

Supplementary Table S6. Comparison of Mycobacterium tuberculosis H37Ra acetylome with other bacterial acetylomes.

BLAST alignments were performed by using BlastP software with BLOSUM62 matrix; the best-scoring homologous protein was selected if the corresponding BLAST E values were lower than 1E-5.

Mycobacterium tuberculosis H37Ra		Salmonella typhimurium	Escherichia coli	Erwinia amylovora	Bacillus subtilis
Protein ID	Description				
qi 148659912	short-chain type dehydrogenase/reductase		qi 26109978	qi 292898248	BSU15910
qi 148660007	3-ketoacyl-ACP reductase		qi 26109978	qi 292898248	BSU15910
qi 148660104	putative iron-sulfur-binding reductase			qi 292899402	
qi 148660013	succinate dehydrogenase flavoprotein subunit		qi 26246691		BSU28440
qi 148660035	acyl-CoA synthetase	sp Q8ZKF6 ACSA_SALTY			BSU28560
qi 148660116	molecular chaperone DnaK	sp POA9X6 MREB_SALTY	qi 75235743		BSU25470
qi 148660129	fructose-bisphosphate aldolase		qi 110643069	qi 292900509	BSU37120
qi 148660204	short chain dehydrogenase		qi 26109978		BSU15910
qi 148660205	molecular chaperone GroEL		qi 99867128	qi 292898143	BSU06030
qi 148660228	dihydrolypoamide dehydrogenase		qi 26106453		BSU14610
qi 148660233	isocitrate lyase Icl	sp P51066 ACEA_SALTY			
qi 148660256	phosphoglyceromutase	sp Q8ZJU8 GPMB_SALTY	qi 13360242	qi 292898912	
qi 148660426	50S ribosomal protein L7/L12			qi 292897959	BSU01050
qi 148660320	acyl-CoA synthetase	sp Q8ZKF6 ACSA_SALTY			BSU28560
qi 148660441	DNA-directed RNA polymerase subunit beta		qi 42818	qi 292897960	BSU01070
qi 148660442	DNA-directed RNA polymerase subunit beta'		qi 223476		BSU01080
qi 148660459	elongation factor G	sp POA1H3 EFG_SALTY	qi 110643581	qi 292900894	BSU01120
qi 148660460	elongation factor Tu	sp POA1W4 LEPA_SALTY	qi 26249935	qi 292900048	BSU01130
qi 148660475	30S ribosomal protein S10			qi 292900892	
qi 148660529	MmsA		qi 75515146		BSU39760
qi 148660637	fatty oxidation complex subunit alpha	sp Q8ZNA7 FADJ_SALTY			
qi 148660667	citrate synthase 2	sp O68883 CISY_SALTY	qi 16128695		BSU29140
qi 148660674	type II citrate synthase	sp O68883 CISY_SALTY	qi 16128695		BSU29140
qi 148660730	succinyl-CoA synthetase subunit beta	sp P66869 SUCC_SALTY			BSU16090
qi 148660799	ribose-phosphate pyrophosphokinase	sp POA1V6 KPRS_SALTY			
qi 148660879	serine hydroxymethyl transferase		qi 26248915	qi 292900198	BSU36900
qi 148660884	fumarate hydratase	sp Q8ZPL7 FUMC_SALTY			BSU06440
qi 148661027	malate dehydrogenase	sp P25077 MDH_SALTY			
qi 148661035	alpha-ketoglutarate decarboxylase	tr Q8ZRT1 Q8ZRT1_SALTY	qi 26246694	qi 292898469	BSU19370
qi 148661113	thioredoxin-related protein		qi 148071	qi 292897894	
qi 148661183	S-adenosylmethionine synthetase		qi 146851		BSU30550
qi 148661240	transaldolase	sp Q8ZN83 TALA_SALTY		qi 292898367	BSU37110
qi 148661276	3-oxoacyl-ACP reductase		qi 26109978	qi 292898248	BSU15910
qi 148661325	acyl-CoA synthetase	sp Q8ZKF6 ACSA_SALTY			BSU28560
qi 148661329	hypothetical protein		qi 146275		
qi 148661425	30S ribosomal protein S1		qi 42900	qi 292899057	BSU22880
qi 148661529	succinic semialdehyde dehydrogenase		qi 75515146		BSU03910
qi 148661643	malate synthase G	tr Q8ZKL4 Q8ZKL4_SALTY			
qi 148661816	20-beta-hydroxysteroid dehydrogenase FabG3		qi 26109978	qi 292898248	BSU15910
qi 148661974	UDP-N-acetylmuramoylalanine-D-glutamate--2,6-diaminopimelate ligase	sp Q8ZRU7 MURE_SALTY			
qi 148662003	long-chain-fatty-acid--CoA ligase	sp Q8ZKF6 ACSA_SALTY			BSU28560
qi 148662032	dihydrolypoamide acetyltransferase	tr Q8ZRT1 Q8ZRT1_SALTY	qi 26246694	qi 292898469	BSU19360
qi 148662065	acyl carrier protein			qi 292899175	
qi 148662038	glutamine synthetase	sp POA1P6 GLNA_SALTY			BSU17460
qi 148662062	pyruvate dehydrogenase subunit E1		qi 83584560		
qi 148662625	polynucleotide phosphorylase		qi 42900	qi 292899057	BSU22880
qi 148662733	elongation factor Ts			qi 292898540	BSU16500
qi 148662734	30S ribosomal protein S2			qi 292898539	BSU16490
qi 148662940	zinc-type alcohol dehydrogenase AdhD			qi 292898783	BSU26970
qi 148662726	ribosome recycling factor	sp P66738 RRF_SALTY	qi 67472290		BSU16520

