH
Rv3699	10.47	SAM-dependent methyltransferases
Rv3735	10.22	Adenosine specific kinase
Rv1003	7.16	Ribosomal RNA small subunit methyltransferase I,also known as rRNA (cytidine-2'-O-)-methyltransferase RsmI; containing putative SAM binding site
Rv3351c	7.03	CoA-transferase
Rv3404c	6.87	Formyltransferase
Rv1603	6.78	HisA. Phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide (ProFAR) isomerase catalyzesthe fourth step in histidine biosynthesis, anisomerisation of the aminoaldose moiety of ProFAR to the aminoketose of PRFAR
Rv2711	6.67	Iron-dependent repressor and activator IdeR
Rv1289	6.47	Hypothetical protein
Rv2121c	6.06	ATP phosphoribosyltransferase HisG
Rv0191	5.70	Predicted arabinose efflux permease involved in transport of drug
Rv0187	5.55	O-methyltransferase, S-adenosylmethionine-dependent methyltransferases(SAM or AdoMet-MTase), class I; AdoMet-MTases are enzymes that use S-adenosyl-L-methionine (SAM or AdoMet) as a substrate for methyltransfer, creating the product S-adenosyl-L-homocysteine
Rv2769c	5.54	PE family protein PE27
Rv1876	5.50	Bacterioferritin BfrA (in fact, BfrB is more important, lacking BfrB would result in highly susceptible to killing by antibiotics,and unable persist in mice)
Rv1377c	5.47	S-adenosylmethionine-dependent methyltransferases (SAM or AdoMet-MTase), class I; AdoMet-MTases are enzymes that use S-

		adenosyl-L-methionine (SAM or AdoMet) as a substrate for methyltransfer, creating the product S-adenosyl-L-homocysteine (AdoHcy)
Rv1581c	5.46	Phage protein
Rv0757	5.36	Two component system response transcriptional positive regulator PhoP (associated with virence)
Rv3455c	5.31	tRNA pseudouridine synthase A
Rv1478	5.14	Peptidoglycan endopeptidase RipB, invasion protein
Rv1613	5.07	Tryptophan synthase subunit alpha
Rv0045c	4.99	Hydrolase
Rv3442c	4.96	30S ribosomal protein S9 RpsI
Rv2115c	4.92	Mycobacterial proteasome ATPase Mpa
Rv0417	4.80	Thiamin biosynthesis protein ThiG. Thiazole synthase (ThiG) is the tetrameric enzyme that is involved in the formation of the thiazole moiety of thiamin pyrophosphate, an essential ubiquitous cofactor that plays an important role in carbohydrate and amino acid metabolism
Rv0120c	4.73	Elongation factor G FusA2 (EF-G)
Rv2525c	4.67	A substrate of the twin arginine translocation (tat) export system
Rv0604	4.65	Lipoprotein LpqO
Rv0116c	4.63	L,D-transpeptidase LdtA (proved to be associated with Mtb persistence)
Rv1718	4.57	Hypothetical protein
Rv2521	4.52	Peroxiredoxin
Rv1719	4.45	Transcriptional regulator
Rv0618	4.34	Galactose-1-phosphate uridylyltransferase
Rv3756c	4.33	Glycine betaine/carnitine/choline/L-proline ABC transporter permease ProZ
Rv1324	4.32	Thioredoxin

Rv3008	4.29	Uncharacterized membrane protein YhiD, involved in acid resistance
Rv3555c	4.24	Superfamily of nucleases including Short Patch Repair (Vsr) Endonucleases, archaeal Holliday junction resolvases, MutH methy-directed DNA mismatch-repair endonucleases
Rv2140c	4.18	PhosphatidylEthanolamine-Binding Protein (PEBP) domain present in bacteria and archaea
Rv1301	4.18	Threonylcarbamoyl-AMP synthase, tRNA threonylcarbamoyl adenosine modification protein
Rv0760c	4.13	Nuclear transport factor 2 (NTF2)
Rv3673c	4.13	Membrane-anchored thioredoxin-like protein, TlpA-like family; composed of TlpA, ResA, DsbE and similar proteins. TlpA, ResA and DsbE are bacterial protein disulfide reductases with important roles in cytochrome maturation. They are membrane-anchored proteins with a soluble TRX domain
Rv0784	4.04	Putative catalytic domain of uncharacterized bacterial proteins from the carbohydrate esterase 4 superfamily
Rv1154c	4.04	Hypothetical protein
Rv3399	3.85	S-adenosylmethionine-dependent methyltransferase, O-Methyltransferase involved in polyketide biosynthesis
Rv3176c	3.85	Epoxide hydrolase MesT
Rv2751	3.84	Methyltransferase
Rv0233	3.80	Ribonucleoside-diphosphate reductase subunit beta NrdB
Rv3283	3.78	Thiosulfate sulfurtransferase SseA
Rv1654	3.75	Probable acetylglutamate kinase ArgB
Rv2172c	3.74	Hypothetical protein
Rv0801	3.74	Glo_EDI_BRP_like superfamily is found in a variety of structurally related metalloproteins, including the type I extradiol dioxygenases, glyoxalase I and a group of antibiotic resistance proteins

