

Gene	Product	EC no.
<i>hdrA</i>	heterodisulfide reductase subunit A	EC:1.8.98.1
<i>hdrB</i>	heterodisulfide reductase subunit B	EC:1.8.98.1
<i>hdrC</i>	heterodisulfide reductase subunit C	EC:1.8.98.1
<i>dsrE</i>	conserved hypothetical protein	
<i>hdrB2</i>	heterodisulfide reductase subunit B	EC:1.8.98.1
<i>rhd</i>	rhodanese; thiosulfate sulfurtransferase	EC:2.8.1.1
<i>doxD</i>	thiosulfate: quinone oxidoreductase	EC:1.8.5.2
<i>sat2</i>	sulfate adenyltransferase subunit 2	EC:2.7.7.4
<i>sat1</i>	sulfate adenyltransferase subunit 1 /adenylsulfate kinase	EC:2.7.7.4 2.7.1.25
<i>sqr</i>	sulfide quinone reductase	EC:1.8.5.-
<i>sqr2</i>	sulfide quinone reductase, putative	EC:1.8.5.-

Ngar Locus	start	end	AA Length	Best BLAST hits in GenBank database
Scaffold_254_gene_1	1	941	313.333333	<i>Hyphomicrobium denitrificans</i> ATCC 51888
Scaffold_254_gene_2	827	2329	501	<i>Rhodobacter</i> sp. SW2
Scaffold_254_gene_3	2500	3246	249	<i>Rhodobacter</i> sp. SW2
Scaffold_254_gene_4	3322	3702	145	<i>Rhodobacter</i> sp. SW2
Scaffold_9_gene_24	22130	22789	220	<i>Rhodobacter</i> sp. SW2
Scaffold_153_gene_17	15215	15748	178	<i>Leptothrix cholodnii</i> SP-6
Scaffold_68_gene_12	9599	10600	334	<i>Gluconobacter oxydans</i> 621H
Scaffold_217_gene_17	14921	15718	266	<i>Gluconacetobacter diazotrophicus</i> PAI 5
Scaffold_217_gene_18	16045	16563	173	<i>Acetobacter aceti</i> NBRC 14818
Scaffold_18_gene_12	14834	16117	428	<i>Bradyrhizobium</i> sp. STM 3809
Scaffold_92_gene_5	4297	5430	378	<i>Acidithiobacillus ferrooxidans</i> ATCC 53993