

The antimicrobial compound reuterin (3-hydroxypropionaldehyde) induces oxidative stress via interaction with thiol groups

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Supplementary Table S1. *E. coli* genes induced and repressed upon exposure to reuterin

See Methods for details of the experiment.

Gene	<i>E. coli</i> MG1655 ORF number	Function	Fold increase in presence of reuterin
<i>bhs</i>	b1112	ORF, hypothetical protein	35.7
<i>marA</i>	b1531	Multiple antibiotic resistance; transcriptional activator of defence systems	23.3
<i>yqhD</i>	b3011	Putative oxidoreductase	21.9
<i>nemR</i>	b1649	ORF, hypothetical protein	20.5
<i>marR</i>	b1530	Multiple antibiotic resistance protein; repressor of mar operon	15.5
<i>grxA</i>	b0849	Glutaredoxin1 redox coenzyme for glutathione-dependent ribonucleotide reductase	14.3
<i>ybiJ</i>	b0802	ORF, hypothetical protein	13.6
<i>nemA</i>	b1650	<i>N</i> -Ethylmaleimide reductase	13.1
<i>yqhC</i>	b3010	Putative ARAC-type regulatory protein	10.3
<i>gloA</i>	b1651	Lactoylglutathione lyase	8.6
<i>ahpF</i>	b0606	Alkyl hydroperoxide reductase, F52a subunit; detoxification of hydroperoxides	8.5
<i>yhcN</i>	b3238	ORF, hypothetical protein	7.4
<i>mdaB</i>	b3028	Modulator of drug activity B	5.2
<i>ahpC</i>	b0605	Alkyl hydroperoxide reductase, C22 subunit; detoxification of hydroperoxides	5.0
<i>yjbM</i>	b4048	ORF, hypothetical protein	4.8
<i>yjgI</i>	b4249	Putative oxidoreductase	4.6

Gene	<i>E. coli</i> MG1655 ORF number	Function	Fold increase in presence of reuterin
<i>emrR</i>	b2684	Regulator of plasmid <i>mcrB</i> operon (microcin B17 synthesis)	4.6
<i>katG</i>	b3942	Catalase; hydroperoxidase HPI(I)	4.6
<i>frmR</i>	b0357	Putative alpha helix chain	4.5
<i>marB</i>	b1532	Multiple antibiotic resistance protein	4.5
<i>adhC</i>	b0356	Alcohol dehydrogenase class III; formaldehyde dehydrogenase, glutathione-dependent	4.1
<i>cysD</i>	b2752	ATP:sulfurylase (ATP:sulfate adenyltransferase), subunit 2	4.1
<i>ibpB</i>	b3686	Heat-shock protein	4.1
<i>rnt</i>	b1652	RNase T, degrades tRNA	4.0
<i>nfnB</i>	b0578	Oxygen-insensitive NAD(P)H nitroreductase	3.9
<i>dkgA</i>	b3012	2,5-Diketo-D-gluconate reductase A	3.9
<i>yafB</i>	b0207	Putative aldose reductase (EC 1.1.1.21)	3.8
<i>yegQ</i>	b2081	ORF, hypothetical protein	3.6
<i>iscR</i>	b2531	Transcriptional repressor for <i>isc</i> operon	3.6
<i>trxC</i>	b2582	Putative thioredoxin-like protein	3.5
<i>iscS</i>	b2530	Putative aminotransferase	3.4
<i>adiY</i>	b4116	Putative ARAC-type regulatory protein	3.3
<i>ibpA</i>	b3687	Heat-shock protein	3.3
<i>nrdH</i>	b2673	Glutaredoxin-like protein; hydrogen donor	3.3
<i>rsmE</i>	b2946	ORF, hypothetical protein	3.2
<i>ybdG</i>	b0577	Putative transporter	3.2
<i>inaA</i>	b2237	pH-inducible protein involved in stress response	3.1
<i>yeiR</i>	b2173	ORF, hypothetical protein	2.9
<i>gshB</i>	b2947	Glutathione synthetase	2.9
<i>lpxT</i>	b2174	ORF, hypothetical protein	2.9
<i>yfhE</i>	b2527	ORF, hypothetical protein	2.9

