

Supporting Information

Diversity of Archaeosine Synthesis in Crenarchaeota

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1. Methods

Media.

Escherichia coli derivatives were routinely grown at 37°C in LB (BD Diagnostic System) supplemented with 0.2% glycerol as a carbon source. Growth media were solidified with 15 g/L agar (BD Diagnostic System) for the preparation of plates. Ampicillin (Amp^r, 100 µg/mL), Thymidine (dT, 300 µM), Kanamycin (Kan^r, 50 µg/mL) and L-arabinose (0.2%) were added when needed. Transformations of *E. coli* were performed following standard procedures (1).

Growth of *Haloquadratum walsbyi*.

H. waslbyi C23 (2) was grown at 37°C static in defined media (DBCM2) (3) containing 200 g NaCl, 29.1 g MgSO₄•7H₂O, 25g MgCl₂•6H₂O, 5.8 g KCl, 5 mM, 5.0 mM NH₄Cl, 1mM K₂HPO₄ pH 7.5, 0.25% HCl, 0.015 g FeCl₂•4H₂O, 0.19 mg CoCl₂•6H₂O, 0.1 mg MnCl₂•4H₂O, 0.07 mg ZnCl₂, 0.006 mg H₃BO₃, 0.036 Na₂MoO₄•2H₂O, 0.024 mg NiCl₂•6H₂O, 0.002 mg CuCl₂•2H₂O, 0.04 mg 4-aminobenzoate, 0.003 mg biotin, 0.09 mg nicotinic acid, 0.05 mg calcium pantothenate, 0.15 mg pyridoxamine hydrochloride, 0.09 mg thiamine chloride hydrochloride, 0.05 cyanocobalamin, 0.03 mg lipoic acid, 0.03 mg riboflavin, 0.012 mg folic acid, and 10 mM pyruvate. The cells were collected by centrifugation (5000 rpm for 5 min at RT) and stored at -20°C for further use.

Growth of *Haloferax volcanii*.

H. volcanii was grown at 45°C and 200 rpm in Hv-YPC rich medium (4) containing: 144 g NaCl, 21 g MgSO₄•7H₂O, 18 g MgCl₂•6H₂O, 4.2 g KCl, 10mM Tris HCl (pH 7.5), 0.5% yeast extract, 0.1% peptone, and 0.1% casamino acids (w/v). The cells were collected by centrifugation (5000 rpm for 5 min at RT) and stored at -20°C for further use.

Archaeal tRNA extraction.

To extract tRNA, the frozen cells were thawed and resuspended in 50 mM Na acetate buffer pH 5.8 (3 mL buffer per 1g of cells). Equal volume of phenol saturated with mildly acid buffer (50 mM NaOAc pH 5.8) was immediately added to the cell suspension and shaken overnight at room temperature. The aqueous phase was recovered by centrifugation (20 min at 5,000 rpm), and another one volume of buffered saturated phenol was added. The phenol:buffer was vigorously shaken again for 2 minutes at room temperature. After centrifugation, as above, one volume of

chloroform was added and mixed vigorously again for 2 minutes at room temperature. The supernatant was recovered by centrifugation and adjusted to 20% isopropanol followed by one hour incubation at -20°C. The pellet containing genomic DNA and long RNA (mRNA and rRNA) was spun down, and the amount of isopropanol was adjusted to 60% final concentration. After one overnight standing at -20°C, the precipitated small RNAs (mostly 'soluble' RNA = tRNA) were recovered by centrifugation at 4°C, washed twice with cold 70% ethanol (to remove the salts from the cellular extract) and then once with cold 80% ethanol, dried and finally resuspended in 5000 µL water. Further purification steps were achieved on DEAE[®]-cellulose (Fisher Scientific cartridge/5 mL) column or on Nucleobond[®] AXR-400 (Clontech Laboratories); both last chromatography steps were performed according to the manufacturer's protocols. All tRNA extractions and analysis were performed at least twice, independently.

Bulk tRNA digestion for LC-MS/MS analysis.

