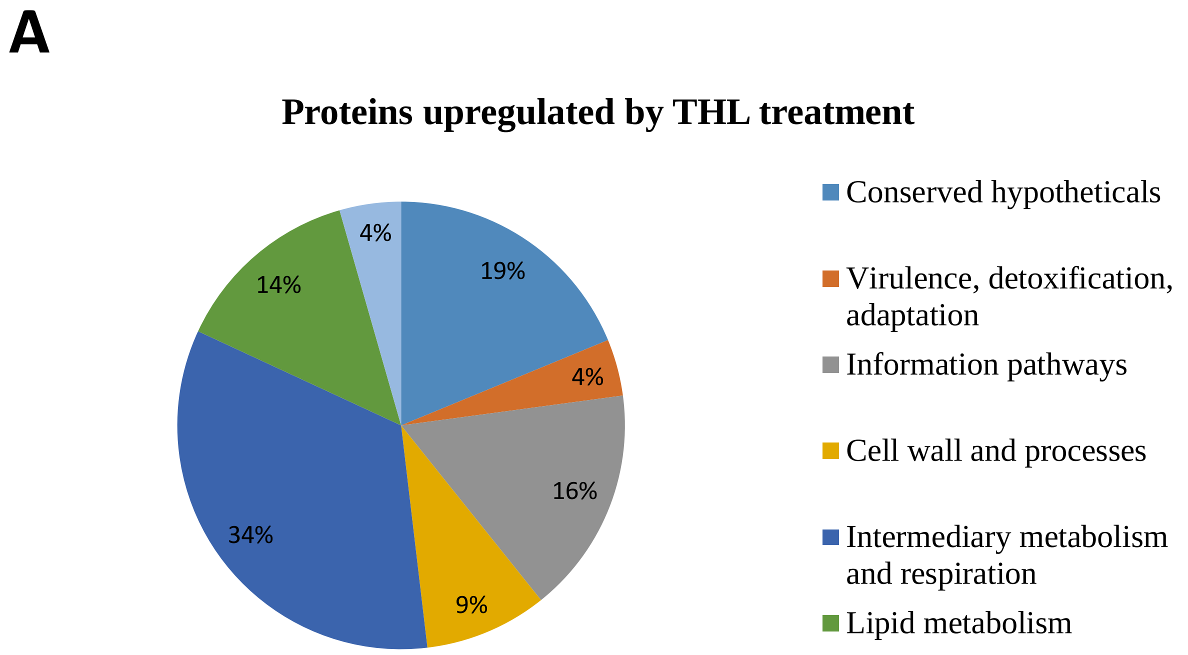
Supplementary figures.



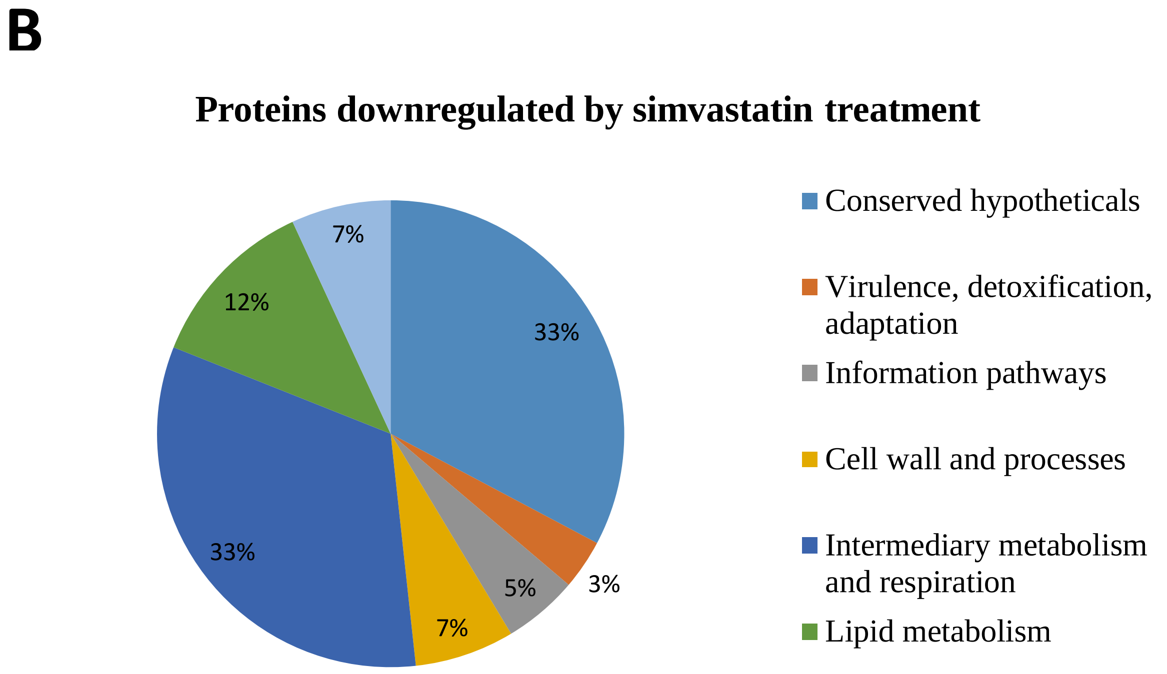


FIG S1 Pie charts representing the percentage, by functional category, of (A) upregulated proteins after 24h THL treatment and (B) downregulated proteins after 24h simvastatin treatment.

