

Online Resource 4 Proteins expressed in the presence and absence of Cr(VI) which are found overexpressed in the presence of Cr(VI).

Bar number ^a	Accession ^b	Protein identification ^b	Protein Length (AA) ^c	Mass (kDa) ^d
Energy production				
1	AIJ13322.1	ATP synthase subunit delta	274	29.147
6	BAC70594.1	putative F-type proton-transporting ATPase alpha chain	529	57.211
39	AIJ13319.1	ATP synthase subunit beta	478	52.127
Biosynthesis				
2	AIJ13934.1	30S ribosomal protein S5	201	20.469
3	AIJ13995.1	50S ribosomal protein L7/L12	127	13.183
4	AIJ13920.1	30S ribosomal protein S9	170	18.669
5	AIJ16455.1	30S ribosomal protein S1	502	54.983
9	AIJ13952.1	30S ribosomal protein S10	102	11.496
13	AIJ13020.1	Translation initiation factor IF-2	613	66.056
14	AIJ13086.1	30S ribosomal protein S2	315	34.023
23	AIJ13335.1	Transcription termination factor Rho	707	76.484
26	BAC73900.1	putative glutamate synthase(NADPH) large subunit	1516	162.882
28	AIJ13083.1	Ribosome-recycling factor	185	20.756
33	AIJ16941.1	30S ribosomal protein S4	204	23.579
34	BAC71850.1	putative phosphoribosyl formylglycinamide synthase II	752	79.836
35	AIJ13926.1	DNA-directed RNA polymerase subunit alpha	340	36.655
38	AIJ13986.1	Elongation factor Tu-1	397	43.735
40	AIJ13993.1	DNA-directed RNA polymerase subunit beta'	1299	144.496
41	AIJ13987.1	Elongation factor G 1	708	77.590
42	AIJ13988.1	30S ribosomal protein S7	156	17.402
Oxide-reduction processes				
11	AIJ13180.1	D-3-phosphoglycerate dehydrogenase	529	54.995
16	AIJ13174.1	3-isopropylmalate dehydrogenase	347	36.664
21	AIJ16273.1	dihydrolipoyl dehydrogenase	462	48.889
27	CBG68387.1	NADP(+)-dependent isocitrate dehydrogenase	739	79.132

29	AIJ16638.1	enoyl-ACP reductase	255	27.118
32	BAC73735.2	putative dihydrolipoamide dehydrogenase	462	48.730
36	AIJ16505.1	Glyceraldehyde-3-phosphate dehydrogenase	336	36.228
Chaperones				
10	AIJ13893.1	60 kDa chaperonin 1	541	57.066
15	AIJ15832.1	Trigger factor	468	51.119
30	AIJ14357.1	60 kDa chaperonin 2	541	56.777
Others				
7	AIJ13849.1	Succinyl-CoA ligase [ADP-forming] subunit beta-1	394	41.559
8	AIJ12642.1	Aconitate hydratase 1	904	90.302
12	AIJ13384.1	Multifunctional 2-oxoglutarate metabolism enzyme	1272	139.103
17	AIJ15373.1	Enolase 1	426	45.437
18	CBG70655.1	serine hydroxymethyltransferase	482	51.679
19	CBG70904.1	cold shock protein	67	7.151
20	AIJ12990.1	Polyribonucleotide nucleotidyltransferase	739	79.292
22	AIJ15811.1	Aminopeptidase N	857	94.347
24	BAC72765.1	putative S-adenosyl-L-homocysteine hydrolase	485	52.958
25	AIJ16063.1	hypothetical protein SLIV_25755	82	8.893
31	AIJ16155.1	hypothetical protein SLIV_26220	196	21.582
37	AIJ12373.1	Acetyl-/propionyl-coenzyme A carboxylase alpha chain	590	62.456

^a The identification of bar is based on at least one peptide identified using tandem mass spectrometry analysis (MS/MS).

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

^c and ^d 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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