Four hundred µg of bulk tRNA was resuspended in 100 µL water. To this solution were added 0.1 volume of 0.01 M ammonium acetate (pH 5.3) and 0.2 units of Nuclease P1. The solution was incubated at 45°C for 2 hours and then briefly cooled on ice. Then, 0.1 volume of ammonium bicarbonate (1.0 M at pH 7.0) was added along with 0.02 units of Phosphodiesterase I and 5.0 units of *E. coli* alkaline phosphatase. The resulting solution was incubated for 2 hours at 37°C. LC-MS/MS analysis was done on a high performance liquid chromatography (HPLC) system coupled to a hybrid triple quadrupole ion trap MS (4000 Q-TRAP; Applied Biosystems, Foster City, CA) equipped with a TurboIonSpray (TIS) interface operated in the positive ion mode at the Donald Danforth Plant Science Center - Mass Spectrometry and Proteomics Facility (St. Louis, MO)

tRNA^{Asp} purification.

tRNA^{Asp} (GUC) was purified from bulk tRNA using biotinylated primers on Streptavidin sepharose resin (GE Healthcare, Pittsburgh, PA) according to Rinehart et al. (5). Four hundred μ g of 5'-biotinylated specific primers (5'-biotin-CCCTGCGTGACAGGCAGG-3') in 6X NTE solution (20X NTE solution is 4.0 M NaCl, 0.1 M Tris-HCl pH 7.5, 50 mM EDTA, 5.0 mM 2-BME) were added to the Hitrap Streptavidin[®] sepharose HP R-10 1 mL column (GE Healthcare). Then, 4.0 mg of total tRNA (10 mg/mL in 6X NTE) were added and incubated at 65°C for 30 min. After incubation, the temperature of the mixture was decreased slowly to 30°C. The tRNA was washed three times with 3X NTE, 1X NTE, and 0.1X NTE until the absorbance ($\lambda=260$ nm) of the wash was zero. The tRNA^{Asp} retained on the beads was eluted with 1 mL of 0.1X NTE at 65°C. 1.0 M NaCl and 80% isopropanol was added to precipitate the tRNA. The pellet was washed with 85% ethanol and dried. The tRNA was resuspended in 50 μ L sterile water.

Strains and plasmids constructions.

The $\Delta queC::Kan^R$ allele was transferred by P1 transduction as described by (6) from the Keio collection strain JW0434-2 (7) into *E. coli* K12 MG1655 to create strain VDC7012 (MG1655 $\Delta queC::Kan^R$). The Kan^R marker was then excised as described by (8) to create VDC2047 (MG1655 $\Delta queC$). The deletion of the *queC* gene was verified by PCR using primers chkybaX.ol1 (5'-AGCATAACGCACATCTACAAT-3') and chkybaX.ol2 (5'-CATAACATCGCCTTCGTCGT-3'). The $\Delta queF::Kan^R$ allele was transferred by P1 transduction from the from the Keio collection strain JW2765-2 (7) into VDC2047 and MG1655 to create VDC3274 and VDC3275, MG1655 $\Delta queC \Delta queF::Kan^R$ and MG1655 $\Delta queF::Kan^R$

respectively. The Kan^R markers were excised from both strains to create VDC3280 (MG1655 $\Delta queC \Delta queF$) and VDC2043 and (MG1655 $\Delta queF$). The deletion of *queF* gene was verified by PCR using primers ckyqcD.ol1 (5'-CAAGGCGTTCCACGCAGCC-3') and ckyqcD.ol2 (TCAGCAGGTGGCTGACAAG).

The plasmid expressing SSO0016 (NP_341593.1) under the P_{BAD} promoter was a pMH4 derivative (Kan^R, ColE1) gift from the Joint Center for Structural Genomics (La Jolla, CA). *P. calidifontis* JCM 11548 genomic DNA was extracted using Nucleobond[®] AXR-400 (Clontech Laboratories) according to manufacturer instructions. The *Pcal_0221* (YP_001055124.1) gene was amplified from genomic DNA by PCR using primers QueFLikepbad24.ol1 (5'-GGCGCCATGGTCAAGGTCTCCAAGTC-3') and QueFLikepbad24.ol2 (5'-GGCGGCATGCTTAGATGTAGACCGGCGGGA-3'). The obtained PCR fragment was digested with *NcoI* and *SphI* and subsequently ligated into pBAD24 (Amp^R, ColE1) (9) after digestion with appropriate endonucleases to give plasmid pGPP358. VDC3280 ($\Delta queC \Delta queF$) was transformed by pMH4::*SSO0016* and pBAD24 to give VDC3282 and VDC3281 respectively. VDC2043 ($\Delta queF$) was transformed with pGP358 and pBAD24 to give VDC3368 and VDC3367 respectively

PCR conditions.

