

Table S9. List of known drug targets mapped on the co-expressed modules.

Arranged in descending order of connectivity (Degree)

Gene ID	Product	Degree	Essentiality	PCC with ME	P-value	Module
<i>Rv1611</i>	Probable indole-3-glycerol phosphate synthase TrpC	156	Essential	0.94	0	turquoise
<i>Rv0545c</i>	Probable low-affinity inorganic phosphate transporter integral membrane protein PitA	107	Not essential	0.95	0	turquoise
<i>Rv2935</i>	Phenolphthiocerol synthesis type-I polyketide synthase PpsE	92	Not essential	-0.74	1.24E-07	turquoise
<i>Rv2244</i>	Meromycolate extension acyl carrier protein AcpM	89	Essential	0.68	3.07E-06	turquoise
<i>Rv2246</i>	3-oxoacyl-[acyl-carrier protein] synthase 2 KasB (beta-ketoacyl-ACP synthase) (KAS I)	88	Essential	0.65	8.78E-06	turquoise
<i>Rv3404c</i>	Conserved hypothetical protein	88	Not essential	0.91	2.89E-15	turquoise
<i>Rv1307</i>	Probable ATP synthase delta chain AtpH	87	Essential	0.80	2.4E-09	turquoise
<i>Rv2245</i>	3-oxoacyl-[acyl-carrier protein] synthase 1 KasA (beta-ketoacyl-ACP synthase) (KAS I)	87	Essential	0.66	5.59E-06	turquoise
<i>Rv2243</i>	Malonyl CoA-acyl carrier protein transacylase FabD (malonyl CoA:ACPM acyltransferase) (MCT)	86	Not essential	0.67	4.67E-06	turquoise
<i>Rv2986c</i>	DNA-binding protein HU homolog HupB (histone-like protein) (HLP) (21-kDa laminin-2-binding protein)	83	Essential	0.77	1.55E-08	turquoise
<i>Rv3458c</i>	30S ribosomal protein S4 RpsD	80	Essential	0.85	1.84E-11	turquoise
<i>Rv0058</i>	Probable replicative DNA helicase DnaB	79	Essential	0.51	0.00104	turquoise
<i>Rv2391</i>	Ferredoxin-dependent sulfite reductase SirA	77	Essential	0.56	0.000288	turquoise
<i>Rv1613</i>	Probable tryptophan synthase	75	Essential	0.88	2.25E-13	turquoise
<i>Rv1181</i>	Probable polyketide beta-ketoacyl synthase Pks4	71	Essential	-0.62	3.9E-05	turquoise
<i>Rv1182</i>	Probable conserved polyketide synthase associated protein PapA3	71	Essential	-0.76	3.7E-08	turquoise
<i>Rv0710</i>	30S ribosomal protein S17 RpsQ	71	Essential	0.55	0.000384	brown
<i>Rv1885c</i>	Chorismate mutase	71	Not essential	0.84	2.77E-11	brown
<i>Rv3135</i>	PPE family protein PPE50	71	Essential	0.65	9.72E-06	brown
<i>Rv0286</i>	PPE family protein PPE4	70	Essential	0.55	0.000376	turquoise
<i>Rv0015c</i>	Transmembrane serine/threonine-protein kinase A PknA	69	Essential	0.93	0	turquoise
<i>Rv2178c</i>	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase AroG (DAHP synthetase)	62	Essential	0.54	0.000485	turquoise
<i>Rv2949c</i>	Chorismate pyruvate lyase	61	Not essential	-0.32	0.050268	turquoise
<i>Rv2939</i>	Possible conserved polyketide synthase associated protein PapA5	59	Not essential	0.54	0.000471	brown

<i>Rv3823c</i>	Conserved integral membrane transport protein MmpL8	58	Essential	-0.27	0.099665	turquoise
