

## **SUPPLEMENTARY INFORMATION**

for

**Feinberg, L.F., R. Srikanth, R.W. Vachet, and J.F. Holden (submitted) “Constraints on anaerobic growth in the hyperthermophilic Archaea *Pyrobaculum islandicum* and *Pyrobaculum aerophilum*”. *Appl. Environ. Microbiol.* (submitted 9/5/07, revised 11/5/07).**

The following information is available at:

<http://www.bio.umass.edu/micro/holden/suppldata-1.html>

and this website is cited in the journal article.

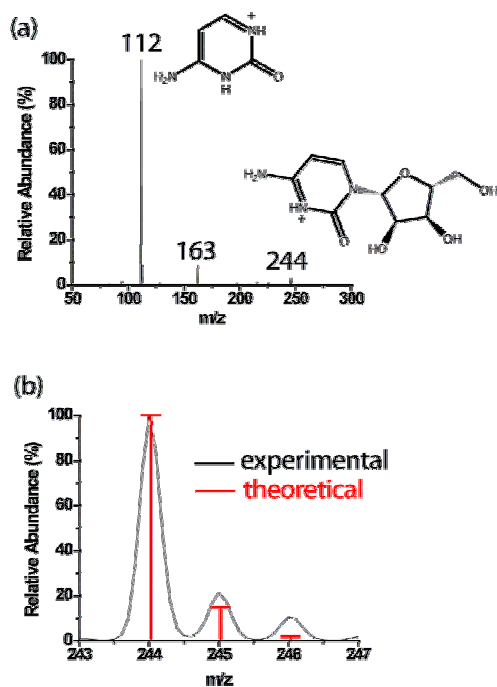


FIG. S1. Electrospray ionization mass spectra of one of the compounds eluting at 3.2 min. The spectra identify this compound as cytidine. (a) MS/MS of m/z 244; the ion at m/z 112 is protonated cytosine, and the mass difference between m/z 244 and 112 is consistent with the neutral loss of a ribose unit. (b) Experimentally measured and theoretically predicted isotope distribution for (M+H)<sup>+</sup> of cytidine.

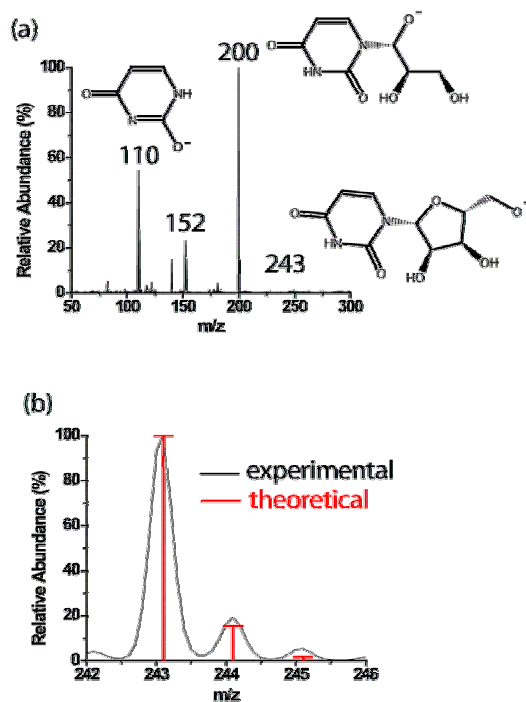


FIG. S2. Electrospray ionization mass spectra of one of the compounds eluting at 3.2 min. The spectra identify this compound as uridine. (a) MS/MS of m/z 243; the ion at m/z 110 is deprotonated uracil, and the mass difference between m/z 243 and 110 is consistent with the neutral loss of a ribose unit. (b) Experimentally measured and theoretically predicted isotope distribution for (M-H)<sup>-</sup> of uridine.