Polymerase chain reactions (PCRs) were performed using Phusion[™] Hot Start, (New England Biolabs, Beverly, MA). For each PCR reaction, 100 ng of template DNA, 0.2 μ M forward primer, 0.2 μ M reverse primer, GC reaction buffer to 1X concentration, 200 μ M dNTP, nuclease free water and 1 – 2 units DNA polymerase per 100 μ l reaction were used. The thermocycling conditions for PCR were: 1 cycle of initial denaturation at 95°C for 1 minute, 30 cycles of

denaturation at 95°C for 15 seconds, annealing at 60°C, extension at 72°C for 30 seconds per kb, and a last cycle of final extension at 72°C for 10 minutes.

RNase T1 Digestion of tRNA and LC-MS/MS.

Purified tRNA^{Asp} was digested with RNase T1 by mixing 1 µg of the sample with 50 U of RNase T1 in 20 mM ammonium acetate and incubating for 2 h at 37 °C. Digestion products were separated using a Thermo Surveyor HPLC system with a Xterra C18 1.0 x 150 mm column (Waters) at room temperature at a flow rate of 40 µL/min. Before each run the column was equilibrated for 15 min at 95% Buffer A (200 mM HFIP, 8.15 mM TEA pH 7.0) and Buffer B (200 mM HFIP, 8.15 mM TEA:methanol, 50:50 v:v, pH 7.0). The gradient used was 5% B for 5 min, 30% B at 7 min and 95% B at 50 min and held at 95% B for 5 min. The eluent was directed into an LTQ-XL (Thermo Scientific) linear ion trap mass spectrometer. Analysis conditions were a capillary temperature of 275 °C, spray voltage of 4.5 kV, sheath gas, auxiliary gas, and sweep gas at 25, 14, and 10 arbitrary units, respectively. Collision induced dissociation (CID) tandem mass spectrometry (normalized collision energy 42%) was used in data-dependent mode to obtain sequence information from the tRNA^{Asp} RNase T1 digestion products. Data-dependent MS/MS, with a Q value of 0.35 for 30 msec, was recorded based on the most abundant ion, and each ion was analyzed for 15 scans or 30 s before being placed on a dynamic exclusion list for 30 s.

2. Supplemental data 1

Gat-QueC Sequences

>gi|327310688|ref|YP_004337585.1| exsB protein [Thermoproteus uzoniensis 768-20]

MCSIGGVLIIFGDLDRERAAAIEAKLRAIAEAATERGRDSFGI AVLDRSGSYRVYKDRRPAPEALKDMP
EM VGVDAVA AIFNNRAEPTTEHVERKTEDDIQPMLGERIAVTHNGTIANDVELERRYGLRRRSRIDTAVLPP
LLEKVVWDGSLLEGLQRILRDEVVGSYALAVLDSARPGRLWLAANFRPLYMWDRLNALFFASSDAYLQGD
VAPWDGNYVKRLEPYTVVEVGVDKTWRASLWKADAEPGRRRRALVVASGGLDSTTAAAALLRQGYEVAL
LHFNYRHVAEDPERRAVREISKALGTPLIEVDMDFFKLAGRSPLLGEINRVDMGREGAEFAHEWVPA
NFVFIALAVLAEAWGYDYVALGINMEEAGAYPDNEMELVRLNQLALPYATGPQRRVQLLMPVGGGLVKHE
IVRLGLEVGAPLHLTWSCYDKGPKHCGRGCPYMRRLAFKINGVRDPVEYDLPPEEEEEFWRGTRPYVWR
PPERRG

>gi|307594719|ref|YP_003901036.1| exsB protein [Vulcanisaeta distributa DSM 14429]