<i>Rv2937</i>	Daunorubicin-dim-transport integral membrane protein ABC transporter DrrB	58	Not essential	0.57	0.000179	brown
<i>Rv2938</i>	Probable daunorubicin-dim-transport integral membrane protein ABC transporter DrrC	58	Essential	0.43	0.007376	brown
<i>Rv3280</i>	Probable propionyl-CoA carboxylase beta chain 5 AccD5 (pccase) (propanoyl-CoA:carbon dioxide ligase)	57	Not essential	0.88	2.77E-13	brown
<i>Rv3139</i>	Probable acyl-CoA dehydrogenase FadE24	54	Essential	0.67	4.71E-06	blue
<i>Rv1304</i>	Probable ATP synthase a chain AtpB (protein 6)	53	Not essential	0.35	0.032548	blue
<i>Rv1305</i>	Probable ATP synthase C chain AtpE (lipid-binding protein) (dicyclohexylcarbodiimide-binding protein)	53	Essential	0.38	0.018526	blue
<i>Rv0643c</i>	Methoxy mycolic acid synthase 3 MmaA3 (methyl mycolic acid synthase 3) (MMA3) (hydroxy mycolic acid synthase)	50	Not essential	0.67	5.24E-06	brown
<i>Rv0652</i>	50S ribosomal protein L7/L12 RplL (SA1)	49	Essential	0.47	0.002979	brown
<i>Rv1461</i>	Conserved protein	48	Essential	0.73	2.02E-07	turquoise
<i>Rv2946c</i>	Probable polyketide synthase Pks1	48	Essential	-0.43	0.007035	brown
<i>Rv0287</i>	ESAT-6 like protein EsxG (conserved protein TB9.8)	47	Not essential	0.25	0.122938	brown
<i>Rv3131</i>	Conserved protein	47	Essential	0.68	2.89E-06	brown
<i>Rv0637</i>	(3R)-hydroxyacyl-ACP dehydratase subunit HadC	46	Essential	0.80	1.66E-09	brown
<i>Rv0636</i>	(3R)-hydroxyacyl-ACP dehydratase subunit HadB	45	Essential	0.51	0.001045	brown
<i>Rv3052c</i>	Probable NrdI protein	45	Not essential	0.62	3.94E-05	brown
<i>Rv1711</i>	Conserved hypothetical protein	44	Essential	0.81	1.08E-09	turquoise
<i>Rv0220</i>	Probable esterase LipC	43	Not essential	0.67	4.64E-06	turquoise
<i>Rv0352</i>	Probable chaperone protein DnaJ1	43	Essential	0.67	4.91E-06	blue
<i>Rv3853</i>	Regulator of RNase E activity a RraA	42	Not essential	-0.42	0.009092	turquoise
<i>Rv2392</i>	Probable 3'-phosphoadenosine 5'-phosphosulfate reductase CysH (PAPS reductase)	42	Essential	0.76	4.32E-08	blue
<i>Rv0186</i>	Probable beta-glucosidase BglS (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase)	41	Not essential	0.73	2.08E-07	turquoise
<i>Rv1465</i>	Possible nitrogen fixation related protein	41	Essential	-0.55	0.000374	turquoise
<i>Rv1221</i>	Alternative RNA polymerase sigma factor SigE	40	Not essential	-0.42	0.008814	turquoise
<i>Rv2195</i>	Probable rieske iron-sulfur protein QcrA	38	Essential	0.71	6.08E-07	blue
<i>Rv2780</i>	Secreted L-alanine dehydrogenase Ald (40 kDa antigen) (TB43)	38	Not essential	0.69	1.92E-06	blue
<i>Rv0285</i>	PE family protein PE5	36	Essential	-0.49	0.001986	blue
<i>Rv3582c</i>	4-diphosphocytidyl-2C-methyl-D-erythritol synthase IspD (MEP cytidyltransferase) (MCT)	35	Essential	0.75	7.48E-08	turquoise

<i>Rv0509</i>	Probable glutamyl-tRNA reductase HemA (GLUTR)	34	Essential	0.89	1.34E-13	turquoise