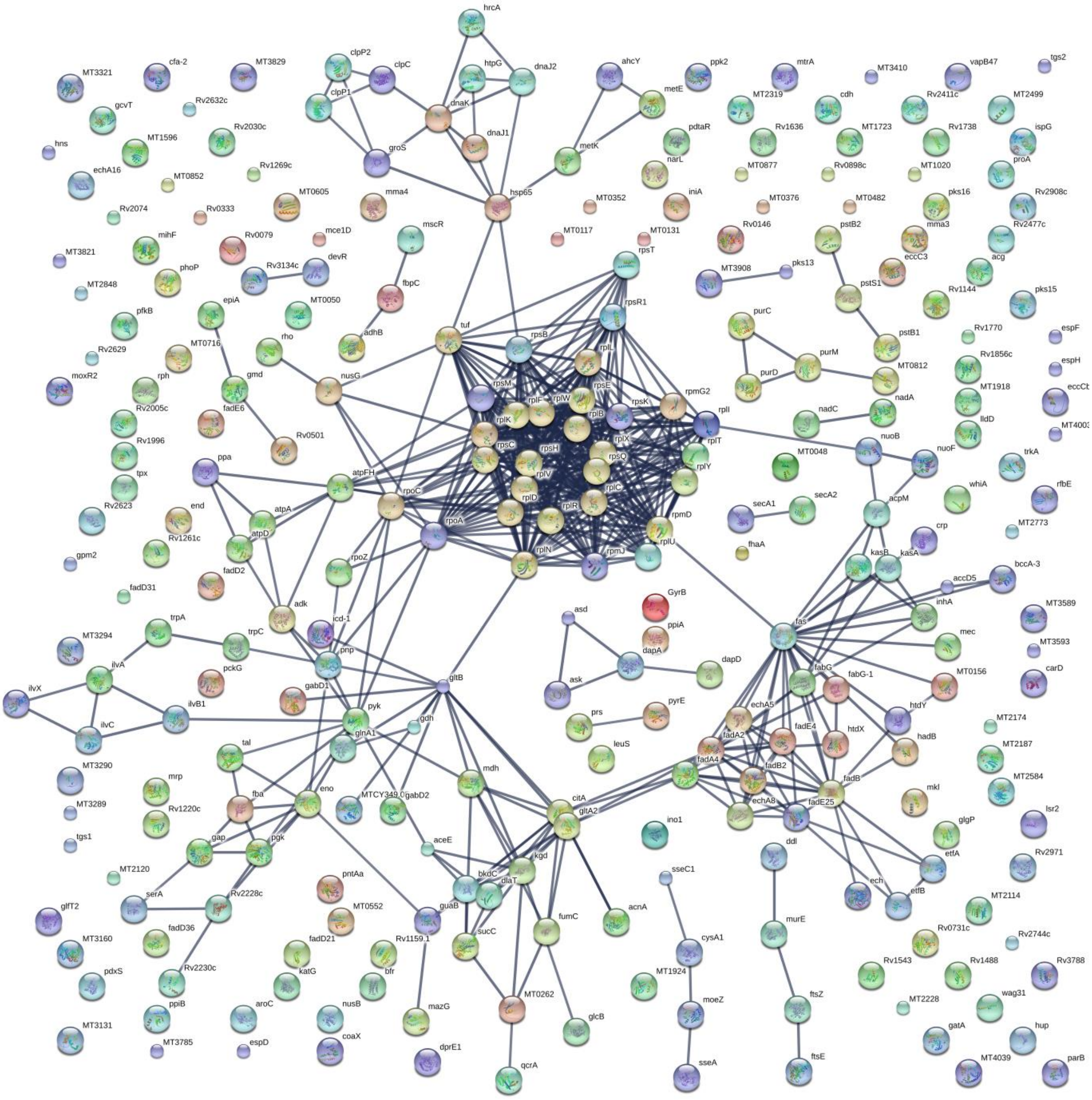


FIG S2 Visualization of network interactions between the 293 up-expressed proteins after 24 h of THL treatment using the STRING database. The figure shows the confidence view and stronger associations, represented by thicker lines. The expected number of edges and the PPI enrichment p-value were 372 and 0, respectively.

TABLE S3

Proteins down- and upexpressed after a 24 h THL treatment

ORF	Gene name	Gene product	Fold change	p-values
Intermediary metabolism and respiration				
Rv0560c		POSSIBLE BENZOQUINONE METHYLTRANSFERASE	0,02	0,02442
Rv0391	*metZ*	PROBABLE O-SUCCINYLHOMOSERINE SULFHYDRYLASE METZ	0,05	0,00356
Rv0077c		PROBABLE OXIDOREDUCTASE	0,08	8,6E-06
Rv2858c	*aldC*	PROBABLE ALDEHYDE DEHYDROGENASE ALDC	0,30	0,0375
Rv2439c	*proB*	PROBABLE GLUTAMATE 5-KINASE PROTEIN PROB	0,36	0,03823
Rv3045	*adhC*	PROBABLE NADP-DEPENDENT ALCOHOL DEHYDROGENASE ADHC	0,58	0,02343
Rv1872c	*lldD*	LACTATE DEHYDROGENASE	1,26	0,02197
Rv1869c		PROBABLE REDUCTASE	1,31	0,02624
RVV2540c	*aroC*	CHORISMATE SYNTHASE	1,32	0,01583
Rv3117	*cysA3*	SULFURTRANSFERASE	1,38	0,03463
Rv3248c	*ahcY*	ADENOSYL HOMOCYSTEINASE	1,43	0,04992
Rv0889	*citA*	CITRATE SYNTHASE 2	1,44	0,02274
Rv1596	*nadC*	NICOTINATE NUCLEOTIDE PYROPHOSPHORYLASE	1,45	0,00622
Rv1144		3 HYDROXY 2 METHYLBUTYRYL COA DEHYDROGENASE	1,46	0,01005
Rv2215	*dlaT*	DIHYDROLIPOAMINE ACETYLTRANSFERASE	1,46	0,00808
Rv0809	*purM*	PROBABLE PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE PURM	1,54	0,02994
Rv0148		PROBABLE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE	1,56	0,00444
Rv0241c	*htdX*	DOUBLE HOTDOG HYDRATASE	1,56	0,02681
Rv1617	*pykA*	PROBABLE PYRUVATE KINASE PYKA	1,56	0,02314
Rv0951	*sucC*	PROBABLE SUCCINYL-CoA SYNTHETASE SUCC	1,56	0,02235
Rv3283	*sseA*	PROBABLE THIOSULFATE SULFURTRANSFERASE SSEA	1,58	0,00826
Rv1307	*atpH*	PROBABLE ATP SYNTHASE DELTA CHAIN ATPH	1,59	0,02304
Rv2509		PROBABLE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE	1,60	0,02337
Rv1511	*gmdA*	GDP-D-MANNOSE DEHYDRATASE GMDA	1,60	0,02323
Rv2476c	*gdh*	PROBABLE NAD-DEPENDENT GLUTAMATE DEHYDROGENASE GDH	1,61	0,01706
Rv1731	*gabD2*	POSSIBLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE GABD2	1,61	0,00171

