

Online Resource 5 Proteins identified specifically in intracellular proteins obtained in the presence of Cr(VI) in the culture media.

| Accession^a | Protein identification^a | Protein Length^b (AA) | Mass^c (kDa) |
|------------------------------|--|--|-------------------------------|
| Energy production (1) | | | |
| BAC70593.1 | putative F-type proton-transporting ATPase gamma chain | 305 | 32.924 |
| Biosynthesis (33) | | | |
| AIJ16970.1 | S-adenosylmethionine synthase | 402 | 43.415 |
| AIJ13951.1 | 50S ribosomal protein L3 | 214 | 22.737 |
| AIJ14567.1 | Phosphoribosylformylglycinamidine synthase 2 | 752 | 79.784 |
| AIJ16924.1 | Pyridoxal biosynthesis lyase PdxS | 303 | 32.163 |
| BAC70793.1 | putative ThiF-family protein | 392 | 42.542 |
| CBG70776.1 | 30S ribosomal protein S3 | 277 | 30.099 |
| AIJ13939.1 | 50S ribosomal protein L5 | 185 | 20.822 |
| AIJ13942.1 | 30S ribosomal protein S17 | 95 | 10.696 |
| BAC72973.1 | putative AraC-family transcriptional regulator | 426 | 45.423 |
| BAC72460.1 | putative arginyl-tRNA synthetase | 590 | 65.130 |
| AIJ13937.1 | 30S ribosomal protein S8 | 132 | 14.250 |
| AIJ15517.1 | DNA-binding protein HU (hs1) | 93 | 9.827 |
| AIJ14419.1 | RNA polymerase-binding transcription factor CarD | 160 | 17.800 |
| AIJ13940.1 | 50S ribosomal protein L24 | 107 | 11.565 |
| AIJ15122.1 | Lsr2-like protein | 111 | 11.754 |
| BAC74533.1 | putative threonyl-tRNA synthetase | 658 | 74.160 |
| AIJ15719.1 | Citrate synthase 1 | 429 | 47.696 |
| AIJ16945.1 | Alanine-tRNA ligase | 890 | 95.709 |
| CBG72899.1 | citrate synthase | 429 | 47.769 |
| AIJ13099.1 | 50S ribosomal protein L19 | 116 | 13.116 |
| BAC69955.1 | putative 1-deoxy-D-xylulose 5-phosphate synthase | 642 | 68.666 |
| AIJ13949.1 | 50S ribosomal protein L23 | 139 | 14.951 |
| AIJ13996.1 | 50S ribosomal protein L10 | 176 | 18.617 |
| CBG73723.1 | putative iron-sulphur cluster biosynthesis protein | 118 | 12.420 |

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| AIJ14816.1 | Methionine-tRNA ligase | 538 | 59.686 |
| BAC69358.1 | putative 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase | 385 | 40.771 |
| CBG69989.1 | 50S ribosomal protein L31 | 73 | 8.037 |
| AIJ12991.1 | 30S ribosomal protein S15 | 95 | 10.766 |
| AIJ16963.1 | Carbamoyl-phosphate synthase large chain | 1102 | 117.817 |
| CBG70764.1 | 50S ribosomal protein L30 | 59 | 6.753 |
| AIJ13936.1 | 50S ribosomal protein L6 | 179 | 19.149 |
| AIJ13194.1 | Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B | 504 | 54.433 |
| CBG74380.1 | translation initiation factor IF-3 | 232 | 25.942 |
| Oxide-reduction processes (8) | | | |
| AIJ11726.1 | Ketol-acid reductoisomerase 2 | 332 | 36.251 |
| AIJ13181.1 | Ketol-acid reductoisomerase 1 | 332 | 36.213 |
| AIJ13716.1 | NADP-dependent alcohol dehydrogenase C 1 | 346 | 36.453 |
| AIJ15377.1 | oxidoreductase | 474 | 51.522 |
| AIJ17728.1 | S-(hydroxymethyl)mycothiol dehydrogenase | 362 | 37.936 |
| BAC69838.1 | putative ferredoxin-nitrite reductase | 564 | 62.698 |
| BAC70921.1 | putative 4-hydroxy-3-methylbut-2-enyl diphosphate reductase | 338 | 36.551 |
| AIJ12540.1 | Sulfite reductase [ferredoxin] | 565 | 62.867 |
| Chaperones (1) | | | |
| CBG70719.1 | 10 kD chaperonin cpn10 | 102 | 11.021 |
| Other (36) | | | |
| AIJ13143.1 | 3-isopropylmalate dehydratase large subunit | 476 | 50.430 |
| AIJ15778.1 | putative ABC transporter ATP-binding protein | 554 | 61.499 |
| AIJ14955.1 | Fructose-bisphosphate aldolase | 343 | 36.859 |
| CBG72153.1 | putative phosphoserine aminotransferase | 372 | 39.553 |
| AIJ16370.1 | Cell division protein FtsZ | 399 | 41.052 |
| AIJ16530.1 | Vegetative protein | 254 | 27.616 |
| BAC74039.1 | putative iron-regulated ABC transporter ATP-binding protein | 260 | 28.267 |
| BAC68872.1 | putative ion channel subunit | 320 | 35.143 |
| BAC71748.1 | hypothetical protein SAV_4036 | 95 | 9.620 |
| AIJ11559.1 | two-component system sensory histidine kinase | 1331 | 142.051 |
| BAG19738.1 | conserved hypothetical protein | 162 | 17.928 |