<i>Rv0848</i>	Possible cysteine synthase a CysK2 (O-acetylserine sulfhydrylase) (O-acetylserine (thiol)-lyase) (CSASE)	33	Not essential	0.46	0.003386	turquoise
<i>Rv2996c</i>	Probable D-3-phosphoglycerate dehydrogenase SerA1 (PGDH)	33	Essential	0.85	2.75E-11	turquoise
<i>Rv3223c</i>	Alternative RNA polymerase sigma-E factor (sigma-24) SigH (RPOE)	33	Not essential	0.83	1.02E-10	brown
<i>Rv3804c</i>	Secreted antigen 85-a FbpA (mycolyl transferase 85A) (fibronectin-binding protein A) (antigen 85 complex A)	33	Not essential	-0.55	0.000341	blue
<i>Rv3680</i>	Probable anion transporter ATPase	33	Essential	-0.94	1.6E-18	red
<i>Rv2225</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase PanB	32	Essential	0.47	0.00296	turquoise
<i>Rv2220</i>	Glutamine synthetase GlnA1 (glutamine synthase) (GS-I)	32	Essential	0.36	0.025853	blue
<i>Rv3229c</i>	Possible linoleoyl-CoA desaturase (delta(6)-desaturase)	32	Not essential	0.68	2.53E-06	blue
<i>Rv3825c</i>	Polyketide synthase Pks2	32	Essential	0.37	0.023032	red
<i>Rv2289</i>	Probable CDP-diacylglycerol pyrophosphatase Cdh (CDP-diacylglycerol diphosphatase) (CDP-diacylglycerol phosphatidylhydrolase)	31	Not essential	-0.28	0.089419	turquoise
<i>Rv2889c</i>	Probable elongation factor Tsf (EF-ts)	31	Essential	0.85	1.08E-11	turquoise
<i>Rv2902c</i>	Probable ribonuclease HII protein RnhB (RNase HII)	30	Not essential	0.75	6.65E-08	turquoise
<i>Rv0046c</i>	myo-inositol-1-phosphate synthase Ino1 (inositol 1-phosphate synthetase) (D-glucose 6-phosphate cycloaldolase) (glucose 6-phosphate cyclase) (glucocycloaldolase)	29	Not essential	0.57	0.000213	turquoise
<i>Rv0703</i>	50S ribosomal protein L23 RplW	28	Essential	0.53	0.00064	red
<i>Rv2601</i>	Probable spermidine synthase SpeE (putrescine aminopropyltransferase) (aminopropyltransferase) (SPDSY)	27	Not essential	0.41	0.009684	turquoise
<i>Rv1300</i>	Probable HemK protein homolog HemK	27	Essential	0.67	4.69E-06	blue
<i>Rv1464</i>	Probable cysteine desulfurase Csd	27	Essential	0.75	4.71E-08	blue
<i>Rv0284</i>	ESX conserved component EccC3. ESX-3 type VII secretion system protein. Possible membrane protein.	27	Essential	0.70	1.01E-06	red
<i>Rv3868</i>	ESX conserved component EccA1. ESX-1 type VII secretion system protein.	27	Essential	-0.58	0.000139	red
<i>Rv2900c</i>	Possible formate dehydrogenase H FdhF (formate-hydrogen-lyase-linked)	26	Not essential	0.51	0.000942	turquoise
<i>Rv0824c</i>	Probable acyl-[acyl-carrier protein] desaturase DesA1 (acyl-[ACP] desaturase) (stearoyl-ACP desaturase) (protein Des)	26	Essential	0.83	1.56E-10	blue
<i>Rv2145c</i>	Diviva family protein Wag31	25	Essential	0.72	3.89E-07	turquoise
<i>Rv2678c</i>	Probable uroporphyrinogen decarboxylase HemE (uroporphyrinogen III decarboxylase) (URO-D) (UPD)	25	Not essential	-0.64	1.83E-05	turquoise
