

1 **The respiratory selenite reductase from *Bacillus selenitireducens* strain MLS10**

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7 **SUPPLEMENTAL MATERIALS**

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9 **Figure S1**

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A) Bsel_1475 Rhodanese domain protein

MKHKWTGLLMGAALLTATACSSDEASVLADEENDNEEQAAVETNVFN^DLMANSAAY
MEDPNFNVITGEALHNKTVFENP^EEDYFILDVRD^TTTFVSGHIPGAVNVPYRV^SGLEQMY
LELPEDKTIYV^VCFSGHTASHTVGMLNALGYDAEALQFGMGGYASGTDLGSN^IPGGPA
ELPVVTTGFELTETHDLPEIMSD^ES^DIR^TIAHEQSQNFLDQEP^PGV^MGAPDLNEMINEGN
LDGHQLIDIRLGEHYEQGHIEGAANLPYNELFNEENLSLLDPEKMTVVIGYNGYDASQV
TRLLGQLEYS^AVPLAYGMSIWSGDES^VVGE^HMFDFSNVYSLPVRELKFDMDAGDIEAG
CR

B) Bsel_1476 Trimethylamine-N-oxide reductase

MPKLR^RSFLKASALTA^AAAAVPFKMTMGDFREASAEAE^EKVIPST^CNG^CASM^CGIYA
HVKNDR^LWYVEGHPVHLKAGGRL^CARGHGMAADIY^GKGRVQGP^MKKVAE^EGEFEPIS
WEQAFKEIG^EKMG^NLRDQYGGNSFLWLEHGVRGKRYADPL^LDRMGSSNYITHYST^RFT
SKTNAWQH^MVGSM^PPAGDHENAKYMIFEG^RNFAGAI^PNGMKKILKAKDNGAKIVVIDP
RYSEIAKVADEWIP^RPGTDLALRLGMAHTLISE^NLYDSAFVKKYV^TDFDEFWSLNKDK
DADWAAEITGIDADTIRRVAREFAEHAPEAFMEPGWHGLHCHYFNSTQTAQMGIILNAL
VGNFFKRGGLMPSANVEFGEYMHTDVEAVEKGP^RADGAGVEGEHMTVEPGRGIAQNV
PDMIDKGR^IKSVFIYHFNPLRTAPDPEYQKKIANAELVVSIPVDWNETSVYAADYILPEN
YYL^RTEVPQAVSGHISHDWPQISIRQ^VT^DPLHDTLPLLDIMRGITKEMGYDNLYDFTV
DDEIAAMLEPTGVTPEELKEKGTVELRTNKVEPKFPVNL^SGEPNLGTFSGKIQFSAEIFKI
DGKRGVPTWIPTMVQPD^LNNPEEFRLIHGKQPYHSHSVTSTNASLLRITEKYNGEAMWI
NTKRAKDLGIEDGDTVSVKSSIANKTVPVHV^TQLIHPECVWIPSA^YGAFSNKIKEGYQLG
INFND^FIPMMIEPYSGSTMSQEVVVNVQKGGEA

C) Bsel_1477 4Fe-4S ferredoxin iron-sulfur binding domain protein

MANYGLLIDTRK^RTG^RHA^RSIA^RSTYNELEPEVSYNRLEFIESGTYPNVKMDIVPVQ^CM
HCDDAP^CVKV^CSTQATFKVEENGIVAFNPDK^CTG^CKAC^CMAAC^CPYDARALNEARLSEK^C
RW^CPEMLTQGKQPS^CAST^CMNEVRLFGDLDDPDSEINKKMAQFNTVQLVPEAGTKPRI
WYIK