Rv3150	*nuoF*	PROBABLE NADH DEHYDROGENASE I (CHAIN F) NUOF	1,61	0,03915
Rv0780	*purC*	PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE PURC	1,62	0,02278
Rv0211	*pckA*	PROBABLE IRON-REGULATED PHOSPHOENOLPYRUVATE CARBOXYKINASE PCKA	1,63	0,00548
Rv3001c	*ilvC*	PROBABLE KETOL-ACID REDUCTOISOMERASE ILVC	1,63	0,00209
Rv2996c	*serA1*	PROBABLE D-3-PHOSPHOGLYCERATE DEHYDROGENASE SERA1	1,65	0,00141
Rv0248c		PROBABLE SUCCINATE DEHYDROGENASE	1,65	0,04814
Rv2211c	*gcvT*	PROBABLE AMINOMETHYLTRANSFERASE GCVT	1,66	0,00439
Rv0338c		PROBABLE IRON-SULFUR-BINDING REDUCTASE	1,68	0,00752
Rv1098c	*fum*	PROBABLE FUMARASE FUM	1,68	0,00028
Rv2971		PROBABLE OXIDOREDUCTASE	1,68	0,01468
Rv1240	*mdh*	PROBABLE MALATE DEHYDROGENASE MDH	1,69	0,0104
Rv3028c	*fixB*	PROBABLE ELECTRON TRANSFER FLAVOPROTEIN FIXB	1,70	0,02823
Rv1436	*gap*	PROBABLE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE GAP	1,71	0,01028
Rv1023	*eno*	PROBABLE ENOLASE ENO	1,71	0,00744
Rv1310	*atpD*	PROBABLE ATP SYNTHASE BETA CHAIN ATPD	1,71	0,00264
Rv1248c	*kgd*	ALPHA-KETOGLUTARATE DECARBOXYLASE	1,72	0,02452
Rv1392	*metK*	PROBABLE S-ADENOSYLMETHIONINE SYNTHETASE METK	1,72	0,00567
Rv0066c	*icd2*	PROBABLE ISOCITRATE DEHYDROGENASE [NADP] ICD2	1,73	0,02631
Rv1559	*ilvA*	PROBABLE THREONINE DEHYDRATASE ILVA	1,73	0,00462
Rv0688		PUTATIVE FERREDOXIN REDUCTASE	1,74	0,00797
Rv3214	*gpm2*	POSSIBLE PHOSPHOGLYCERATE MUTASE GPM2	1,74	0,01569
Rv1512	*epiA*	PROBABLE NUCLEOTIDE-SUGAR EPIMERASE EPIA	1,75	0,01474
Rv3411c	*guaB2*	PROBABLE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE GUAB2	1,75	0,00012
Rv1133c	*metE*	PROBABLE5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE METE	1,76	0,01419
Rv3206c	*moeB1*	PROBABLE MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN MOEB1	1,77	0,00817
Rv1448c	*tal*	PROBABLE TRANSALDOLASE TAL	1,77	0,00351
Rv2753c	*dapA*	PROBABLE DIHYDRODIPICOLINATE SYNTHASE DAPA	1,78	0,01917
Rv2259	*mscR*	S-NITROSOMYCOTHIOL REDUCTASE MSCR	1,80	0,02769
Rv1017c	*prsA*	PROBABLE RIBOSE-PHOSPHATE PYROPHOSPHOKINASE PRSA	1,81	0,00805

Rv3029c	*fixA*	PROBABLE ELECTRON TRANSFER FLAVOPROTEIN FIXA	1,81	0,00618
Rv2029c	*pfkB*	PROBABLE PHOSPHOFRUCTOKINASE PFKB	1,85	0,03022
Rv1201c		PROBABLE TRANSFERASE	1,86	0,01838
Rv3596c	*clpC1*	PROBABLE ATP-DEPENDENT PROTEASE ATP-BINDING SUBUNIT CLPC1	1,86	0,0011
Rv0234c	*gabD1*	SUCCINATE SEMIALDEHYDE DESHYDROGENASE	1,86	0,03506
Rv0636		SINGLE HOTDOG HYDRATASE, HOMODIMER	1,86	0,02617
Rv0382c	*pyrE*	PROBABLE OROTATE PHOSPHORIBOSYLTRANSFERASE PYRE	1,89	0,02032
Rv3224		POSSIBLE IRON-REGULATED SHORT-CHAIN DEHYDROGENASE/REDUCTASE	1,90	0,00089
Rv3726		POSSIBLE DEHYDROGENASE	1,91	0,04217
Rv2606c	*snzP*	POSSIBLE PYRIDOXINE BIOSYNTHESIS PROTEIN SNZP	1,91	0,00176
Rv0155	*pntAa*	PROBABLE NAD(P) TRANSHYDROGENASE (SUBUNIT ALPHA) PNTAA	1,92	0,02227
Rv2241	*aceE*	PYRUVATE DESHYDROGENASE E1 COMPONENT	1,92	0,00994
Rv3232c	*ppk2*	POLYPHOSPHATE KINASE	1,94	0,02743
Rv2220	*glnA1*	GLUTAMINE SYNTHETASE GLNA1	1,95	0,00512
Rv2460c	*clpP2*	PROBABLE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 2 CLPP2	1,96	0,0055
Rv3708c	*asd*	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE ASD	1,97	0,00166
Rv3709c	*ask*	ASPARTOKINASE ASK	1,99	0,01958
Rv1328	*glgP*	PROBABLE GLYCOGEN PHOSPHORYLASE GLGP	2,04	0,00059
Rv1837c	*glcB*	PROBABLE MALATE SYNTHASE G GLCB	2,05	0,02906
Rv1229c	*mrp*	SODIUM:POTON ANTIPORTER	2,06	0,00265
Rv0733	*adk*	PROBABLE ADENYLATE KINASE ADK	2,08	0,02456
Rv0363c	*fba*	PROBABLE FRUCTOSE-BISPHOSPHATE ALDOLASE FBA	2,11	0,0021
Rv1475c	*acnA*	PROBABLE IRON-REGULATED ACONITATE HYDRATASE ACN	2,11	0,01704
Rv3628	*ppa*	INORGANIC PYROPHOSPHATASE PPA	2,12	0,02801
Rv1611	*trpC*	PROBABLE INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE TRPC	2,13	0,00369
Rv1613	*trpA*	PROBABLE TRYPTOPHAN SYNTHASE, ALPHA SUBUNIT TRPA	2,14	0,04889
Rv2195	*qcrA*	PROBABLE RIESKE IRON-SULFUR PROTEIN QCRA	2,15	0,002
Rv2129c		PROBABLE OXYDREDUCTASE	2,16	0,02013
Rv2461c	*clpP1*	PROBABLE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1 CLPP1	2,28	0,01072
Rv0044c		POSSIBLE OXIDOREDUCTASE	2,29	0,00769
Rv3509c	*ilvX*	PROBABLE ACETOHYDROXYACID SYNTHASE ILVX	2,38	5,7E-05
Rv0046c	*ino1*	MYO-INOSITOL-1-PHOSPHATE SYNTHASE INO1	2,40	0,00177