<i>Rv3858c</i>	Probable NADH-dependent glutamate synthase (small subunit) GltD (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH)) (GLTS beta chain) (NADPH-GOGAT)	25	Essential	0.81	1.02E-09	turquoise

<i>Rv3282</i>	Conserved hypothetical protein	25	Not essential	0.73	2.35E-07	brown
<i>Rv3332</i>	Probable N-acetylglucosamine-6-phosphate deacetylase NagA (GlcNAc 6-P deacetylase)	24	Essential	-0.53	0.000602	turquoise
<i>Rv2992c</i>	Glutamyl-tRNA synthetase GltS (glutamate--tRNA ligase) (glutamyl-tRNA synthase) (GLURS)	23	Essential	0.68	2.73E-06	turquoise
<i>Rv3266c</i>	dTDP-6-deoxy-L-lyxo-4-hexulose reductase RmlD (dTDP-rhamnose modification protein) (dTDP-rhamnose biosynthesis protein) (dTDP-rhamnose synthase)	23	Not essential	0.80	2.29E-09	brown
<i>Rv3283</i>	Probable thiosulfate sulfurtransferase SseA (rhodanese) (thiosulfate cyanide transsulfurase) (thiosulfate thiotransferase)	22	Not essential	0.82	3.18E-10	brown
<i>Rv1631</i>	Probable dephospho-CoA kinase CoaE (dephosphocoenzyme a kinase)	22	Essential	0.70	1.17E-06	blue
<i>Rv3842c</i>	Probable glycerophosphoryl diester phosphodiesterase GlpQ1 (glycerophosphodiester phosphodiesterase)	22	Not essential	0.68	2.16E-06	blue
<i>Rv2152c</i>	Probable UDP-N-acetylmuramate-alanine ligase MurC	20	Essential	0.86	3.8E-12	turquoise
<i>Rv1484</i>	NADH-dependent enoyl-[acyl-carrier-protein] reductase InhA (NADH-dependent enoyl-ACP reductase)	19	Not essential	0.83	1.57E-10	turquoise
<i>Rv2837c</i>	Conserved protein	19	Essential	0.87	1.39E-12	turquoise
<i>Rv2136c</i>	Possible conserved transmembrane protein	16	Not essential	0.40	0.01301	brown
<i>Rv3284</i>	Conserved hypothetical protein	16	Not essential	0.91	1.33E-15	brown
<i>Rv3002c</i>	Probable acetolactate synthase (small subunit) IlvN (acetohydroxy-acid synthase) (AHAS) (ALS)	14	Essential	0.63	2.72E-05	brown
<i>Rv3859c</i>	Probable ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH))(NADPH-GOGAT)	14	Essential	0.71	6.56E-07	brown
<i>Rv3048c</i>	Ribonucleoside-diphosphate reductase (beta chain) NrdF2 (ribonucleotide reductase small subunit) (R2F protein)	14	Essential	0.42	0.008347	red
<i>Rv3137</i>	Probable monophosphatase	14	Essential	0.36	0.026572	red
<i>Rv3679</i>	Probable anion transporter ATPase	14	Essential	-0.89	1.16E-13	red
<i>Rv3887c</i>	ESX conserved component EccD2. ESX-2 type VII secretion system protein. Probable transmembrane protein.	13	Essential	0.73	1.97E-07	turquoise
<i>Rv3782</i>	UDP-galactofuranosyl transferase GltT1	12	Essential	0.79	4.45E-09	turquoise
<i>Rv3031</i>	Conserved protein	12	Essential	0.51	0.000952	brown
<i>Rv2069</i>	RNA polymerase sigma factor	12	Not essential	0.50	0.001372	blue
<i>Rv1264</i>	Adenylyl cyclase (ATP pyrophosphate-lyase) (adenylate cyclase)	11	Not essential	0.81	6.76E-10	turquoise