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|-------------------|---|------|---------|
| AIJ13848.1 | Succinyl-CoA ligase [ADP-forming] subunit alpha-1 | 294 | 30.202 |
| AIJ16874.1 | Argininosuccinate lyase | 475 | 50.920 |
| AIJ12546.1 | lipoprotein | 367 | 38.415 |
| BAC74201.1 | putative hydrolase | 342 | 35.068 |
| AIJ16337.1 | Phospho-2-dehydro-3-deoxyheptonate aldolase | 448 | 49.621 |
| CBG74079.1 | cob(I)yrinic acid a,c-diamide adenosyltransferase (EC 2.5.1.17) | 199 | 22.378 |
| AIJ12753.1 | Ornithine carbamoyltransferase | 335 | 36.649 |
| AIJ17905.1 | Catalase-peroxidase | 740 | 80.776 |
| CBG74770.1 | putative adenylosuccinate lyase | 480 | 51.926 |
| BAC74834.1 | putative 6-phosphofructokinase | 341 | 36.385 |
| BAC74125.1 | putative magnesium-chelatase subunit | 689 | 72.062 |
| BAC73188.1 | hypothetical protein SAV_5476 | 376 | 41.004 |
| BAC72227.1 | hypothetical protein SAV_4515 | 175 | 19.949 |
| CBG69102.1 | sulfate adenylyltransferase subunit 1 | 444 | 47.712 |
| BAC73079.1 | putative ABC transporter ATP-binding protein | 547 | 60.516 |
| AIJ13102.1 | hypothetical protein SLIV_10510 | 79 | 8.660 |
| BAG18517.1 | putative M16-family peptidase | 457 | 49.448 |
| BAG23527.1 | putative ABC transporter permease protein | 553 | 56.997 |
| AIJ17150.1 | hypothetical protein SLIV_31310 | 562 | 62.477 |
| BAG19549.1 | putative integral membrane protein | 608 | 60.155 |
| AIJ14612.1 | ATP binding protein | 156 | 17.277 |
| AIJ12950.1 | Glutamate transport ATP-binding protein GluA | 258 | 28.098 |
| AIJ14744.1 | DNA-binding protein | 182 | 19.284 |
| AIJ18085.1 | secreted protein | 242 | 25.135 |
| BAC70569.1 | putative M protein | 1258 | 138.096 |

^a and ^{a'} Function annotations were retrieved from NCBIInr (<http://www.ncbi.nlm.nih.gov>).

^b and ^c Information obtained from ProteoIQ program (local license)

Intracellular proteomic analysis of *Streptomyces* sp. MC1 when exposed to Cr(VI) by gel-based and gel-free methods. Current Microbiology. José O. Bonilla, Eduardo A. Callegari, María C. Estevez, Liliana B. Villegas.
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