MCTIGGVLIIFGDLDRDRAKRIEEVLRMIVVKGEERGRDSFGIVALDKNGELNVFKSRDRPSIAVSRMPS
IINENTVAAIFNNRAEPTTEYVRAKTEDDIQPMIGEHVVAHNGTIANDKDLETKFNLTRRSRIDTAILP
PLLERLWDGSLNGLRDVLIHVIGSYALAIMDTRRPGKVLATNFKPLYMAWYSDLKALFFASLDDYLVN
DQGRPIWDMPTIRRVPEPYTAMEIGIDGTWSTVSLRREEQGRRRRVLVIASGGLDSTTAATYLLKQGYDVA
LLHFNYGHRAETQEDRAIRRIAFLGVPLLEVSMDFFKVVRHSPLLGDGEINRVDEGREGAEFAHEWVPA
RNFVFIALATAIAEAYGYDYIATGINLEEAGAYPDNEMEFIRLLNKVMPYAVGPNKHVELLMPVGHVVKH
EIVKLGLEVGAPLHLTWSCYDNGERHCGRCGCPYMRRLAFKINGVRDPVEYDLPVEVEEEFWRDARPYKI
PKRPSK

>gi|325969442|ref|YP_004245634.1| exsB protein [Vulcanisaeta moutnovskia 768-28]

MCTIGGVLIIFGDLDEDRAKRIEEVLRMVIIKGEERGRDSFGIVSLSRDGELNVFKSKERPSVAVSKMPR
MITEDTVA AIFNNRAEPTTEYVVKKNEDDIQPMIGERIVVAHNGTIANDKDLESKFGLIRRSKIDTAILP
PLLEKFWGSLNGLFRDVLVNYVVGSYALAIMDTRRPGRVLWLNFKPLYMAWYGDGLKTLFFASLDDYLVN
DWNKPIWGMPIVIRRVPEPYTAMEIGIDGTWSTVSLRKEGQVKKRVLVIASGGLDSTTAATYLLKQGYDVAL
LHFNYGHRAETQEDRAIKRIAFLVHNPLFEVNMDFFKIVRHSPLLGDGEINRVDEGREGAEFAHEWVPA
NFVFIALATAIAEAYGYDYIATGINLEESGAYPDNEMEFIRLLNRVMPYAVGPNKHVELLMPVGHVVKH
EIVKLGLEVDAPLHLTWSCYDNGEKHCGRGCPYMRRLAFKINGVVKDPVEYELPKEIEEEFWMGARPYEVP
KRPQG

>gi|159041826|ref|YP_001541078.1| exsB protein [Caldivirga maquilensis IC-167]

MVECSVSGVLIFGEPDEARIRGIEDKLRSIVMRAEERGRDSWGIVTMSRDGGIKSFKSLGKASETLPKYS
RLLDTDTVVAIANNRAEPTTEYVKEKGINDIQPMISEYVVVSHNGTIANDIELEGKYGIRKMSKIDSSIL
PPLLEKAWDGSLEGLQKILRDEIIGSFALAIIDRRRPGRLWLVNFKPLYMWDRELNALFFSSLDTYLE
DPDKPPWETNVVKRIEPIVSVIEVSREGGWRRSLWRVDSKPRRVLVVASGGLDSTTSATQLIKQGYDVT
LLHFNYGHVAEGPEENAVRRIAFLNVPLLEVNMDFFKIVKHSPLLGDGEINRRREGITGAFAHEWVPA
RNLVFIALAVIAEAMGYDYVATGVNLEEAGAYPDNEMEFIRLLNQVMPYAVGPNKHVELLMPVGHVVKH
EIVKLGLEIGAPLHLTWSCYDKGPKHCGRGCPYMRRLAFKINGVRDPVEYDLPPEVEEEYWRGTPYRT
PLPVGKRELQH

>gi|332797158|ref|YP_004458658.1| exsB protein [Acidianus hospitalis W1]

MCSVSGALILNSKNYDKIERKFAEILKNAEDRGKDSFGIIVVQSDGTTKSVKSLGRPSEQEELKYLILDE
KSRVVIANNRAEPTTEFVNKKTEDIQPFEGEFIVTHNGIANDKELEKKFGVKRESNIDTAVIPPILD
KFWKGLDPLTKDLLSEIRGSFAFIITDKKNPNEIYIAQNFKPVYMMYDYELGAIFFTSLDDYFSQNPLDK
VNITKLEPYSIVSVDSNLKIEKIDLIKPKDKKKVLVIASGGLDSTVAATYLLRQGHIEITLLHFNYRHKAE

