**Supplementary Fig. 1.** Selected bands for in-gel digestion in anti-OmcA and anti-MtrC IP of unlabeled cell lysates.

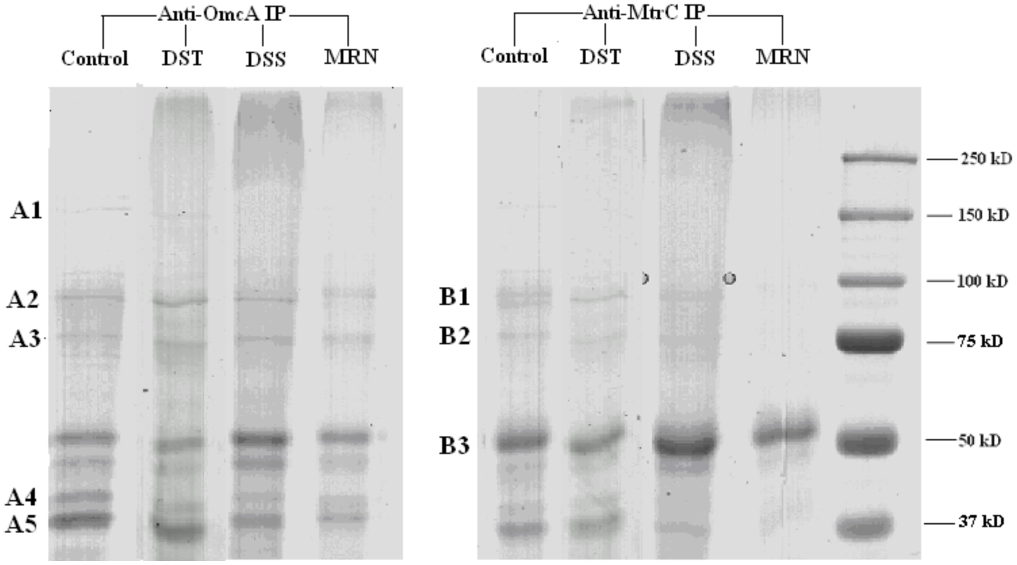
**Supplementary Fig. 2.** Protein mass distribution in *S. oneidensis* MR-1 cells. Genome database (4,854 ORFs) was downloaded from The Institute for Genomic Research (TIGR) (http://www.tigr.org/).

**Supplementary Fig. 3.** SDS-PAGE analysis of the proteins immunoprecipitated with anti-OmcA and anti-MtrC from *mtrC* and *omcA* mutant cells *in vivo* cross-linked by DSS and MRN. IP of uncross-linked mutant cells served as a control.

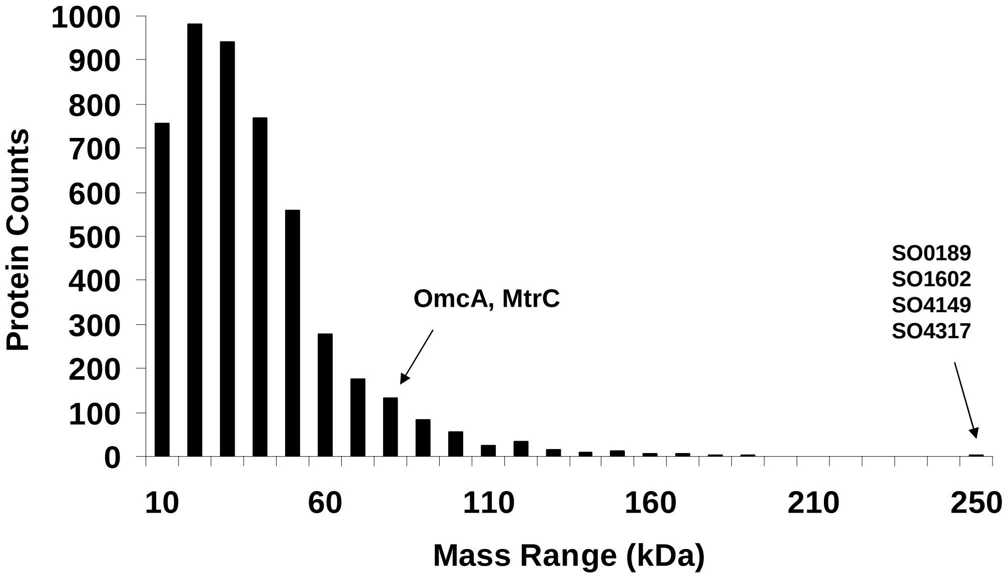
**Supplementary Fig. 4.** SDS-PAGE analysis of the proteins immunoprecipitated with anti-OmcA from cell lysates cross-linked by DSS or MRN. IP of uncross-linked cells served as a control.

**Supplementary Table I** Protein identifications of selected bands in anti-OmcA and anti-MtrC IP of unlabeled cell lysates.

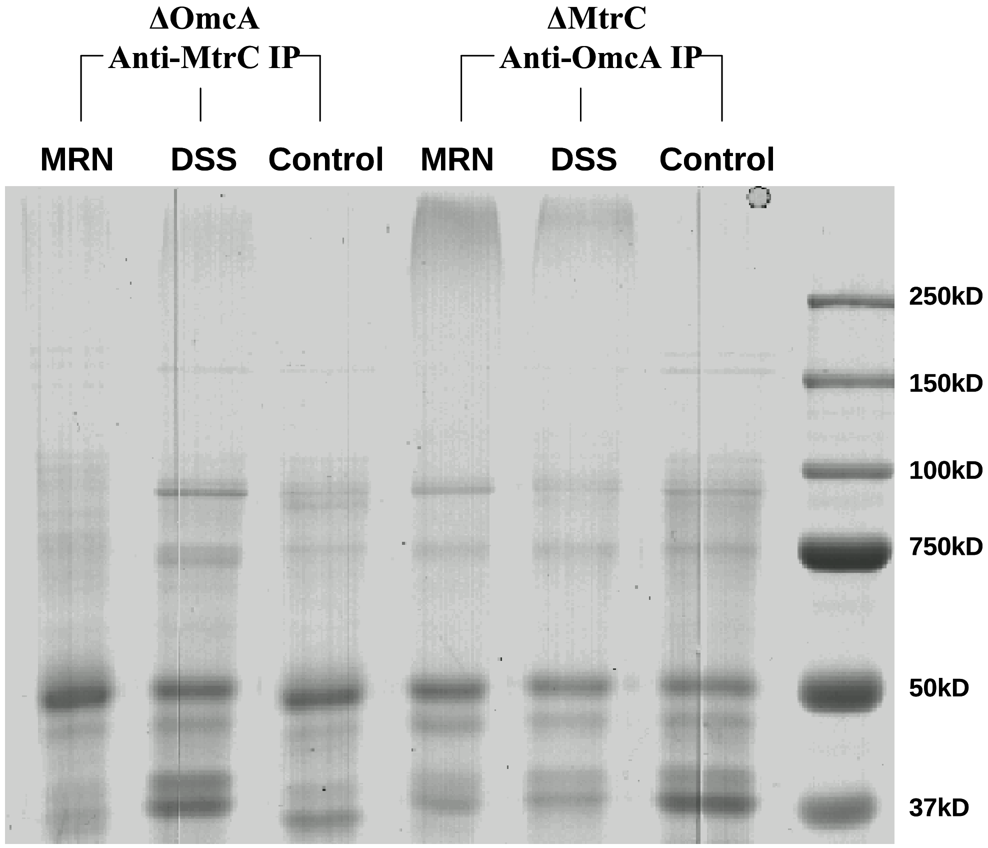
**Supplementary Table II.** Peptide details for all identified proteins.



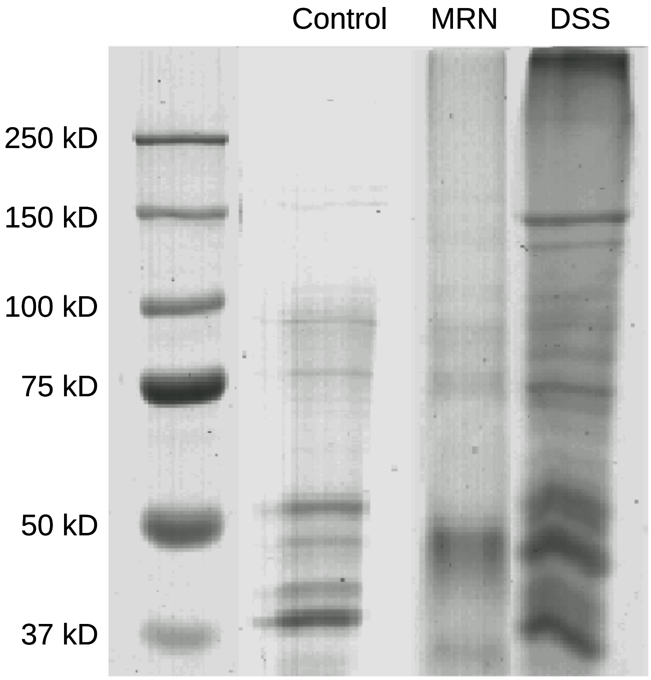
**Supplementary Fig. 1**



**Supplementary Fig. 2**



Supplementary Fig. 3



Supplementary Fig. 4

## Supplementary Table I

**A1**

| Gene | Mascot Score | Annotation | Category[a] | MW (kDa) |
|---|---|---|---|---|
| SO0224 | 1067 | DNA-directed RNA polymerase, beta subunit, RpoB | C | 150 |
| SO0225 | 873 | DNA-directed RNA polymerase, beta subunit, RpoC | C | 156 |
| SOa0110 | 821 | lipoprotein, putative | OM | 146 |
| SO2593 | 86 | NAD-glutamate dehydrogenase family protein | C | 183 |

**A2**

| Gene | Mascot Score | Annotation | Category[a] | MW (kDa) |
|---|---|---|---|---|
| SO0432 | 1250 | aconitate hydratase 2, AcnB | C | 94 |
| SO2427 | 1122 | TonB-dependent receptor | OM | 92 |
| SO0424 | 543 | pyruvate dehydrogenase, E1 component, AceE | C | 100 |
| SO1429 | 474 | anaerobic dimethyl sulfoxide reductase | OM | 92 |
| SO2907 | 396 | TonB-dependent receptor domain protein | OM | 96 |
| SO1521 | 394 | respiratory FAD-dependent D-lactate dehydrogenase | C | 103 |
| SO3935 | 355 | ribonuclease R, Rnr | C | 91 |
| SO0781 | 216 | glycine dehydrogenase (decarboxylating), GcvP | C | 105 |
| SO3193 | 214 | polysaccharide biosynthesis/export protein, OtnA | OM | 100 |
| SO4692 | 209 | acridine efflux pump, AcrB/AcrD/AcrF family | IM | 112 |
| SO2606 | 114 | PqiB family protein | IM | 93 |
| SO1482 | 106 | TonB-dependent receptor | OM | 90 |
| SO1637 | 96 | outer membrane protein assembly factor, YaeT | OM | 92 |
| SO1174 | 66 | leucyl-tRNA synthetase, LeuS | C | 97 |
| SO3560 | 64 | subfamily M16B unassigned peptidases | OM | 105 |

**A3**

| Gene | Mascot Score | Annotation | Category[a] | MW (kDa) |
|---|---|---|---|---|
| SO0021 | 1050 | fatty oxidation complex, alpha subunit, FadB | C | 77 |
| SO1779 | 861 | Decaheme cytochrome c, OmcA | OM | 80 |
| SO1126 | 789 | chaperone protein, DnaK | C | 69 |
| SO3669 | 664 | TonB-dependent haem/haemoglobin receptor, HmuA | OM | 76 |
| SO1776 | 588 | outer membrane protein, MtrB | OM | 76 |
| SO0314 | 539 | ornithine decarboxylase, SpeF | C | 82 |
| SO1209 | 466 | polyribonucleotide nucleotidyltransferase, PnpA | C | 76 |
| SO0842 | 368 | translation elongation factor G, FusA_2 | C | 77 |
| SO2492 | 317 | oxidoreductase, acyl-CoA dehydrogenase family | IM | 83 |
| SO3033 | 300 | ferric alcaligin siderophore receptor, FauA | OM | 78 |
| SO4523 | 215 | TonB-dependent adherence-conferring protein, IrgA | OM | 73 |

| | | | | |
|---|---|---|---|---|
| SO0425 | 200 | dihydrolipoamide acetyltransferase, AceF | C | 70 |
| SO2912 | 208 | pyruvate formate-lyase, PflB | C | 85 |
| SO0228 | 154 | translation elongation factor G, FusA_1 | C | 77 |
| SO1894 | 119 | methylcrotonyl-CoA carboxylase, MccA | C | 76 |
| SO4743 | 82 | TonB-dependent receptor | OM | 76 |
| SO3844 | 73 | oligopeptidase lipoprotein, M13 family | OM | 77 |

**A4**

| Gene | Mascot Score | Annotation | Category[a] | MW (kDa) |
|---|---|---|---|---|
| SO3545 | 1469 | OmpA family protein | OM | 40 |
| SO1821 | 467 | outer membrane porin | OM | 44 |
| SO0256 | 217 | DNA-directed RNA polymerase, alpha subunit, RpoA | C | 36 |
| SO4693 | 134 | type I secretion membrane fusion protein, HlyD | OM | 40 |
| SO3896 | 109 | outer membrane porin, putative | OM | 40 |
| SO1164 | 56 | D-alanyl-D-alanine carboxypeptidase, DacA | P | 43 |

**A5**

| Gene | Mascot Score | Annotation | Category[a] | MW (kDa) |
|---|---|---|---|---|
| SO3896 | 7512 | Outer membrane porin, putative | OM | 40 |
| SO3545 | 645 | OmpA family protein | OM | 40 |
| SO2929 | 76 | expressed protein of unknown function | C | 41 |

**B1**

| Gene | Mascot Score | Annotation | Category[a] | MW (kDa) |
|---|---|---|---|---|
| SO3935 | 1135 | ribonuclease R, Rnr | C | 91 |
| SO2427 | 566 | TonB-dependent receptor | OM | 92 |
| SO0432 | 483 | aconitate hydratase 2, AcnB | C | 94 |
| SO1930 | 393 | 2-oxoglutarate dehydrogenase, E1 component, SucA | C | 105 |
| SO0424 | 327 | pyruvate dehydrogenase, E1 component, AceE | C | 100 |
| SO1521 | 177 | respiratory FAD-dependent D-lactate dehydrogenase | C | 103 |
| SO3193 | 151 | polysaccharide biosynthesis/export protein, OtnA | OM | 100 |
| SO2907 | 120 | TonB-dependent receptor domain protein | OM | 96 |
| SO4211 | 117 | preprotein translocase ATPase subunit, SecA | C | 103 |
| SO2411 | 62 | DNA gyrase subunit, GyrA | C | 102 |

**B2**

| Gene | Mascot Score | Annotation | Category[a] | MW (kDa) |
|---|---|---|---|---|
| SO1126 | 490 | chaperone protein, DnaK | C | 69 |
| SO1776 | 450 | outer membrane protein, MtrB | OM | 78 |
| SO1779 | 410 | Decaheme cytochrome c, OmcA | OM | 80 |

| | | | | |
|---|---|---|---|---|
| SO3669 | 335 | TonB-dependent haem/haemoglobin receptor, HmuA | OM | 76 |
| SO1778 | 332 | Decaheme cytochrome c, MtrC | OM | 72 |
| SO0314 | 291 | ornithine decarboxylase, SpeF | C | 82 |
| SO0021 | 188 | fatty oxidation complex, alpha subunit, FadB | C | 77 |
| SO2402 | 178 | ribosomal protein S1, RpsA | C | 61 |
| SO3844 | 141 | oligopeptidase lipoprotein, M13 family | OM | 77 |
| SO3033 | 140 | ferric alcaligin siderophore receptor, FauA | OM | 78 |
| SO2912 | 129 | pyruvate formate-lyase, PflB | C | 85 |
| SO2492 | 128 | oxidoreductase, acyl-CoA dehydrogenase family | IM | 84 |
| SO1209 | 124 | polyribonucleotide nucleotidyltransferase, PnpA | C | 76 |
| SO4743 | 101 | TonB-dependent receptor | OM | 77 |
| SO3142 | 97 | peptidyl-dipeptidase, Dcp_1 | OM | 80 |
| SO2629 | 76 | isocitrate dehydrogenase, NADP-dependent, Icd | C | 81 |

**B3**[b]

| **Gene** | **Mascot Score** | **Annotation** | **Category** | **MW (kDa)** |
|---|---|---|---|---|
| TRPGTR | 205 | Trypsin precursor | | 25 |
| I46732 | 171 | IG gamma heavy chain comstant region | | 21 |
| GHRB | 145 | IG gamma chain C region | | 36 |

[a] OM denotes outer membrane; P denotes periplasmic; IM denotes inner membrane; and C denotes cytoplasmic.

[b] B3 identification was performed using MSDB database with a mammalian taxonomy.

**Supplementary Table II - Peptide details for all identified proteins**

**Anti-OmcA IP / MRN**

| Gene | Annotation | Mascot_Score | MW (kDa) | Coverage% | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO1779** | Decaheme cytochrome c, OmcA | 789 | 79 | 30.0 | 468.31 | 934.61 | 934.49 | 0.12 | 0 | 31 | 0.017 | VPTSFAWK | |
| | | | | | 483.31 | 964.61 | 964.50 | 0.11 | 0 | 39 | 0.0022 | AWLYGDIK | |
| | | | | | 537.34 | 1072.67 | 1072.63 | 0.04 | 0 | 73 | 1.1e-006 | FGIAQLTPVK | |
| | | | | | 543.83 | 1085.64 | 1085.62 | 0.02 | 0 | 94 | 8e-009 | SNVVTGIALGR | |
| | | | | | 629.78 | 1257.54 | 1256.59 | 0.94 | 0 | 25 | 0.11 | EFISDPSAYTK | |
| | | | | | 650.76 | 1299.51 | 1299.62 | -0.11 | 0 | 77 | 3e-007 | YAYIQDQPFR | |
| | | | | | 670.78 | 1339.54 | 1339.66 | -0.12 | 0 | 53 | 0.0001 | TFTIDSTNSNLK | |
| | | | | | 671.30 | 1340.59 | 1340.65 | -0.06 | 0 | 48 | 0.00022 | GYQWQAYINAK | |
| | | | | | 535.25 | 1602.72 | 1601.78 | 0.94 | 0 | 46 | 0.00083 | HTFDATGAQVPAPYK | |
| | | | | | 802.73 | 1603.45 | 1603.82 | -0.37 | 0 | 95 | 5.8e-009 | NNALTFDVQILDNK | |
| | | | | | 696.25 | 2085.74 | 2086.05 | -0.31 | 0 | 54 | 5.2e-005 | DGEDGKPGVVGVNINSTSTLK | |
| | | | | | 714.61 | 2140.80 | 2140.05 | 0.75 | 0 | 66 | 7.6e-006 | SHIETNGGILNGTSAADVQTR | |
| | | | | | 748.28 | 2241.83 | 2242.16 | -0.33 | 1 | 21 | 0.091 | NNALTFDVQILDNKDQPIGK | |
| | | | | | 976.49 | 2926.45 | 2927.43 | -0.97 | 1 | 74 | 2.9e-007 | KEPGTVPSGVDNLNPSTQFQANVESANK | |
| **SO1778** | Decaheme cytochrome c, MtrC | 378 | 72 | 15.0 | 538.83 | 1075.64 | 1075.58 | 0.06 | 0 | 22 | 0.12 | VFNAQLTQR | |
| | | | | | 547.32 | 1092.63 | 1092.58 | 0.05 | 0 | 70 | 1.7e-006 | ADLAFATLSGK | |
| | | | | | 726.75 | 1451.48 | 1451.71 | -0.23 | 0 | 104 | 6.5e-010 | ETLESFGAVVDGTK | |
| | | | | | 878.15 | 1754.28 | 1754.78 | -0.50 | 0 | 80 | 1.5e-007 | FVDCADPAFDGVDVTK | |
| | | | | | 818.19 | 2451.55 | 2452.23 | -0.69 | 0 | 24 | 0.045 | ALQLIPEGATGPGNSANWQGLGSSK | |
| | | | | | 951.51 | 2851.51 | 2852.32 | -0.81 | 0 | 57 | 3.8e-005 | LADGTTVPVAEMVEDFDGQGNAPQYTK | |
| **SOa0110** | Lipoprotein, putative | 253 | 145 | 6.0 | 669.25 | 1336.49 | 1336.72 | -0.23 | 0 | 39 | 0.0035 | VIDSTTSAFAVVK | |
| | | | | | 699.28 | 1396.54 | 1396.74 | -0.19 | 0 | 69 | 2.4e-006 | VIYSTNNAFAAVK | |
| | | | | | 714.28 | 1426.55 | 1427.69 | -1.14 | 0 | 37 | 0.0053 | GVDQFTYLVSDGK | |
| | | | | | 720.21 | 1438.41 | 1438.72 | -0.31 | 0 | 36 | 0.0038 | QGATGITYTPGAFR | |
| | | | | | 721.78 | 1441.55 | 1441.71 | -0.16 | 0 | 99 | 2.5e-009 | GVDQFTYVITDGK | |
| | | | | | 722.90 | 1443.78 | 1443.80 | -0.02 | 0 | 40 | 0.0026 | LAPNLFLIETSIN | |
| | | | | | 735.19 | 1468.36 | 1468.66 | -0.30 | 0 | 68 | 3.5e-006 | ENASVDYTPGNFR | |
| **SO3545** | OmpA family protein | 228 | 40 | 18.0 | 755.31 | 1508.61 | 1508.85 | -0.23 | 0 | 41 | 0.0011 | GATLGLVGVWPLGNR | |
| | | | | | 903.64 | 1805.27 | 1805.88 | -0.61 | 0 | 48 | 0.00034 | QEDVGSIQFANDSAVVK | |
| | | | | | 602.98 | 1805.92 | 1804.97 | 0.95 | 0 | 70 | 1.4e-006 | VTSNGYGITKPLVAGNSK | |
| | | | | | 932.11 | 1862.21 | 1862.86 | -0.65 | 0 | 101 | 1.8e-009 | DLGSADWTTGGISNDAGVK | |
| | | | | | 645.63 | 1933.87 | 1933.97 | -0.11 | 1 | 32 | 0.0069 | KQEDVGSIQFANDSAVVK | |
| **SO3896** | Outer membrane porin, putative | 149 | 39 | 9.0 | 468.30 | 934.59 | 934.49 | 0.10 | 0 | 30 | 0.035 | GIAGIDAYR | |
| | | | | | 636.44 | 1270.86 | 1271.58 | -0.72 | 0 | 47 | 0.00061 | SADGVWYYSPK | |
| | | | | | 835.18 | 1668.34 | 1668.82 | -0.48 | 0 | 92 | 1.1e-008 | TNESLYALSATLGDSK | |
| **SO1295** | major outer membrane lipoprotein | 126 | 9 | 13.0 | 631.32 | 1260.63 | 1260.66 | -0.03 | 0 | 79 | 2.3e-007 | VDQLSADVSSLK | |
| **SO0404** | hypothetical protein | 112 | 129 | 4.0 | 807.73 | 1613.44 | 1613.81 | -0.37 | 0 | 53 | 8e-005 | FATTFEPYDLAALR | |
| | | | | | 819.73 | 1637.45 | 1637.82 | -0.37 | 0 | 43 | 0.00077 | FGALYNIEQNNSLR | |
| | | | | | 726.93 | 2177.78 | 2178.05 | -0.26 | 0 | 53 | 0.00018 | AQFEPGEVISQFSDSPEALK | |
| **SO1429** | anaerobic dimethyl sulfoxide reductase | 58 | 91 | 5.0 | 601.33 | 1200.65 | 1200.66 | -0.02 | 0 | 28 | 0.048 | APFIVTGAGVNR | |
| | | | | | 693.73 | 1385.44 | 1385.70 | -0.27 | 0 | 37 | 0.0036 | GTADLDTPLGADIK | |
| | | | | | 690.29 | 2067.86 | 2067.09 | 0.77 | 0 | 38 | 0.0039 | VAPGVVALGQGAWYQPDIAR | |
| **SO3099** | long chain fatty acid transport, putative | 57 | 47 | 4.0 | 845.35 | 1688.68 | 1689.87 | -1.19 | 0 | 42 | 0.0014 | AFAGDAVIADNATVLSR | |
| | | | | | 735.19 | 1468.36 | 1468.66 | -0.30 | 0 | 68 | 3.5e-006 | ENASVDYTPGNFR | |
| **SO2001** | 5-nucleotidase | 46 | 61 | 4.0 | 665.78 | 1329.54 | 1330.73 | -1.19 | 0 | 35 | 0.01 | IAVIGLTTEDTAK | |
| | | | | | 783.70 | 1565.38 | 1565.77 | -0.39 | 0 | 36 | 0.0039 | IGNPEYISELEFR | |
| **SO1824** | conserved hypothetical | 134 | 25 | 22.0 | 617.82 | 1233.62 | 1234.66 | -1.03 | 0 | 34 | 0.0079 | VALYAQSLDQK | |
| | | | | | 651.30 | 1300.59 | 1300.72 | -0.13 | 0 | 40 | 0.0018 | LLNTAEVTLAEK | |
| | | | | | 654.83 | 1307.65 | 1307.69 | -0.04 | 0 | 61 | 1.2e-005 | EVLVDFFNLGR | |
| | | | | | 850.24 | 1698.46 | 1699.81 | -1.35 | 0 | 27 | 0.049 | SYNDYVASLVADQQK | |
| **SO1825** | MotA/TolQ/ExbB proton channel protein | 174 | 48 | 9.0 | 654.29 | 1306.57 | 1307.67 | -1.10 | 0 | 43 | 0.0014 | FQGSVTAIDGSVK | |
| | | | | | 726.22 | 1450.42 | 1450.71 | -0.29 | 0 | 29 | 0.019 | TAQGDLGEMFGVVK | |
| | | | | | 865.17 | 1728.33 | 1728.78 | -0.46 | 0 | 92 | 1.1e-008 | FWQEQLFEMAESGK | |
| **SO3286** | cytochrome c ubiquinol oxidase | 105 | 58 | 10.0 | 596.35 | 1190.69 | 1190.65 | 0.05 | 0 | 33 | 0.01 | IPYAMGIVATR | |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | 660.30 | 1318.60 | 1318.68 | -0.08 | 0 | 29 | 0.039 | MIVEEVVELSR | Oxidation (M) |
| | | | | | 812.18 | 1622.35 | 1622.78 | -0.43 | 0 | 28 | 0.041 | YTNNVVDATEEQIK | |
| | | | | | 726.27 | 2175.79 | 2176.08 | -0.29 | 0 | 78 | 4.7e-007 | SLDEQVTGIHDLISEHEVR | |
| **SO4747** | ATP synthase F1, beta subunit | 100 | 49 | 5.0 | 683.29 | 1364.57 | 1365.73 | -1.16 | 0 | 48 | 0.00021 | DVLLFVDNIYR | |
| | | | | | 725.81 | 1449.61 | 1449.78 | -0.17 | 0 | 67 | 5.6e-006 | YTLAGTEVSALLGR | |
| **SO0217** | Translation elongation factor Tu | 79 | 43 | 11.0 | 593.34 | 1184.66 | 1184.64 | 0.02 | 0 | 32 | 0.019 | VGDEVEIVGIR | |
| | | | | | 950.16 | 1898.32 | 1899.00 | -0.68 | 0 | 39 | 0.0016 | ILELAAALDSYIPEPER | |
| | | | | | 726.97 | 2177.88 | 2178.10 | -0.22 | 0 | 53 | 0.00016 | DIDKPFLMPIEDVFSISGR | |
| **SO4749** | ATP synthase F1, alpha subunit | 54 | 55 | 12.0 | 661.76 | 1321.50 | 1321.65 | -0.15 | 0 | 28 | 0.031 | IEQFEVVSESR | |
| | | | | | 722.24 | 1442.46 | 1442.77 | -0.31 | 0 | 36 | 0.004 | NEGTIVAVSDGIIR | |
| | | | | | 928.69 | 1855.36 | 1855.86 | -0.50 | 0 | 30 | 0.024 | ELAAFSQFASDLDDATR | |
| | | | | | 765.95 | 2294.81 | 2294.13 | 0.69 | 0 | 27 | 0.057 | VGDFEAALLSYMNSEHAALIK | Oxidation (M) |