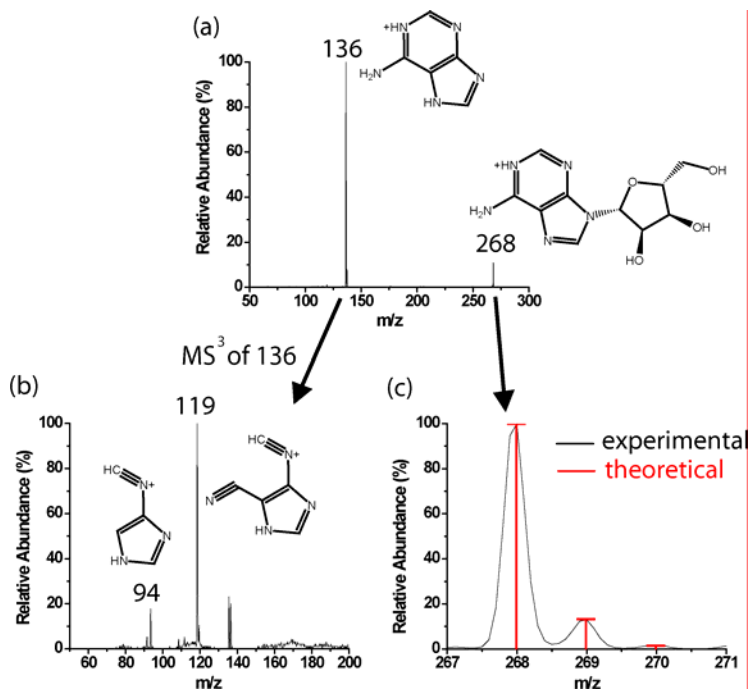


FIG. S3. Electrospray ionization mass spectra of one of the compounds eluting at 3.4 min. The spectra identify this compound as adenosine. (a) MS/MS of m/z 268; the ion at m/z 136 is protonated adenine, and the mass difference between m/z 268 and 136 is consistent with the neutral loss of a ribose unit. (b) MS<sup>3</sup> of the product ion at m/z 136, confirming the structure of adenine (Nelson and McCloskey, 1992). (c) Experimentally measured and theoretically predicted isotope distribution for (M+H)<sup>+</sup> of adenosine.

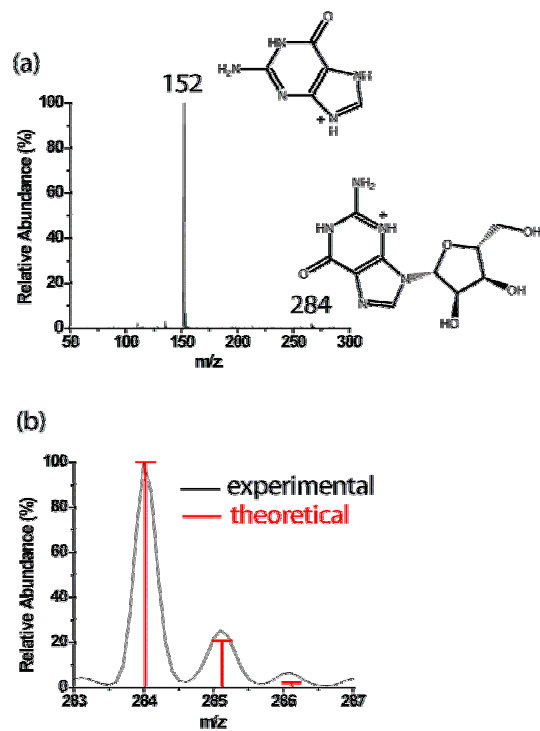


FIG. S4. Electrospray ionization mass spectra of one of the compounds eluting at 3.4 min. The spectra identify this compound as guanosine. (a) MS/MS of m/z 284; the ion at m/z 152 is protonated guanine, and the mass difference between m/z 284 and 152 is consistent with the neutral loss of a ribose unit. (b) Experimentally measured and theoretically predicted isotope distribution for (M+H)<sup>+</sup> of guanosine.

TABLE 1. Peptide masses measured from the trypsin-digested 120-kDa protein from thiosulfate-grown cultures compared with the predicted trypsin-digested masses of the  $\alpha$  subunit of thiosulfate reductase (Pisl\_0266) and a solute binding protein (Pisl\_0913)

Measured m/z	Predicted m/z	$\Delta$ m/z	Amino acid sequence
Thiosulfate reductase, $\alpha$ subunit (Pisl_0266):			
1495.6	1495.7	0.1	YSVDLEEELWR (806-816)
2208.8	2209.0	0.2	DYMEAAAREADVNDLRR (415-433)
2413.9	2414.1	0.2	FADTYGGGVITFDNPYCTYPR (193-213)
3013.7	3014.6	0.9	DVVVRVHVYKPKYSVDLEEELWR (793-816)
3060.3	3060.4	0.1	DGTEWSQNMPVGMITEEGIFPIPNER (711-737)
3250.6	3250.7	0.1	IVDEAGNVRAPTVEDIYKMGGYMLVPTGR (748-777)
3616.9	3616.9	0	VHVYKPKYSVDLEEELWRTHIYNPMPAR (798-826)

Predicted amino acid sequence (matches are in red):