Rv3389c	*htdY*	DOUBLE HOTDOG HYDRATASE	2,41	0,00057
Rv3859c	*gltB*	PROBABLE FERRODOXIN-DEPENDENT GLUTAMATE SYNTHASE GLTB	2,50	0,03912
Rv1856c		POSSIBLE OXIDOREDUCTASE	2,56	0,00161
Rv2427c	*proA*	PROBABLE GAMMA-GLUTAMYL PHOSPHATE REDUCTASE PROTEIN PROA	2,64	0,00682
Rv3485c		PROBABLE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE	2,74	0,01823
Rv1437	*pgk*	PROBABLE PHOSPHOGLYCERATE KINASE PGK	2,81	0,0298
Rv1594	*nadA*	PROBABLE QUINOLINATE SYNTHETASE NADA	2,83	0,00044
Rv1308	*atpA*	PROBABLE ATP SYNTHASE ALPHA CHAIN ATPA	2,88	0,0336
Rv0761c	*adhB*	POSSIBLE ZINC-CONTAINING ALCOHOL DEHYDROGENASE NAD DEPENDENT ADHB	2,95	0,00014
Rv3003c	*ilvB1*	ACETOLACTATE SYNTHASE ilvB1	3,03	0,00222
Rv0501	*galE2*	POSSIBLE UDP-GLUCOSE 4-EPIMERASE GALE2	3,05	0,04452
Rv3146	*nuoB*	PROBABLE NADH DEHYDROGENASE I (CHAIN B) NUOB	3,10	0,03522
Rv1220c		METHYLTRASFERASE	3,32	0,01155
Rv3118	*sseC1*	CONSERVED HYPOTHETICAL PROTEIN	3,60	0,04349
Rv0896	*gltA2*	PROBABLE CITRATE SYNTHASE I GLTA2	3,95	0,01594
Rv0772	*purD*	PROBABLE PHOSPHORIBOSYLAMINE--GLYCINE LIGASE PURD	3,98	0,04212
Rv1876	*bfrA*	PROBABLE BACTERIOFERRITIN BFRA	4,48	0,00319
Rv1334	*mec*	POSSIBLE HYDROLASE	4,68	0,00618
Lipid metabolism				
Rv0860	*fadB*	3 HYDROXYL COA DEHYDROGENASE	1,24	0,04974
Rv0731c		S-ADENOSYL-L-METHIONINE-DEPENDANT METHYLTRANSFERASE	1,43	0,04865
Rv0146		S-ADENOSYL-L-METHIONINE-DEPENDANT METHYLTRANSFERASE	1,47	0,01735
Rv1683		ACYL COA SYNTHETASE	1,47	0,00035
Rv0270	*fadD2*	PROBABLE FATTY-ACID-CoA LIGASE FADD2	1,52	0,04728
Rv0675	*echA5*	PROBABLE ENOYL-CoA HYDRATASE ECHA5	1,55	0,00526
Rv0243	*fadA2*	PROBABLE ACETYL-CoA ACYLTRANSFERASE FADA2	1,60	0,01241
Rv3774	*echA21*	POSSIBLE ENOYL-CoA HYDRATASE ECHA21	1,65	0,0218
Rv1925	*fadD31*	PROBABLE ACYL-CoA LIGASE FADD31	1,67	7,2E-05
Rv2524c	*fas*	PROBABLE FATTY ACID SYNTHASE FAS	1,68	0,01709
Rv3274c	*fadE25*	PROBABLE ACYL-CoA DEHYDROGENASE FADE25	1,72	0,01243
Rv0242c	*fabG4*	PROBABLE 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE FABG4	1,73	0,00288
Rv1544		POSSIBLE KETOACYL REDUCTASE	1,74	0,00017
Rv0271c	*fadE6*	PROBABLE ACYL-CoA DEHYDROGENASE FADE6	1,79	0,01564
Rv1484	*inhA*	NADH-DEPENDENT ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE INHA	1,79	0,00026

Rv3801c	*fadD32*	FATTY ACID COA LIGASE	1,79	0,00044
Rv2831	*echA16*	PROBABLE ENOYL-CoA HYDRATASE ECHA16	1,80	0,02105
Rv3800c	*pks13*	POLYKETIDE SYNTHASE PKS13	1,81	0,00024
Rv3280	*accD5*	PROBABLE PROPIONYL-CoA CARBOXYLASE BETA CHAIN 5 ACCD5	1,82	0,00201
Rv0468	*fadB2*	PROBABLE 3-HYDROXYBUTYRYL-CoA DEHYDROGENASE FADB2	2,00	0,00813
Rv2246	*kasB*	3-OXOACYL-ACP SYNTHASE	2,01	0,00016
Rv0129c	*fbpC*	SECRETED ANTIGEN 85-C FBPC	2,03	0,00992
Rv1483	*fabG1*	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE FABG1	2,05	0,03438
Rv2245	*kasA*	3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE 1 KASA	2,05	0,02594
Rv3285	*accA3*	PROBABLE BIFUNCTIONAL PROTEIN ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE accA3	2,08	0,00046
Rv0642c	*mmaA4*	METHOXY MYCOLIC ACID SYNTHASE 4 MMAA4	2,13	0,03725
Rv1323	*fadA4*	ACETYL COA ACETYLTRANSFERASE	2,19	0,00695
Rv2244	*acpM*	MEROMYCOLATE EXTENSION ACYL CARRIER PROTEIN ACPM	2,23	0,00133
Rv1193	*fadD36*	PROBABLE FATTY-ACID-CoA LIGASE FADD36	2,30	0,01604
Rv1013	*pks16*	PUTATIVE POLYKETIDE SYNTHASE PKS16	2,49	0,01062
Rv1070c	*echA8*	ENOYL-COA HYDRATASE ECHA8	2,64	0,0461
Rv1185c	*fadD21*	PROBABLE FATTY-ACID--CoA LIGASE FADD21	2,72	0,04212
Rv2289	*cdh*	PROBABLE CDP-DIACYLGLYCEROL PYROPHOSPHATASE CDH	2,75	0,02922
Rv3720		POSSIBLE FATTY ACID SYNTHASE	2,77	0,0339
Rv1543		POSSIBLE FATTY ACYL-CoA REDUCTASE	3,17	0,05053
Rv2947c	*pks15*	PROBABLE POLYKETIDE SYNTHASE PKS15	3,24	0,00153
Rv2982c	*gpdA2*	PROBABLE GLYCEROL-3-PHOSPHATE DEHYDROGENASE gpdA2	3,36	0,01406
Rv0231	*fadE4*	PROBABLE ACYL-CoA DEHYDROGENASE FADE4	4,72	0,02354
Rv3130c	*tgs1*	TRIACYLGLYCEROL SYNTHASE	5,36	0,0011
Rv0643c	*mmaA3*	METHOXY MYCOLIC ACID SYNTHASE 3 MMAA3	7,63	0,01072
Information pathways				
Rv1020	*mfd*	PROBABLE TRANSCRIPTION-REPAIR COUPLING FACTOR MFD	0,40	0,00282
Rv3852	*hns*	NUCLEOTIDESTRUCTURING PROTEIN HNS	1,48	0,00439
Rv0685	*tuf*	ELONGATION FACTOR TU	1,49	0,0138
Rv0639	*nusG*	PROBABLE TRANSCRIPTION ANTITERMINATION PROTEIN NUSG	1,52	0,02598
Rv2890c	*rpsB*	PROBABLE 30S RIBOSOMAL PROTEIN S2 RPSB	1,53	0,00704
RV2495c	*bkdC*	PROBABLE BRANCHED-CHAIN KETO ACID DEHYDROGENASE E2 COMPONENT BKDC	1,56	0,00072
Rv2412	*rpsT*	PROBABLE 30S RIBOSOMAL PROTEIN S20 RPST	1,60	0,01752