**Anti-MtrC IP / MRN**

| Gene | Annotation | Mascot_Score | MW (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO1779** | Decaheme cytochrome c, OmcA | 811 | 79 | 31.00 | 468.28 | 934.55 | 934.49 | 0.06 | 0 | 39 | 0.004 | VPTSFAWK | |
| | | | | | 483.28 | 964.54 | 964.50 | 0.04 | 0 | 30 | 0.023 | AWLYGDIK | |
| | | | | | 537.32 | 1072.62 | 1072.63 | -0.01 | 0 | 69 | 3.7e-006 | FGIAQLTPVK | |
| | | | | | 543.79 | 1085.57 | 1085.62 | -0.05 | 0 | 91 | 2.1e-008 | SNVVTGIALGR | |
| | | | | | 629.26 | 1256.50 | 1256.59 | -0.09 | 0 | 29 | 0.033 | EFISDPSAYTK | |
| | | | | | 650.75 | 1299.48 | 1299.62 | -0.15 | 0 | 69 | 2.6e-006 | YAYIQDQPFR | |
| | | | | | 670.71 | 1339.40 | 1339.66 | -0.27 | 0 | 38 | 0.0038 | TFTIDSTNSNLK | |
| | | | | | 671.24 | 1340.46 | 1340.65 | -0.20 | 0 | 53 | 0.00012 | GYQWQAYINAK | |
| | | | | | 534.87 | 1601.57 | 1601.78 | -0.21 | 0 | 54 | 0.00019 | HTFDATGAQVPAPYK | |
| | | | | | 802.70 | 1603.38 | 1603.82 | -0.44 | 0 | 95 | 1.2e-008 | NNALTFDVQILDNK | |
| | | | | | 942.03 | 1882.04 | 1882.84 | -0.79 | 0 | 37 | 0.0031 | GGYGVEDVVATPCSTDTR | |
| | | | | | 696.21 | 2085.59 | 2086.05 | -0.46 | 0 | 60 | 1.4e-005 | DGEDGKPGVVGVNINSTSTLK | |
| | | | | | 714.51 | 2140.50 | 2140.05 | 0.45 | 0 | 26 | 0.098 | SHIETNGGILNGTSAADVQTR | |
| | | | | | 748.24 | 2241.69 | 2242.16 | -0.47 | 1 | 31 | 0.024 | NNALTFDVQILDNKDQPIGK | |
| | | | | | 891.43 | 2671.27 | 2670.27 | 1.00 | 0 | 48 | 0.00047 | ATMELELPQLAANAHFDWQPSTGK | |
| | | | | | 976.39 | 2926.14 | 2927.43 | -1.28 | 1 | 69 | 1.2e-006 | KEPGTVPSGVDNLNPSTQFQANVESANK | |
| **SO1778** | Decaheme cytochrome c, MtrC | 343 | 72 | 7.0 | 538.76 | 1075.50 | 1075.58 | -0.08 | 0 | 74 | 1.1e-006 | VFNAQLTQR | |
| | | | | | 547.28 | 1092.55 | 1092.58 | -0.03 | 0 | 54 | 0.0001 | ADLAFATLSGK | |
| | | | | | 726.71 | 1451.40 | 1451.71 | -0.31 | 0 | 85 | 7.5e-008 | ETLESFGAVVDGTK | |
| | | | | | 878.08 | 1754.15 | 1754.78 | -0.63 | 0 | 87 | 3.5e-008 | FVDCADPAFDGVDVTK | |
| **SOa0110** | Lipoprotein, putative | 322 | 145 | 8.0 | 675.17 | 1348.32 | 1348.70 | -0.38 | 0 | 48 | 0.00072 | VIDSTNNAFAAVK | |
| | | | | | 678.73 | 1355.45 | 1355.71 | -0.26 | 0 | 46 | 0.00097 | VIYSNSSAFAAVK | |
| | | | | | 699.23 | 1396.44 | 1396.74 | -0.30 | 0 | 74 | 7.9e-007 | VIYSTNNAFAAVK | |
| | | | | | 720.20 | 1438.38 | 1438.72 | -0.34 | 0 | 59 | 3e-005 | QGATGITYTPGAFR | |
| | | | | | 721.70 | 1441.39 | 1441.71 | -0.32 | 0 | 98 | 3.3e-009 | GVDQFTYVITDGK | |
| | | | | | 735.10 | 1468.18 | 1468.66 | -0.48 | 0 | 30 | 0.023 | ENASVDYTPGNFR | |
| | | | | | 964.51 | 1927.00 | 1926.90 | 0.11 | 0 | 27 | 0.032 | STGETYIPTAADDGFNIR | |
| | | | | | 738.23 | 2211.68 | 2213.11 | -1.43 | 0 | 32 | 0.024 | LIADADGDALSIAHIYTANNR | |
| **SO3545** | OmpA family protein | 123 | 40 | 17 | 742.14 | 1482.27 | 1482.70 | -0.44 | 0 | 37 | 0.0037 | VDSVGCTLYENVK | |
| | | | | | 755.28 | 1508.55 | 1508.85 | -0.30 | 0 | 48 | 0.00052 | GATLGLVGVWPLGNR | |
| | | | | | 903.60 | 1805.19 | 1805.88 | -0.69 | 0 | 26 | 0.053 | QEDVGSIQFANDSAVVK | |
| | | | | | 932.08 | 1862.15 | 1862.86 | -0.72 | 0 | 55 | 6.3e-005 | DLGSADWTTGGISNDAGVK | |
| **SO3896** | Outer membrane porin, putative | 90 | 39 | 11.0 | 636.69 | 1271.36 | 1271.58 | -0.22 | 0 | 62 | 2.5e-005 | SADGVWYYSPK | |
| | | | | | 835.16 | 1668.31 | 1668.82 | -0.52 | 0 | 36 | 0.0043 | TNESLYALSATLGDSK | |
| | | | | | 587.61 | 1759.81 | 1759.97 | -0.17 | 0 | 44 | 0.0019 | YTEVQIIDGKPTVVAK | |
| **SO1295** | major outer membrane lipoprotein | 153 | 9 | 13.0 | 631.26 | 1260.51 | 1260.66 | -0.15 | 0 | 83 | 1.3e-007 | VDQLSADVSSLK | |
| **SO3286** | cytochrome c ubiquinol oxidase | 126 | 58 | 9.0 | 545.82 | 1089.62 | 1089.64 | -0.02 | 0 | 29 | 0.053 | VDLGYGLLLK | |
| | | | | | 604.27 | 1206.53 | 1206.64 | -0.11 | 0 | 49 | 0.00033 | IPYAMGIVATR | Oxidation (M) |
| | | | | | 660.22 | 1318.43 | 1318.68 | -0.25 | 0 | 50 | 0.00027 | MIVEEVVELSR | Oxidation (M) |
| | | | | | 726.31 | 2175.90 | 2176.08 | -0.18 | 0 | 52 | 0.0001 | SLDEQVTGIHDLISEHEVR | |
| **SO0217** | Translation elongation factor Tu | 91 | 43 | 7.0 | 592.73 | 1183.45 | 1184.64 | -1.19 | 0 | 62 | 1.5e-005 | VGDEVEIVGIR | |
| | | | | | 732.22 | 2193.63 | 2194.10 | -0.47 | 0 | 29 | 0.046 | DIDKPFLMPIEDVFSISGR | Oxidation (M) |

**Anti-OmcA IP / DSS**

| Gene | Annotation | Mascot_Score | MW (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO1779** | Decaheme cytochrome c, OmcA | 432 | 79 | 16.0 | 537.78 | 1073.54 | 1072.63 | 0.92 | 0 | 63 | 2.2e-005 | R.FGIAQLTPVK.E | |
| | | | | | 543.71 | 1085.40 | 1085.62 | -0.22 | 0 | 89 | 5.4e-008 | K.SNVVTGIALGR.S | |
| | | | | | 629.72 | 1257.43 | 1256.59 | 0.84 | 0 | 33 | 0.019 | K.EFISDPSAYTK.S | |
| | | | | | 650.71 | 1299.41 | 1299.62 | -0.22 | 0 | 60 | 4e-005 | R.YAYIQDQPFR.F | |
| | | | | | 670.64 | 1339.27 | 1339.66 | -0.40 | 0 | 49 | 0.00047 | K.TFTIDSTNSNLK.L | |
| | | | | | 535.18 | 1602.52 | 1601.78 | 0.73 | 0 | 46 | 0.00099 | R.HTFDATGAQVPAPYK.I | |
| | | | | | 696.18 | 2085.51 | 2086.05 | -0.55 | 0 | 40 | 0.0029 | K.DGEDGKPGVVGVNINSTSTLK.A | |
| | | | | | 977.02 | 2928.05 | 2927.43 | 0.63 | 1 | 51 | 0.00028 | K.KEPGTVPSGVDNLNPSTQFQANVESANK.C | |
| **SO1778** | Decaheme cytochrome c, MtrC | 49 | 72 | 3.0 | 547.27 | 1092.53 | 1092.58 | -0.05 | 0 | 33 | 0.023 | K.ADLAFATLSGK.A | |
| | | | | | 726.64 | 1451.27 | 1451.71 | -0.44 | 0 | 36 | 0.0099 | K.ETLESFGAVVDGTK.D | |
| **SO3545** | OmpA family protein | 45 | 40 | 8.0 | 742.66 | 1483.31 | 1482.70 | 0.61 | 0 | 32 | 0.024 | K.VDSVGCTLYENVK.K | |
| | | | | | 602.91 | 1805.72 | 1804.97 | 0.75 | 0 | 34 | 0.016 | R.VTSNGYGITKPLVAGNSK.E | |
| **SO3896** | Outer membrane porin, putative | 67 | 39 | 7.0 | 636.69 | 1271.36 | 1271.58 | -0.22 | 0 | 49 | 0.00047 | R.SADGVWYYSPK.I | |
| | | | | | 587.60 | 1759.77 | 1759.97 | -0.21 | 0 | 37 | 0.0077 | K.YTEVQIIDGKPTVVAK.S | |
| **SO1295** | major outer membrane lipoprotein | 78 | 9 | 13.0 | 631.26 | 1260.50 | 1260.66 | -0.16 | 0 | 61 | 3e-005 | K.VDQLSADVSSLK.S | |
| **SO1824** | conserved hypothetical | 51 | 25 | 9.0 | 596.76 | 1191.50 | 1191.65 | -0.15 | 0 | 30 | 0.043 | R.LILDAYSIER.D | |
| | | | | | 618.16 | 1234.31 | 1234.66 | -0.34 | 0 | 39 | 0.0042 | R.VALYAQSLDQK.T | |
| **SO1825** | MotA/TolQ/ExbB proton channel protein | 103 | 48 | 7.0 | 655.22 | 1308.43 | 1307.67 | 0.76 | 0 | 67 | 6e-006 | K.FQGSVTAIDGSVK.T | |
| | | | | | 726.22 | 1450.42 | 1450.71 | -0.29 | 0 | 29 | 0.019 | K.TAQGDLGEMFGVVK.S | |
| **SO0217** | Translation elongation factor Tu | 94 | 43 | 6.0 | 592.91 | 1183.82 | 1184.64 | -0.82 | 0 | 62 | 2.6e-005 | R.VGDEVEIVGIR.T | |
| | | | | | 732.22 | 2193.63 | 2194.10 | -0.47 | 0 | 29 | 0.046 | K.DIDKPFLMPIEDVFSISGR.E | Oxidation (M) |
| **SO0237** | ribosomal protein S3 | 141 | 25 | 11.0 | 672.21 | 1342.40 | 1341.73 | 0.67 | 0 | 77 | 5.8e-007 | K.LVADSIAQQLER.R | |
| | | | | | 734.16 | 1466.32 | 1465.83 | 0.49 | 0 | 46 | 0.00087 | K.LAGTPAQINIAEIR.K | |

**Anti-MtrC IP / DSS**

| **Gene** | **Annotation** | **Mascot_Score** | **MW (kDa)** | **Coverage** | **Observed m/z** | **Mr(expt)** | **Mr(calc)** | **Delta** | **Miss** | **Score** | **Expect** | **Peptide** | **Var_Mod** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO1779** | Decaheme cytochrome c, OmcA | 132 | 79 | 4.0 | 537.29 | 1072.56 | 1072.63 | -0.07 | 0 | 67 | 8.6e-006 | R.FGIAQLTPVK.E | |
| | | | | | 651.24 | 1300.47 | 1299.62 | 0.85 | 0 | 46 | 0.0013 | R.YAYIQDQPFR.F | |
| | | | | | 670.77 | 1339.52 | 1339.66 | -0.14 | 0 | 34 | 0.009 | K.TFTIDSTNSNLK.L | |
| **SO1778** | Decaheme cytochrome c, MtrC | 307 | 72 | 6.0 | 547.31 | 1092.60 | 1092.58 | 0.02 | 0 | 74 | 7.5e-007 | K.ADLAFATLSGK.A | |
| | | | | | 726.74 | 1451.46 | 1451.71 | -0.25 | 0 | 82 | 1.5e-007 | K.ETLESFGAVVDGTK.D | |
| | | | | | 878.11 | 1754.20 | 1754.78 | -0.58 | 0 | 84 | 1.5e-007 | K.FVDCADPAFDGVDVTK.Y | |
| **SO1295** | major outer membrane lipoprotein | 96 | 9 | 13.0 | 631.33 | 1260.64 | 1260.66 | -0.02 | 0 | 64 | 9.2e-006 | K.VDQLSADVSSLK.S | |
| **SO1825** | MotA/TolQ/ExbB proton channel protein | 87 | 48 | 5.0 | 654.79 | 1307.57 | 1307.67 | -0.10 | 0 | 55 | 6.2e-005 | K.FQGSVTAIDGSVK.T | |
| | | | | | 733.76 | 1465.51 | 1466.71 | -1.19 | 0 | 32 | 0.03 | K.TAQGDLGEMFGVVK.G | Oxidation (M) |
| **SO0217** | Translation elongation factor Tu | 146 | 43 | 11.0 | 593.34 | 1184.66 | 1184.64 | 0.02 | 0 | 90 | 4.3e-008 | R.VGDEVEIVGIR.T | |
| | | | | | 601.97 | 1802.88 | 1802.88 | -0.00 | 0 | 31 | 0.02 | R.GITINTSHIEYDTPSR.H | |
| | | | | | 732.53 | 2194.57 | 2194.10 | 0.47 | 0 | 39 | 0.0025 | R.DIDKPFLMPIEDVFSISGR.G | Oxidation (M) |
| **SO0237** | ribosomal protein S3 | 125 | 25 | 11.0 | 671.27 | 1340.53 | 1341.73 | -1.20 | 0 | 71 | 2.8e-006 | K.LVADSIAQQLER.R | |
| | | | | | 733.78 | 1465.55 | 1465.83 | -0.28 | 0 | 78 | 4e-007 | K.LAGTPAQINIAEIR.K | |

**Anti-OmcA IP / DST**

| **Gene** | **Annotation** | **Mascot_Score** | **MW (kDa)** | **Coverage** | **Observed m/z** | **Mr(expt)** | **Mr(calc)** | **Delta** | **Miss** | **Score** | **Expect** | **Peptide** | **Var_Mod** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO1779** | Decaheme cytochrome c, OmcA | 523 | 79 | 12.0 | 537.29 | 1072.57 | 1072.63 | -0.05 | 0 | 68 | 3.7e-006 | R.FGIAQLTPVK.E | |
| | | | | | 543.78 | 1085.55 | 1085.62 | -0.07 | 0 | 90 | 5.3e-008 | K.SNVVTGIALGR.S | |
| | | | | | 650.22 | 1298.43 | 1299.62 | -1.20 | 0 | 54 | 8.7e-005 | R.YAYIQDQPFR.F | |
| | | | | | 670.69 | 1339.37 | 1339.66 | -0.29 | 0 | 48 | 0.00044 | K.TFTIDSTNSNLK.L | |
| | | | | | 801.64 | 1601.27 | 1601.78 | -0.52 | 0 | 36 | 0.0075 | R.HTFDATGAQVPAPYK.I | |
| | | | | | 802.69 | 1603.36 | 1603.82 | -0.46 | 0 | 94 | 1.3e-008 | K.NNALTFDVQILDNK.D | |
| | | | | | 714.87 | 2141.59 | 2140.05 | 1.53 | 0 | 56 | 0.00012 | K.SHIETNGGILNGTSAADVQTR.A | |
| **SO1778** | Decaheme cytochrome c, MtrC | 118 | 72 | 3.0 | 547.29 | 1092.56 | 1092.58 | -0.02 | 0 | 60 | 4.5e-005 | K.ADLAFATLSGK.A | |
| | | | | | 726.72 | 1451.43 | 1451.71 | -0.29 | 0 | 61 | 2e-005 | K.ETLESFGAVVDGTK.D | |
| **SO3545** | OmpA family protein | 376 | 40 | 22.0 | 742.15 | 1482.29 | 1482.70 | -0.41 | 0 | 72 | 1.7e-006 | K.VDSVGCTLYENVK.K | |
| | | | | | 754.98 | 1507.95 | 1508.85 | -0.89 | 0 | 58 | 7.6e-005 | K.GATLGLVGVWPLGNR.W | |
| | | | | | 903.58 | 1805.14 | 1805.88 | -0.74 | 0 | 75 | 1.5e-006 | K.QEDVGSIQFANDSAVVK.K | |
| | | | | | 602.93 | 1805.77 | 1804.97 | 0.80 | 0 | 68 | 3.5e-006 | R.VTSNGYGITKPLVAGNSK.E | |
| | | | | | 932.09 | 1862.17 | 1862.86 | -0.70 | 0 | 105 | 8.2e-010 | R.DLGSADWTTGGISNDAGVK.G | |
| | | | | | 645.59 | 1933.74 | 1933.97 | -0.23 | 1 | 98 | 9e-009 | K.KQEDVGSIQFANDSAVVK.K | |
| **SO1295** | major outer membrane lipoprotein | 202 | 9 | 13.0 | 631.27 | 1260.53 | 1260.66 | -0.12 | 0 | 83 | 1.3e-007 | K.VDQLSADVSSLK.S | |
| **SO3286** | cytochrome c ubiquinol oxidase | 76 | 58 | 5.0 | 596.18 | 1190.34 | 1190.65 | -0.31 | 0 | 52 | 0.00035 | K.IPYAMGIVATR.S | |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  |  |  |  |  | 726.28 | 2175.83 | 2176.08 | -0.25 | 0 | 52 | 0.00017 | R.SLDEQVTGIHDLISEHEVR.I |  |
| **SO0217** | Translation elongation factor Tu | 231 | 43 | 21.0 | 593.28 | 1184.54 | 1184.64 | -0.10 | 0 | 100 | 4.9e-009 | R.VGDEVEIVGIR.T |  |
|  |  |  |  |  | 794.20 | 1586.39 | 1586.82 | -0.42 | 0 | 31 | 0.042 | K.VTLICPIAMDEGLR.F |  |
|  |  |  |  |  | 950.15 | 1898.28 | 1899.00 | -0.72 | 0 | 38 | 0.0071 | K.ILELAAALDSYIPEPER.D |  |
|  |  |  |  |  | 732.53 | 2194.58 | 2194.10 | 0.48 | 0 | 72 | 3.2e-006 | R.DIDKPFLMPIEDVFSISGR.G |  |
|  |  |  |  |  | 802.58 | 2404.72 | 2405.20 | -0.48 | 0 | 54 | 0.00022 | R.ELLSEYDFPGDDLPVIQGSALK.A |  |
| **SO1930** | 2-oxoglutarate dehydrogenase, sucA | 72 | 105 | 2.0 | 678.72 | 1355.43 | 1355.73 | -0.30 | 0 | 50 | 0.00051 | R.ILEGLNAAEGIEK.Y |  |
|  |  |  |  |  | 846.99 | 1691.96 | 1692.76 | -0.81 | 0 | 45 | 0.0015 | R.EWDEAYDASLPIER.L |  |