<i>Rv3255c</i>	Probable mannose-6-phosphate isomerase ManA (phosphomannose isomerase) (phosphomannoisomerase) (PMI) (phosphohexoisomerase) (phosphohexomutase)	11	Essential	0.81	4.75E-10	brown
<i>Rv3849</i>	ESX-1 transcriptional regulatory protein EspR	11	Not essential	0.59	9.28E-05	blue
<i>Rv1294</i>	Probable homoserine dehydrogenase ThrA	10	Essential	0.76	3.74E-08	turquoise

<i>Rv2139</i>	Probable dihydroorotate dehydrogenase PyrD	10	Not essential	0.73	2.32E-07	turquoise
<i>Rv0243</i>	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)	10	Not essential	0.84	5E-11	blue
<i>Rv0542c</i>	Possible O-succinylbenzoic acid--CoA ligase MenE (OSB-CoA synthetase) (O-succinylbenzoate-CoA synthase)	10	Essential	0.80	2.26E-09	blue
<i>Rv1872c</i>	Possible L-lactate dehydrogenase (cytochrome) LldD2	10	Not essential	0.62	3.13E-05	blue
<i>Rv2726c</i>	Probable diaminopimelate epimerase DapF (DAP epimerase)	9	Essential	0.79	5.06E-09	turquoise
<i>Rv3778c</i>	Possible aminotransferase	9	Essential	0.77	1.15E-08	turquoise
<i>Rv1257c</i>	Probable oxidoreductase	8	Not essential	0.80	1.77E-09	turquoise
<i>Rv1701</i>	Probable integrase/recombinase	8	Essential	0.70	1.23E-06	turquoise
<i>Rv2101</i>	Probable helicase HelZ	8	Not essential	0.86	4.27E-12	turquoise
<i>Rv1857</i>	Probable molybdate-binding lipoprotein ModA	8	Not essential	0.61	5.11E-05	brown
<i>Rv0526</i>	Possible thioredoxin protein (thiol-disulfide interchange protein)	8	Essential	0.78	6.16E-09	blue
<i>Rv0557</i>	Mannosyltransferase MgtA	8	Essential	0.80	1.16E-09	red
<i>Rv3220c</i>	Probable two component sensor kinase	7	Not essential	0.85	1.32E-11	brown
<i>Rv3246c</i>	Two component sensory transduction transcriptional regulatory protein MtrA	7	Not essential	0.74	1.18E-07	brown
<i>Rv1295</i>	Threonine synthase ThrC (ts)	6	Essential	0.36	0.024498	turquoise
<i>Rv1483</i>	3-oxoacyl-[acyl-carrier protein] reductase FabG1 (3-ketoacyl-acyl carrier protein reductase) (mycolic acid biosynthesis a protein)	6	Essential	0.68	2.65E-06	turquoise
<i>Rv3343c</i>	PPE family protein PPE54	6	Essential	0.79	3.58E-09	brown
<i>Rv0363c</i>	Probable fructose-bisphosphate aldolase Fba	5	Not essential	0.51	0.001204	turquoise
<i>Rv1485</i>	Ferrochelatase HemZ (protoheme ferro-lyase) (heme synthetase)	5	Essential	0.60	7.84E-05	turquoise
<i>Rv2763c</i>	Dihydrofolate reductase DfrA (DHFR) (tetrahydrofolate dehydrogenase)	5	Not essential	-0.56	0.000267	turquoise
<i>Rv3121</i>	Probable cytochrome P450 141 Cyp141	5	Essential	0.71	4.62E-07	brown
<i>Rv0256c</i>	PPE family protein PPE2	5	Essential	-0.55	0.000567	blue
<i>Rv1178</i>	Probable aminotransferase	5	Not essential	0.77	1.15E-08	blue
<i>Rv3581c</i>	Probable 2C-methyl-D-erythritol 2	5	Essential	0.82	2.97E-10	blue
<i>Rv0014c</i>	Transmembrane serine/threonine-protein kinase B PknB (protein kinase B) (STPK B)	4	Essential	0.51	0.001039	blue
