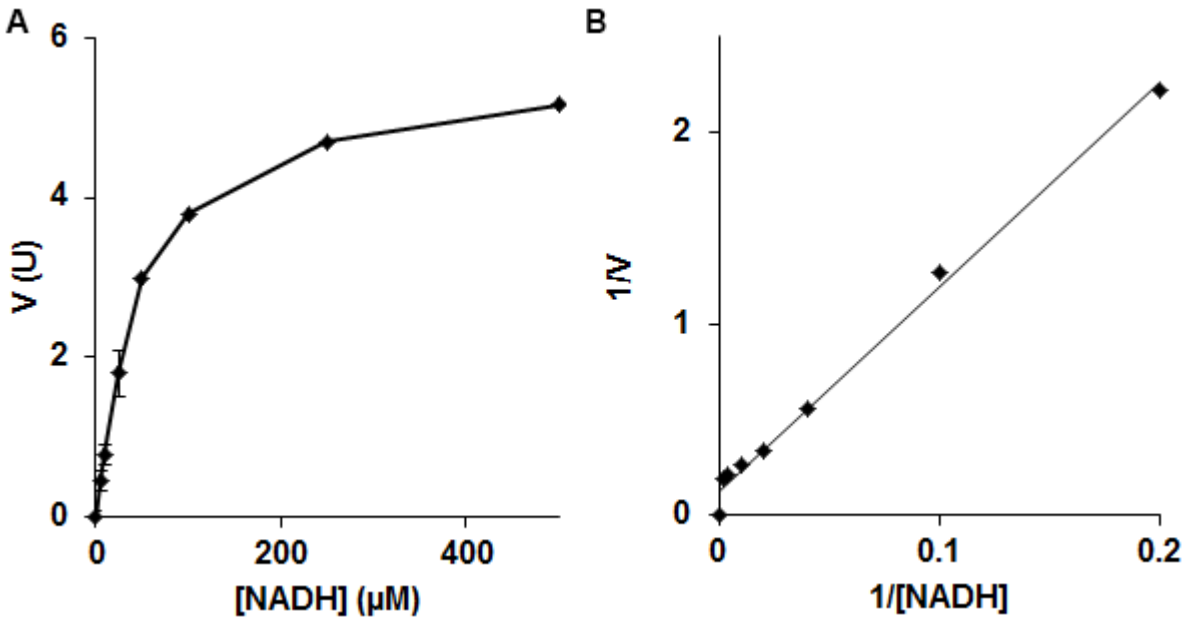


Figure S1. Michaelis–Menten (A) and Lineweaver–Burk (B) plots of the electron donor NADH for tellurite reduction. The reaction was carried out at 28 ºC, pH 7.0. Error bars represent one standard deviation.

>gi|563284320|gb|ESZ88862.1| molecular chaperone GroEL [*Blastomonas* sp. CACIA14H2]

MAAKDVKFGRDARERILRGVDILADAVKVTLGPKGRNVVIDKSFGAPRITKDGV
SVAKEIELKDKFENMGAQMVKEVASKTNDIAGDGTTTATVLAQAIVREGMKSV
AAGMNPMDLKRGIDLAVTKVVENLKSRSKDVAGSNEIAQVGIISANGDREVGEK
IAEAMERVGKEGVITVEEAKGLEFELDVVEGMQFDRGYLSPYFITNPDKMTVEL
DNPYILIHEKKLSNLQAMLPILEAVVQTGRPLLIIAEDIEGEALATLVVNKLRGGL
KVAAVKAPGFGDRRKAMLEDIAILSKGEMISEDLGIKLENVTLGMLGQAKRVSI
DKDNTTIVDGAGEADAIKARVEAIRTQIDNTTSDYDREKLQERLAKLAGGVAVI
KVGGASEVEVKEKKDRVDDALHATRAAVEEGIVPGGGTALLYATSALEGLTGE
NDDQTRGIDIIRKALFAPVRQIAQNAGHDGAVVSGKLLDGNDPTLGFNAATDTY
ENLVAAGVIDPTKVVRAALQDAASVAGLLITTEAAICDAPEDKAAAGGMGGMP
GGMGGMGGMDF

Figure S2. MS sequence analysis of the membrane associated tellurite/tellurate reductase from strain KR99 compared to its nearest match GroEL from *Blastomonas* sp. CACIA14H2. Sequence identified by data matching is underlined.

Table S1. Comparison of ions from the tryptic digest of KR99 tellurite reductase to those expected from a similar digest of the GroEL protein from *Blastomonas* sp. CACIA14H2 (NCBI gi|563284320).

Observed ions	Expected ions	Peptide		MS/MS[1]	Sequence of *Blastomonas* GroEL
1302.687	1302.717	37	48	okay	NVVIDKSFGAPR
1498.822	1498.884	119	132		GIDLAVTKVVENLK
1514.722	1514.753	198	210	poor	GYLSPYFITNPDK
1595.906	1595.937	19	34	poor	GVDILADAVKVTLGPK
1741.917	1742.018	119	134		GIDLAVTKVVENLKSR
1814.905	1814.936	211	225		MTVELDNPYILIHEK
1883.854	1883.885	182	197		GLEFELDVVEGMQFDR
1978.157	1978.206	16	34	no match	ILRGVDILADAVKVTLGPK
1985.871	1985.989	137	156		DVAGSNEIAQVGIISANGDR
2088.049	2088.094	81	101	poor	TNDIAGDGTTTATVLAQAIVR
2132.028	2132.072	323	343		VSIDKDNTTIVDGAGEADAIK
2306.167	2306.237	446	468	poor	ALFAPVRQIAQNAGHDGAVVSGK
2714.309	2714.356	503	529		AALQDAASVAGLLITTEAAICDAPEDK
2743.333	2743.386	135	161		SKDVAGSNEIAQVGIISANGDREVGEK
3311.612	3310.671	198	225		GYLSPYFITNPDKMTVELDNPYILIHEK
3375.608	3375.656	405	438	excellent	AAVEEGIVPGGGTALLYATSALEGLTGENDDQTR
3559.763	3559.828	469	502	good	LLDGNDPTLGFNAATDTYENLVAAGVIDPTKVVR
4172.104	4171.152	405	445		AAVEEGIVPGGGTALLYATSALEGLTGENDDQTRGIDIIRK

[1]Tandem mass spectrometry to test whether the sequence of the peptides matched the expected.