**Anti-MtrC IP / DST**

| **Gene** | **Annotation** | **Mascot_Score** | **MW (kDa)** | **Coverage** | **Observed m/z** | **Mr(expt)** | **Mr(calc)** | **Delta** | **Miss** | **Score** | **Expect** | **Peptide** | **Var_Mod** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO1778** | Decaheme cytochrome c, MtrC | 136 | 72 | 4.0 | 726.78 | 1451.54 | 1451.71 | -0.18 | 0 | 75 | 1.4e-006 | K.ETLESFGAVVDGTK.D |  |
|  |  |  |  |  | 878.12 | 1754.23 | 1754.78 | -0.56 | 0 | 54 | 9e-005 | K.FVDCADPAFDGVDVTK.Y |  |
| **SO3545** | OmpA family protein | 189 | 40 | 18.0 | 742.15 | 1482.30 | 1482.70 | -0.41 | 0 | 51 | 0.00044 | K.VDSVGCTLYENVK.K |  |
|  |  |  |  |  | 602.99 | 1805.96 | 1804.97 | 0.99 | 0 | 53 | 0.00028 | R.VTSNGYGITKPLVAGNSK.E |  |
|  |  |  |  |  | 932.05 | 1862.08 | 1862.86 | -0.78 | 0 | 77 | 8.9e-007 | R.DLGSADWTTGGISNDAGVK.G |  |
|  |  |  |  |  | 645.36 | 1933.05 | 1933.97 | -0.93 | 1 | 66 | 5.8e-006 | K.KQEDVGSIQFANDSAVVK.K |  |
| **SO3896** | Outer membrane porin, putative | 97 | 39 | 4.0 | 636.15 | 1270.28 | 1271.58 | -1.30 | 0 | 70 | 5.8e-006 | R.SADGVWYYSPK.I |  |
|  |  |  |  |  | 587.60 | 1759.77 | 1759.97 | -0.21 | 0 | 37 | 0.0077 | K.YTEVQIIDGKPTVVAK.S |  |
| **SO1295** | major outer membrane lipoprotein | 153 | 9 | 13.0 | 631.27 | 1260.54 | 1260.66 | -0.12 | 0 | 82 | 1.4e-007 | K.VDQLSADVSSLK.S |  |
| **SO0217** | Translation elongation factor Tu | 120 | 43 | 8.0 | 593.83 | 1185.65 | 1184.64 | 1.01 | 0 | 88 | 3.3e-008 | R.VGDEVEIVGIR.T |  |
|  |  |  |  |  | 802.57 | 2404.69 | 2405.20 | -0.51 | 0 | 31 | 0.041 | R.ELLSEYDFPGDDLPVIQGSALK.A |  |

**ΔMtrC / Anti-OmcA IP / MRN**

| **Gene** | **Annotation** | **Mascot_Score** | **MW (kDa)** | **Coverage** | **Observed m/z** | **Mr(expt)** | **Mr(calc)** | **Delta** | **Miss** | **Score** | **Expect** | **Peptide** | **Var_Mod** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO1779** | Decaheme cytochrome c, OmcA | 971 | 79 | 24.0 | 537.32 | 1072.62 | 1072.63 | -0.01 | 0 | 63 | 1.2e-005 | R.FGIAQLTPVK.E |  |
|  |  |  |  |  | 543.81 | 1085.60 | 1085.62 | -0.02 | 0 | 96 | 5.7e-009 | K.SNVVTGIALGR.S |  |
|  |  |  |  |  | 650.76 | 1299.50 | 1299.62 | -0.12 | 0 | 55 | 8.6e-005 | R.YAYIQDQPFR.F |  |
|  |  |  |  |  | 670.74 | 1339.46 | 1339.66 | -0.20 | 0 | 45 | 0.00072 | K.TFTIDSTNSNLK.L |  |
|  |  |  |  |  | 671.27 | 1340.52 | 1340.65 | -0.13 | 0 | 62 | 1.2e-005 | R.GYQWQAYINAK.K |  |
|  |  |  |  |  | 534.93 | 1601.78 | 1601.78 | -0.00 | 0 | 69 | 5.3e-006 | R.HTFDATGAQVPAPYK.I |  |
|  |  |  |  |  | 802.71 | 1603.41 | 1603.82 | -0.41 | 0 | 125 | 1e-011 | K.NNALTFDVQILDNK.D |  |
|  |  |  |  |  | 942.09 | 1882.16 | 1882.84 | -0.68 | 0 | 59 | 2.5e-005 | K.GGYGVEDVVATPCSTDTR.Y |  |
|  |  |  |  |  | 696.26 | 2085.74 | 2086.05 | -0.31 | 0 | 57 | 3.6e-005 | K.DGEDGKPGVVGVNINSTSTLK.A |  |
|  |  |  |  |  | 714.18 | 2139.52 | 2140.05 | -0.53 | 0 | 44 | 0.0021 | K.SHIETNGGILNGTSAADVQTR.A |  |
|  |  |  |  |  | 748.24 | 2241.69 | 2242.16 | -0.47 | 1 | 31 | 0.038 | K.NNALTFDVQILDNKDQPIGK.E |  |
|  |  |  |  |  | 976.49 | 2926.44 | 2927.43 | -0.98 | 1 | 70 | 3.7e-006 | K.KEPGTVPSGVDNLNPSTQFQANVESANK.C |  |
| **SOa0110** | Lipoprotein, putative | 308 | 145 | 7.0 | 669.29 | 1336.57 | 1336.72 | -0.15 | 0 | 47 | 0.00085 | K.VIDSTTSAFAVVK.E |  |
|  |  |  |  |  | 678.79 | 1355.57 | 1355.71 | -0.14 | 0 | 34 | 0.015 | K.VIYSNSSAFAAVK.Q |  |
|  |  |  |  |  | 699.28 | 1396.55 | 1396.74 | -0.19 | 0 | 73 | 1.1e-006 | K.VIYSTNNAFAAVK.E |  |
|  |  |  |  |  | 714.76 | 1427.51 | 1427.69 | -0.18 | 0 | 68 | 3.1e-006 | R.GVDQFTYLVSDGK.G |  |
|  |  |  |  |  | 720.22 | 1438.43 | 1438.72 | -0.29 | 0 | 56 | 5.5e-005 | K.QGATGITYTPGAFR.G |  |
|  |  |  |  |  | 721.74 | 1441.47 | 1441.71 | -0.24 | 0 | 94 | 9.5e-009 | R.GVDQFTYVITDGK.D |  |
|  |  |  |  |  | 722.49 | 1442.96 | 1443.80 | -0.84 | 0 | 40 | 0.0045 | K.LAPNLFLIETSIN.- |  |
|  |  |  |  |  | 735.18 | 1468.35 | 1468.66 | -0.30 | 0 | 54 | 0.00012 | K.ENASVDYTPGNFR.G |  |
| **SO3545** | OmpA family protein | 472 | 40 | 17.0 | 742.22 | 1482.42 | 1482.70 | -0.28 | 0 | 77 | 4.2e-007 | K.VDSVGCTLYENVK.K |  |
|  |  |  |  |  | 755.28 | 1508.54 | 1508.85 | -0.30 | 0 | 90 | 1.9e-008 | K.GATLGLVGVWPLGNR.W |  |
|  |  |  |  |  | 903.65 | 1805.28 | 1805.88 | -0.60 | 0 | 87 | 4.8e-008 | K.QEDVGSIQFANDSAVVK.K |  |
|  |  |  |  |  | 932.12 | 1862.23 | 1862.86 | -0.63 | 0 | 133 | 9e-013 | R.DLGSADWTTGGISNDAGVK.G |  |
|  |  |  |  |  | 645.62 | 1933.82 | 1933.97 | -0.15 | 1 | 90 | 1.8e-008 | K.KQEDVGSIQFANDSAVVK.K |  |
| **SO3896** | Outer membrane porin, putative | 100 | 39 | 11.0 | 636.76 | 1271.50 | 1271.58 | -0.08 | 0 | 47 | 0.00081 | R.SADGVWYYSPK.I |  |
|  |  |  |  |  | 835.17 | 1668.34 | 1668.82 | -0.49 | 0 | 45 | 0.00077 | K.TNESLYALSATLGDSK.F |  |
|  |  |  |  |  | 587.59 | 1759.76 | 1759.97 | -0.21 | 0 | 47 | 0.00044 | K.YTEVQIIDGKPTVVAK.S |  |
| **SO1295** | major outer membrane lipoprotein | 183 | 9 | 13.0 | 631.28 | 1260.56 | 1260.66 | -0.10 | 0 | 82 | 1.3e-007 | K.VDQLSADVSSLK.S |  |
| **SO1824** | conserved hypothetical | 69 | 25 | 10.0 | 651.24 | 1300.47 | 1300.72 | -0.25 | 0 | 28 | 0.079 | R.LLNTAEVTLAEK.Y |  |
|  |  |  |  |  | 654.30 | 1306.59 | 1307.69 | -1.09 | 0 | 69 | 2.4e-006 | K.EVLVDFFNLGR.V |  |
| **SO3286** | cytochrome c ubiquinol oxidase | 68 | 58 | 5.0 | 596.37 | 1190.73 | 1190.65 | 0.08 | 0 | 32 | 0.03 | K.IPYAMGIVATR.S |  |
|  |  |  |  |  | 726.63 | 2176.86 | 2176.08 | 0.78 | 0 | 57 | 3.9e-005 | R.SLDEQVTGIHDLISEHEVR.I |  |
| **SO4747** | ATP synthase F1, beta subunit | 108 | 49 | 5.0 | 683.76 | 1365.51 | 1365.73 | -0.22 | 0 | 37 | 0.0031 | R.DVLLFVDNIYR.Y |  |
|  |  |  |  |  | 725.78 | 1449.56 | 1449.78 | -0.23 | 0 | 93 | 2.2e-008 | R.YTLAGTEVSALLGR.M |  |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO0217** | Translation elongation factor Tu | 82 | 43 | 4.0 | 593.34 | 1184.66 | 1184.64 | 0.02 | 0 | 82 | 1.1e-007 | R.VGDEVEIVGIR.T | |
| | | | | | 601.97 | 1802.88 | 1802.88 | -0.00 | 0 | 31 | 0.02 | R.GITINTSHIEYDTPSR.H | |

**ΔOmcA / Anti-MtrC IP / MRN**

| Gene | Annotation | Mascot_Score | MW (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO1778** | Decaheme cytochrome c, MtrC | 333 | 72 | 6.0 | 547.28 | 1092.55 | 1092.58 | -0.03 | 0 | 81 | 1.6e-007 | K.ADLAFATLSGK.A | |
| | | | | | 726.69 | 1451.36 | 1451.71 | -0.35 | 0 | 97 | 5.8e-009 | K.ETLESFGAVVDGTK.D | |
| | | | | | 878.08 | 1754.15 | 1754.78 | -0.63 | 0 | 76 | 5.4e-007 | K.FVDCADPAFDGVDVTK.Y | |
| **SO1295** | major outer membrane lipoprotein | 179 | 9 | 13.0 | 631.25 | 1260.48 | 1260.66 | -0.17 | 0 | 82 | 1.6e-007 | K.VDQLSADVSSLK.S | |

**ΔMtrC / Anti-OmcA IP / DSS**

| Gene | Annotation | Mascot_Score | MW (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO1779** | Decaheme cytochrome c, OmcA | 476 | 79 | 17.0 | 537.33 | 1072.64 | 1072.63 | 0.01 | 0 | 80 | 2.4e-007 | R.FGIAQLTPVK.E | |
| | | | | | 543.84 | 1085.67 | 1085.62 | 0.05 | 0 | 96 | 6.4e-009 | K.SNVVTGIALGR.S | |
| | | | | | 629.29 | 1256.57 | 1256.59 | -0.03 | 0 | 32 | 0.014 | K.EFISDPSAYTK.S | |
| | | | | | 650.74 | 1299.47 | 1299.62 | -0.16 | 0 | 61 | 3.9e-005 | R.YAYIQDQPFR.F | |
| | | | | | 670.78 | 1339.54 | 1339.66 | -0.12 | 0 | 43 | 0.0013 | K.TFTIDSTNSNLK.L | |
| | | | | | 671.25 | 1340.49 | 1340.65 | -0.16 | 0 | 34 | 0.007 | R.GYQWQAYINAK.K | |
| | | | | | 802.69 | 1603.37 | 1603.82 | -0.45 | 0 | 71 | 2.2e-006 | K.NNALTFDVQILDNK.D | |
| | | | | | 714.54 | 2140.60 | 2140.05 | 0.55 | 0 | 42 | 0.0027 | K.SHIETNGGILNGTSAADVQTR.A | |
| | | | | | 934.08 | 2799.22 | 2799.33 | -0.11 | 0 | 26 | 0.085 | K.EPGTVPSGVDNLNPSTQFQANVESANK.C | |
| **SO3545** | OmpA family protein | 149 | 40 | 22.0 | 742.22 | 1482.42 | 1482.70 | -0.28 | 0 | 33 | 0.012 | K.VDSVGCTLYENVK.K | |
| | | | | | 755.26 | 1508.51 | 1508.85 | -0.34 | 0 | 73 | 1.1e-006 | K.GATLGLVGVWPLGNR.W | |
| | | | | | 602.52 | 1804.55 | 1804.97 | -0.42 | 0 | 32 | 0.032 | R.VTSNGYGITKPLVAGNSK.E | |
| | | | | | 932.13 | 1862.24 | 1862.86 | -0.63 | 0 | 58 | 2.9e-005 | R.DLGSADWTTGGISNDAGVK.G | |
| | | | | | 645.63 | 1933.88 | 1933.97 | -0.09 | 1 | 52 | 0.00012 | K.KQEDVGSIQFANDSAVVK.K | |
| **SO3896** | Outer membrane porin, putative | 125 | 39 | 11.0 | 636.30 | 1270.59 | 1271.58 | -0.99 | 0 | 54 | 0.00016 | R.SADGVWYYSPK.I | |
| | | | | | 835.19 | 1668.36 | 1668.82 | -0.46 | 0 | 62 | 1.5e-005 | K.TNESLYALSATLGDSK.F | |
| | | | | | 587.73 | 1760.18 | 1759.97 | 0.21 | 0 | 31 | 0.018 | K.YTEVQIIDGKPTVVAK.S | |
| **SO1295** | major outer membrane lipoprotein | 153 | 9 | 13.0 | 631.32 | 1260.62 | 1260.66 | -0.04 | 0 | 88 | 3.4e-008 | K.VDQLSADVSSLK.S | |
| **SO0237** | ribosomal protein S3 | 105 | 25 | 11.0 | 671.80 | 1341.58 | 1341.73 | -0.14 | 0 | 64 | 8.5e-006 | K.LVADSIAQQLER.R | |
| | | | | | 733.18 | 1464.35 | 1465.83 | -1.48 | 0 | 46 | 0.00098 | K.LAGTPAQINIAEIR.K | |

**ΔOmcA / Anti-MtrC IP / DSS**

| Gene | Annotation | Mascot_Score | MW (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO1778** | Decaheme cytochrome c, MtrC | 312 | 72 | 6.0 | 547.29 | 1092.57 | 1092.58 | -0.01 | 0 | 72 | 1.2e-006 | K.ADLAFATLSGK.A | |
| | | | | | 726.75 | 1451.48 | 1451.71 | -0.23 | 0 | 92 | 1.5e-008 | K.ETLESFGAVVDGTK.D | |
| | | | | | 878.13 | 1754.24 | 1754.78 | -0.55 | 0 | 71 | 1.6e-006 | K.FVDCADPAFDGVDVTK.Y | |
| **SO1295** | major outer membrane lipoprotein | 106 | 9 | 13.0 | 631.35 | 1260.68 | 1260.66 | 0.02 | 0 | 68 | 3.4e-006 | K.VDQLSADVSSLK.S | |
| **SO1490** | alcohol dehydrogenase II, AdhB | 306 | 40 | 29.0 | 537.30 | 1072.58 | 1072.54 | 0.04 | 0 | 66 | 1.2e-005 | K.GAVDDAIGDIK.T | |
| | | | | | 562.76 | 1123.51 | 1123.53 | -0.02 | 0 | 24 | 0.071 | R.FCIITDEAR.H | |
| | | | | | 600.88 | 1199.74 | 1199.69 | 0.06 | 0 | 35 | 0.014 | K.GIALVATNGGSIK.D | |
| | | | | | 685.78 | 1369.54 | 1369.71 | -0.17 | 0 | 73 | 1e-006 | K.AEDIPTLADNALK.D | |
| | | | | | 741.32 | 1480.62 | 1480.86 | -0.24 | 0 | 55 | 6e-005 | K.AIELIQGNLVNAVK.Q | |
| | | | | | 753.72 | 1505.43 | 1505.74 | -0.31 | 0 | 95 | 5.9e-009 | K.MTDEQGAAAAITAIK.T | Oxidation (M) |
| | | | | | 608.62 | 1822.82 | 1822.95 | -0.13 | 0 | 36 | 0.011 | K.HTTPILSVNDPELMLK.K | Oxidation (M) |
| | | | | | 801.51 | 2401.51 | 2402.25 | -0.74 | 0 | 32 | 0.012 | K.STKPQLPLVAINTTAGTASEMTR.F | Oxidation (M) |
| **SO0217** | Translation elongation factor Tu | 179 | 43 | 20.0 | 593.29 | 1184.58 | 1184.64 | -0.06 | 0 | 69 | 2.5e-006 | R.VGDEVEIVGIR.T | |
| | | | | | 710.73 | 1419.44 | 1419.63 | -0.19 | 0 | 29 | 0.034 | K.DFSQIDNAPEER.E | |
| | | | | | 633.99 | 1898.94 | 1899.00 | -0.06 | 0 | 32 | 0.023 | K.ILELAAALDSYIPEPER.D | |
| | | | | | 732.23 | 2193.65 | 2194.10 | -0.44 | 0 | 67 | 8.7e-006 | R.DIDKPFLMPIEDVFSISGR.G | Oxidation (M) |
| | | | | | 802.53 | 2404.56 | 2405.20 | -0.64 | 0 | 52 | 0.00012 | R.ELLSEYDFPGDDLPVIQGSALK.A | |
| **SO0314** | Ornithine Decarboxylase | 57 | 82 | 3.0 | 731.75 | 1461.49 | 1461.77 | -0.28 | 0 | 38 | 0.0039 | K.FLLTTPGIDAETGK.Y | |
| | | | | | 781.17 | 1560.32 | 1560.76 | -0.44 | 0 | 35 | 0.013 | K.VMDPQEANLEFIR.G | |