EKEREAVRKISEYLQVPYIEIDTDLFKI IGHITLLKGGGEIVKERQGEEGAFAHEWVPARNLIFFSVAL
AIAEAYGFDAIASGINLEEAGAYPDNEMEFVRLFSKLSPYATGPNKKIEVMMPVGNLVKHEIVKLGVEIG
APLHLTWSCYEGGKHCCKGKGCPCYMRKMAFKINGLKDPEYEN

>gi|70606119|ref|YP_254989.1| hypothetical protein Saci_0280 [Sulfolobus
acidocaldarius DSM 639]

MCSVTGVLILNPNHYKEIEKKLAKILIRAEDRGRDSFGIVVIQKDGSTKSSKHVKGPSLQEEKLYGILDE
NSKVVIANNRAEPTTEYVRRKTENDIQPFEGEFVVTTHNGIIANDMELEKKYKVSKLSRIDSSVLPPVLD
RSWNGNLDLSEILNSIRGSFALVIGDKKNPDRIFIAQNFKPVYMMYDRDLGAVFFTSLDDYFDATLNDN
VTKLDPYSVVMVDDKLEIRKVPLLKEKNKRILVVASGGLDSTVAATYLVRQGHVETLLHFNYHHKAEK
EREAVRKISEYLNVPFVEIDTDLFKIVGHSTLIKGSSEIVKDRKGEEGAFAHEWVPARNLIFFSVALA
MAEAYGFDAIASGINLEEAGAYPDNEMEFVRFMSRLVPYAVGPNKKVEVLMMPVGNLVKHEIVKLGVEIG
PLHLTWSCYEGGNKHCCKGKGCPCYMRKVAFAEVNGLKDPVEYEA

>gi|15922650|ref|NP_378319.1| succinoglycan biosynthesis regulator
[Sulfolobus tokodaii str. 7]

MCSVTGVLIIKPENYEKIEKKLIQILKRAEDRGRDSFGVIVIEKDGSVRKKVKGALGRPSTQEEKLYGILDE
NSKVI IANNRAEPTTEYVRQKTEEDIQPFEGERYIVTHNGIIANDLELEKKNVIRRTKIDS AVVPPILD
KYWNGEIEQLKKILNDIKGSFAFIIGDKKRPNRIYIAQNFKPVYMMYDRELGAIFFTSLDDYFDASAFDS
VTKLDPYSIVEVNDNLEIRKIQLLDKKIKKVLVIASGGLDSTVAATYLLRQGYEITLLHFNYHHKAEERE
REAVKIIAEYLQVPLIEIDTDLFKI IGHITLLKGGGEIVKDRKGEEGAFAHEWVPARNLIFFSVALALA
EAYGYDAIASGINLEEAGAYPDNEMEFVRLFAKLSPYATGPNKKVEVMMPVGNLVKHEIVKLGVEIGAPL
HLTWSCYEGGQKHCCKGKGCPCYMRKMAFRINGLNDPVEYEN

>gi|227831113|ref|YP_002832893.1| exsB protein [Sulfolobus islandicus
L.S.2.15]

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KTWDGNIGTLKGILEQIRGSFALVIGDKRNHDIRIFLAQNFKPLYMAYDYSLESIFFTSLDEYFDVKKPFDL
VNVTKLEPYSVVMVSSNKQITTLPIIEKRKKHKVLVVASGGLDSTVAATKLLREGHEVTLIHFNYHHKAE
EREREAVRNIAEHLQVPLIEINTDLFKMIGHATLIKGGGEIVKDRKGEEGAFAHEWVPARNLIFFSAAL
AIAEAYGYDAIASGINLEEAGAYPDNEMEFIRMLSKLSPYATGPNKKVEVLMMPVGNLVKHEIVKLGVEIG
APLHLTWSCYEGGQKHCCKGKGCPCYMRVAFKINGLRDPVEYAE

>gi|229579998|ref|YP_002838398.1| exsB protein [Sulfolobus islandicus
Y.G.57.14]

