Gene	Name / Function	fold change	p value
cysD	Sulfate adenylyltransferase	8.74	0.00
katG	Catalase hydrogen peroxidase I	7.83	0.00
cysJ	Sulfite reductase, beta-subunit	7.62	0.01
cysC	Adenylylsulfate kinase	5.97	0.00
ibpA	Small heat shock protein	5.92	0.00
mcbA	Colanic acid production	5.76	0.01
acpD	ACP phosphodiesterase	5.67	0.02
cysP	Periplasmic sulfate binding protein	5.63	0.01
ybiJ	Function unknown	5.58	0.03
cysW	Sulfate transport system permease	5.57	0.01
cysA	Sulfate-transporting ATPase	5.37	0.01
cysK	Cysteine synthase A	5.32	0.01
cysU	Sulfate transport system permease	5.24	0.00
grxA	Glutaredoxin 1	5.23	0.00
argI	Ornithine transcarbamylase	5.06	0.01
cbl	HTH-type transcriptional regulator	4.99	0.00
cysN	Sulfate adenylyltransferase subunit I	4.92	0.00
yeeE	UPF0394 inner membrane protein	4.46	0.01
ylaC	Inner membrane protein	4.22	0.01
ygbE	Inner membrane protein	4.15	0.02
sufE	Cysteine desulfuration protein	3.87	0.01
pstS	Phosphate-transport protein	3.81	0.04
pstB	phosphate import ATP-binding protein	3.80	0.05
iscR	HTH-type transcriptional regulator	3.77	0.02
yeaJ	Function unknown	3.72	0.01
ahpF	Alkyl hydroperoxide reductase	3.52	0.02
sufS	Cysteine desulfurase	3.52	0.02
nlpA	Lipoprotein 28	3.44	0.02
iscS	Cysteine desulfurase	3.27	0.02
gsiD	Glutathione transport system permease	3.22	0.03
ydjN	Uncharacterised symporter	3.21	0.01
argA	Amino-acid acetyltransferase	3.18	0.04
yciW	Function unknown	3.05	0.01
bhsA	Multiple stress resistance protein	2.99	0.04
iscU	nifU-like protein	2.93	0.04
norR	NO reductase transcription regulator	2.89	0.04
ahpC	Alkyl hydroperoxide reductase	2.85	0.02
fliY	Cystine-binding protein	2.79	0.05
rnfE	Electron transport complex protein	2.79	0.01
pstC	Phosphate transport system permease	2.72	0.01
yncE	Function unknown	2.70	0.00
iaaA	Isoaspartyl peptidase	2.69	0.04
argD	Acetylornithine aminotransferase	2.68	0.04
pstA	Phosphate transport system permease	2.58	0.03
mltD	Murein hydrolase D	2.54	0.03
argC	N-acetyl-γ-glutamyl-phosphate reductase	2.49	0.01
argB	Acetylglutamate kinase	2.47	0.02
ykgI	Function unknown	2.47	0.05
fabA	β-hydroxydecanoylthioester dehydrase	2.41	0.00
argE	Acetylornithine deacetylase	2.25	0.04
rnfC	Electron transport complex protein	2.25	0.01
rplS	50S ribosomal protein L19	2.18	0.04
marA	Multiple antibiotic resistance protein	2.13	0.05
lon	ATP-dependent protease La	2.05	0.03
rsxP	Inner membrane protein	2.03	0.04

Supplemental Table 1. Full microarray list of the genes upregulated in response to peroxynitrite exposure. The mean fold change in individual gene expression after exposure to 300 μM peroxynitrite compared with unstressed controls grown aerobically is shown for upregulated genes over the threshold of 2-fold change.