Gene	<i>E. coli</i> MG1655 ORF number	Function	Fold increase in presence of reuterin
<i>astD</i>	b1746	Putative aldehyde dehydrogenase	2.8
<i>iscA</i>	b2528	Iron–sulfur cluster assembly protein	2.8
<i>ribE</i>	b1662	Riboflavin synthase, alpha chain	2.8
<i>sodA</i>	b3908	Superoxide dismutase, manganese	2.8
<i>iscU</i>	b2529	Iron–sulfur cluster assembly scaffold protein	2.8
<i>htrB</i>	b1054	Heat-shock protein	2.8
<i>hemB</i>	b0369	5-aminolevulinate dehydratase = porphobilinogen synthase	2.7
<i>yhbW</i>	b3160	Putative enzyme	2.7
<i>rzpQ</i>	b1553	ORF, hypothetical protein	2.7
<i>cysH</i>	b2762	3'-phosphoadenosine 5'-phosphosulfate reductase	2.7
<i>cysJ</i>	b2764	Sulfite reductase (NADPH), flavoprotein beta subunit	2.7
<i>ytfI</i>	b4215	ORF, hypothetical protein	2.6
<i>iscX</i>	b2524	Iron–sulfur cluster assembly protein	2.6
<i>yjgH</i>	b4248	ORF, hypothetical protein	2.6
<i>fdx</i>	b2525	[2FE–2S] ferredoxin, electron carrier protein	2.6
<i>fur</i>	b0683	Negative regulator	2.6
<i>ytfG</i>	b4211	Putative oxidoreductase	2.6
<i>cysI</i>	b2763	Sulfite reductase, alpha subunit	2.6
<i>ribA</i>	b1277	GTP cyclohydrolase II	2.5
<i>ycaM</i>	b0899	Putative transport	2.5
<i>hemF</i>	b2436	Coproporphyrinogen III oxidase	2.4
<i>amiA</i>	b2435	<i>N</i> -acetylmuramoyl-L-alanine amidase I	2.4
<i>yciW</i>	b1287	Putative oxidoreductase	2.4
<i>hscA</i>	b2526	Heat-shock protein, chaperone, member of Hsp70 protein family	2.3
<i>yffQ</i>	b2448	ORF, hypothetical protein	2.3
<i>poxB</i>	b0871	Pyruvate oxidase	2.3

Gene	<i>E. coli</i> MG1655 ORF number	Function	Fold increase in presence of reuterin
<i>ybcC</i>	b0920	ORF, hypothetical protein	2.3
<i>yadR</i>	b0156	ORF, hypothetical protein	2.3
<i>ygfZ</i>	b2898	ORF, hypothetical protein	2.3
<i>yaiM</i>	b0355	Putative esterase (EC 3.1.1.1)	2.3
<i>nrdA</i>	b2234	Ribonucleoside diphosphate reductase 1, alpha subunit, B1	2.3
<i>yhgI</i>	b3414	ORF, hypothetical protein	2.3
<i>yncJ</i>	b1436	ORF, hypothetical protein	2.2
<i>xthA</i>	b1749	Exonuclease III	2.2
<i>cysA</i>	b2422	ATP-binding component of sulfate permease A protein; chromate resistance	2.2
<i>yeeD</i>	b2012	ORF, hypothetical protein	2.1
<i>emrA</i>	b2685	Multidrug resistance secretion protein	2.1
<i>yqfE</i>	b2915	ORF, hypothetical protein	2.1
<i>cydB</i>	b0734	Cytochrome <i>d</i> terminal oxidase polypeptide subunit II	2.1
<i>ybdJ</i>	b0580	ORF, hypothetical protein	2.1
<i>folE</i>	b2153	GTP cyclohydrolase I	2.1
<i>yljA</i>	b0881	ORF, hypothetical protein	2.1
<i>ybhT</i>	b0762	ORF, hypothetical protein	2.1
<i>fruB</i>	b2169	PTS system, fructose-specific IIA/fpr component	2.1
<i>mdaA</i>	b0851	Modulator of drug activity A	2.1
<i>yggR</i>	b2950	Putative protein transport	2.1
<i>add</i>	b1623	Adenosine deaminase	2.1
<i>cysK</i>	b2414	Cysteine synthase A, O-acetylserine sulfhydrylase A	2.1
<i>def</i>	b3287	Peptide deformylase	2.1
<i>pepE</i>	b4021	Peptidase E, a dipeptidase where amino-terminal residue is aspartate	2.1