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KTWDGNIGTLKGILEQIRGSFALVIGDKRNHDIRIFLAQNFKPLYMAYDYSLESIFFTSLDEYFDVKKPFDL
VNVTKLEPYSVVMVSSNKQITTLPIIEKRKKHKVLVVASGGLDSTVAATKLLREGHEVTLIHFNYHHKAE
EREREAVRKIAEHLQVPLIEINTDLFKMIGHATLIKGGGEIVKDRKGEEGAFAHEWVPARNLIFFSAAL
AIAEAYGYDAIASGINLEEAGAYPDNEMEFIRMLSKLSPYATGPNKKVEVLMMPVGNLVKHEIVKLGVEIG
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>gi|323475431|gb|ADX86037.1| exsB protein [Sulfolobus islandicus REY15A]

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KTWDGNIGTLKGILEQIRGSFALVIGDKRNHDIRIFLAQNFKPLYMAYDYSLESIFFTSLDEYFDVKKPFDL
VNVTKLEPYSVVMVSSNKQITTLPIIEKRKKHKVLVVASGGLDSTVAATKLLREGHEVTLIHFNYHHKAE
EREREAVRKIAEHLQVPLIEINTDLFKMIGHATLIKGGGEIVKDRKGEEGAFAHEWVPARNLIFFSAAL
AIAEAYGYDAIASGINLEEAGAYPDNEMEFIRMLSKLSPYATGPNKKVEVLMMPVGNLMKHEIVKLGVEIG
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>gi|227828356|ref|YP_002830136.1| exsB protein [Sulfolobus islandicus
M.14.25]

MCSVSGVLILNPKNFDKVERKLADILKRAEDRGRDSFGIVVIQKDGTVKVRKSVGKPSSEKEELLYGILDE
DSRVVIANNRAEPTTEYVRQKTEEDIQPFIGDRYIVTHNGIIANDLELEKKYELKRKTKIDSAILPSLLD

KTWDGNLGLTKGILEQIRGSFALVIGDKRNHDRIFLAQNFKPLYMAYDYSLESIFFTSLDEYFDVKPFDL
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EREREAVRKIAEHLQVPLIEINTDLFKMIGHATLIKGGGEIVKDRKGEEGAFAHEWVPARNLIFFSAAL
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>gi|15896988|ref|NP_341593.1| transcription regulator (exsB) related protein
[Sulfolobus solfataricus P2]

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VNITKLEPYSVVMVTSNKLIITLPIIMEKRKKYRVLVVASGGLDSTVAATKLLREGHEVTLIHFNYHHKAE
EKEREAVRKIAEYLQIPLLEINTDLFKIIGHATLIKGGGEIVKDRKGEEGAFAHEWVPARNLIFFSVSL
AIAEAYGYDAIASGINLEEAGAYPDNEMEFIRMLNKLSPYATGPNKRIEILMPVGNLVKHEIVKLGYEIG
APLHLTWSCYEGGQKHCCKGCPYMRKMAFRINGLKDPVEYDEE

>gi|330835407|ref|YP_004410135.1| exsB protein [Metallosphaera cuprina Ar-4]

MCSVTGVLILDPSTYLDVESKLSILIKAEDRGRDSFGIVSINVDGSVNQVKSLSGRPSKNQEKLGIVSE
KTRVIVANNRAEPTTEFVRFKTEKDIQPFVGNRFVITHNGI IANDMEIEKKYEINRTTKIDSAILPPFLE
KKWDGSLEGLRNSLKEKLSYALVIGDRLKPDRIFLAQNFKPIYMAYDFKLRAIFFFTSLDDYFDVQPFDE
VNVKLEPYSVVEVSNKKEFRTL SLYDKPKRRALVIASGGLDSTVAATKMVKDGYQVTL LHFNYHHKAAE
REREATRKIASYLNVDLIEVNTDVFTLIGESPLLKAGGEIVKERKGEEGAFAHEWVPARNSIFFTVAMA
IAEARGYDTLVSGINLEEAGAYPDNEMEFVRFQRLSPYAVGPNKRVDIVMPVGNLVKHEIVKLGLDIGA
PLHLTWSCYEGGEKHCGRGCPYMRKTAFEINGVKDPIEYQD

>gi|146303330|ref|YP_001190646.1| exsB protein [Metallosphaera sedula DSM
5348]