**Cell lysate / Anti-OmcA IP / DSS**

| Gene | Annotation | Mascot_Score | MW (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO0225** | DNA-directed RNA polymerase, rpoC | 1928 | 156 | 33.0 | 521.78 | 1041.55 | 1041.62 | -0.07 | 0 | 37 | 0.0056 | R.SVITVGPTLR.L | |
| | | | | | 527.78 | 1053.55 | 1053.62 | -0.07 | 0 | 74 | 8.6e-007 | K.IGLASPDLIR.S | |
| | | | | | 601.29 | 1200.56 | 1200.65 | -0.09 | 0 | 105 | 7.4e-010 | K.MGAEAVLELLR.A | |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | 615.75 | 1229.49 | 1229.62 | -0.13 | 0 | 74 | 1.1e-006 | K.AYATGAAELHAR.V | |
| | | | | | 623.25 | 1244.49 | 1244.64 | -0.15 | 0 | 46 | 0.0013 | K.VIDIWASANEK.V | |
| | | | | | 637.22 | 1272.42 | 1273.61 | -1.19 | 0 | 33 | 0.013 | R.EELPSINSETR.R | |
| | | | | | 645.71 | 1289.40 | 1289.68 | -0.27 | 0 | 39 | 0.0054 | R.LIPAGTGYAYHK.T | |
| | | | | | 651.75 | 1301.48 | 1301.68 | -0.21 | 0 | 109 | 3.6e-010 | R.SSELAIIDELGR.E | |
| | | | | | 654.82 | 1307.62 | 1307.78 | -0.16 | 0 | 59 | 2.3e-005 | R.LLDLAAPDIIVR.N | |
| | | | | | 657.72 | 1313.42 | 1313.63 | -0.21 | 0 | 84 | 9.7e-008 | R.FATSDLNDLYR.R | |
| | | | | | 692.74 | 1383.47 | 1383.65 | -0.19 | 0 | 77 | 4.9e-007 | K.FVDMIDGVTMTR.Q | |
| | | | | | 695.20 | 1388.38 | 1388.68 | -0.30 | 0 | 55 | 7.9e-005 | R.ITETIIDENGER.S | |
| | | | | | 757.26 | 1512.50 | 1512.86 | -0.35 | 0 | 56 | 5.9e-005 | R.LGIQAFEPVLIEGK.A | |
| | | | | | 780.66 | 1559.31 | 1559.76 | -0.46 | 0 | 46 | 0.00073 | R.MLQESVDALLDNGR.R | |
| | | | | | 788.65 | 1575.28 | 1575.69 | -0.42 | 0 | 70 | 5.5e-006 | R.GEGMYFMSVAEVEK.A | |
| | | | | | 804.63 | 1607.24 | 1607.76 | -0.53 | 0 | 95 | 1.6e-008 | K.AMMENLSTETVINR.D | |
| | | | | | 831.63 | 1661.25 | 1661.84 | -0.58 | 0 | 75 | 7.5e-007 | R.GEVIADGPEAAHDILR.L | |
| | | | | | 836.20 | 1670.38 | 1670.85 | -0.47 | 0 | 92 | 1.8e-008 | R.EVAEVWDVLDEVIR.E | |
| | | | | | 602.27 | 1803.80 | 1803.93 | -0.13 | 0 | 47 | 0.001 | R.EGLNVLQYFISTHGAR.K | |
| | | | | | 973.63 | 1945.25 | 1946.01 | -0.76 | 0 | 71 | 1.6e-006 | R.VVAVDVFYPGTEDVLAPR.N | |
| | | | | | 655.96 | 1964.86 | 1964.03 | 0.82 | 0 | 73 | 2e-006 | R.MGHIELASPVAHIWFLK.S | Oxidation (M) |
| | | | | | 995.55 | 1989.08 | 1988.98 | 0.11 | 0 | 66 | 6e-006 | R.LVITPADGGEQYEEMIPK.W | |
| | | | | | 674.96 | 2021.86 | 2022.20 | -0.34 | 0 | 35 | 0.0076 | K.VLPVLPPDLRPLVPLDGGR.F | |
| | | | | | 1018.60 | 2035.19 | 2036.01 | -0.83 | 0 | 60 | 2.4e-005 | R.YATISGASVGIDDMVIPAEK.Y | |
| | | | | | 701.87 | 2102.57 | 2102.05 | 0.52 | 0 | 65 | 1.5e-005 | R.GIHNVANYIVNEVQDVYR.L | |
| | | | | | 709.93 | 2126.76 | 2128.13 | -1.37 | 0 | 56 | 8e-005 | R.GLMAKPDGSIIETPIVANFR.E | |
| | | | | | 725.23 | 2172.66 | 2172.05 | 0.61 | 0 | 30 | 0.053 | K.ITASEAEQNLADLLNLAGSQD.- | |
| | | | | | 714.74 | 2854.91 | 2855.47 | -0.56 | 0 | 48 | 0.00042 | R.GHIINHGEAIGVVAAQSIGEPGTQLTMR.T | |
| | | | | | 1022.77 | 3065.28 | 3065.52 | -0.24 | 0 | 114 | 2.3e-010 | K.YTLVADAEAEVLEIQEQFQSGLVTAGER.Y | |
| | | | | | 828.59 | 3310.31 | 3311.67 | -1.35 | 0 | 29 | 0.03 | K.LEEASVEAGDIIANWDPHTHPIITEVAGSIK.F | |
| **SO0224** | DNA-directed RNA polymerase, rpoB | 1431 | 150 | 32.0 | 521.25 | 1040.49 | 1040.60 | -0.11 | 0 | 59 | 2.2e-005 | R.ISALGPGGLTR.E | |
| | | | | | 576.15 | 1150.29 | 1150.56 | -0.28 | 0 | 35 | 0.015 | R.GGVIDYVDASR.I | |
| | | | | | 608.67 | 1215.33 | 1215.61 | -0.28 | 0 | 46 | 0.0014 | K.DAEGTVLVEAGR.R | |
| | | | | | 634.17 | 1266.32 | 1266.57 | -0.24 | 0 | 69 | 2.3e-006 | R.SVGEMAENQFR.V | |
| | | | | | 637.25 | 1272.48 | 1272.67 | -0.20 | 0 | 49 | 0.00032 | K.DTLVMTLVPER.L | |
| | | | | | 650.74 | 1299.47 | 1299.68 | -0.22 | 0 | 50 | 0.00026 | K.GGIPVATPAFDGAK.E | |
| | | | | | 654.24 | 1306.46 | 1306.66 | -0.20 | 1 | 38 | 0.0033 | K.RGGVIDYVDASR.I | |
| | | | | | 663.71 | 1325.41 | 1325.72 | -0.31 | 0 | 62 | 1.5e-005 | K.ITQGDDLAPGVLK.I | |
| | | | | | 670.73 | 1339.45 | 1339.61 | -0.16 | 0 | 64 | 1.1e-005 | R.GSWLDFEFDPK.D | |
| | | | | | 708.69 | 1415.36 | 1415.71 | -0.35 | 0 | 48 | 0.00049 | R.LSIPDDEGSGVLSK.E | |
| | | | | | 724.20 | 1446.38 | 1446.68 | -0.30 | 0 | 71 | 2.5e-006 | R.TNSYGFLETPYR.K | |
| | | | | | 727.74 | 1453.46 | 1453.81 | -0.35 | 1 | 42 | 0.0017 | R.KITQGDDLAPGVLK.I | |
| | | | | | 732.14 | 1462.27 | 1462.71 | -0.43 | 0 | 88 | 5.2e-008 | K.QVYELGDEVQQR.V | |
| | | | | | 736.22 | 1470.42 | 1470.79 | -0.38 | 1 | 88 | 4.3e-008 | R.KDVLVQVIDDEAK.Q | |
| | | | | | 755.79 | 1509.57 | 1509.76 | -0.19 | 0 | 43 | 0.00095 | R.AIEIEEMHIAQAR.K | |
| | | | | | 769.18 | 1536.34 | 1536.73 | -0.39 | 0 | 85 | 1e-007 | R.VDIDSFTDDELLR.L | |
| | | | | | 793.23 | 1584.44 | 1584.85 | -0.41 | 0 | 76 | 5.7e-007 | K.QMLELAGLPTSGQLK.L | |
| | | | | | 804.59 | 1607.17 | 1607.75 | -0.58 | 0 | 70 | 2.2e-006 | K.SFSGNSELQYVSYK.L | |
| | | | | | 811.65 | 1621.28 | 1621.83 | -0.55 | 0 | 73 | 1.3e-006 | R.STGSYSLVTQQPLGGK.A | |
| | | | | | 572.89 | 1715.64 | 1714.75 | 0.88 | 0 | 36 | 0.0054 | R.NGFDEVDDIDHLGNR.R | |
| | | | | | 896.15 | 1790.28 | 1790.93 | -0.65 | 0 | 48 | 0.00037 | K.TNTTELEVPVEYIVGK.Y | |
| | | | | | 608.90 | 1823.68 | 1823.89 | -0.21 | 0 | 38 | 0.0088 | K.QTELEQLAEQHEELK.A | |
| | | | | | 624.26 | 1869.76 | 1870.03 | -0.27 | 0 | 50 | 0.00048 | R.NLLLSAGFSEAQIAALPR.K | |
| | | | | | 987.09 | 1972.17 | 1972.98 | -0.80 | 0 | 83 | 1.1e-007 | R.ALEYSTQEILDLFFER.V | |
| | | | | | 1015.09 | 2028.17 | 2029.02 | -0.86 | 0 | 59 | 3e-005 | K.LGSEEITADIPNVGESALSK.L | |
| | | | | | 731.54 | 2191.60 | 2192.08 | -0.49 | 0 | 28 | 0.041 | K.VVDGVITDEVEYLSAIEEGR.Y | |
| | | | | | 748.93 | 2243.76 | 2244.25 | -0.49 | 0 | 69 | 3.9e-006 | K.RPQVLDIPYLLSIQLDSFK.K | |
| | | | | | 749.18 | 2244.53 | 2245.12 | -0.59 | 0 | 97 | 6.4e-009 | K.VNEDELRPGEAGIDIYNLTK.Y | |
| | | | | | 774.18 | 2319.52 | 2320.18 | -0.66 | 1 | 52 | 0.00016 | R.KVVDGVITDEVEYLSAIEEGR.Y | |
| | | | | | 800.86 | 2399.56 | 2401.14 | -1.58 | 0 | 29 | 0.07 | R.IAFMPWNGYNFEDSILISER.V | |
| | | | | | 808.15 | 2421.44 | 2422.20 | -0.76 | 0 | 40 | 0.0055 | K.ELSTLYINELDHGAYISDTLR.I | |
| | | | | | 823.46 | 2467.36 | 2467.20 | 0.16 | 0 | 44 | 0.0018 | K.NIVDGNHQMQPGMPESFNVLLK.E | |
| **SO1490** | alcohol dehydrogenase II, AdhB | 987 | 40 | 55.0 | 537.21 | 1072.40 | 1072.54 | -0.14 | 0 | 75 | 7.2e-007 | K.GAVDDAIGDIK.T | |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | 562.73 | 1123.44 | 1123.53 | -0.09 | 0 | 37 | 0.0038 | R.FCIITDEAR.H | |
| | | | | | 601.24 | 1200.46 | 1199.69 | 0.77 | 0 | 38 | 0.0042 | K.GIALVATNGGSIK.D | |
| | | | | | 610.83 | 1219.65 | 1219.70 | -0.05 | 0 | 38 | 0.0041 | K.FFIPSVNVLGK.G | |
| | | | | | 685.73 | 1369.45 | 1369.71 | -0.26 | 0 | 59 | 2.7e-005 | K.AEDIPTLADNALK.D | |
| | | | | | 741.26 | 1480.50 | 1480.86 | -0.36 | 0 | 102 | 1.2e-009 | K.AIELIQGNLVNAVK.Q | |
| | | | | | 753.67 | 1505.32 | 1505.74 | -0.42 | 0 | 123 | 1.4e-011 | K.MTDEQGAAAAITAIK.T | Oxidation (M) |
| | | | | | 858.62 | 1715.23 | 1715.83 | -0.60 | 0 | 35 | 0.007 | K.QATHAEICQIFTNAL.- | |
| | | | | | 608.63 | 1822.85 | 1822.95 | -0.10 | 0 | 62 | 3.5e-005 | K.HTTPILSVNDPELMLK.K | Oxidation (M) |
| | | | | | 711.48 | 2131.40 | 2131.94 | -0.54 | 0 | 78 | 3.6e-007 | K.ANQCDFVISLGGGSPHDCAK.G | |
| | | | | | 726.58 | 2176.72 | 2177.27 | -0.55 | 0 | 61 | 2.6e-005 | R.ALIVTDKPLVNIGLVGEVAEK.L | |
| | | | | | 796.50 | 2386.48 | 2386.25 | 0.23 | 0 | 60 | 4e-005 | K.STKPQLPLVAINTTAGTASEMTR.F | |
| | | | | | 1037.10 | 3108.28 | 3108.65 | -0.36 | 0 | 94 | 1.6e-008 | K.LGQNGITSTVFDGVQPNPTVGNVEAGLALLK.A | |
| **SO0229** | translation elongation factor Tu, TufA | 928 | 43 | 54.0 | 593.25 | 1184.49 | 1184.64 | -0.15 | 0 | 122 | 1.3e-011 | R.VGDEVEIVGIR.T | |
| | | | | | 629.73 | 1257.45 | 1257.59 | -0.14 | 0 | 41 | 0.0018 | K.ALEGEPEWEAK.I | |
| | | | | | 663.31 | 1324.60 | 1324.77 | -0.17 | 0 | 85 | 7.2e-008 | K.TTLTAAISHVLAK.T | |
| | | | | | 710.66 | 1419.31 | 1419.63 | -0.32 | 0 | 68 | 5.8e-006 | K.DFSQIDNAPEER.E | |
| | | | | | 754.26 | 1506.50 | 1506.83 | -0.33 | 0 | 29 | 0.056 | R.QVGVPFIIVFMNK.C | |
| | | | | | 590.22 | 1767.62 | 1767.78 | -0.16 | 0 | 47 | 0.00088 | R.HYAHVDCPGHADYVK.N | |
| | | | | | 902.09 | 1802.17 | 1802.88 | -0.71 | 0 | 87 | 4.9e-008 | R.GITINTSHIEYDTPSR.H | |
| | | | | | 917.74 | 1833.46 | 1832.92 | 0.54 | 0 | 92 | 1.5e-008 | K.MVVTLICPIAMDEGLR.F | Oxidation (M) |
| | | | | | 950.13 | 1898.25 | 1899.00 | -0.75 | 0 | 52 | 0.00016 | K.ILELAAALDSYIPEPER.D | |
| | | | | | 732.25 | 2193.72 | 2194.10 | -0.38 | 0 | 68 | 6.7e-006 | R.DIDKPFLMPIEDVFSISGR.G | |
| | | | | | 802.56 | 2404.65 | 2405.20 | -0.55 | 0 | 81 | 4.5e-007 | R.ELLSEYDFPGDDLPVIQGSALK.A | |
| | | | | | 859.79 | 2576.35 | 2577.22 | -0.86 | 0 | 72 | 2.7e-006 | R.TTDVTGTIELPEGVEMVMPGDNIK.M | Oxidation (M) |
| | | | | | 906.35 | 2716.02 | 2716.41 | -0.39 | 0 | 36 | 0.0063 | R.GQVLSKPGSINPHTTFESEVYVLSK.E | |
| **SO0217** | translation elongation factor Tu, TufB | 888 | 43 | 53.0 | 593.25 | 1184.49 | 1184.64 | -0.15 | 0 | 122 | 1.3e-011 | R.VGDEVEIVGIR.T | |
| | | | | | 629.73 | 1257.45 | 1257.59 | -0.14 | 0 | 41 | 0.0018 | K.ALEGEPEWEAK.I | |
| | | | | | 663.31 | 1324.60 | 1324.77 | -0.17 | 0 | 85 | 7.2e-008 | K.TTLTAAISHVLAK.T | |
| | | | | | 710.66 | 1419.31 | 1419.63 | -0.32 | 0 | 68 | 5.8e-006 | K.DFSQIDNAPEER.E | |
| | | | | | 754.26 | 1506.50 | 1506.83 | -0.33 | 0 | 29 | 0.056 | R.QVGVPFIIVFMNK.C | |
| | | | | | 794.16 | 1586.30 | 1586.82 | -0.51 | 0 | 74 | 1.4e-006 | K.VTLICPIAMDEGLR.F | |
| | | | | | 590.22 | 1767.62 | 1767.78 | -0.16 | 0 | 47 | 0.00088 | R.HYAHVDCPGHADYVK.N | |
| | | | | | 902.09 | 1802.17 | 1802.88 | -0.71 | 0 | 87 | 4.9e-008 | R.GITINTSHIEYDTPSR.H | |
| | | | | | 950.13 | 1898.25 | 1899.00 | -0.75 | 0 | 52 | 0.00016 | K.ILELAAALDSYIPEPER.D | |
| | | | | | 732.25 | 2193.72 | 2194.10 | -0.38 | 0 | 68 | 6.7e-006 | R.DIDKPFLMPIEDVFSISGR.G | |
| | | | | | 802.56 | 2404.65 | 2405.20 | -0.55 | 0 | 81 | 4.5e-007 | R.ELLSEYDFPGDDLPVIQGSALK.A | |
| | | | | | 859.79 | 2576.35 | 2577.22 | -0.86 | 0 | 72 | 2.7e-006 | R.TTDVTGTIELPEGVEMVMPGDNIK.M | Oxidation (M) |
| | | | | | 906.35 | 2716.02 | 2716.41 | -0.39 | 0 | 36 | 0.0063 | R.GQVLSKPGSINPHTTFESEVYVLSK.E | |
| **SO4749** | ATP synthase F1, alpha subunit | 467 | 55 | 23.0 | 621.19 | 1240.37 | 1240.67 | -0.30 | 0 | 25 | 0.06 | R.VVNTLGEPIDGK.G | |
| | | | | | 658.16 | 1314.31 | 1315.69 | -1.38 | 0 | 54 | 0.0002 | K.TAMAIDAIINQR.D | |
| | | | | | 661.25 | 1320.48 | 1321.65 | -1.17 | 0 | 86 | 7.3e-008 | R.IEQFEVVSESR.N | |
| | | | | | 722.18 | 1442.35 | 1442.77 | -0.42 | 0 | 106 | 8.8e-010 | R.NEGTIVAVSDGIIR.I | |
| | | | | | 777.05 | 1552.08 | 1552.73 | -0.65 | 0 | 59 | 5.6e-005 | R.EAYPGDVFYLHSR.L | |
| | | | | | 928.56 | 1855.11 | 1855.86 | -0.75 | 0 | 56 | 5.2e-005 | R.ELAAFSQFASDLDDATR.A | |
| | | | | | 661.44 | 1981.29 | 1981.00 | 0.29 | 0 | 61 | 3.9e-005 | K.QYAPMSVAAQAVSIFAAEK.G | |
| | | | | | 760.24 | 2277.71 | 2278.13 | -0.42 | 0 | 106 | 6.6e-010 | K.VGDFEAALLSYMNSEHAALIK.L | |
| **SO1142** | carbamoyl-phosphate synthase, CarB | 321 | 119 | 9.0 | 680.25 | 1358.49 | 1358.76 | -0.27 | 0 | 63 | 1.1e-005 | K.GVIVQYGGQTPLK.L | |
| | | | | | 708.23 | 1414.45 | 1414.77 | -0.32 | 0 | 41 | 0.0043 | K.ELLIDESLIGWK.E | |
| | | | | | 746.15 | 1490.29 | 1490.72 | -0.43 | 0 | 83 | 1.6e-007 | K.NNEIYMIEVNPR.A | |
| | | | | | 819.16 | 1636.31 | 1636.83 | -0.53 | 0 | 72 | 1.6e-006 | R.TPASFEPAIDYVVTK.V | |
| | | | | | 623.56 | 1867.66 | 1867.89 | -0.23 | 0 | 45 | 0.00073 | R.HGLDPITDMSKPEAMAR.I | |
| | | | | | 961.09 | 1920.17 | 1920.96 | -0.79 | 0 | 50 | 0.00046 | K.LAVGFTLDELMNDITGGR.T | |
| | | | | | 967.69 | 1933.36 | 1934.04 | -0.68 | 0 | 66 | 6.5e-006 | R.LYFEPVTLEDVLEIVR.I | |
| **SO4747** | ATP synthase F1, beta subunit | 238 | 50 | 15.0 | 683.77 | 1365.52 | 1365.73 | -0.21 | 0 | 58 | 2.8e-005 | R.DVLLFVDNIYR.Y | |
| | | | | | 725.72 | 1449.43 | 1449.78 | -0.35 | 0 | 98 | 3.5e-009 | R.YTLAGTEVSALLGR.M 597 | |
| | | | | | 774.46 | 2320.35 | 2321.10 | -0.76 | 0 | 28 | 0.075 | R.MPSAVGYQPTLAEEMGVLQER.I | Oxidation (M) |
| | | | | | 994.10 | 2979.27 | 2980.42 | -1.14 | 0 | 66 | 1.3e-005 | K.GILSGEFDHIPEQAFYMVGSIDEAVEK.A | |
| **SO2638** | leucine dehydrogenase, Ldh | 170 | 37 | 14.0 | 757.64 | 1513.27 | 1513.77 | -0.50 | 0 | 96 | 7.9e-009 | K.IVAGCANNQLAEVR.H | |
| | | | | | 862.13 | 1722.26 | 1722.88 | -0.63 | 0 | 66 | 1.1e-005 | K.SGDPSPFTALGTYLGIK.A | |
| | | | | | 611.93 | 1832.77 | 1832.97 | -0.20 | 0 | 36 | 0.0098 | K.AIIAIHNTNLGPAVGGCR.M | |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO0314** | ornithine decarboxylase, SpeF | 161 | 82 | 7.0 | 731.76 | 1461.50 | 1461.77 | -0.27 | 0 | 52 | 0.0003 | K.FLLTTPGIDAETGK.Y |
| | | | | | 777.21 | 1552.40 | 1552.74 | -0.34 | 0 | 59 | 3e-005 | R.QFFDFFGETIFR.S |
| | | | | | 780.66 | 1559.31 | 1560.76 | -1.46 | 0 | 46 | 0.00067 | K.VMDPQEANLEFIR.G |
| | | | | | 845.16 | 1688.30 | 1688.91 | -0.61 | 0 | 34 | 0.011 | K.LGDLLIHEGAPLDAQK.Y |
| **SO3032** | NTP-dependent alcaligin synthetase | 160 | 69 | 7.0 | 577.24 | 1152.47 | 1151.60 | 0.87 | 0 | 50 | 0.00046 | R.TFFNLSAPQK.C |
| | | | | | 651.72 | 1301.43 | 1301.73 | -0.30 | 0 | 48 | 0.00039 | K.LITPQIYAQGAK.V |
| | | | | | 674.82 | 1347.63 | 1347.69 | -0.07 | 0 | 64 | 2.3e-005 | R.FAGGLDNPLAAFR.Q |
| | | | | | 790.18 | 1578.34 | 1579.70 | -1.36 | 0 | 60 | 4.8e-005 | R.YYEEALTQDSAYK.K |
| **SOA0112** | Lipoprotein, putative | 117 | 146 | 1.0 | 699.24 | 1396.47 | 1396.74 | -0.26 | 0 | 73 | 1.2e-006 | K.VIYSTNNAFAAVK.E |
| | | | | | 720.16 | 1438.30 | 1438.72 | -0.42 | 0 | 27 | 0.11 | K.QGATGITYTPGAFR.G |
| **SO1521** | conserved hypothetical protein | 100 | 103 | 6.0 | 675.72 | 1349.42 | 1349.60 | -0.19 | 0 | 37 | 0.0095 | R.FAWSTDASYFR.I |
| | | | | | 684.42 | 1366.82 | 1367.80 | -0.98 | 0 | 44 | 0.0017 | R.TLPEVVVTLLER.A |
| | | | | | 753.25 | 1504.49 | 1505.79 | -1.31 | 0 | 58 | 3.7e-005 | K.IPVLVDALSCTYR.T |
| | | | | | 774.80 | 2321.38 | 2322.25 | -0.87 | 0 | 31 | 0.038 | R.AIPLINGESVSAAELLDWPSIK.A |
| **SO3532** | isoleucyl-tRNA synthetase, IleS | 91 | 106 | 9.0 | 734.71 | 1467.41 | 1467.80 | -0.40 | 0 | 52 | 0.00018 | K.SIGNVIAPQQVTNK.L |
| | | | | | 797.65 | 1593.29 | 1593.79 | -0.50 | 0 | 36 | 0.0062 | K.FTLNLPETEFPMR.G |
| | | | | | 955.14 | 1908.27 | 1909.01 | -0.74 | 0 | 37 | 0.0042 | R.ALSISPELDYSLVEFVK.D |
| | | | | | 690.95 | 2069.82 | 2070.11 | -0.29 | 0 | 30 | 0.026 | K.VLPLVDATSDAVETELASLK.L |
| | | | | | 800.43 | 3197.67 | 3197.55 | 0.13 | 0 | 25 | 0.072 | K.YGLEVANPVGDNGVYKPDTEFFAGQHVFK.A |
| **SO0021** | fatty oxidation complex, alpha subunit | 86 | 77 | 5.0 | 723.75 | 1445.49 | 1445.76 | -0.27 | 0 | 43 | 0.0013 | R.ETLASLDAALDSIK.Q |
| | | | | | 731.94 | 2192.81 | 2193.21 | -0.40 | 0 | 70 | 5e-006 | K.VGAVDAVVAPEALEVAAIQMLK.D |
| **SO0256** | DNA-directed RNA polymerase, RpoA | 81 | 36 | 7.0 | 637.22 | 1272.42 | 1272.67 | -0.24 | 0 | 44 | 0.0012 | R.LVDIEQVNSTR.A |
| | | | | | 863.24 | 1724.47 | 1724.96 | -0.48 | 0 | 54 | 0.00019 | K.EGVQEDILEILLNLK.G |
| **SO4030** | excinuclease ABC, A subunit, UvrA | 73 | 106 | 3.0 | 755.21 | 1508.40 | 1509.85 | -1.45 | 0 | 40 | 0.0054 | R.VITNPELSLAGGAIR.G |
| | | | | | 816.16 | 1630.31 | 1629.82 | 0.48 | 0 | 57 | 0.00011 | R.STVGTITEIYDYLR.L |
| **SO1295** | major outer membrane lipoprotein | 68 | 9 | 13.0 | 630.73 | 1259.45 | 1260.66 | -1.21 | 0 | 50 | 0.00049 | K.VDQLSADVSSLK.S |
| **SO3440** | enolase, Eno | 56 | 42 | 7.0 | 781.55 | 1561.08 | 1561.84 | -0.76 | 0 | 31 | 0.036 | K.IQLVGDDLFVTNTK.I |
| | | | | | 817.58 | 1633.14 | 1632.88 | 0.25 | 0 | 47 | 0.00095 | K.FNQIGSLTETLAAIR.M |
| **SO1779** | Decaheme cytochrome c, OmcA | 41 | 80 | 2.0 | 650.21 | 1298.40 | 1299.62 | -1.23 | 0 | 33 | 0.027 | R.YAYIQDQPFR.F |
| | | | | | 670.72 | 1339.43 | 1339.66 | -0.23 | 0 | 32 | 0.017 | K.TFTIDSTNSNLK.L |