Gene	<i>E. coli</i> MG1655 ORF number	Function	Fold increase in presence of reuterin
<i>ycaK</i>	b0901	ORF, hypothetical protein	2.1
<i>fryB</i>	b2387	Putative PTS system enzyme IIB component	2.1
<i>soxS</i>	b4062	Regulation of superoxide response regulon	2.1
<i>cysP</i>	b2425	Thiosulfate binding protein	2.0
<i>ompX</i>	b0814	Outer-membrane protein X	2.0
<i>adiA</i>	b4117	Biodegradative arginine decarboxylase	2.0
<i>zwf</i>	b1852	Glucose-6-phosphate dehydrogenase	2.0
<i>ydjN</i>	b1729	Part of a kinase	2.0
<i>mioC</i>	b3742	Initiation of chromosome replication	2.0
<i>idi</i>	b2889	Putative enzyme	2.0
<i>ymfD</i>	b1137	ORF, hypothetical protein	2.0
<i>arrQ</i>	b1554	Putative lysozyme	1.9
<i>hemH</i>	b0475	Ferrochelatase: final enzyme of haem biosynthesis	1.9
<i>arsC</i>	b3503	Arsenate reductase	1.9
<i>yceE</i>	b1053	ORF, hypothetical protein	1.9
<i>aceA</i>	b4015	Isocitrate lyase	1.9
<i>ycgC</i>	b1198	Putative PTS system enzyme I	1.9
<i>clpA</i>	b0882	ATP-binding component of serine protease	1.9
<i>ycjY</i>	b1327	ORF, hypothetical protein	1.9
<i>cstC</i>	b1748	Acetylornithine delta-aminotransferase	1.9
<i>cadA</i>	b4131	Lysine decarboxylase 1	1.9
<i>hyaA</i>	b0972	Hydrogenase-1 small subunit	-11.6
<i>hyaB</i>	b0973	Hydrogenase-1 large subunit	-9.7
<i>gadA</i>	b3517	Glutamate decarboxylase isozyme	-8.5
<i>tdcB</i>	b3117	Threonine dehydratase, catabolic	-8.2
<i>gadB</i>	b1493	Glutamate decarboxylase isozyme	-7.3

Gene	<i>E. coli</i> MG1655 ORF number	Function	Fold increase in presence of reuterin
<i>tdcE</i>	b3114	Probable formate acetyltransferase 3	-7.1
<i>hyaD</i>	b0975	Processing of HyaA and HyaB proteins	-6.9
<i>yhiM</i>	b3491	ORF, hypothetical protein	-6.6
<i>frvR</i>	b3897	Putative DNA transposition protein	-6.2
<i>cnu</i>	b1625	ORF, hypothetical protein	-5.8
<i>yciD</i>	b1256	Putative outer-membrane protein	-5.4
<i>tnaA</i>	b3708	Tryptophanase	-5.3
<i>xasA</i>	b1492	Acid sensitivity protein, putative transporter	-5.1
<i>ompC</i>	b2215	Outer-membrane protein 1b (Ib;c)	-4.7
<i>yehZ</i>	b2131	Putative transport system permease protein	-4.6
<i>yjiH</i>	b4330	ORF, hypothetical protein	-4.5
<i>yhiE</i>	b3512	ORF, hypothetical protein	-4.3
<i>hyaC</i>	b0974	Probable Ni/Fe-hydrogenase 1 <i>b</i> -type cytochrome subunit	-4.2
<i>glpC</i>	b2243	sn-glycerol-3-phosphate dehydrogenase (anaerobic), K-small subunit	-4.2
<i>hyaE</i>	b0976	Processing of HyaA and HyaB proteins	-4.2
<i>pheA</i>	b2599	Chorismate mutase-P and prephenate dehydratase	-4.1
<i>hns</i>	b1237	DNA-binding protein HLP-II (HU, BH2, HD, NS); pleiotropic regulator	-4.0
<i>hdeA</i>	b3510	ORF, hypothetical protein	-4.0
<i>yeaU</i>	b1800	Putative tartrate dehydrogenase	-3.9
<i>tnaL</i>	b3707	Tryptophanase leader peptide	-3.9
<i>ansB</i>	b2957	Periplasmic L-asparaginase II	-3.8
<i>glpA</i>	b2241	sn-glycerol-3-phosphate dehydrogenase (anaerobic), large subunit	-3.7
<i>yibP</i>	b3613	Putative membrane protein	-3.7
<i>tdcC</i>	b3116	Anaerobically inducible L-threonine, L-serine permease	-3.6