MSRFFLLMEISRREVLKAGATIGLIGVSGILLKAAVEQSKAEAAASAVTSVPSICGMCMAQCAIYIDV  
VDGKPVIRPNTNAPTSAGKICARGVAGTFNAWLNPDIAIKKPMARRALVDWAQKISWEEAKRQL  
VTNRGKYDDMVEVDWNTAIDIIAKKLKELADNNERHAFTFLFGAWGPVASMRAVPLMR**FADTY  
GGGVITFDNPYCTYPR**YLGHWLWGHGHQAHVACIDYGEAEAVLVVRRNVIGAGVVTTETWRFME  
AVRRGAKLVVLSVDFDETASYADVWLPVKPGTDLAVLLAFIKYVLDNGYYMAEYLRRFTNAPFLIK  
PDGLPLLAASEVDWGKYGVKEPAFAYVWDEAAGGPAPDNAAQRAALFGEYEVALKDGSVVKAKT  
ALQILKEWVDANLSALAQKHGVK**DYMEAAAREADVNDLRR**AAEIVAKYRAVSPIGWHDPYRS  
NSPQTWRAVGVLMALLGRIQQGGFLLLTHLIMPYADVTKVMKYTKKDVPYKTIRGLTFGEYVS  
ANLRGIYVIPIAPPLPGPSDRDAPPVKSLETVWGEAAEKKGYPYDTPVQALYESVVHKGKPFKIKVV  
FITGSNPIPRIGNSRLVEEIFRNLELVIVHDIQFNDTAFADVLPDLPYLERLDLALPGPFSPFAISVRF  
PWYEEYKLLAAGGKPGELDKAFRSRDGRATAFEVLLMIARRLSQLGVKPR**DGTEWSQNMPVGM  
ITEEGIFPIPNER**FINAQLRRVR**IVDEAGNVRAPTVEDIYKMGGYMLVPTGR**VEAVKDELWSKALG  
RDVVVRVHVYKPKYSVDLEEELWRTHIYNPMPARGEVPLPTPSGRVEIYSINLAYDVRVFGKPA  
TSIDPSDLEGGKSGVDPLFSPVPLYAGMARPDYMWATGPATEDVEINGLVPPEPPKRLLLVYRHGPY  
THTHSNTQNNLLDTLTSELSSAWIHPDTAAALGVKDGDWIEVRPAAPKVAKQLESVGVKEVPTA  
RFRVVRVPMVRRDVVAIYHYWLVPRGRLRVKAWKLADVRAGYSDDNYLGPMLAGKLGTPGAMG  
NTVVEVSRVGG

Solute binding protein (Pisl\_0913):

1345.7	1345.8	0.1	YNVPWLSLILK (584-594)
1581.7	1581.8	0.1	YASFQEYIELYR (302-313)
2024.9	2025.0	0.1	DIGDAFASALEQLGFTVDR (203-221)
2153.0	2153.1	0.1	KDIGDAFASALEQLGFTVDR (202-221)
2318.0	2318.2	0.2	YSHMISQGPFFLYAIDTAK (645-664)
2423.0	2423.1	0.1	MMYDPAVWNHPFTGEPMPFR (403-422)
2617.5	2618.5	1.0	AINVPTVVVGQPATISVSLEVPAGGR (696-722)
3013.7	3013.6	0.1	AYKFWVLTYAENVPIVSEATQVFIPK (768-793)
3631.8	3629.8	2.0	GDPSVVLTYAAAGFNDIILNPAPSNPPCANPFSSR (70-104)
4383.5	4380.2	3.3	AAQAAPLKGDPVVLTYAAAGFNDIILNPAPSNPPCANPFSSR (62-104)

Predicted amino acid sequence (matches are in red):

MRLRTVLLAMLLGIVLFAQYTPHTNPGPATDRIVGKSVPIAQAGAAKAGDIDVYIFGMR**AAQAA  
PLKGDPSVVLTYAAAGFNDIILNPAPSNPPCANPFSSR**AIRYAMQFVIDRDYVANEIFKGFVPMYIW  
LSQYDPTYISVADIISQLGIRYDLDYAKTIVESEMPKLGATKGPDKWYCKGKLVTVIGLIRVEDERK

DIGDAFASALEQLGFTVDRKYVTFDVAIQTVYGTDPAQFQWHFYTEGWGKSGIDRWDTSSIAQYCA  
SWFGYMPGWGTTGWYNFANATIDEITDKLYKGGK~~YASFQEYIELYR~~KATLMCIQESVRVFNNTLN  
AFVASPQLKGVTVDLGAGLRASVYNARNWYVPGKDVVNVGHLWVWTASSAWNVPVQGGFTDVY  
SVDWFR~~MMYDPAVWNHPFTGEPMPFR~~ATYVETKGPAGYFDVPADAYRWDAKQKAWVSAGGA  
KAKSKVVFNYAKYIGAKWHHGQPIKLADVLFYAFLOWDIANDPQKVARESGVASVNSTMNLKGI  
RIINDTSIEVYIDYWHFDPNYIAAMAVTPDMPWEVYYAVDQLVYVKQTYAASRASATK~~YNVPWL~~  
~~SLILK~~DHAKAAADVLDALNKGIYPESWFKIGDKTLLTKDEALARYRAAVDWFNK~~YSHMIISQGP~~  
~~YLYAIDTAK~~QYIELRAYRDPSYPYKPGAFYFGVATPVSVK~~AINVPTVVVGQPATISVSLEVP~~SGAGRI  
YYK WGIVDPTTGRFLYMSEEGTTAAAPININVPADVSSKLTANR~~AYKFWVLTYAENVPIVSEATQVF~~  
~~IPK~~AAAPATTPPTPTTPPPATTPPPQPTVVTTTAPATGTTEALAAAIVGILAVLVALAFALRKKSGE  
TKQETKVYR