**Cell lysate / Anti-OmcA IP / MRN**

| Gene | Annotation | Mascot_Score | MW (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SO0224** | DNA-directed RNA polymerase, rpoB | 74 | 150 | 3.0 | 650.78 | 1299.54 | 1299.68 | -0.14 | 0 | 35 | 0.0088 | K.GGIPVATPAFDGAK.E | |
| | | | | | 724.23 | 1446.44 | 1446.68 | -0.24 | 0 | 50 | 0.00062 | R.TNSYGFLETPYR.K | |
| | | | | | 811.67 | 1621.32 | 1621.83 | -0.51 | 0 | 28 | 0.074 | R.STGSYSLVTQQPLGGK.A | |
| **SO0229** | translation elongation factor Tu, TufA | 359 | 43 | 21.0 | 593.79 | 1185.57 | 1184.64 | 0.93 | 0 | 104 | 8.3e-010 | R.VGDEVEIVGIR.T | |
| | | | | | 909.73 | 1817.44 | 1816.92 | 0.52 | 0 | 28 | 0.09 | K.MVVTLICPIAMDEGLR.F | |
| | | | | | 950.15 | 1898.29 | 1899.00 | -0.71 | 0 | 35 | 0.0079 | K.ILELAAALDSYIPEPER.D | |
| | | | | | 732.27 | 2193.79 | 2194.10 | -0.31 | 0 | 47 | 0.00087 | R.DIDKPFLMPIEDVFSISGR.G | Oxidation (M) |
| | | | | | 802.54 | 2404.61 | 2405.20 | -0.59 | 0 | 53 | 0.00011 | R.ELLSEYDFPGDDLPVIQGSALK.A | |
| **SO0217** | translation elongation factor Tu, TufB | 367 | 43 | 21.0 | 593.79 | 1185.57 | 1184.64 | 0.93 | 0 | 104 | 8.3e-010 | R.VGDEVEIVGIR.T | |
| | | | | | 802.65 | 1603.29 | 1602.81 | 0.48 | 0 | 38 | 0.0099 | K.VTLICPIAMDEGLR.F | Oxidation (M) |
| | | | | | 950.15 | 1898.29 | 1899.00 | -0.71 | 0 | 35 | 0.0079 | K.ILELAAALDSYIPEPER.D | |
| | | | | | 732.27 | 2193.79 | 2194.10 | -0.31 | 0 | 47 | 0.00087 | R.DIDKPFLMPIEDVFSISGR.G | Oxidation (M) |
| | | | | | 802.54 | 2404.61 | 2405.20 | -0.59 | 0 | 53 | 0.00011 | R.ELLSEYDFPGDDLPVIQGSALK.A | |
| **SO1142** | carbamoyl-phosphate synthase, CarB | 88 | 119 | 3.0 | 680.25 | 1358.48 | 1358.76 | -0.27 | 0 | 38 | 0.0043 | K.GVIVQYGGQTPLK.L | |
| | | | | | 746.75 | 1491.49 | 1490.72 | 0.77 | 0 | 36 | 0.011 | K.NNEIYMIEVNPR.A | |
| | | | | | 819.20 | 1636.38 | 1636.83 | -0.45 | 0 | 58 | 4.6e-005 | R.TPASFEPAIDYVVTK.V | |
| **SO4747** | ATP synthase F1, beta subunit | 45 | 50 | 5.0 | 683.61 | 1365.20 | 1365.73 | -0.53 | 0 | 39 | 0.006 | R.DVLLFVDNIYR.Y | |
| | | | | | 726.38 | 1450.76 | 1449.78 | 0.97 | 0 | 33 | 0.025 | R.YTLAGTEVSALLGR.M | |
| **SO0314** | ornithine decarboxylase, SpeF | 130 | 82 | 8.0 | 731.74 | 1461.46 | 1461.77 | -0.31 | 0 | 44 | 0.0011 | K.FLLTTPGIDAETGK.Y | |
| | | | | | 755.76 | 1509.51 | 1509.82 | -0.30 | 0 | 38 | 0.0031 | R.GNVELVPLSQIEGR.I | |
| | | | | | 781.23 | 1560.44 | 1560.76 | -0.32 | 0 | 55 | 7.2e-005 | K.VMDPQEANLEFIR.G | |
| | | | | | 733.95 | 2198.84 | 2199.11 | -0.27 | 0 | 39 | 0.0032 | K.LVDEDAPLSEVLPNVYNANK.A | |
| **SO1295** | major outer membrane lipoprotein | 138 | 9 | 13.0 | 630.81 | 1259.60 | 1260.66 | -1.06 | 0 | 65 | 8.7e-006 | K.VDQLSADVSSLK.S | |
| **SO1779** | OmcA | 140 | 80 | 4.0 | 537.33 | 1072.64 | 1072.63 | 0.02 | 0 | 70 | 4.8e-006 | R.FGIAQLTPVK.E | |
| | | | | | 650.53 | 1299.04 | 1299.62 | -0.58 | 0 | 50 | 0.0006 | R.YAYIQDQPFR.F | |
| | | | | | 671.26 | 1340.51 | 1339.66 | 0.85 | 0 | 41 | 0.0037 | K.TFTIDSTNSNLK.L | |

**A1**

| Gene | Annotation | Mascot Score | Mass (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SO0224 | DNA-directed RNA polymerase, RpoB | 1067 | 150 | 24.0 | 521.42 | 1040.83 | 1040.60 | 0.23 | 0 | 26 | 0.037 | R.ISALGPGGLTR.E | |
| | | | | | 553.39 | 1104.76 | 1104.62 | 0.15 | 0 | 50 | 0.00019 | R.LEALVEIYR.M | |
| | | | | | 634.27 | 1266.52 | 1266.57 | -0.04 | 0 | 50 | 0.00013 | R.SVGEMAENQFR.V | |
| | | | | | 637.31 | 1272.60 | 1272.67 | -0.08 | 0 | 50 | 0.00017 | K.DTLVMTLVPER.L | |
| | | | | | 650.80 | 1299.58 | 1299.68 | -0.10 | 0 | 40 | 0.0016 | K.GGIPVATPAFDGAK.E | |
| | | | | | 663.82 | 1325.62 | 1325.72 | -0.10 | 0 | 65 | 7.2e-006 | K.ITQGDDLAPGVLK.I | |
| | | | | | 670.75 | 1339.48 | 1339.61 | -0.12 | 0 | 68 | 3.3e-006 | R.GSWLDFEFDPK.D | |
| | | | | | 708.79 | 1415.57 | 1415.71 | -0.14 | 0 | 50 | 0.00021 | R.LSIPDDEGSGVLSK.E | |
| | | | | | 724.28 | 1446.55 | 1446.68 | -0.13 | 0 | 70 | 2.1e-006 | R.TNSYGFLETPYR.K | |
| | | | | | 732.26 | 1462.50 | 1462.71 | -0.21 | 0 | 79 | 2e-007 | K.QVYELGDEVQQR.V | |
| | | | | | 736.31 | 1470.61 | 1470.79 | -0.19 | 1 | 30 | 0.019 | R.KDVLVQVIDDEAK.Q | |
| | | | | | 769.25 | 1536.48 | 1536.73 | -0.26 | 0 | 79 | 1.8e-007 | R.VDIDSFTDDELLR.L | |
| | | | | | 793.29 | 1584.57 | 1584.85 | -0.28 | 0 | 31 | 0.01 | K.QMLELAGLPTSGQLK.L | |
| | | | | | 804.71 | 1607.41 | 1607.75 | -0.34 | 0 | 75 | 5.8e-007 | K.SFSGNSELQYVSYK.L | |
| | | | | | 811.71 | 1621.41 | 1621.83 | -0.42 | 0 | 28 | 0.026 | R.STGSYSLVTQQPLGGK.A | |
| | | | | | 896.21 | 1790.40 | 1790.93 | -0.53 | 0 | 25 | 0.053 | K.TNTTELEVPVEYIVGK.Y | |
| | | | | | 935.76 | 1869.51 | 1870.03 | -0.52 | 0 | 26 | 0.054 | R.NLLLSAGFSEAQIAALPR.K | |
| | | | | | 943.64 | 1885.27 | 1885.88 | -0.62 | 0 | 80 | 1.4e-007 | K.DAAEALFQNLFFSEER.Y | |
| | | | | | 743.92 | 2228.73 | 2230.05 | -1.32 | 0 | 30 | 0.012 | R.GDVLADGPSTDLGDLALGQNMR.I | Oxidation (M) |
| | | | | | 749.26 | 2244.77 | 2245.12 | -0.35 | 0 | 27 | 0.025 | K.VNEDELRPGEAGIDIYNLTK.Y | |
| | | | | | 774.59 | 2320.74 | 2320.18 | 0.56 | 1 | 53 | 0.00016 | R.KVVDGVITDEVEYLSAIEEGR.Y | |
| | | | | | 808.24 | 2421.70 | 2422.20 | -0.51 | 0 | 63 | 1.5e-005 | K.ELSTLYINELDHGAYISDTLR.I | |
| SO0225 | DNA-directed RNA polymerase, RpoC | 873 | 156 | 17.0 | 521.46 | 1040.90 | 1041.62 | -0.72 | 0 | 30 | 0.033 | R.SVITVGPTLR.L | |
| | | | | | 527.92 | 1053.82 | 1053.62 | 0.20 | 0 | 52 | 0.00011 | K.IGLASPDLIR.S | |
| | | | | | 597.33 | 1192.65 | 1193.61 | -0.97 | 0 | 45 | 0.0011 | R.IGLMLDMTLR.D | Oxidation (M) |
| | | | | | 609.45 | 1216.88 | 1216.65 | 0.23 | 0 | 74 | 1.3e-006 | K.MGAEAVLELLR.A | |
| | | | | | 623.33 | 1244.64 | 1244.64 | -0.00 | 0 | 60 | 2e-005 | K.VIDIWASANEK.V | |
| | | | | | 651.85 | 1301.69 | 1301.68 | 0.00 | 0 | 79 | 2.4e-007 | R.SSELAIIDELGR.E | |
| | | | | | 654.89 | 1307.77 | 1307.78 | -0.01 | 0 | 52 | 9e-005 | R.LLDLAAPDIIVR.N | |
| | | | | | 657.81 | 1313.60 | 1313.63 | -0.02 | 0 | 60 | 1.8e-005 | R.FATSDLNDLYR.R | |
| | | | | | 695.28 | 1388.54 | 1388.68 | -0.14 | 0 | 50 | 0.00016 | R.ITETIIDENGER.S | |
| | | | | | 700.76 | 1399.50 | 1399.65 | -0.15 | 0 | 29 | 0.023 | K.FVDMIDGVTMTR.Q | Oxidation (M) |
| | | | | | 757.31 | 1512.61 | 1512.86 | -0.24 | 0 | 38 | 0.0024 | R.LGIQAFEPVLIEGK.A | |
| | | | | | 796.70 | 1591.39 | 1591.69 | -0.30 | 0 | 40 | 0.0015 | R.GEGMYFMSVAEVEK.A | Oxidation (M) |
| | | | | | 831.74 | 1661.46 | 1661.84 | -0.38 | 0 | 32 | 0.009 | R.GEVIADGPEAAHDILR.L | |
| | | | | | 836.23 | 1670.45 | 1670.85 | -0.40 | 0 | 61 | 1.4e-005 | R.EVAEVWDVLDEVIR.E | |
| | | | | | 973.68 | 1945.35 | 1946.01 | -0.66 | 0 | 71 | 1.1e-006 | R.VVAVDVFYPGTEDVLAPR.N | |
| | | | | | 1003.15 | 2004.29 | 2004.97 | -0.69 | 0 | 25 | 0.058 | R.LVITPADGGEQYEEMIPK.W | Oxidation (M) |
| | | | | | 682.03 | 2043.08 | 2043.08 | -0.00 | 0 | 39 | 0.0038 | R.QTDELTGLSSIVILDVGQR.G | |
| | | | | | 899.46 | 2695.35 | 2696.17 | -0.82 | 0 | 38 | 0.0034 | R.GQMLTEETYLDALEEYGDEFEAK.M | Oxidation (M) |
| SOa0110 | lipoprotein, putative | 821 | 146 | 13.0 | 655.32 | 1308.62 | 1308.69 | -0.08 | 0 | 78 | 4.6e-007 | K.VIDSTSSAFAAIK.E | |
| | | | | | 669.36 | 1336.70 | 1336.72 | -0.03 | 0 | 64 | 6.6e-006 | K.VIDSTTSAFAVVK.E | |
| | | | | | 678.82 | 1355.62 | 1355.71 | -0.09 | 0 | 71 | 1.2e-006 | K.VIYSNSSAFAAVK.Q | |
| | | | | | 686.33 | 1370.65 | 1370.71 | -0.06 | 0 | 26 | 0.032 | K.VIDSTYSAFAAVK.E | |
| | | | | | 699.31 | 1396.61 | 1396.74 | -0.13 | 0 | 89 | 2.1e-008 | K.VIYSTNNAFAAVK.E | |
| | | | | | 714.78 | 1427.55 | 1427.69 | -0.14 | 0 | 75 | 4.9e-007 | R.GVDQFTYLVSDGK.G | |
| | | | | | 720.27 | 1438.53 | 1438.72 | -0.19 | 0 | 70 | 1.5e-006 | K.QGATGITYTPGAFR.G | |
| | | | | | 721.77 | 1441.53 | 1441.71 | -0.18 | 0 | 78 | 2.8e-007 | R.GVDQFTYVITDGK.D | |
| | | | | | 722.84 | 1443.66 | 1443.80 | -0.13 | 0 | 66 | 4.4e-006 | K.LAPNLFLIETSIN.- | |
| | | | | | 735.24 | 1468.46 | 1468.66 | -0.20 | 0 | 62 | 1.1e-005 | K.ENASVDYTPGNFR.G | |
| | | | | | 861.17 | 1720.32 | 1720.84 | -0.51 | 0 | 76 | 7.1e-007 | K.VETIFSDMYAFAALK.T | Oxidation (M) |
| | | | | | 619.31 | 1854.90 | 1855.93 | -1.03 | 0 | 45 | 0.00086 | K.ISDVDGDTLSITLHGSAR.F | |
| | | | | | 738.63 | 2212.87 | 2213.11 | -0.24 | 0 | 27 | 0.06 | R.LIADADGDALSIAHIYTANNR.A | |
| SO2593 | NAD-glutamate dehydrogenase family prot | 86 | 183 | 2.0 | 831.73 | 1661.44 | 1661.81 | -0.37 | 0 | 26 | 0.039 | R.ALEFLPSEEELTER.L | |
| | | | | | 806.27 | 2415.79 | 2414.32 | 1.47 | 0 | 65 | 3.8e-006 | R.ALLDITDNILNGEIVHPVDVVR.H | |

**A2**

| Gene | Annotation | Mascot Score | Mass (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SO0432 | aconitate hydratase 2, AcnB | 1250 | 94 | 36.0 | 391.40 | 780.78 | 780.52 | 0.26 | 0 | 31 | 0.011 | R.IPLIIGR.G | |