Rv3709c	3.66	Aspartate kinase, Amino Acid Kinase Superfamily(AAK),
Rv1460	3.63	Transcriptional regulator, ArsR family, Arsenical Resistance Operon Repressor and similar prokaryotic, metal regulated homodimeric repressors. ARSR subfamily of helix-turn-helix bacterial transcription regulatory proteins (winged helix topology)
Rv1337	3.57	Integral membrane protein
Rv1857	3.53	Molybdate-binding lipoprotein ModA
Rv1879	3.50	Predicted metal-dependent hydrolase, TIM-barrel fold
Rv1667c	3.49	Second part of macrolide-transport ATP-binding protein ABC transporter
Rv3268	3.49	Hypothetical protein
Rv3563	3.46	Acyl-CoA dehydrogenase FadE32
Rv1078	3.45	Hypothetical protein
Rv2245	3.45	3-oxoacyl-ACP synthase 1, Beta-ketoacyl-acyl carrier protein (ACP) synthase(KAS), type I and II. KASs are responsible for the elongation steps in fatty acid biosynthesis.
Rv3382c	3.41	LYTB-related protein LytB1,4-hydroxy-3-methylbut-2-enyl diphosphate reductase
Rv1712	3.40	Cytidylate kinase
Rv3837c	3.38	Phosphoglycerate mutase
Rv2857c	3.37	Short-chain type dehydrogenase/reductase,Rossmann-fold NAD(P)(+)-binding proteins
Rv1919c	3.33	Pyrabactin resistance 1 (PYR1), PYR1-like (PYL), regulatory component of abscisic acid receptors (RCARs), and related proteins
Rv1597	3.29	S-adenosylmethionine-dependent methyltransferases (SAM or AdoMet-MTase)
Rv3378c	3.28	Diterpene synthase
Rv2965c	3.24	Phosphopantetheine adenylyltransferase
Rv3305c	3.21	N-acyl-L-amino acid amidohydrolase AmiA

Rv2895c	3.20	Mycobactin utilization protein ViuB
Rv1083	3.19	N-acetylmuramic acid-6-phosphate etherase
Rv0421c	3.19	Hydrolase of the alpha/beta-hydrolase fold
Rv1056	3.14	Hypothetical protein
Rv0134	3.10	Epoxide hydrolase EphF
Rv0283	3.09	ESX-3 secretion system protein EccB3, type VII secretion protein EccB, Actinobacterial
Rv3154	3.07	NADH-quinone oxidoreductase subunit J
Rv2821c	3.06	CRISPR type III-associated RAMP protein Csm3
Rv1949c	3.05	Carboxyl transferase
Rv3089	3.05	Long chain-fatty-acid--CoA ligase FadD13
Rv0459	3.03	Hypothetical protein
Rv3420c	3.03	Ribosomal-protein-alanine acetyltransferase, RimI
Rv0503c	3.02	Cyclopropane mycolic acid synthase,S-adenosylmethionine-dependent methyltransferases (SAM or AdoMet-MTase), class I; AdoMet-MTases are enzymes that use S-adenosyl-L-methionine (SAM or AdoMet) as a substrate for methyltransfer, creating the product S-adenosyl-L-homocysteine (AdoHcy)
Rv0414c	3.02	Thiamine-phosphate pyrophosphorylase ThiE (TMP pyrophosphorylase) (TMP-PPASE) (thiamine-phosphate synthase)
Rv3174	3.01	Short-chain dehydrogenase/reductase, Rossmann-fold NAD(P)(+)-binding proteins
Rv2049c	3.01	Hypothetical protein

SNR: signal to noise ratio.