MCSVTGVLIMDP SKYAEVNQKLKLSILIRAEDRGRDSFGVIAVEEDGHVRSVKSLSGRPSLNQEKLDGIITE
KTRVLVANNRAEPTTEFVRFKMERDIQPF LGDRFIVSHNGI IANDKEIEKKYEIKRLTTIDSAILPPLLD
KKWDGKLETLRDILKELRGSYALVIADRERPDRIFLGQNFKPLYMAYDVLNAVFFFTSLDDYFDVKPFDH
VNVKLEPYSVVEVTLNKEFRTL SLYAQPRRRALVIASGGLDSTVAATKMIREGYQVTL LHFNYHHKAAE
KEREAVRKIASYLNADLMEINTDLFSLIGNATLLKGGGEIVKDRKGEEGAFAHEWVPARNAIFFTVAMA
IAEAKGYDAIVSGINLEEAGAYPDNEMEFVRFQRLSPYAVGPEKRV DVLMPVGNLVKHEIVKLGLEIGA
PLHLTWSCYEGGEKHCCKGCPYMRVAFEINGVKDPVEYESLDDQSRH

List of QueF-like and QueF sequences used for alignment

QueF-like sequences

>gi|118431468|ref|NP_147965.2| putative GTP cyclohydrolase I [Aeropyrum
pernix K1]

MLETAVDAVCPFTGAPDSYDVEIEYVSRDACLEALSLASWLESFRGVKISQEQLAHEIALTLKELLKPEY
VCVKLTGSHGRVGMVVERCEDTSPTEDMGPI

>gi|124027916|ref|YP_001013236.1| GTP cyclohydrolase I [Hyperthermus
butylicus DSM 5456]

MQHKELRVVEGEACVEKVVLTGSVEAVCPVTGMVDLYRVIVEYKPSAGRVCRYIEALS FHFY LQSYKGR
KILQEELTATIVRDFCEALGGGEVKVVTEGYHGPVGMRAEASGRCGGSA

>gi|18311862|ref|NP_558529.1| GTP cyclohydrolase I, conjectural [Pyrobaculum
aerophilum str. IM2]

MLKLSKNPQLVRLKTRGESVCPISKTVDSFEVTVEYIPRGAALAIIEEFKKIVDSYRGREILHEELAVDIM
EKIKA AVNPPYVKVTVKSYIIGVEVEVVAESGGVQPLYI

>gi|145592346|ref|YP_001154348.1| GTP cyclohydrolase I [Pyrobaculum arsenaticum DSM 13514]
MLKLSKNPQLVRLKTRGESVCPISKTVDSFEVTLEYIPRGVALAIEEFKKMVDSYRGREILHEELAVDLL
EKVKSVVNPPYVKVTLKSFYAGVEVEVVAESGGTQPLYI

>gi|126458846|ref|YP_001055124.1| GTP cyclohydrolase I [Pyrobaculum calidifontis JCM 11548]
MLKVSKSPSLVRLKTRGESVCPISKTVDSFEVSVVEYIPRGAVLAIEEFKKMVDSYRGREILHEELAVDLL
EKVKA AVNPPYVKVTVKSYIIGVEVEVVAESGGVPPVYI

>gi|171185538|ref|YP_001794457.1| GTP cyclohydrolase I [Thermoproteus neutrophilus V24Sta]
MAHQPVLLKLSRPTLVRLKTRGEAVCPISKVVDSFEVTVEYMPRGGALAIEEFKRMVDSYRGREILHEEL
AVDLMEKIKAAVNPPYVKVVLKSVYIGVEVEVVAESGGVPPVYI

>gi|119873451|ref|YP_931458.1| GTP cyclohydrolase I [Pyrobaculum islandicum DSM 4184]
MLKLSKNPSLVRLKTRGESICPISKVVDSFEISLEYIPRGVALSIEEFKKMVDSYRGREILHEELAVDIM
ERVKA AVNPPYVKVVVKSIIYMGVEVEVIAESGGVPPVYI

>gi|307596129|ref|YP_003902446.1| GTP cyclohydrolase I/Nitrile oxidoreductase [Vulcanisaeta distributa DSM 14429]
MIRTIKAGPVDYVHLETFSFAICPVDHNIDNYVIEVDYKPTCSGGCIYMEINSLREYLDGFKDRVIYHE
DLINELINEFVRTLNPIEITVTLTSNYKGIKYVIRRSINKRDSQHAP