|  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  |  |  |  |  | 530.33 | 1058.64 | 1058.56 | 0.08 | 0 | 75 | 5.3e-007 | K.TDVLLDEVR.A |  |
|  |  |  |  |  | 602.35 | 1202.69 | 1202.66 | 0.03 | 0 | 61 | 1.5e-005 | K.AIELGMLTVEK.K |  |
|  |  |  |  |  | 607.35 | 1212.68 | 1212.52 | 0.16 | 0 | 25 | 0.053 | K.WMIAEGYGDR.R | Oxidation (M) |
|  |  |  |  |  | 613.28 | 1224.55 | 1224.56 | -0.01 | 0 | 44 | 0.00065 | K.ELDATAADTYR.Y |  |
|  |  |  |  |  | 615.33 | 1228.64 | 1228.69 | -0.05 | 0 | 73 | 7.9e-007 | R.VLEIEGLESLK.V |  |
|  |  |  |  |  | 629.84 | 1257.66 | 1257.66 | -0.00 | 0 | 45 | 0.0007 | R.IPPGVDEAAYVK.A |  |
|  |  |  |  |  | 724.27 | 1446.52 | 1446.70 | -0.18 | 0 | 58 | 3.2e-005 | R.HGSDEVISEFSLK.T |  |
|  |  |  |  |  | 727.27 | 1452.53 | 1452.75 | -0.22 | 0 | 78 | 2.6e-007 | R.DGIEPDVAGSVGPIK.K |  |
|  |  |  |  |  | 735.27 | 1468.52 | 1468.71 | -0.19 | 0 | 67 | 3.7e-006 | R.LPTVEEYQEYAK.E |  |
|  |  |  |  |  | 753.75 | 1505.48 | 1505.70 | -0.22 | 0 | 72 | 7.4e-007 | R.YLNFDQIDSYTK.K |  |
|  |  |  |  |  | 776.21 | 1550.41 | 1550.72 | -0.31 | 0 | 113 | 9.8e-011 | K.VEQAFELSDASAER.S |  |
|  |  |  |  |  | 552.80 | 1655.39 | 1655.79 | -0.40 | 0 | 40 | 0.0016 | R.MLLPDTVGTGGDSHTR.F |  |
|  |  |  |  |  | 855.24 | 1708.46 | 1708.88 | -0.42 | 0 | 119 | 1.9e-011 | K.GFPLVYVGDVVGTGSSR.K |  |
|  |  |  |  |  | 950.16 | 1898.32 | 1898.92 | -0.60 | 0 | 48 | 0.00022 | K.MEMGDVIDIYPYAGVVK.R |  |
|  |  |  |  |  | 674.63 | 2020.86 | 2020.92 | -0.06 | 1 | 73 | 1.8e-006 | K.MDKDQLTEEGYYGIFGR.V |  |
|  |  |  |  |  | 691.05 | 2070.14 | 2070.15 | -0.01 | 0 | 55 | 8.8e-005 | R.AAEGVVPKPLDAHQVAELVK.L |  |
|  |  |  |  |  | 696.92 | 2087.73 | 2088.03 | -0.30 | 0 | 26 | 0.078 | K.ALAHTLLMFDSFHDVVEK.M | Oxidation (M) |
|  |  |  |  |  | 766.28 | 2295.83 | 2295.22 | 0.60 | 0 | 43 | 0.00056 | R.AVLGLPASEVFVRPQDIADNGK.G |  |
|  |  |  |  |  | 836.22 | 2505.62 | 2506.27 | -0.64 | 0 | 55 | 8.6e-005 | K.IAPIFFNTMEDAGALPIELDVSK.M | Oxidation (M) |
|  |  |  |  |  | 833.98 | 3331.90 | 3332.63 | -0.73 | 0 | 26 | 0.014 | K.VSGETNTDDLSPAPDAWSRPDIPLHALAMLK.N | Oxidation (M) |
| SO2427 | TonB-dependent receptor | 1122 | 92 | 30 | 905.59 | 905.50 | 0.10 | 0 | 57 | .4e-005 | 1 |  |  |
|  |  |  |  |  | 577.37 | 1152.72 | 1152.60 | 0.12 | 0 | 46 | 0.0004 | K.VSNDTTYLIK.F |  |
|  |  |  |  |  | 656.28 | 1310.55 | 1310.59 | -0.04 | 0 | 69 | 2.3e-006 | R.IYNQDTDTWR.L |  |
|  |  |  |  |  | 698.84 | 1395.66 | 1395.75 | -0.09 | 0 | 61 | 1.2e-005 | R.SNQQLAAQPAQIK.L |  |
|  |  |  |  |  | 791.76 | 1581.50 | 1581.81 | -0.31 | 0 | 92 | 8.8e-009 | K.IGLTYTATDELMVR.T |  |
|  |  |  |  |  | 930.20 | 1858.38 | 1858.93 | -0.56 | 0 | 127 | 3.6e-012 | R.QDMETASPVTVIDAAAIK.A |  |
|  |  |  |  |  | 673.98 | 2018.93 | 2020.05 | -1.12 | 0 | 99 | 1.9e-009 | K.DGASAVYGSDAIAGVVNIITK.K |  |
|  |  |  |  |  | 1107.54 | 2213.07 | 2213.94 | -0.87 | 0 | 37 | 0.0023 | R.TETYDYSNDVYFQTPSER.R |  |
|  |  |  |  |  | 1154.50 | 2306.99 | 2308.00 | -1.01 | 0 | 74 | 4.7e-007 | R.SMTDVYTDYDANDNPFVAVR.G | Oxidation (M) |
|  |  |  |  |  | 770.20 | 2307.57 | 2307.97 | -0.40 | 0 | 84 | 5.4e-008 | K.FEQDGENYTGTIDGNMGAYAR.V |  |
|  |  |  |  |  | 790.85 | 2369.53 | 2370.04 | -0.51 | 1 | 75 | 4.2e-007 | K.RTETYDYSNDVYFQTPSER.R |  |
|  |  |  |  |  | 797.91 | 2390.71 | 2390.16 | 0.56 | 0 | 85 | 3.8e-008 | R.MVNSGSGADSAVDLNSIPVAMIAR.V | Oxidation (M) |
|  |  |  |  |  | 924.57 | 2770.69 | 2771.34 | -0.66 | 0 | 67 | 4.3e-006 | R.SLFANMTQELGNDVVLTADAIYTNR.R | Oxidation (M) |
|  |  |  |  |  | 1003.79 | 3008.36 | 3008.47 | -0.12 | 0 | 68 | 1.2e-006 | K.NLTDEKPLYVTNGSDAGTVPQVYDTVGR.T |  |
|  |  |  |  |  | 1034.77 | 3101.29 | 3102.53 | -1.23 | 1 | 50 | 6.8e-005 | R.GVIQGDRDWYDPLDNTSSIIPTGTLNQK.V |  |
| SO0424 | pyruvate dehydrogenase, E1 component, A | 543 | 100 | 17.0 | 517.33 | 1032.65 | 1032.54 | 0.11 | 0 | 41 | 0.0016 | R.YWDPLLAR.D |  |
|  |  |  |  |  | 529.35 | 1056.68 | 1056.51 | 0.17 | 0 | 23 | 0.087 | R.TFGMEGLFR.Q |  |
|  |  |  |  |  | 570.82 | 1139.62 | 1139.56 | 0.06 | 0 | 41 | 0.0014 | R.EISSTMAFVR.V |  |
|  |  |  |  |  | 596.81 | 1191.60 | 1191.59 | 0.01 | 0 | 69 | 2.6e-006 | R.LSEDQLANFR.Q |  |
|  |  |  |  |  | 617.35 | 1232.69 | 1232.64 | 0.05 | 0 | 49 | 0.00032 | K.IIQELEGEFR.G |  |
|  |  |  |  |  | 618.33 | 1234.65 | 1235.69 | -1.04 | 0 | 22 | 0.11 | K.NIVPIIPDEAR.T |  |
|  |  |  |  |  | 639.33 | 1276.65 | 1276.66 | -0.01 | 0 | 43 | 0.0011 | K.FSEELEVPSLK.I |  |
|  |  |  |  |  | 641.38 | 1280.75 | 1280.73 | 0.02 | 0 | 42 | 0.00091 | K.ELPVDVLANAIK.E |  |
|  |  |  |  |  | 647.29 | 1292.56 | 1292.56 | -0.00 | 0 | 52 | 0.00012 | R.IGDMAWAAGDMR.A |  |
|  |  |  |  |  | 653.79 | 1305.57 | 1305.67 | -0.10 | 0 | 37 | 0.003 | K.IFDSILQGSNGR.E |  |
|  |  |  |  |  | 798.67 | 1595.34 | 1595.75 | -0.41 | 1 | 38 | 0.0029 | K.EYGIDADKINPQYA.- |  |
|  |  |  |  |  | 801.70 | 1601.38 | 1602.73 | -1.35 | 0 | 51 | 0.00016 | K.YVPQDSDQVAYYR.E |  |
|  |  |  |  |  | 1004.15 | 3009.43 | 3010.42 | -0.99 | 0 | 37 | 0.004 | R.FNIPIPDDQLEDLPFYHPGPDSEEVK.Y |  |
| SO1429 | anaerobic dimethyl sulfoxide reductase | 474 | 92 | 19.0 | 601.30 | 1200.60 | 1200.66 | -0.07 | 0 | 48 | 0.00029 | K.APFIVTGAGVNR.H |  |
|  |  |  |  |  | 617.28 | 1232.55 | 1233.62 | -1.07 | 0 | 58 | 4.9e-005 | K.LVAEFTASGDPK.K |  |
|  |  |  |  |  | 634.86 | 1267.71 | 1267.65 | 0.07 | 0 | 31 | 0.012 | K.VEIYSLSMAQK.G |  |
|  |  |  |  |  | 644.26 | 1286.51 | 1286.58 | -0.07 | 0 | 38 | 0.0042 | R.QSGSGEGYDFLK.A |  |
|  |  |  |  |  | 693.79 | 1385.57 | 1385.70 | -0.14 | 0 | 58 | 2.3e-005 | R.GTADLDTPLGADIK.A |  |
|  |  |  |  |  | 724.31 | 1446.61 | 1446.77 | -0.16 | 0 | 46 | 0.00055 | K.TPVLALDSYINGGK.A |  |
|  |  |  |  |  | 843.21 | 1684.41 | 1684.81 | -0.40 | 0 | 62 | 1.1e-005 | K.ESISFFTWAEAIER.G |  |
|  |  |  |  |  | 894.66 | 1787.30 | 1787.84 | -0.54 | 0 | 23 | 0.082 | K.TQYLPYIDVEDNYR.N |  |
|  |  |  |  |  | 689.68 | 2066.01 | 2067.09 | -1.08 | 0 | 80 | 1.1e-007 | R.VAPGVVALGQGAWYQPDIAR.I |  |
|  |  |  |  |  | 1060.14 | 2118.26 | 2119.06 | -0.80 | 0 | 77 | 2.6e-007 | K.FVPISWDEAASTIASEIQR.I |  |
|  |  |  |  |  | 801.22 | 2400.63 | 2401.10 | -0.47 | 1 | 42 | 0.0019 | K.EAEYTEGKDEAAWLEELYQK.T |  |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SO2907 | TonB-dependent receptor domain protein | 396 | 96 | 14.0 | 542.82 | 1083.62 | 1083.52 | 0.09 | 0 | 46 | 0.00043 | K.TFDGLAFDAK.F | |
| | | | | | 603.36 | 1204.70 | 1204.65 | 0.05 | 0 | 65 | 7.5e-006 | R.YEALDNLVLR.A | |
| | | | | | 610.31 | 1218.61 | 1218.53 | 0.07 | 0 | 43 | 0.001 | K.DSVFSNMTYR.I | |
| | | | | | 904.62 | 1807.22 | 1806.90 | 0.32 | 0 | 45 | 0.00048 | R.ITDELEWFGQAIVMR.D | |
| | | | | | 636.39 | 1906.15 | 1906.06 | 0.09 | 0 | 55 | 0.00011 | K.AAFVELELPVLDHLNVK.L | |
| | | | | | 995.14 | 1988.27 | 1989.00 | -0.73 | 0 | 61 | 1.1e-005 | R.TDMESALPVTVLSAEDIAK.T | |
| | | | | | 1086.04 | 2170.06 | 2170.97 | -0.90 | 0 | 44 | 0.00047 | K.YIDSYDGETPQQQEVGTNK.Q | |
| | | | | | 829.28 | 2484.81 | 2486.25 | -1.44 | 0 | 39 | 0.0017 | R.IAPSATFGGDATNLNLIPMDAIER.I | |
| SO1521 | respiratory FAD-dependent D-lactate dehy | 394 | 103 | 8.0 | 600.84 | 1199.66 | 1199.69 | -0.03 | 1 | 35 | 0.0061 | K.RQELIDVLSK.M | |
| | | | | | 625.30 | 1248.58 | 1248.64 | -0.06 | 0 | 48 | 0.00025 | K.ITGDGITNALMK.T | Oxidation (M) |
| | | | | | 675.78 | 1349.55 | 1349.60 | -0.05 | 0 | 60 | 3e-005 | R.FAWSTDASYFR.I | |
| | | | | | 684.85 | 1367.69 | 1367.80 | -0.11 | 0 | 73 | 6.6e-007 | R.TLPEVVVTLLER.A | |
| | | | | | 695.79 | 1389.56 | 1390.66 | -1.10 | 0 | 26 | 0.053 | K.EVPYWNPDFPK.G | |
| | | | | | 877.97 | 2630.90 | 2631.37 | -0.47 | 0 | 91 | 2.1e-008 | K.QVFDPQGILNPGVILNDDSNIHVK.N | |
| SO3935 | ribonuclease R, Rnr | 355 | 91 | 10.0 | 607.84 | 1213.67 | 1213.67 | 0.00 | 0 | 50 | 0.00021 | R.QGDVVVVELTR.R | |
| | | | | | 693.31 | 1384.61 | 1384.72 | -0.11 | 0 | 90 | 1.5e-008 | R.SLPLVTIDGEDAR.D | |
| | | | | | 694.31 | 1386.60 | 1386.74 | -0.14 | 0 | 50 | 0.00017 | R.ITQEILIASEDR.N | |
| | | | | | 746.34 | 1490.66 | 1489.73 | 0.93 | 0 | 37 | 0.005 | K.QMAPGMEIEIALR.N | |
| | | | | | 953.22 | 1904.42 | 1904.97 | -0.55 | 0 | 30 | 0.027 | R.GNSVYFPSQVIPMLPEK.I | |
| | | | | | 754.58 | 2260.71 | 2262.02 | -1.31 | 0 | 35 | 0.0036 | K.EGYGFFKPDEGGDDLFISNR.D | |
| SO0781 | glycine dehydrogenase (decarboxylating), ( | 216 | 105 | 4.0 | 609.37 | 1216.73 | 1216.68 | 0.05 | 0 | 69 | 2.2e-006 | R.FADILAAGLQAK.G | |
| | | | | | 777.24 | 1552.47 | 1552.79 | -0.32 | 0 | 69 | 1.8e-006 | K.STQTALLNANYVMK.K | |
| | | | | | 886.67 | 1771.32 | 1771.88 | -0.56 | 0 | 43 | 0.0013 | R.FGQITDFTDLFAELR.A | |
| SO3193 | polysaccharide biosynthesis/export protei | 214 | 100 | 4.0 | 585.32 | 1168.62 | 1168.68 | -0.06 | 0 | 36 | 0.0073 | K.VNDLIVAAGGLK.E | |
| | | | | | 746.81 | 1491.61 | 1491.76 | -0.16 | 0 | 71 | 1.2e-006 | K.MLANLFDDAELLK.L | |
| | | | | | 765.00 | 2291.98 | 2292.13 | -0.15 | 0 | 42 | 0.0016 | K.DGTVVNYADAQLMLADLENIK.A | |
| SO4692 | acridine efflux pump, AcrB/AcrD/AcrF fam | 209 | 112 | 6.0 | 754.71 | 1507.41 | 1507.73 | -0.32 | 0 | 70 | 1.5e-006 | K.SDTSGANVFLGDVAR.V | |
| | | | | | 758.26 | 1514.52 | 1514.79 | -0.28 | 0 | 48 | 0.00026 | K.IVEDSVTQVIEQR.M | |
| | | | | | 759.27 | 1516.52 | 1517.74 | -1.22 | 0 | 36 | 0.0048 | R.VMSEEGLSPLEATR.K | |
| | | | | | 752.24 | 2253.69 | 2254.16 | -0.47 | 0 | 31 | 0.025 | K.LQGAMTLLPQEVQAQGVDVNK.S | Oxidation (M) |
| SO2606 | PqiB family protein | 114 | 93 | 2.0 | 616.74 | 1231.47 | 1232.68 | -1.21 | 0 | 38 | 0.0053 | K.ETLFWLVTPK.A | |
| | | | | | 804.18 | 1606.35 | 1607.80 | -1.45 | 0 | 49 | 0.00041 | K.LVESSYANVAEDALK.F | |
| SO1482 | TonB-dependent receptor | 106 | 90 | 4.0 | 816.23 | 1630.44 | 1630.81 | -0.37 | 0 | 52 | 0.00018 | K.AFDDQMLASLVFFK.S | |
| | | | | | 834.73 | 1667.45 | 1667.84 | -0.39 | 0 | 30 | 0.03 | R.LEQFSIYDADQVIK.D | |
| | | | | | 658.81 | 1315.61 | 1316.72 | -1.11 | 0 | 49 | 0.00045 | R.SLTNVESVEVLK.G | |
| SO1637 | outer membrane protein assembly factor, Y | 96 | 92 | 6.0 | 626.44 | 1250.87 | 1250.80 | 0.07 | 0 | 64 | 7.7e-006 | R.VALGAALLSLPVK.V | |
| | | | | | 778.72 | 1555.43 | 1555.71 | -0.28 | 0 | 39 | 0.0034 | K.DYVAWWDLFGER.R | |
| | | | | | 833.17 | 1664.32 | 1664.75 | -0.43 | 0 | 32 | 0.012 | K.TDFDTNYYFPINR.S | |
| | | | | | 583.61 | 1747.82 | 1747.91 | -0.09 | 0 | 22 | 0.084 | K.VTERPTISAVTFEGNK.D | |
| SO3560 | subfamily M16B unassigned peptidases | 64 | 105 | 2.0 | 659.82 | 1317.63 | 1318.69 | -1.06 | 0 | 31 | 0.016 | R.ILASINEFEQR.G | |
| | | | | | 763.25 | 1524.49 | 1525.72 | -1.23 | 0 | 26 | 0.045 | K.LFEPAFNEADFAR.V | |

**A3**

| Gene | Annotation | Mascot Score | Mass (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SO0021 | fatty oxidation complex, alpha subunit, Fad | 1050 | 77 | 38.0 | 478.89 | 955.77 | 955.55 | 0.21 | 0 | 34 | 0.0085 | K.MPLVEVIR.G | |
| | | | | | 560.84 | 1119.66 | 1119.56 | 0.11 | 0 | 34 | 0.0061 | K.AFDADEIIAR.T | |
| | | | | | 582.32 | 1162.62 | 1163.52 | -0.90 | 0 | 51 | 0.00012 | K.GFYAYSVDSR.G | |
| | | | | | 622.27 | 1242.53 | 1241.57 | 0.96 | 0 | 36 | 0.004 | R.ALAANNGSYYQA.- | |
| | | | | | 668.31 | 1334.61 | 1334.69 | -0.09 | 0 | 40 | 0.0014 | R.TMIPMIIETVR.C | Oxidation (M) |
| | | | | | 701.32 | 1400.62 | 1400.76 | -0.14 | 0 | 36 | 0.0068 | K.LEDLPFPTASAIK.G | |
| | | | | | 723.81 | 1445.61 | 1445.76 | -0.15 | 0 | 87 | 3.8e-008 | R.ETLASLDAALDSIK.Q | |
| | | | | | 739.33 | 1476.64 | 1476.83 | -0.19 | 0 | 27 | 0.031 | K.ALIGIFLNDQFVK.G | |
| | | | | | 743.82 | 1485.62 | 1485.82 | -0.19 | 0 | 63 | 1.2e-005 | K.QQSNIQALVLTSGK.D | |
| | | | | | 750.26 | 1498.51 | 1498.78 | -0.27 | 0 | 47 | 0.00029 | R.SDALQIEHQAFIK.L | |
| | | | | | 819.73 | 1637.45 | 1637.86 | -0.41 | 0 | 51 | 0.00012 | K.DIAQPALDLGLNEAAK.L | |
| | | | | | 821.27 | 1640.52 | 1640.91 | -0.39 | 0 | 61 | 1.2e-005 | K.VLNNITPALEYAPVK.H | |
| | | | | | 864.22 | 1726.43 | 1726.86 | -0.43 | 0 | 111 | 1.4e-010 | R.YLDTMGVANFVALADK.Y | |
| | | | | | 867.69 | 1733.37 | 1733.86 | -0.48 | 0 | 64 | 8.4e-006 | K.TPIVVNDCPGFFVNR.V | |
| | | | | | 622.63 | 1864.87 | 1863.88 | 0.98 | 0 | 66 | 3.9e-006 | R.GEHSSEETIASVVAYASK.M | |
| | | | | | 637.98 | 1910.93 | 1911.95 | -1.02 | 0 | 73 | 5.8e-007 | K.HYPAPMAAVNVVEQAATK.G | Oxidation (M) |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | 993.63 | 1985.25 | 1985.98 | -0.74 | 0 | 50 | 0.00012 | R.VIGADNALEWITTGNEQR.A | |
| | | | | | 737.66 | 2209.95 | 2209.20 | 0.75 | 0 | 68 | 5.5e-006 | K.VGAVDAVVAPEALEVAAIQMLK.D | Oxidation (M) |
| | | | | | 740.66 | 2218.96 | 2220.13 | -1.17 | 0 | 56 | 2.6e-005 | -.MIYQSPTIQVELLEDNIAK.L | Oxidation (M) |
| SO1779 | Decaheme cytochrome c, OmcA | 861 | 80 | 23.0 | 468.32 | 934.63 | 934.49 | 0.14 | 0 | 43 | 0.00096 | K.VPTSFAWK.A | |
| | | | | | 483.33 | 964.65 | 964.50 | 0.15 | 0 | 26 | 0.043 | R.AWLYGDIK.N | |
| | | | | | 543.85 | 1085.68 | 1085.62 | 0.06 | 0 | 100 | 1.8e-009 | K.SNVVTGIALGR.S | |
| | | | | | 629.31 | 1256.60 | 1256.59 | 0.00 | 0 | 59 | 2.7e-005 | K.EFISDPSAYTK.S | |
| | | | | | 650.80 | 1299.58 | 1299.62 | -0.05 | 0 | 54 | 6e-005 | R.YAYIQDQPFR.F | |
| | | | | | 670.78 | 1339.55 | 1339.66 | -0.12 | 0 | 62 | 1.3e-005 | K.TFTIDSTNSNLK.L | |
| | | | | | 671.32 | 1340.62 | 1340.65 | -0.04 | 0 | 32 | 0.019 | R.GYQWQAYINAK.K | |
| | | | | | 802.21 | 1602.40 | 1601.78 | 0.62 | 0 | 52 | 0.00012 | R.HTFDATGAQVPAPYK.I | |
| | | | | | 802.74 | 1603.47 | 1603.82 | -0.35 | 0 | 109 | 2.6e-010 | K.NNALTFDVQILDNK.D | |
| | | | | | 714.60 | 2140.76 | 2140.05 | 0.71 | 0 | 45 | 0.001 | K.SHIETNGGILNGTSAADVQTR.A | |
| | | | | | 890.86 | 2669.55 | 2670.27 | -0.72 | 0 | 48 | 0.00034 | R.ATMELELPQLAANAHFDWQPSTGK.T | |
| | | | | | 976.45 | 2926.33 | 2927.43 | -1.09 | 1 | 94 | 2.9e-009 | K.KEPGTVPSGVDNLNPSTQFQANVESANK.C | |
| SO1126 | chaperone protein, DnaK | 789 | 69 | 23.0 | 620.34 | 1238.67 | 1238.63 | 0.04 | 0 | 72 | 1.8e-006 | K.VQEAVTNFFGK.E | |
| | | | | | 660.32 | 1318.62 | 1318.68 | -0.06 | 0 | 79 | 2.4e-007 | K.IEAAMSAVETAVK.G | |
| | | | | | 677.33 | 1352.64 | 1352.73 | -0.09 | 1 | 33 | 0.012 | R.LINYLADEFKK.E | |
| | | | | | 749.84 | 1497.67 | 1497.88 | -0.21 | 1 | 73 | 8.6e-007 | R.AKLESLVEDLIIR.T | |
| | | | | | 758.84 | 1515.67 | 1515.73 | -0.06 | 0 | 90 | 3.4e-008 | K.IIAADNGDAWVESR.G | |
| | | | | | 782.75 | 1563.48 | 1563.80 | -0.32 | 0 | 56 | 3.1e-005 | R.QAVTNPNNTFFAIK.R | |
| | | | | | 796.69 | 1591.37 | 1591.75 | -0.38 | 0 | 95 | 5.2e-009 | K.ASSGLSEEEVAQMVR.D | |
| | | | | | 807.23 | 1612.44 | 1612.82 | -0.38 | 0 | 74 | 7e-007 | K.SLGQFNLDGIEPAPR.G | |
| | | | | | 830.25 | 1658.49 | 1658.89 | -0.39 | 0 | 112 | 1e-010 | R.IINEPTAAALAYGIDK.K | |
| | | | | | 808.25 | 2421.74 | 2422.27 | -0.53 | 1 | 105 | 4e-010 | R.KDVNPDEAVAVGAAIQAGVLSGDVK.D | |
| SO3669 | TonB-dependent haem/haemoglobin recep | 664 | 76 | 26.0 | 522.33 | 1042.64 | 1042.51 | 0.13 | 0 | 30 | 0.019 | K.LTYGVDGYR.D | |
| | | | | | 658.27 | 1314.53 | 1314.62 | -0.08 | 0 | 40 | 0.0017 | R.GSYFMDPELLK.S | |
| | | | | | 675.27 | 1348.53 | 1348.65 | -0.12 | 0 | 74 | 7.2e-007 | R.VDFAIENIGDEK.Y | |
| | | | | | 705.22 | 1408.43 | 1408.63 | -0.20 | 0 | 51 | 0.00023 | R.NTGDYIEGMPANK.F | |
| | | | | | 725.28 | 1448.54 | 1448.71 | -0.17 | 0 | 40 | 0.0026 | K.GLCNTFATNPNLK.S | |
| | | | | | 830.24 | 1658.47 | 1658.86 | -0.39 | 0 | 56 | 8.3e-005 | R.TVGINLNNSSQLGNTK.L | |
| | | | | | 842.16 | 1682.30 | 1682.76 | -0.46 | 0 | 106 | 5e-010 | K.FNVDLSQGIMEGDMK.L | |
| | | | | | 929.17 | 1856.33 | 1856.89 | -0.57 | 0 | 42 | 0.0011 | K.SAQDFLAPNETFGGYLK.Q | |
| | | | | | 943.66 | 1885.31 | 1885.94 | -0.63 | 0 | 60 | 1.6e-005 | R.VTYVASQTNTPTGYSVAK.Y | |
| | | | | | 954.65 | 1907.29 | 1907.90 | -0.61 | 0 | 72 | 1.6e-006 | R.NDVDDFIVQQVSNPYR.G | |
| | | | | | 1068.18 | 2134.36 | 2135.16 | -0.80 | 0 | 23 | 0.058 | K.INELVPSNPSAAVSSSVPLVR.R | |
| | | | | | 806.90 | 2417.68 | 2418.16 | -0.48 | 0 | 71 | 1e-006 | K.GQVGQRPEDIDGETTVWGAFTR.A | |
| SO1776 | outer membrane protein, MtrB | 588 | 76 | 23.0 | 626.77 | 1251.52 | 1251.54 | -0.02 | 0 | 59 | 2.2e-005 | R.LTGSYDYYDR.D | |
| | | | | | 677.79 | 1353.56 | 1353.64 | -0.08 | 0 | 38 | 0.0024 | K.QGQYNVNVNYR.Q | |
| | | | | | 711.75 | 1421.49 | 1421.68 | -0.19 | 0 | 43 | 0.001 | R.YANQLNTDAVDAK.V | |
| | | | | | 717.76 | 1433.50 | 1433.65 | -0.15 | 0 | 31 | 0.016 | R.QGITGDYGDYFAK.V | |
| | | | | | 720.24 | 1438.47 | 1438.65 | -0.19 | 0 | 86 | 4.2e-008 | R.ASVDAYQLGMDGGR.L | |
| | | | | | 764.25 | 1526.48 | 1526.69 | -0.21 | 0 | 84 | 5.2e-008 | R.VNSFDTWDMWVK.G | |
| | | | | | 570.30 | 1707.89 | 1707.92 | -0.03 | 0 | 37 | 0.0051 | R.ITHSPLESLTIDVGAR.Y | |
| | | | | | 952.15 | 1902.29 | 1902.91 | -0.62 | 0 | 80 | 1.6e-007 | R.YALDDYTDTVIGLTESK.D | |
| | | | | | 966.62 | 1931.22 | 1931.89 | -0.67 | 0 | 57 | 4e-005 | R.LGLDYTYSNSDSNTQVR.Q | |
| | | | | | 690.28 | 2067.82 | 2067.99 | -0.17 | 0 | 34 | 0.011 | R.ILTGQMSQDQALVTDNYR.Y | Oxidation (M) |
| | | | | | 753.54 | 2257.60 | 2258.01 | -0.41 | 0 | 39 | 0.0017 | R.DGSQYQASEWTSSETNSLLR.K | |
| SO0314 | ornithine decarboxylase, SpeF | 539 | 82 | 20.0 | 467.31 | 932.61 | 933.49 | -0.88 | 0 | 51 | 0.00015 | K.GDLVLFDR.N | |
| | | | | | 564.80 | 1127.59 | 1127.53 | 0.06 | 0 | 25 | 0.048 | R.FFEFEPGQK.W | |
| | | | | | 709.76 | 1417.50 | 1416.69 | 0.81 | 0 | 79 | 3.1e-007 | K.TYFVLNGTSSSNK.V | |
| | | | | | 731.80 | 1461.59 | 1461.77 | -0.19 | 0 | 48 | 0.00027 | K.FLLTTPGIDAETGK.Y | |
| | | | | | 755.78 | 1509.55 | 1509.82 | -0.27 | 0 | 45 | 0.00039 | R.GNVELVPLSQIEGR.I | |
| | | | | | 777.23 | 1552.44 | 1552.74 | -0.29 | 0 | 60 | 1.5e-005 | R.QFFDFFGETIFR.S | |
| | | | | | 781.24 | 1560.47 | 1560.76 | -0.29 | 0 | 71 | 1.3e-006 | K.VMDPQEANLEFIR.G | |
| | | | | | 812.27 | 1622.52 | 1622.87 | -0.35 | 0 | 24 | 0.054 | K.YEQALLPPFFGTLK.K | |
| | | | | | 845.25 | 1688.49 | 1688.91 | -0.42 | 0 | 39 | 0.0021 | K.LGDLLIHEGAPLDAQK.Y | |
| | | | | | 941.19 | 1880.37 | 1881.00 | -0.63 | 0 | 58 | 4.3e-005 | R.LAIIQLGTYDGTIYNAR.Q | |
| | | | | | 734.02 | 2199.04 | 2199.11 | -0.06 | 0 | 44 | 0.001 | K.LVDEDAPLSEVLPNVYNANK.A | |
| SO1209 | polyribonucleotide nucleotidyltransferase, | 466 | 76 | 20.0 | 581.81 | 1161.60 | 1161.64 | -0.05 | 0 | 49 | 0.00043 | K.TSVAGIAMGLVK.E | Oxidation (M) |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | 608.83 | 1215.65 | 1215.63 | 0.01 | 0 | 36 | 0.0044 | R.EVDNLLGSLEK.K | |
| | | | | | 698.81 | 1395.61 | 1395.74 | -0.13 | 0 | 74 | 1.2e-006 | K.EALLAANPDVDLR.E | |
| | | | | | 750.77 | 1499.52 | 1499.73 | -0.21 | 0 | 33 | 0.0071 | R.DFFPLTVNYQEK.T | |
| | | | | | 804.71 | 1607.41 | 1607.80 | -0.39 | 0 | 35 | 0.0056 | K.EIMEIALQQAYGAR.V | |
| | | | | | 833.73 | 1665.45 | 1664.88 | 0.57 | 0 | 77 | 3.5e-007 | R.VGYINGEYVLNPTVK.Q | |
| | | | | | 933.64 | 1865.28 | 1865.90 | -0.62 | 0 | 39 | 0.0019 | R.GINAVMPSAEEFPYSVR.V | |
| | | | | | 875.52 | 2623.54 | 2624.31 | -0.77 | 0 | 53 | 4.8e-005 | K.AEAGKPTWDWTAPVEDEALVAQIK.E | |
| | | | | | 899.48 | 2695.41 | 2696.18 | -0.77 | 0 | 73 | 5.1e-007 | K.EGDDFVVLSDILGDEDHLGDMDFK.V | Oxidation (M) |
| SO0842 | translation elongation factor G, FusA_2 | 368 | 77 | 19.0 | 455.33 | 908.66 | 909.51 | -0.85 | 0 | 56 | 4.9e-005 | R.FGALTFVR.I | |
| | | | | | 825.18 | 1648.35 | 1648.78 | -0.43 | 0 | 75 | 5.5e-007 | K.DVPANMVDLVEEYR.E | |
| | | | | | 877.71 | 1753.40 | 1753.87 | -0.48 | 0 | 74 | 1e-006 | K.ADVPLSEMFGYIGSLR.T | |
| | | | | | 897.21 | 1792.40 | 1792.94 | -0.53 | 0 | 38 | 0.0024 | R.TYGVELIVGEPQVAYR.E | |
| | | | | | 934.64 | 1867.27 | 1867.86 | -0.59 | 0 | 36 | 0.0062 | K.AYVWDDSGIPENFEVK.D | |
| | | | | | 1023.12 | 2044.23 | 2044.97 | -0.74 | 0 | 65 | 4.3e-006 | K.VDVFSPDDNVGDVIGDLNR.R | |
| | | | | | 750.54 | 2248.61 | 2248.99 | -0.38 | 0 | 52 | 9.2e-005 | K.IGEVHDGESTTDFMVQEAER.G | |
| | | | | | 845.54 | 2533.60 | 2534.19 | -0.59 | 0 | 25 | 0.068 | K.VLDGGIAVFCGSGGVEPQSETNWR.Y | |
| SO2492 | oxidoreductase, acyl-CoA dehydrogenase fa | 317 | 83 | 11.0 | 567.88 | 1133.75 | 1133.65 | 0.11 | 0 | 62 | 1.1e-005 | K.EGFFALIIPK.K | |
| | | | | | 645.29 | 1288.56 | 1288.67 | -0.11 | 0 | 48 | 0.00024 | R.LAAINVNDFEAL.- | |
| | | | | | 646.29 | 1290.56 | 1290.65 | -0.09 | 0 | 55 | 5.3e-005 | R.GEFNGEEVLGLK.L | |
| | | | | | 681.82 | 1361.63 | 1361.73 | -0.10 | 0 | 54 | 6.1e-005 | R.IIANTYQLEAAR.R | |
| | | | | | 711.77 | 1421.53 | 1421.69 | -0.16 | 0 | 30 | 0.019 | K.DLPPELWDYFK.K | |
| | | | | | 856.23 | 1710.45 | 1710.89 | -0.43 | 0 | 44 | 0.00066 | R.MGDVLSQLYLGSATLK.L | Oxidation (M) |
| | | | | | 574.01 | 1719.00 | 1718.87 | 0.13 | 0 | 24 | 0.047 | K.MATELVSGMLKPSPAR.E | Oxidation (M) |
| SO3033 | ferric alcaligin siderophore receptor, FauA | 300 | 78 | 13.0 | 617.34 | 1232.67 | 1232.65 | 0.02 | 0 | 49 | 0.0002 | R.VYQTVNSPLGR.V | |
| | | | | | 744.79 | 1487.57 | 1487.80 | -0.23 | 0 | 51 | 0.00012 | R.TGDVLPGTTIPVYR.E | |
| | | | | | 811.21 | 1620.40 | 1620.78 | -0.38 | 0 | 68 | 3e-006 | R.GMVDLSSGLTDSGNIR.G | |
| | | | | | 902.16 | 1802.30 | 1802.85 | -0.55 | 0 | 60 | 1.9e-005 | R.FNYGDNLIDTAIYER.V | |
| | | | | | 1021.13 | 2040.24 | 2041.04 | -0.80 | 0 | 35 | 0.0038 | R.GIAVTSILYDGVPTTYDTR.F | |
| | | | | | 805.92 | 2414.73 | 2415.15 | -0.42 | 0 | 37 | 0.0065 | R.QEFANPYYYPTAAVPPLGDFR.D | |
| SO4523 | TonB-dependent adherence-conferring pro | 215 | 73 | 9.0 | 616.84 | 1231.66 | 1231.59 | 0.07 | 0 | 27 | 0.072 | K.FSAGIYNAFDK.E | |
| | | | | | 666.78 | 1331.54 | 1331.60 | -0.06 | 0 | 23 | 0.084 | R.WDFGTSDTYIK.H | |
| | | | | | 717.30 | 1432.59 | 1432.77 | -0.17 | 0 | 62 | 9.3e-006 | R.IVVTASGFEQQVR.D | |
| | | | | | 749.23 | 1496.45 | 1496.75 | -0.30 | 0 | 51 | 0.00026 | R.GMGSQYTLILVDGK.R | Oxidation (M) |
| | | | | | 548.57 | 1642.70 | 1642.72 | -0.02 | 0 | 56 | 8.2e-005 | R.LDDDENFGEHLSPR.I | |
| SO0425 | dihydrolipoamide acetyltransferase, AceF | 200 | 70 | 6.0 | 638.29 | 1274.56 | 1274.65 | -0.09 | 0 | 50 | 0.00021 | K.FGEVEEIPLSR.I | |
| | | | | | 733.28 | 1464.55 | 1464.72 | -0.17 | 0 | 76 | 3.7e-007 | R.EFGVDLTQVTGSGR.K | |
| | | | | | 808.88 | 2423.62 | 2424.22 | -0.60 | 0 | 55 | 3.7e-005 | K.TLQQFPVFNSSLSSDGESLIQK.K | |
| SO2912 | pyruvate formate-lyase, PflB | 208 | 85 | 7.0 | 653.30 | 1304.59 | 1304.67 | -0.09 | 0 | 43 | 0.00075 | K.SGVLTGLPDAYGR.G | |
| | | | | | 672.32 | 1342.62 | 1342.68 | -0.06 | 0 | 75 | 4.8e-007 | R.TSSFLDIYIER.D | |
| | | | | | 589.95 | 1766.84 | 1767.97 | -1.14 | 1 | 21 | 0.1 | K.DLETIVGLQTDAPLKR.A | |
| | | | | | 749.59 | 2245.75 | 2246.13 | -0.38 | 1 | 72 | 1.8e-006 | R.EMLEDAVVNPDKYPQLTIR.V | Oxidation (M) |
| SO0228 | translation elongation factor G, FusA_1 | 154 | 77 | 7.0 | 775.77 | 1549.52 | 1549.85 | -0.33 | 0 | 48 | 0.00026 | K.IATDPFVGTLTFIR.V | |
| | | | | | 872.68 | 1743.34 | 1743.87 | -0.53 | 0 | 54 | 0.00011 | R.VYSGVLESGSGVYNSVK.Q | |
| | | | | | 810.63 | 2428.86 | 2429.22 | -0.36 | 0 | 52 | 0.00017 | K.LEPNEEGAGYEFINAIVGGVVPR.E | |
| SO1894 | methylcrotonyl-CoA carboxylase, MccA | 119 | 76 | 10.0 | 791.22 | 1580.42 | 1580.80 | -0.39 | 0 | 29 | 0.018 | K.VVEEAPAPGLSDELR.A | |
| | | | | | 578.68 | 1733.03 | 1732.94 | 0.09 | 0 | 34 | 0.015 | K.AGELVSDGAVLLHVEPK.A | |
| | | | | | 680.31 | 2037.90 | 2038.04 | -0.14 | 0 | 21 | 0.088 | R.LQVEHPVTEMVTGQDLVK.W | Oxidation (M) |
| | | | | | 754.93 | 2261.76 | 2262.08 | -0.32 | 0 | 40 | 0.0012 | K.AQAQAIHPGYGFLSENADFAR.K | |
| SO4743 | TonB-dependent receptor | 82 | 76 | 7.0 | 552.33 | 1102.65 | 1101.55 | 1.11 | 0 | 26 | 0.076 | K.AGIDAGGWLDK.Q | |
| | | | | | 852.70 | 1703.38 | 1703.83 | -0.45 | 0 | 26 | 0.045 | R.LDSAPSLIEGSEDPFK.D | |
| | | | | | 989.43 | 2965.27 | 2966.48 | -1.20 | 0 | 30 | 0.011 | R.VIPGQPIIQQDLDYHQGQLSNPSEYK.Y | |