Gene	<i>E. coli</i> MG1655 ORF number	Function	Fold increase in presence of reuterin
<i>ydfZ</i>	b1541	ORF, hypothetical protein	-3.5
<i>hdeB</i>	b3509	ORF, hypothetical protein	-3.5
<i>tdcD</i>	b3115	Putative kinase	-3.4
<i>yobF</i>	b1824	ORF, hypothetical protein	-3.4
<i>argT</i>	b2310	lysine-, arginine-, ornithine-binding periplasmic protein	-3.4
<i>ybaS</i>	b0485	Putative glutaminase	-3.4
<i>appA</i>	b0980	Phosphoanhydride phosphorylase; pH 2.5 acid phosphatase; periplasmic	-3.3
<i>hycA</i>	b2725	Transcriptional repression of <i>hyc</i> and <i>hyp</i> operons	-3.2
<i>fumB</i>	b4122	Phage transposase	-3.2
<i>slp</i>	b3506	Outer-membrane protein induced after carbon starvation	-3.1
<i>ybjZ</i>	b0879	Putative ATP-binding component of a transport system	-3.1
<i>glpB</i>	b2242	sn-glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit	-3.1
<i>hydN</i>	b2713	Involved in electron transport from formate to hydrogen, Fe-S centres	-3.1
<i>lldD</i>	b3605	L-lactate dehydrogenase	-3.0
<i>hycH</i>	b2718	Processing of large subunit (HycE) of hydrogenase 3 (part of the FHL complex)	-3.0
<i>stfR</i>	b1372	Unknown protein encoded by prophage CP-933X	-3.0
<i>cbpA</i>	b1000	Curved DNA-binding protein; functions closely related to DnaJ	-3.0
<i>evgA</i>	b2369	Putative positive transcription regulator (sensor EvgS)	-3.0
<i>yehL</i>	b2119	ORF, hypothetical protein	-2.9
<i>hyaF</i>	b0977	Nickel incorporation into hydrogenase-1 proteins	-2.9
<i>hdeD</i>	b3511	ORF, hypothetical protein	-2.9
<i>wrbA</i>	b1004	trp repressor binding protein; affects association of trp repressor and operator	-2.9

Gene	<i>E. coli</i> MG1655 ORF number	Function	Fold increase in presence of reuterin
<i>hypA</i>	b2726	Pleiotropic effects on three hydrogenase isozymes	-2.9
<i>hemD</i>	b3804	Uroporphyrinogen III synthase	-2.9
<i>hycF</i>	b2720	Probable iron-sulfur protein of hydrogenase 3 (part of FHL complex)	-2.8
<i>yheN</i>	b3345	Putative citrate permease	-2.8
<i>ybaT</i>	b0486	Putative amino acid/amine transport protein	-2.8
<i>viaZ</i>	b3556a	Putative membrane-permeability-altering protein	-2.8
<i>None</i>	b4103	Membrane channel protein component of Pn transporter	-2.8
<i>yfiQ</i>	b2584	ORF, hypothetical protein	-2.8
<i>tnaB</i>	b3709	Low-affinity tryptophan permease	-2.8
<i>appC</i>	b0978	Probable third cytochrome oxidase, subunit I	-2.7
<i>yjcC</i>	b4061	Hypothetical protein	-2.7
<i>malP</i>	b3417	Maltodextrin phosphorylase	-2.7
<i>yjiG</i>	b4329	ORF, hypothetical protein	-2.6
<i>yhaP</i>	b3111	Putative L-serine dehydratase	-2.6
<i>treB</i>	b4240	PTS system enzyme II, trehalose-specific	-2.6
<i>treC</i>	b4239	Trehalase 6-P hydrolase	-2.6
<i>frdA</i>	b4154	Fumarate reductase, anaerobic, flavoprotein subunit	-2.6
<i>hycE</i>	b2721	Large subunit of hydrogenase 3 [part of formate hydrogenlyase (FHL) complex]	-2.6
<i>hycD</i>	b2722	Membrane-spanning protein of hydrogenase 3 [part of formate hydrogenlyase (FHL) complex]	-2.6
<i>hycB</i>	b2724	Probable small subunit of hydrogenase-3, iron-sulfur protein [part of formate hydrogenlyase (FHL) complex]	-2.5
<i>glpT</i>	b2240	sn-glycerol-3-phosphate permease	-2.5
<i>ynaF</i>	b1376	Putative filament protein	-2.5
<i>hisG</i>	b2019	ATP phosphoribosyltransferase	-2.5