Rv2783c	*gpsI*	BIFUNCTIONAL PROTEIN POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE GPSI: GUANOSINE PENTAPHOSPHATE SYNTHETASE + POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE	1,60	0,04032
Rv1340	*rphA*	PROBABLE RIBONUCLEASE RPHA	1,61	0,01368
Rv3457c	*rpoA*	PROBABLE DNA-DIRECTED RNA POLYMERASE (ALPHA CHAIN) RPOA	1,63	0,04996
Rv0670	*end*	PROBABLE ENDONUCLEASE IV END	1,64	0,02439
Rv2986c	*hupB*	PROBABLE DNA-BINDING PROTEIN HU HOMOLOG HUPB	1,65	0,00631
Rv2533c	*nusB*	N UTILIZATION SUBSTANCE PROTEIN NUSB	1,66	0,04288
Rv0719	*rplF*	PROBABLE 50S RIBOSOMAL PROTEIN L6 RPLF	1,67	0,01059
Rv2442c	*rplU*	PROBABLE 50S RIBOSOMAL PROTEIN L21 RPLU	1,67	0,01946
Rv1641	*infC*	PROBABLE INITIATION FACTOR IF-3 INFC	1,71	0,02626
Rv0707	*rpsC*	PROBABLE 30S RIBOSOMAL PROTEIN S3 RPSC	1,72	0,01722
Rv1015c	*rplY*	PROBABLE 50S RIBOSOMAL PROTEIN L25 RPLY	1,76	0,01911
Rv0718	*rpsH*	PROBABLE 30S RIBOSOMAL PROTEIN S8 RPSH	1,77	0,01502
Rv0009	*ppiA*	PROBABLE IRON-REGULATED PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A PPIA	1,82	0,01293
Rv0056	*rplI*	PROBABLE 50S RIBOSOMAL PROTEIN L9 RPLI	1,86	0,03289
Rv0704	*rplB*	PROBABLE 50S ribosomal protein L2 RPLB	1,89	0,02032
Rv0702	*rplD*	PROBABLE 50S RIBOSOMAL PROTEIN L4 RPLD	1,89	0,00479
Rv1297	*rho*	PROBABLE TRANSCRIPTION TERMINATION FACTOR RHO HOMOLOG	1,89	0,00142
Rv0714	*rplN*	PROBABLE 50S RIBOSOMAL PROTEIN L14 RPLN	1,89	0,02058
Rv0005	*gyrB*	DNA GYRASE (SUBUNIT B) GYRB	1,91	0,00161
Rv0640	*rplK*	PROBABLE 50S RIBOSOMAL PROTEIN L11 RPLK	1,91	0,0073
Rv0701	*rplC*	PROBABLE 50S RIBOSOMAL PROTEIN L3 RPLC	1,92	0,01161
Rv0721	*rpsE*	PROBABLE 30S RIBOSOMAL PROTEIN S5 RPSE	1,92	0,0126
Rv0668	*rpoC*	DNA-DIRECTED RNA POLYMERASE (BETA' CHAIN) RPOC	1,94	0,00353
Rv0652	*rplL*	PROBABLE 50S RIBOSOMAL PROTEIN L7/L12 RPLL	1,96	0,01398
Rv0710	*rpsQ*	PROBABLE 30S RIBOSOMAL PROTEIN S17 RPSQ	2,01	0,0402
Rv0715	*rplX*	PROBABLE 50S RIBOSOMAL PROTEIN L24 RPLX	2,01	0,04266
Rv0706	*rplV*	PROBABLE 50S RIBOSOMAL PROTEIN L22 RPLV	2,01	0,01763
Rv0703	*rplW*	PROBABLE 50S RIBOSOMAL PROTEIN L23 RPLW	2,02	0,01458
Rv0720	*rplR*	PROBABLE 50S RIBOSOMAL PROTEIN L18 RPLR	2,07	0,04529
Rv1388	*mihF*	PUTATIVE INTEGRATION HOST FACTOR MIHF	2,09	0,00495
Rv0634B	*rpmG2*	PROBABLE 50S RIBOSOMAL PROTEIN L33 RPMG2	2,12	0,01083
Rv3459c	*rpsK*	PROBABLE 30S RIBOSOMAL PROTEIN S11 RPSK	2,39	0,01416
Rv0722	*rpmD*	PROBABLE 50S RIBOSOMAL PROTEIN L30 RPMD	2,40	0,0474
Rv0055	*rpsR1*	PROBABLE 30S RIBOSOMAL PROTEIN S18-1 RPSR1	2,41	0,00616
Rv1643	*rplT*	PROBABLE 50S RIBOSOMAL PROTEIN L20 RPLT	2,51	0,00766
Rv3460c	*rpsM*	PROBABLE 30S RIBOSOMAL PROTEIN S13 RPSM	2,62	0,03019