qi 148662987	two component transcriptional regulatory protein DevR	sp P27667 UHPA_SALTY		qi 292900804	BSU28560
qi 148663086	short chain dehydrogenase		qi 26109978		BSU15910
qi 148663109	two component sensory transduction transcriptional regulatory protein MtrA	sp P66795 QSEB_SALTY		qi 292900804	BSU23120
qi 148663251	hypothetical protein MRA_3428A			qi 292899402	
qi 148663281	molecular chaperone GroEL		qi 99867128	qi 292898143	BSU06030
qi 148663282	co-chaperonin GroES			qi 292898142	BSU06020
qi 148663444	cysteinyI-tRNA synthetase	sp Q8ZR68 SYC_SALTY			
qi 148663491	inorganic pyrophosphatase	sp P65748 IPYR_SALTY		qi 292898185	
qi 148663642	enoyl-CoA hydratase	sp Q8ZNA7 FADJ_SALTY		qi 292900048	
qi 148663668	polyketide synthase Pks13			qi 292900669	BSU03510
qi 148660731	succinyl-CoA synthetase subunit alpha				BSU16100
qi 148660908	6-phosphogluconate dehydrogenase				BSU23860
qi 148661096	ATP synthase FOF1 subunit alpha				BSU36810
qi 148661098	ATP synthase FOF1 subunit beta				BSU36810
qi 148661268	aconitate hydratase				BSU18000
qi 148661317	acyl-CoA synthetase				BSU28560
qi 148661431	hypothetical protein				BSU39250
qi 148661454	argininosuccinate synthase				BSU29450
qi 148663669	long-chain-fatty-acid--CoA ligase				BSU28560
qi 148663323	30S ribosomal protein S4				BSU29660
qi 148663322	DNA-directed RNA polymerase subunit alpha				BSU01430
qi 148661733	fatty-acid--CoA ligase				BSU28560
qi 148662028	glycine cleavage system aminomethyltransferase T				BSU24570
qi 148662295	ATP-dependent Clp protease proteolytic subunit				BSU34540
qi 148662446	pyridoxal biosynthesis lyase PdxS				BSU00110
qi 148662852	ketol-acid reductoisomerase				BSU28290