**A4**

| Gene | Annotation | Mascot Score | Mass (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SO3545 | OmpA family protein | 1469 | 40 | 41.0 | 552.83 | 1103.65 | 1103.61 | 0.04 | 0 | 58 | 3.7e-005 | R.IEAIVTTTEK.Q | |
| | | | | | 630.85 | 1259.69 | 1259.71 | -0.02 | 1 | 73 | 1.3e-006 | R.RIEAIVTTTEK.Q | |
| | | | | | 742.22 | 1482.43 | 1482.70 | -0.27 | 0 | 88 | 3.9e-008 | K.VDSVGCTLYENVK.K | |
| | | | | | 755.32 | 1508.62 | 1508.85 | -0.22 | 0 | 59 | 6e-005 | K.GATLGLVGVWPLGNR.W | |
| | | | | | 903.67 | 1805.33 | 1805.88 | -0.55 | 0 | 107 | 5.9e-010 | K.QEDVGSIQFANDSAVVK.K | |
| | | | | | 603.00 | 1805.97 | 1804.97 | 1.00 | 0 | 65 | 6.1e-006 | R.VTSNGYGITKPLVAGNSK.E | |
| | | | | | 932.12 | 1862.23 | 1862.86 | -0.64 | 0 | 132 | 1.5e-012 | R.DLGSADWTTGGISNDAGVK.G | |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | 645.46 | 1933.35 | 1933.97 | -0.62 | 1 | 94 | 9.1e-009 | K.KQEDVGSIQFANDSAVVK.K | |
| | | | | | 688.32 | 2061.95 | 2062.07 | -0.12 | 2 | 57 | 4.1e-005 | K.KQEDVGSIQFANDSAVVKK.E | |
| | | | | | 737.34 | 2945.34 | 2944.41 | 0.93 | 0 | 24 | 0.097 | R.FGTPAAAAPVAAAVVAAAPVDSDNDGVYDDK.D | |
| | | | | | 1048.01 | 3140.99 | 3142.37 | -1.37 | 0 | 47 | 0.0009 | R.YENLDDTDFNTIEADSNYWGLELSYR.F | |
| | | | | | 1100.34 | 3298.00 | 3298.47 | -0.46 | 1 | 30 | 0.022 | R.RYENLDDTDFNTIEADSNYWGLELSYR.F | |
| SO1821 | outer membrane porin | 467 | 44 | 31.0 | 618.71 | 1235.40 | 1236.58 | -1.18 | 0 | 61 | 4.2e-005 | R.ELSDGWNAFAK.L | |
| | | | | | 640.83 | 1279.64 | 1279.67 | -0.03 | 0 | 86 | 4.8e-008 | K.EAVGAETLLSYK.F | |
| | | | | | 695.31 | 1388.60 | 1388.70 | -0.10 | 0 | 46 | 0.0011 | R.YFVSYNILDAGK.D | |
| | | | | | 790.68 | 1579.35 | 1579.69 | -0.34 | 0 | 67 | 5.9e-006 | R.FESVQDEFFYNR.L | |
| | | | | | 837.17 | 1672.33 | 1672.84 | -0.50 | 0 | 65 | 8.7e-006 | R.VINTQGETEVVNGASR.I | |
| | | | | | 1005.25 | 2008.49 | 2008.03 | 0.46 | 0 | 33 | 0.026 | K.DYVIQPNLPIYANDVFK.R | |
| | | | | | 1010.16 | 2018.30 | 2017.99 | 0.31 | 0 | 47 | 0.00047 | K.LEWGVNPVGNSDIVYSNR.F | |
| | | | | | 953.53 | 2857.57 | 2858.33 | -0.76 | 1 | 39 | 0.0048 | R.KDFSDFTGVDEAAMALSEDDGIAIGIR.Y | Oxidation (M) |
| SO0256 | DNA-directed RNA polymerase, alpha subu | 217 | 36 | 11.0 | 637.31 | 1272.61 | 1272.67 | -0.06 | 0 | 65 | 9e-006 | R.LVDIEQVNSTR.A | |
| | | | | | 638.30 | 1274.58 | 1273.70 | 0.88 | 0 | 61 | 3.7e-005 | R.LLVDASFSPVAR.I | |
| | | | | | 863.26 | 1724.51 | 1724.96 | -0.45 | 0 | 83 | 1.5e-007 | K.EGVQEDILEILLNLK.G | |
| SO4693 | type I secretion membrane fusion protein, | 134 | 40 | 24.0 | 586.31 | 1170.60 | 1170.64 | -0.03 | 0 | 28 | 0.035 | K.AALVSANADLAR.A | |
| | | | | | 829.75 | 1657.48 | 1657.89 | -0.41 | 0 | 74 | 1.2e-006 | K.EALASVTVAEAAINTAK.I | |
| | | | | | 837.71 | 1673.41 | 1673.90 | -0.49 | 0 | 40 | 0.0033 | K.INLEYTEVLAPISGR.I | |
| | | | | | 891.71 | 1781.41 | 1781.93 | -0.53 | 0 | 40 | 0.0053 | R.AMLNAGTDPQAILVPQK.A | Oxidation (M) |
| | | | | | 937.65 | 1873.29 | 1873.94 | -0.65 | 0 | 35 | 0.0072 | R.AEFPNPDGVLLPGMYVR.A | |
| | | | | | 629.16 | 1884.45 | 1884.05 | 0.41 | 0 | 28 | 0.051 | K.AFLEAEVRPQVNGIITK.R | |
| SO3896 | outer membrane porin, putative | 109 | 40 | 11.0 | 636.17 | 1270.32 | 1271.58 | -1.26 | 0 | 46 | 0.0015 | R.SADGVWYYSPK.I | |
| | | | | | 835.27 | 1668.53 | 1668.82 | -0.29 | 0 | 42 | 0.0029 | K.TNESLYALSATLGDSK.F | |
| | | | | | 587.70 | 1760.09 | 1759.97 | 0.12 | 0 | 48 | 0.00073 | K.YTEVQIIDGKPTVVAK.S | |

**A5**

| Gene | Annotation | Mascot Score | Mass (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SO3896 | Outer membrane porin, putative | 7512 | 40 | 59.0 | 396.78 | 791.55 | 791.45 | 0.09 | 0 | 24 | 0.093 | R.NTFLGLK.T | |
| | | | | | 468.32 | 934.63 | 934.49 | 0.15 | 0 | 64 | 9.7e-006 | K.GIAGIDAYR.G | |
| | | | | | 636.71 | 1271.40 | 1271.58 | -0.18 | 0 | 89 | 3.1e-008 | R.SADGVWYYSPK.I | |
| | | | | | 731.20 | 1460.39 | 1460.69 | -0.31 | 0 | 104 | 1.2e-009 | K.DQNYYLAVAYNK.G | |
| | | | | | 743.19 | 1484.37 | 1484.64 | -0.27 | 0 | 90 | 2.6e-008 | K.STMVYGQYSMYR.G | |
| | | | | | 781.72 | 1561.43 | 1561.77 | -0.35 | 0 | 89 | 3e-008 | K.VDLQDDNVFSVGVR.Y | |
| | | | | | 835.17 | 1668.33 | 1668.82 | -0.49 | 0 | 112 | 1.8e-010 | K.TNESLYALSATLGDSK.F | |
| | | | | | 587.64 | 1759.91 | 1759.97 | -0.06 | 0 | 66 | 1.4e-005 | K.YTEVQIIDGKPTVVAK.S | |
| | | | | | 967.57 | 1933.12 | 1933.88 | -0.76 | 0 | 84 | 9e-008 | K.QAEGNVDVFGNTNADIDR.L | |
| | | | | | 1022.58 | 2043.15 | 2043.95 | -0.80 | 0 | 101 | 3.5e-009 | K.STTGTDISVQNFNVGADYR.F | |
| | | | | | 708.55 | 2122.63 | 2122.92 | -0.30 | 0 | 95 | 9.3e-009 | K.AEYGVDEAGFGNYYNNVNK.Y | |
| | | | | | 771.90 | 2312.69 | 2313.14 | -0.44 | 0 | 102 | 3.1e-009 | K.IADLVTLNATYLFDDNDTTAK.T | |
| | | | | | 1216.01 | 2430.01 | 2431.13 | -1.12 | 0 | 72 | 1.2e-006 | K.NYADENNGGTYLENNFSLLGVK.G | |
| | | | | | 811.94 | 2432.81 | 2433.22 | -0.41 | 0 | 77 | 4.9e-007 | R.LELALTNTETGATLQSGTNGVDTK.N | |
| SO3545 | OmpA family protein | 645 | 40 | 21.0 | 630.88 | 1259.75 | 1259.71 | 0.04 | 1 | 45 | 0.0018 | R.RIEAIVTTTEK.Q | |
| | | | | | 742.22 | 1482.43 | 1482.70 | -0.27 | 0 | 58 | 8.8e-005 | K.VDSVGCTLYENVK.K | |
| | | | | | 903.66 | 1805.31 | 1805.88 | -0.57 | 0 | 63 | 1.6e-005 | K.QEDVGSIQFANDSAVVK.K | |
| | | | | | 603.00 | 1805.96 | 1804.97 | 0.99 | 0 | 73 | 2.5e-006 | R.VTSNGYGITKPLVAGNSK.E | |
| | | | | | 932.12 | 1862.23 | 1862.86 | -0.63 | 0 | 129 | 3.2e-012 | R.DLGSADWTTGGISNDAGVK.G | |
| | | | | | 645.63 | 1933.87 | 1933.97 | -0.11 | 1 | 100 | 2e-009 | K.KQEDVGSIQFANDSAVVK.K | |
| SO2929 | expressed protein of unknown function | 76 | 41 | 6.0 | 617.35 | 1232.68 | 1232.68 | -0.00 | 0 | 40 | 0.0044 | R.IVFLATGDEIR.S | |
| | | | | | 682.26 | 1362.51 | 1362.69 | -0.18 | 0 | 65 | 1.6e-005 | R.VQEFLNELMPK.L | Oxidation (M) |