Rv3011c	*gatA*	PROBABLE GLUTAMYL-TRNA(GLN) AMIDOTRANSFERASE (SUBUNIT A) GATA	2,63	0,00902
Rv2582	*ppiB*	PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PPIB	2,80	0,0124
Rv0041	*leuS*	PROBABLE LEUCYL-tRNA SYNTHETASE LEUS	3,05	0,04344
Rv3461c	*rpmJ*	PROBABLE 50S RIBOSOMAL PROTEIN L36 RPMJ	3,22	0,00382
Rv1390	*rpoZ*	PROBABLE DNA-DIRECTED RNA POLYMERASE RPOZ	3,66	0,04035
Rv2975A	*rpmB*	50S RIBOSOMAL PROTEIN L28	3,87	0,01394
Virulence, detoxification, adaptation				
Rv0440	*hsp65*	60KDA CHAPERONINE	1,34	0,00177
Rv3418c	*groS*	10KDA CHAPERONINE	1,41	0,00032
Rv1908c	*katG*	CATALASE PEROXYDASE	1,43	0,04957
Rv3407	*vapB47*	CONSERVED HYPOTHETICAL PROTEIN, ANTITOXIN vapB47	1,51	0,02108
Rv0350	*dnaK*	PROBABLE CHAPERONE PROTEIN DNAK	1,53	0,01644
Rv1932	*tpx*	PROBABLE THIOL PEROXIDASE TPX	1,60	0,0199
Rv0352	*dnaJ1*	PROBABLE CHAPERONE PROTEIN DNAJ1	1,84	0,0114
Rv2373c	*dnaJ2*	PROBABLE CHAPERONE PROTEIN DNAJ2	1,85	0,00404
Rv2299c	*htpG*	PROBABLE CHAPERONE PROTEIN HTPG	1,89	0,00146
Rv0171	*mce1C*	MCE-FAMILY PROTEIN MCE1C	3,19	0,03676
Rv2374c	*hrcA*	PROBABLE HEAT SHOCK PROTEIN TRANSCRIPTIONAL REPRESSOR HRCA	4,35	0,01172
Rv3134c		CONSERVED HYPOTHETICAL PROTEIN	7,33	0,00171
Cell wall and processes				
Rv2981c	*ddl*	D ALANINE LIGASE	1,35	0,04392
Rv3888c		MEMBRANE PROTEIN	1,39	0,04985
Rv3867	*espH*	SECRETION PROTEIN ESPH	1,43	0,02712
Rv3808c	*glfT2*	GLYCOSYL TRANSFERASE	1,43	0,03764
Rv2692	*trkA*	POTASSIUM TRANSPORTER TRKA	1,49	0,00206
Rv3102c	*ftsE*	CELL DIVISION ATP BINDING PROTEIN	1,49	0,00445
Rv3614	*espD*	SECRETION PROTEIN	1,51	0,01001
Rv0284		POSSIBLE CONSERVED MEMBRANE PROTEIN	1,57	0,03675
Rv2158c	*murE*	UDP-N-ACETYLMURANYL-TRIPEPTIDE SYNTHETASE	1,59	0,0056
Rv3240c	*secA1*	PROBABLE PREPROTEIN TRANSLOCASE SECA1 1 SUBUNIT	1,61	0,03592
Rv2477c		PROBABLE MACROLIDE-TRANSPORT ATP-BINDING PROTEIN ABC TRANSPORTER	1,62	0,00147
Rv2145c	*wag31*	CONSERVED HYPOTHETICAL PROTEIN WAG31	1,63	0,03999
Rv0655	*mkl*	ABC TRANSPORTER	1,80	0,00239
Rv3917c	*parB*	PROBABLE CHROMOSOME PARTITIONING PROTEIN PARB	1,82	0,04963

Rv1821	*secA2*	POSSIBLE PREPROTEIN TRANSLOCASE ATPase SECA2	1,88	0,03665
Rv0933	*pstB*	PHOSPHATE-TRANSPORT ATP-BINDING PROTEIN ABC TRANSPORTER PSTB	1,89	0,01943
Rv0820	*phoT*	PHOSPHATE ABC TRANSPORTER ATP BINDING PROTEIN PHOT	2,04	0,01701
Rv3197		PROBABLE CONSERVED ATP-BINDING PROTEIN ABC TRANSPORTER	2,22	0,01669
Rv3781	*rfbE*	PROBABLE O-ANTIGEN/LIPOPOLYSACCHARIDE TRANSPORT ATP-BINDING PROTEIN ABC TRANSPORTER RFBE	2,57	0,02278
Rv1488		POSSIBLE EXPORTED CONSERVED PROTEIN	2,66	0,00645
Rv2150c	*FtsZ*	CELL DIVISION PROTEIN FTSZ	3,23	0,00688
Rv0934	*pstS1*	PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS1	3,95	0,00033
Rv0342	*iniA*	ISONIAZID INDUCTIBLE GENE PROTEIN INIA	4,39	0,00053
Rv0341	*iniB*	ISONIAZID INDUCTIBLE GENE PROTEIN INIB	5,23	0,02819
Rv3200c		POSSIBLE TRANSMEMBRANE CATION TRANSPORTER	8,50	0,01032
Rv1269c		CONSERVED PROBABLE SECRETED PROTEIN	28,74	0,02618
Regulatory proteins				
Rv1626		TRANSCRIPTIONAL REGULATORY PROTEIN	1,44	0,01665
Rv3692	*moxR2*	PROBABLE METHANOL DEHYDROGENASE TRANSCRIPTIONAL REGULATORY PROTEIN MOXR2	1,53	0,01628
Rv0020c	*fhaA*	CONSERVED HYPOTHETICAL PROTEIN WITH FHA DOMAIN, FHAA	1,54	0,02354
Rv0844c	*narL*	POSSIBLE NITRATE/NITRITE RESPONSE TRANSCRIPTIONAL REGULATORY PROTEIN NARL	1,70	0,01024
Rv0576		PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN	1,83	0,00924
Rv1423	*whiA*	PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN WHIA	1,87	0,00189
Rv3246c	*mtrA*	TWO COMPONENT SENSORY TRANSDUCTION TRANSCRIPTIONAL REGULATORY PROTEIN MTRA	1,88	0,00378
Rv2258c		POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN	1,90	0,04391
Rv3676	*crp*	TRANSCRIPTIONAL REGULATORY PROTEIN CRP	2,21	0,00683
Rv0042c		POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN	2,59	0,00348
Rv3133c	*devR*	TWO COMPONENT TRANSCRIPTIONAL REGULATORY PROTEIN DEVR	3,04	0,01623
Rv3583c		POSSIBLE TRANSCRIPTION FACTOR	3,13	0,02759
Rv0757	*phoP*	ALCALINE PHOSPHATASE PHOP	8,67	0,00106