D) Bsel_1478 Polysulfide reductase NrfD

MLNRNLWYGITGIMIIFGIIGNIFIHGEHVMGTSNYVPWGS^LLIGAYVFFVAISTGLTFLS
SMVHVFKMKQFEFLTKRLTLASIA^TLLMGFVMIGVELGNPLAMVYILVTPNVMAPIFW
MGAFYGLYLVLHII^EFFFQIKDNHKIVNTISPFVLVVGIAAQSTLGA^VFGLSVARGIWN^SA
YLSIFFLIMAFVSGLAVAMIMAFFLSKGNVMKQEDREKLPGLYPFMSKLTMGLLAVGII^F
VTWNWIYGLHSGNPNRMASMEMLNGPLAVPYWVLEVG^FVFLIPLLILGLVKAKKAAT
MLTTGVVLLIGLFAMRIILTFAGQMVPLEVVTGSLTMNELRDVSILWSEWATMIFGVGG
SILYMLGERFLNLDVTEHGS^HGTHDKKATQAS

51 **E) Bsel_1479 Chaperon protein NarJ**

52 MNKTDREKETYTELIRLLGELYKFPDDEVEQAIAEGVLDQEIDDYLSLFPEIRIENKQSFSS
53 LRDKELTAKKQYMTAYSGITTPFHPPVESLYKPWSVDPKDQTGLYNKTGYMGMGDAAL
54 HMKHLLQHYEIEVPKDYEMMPDHLAISLEFYAMLLERDTEAAEAFHQDHFDFWLKAFH
55 KKHQEIDDVPFYDYLLRVLIAVTAVSPRELT
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57 **F) Bsel_1480 Rhodanese domain protein**

58 MKKWAIGLLSLAGMITLSACGTSQASETEPTSFLPMEPDVSPYIVVEEEAEEEGQDHVPYH
59 ENWNYIDTVQLTRLMDGLPEISQDRESYDQVPP**EWGDVALIDSRPPGVYAAGHINGAINI**
60 **PDSEFDDYKHLLPEDKDTQLIFYCGGLHCALSGNSSEKAMDMGYENSYVYQEGTPAWK**
61 **SAGNYFTVTPEYVEEQILES NVARD**DTDPVMIIDTRTYAGYFAEHIPTAVFWDDTQYGT
62 **KYQGFAPENKDAEIIYCGGFFCHKSPALADDLLGDGYTNVKVLSGGMPAWKQAGLPT**
63 **FGMETADADFDVSAGKVDRSVSAEDFEDLIASGATVVDVRGDGEVANGMIDGALH**
64 **VPDGDIIHANDPSVEETLPDDKSTLLIHCASGARASGVVEKIADLGYEEVYYWNGGISIS**
65 **DDGSYTLN**
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68 **Figure S1. Structural motifs predicted in proteins of the MLS10 Srr operon *srrEABCF***
69 **(Bsel 1475 – Bsel_1480).** The annotation is that provided by the Joint Genome Institute
70 Integrated Genome who sequenced the genome. A) SrrE, Rhodanese domain protein. The
71 putative lipoprotein motif anchoring the protein to the membrane is highlighted in grey. The
72 putative rhodanese domains are highlighted in purple. One rhodanese domain has a predicted
73 catalytically active cysteine residue, highlighted in teal. B) SrrA, Trimethylamine-N-oxide
74 reductase. The putative twin arginine translocation motif is highlighted in teal. The putative
75 4Fe-4S cluster is highlighted in yellow. The cysteine residue predicted to coordinate the guanine
76 dinucleotide molybdopterin cofactor is highlighted in red. C) SrrB, 4Fe-4S ferredoxin iron-sulfur
77 binding domain protein. The four predicted 4Fe-4S iron clusters are highlighted. The first 4Fe-
78 4S cluster is highlighted in red. The second 4Fe-4S cluster is highlighted in purple. The third
79 4Fe-4S cluster is highlighted in teal. The fourth 4Fe-4S cluster is highlighted in yellow.
80 D) SrrC, Polysulfide reductase NrfD. E) SrrD, Chaperon protein NarJ. F). SrrF, Rhodanese
81 domain protein. The putative lipoprotein motif anchoring the protein to the membrane is
82 highlighted in grey. The putative rhodanese domains are highlighted in purple. All three
83 rhodanese domains have predicted catalytically active cysteine residues, highlighted in teal.