**B1**

| Gene | Annotation | Mascot Score | Mass (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SO3935 | ribonuclease R, Rnr | 1135 | 91 | 27.0 | 607.77 | 1213.52 | 1213.67 | -0.14 | 0 | 75 | 6.3e-007 | R.QGDVVVVELTR.R | |
| | | | | | 643.75 | 1285.49 | 1285.67 | -0.18 | 0 | 85 | 6.1e-008 | K.MDLISGTVLGHK.E | |
| | | | | | 670.23 | 1338.44 | 1338.62 | -0.18 | 0 | 39 | 0.0025 | R.QIDLMMLGDSGK.G | |
| | | | | | 693.22 | 1384.42 | 1384.72 | -0.30 | 0 | 81 | 1.2e-007 | R.SLPLVTIDGEDAR.D | |
| | | | | | 694.21 | 1386.41 | 1386.74 | -0.32 | 0 | 60 | 1.6e-005 | R.ITQEILIASEDR.N | |
| | | | | | 707.18 | 1412.36 | 1412.65 | -0.29 | 0 | 80 | 1.8e-007 | R.LCMVAEMTISAR.G | |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | 745.67 | 1489.32 | 1489.73 | -0.40 | 0 | 55 | 7e-005 | K.QMAPGMEIEIALR.N | |
| | | | | | 528.35 | 1582.03 | 1580.77 | 1.26 | 0 | 43 | 0.0015 | K.ISNGLCSLNPHVDR.L | |
| | | | | | 839.15 | 1676.28 | 1676.85 | -0.56 | 0 | 78 | 2.7e-007 | K.IIEECMILANVSAAK.F | |
| | | | | | 608.79 | 1823.35 | 1822.87 | 0.48 | 1 | 27 | 0.031 | R.FHVDSGMAFVIADDKR.I | Oxidation (M) |
| | | | | | 637.90 | 1910.68 | 1910.88 | -0.20 | 0 | 85 | 9.6e-008 | R.DFDDAVYAEVKPSGGWR.L | |
| | | | | | 961.10 | 1920.18 | 1920.97 | -0.78 | 0 | 65 | 4e-006 | R.GNSVYFPSQVIPMLPEK.I | |
| | | | | | 680.33 | 2037.95 | 2039.07 | -1.12 | 0 | 56 | 2.9e-005 | R.LIGEHTGQVYQVGDPVTVK.V | |
| | | | | | 700.58 | 2098.71 | 2099.03 | -0.32 | 0 | 91 | 2.6e-008 | R.GAIAFETIETQFIFNDQR.K | |
| | | | | | 754.81 | 2261.42 | 2262.02 | -0.60 | 0 | 39 | 0.0013 | K.EGYGFFKPDEGGDDLFISNR.D | |
| SO2427 | TonB-dependent receptor | 566 | 92 | 24.0 | 453.73 | 905.44 | 905.50 | -0.06 | 0 | 30 | 0.044 | K.LTGEFALR.L | |
| | | | | | 558.71 | 1115.41 | 1114.58 | 0.83 | 0 | 33 | 0.016 | K.VIDANGNWVK.R | |
| | | | | | 656.18 | 1310.35 | 1310.59 | -0.24 | 0 | 51 | 0.00024 | R.IYNQDTDTWR.L | |
| | | | | | 698.76 | 1395.50 | 1395.75 | -0.24 | 0 | 37 | 0.0035 | R.SNQQLAAQPAQIK.L | |
| | | | | | 799.64 | 1597.27 | 1597.80 | -0.53 | 0 | 33 | 0.0087 | K.IGLTYTATDELMVR.T | Oxidation (M) |
| | | | | | 625.90 | 1874.69 | 1874.93 | -0.24 | 0 | 67 | 6.8e-006 | R.QDMETASPVTVIDAAAIK.A | Oxidation (M) |
| | | | | | 734.86 | 2201.56 | 2202.07 | -0.51 | 0 | 48 | 0.00048 | R.VQDPTAGCLTLDQGMIDAGIK.A | |
| | | | | | 738.65 | 2212.92 | 2213.94 | -1.02 | 0 | 29 | 0.042 | R.TETYDYSNDVYFQTPSER.R | |
| | | | | | 1146.42 | 2290.83 | 2292.00 | -1.17 | 0 | 77 | 3.9e-007 | R.SMTDVYTDYDANDNPFVAVR.G | |
| | | | | | 775.74 | 2324.18 | 2323.97 | 0.22 | 0 | 77 | 4.8e-007 | K.FEQDGENYTGTIDGNMGAYAR.V | Oxidation (M) |
| | | | | | 790.79 | 2369.35 | 2370.04 | -0.69 | 1 | 25 | 0.072 | K.RTETYDYSNDVYFQTPSER.R | |
| | | | | | 803.16 | 2406.46 | 2406.15 | 0.31 | 0 | 50 | 0.0001 | R.MVNSGSGADSAVDLNSIPVAMIAR.V | Oxidation (M) |
| | | | | | 1003.72 | 3008.13 | 3008.47 | -0.34 | 0 | 53 | 0.00013 | K.NLTDEKPLYVTNGSDAGTVPQVYDTVGR.T | |
| SO0432 | aconitate hydratase 2, AcnB | 483 | 94 | 17.0 | 599.25 | 1196.49 | 1196.53 | -0.04 | 0 | 26 | 0.071 | K.WMIAEGYGDR.R | |
| | | | | | 615.29 | 1228.56 | 1228.69 | -0.13 | 0 | 56 | 4.7e-005 | R.VLEIEGLESLK.V | |
| | | | | | 629.76 | 1257.50 | 1257.66 | -0.16 | 0 | 33 | 0.0099 | R.IPPGVDEAAYVK.A | |
| | | | | | 727.18 | 1452.35 | 1452.75 | -0.40 | 0 | 66 | 9.5e-006 | R.DGIEPDVAGSVGPIK.K | |
| | | | | | 734.71 | 1467.40 | 1468.71 | -1.31 | 0 | 52 | 0.00013 | R.LPTVEEYQEYAK.E | |
| | | | | | 776.13 | 1550.24 | 1550.72 | -0.48 | 0 | 93 | 1e-008 | K.VEQAFELSDASAER.S | |
| | | | | | 824.11 | 1646.21 | 1646.76 | -0.55 | 0 | 86 | 6.2e-008 | K.DQLTEEGYYGIFGR.V | |
| | | | | | 855.19 | 1708.37 | 1708.88 | -0.51 | 0 | 92 | 1.8e-008 | K.GFPLVYVGDVVGTGSSR.K | |
| | | | | | 742.56 | 2224.65 | 2223.15 | 1.50 | 0 | 67 | 5.8e-006 | K.LVQNPPAGEEAFVLDLLENR.I | |
| | | | | | 836.08 | 2505.23 | 2506.27 | -1.04 | 0 | 29 | 0.028 | K.IAPIFFNTMEDAGALPIELDVSK.M | Oxidation (M) |
| SO0424 | pyruvate dehydrogenase, E1 component, A | 327 | 100 | 12.0 | 516.76 | 1031.51 | 1032.54 | -1.03 | 0 | 35 | 0.0062 | R.YWDPLLAR.D | |
| | | | | | 596.76 | 1191.51 | 1191.59 | -0.08 | 0 | 85 | 6.2e-008 | R.LSEDQLANFR.Q | |
| | | | | | 617.23 | 1232.44 | 1232.64 | -0.20 | 0 | 62 | 1e-005 | K.IIQELEGEFR.G | |
| | | | | | 639.25 | 1276.49 | 1276.66 | -0.16 | 0 | 75 | 7.4e-007 | K.FSEELEVPSLK.I | |
| | | | | | 654.23 | 1306.45 | 1305.67 | 0.79 | 0 | 52 | 8.7e-005 | K.IFDSILQGSNGR.E | |
| | | | | | 801.61 | 1601.20 | 1602.73 | -1.54 | 0 | 76 | 4.5e-007 | K.YVPQDSDQVAYYR.E | |
| | | | | | 786.79 | 2357.34 | 2358.14 | -0.81 | 0 | 24 | 0.1 | K.QAYISQVISSDAPAIAATDYMK.I | Oxidation (M) |
| | | | | | 1004.03 | 3009.08 | 3010.42 | -1.35 | 0 | 27 | 0.045 | R.FNIPIPDDQLEDLPFYHPGPDSEEVK.Y | |
| SO1521 | respiratory FAD-dependent D-lactate dehy | 177 | 103 | 9.0 | 570.75 | 1139.48 | 1139.62 | -0.14 | 0 | 32 | 0.011 | K.IGPDPATIASAK.I | |
| | | | | | 625.27 | 1248.53 | 1248.64 | -0.11 | 0 | 61 | 1.4e-005 | K.ITGDGITNALMK.T | Oxidation (M) |
| | | | | | 675.65 | 1349.29 | 1349.60 | -0.32 | 0 | 45 | 0.00055 | R.FAWSTDASYFR.I | |
| | | | | | 753.76 | 1505.51 | 1505.79 | -0.28 | 0 | 53 | 0.00011 | K.IPVLVDALSCTYR.T | |
| | | | | | 635.88 | 1904.63 | 1904.88 | -0.25 | 0 | 52 | 0.0002 | R.ADDAQTLEHYTQDVTAK.L | |
| | | | | | 812.40 | 2434.17 | 2433.17 | 1.00 | 0 | 24 | 0.085 | K.LAGFDFIRPMEFSTNPAVYDK.Y | Oxidation (M) |
| SO3193 | polysaccharide biosynthesis/export protei | 151 | 100 | 4.0 | 713.21 | 1424.40 | 1424.77 | -0.38 | 0 | 45 | 0.00056 | R.AGAGIQVVGVDGQVR.L | |
| | | | | | 754.72 | 1507.43 | 1507.76 | -0.33 | 0 | 81 | 2.1e-007 | K.MLANLFDDAELLK.L | Oxidation (M) |
| | | | | | 776.68 | 1551.35 | 1551.77 | -0.42 | 0 | 72 | 1.4e-006 | K.VIVFNFSDDVQNR.F | |
| SO2907 | TonB-dependent receptor domain protein | 120 | 96 | 4.0 | 542.73 | 1083.44 | 1083.52 | -0.08 | 0 | 43 | 0.00072 | K.TFDGLAFDAK.F | |
| | | | | | 602.79 | 1203.57 | 1204.65 | -1.07 | 0 | 83 | 2e-007 | R.YEALDNLVLR.A | |
| | | | | | 767.39 | 2299.15 | 2299.98 | -0.83 | 0 | 38 | 0.0045 | K.AGSACGFNHFDGTDYLPDQTK.D | |

**B2**

| Gene | Annotation | Mascot Score | Mass (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SO1126 | chaperone protein, DnaK | 490 | 69 | 23.0 | 613.24 | 1224.47 | 1224.64 | -0.17 | 0 | 51 | 0.00027 | R.LINYLADEFK.K | |
| | | | | | 620.25 | 1238.48 | 1238.63 | -0.15 | 0 | 61 | 1.1e-005 | K.VQEAVTNFFGK.E | |
| | | | | | 649.67 | 1297.33 | 1298.69 | -1.36 | 0 | 43 | 0.0014 | K.MAPPQVSAEILK.K | Oxidation (M) |
| | | | | | 650.28 | 1298.54 | 1298.74 | -0.20 | 0 | 45 | 0.00042 | K.LESLVEDLIIR.T | |
| | | | | | 660.27 | 1318.52 | 1318.68 | -0.16 | 0 | 71 | 1.7e-006 | K.IEAAMSAVETAVK.G | |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | 758.66 | 1515.30 | 1515.73 | -0.43 | 0 | 79 | 3.9e-007 | K.IIAADNGDAWVESR.G | |
| | | | | | 782.72 | 1563.42 | 1563.80 | -0.38 | 0 | 41 | 0.002 | R.QAVTNPNNTFFAIK.R | |
| | | | | | 804.60 | 1607.19 | 1607.75 | -0.55 | 0 | 54 | 6e-005 | K.ASSGLSEEEVAQMVR.D | Oxidation (M) |
| | | | | | 806.66 | 1611.32 | 1612.82 | -1.51 | 0 | 63 | 9.9e-006 | K.SLGQFNLDGIEPAPR.G | |
| | | | | | 830.16 | 1658.31 | 1658.89 | -0.58 | 0 | 89 | 2.3e-008 | R.IINEPTAAALAYGIDK.K | |
| | | | | | 1060.09 | 2118.17 | 2119.07 | -0.90 | 0 | 34 | 0.0067 | R.TTPSIIAYTDDETIVGQPAK.R | |
| SO1776 | outer membrane protein, MtrB | 450 | 78 | 13.0 | 626.69 | 1251.37 | 1251.54 | -0.17 | 0 | 47 | 0.00034 | R.LTGSYDYYDR.D | |
| | | | | | 677.69 | 1353.36 | 1353.64 | -0.28 | 0 | 37 | 0.0035 | K.QGQYNVNVNYR.Q | |
| | | | | | 717.66 | 1433.32 | 1433.65 | -0.33 | 0 | 75 | 6.1e-007 | R.QGITGDYGDYFAK.V | |
| | | | | | 728.14 | 1454.27 | 1454.65 | -0.38 | 0 | 65 | 8.6e-006 | R.ASVDAYQLGMDGGR.L | |
| | | | | | 772.15 | 1542.29 | 1542.68 | -0.39 | 0 | 84 | 7.2e-008 | R.VNSFDTWDMWVK.G | |
| | | | | | 952.09 | 1902.16 | 1902.91 | -0.75 | 0 | 74 | 6.3e-007 | R.YALDDYTDTVIGLTESK.D | |
| | | | | | 1034.48 | 2066.95 | 2067.99 | -1.04 | 0 | 69 | 1.5e-006 | R.ILTGQMSQDQALVTDNYR.Y | Oxidation (M) |
| SO1779 | Decaheme cytochrome c, OmcA | 410 | 80 | 12.0 | 468.32 | 934.63 | 934.49 | 0.14 | 0 | 43 | 0.00096 | K.VPTSFAWK.A | |
| | | | | | 483.33 | 964.65 | 964.50 | 0.15 | 0 | 26 | 0.043 | R.AWLYGDIK.N | |
| | | | | | 543.85 | 1085.68 | 1085.62 | 0.06 | 0 | 100 | 1.8e-009 | K.SNVVTGIALGR.S | |
| | | | | | 629.31 | 1256.60 | 1256.59 | 0.00 | 0 | 59 | 2.7e-005 | K.EFISDPSAYTK.S | |
| | | | | | 650.80 | 1299.58 | 1299.62 | -0.05 | 0 | 54 | 6e-005 | R.YAYIQDQPFR.F | |
| | | | | | 670.78 | 1339.55 | 1339.66 | -0.12 | 0 | 62 | 1.3e-005 | K.TFTIDSTNSNLK.L | |
| SO3669 | TonB-dependent haem/haemoglobin recep | 335 | 76 | 22.0 | 522.26 | 1042.50 | 1042.51 | -0.01 | 0 | 27 | 0.039 | K.LTYGVDGYR.D | |
| | | | | | 658.20 | 1314.39 | 1314.62 | -0.23 | 0 | 44 | 0.00067 | R.GSYFMDPELLK.S | |
| | | | | | 675.22 | 1348.42 | 1348.65 | -0.23 | 0 | 71 | 1.3e-006 | R.VDFAIENIGDEK.Y | |
| | | | | | 725.17 | 1448.32 | 1448.71 | -0.39 | 0 | 66 | 5.6e-006 | K.GLCNTFATNPNLK.S | |
| | | | | | 830.14 | 1658.26 | 1658.86 | -0.60 | 0 | 52 | 0.00012 | R.TVGINLNNSSQLGNTK.L | |
| | | | | | 929.09 | 1856.17 | 1856.89 | -0.72 | 0 | 28 | 0.023 | K.SAQDFLAPNETFGGYLK.Q | |
| | | | | | 943.57 | 1885.12 | 1885.94 | -0.83 | 0 | 51 | 0.00012 | R.VTYVASQTNTPTGYSVAK.Y | |
| | | | | | 636.92 | 1907.73 | 1907.90 | -0.18 | 0 | 39 | 0.0016 | R.NDVDDFIVQQVSNPYR.G | |
| | | | | | 722.55 | 2164.64 | 2165.05 | -0.41 | 0 | 74 | 5e-007 | K.SAEQGVVETEFDEVLVSATR.L | |
| | | | | | 806.79 | 2417.36 | 2418.16 | -0.79 | 0 | 39 | 0.0014 | K.GQVGQRPEDIDGETTVWGAFTR.A | |
| SO1778 | Decaheme cytochrome c, MtrC | 332 | 72 | 10.0 | 547.26 | 1092.51 | 1092.58 | -0.07 | 0 | 71 | 1.3e-006 | K.ADLAFATLSGK.A | |
| | | | | | 726.71 | 1451.40 | 1451.71 | -0.32 | 0 | 103 | 1e-009 | K.ETLESFGAVVDGTK.D | |
| | | | | | 878.06 | 1754.10 | 1754.78 | -0.68 | 0 | 96 | 3.6e-009 | K.FVDCADPAFDGVDVTK.Y | |
| | | | | | 957.05 | 2868.13 | 2868.31 | -0.18 | 0 | 27 | 0.045 | K.LADGTTVPVAEMVEDFDGQGNAPQYTK.N | Oxidation (M) |
| SO0314 | ornithine decarboxylase, SpeF | 291 | 82 | 14.0 | 467.77 | 933.53 | 933.49 | 0.04 | 0 | 38 | 0.0033 | K.GDLVLFDR.N | |
| | | | | | 564.70 | 1127.39 | 1127.53 | -0.14 | 0 | 29 | 0.04 | R.FFEFEPGQK.W | |
| | | | | | 709.70 | 1417.38 | 1416.69 | 0.69 | 0 | 72 | 1.5e-006 | K.TYFVLNGTSSSNK.V | |
| | | | | | 731.72 | 1461.43 | 1461.77 | -0.34 | 0 | 63 | 7.6e-006 | K.FLLTTPGIDAETGK.Y | |
| | | | | | 755.71 | 1509.41 | 1509.82 | -0.40 | 0 | 40 | 0.0014 | R.GNVELVPLSQIEGR.I | |
| | | | | | 781.16 | 1560.31 | 1560.76 | -0.46 | 0 | 76 | 4.7e-007 | K.VMDPQEANLEFIR.G | |
| | | | | | 812.19 | 1622.36 | 1622.87 | -0.51 | 0 | 28 | 0.046 | K.YEQALLPPFFGTLK.K | |
| | | | | | 734.19 | 2199.55 | 2199.11 | 0.44 | 0 | 45 | 0.00097 | K.LVDEDAPLSEVLPNVYNANK.A | |
| SO0021 | fatty oxidation complex, alpha subunit, Fad | 188 | 77 | 15.0 | 560.24 | 1118.47 | 1119.56 | -1.08 | 0 | 38 | 0.0056 | K.AFDADEIIAR.T | |
| | | | | | 701.24 | 1400.47 | 1400.76 | -0.29 | 0 | 46 | 0.00037 | K.LEDLPFPTASAIK.G | |
| | | | | | 723.75 | 1445.48 | 1445.76 | -0.28 | 0 | 74 | 8.6e-007 | R.ETLASLDAALDSIK.Q | |
| | | | | | 819.66 | 1637.30 | 1637.86 | -0.56 | 0 | 45 | 0.00051 | K.DIAQPALDLGLNEAAK.L | |
| | | | | | 621.96 | 1862.87 | 1863.88 | -1.02 | 0 | 25 | 0.096 | R.GEHSSEETIASVVAYASK.M | |
| | | | | | 662.93 | 1985.77 | 1985.98 | -0.21 | 0 | 28 | 0.052 | R.VIGADNALEWITTGNEQR.A | |
| | | | | | 736.89 | 2207.64 | 2209.20 | -1.57 | 0 | 42 | 0.002 | K.VGAVDAVVAPEALEVAAIQMLK.D | Oxidation (M) |
| SO2402 | ribosomal protein S1, RpsA | 178 | 61 | 17.0 | 616.71 | 1231.41 | 1231.61 | -0.20 | 0 | 26 | 0.044 | K.SESPIPAEQFK.N | |
| | | | | | 707.69 | 1413.36 | 1413.71 | -0.35 | 0 | 57 | 3.9e-005 | K.QLGEDPWLEISK.R | |
| | | | | | 764.21 | 1526.41 | 1526.79 | -0.39 | 0 | 68 | 4.9e-006 | R.DALLENLQEGQAVK.G | |
| | | | | | 797.40 | 1592.78 | 1591.81 | 0.97 | 0 | 27 | 0.044 | K.AYEDAETVIGIINGK.V | |
| | | | | | 813.60 | 1625.19 | 1625.72 | -0.53 | 0 | 42 | 0.001 | K.QTEDDPFNAYLADK.K | |
| | | | | | 820.16 | 1638.30 | 1638.76 | -0.46 | 0 | 23 | 0.079 | K.QEDAVISNAMAEAFK.A | |
| | | | | | 884.04 | 1766.07 | 1766.86 | -0.79 | 0 | 31 | 0.018 | R.IEDASTVYSVGDAIEAK.F | |
| SO3844 | oligopeptidase lipoprotein, M13 family | 141 | 77 | 8.0 | 685.23 | 1368.45 | 1367.78 | 0.67 | 0 | 43 | 0.0013 | R.GVAAVNGVLGEVVGK.V | |
| | | | | | 685.73 | 1369.45 | 1369.68 | -0.23 | 0 | 50 | 0.00014 | K.EAPVIDGLTGDQR.F | |
| | | | | | 713.72 | 1425.43 | 1425.68 | -0.25 | 0 | 82 | 1.1e-007 | K.ALGSGIEFENFDK.S | |
| | | | | | 709.54 | 2125.59 | 2126.07 | -0.49 | 0 | 38 | 0.0027 | K.AIIEEVAATPNLVEGTDEQK.V | |
| SO3033 | ferric alcaligin siderophore receptor, FauA | 140 | 78 | 7.0 | 560.80 | 1119.58 | 1119.58 | 0.00 | 0 | 47 | 0.00087 | R.IDASYIDPVK.G | |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | 585.77 | 1169.52 | 1169.67 | -0.15 | 0 | 35 | 0.0049 | K.DIEIINVVGAK.D | |
| | | | | | 744.71 | 1487.41 | 1487.80 | -0.38 | 0 | 47 | 0.00034 | R.TGDVLPGTTIPVYR.E | |
| | | | | | 902.12 | 1802.22 | 1802.85 | -0.62 | 0 | 80 | 2.6e-007 | R.FNYGDNLIDTAIYER.V | |
| SO2912 | pyruvate formate-lyase, PflB | 129 | 85 | 8.0 | 643.38 | 1284.74 | 1284.68 | 0.06 | 0 | 25 | 0.08 | R.VALYGIDFLMK.D | Oxidation (M) |
| | | | | | 652.70 | 1303.38 | 1303.61 | -0.22 | 0 | 30 | 0.031 | R.VDDIACDLVER.F | |
| | | | | | 653.23 | 1304.45 | 1304.67 | -0.22 | 0 | 65 | 5.1e-006 | K.SGVLTGLPDAYGR.G | |
| | | | | | 672.23 | 1342.44 | 1342.68 | -0.24 | 0 | 30 | 0.034 | R.TSSFLDIYIER.D | |
| | | | | | 806.66 | 1611.32 | 1611.87 | -0.56 | 0 | 32 | 0.013 | K.DLETIVGLQTDAPLK.R | |
| SO2492 | oxidoreductase, acyl-CoA dehydrogenase fa | 128 | 84 | 4.0 | 567.83 | 1133.64 | 1133.65 | -0.01 | 0 | 29 | 0.023 | K.EGFFALIIPK.K | |
| | | | | | 646.26 | 1290.50 | 1290.65 | -0.15 | 0 | 62 | 1.1e-005 | R.GEFNGEEVLGLK.L | |
| | | | | | 681.75 | 1361.49 | 1361.73 | -0.24 | 0 | 60 | 1.6e-005 | R.IIANTYQLEAAR.R | |
| SO1209 | polyribonucleotide nucleotidyltransferase, | 124 | 76 | 8.0 | 608.75 | 1215.49 | 1215.63 | -0.14 | 0 | 26 | 0.044 | R.EVDNLLGSLEK.K | |
| | | | | | 698.74 | 1395.47 | 1395.74 | -0.27 | 0 | 79 | 2e-007 | K.EALLAANPDVDLR.E | |
| | | | | | 750.70 | 1499.38 | 1499.73 | -0.35 | 0 | 34 | 0.0067 | R.DFFPLTVNYQEK.T | |
| | | | | | 899.36 | 2695.06 | 2696.18 | -1.12 | 0 | 51 | 0.00019 | K.EGDDFVVLSDILGDEDHLGDMDFK.V | Oxidation (M) |
| SO4743 | TonB-dependent receptor | 101 | 77 | 4.0 | 787.10 | 1572.18 | 1572.69 | -0.52 | 0 | 64 | 1.2e-005 | R.NLFDTEYLDGGSDK.M | |
| | | | | | 852.63 | 1703.26 | 1703.83 | -0.57 | 0 | 58 | 2.4e-005 | R.LDSAPSLIEGSEDPFK.D | |
| SO3142 | peptidyl-dipeptidase, Dcp_1 | 97 | 80 | 3.0 | 642.27 | 1282.53 | 1282.68 | -0.15 | 0 | 73 | 6.7e-007 | R.VLEDGVFYTLK.E | |
| | | | | | 676.66 | 1351.31 | 1352.69 | -1.39 | 0 | 46 | 0.00078 | K.VTYPSLSGTSVSR.D | |
| SO2629 | isocitrate dehydrogenase, NADP-dependen | 76 | 81 | 4.0 | 704.19 | 1406.37 | 1406.64 | -0.26 | 0 | 31 | 0.016 | K.GYDIPNYPDEPK.T | |
| | | | | | 916.09 | 1830.17 | 1830.94 | -0.77 | 0 | 66 | 3.1e-006 | K.TFEIPADGVVNVIDASGK.V | |

**B3**

| Gene | Annotation | Mascot Score | Mass (kDa) | Coverage | Observed m/z | Mr(expt) | Mr(calc) | Delta | Miss | Score | Expect | Peptide | Var_Mod |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TRPGTR | Trypsin precursor | 205 | 25 | 20.0 | 421.87 | 841.72 | 841.50 | 0.22 | 0 | 44 | 0.05 | R.VATVSLPR.S | |
| | | | | | 737.45 | 2209.32 | 2210.10 | -0.78 | 0 | 110 | 6.6e-009 | R.LGEHNIDVLEGNEQFINAAK.I | |
| | | | | | 761.57 | 2281.69 | 2282.17 | -0.48 | 0 | 75 | 2.6e-005 | K.IITHPNFNGNTLDNDIMLIK.L | |
| I46732 | IG gamma heavy chain comstant region | 171 | 21 | 13.0 | 601.77 | 1201.53 | 1201.61 | -0.08 | 0 | 77 | 2.3e-005 | K.LSVPTSEWQR.G | |
| | | | | | 817.71 | 1633.40 | 1633.89 | -0.49 | 0 | 71 | 8.4e-005 | R.VVSTLPIAHQDWLR.G | |
| GHRB | IG gamma chain C region | 145 | 36 | 9.0 | 601.77 | 1201.53 | 1201.61 | -0.08 | 0 | 77 | 2.3e-005 | K.LSVPTSEWQR.G | |
| | | | | | 1131.09 | 2260.17 | 2260.15 | 0.02 | 0 | 45 | 0.034 | K.GYLPEPVTVTWNSGTLTNGVR.T | |