Conserved hypotheticals

Rv0074		CONSERVED HYPOTHETICAL PROTEIN	0,34	0,03426
Rv0678		CONSERVED HYPOTHETICAL PROTEIN	0,36	0,00075
Rv1875		UNKNOWN PROTEIN	1,33	0,02118
Rv1261c		CONSERVED HYPOTHETICAL PROTEIN	1,44	0,0294
Rv3075c		HYPOTHETICAL PROTEIN	1,46	0,04643
Rv3683		CONSERVED HYPOTHETICAL PROTEIN	1,51	0,02673
Rv0787A		CONSERVED HYPOTHETICAL PROTEIN	1,52	0,00639
Rv0831c		CONSERVED HYPOTHETICAL PROTEIN	1,55	0,01236
Rv1159A		HYPOTHETICAL PROTEIN	1,57	0,03004
Rv1636	*TB 15.3*	IRON-REGULATED CONSERVED HYPOTHETICAL PROTEIN TB15.3	1,59	0,01655
Rv2061c		CONSERVED HYPOTHETICAL PROTEIN	1,60	0,01521
Rv0854		CONSERVED HYPOTHETICAL PROTEIN	1,62	0,04899
Rv2172c		CONSERVED HYPOTHETICAL PROTEIN	1,62	0,00609
Rv2778c		CONSERVED HYPOTHETICAL PROTEIN	1,62	0,0212
Rv3046c		CONSERVED HYPOTHETICAL PROTEIN	1,66	0,03544
Rv2699c		CONSERVED HYPOTHETICAL PROTEIN	1,69	0,00323
Rv2054		CONSERVED HYPOTHETICAL PROTEIN	1,74	0,00184
Rv0333		HYPOTHETICAL PROTEIN	1,74	0,01082
Rv0466		CONSERVED HYPOTHETICAL PROTEIN	1,74	0,00411
Rv2228c		CONSERVED HYPOTHETICAL PROTEIN	1,75	0,03292
Rv2868c	*gcpE*	PROBABLE GCPE PROTEIN	1,78	0,00106
Rv2074		POSSIBLE PYRIDOXAMINE 5' PHOSPHATE OXYDASE	1,81	0,0426
Rv0123		HYPOTHETICAL PROTEIN	1,81	0,01847
Rv3718c		CONSERVED HYPOTHETICAL PROTEIN	1,85	0,03225
Rv2632c		CONSERVED HYPOTHETICAL PROTEIN	1,92	0,00859
Rv2744c	*35kd_ag*	CONSERVED 35 KDA ALANINE RICH PROTEIN	1,92	0,00905
Rv3600c		CONSERVED HYPOTHETICAL PROTEIN	1,93	0,00904
Rv0898c		CONSERVED HYPOTHETICAL PROTEIN	1,94	0,01905
Rv3734c	*Tgs2*	PUTATIVE TRIACYLGLYCEROL SYNTHASE TGS2	1,95	0,03412
Rv3597c	*Lsr2*	PROBABLE IRON-REGULATED LSR2 PROTEIN PRECURSOR	1,95	8,6E-05
Rv3920c		HYPOTHETICAL PROTEIN SIMILAR TO JAG PROTEIN	2,03	0,04132
Rv2114		HYPOTHETICAL PROTEIN	2,06	0,0035
Rv1021		CONSERVED HYPOTHETICAL PROTEIN	2,07	0,0009
Rv2908c		CONSERVED HYPOTHETICAL PROTEIN	2,08	0,00542
Rv3790	*dprE1*	DECAPRENYLPHOSPHORYL-BET-D-RIBOSE OXYDASE	2,13	0,04643
Rv0991c		CONSERVED HYPOTHETICAL SERINE RICH PROTEIN	2,20	0,00012
Rv0360c		CONSERVED HYPOTHETICAL PROTEIN	2,32	0,0254
Rv1996		CONSERVED HYPOTHETICAL PROTEIN	2,40	0,01274

Rv2230c		CONSERVED HYPOTHETICAL PROTEIN	2,43	0,01759
Rv3489		HYPOTHETICAL PROTEIN	2,55	0,00459
Rv2426c		CONSERVED HYPOTHETICAL PROTEIN	2,56	0,00361
Rv1770		CONSERVED HYPOTHETICAL PROTEIN	2,57	0,00037
Rv0530		CONSERVED HYPOTHETICAL PROTEIN	2,63	0,01837
Rv3788		HYPOTHETICAL PROTEIN	2,69	0,04121
Rv3196A		HYPOTHETICAL PROTEIN	2,71	0,02928
Rv3865	*espF*	ESX-1-SECRETION-ASSOCIATED PROTEIN ESPF	2,99	0,00184
Rv3311		CONSERVED HYPOTHETICAL PROTEIN	3,14	0,00191
Rv0079		HYPOTHETICAL PROTEIN	3,54	0,0057
Rv2005c		CONSERVED HYPOTHETICAL PROTEIN	3,65	0,00121
Rv2030c		CONSERVED HYPOTHETICAL PROTEIN	3,81	0,00845
Rv2629		CONSERVED HYPOTHETICAL PROTEIN	4,21	0,00349
Rv0108c		HYPOTHETICAL PROTEIN	4,94	1,9E-05
Rv2411c		CONSERVED HYPOTHETICAL PROTEIN	4,96	0,02186
Rv2623		CONSERVED HYPOTHETICAL PROTEIN TB31.7	5,01	0,01997
Rv2032	*acg*	CONSERVED HYPOTHETICAL PROTEIN ACG	5,31	0,02419
Rv3871	*eccCb1*	ESX CONSERVED COMPONENT ECCCB1	6,39	0,00047
Rv1738		CONSERVED HYPOTHETICAL PROTEIN	20,06	0,00015

Proteins down- and upexpressed after a 24 h simvastatin treatment

ORF	Gene name	Gene product	Fold change	p-values
Intermediary metabolism and respiration				
Rv0560c		POSSIBLE BENZOQUINONE METHYLTRANSFERASE	0,04	0,02592
Rv0077c		PROBABLE OXIDOREDUCTASE	0,05	2,8E-06
Rv2858c	*aldC*	PROBABLE ALDEHYDE DEHYDROGENASE ALDC	0,25	0,02522
Rv3778c		POSSIBLE AMINOTRANSFERASE	0,32	0,02681
Rv1652	*argC*	PROBABLE N-ACETL-GAMMA-GLUTAMYL-PHOSHATE REDUCTASE ARGC	0,36	0,04607
Rv0189c	*ilvD*	PROBABLE DIHYDROXY-ACID DEHYDRATASE ILVD	0,38	0,04197
Rv2439c	*proB*	PROBABLE GLUTAMATE 5-KINASE PROTEIN PROB	0,38	0,01857
Rv1380	*pyrB*	PROBABLE ASPARTATE CARBAMOYLTRANSFERASE PYRB	0,43	0,02299
Rv0803	*purL*	PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE II PURL	0,50	0,02455
Rv2161c		CONSERVED HYPOTHETICAL PROTEIN	0,51	0,00063
Rv3042c	*serB2*	PROBABLE PHOSPHOSERINE PHOSPHATASE SERB2	0,53	0,04512
Rv3275c	*purE*	PROBABLE PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE CATALYTIC SUBUNIT PURE	0,57	0,02338
Rv1612	*trpB*	PROBABLE TRYPTOPHAN SYNTHASE, BETA SUBUNIT TRPB	0,60	0,03615