<i>Rv2157c</i>	Probable UDP-N-acetylmuramoylalanyl-D-glutamyl-2	4	Essential	0.64	1.28E-05	blue
<i>Rv3579c</i>	Possible tRNA/rRNA methyltransferase	4	Essential	0.77	1.98E-08	blue
<i>Rv1650</i>	Probable phenylalanyl-tRNA synthetase	3	Essential	0.64	1.52E-05	turquoise

<i>Rv2702</i>	Polyphosphate glucokinase PpgK (polyphosphate-glucose phosphotransferase)	3	Essential	0.45	0.004486	turquoise
<i>Rv0018c</i>	Phosphoserine/threonine phosphatase PstP	3	Not essential	0.63	1.92E-05	blue
<i>Rv2957</i>	Possible glycosyl transferase	3	Not essential	-0.67	3.64E-06	blue
<i>Rv1385</i>	Probable orotidine 5'-phosphate decarboxylase PyrF (OMP decarboxylase) (ompdecase)	2	Not essential	0.45	0.004733	turquoise
<i>Rv2071c</i>	Precorrin-3 methylase CobM (precorrin-4 C11-methyltransferase)	2	Not essential	-0.65	1.04E-05	turquoise
<i>Rv3265c</i>	dTDP-RHA:a-D-GlcNAc-diphosphoryl polyprenol	2	Essential	0.41	0.0101	brown
<i>Rv3285</i>	Probable bifunctional protein acetyl-/propionyl-coenzyme A carboxylase (alpha chain) AccA3: biotin carboxylase + biotin carboxyl carrier protein (BCCP)	2	Essential	0.52	0.000721	brown
<i>Rv0894</i>	Possible transcriptional regulatory protein (possibly LuxR-family)	2	Essential	-0.66	5.6E-06	blue
<i>Rv1094</i>	Possible acyl-[acyl-carrier protein] desaturase DesA2 (acyl-[ACP] desaturase) (stearoyl-ACP desaturase)	2	Essential	0.61	4.86E-05	blue
<i>Rv2444c</i>	Possible ribonuclease E Rne	1	Essential	0.63	1.91E-05	turquoise
<i>Rv2482c</i>	Probable glycerol-3-phosphate acyltransferase PlsB2 (GPAT)	1	Not essential	-0.51	0.001012	turquoise
<i>Rv2787</i>	Conserved hypothetical alanine rich protein	1	Not essential	-0.54	0.000534	turquoise
<i>Rv3917c</i>	Probable chromosome partitioning protein ParB	1	Essential	0.66	6.53E-06	turquoise
<i>Rv0503c</i>	Cyclopropane-fatty-acyl-phospholipid synthase 2 CmaA2 (cyclopropane fatty acid synthase) (CFA synthase) (cyclopropane mycolic acid synthase 2) (mycolic acid trans-cyclopropane synthetase)	1	Not essential	0.67	3.47E-06	brown
<i>Rv3755c</i>	Conserved protein	1	Not essential	0.67	3.53E-06	brown
<i>Rv0196</i>	Possible transcriptional regulatory protein	1	Not essential	-0.48	0.002161	blue
<i>Rv2221c</i>	Glutamate-ammonia-ligase adenyltransferase GlnE (glutamine-synthetase adenyltransferase)	1	Essential	0.55	0.000378	blue
<i>Rv2533c</i>	N utilization substance protein NusB (NusB protein)	1	Essential	0.66	7.38E-06	blue
<i>Rv0558</i>	Probable ubiquinone/menaquinone biosynthesis methyltransferase MenH (2-heptaprenyl-1	1	Essential	0.73	1.71E-07	red
<i>Rv1981c</i>	Ribonucleoside-diphosphate reductase (beta chain) NrdF1 (ribonucleotide reductase small subunit) (R2F protein)	1	Not essential	0.49	0.002027	red
<i>Rv2349c</i>	Probable phospholipase C 3 PlcC	1	Not essential	-0.47	0.002842	black
<i>Rv2959c</i>	Possible methyltransferase (methylase)	1	Not essential	-0.54	0.000462	black