Gene	<i>E. coli</i> MG1655 ORF number	Function	Fold increase in presence of reuterin
<i>ynfK</i>	b1593	ORF, hypothetical protein	-2.5
<i>yehH</i>	b1205	ORF, hypothetical protein	-2.5
<i>yhaQ</i>	b3112	Putative L-serine dehydratase	-2.4
<i>yhiU</i>	b3513	Putative membrane protein	-2.4
<i>glpF</i>	b3927	Facilitated diffusion of glycerol	-2.4
<i>None</i>	b3808	ORF, hypothetical protein	-2.4
<i>pheL</i>	b2598	Leader peptide of chorismate mutase-P-prephenate dehydratase	-2.3
<i>hycG</i>	b2719	Hydrogenase activity	-2.3
<i>narG</i>	b1224	Nitrate reductase 1, alpha subunit	-2.3
<i>ydfD</i>	b1576	ORF, hypothetical protein	-2.2
<i>rob</i>	b4396	Right origin-binding protein	-2.2
<i>dpdA</i>	b2146	Putative oxidoreductase	-2.2
<i>aidB</i>	b4187	Putative acyl coenzyme A dehydrogenase	-2.2
<i>glpQ</i>	b2239	Glycerophosphodiester phosphodiesterase, periplasmic	-2.2
<i>fimB</i>	b4312	Recombinase involved in phase variation; regulator for fimA	-2.2
<i>yhiV</i>	b3514	Putative transport system permease protein	-2.2
<i>glpX</i>	b3925	Unknown protein encoded by prophage CP-933N	-2.2
<i>pckA</i>	b3403	Phosphoenolpyruvate carboxykinase	-2.2
<i>pspF</i>	b1303	Psp operon transcriptional activator	-2.2
<i>yffQ</i>	b2633	ORF, hypothetical protein	-2.1
<i>dnaK</i>	b0014	Chaperone Hsp70; DNA biosynthesis; autoregulated heat-shock proteins	-2.1
<i>mviN</i>	b1069	Putative virulence factor	-2.1
	b1586	ORF, hypothetical protein	-2.1
<i>dpdB</i>	b2147	Putative oxidoreductase	-2.1
<i>rbsB</i>	b3751	D-ribose periplasmic binding protein	-2.1

Gene	<i>E. coli</i> MG1655 ORF number	Function	Fold increase in presence of reuterin
<i>hypB</i>	b2727	Guanine-nucleotide binding protein, functions as nickel donor for large subunit of hydrogenase 3	-2.1
<i>lamB</i>	b4036	Phage lambda receptor protein; maltose high-affinity receptor	-2.1
<i>yjiE</i>	b4327	Putative transcriptional regulator LYSR-type	-2.1
<i>yecI</i>	b1902	Ferritin-like protein	-2.1
<i>yjeF</i>	b4167	ORF; Unknown function	-2.1
<i>bssR</i>	b0836	Putative receptor	-2.1
<i>hypC</i>	b2728	Pleiotrophic effects on three hydrogenase isozymes	-2.1
<i>hdhA</i>	b1619	NAD-dependent 7alpha-hydroxysteroid dehydrogenase, dehydroxylation of bile acids	-2.1
<i>hypD</i>	b2729	Pleiotrophic effects on three hydrogenase isozymes	-2.1
<i>ychM</i>	b1206	ORF, hypothetical protein	-2.1
<i>yhiF</i>	b3507	ORF, hypothetical protein	-2.1