Online Resource 2

Table S1 Processing parameters used for the analysis

Processing parameters	Attribute	Value
Mass Accuracy		
Electrospray Survey	Perform Lock Mass Calibration	Yes
	Lock Spray Lock Mass	785.8427 Da/e
	Lock Spray Scans	10
	Lock Mass Tolerance	0.1 Da
MSMS	Perform Lock Mass Calibration	Yes
	Lock Spray Lock Mass	785.8427 Da/e
	Lock Spray Scans	10
	Lock Mass Tolerance	0.1 Da
Noise Reduction		
Electrospray Survey	Background Subtract Type	Normal
	Background Threshold	35.00%
	Background Polynomial	5
	Perform Smoothing	Yes
	Smoothing Type	Savitzky-Golay
	Smoothing Iterations	2
	Smoothing Window	3 channels
MSMS	Background Subtract Type	Normal
	Background Threshold	35.00%
	Background Polynomial	5
	Perform Smoothing	Yes
	Smoothing Type	Savitzky-Golay
	Smoothing Iterations	2
	Smoothing Window	3 channels
Deisotoping and Centroiding		
Electrospray Survey	Perform Deisotoping	Yes
	Deisotoping Type	Fast
	Iterations (default)	30
	Automatic Thresholds (default)	No
	Threshold (default)	3%
	Minimum Peak Width	4 Channels
	Centroid Top	80%
	TOF Resolution	10000
	NP Multiplier	70%
MSMS	Perform Deisotoping	Yes
	Deisotoping Type	Fast
	Iterations (default)	30
	Automatic Thresholds (default)	No
	Threshold (default)	3%
	Minimum Peak Width	4 Channels
	Centroid Top	80%
	TOF Resolution	10000
	NP Multiplier	70%

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.
Corresponding author: Liliana B. Villegas. Instituto de Química San Luis (INQUISAL), CONICET. Chacabuco 917, 5700, San Luis, Argentina. T: +54 266 4520300 (6108). e-mail: lbvilleg@hotmail.com, lbvillegas@unsl.edu.ar