

NCBI Genome ID NC011761	Gene	Function	Median (Stats)	One Sample t-Test (Adv)	S induced
petII operon					
AFE_2732	<i>hip</i>	high potential iron sulfur protein	-1.845	0.000001	*
AFE_2731	<i>petC2</i>	ubiquinol--cytochrome c reductase, cytochrome c1 subunit	-0.293	0.085725	
AFE_2730	<i>petB2</i>	ubiquinol--cytochrome c reductase, cytochrome b subunit	-1.696	0.00064	*
AFE_2729	<i>petA2</i>	ubiquinol--cytochrome c reductase, iron-sulfur subunit	-1.94	0.000533	*
AFE_2728	<i>sdrA2</i>	oxidoreductase, short-chain dehydrogenase/reductase family	-1.139	0.001041	*
AFE_2727	<i>cycA2</i>	cytochrome c4	-0.497	0.168308	
Heterodisulfide reductase complex operon					
AFE_2586	<i>hdrB</i>	heterodisulfide reductase subunit B, homolog	-1.488	0.000002	*
AFE_2558	<i>pspE</i>	rhodanese-like domain protein	0.106	0.376134	
AFE_2557	<i>sirA</i>	conserved hypothetical protein	-2.387	0.000317	*
AFE_2556	<i>dsrE</i>	conserved hypothetical protein	-2.105	0.000005	*
AFE_2555	<i>hdrC</i>	iron-sulfur cluster-binding protein	-2.103	0.000233	*
AFE_2554	<i>hdrB</i>	heterodisulfide reductase subunit B, homolog	-1.968	0.000086	*
AFE_2553	<i>hdrA</i>	pyridine nucleotide-disulfide oxidoreductase	-2.576	0.000646	*
AFE_2552	<i>orf2</i>	conserved hypothetical protein			
AFE_2551	<i>hdrC</i>	iron-sulfur cluster-binding protein	-2.387	0.000004	*
AFE_2550	<i>hdrB</i>	succinate dehydrogenase/fumarate reductase, C subunit	-1.857	0.000102	*
Sulfide-quinone reductase					
AFE_1792	<i>sqr</i>	sulfide-quinone reductase, putative	-1.558	0.000064	*
Cytochrome bd ubiquinol oxidase					
AFE_0955	<i>cydA</i>	cytochrome d ubiquinol oxidase, subunit I	-1.989	0	*
AFE_0954	<i>cydB</i>	cytochrome d ubiquinol oxidase, subunit II	-2.593	0	*
Cytochrome bo 3 ubiquinol oxidase					
AFE_0634	<i>cyoD</i>	cytochrome o ubiquinol oxidase, subunit IV	-2.25	0.000217	*
AFE_0633	<i>cyoC</i>	cytochrome o ubiquinol oxidase, subunit III	-2.964	0.000023	*
AFE_0632	<i>cyoB</i>	cytochrome o ubiquinol oxidase, subunit I	-2.736	0.000377	*
AFE_0631	<i>cyoA</i>	cytochrome o ubiquinol oxidase, subunit II	-3.157	0.000008	*
Sulfate adenylyltransferase					
AFE_0539	<i>sat</i>	sulfate adenylyltransferase, putative/adenylylsulfate kinase	0.713	0.000814	
Thiosulfate-quinone oxidoreductase complex operon					
AFE_0046		conserved hypothetical protein	-1.69	0.00009	*
AFE_0045		sulfur/pyrite/thiosulfate/sulfide-induced protein	-1.058	0.004411	*
AFE_0044	<i>doxDA</i>	Thiosulfate-quinone oxidoreductase, DoxD-like family protein	-2.257	0.000013	*
AFE_0043		periplasmic solute-binding protein, putative	-2.242	0.000001	*

AFE_0042		Tat (twin-arginine translocation) pathway signal sequence domain protein	-1.544	0.000372	*
AFE_0041		C4-dicarboxylate transporter/malic acid transport protein	-1.497	0.000001	*
Tetrathionate hydrolase					
AFE_0029	<i>tetH</i>	Tetrathionate hydrolase	-0.638	0.223567	*