Rv1133c	*metE*	5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE-HOMOCYSTEINE METHYLTRANSFERASE	0,67	0,04245
Rv1144		3 HYDROXY-2-METHYLBUTYRYL-COA DEHYDROGENASE	0,68	0,03472
Rv0458		ALDEHYDE DEHYDROGENASE	0,71	0,02484
Rv0730		GCN-5-RELATED N-ACETYLTRANSFERASE	0,75	0,04879
Rv3117		SULFURTRANSFERASE	0,77	0,04603
Rv1596	*nadC*	NICOTINATE NUCLEOTIDE PYROPHOSPHORYLASE	0,83	0,03576
Rv3161c		POSSIBLE DIOXYGENASE	2,91	0,00441
Rv0247c		PROBABLE SUCCINATE DEHYDROGENASE	3,93	0,02276
Rv3432c	*gadB*	PROBABLE GLUTAMATE DECARBOXYLASE GADB	4,01	0,00902
Rv1383	*carA*	PROBABLE CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN CARA	4,30	0,01159
Lipid metabolism				
Rv0873	*fadE10*	PROBABLE ACYL-CoA DEHYDROGENASE FADE10	0,27	0,02388
Rv0632c	*echA3*	PROBABLE ENOYL-CoA HYDRATASE ECHA3	0,46	0,00161
Rv3774	*echA21*	POSSIBLE ENOYL-CoA HYDRATASE ECHA21	0,51	0,02639
Rv0469	*umaA*	POSSIBLE MYCOLIC ACID SYNTHASE UMAA	0,54	0,00531
Rv2002	*fabG3*	POSSIBLE 20-BETA-HYDROXYSTEROID DEHYDROGENASE FABG3	0,58	0,02601
Rv0860	*fadB*	PROBABLE FATTY OXIDATION PROTEIN FADB	0,63	0,02238
Rv0905	*echA6*	ENOYL-COA-HYDRATASE	0,80	0,04345
Rv1543		OXYDOREDUCTASE	1,37	0,01025
Rv1886c	*fbpB*	SECRETED ANTIGEN 85-B FBPB	3,44	0,00205
Information pathways				
Rv0670	*end*	PROBABLE ENDONUCLEASE IV END	0,25	0,00117
Rv3051c	*nrdE*	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE NRDE	0,33	0,03722
Rv1340	*rphA*	PROBABLE RIBONUCLEASE RPHA	0,56	0,00372
Rv0703	*rplW*	50S RIBOSOMAL PROTEIN L23	1,42	0,01976
Rv3461c	*rpmJ*	50S RIBOSOMAL PROTEIN L36	1,44	0,01011
Rv3834c	*serS*	SERYL-TRNA SYNTHETASE SERS	2,00	0,04965
Rv2582	*ppiB*	PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PPIB	2,15	0,0274
Virulence, detoxification, adaptation				
Rv2493	*vapB38*	POSSIBLE ANTITOXIN VAPB38	0,11	0,00175
Rv1908c	*katG*	CATALASE-PEROXIDASE-PEROXYNITRITASE T KATG	0,59	0,02463
Rv2063	*mazE7*	ANTITOXIN MAZE7	1,92	0,04555
Cell wall and processes				
Rv1987		POSSIBLE CHITINASE	0,31	0,02895

Rv1038c	*esxJ*	ESAT-6 LIKE PROTEIN ESXJ	0,35	0,00851
Rv3809c	*glf*	UDP-GALACTOPYRANOSE MUTASE	0,39	0,01595
Rv3874	*esxB*	10 KDA CULTURE FILTRATE ANTIGEN ESXB	0,62	0,01943
Regulatory proteins				
Rv3143		PROBABLE RESPONSE REGULATOR	0,26	0,01309
Rv1267c	*embR*	PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN EMBR	0,27	0,03298
Rv0015c	*pknA*	TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE A PKNA	0,29	0,03018
Rv0903c	*prrA*	TRANSCRIPTIONAL REGULATOR	0,68	0,02181
Conserved hypotheticals				
Rv1637c		CONSERVED HYPOTHETICAL PROTEIN	0,12	0,03102
Rv1769		CONSERVED HYPOTHETICAL PROTEIN	0,25	0,0497
Rv3547		CONSERVED HYPOTHETICAL PROTEIN	0,36	0,02813
Rv0074		CONSERVED HYPOTHETICAL PROTEIN	0,37	0,02476
Rv1893		CONSERVED HYPOTHETICAL PROTEIN	0,44	0,00018
Rv2302		CONSERVED HYPOTHETICAL PROTEIN	0,47	0,01501
Rv0577	*TB27.3*	CONSERVED HYPOTHETICAL PROTEIN	0,52	0,0377
Rv3678c		CONSERVED HYPOTHETICAL PROTEIN	0,52	0,02992
Rv0678	*mmpR5*	CONSERVED HYPOTHETICAL PROTEIN	0,52	0,00238
Rv2475c		CONSERVED HYPOTHETICAL PROTEIN	0,58	0,04676
Rv2159c		CONSERVED HYPOTHETICAL PROTEIN	0,61	0,01673
Rv0145		POSSIBLE S-ADENOSYLMETHIONINE-DEPENDENT METHYLTRANSFERASE	0,62	0,02184
Rv1827	*garA*	CONSERVED HYPOTHETICAL PROTEIN WITH FHA DOMAIN	0,64	0,00959
Rv1498A		CONSERVED HYPOTHETICAL PROTEIN	0,67	0,02886
Rv3046c		CONSERVED HYPOTHETICAL PROTEIN	0,68	0,04952
Rv3600c	*coaX*	TYPE III PANTOTHENATE KINASE	0,69	0,00194
Rv1919c		CONSERVED HYPOTHETICAL PROTEIN	0,71	0,01704
Rv3208A	*TTB9.4*	CONSERVED PROTEIN TB9.4	0,75	0,04714
Rv1261c		NITROREDUCTASE	0,82	0,02658
Rv2821c	*cmr4*	CRISPR ASSOCIATED PROTEIN	1,25	0,0415
Rv1894c		MONOOXYGENASE	1,46	0,03288
Rv1021		CONSERVED HYPOTHETICAL PROTEIN	1,62	0,00016
Rv2426c		CONSERVED HYPOTHETICAL PROTEIN	1,97	0,03874
Rv1738		CONSERVED HYPOTHETICAL PROTEIN	2,30	0,04828