7-cyano-7-deazaguanine reductase -NADPH dependent- oxidoreductase (QueF)

>gi|16130701|ref|NP_417274.1| 7-cyano-7-deazaguanine reductase (NADPH-dependent) [Escherichia coli str. K-12 substr. MG1655]
MSSYANHQALAGLTLGKSTDYRDYDASLLQGVPRSLNRDPLGLKADNLPFHGTDIWTLTYELSWLNAKGL
PQVAVGHVELDYTSVNLIIESKSFKLYLNSFNQTRFNNWDEVQRQTLERDLSTCAQGGKISVALYRLDELEGQ
PIGHFNQTCIDDQDITIDNYEFTTDYLENATCGEKVVEETLVSHLLKSNCLITHQPDWGSLLQIQYRGRQI
DREKLLRYLVSFRHHNEFHQCVERIFNDLLRFCQPEKLSVYARYTRRGGLDINPWRNSNSDFVPSTTRLV
RQ

>gi|15598002|ref|NP_251496.1| 7-cyano-7-deazaguanine reductase [Pseudomonas aeruginosa PAO1]
MQHPAEHSPLGKTSEYVSSYTPSLLPFISRTAKWAEGLSAETLPYRGVDIWNICYELSWLTPAGKPVVAI
GEFSIPADSPNIIIESKSFKLYLNSLNQSAFDSREALRAVLQKDLAAVAVGAPVGVRLRSLDEVAEEGIGRL
PGRCIDELDIAVDGYEQPRPELLRCDAGRIVEEQLYSHLLKSNCPVTGQPDWGTLVVDYRGPALDPASLL
AYLVSFRQHQDFHEQCVERIFLDLQRLQALSVYARYVRRGGLDINPYRSLAEVAPDNRRLLVRQ

>gi|37524663|ref|NP_928007.1| 7-cyano-7-deazaguanine reductase [Photorhabdus luminescens subsp. laumondii TT01]
MSLYRDHQALEQLTLGKTTLYRDQYDASLLQAVPRNMNREPLEIFPDNLPFHGADIWTLTYELSWLNNRGL
PQVAVGHVSLNAASTNLIIESKSFKLYLNSFNQTRFENWQAVEETLQRDLAACAEGEVEVALHHLDFHNNQ
PISTFTGECIDDQDIEVTEYDFNRHYLQNAAQGPQVEEVLVSHLLKSNCLITHQPDWGSVQIHYKGSKIN
REALLRYLVSFRHHNEFHQCVERIFSDLQQLCAPEKLSVYARYTRRGGLDINPWRTNSEGFVPATGRLA
RQ

>gi|22127023|ref|NP_670446.1| 7-cyano-7-deazaguanine reductase [Yersinia pestis KIM 10]
MSSYQNHKALAEELTLGKPTAYCDYDATLLQAVPRSMNREPLGLYPDNLPHGADIWTLTYELSWLNSNGL
PQVAVGEISLNADSNLIESKSFKLYLNSFNQTFADKESVRMTLQRDLAACAQGNVSVLYDLDEITGQ
PISNFGNCELDKQDIRIDSYEFNADYLQGAAGKDHVESLVSHLLKSNCLITHQPDWGSVQIHYRGPQID
HEALLRYLVSFRHHNEFHQCVERIFNDIMRFCQPETLTVYARYTRRGGLDINPWRNSNTDFVPLTGLRLAR

Q

>gi|229846813|ref|ZP_04466920.1| 7-cyano-7-deazaguanine reductase [Haemophilus influenzae 7P49H1]

MNYQDNSLKSLKLGQKTEYASQYDRTLLQPVPRALNRDGLGITQNQPFTIGADIWTAYEISWLNEKGLPQ
VAIADIYLDYQSQNLIIESKSFKLYLNSFNQSKFTDFNAVQQTMRDLIECAQGDVVKVRLNPVAVYDAQKI
EHLQGDICIDEQDIEITSYEFNANWLKDCVSDEIVEEKLVSHELLKSNCLITNQPDWGTLHIHYVGKINQE
KLLRYVVSFRQHNEFHEQCVERIFCDLMHYAKPEKLTVYARYTRRGGLDINPFRSNFENLPENLRLARQ

>gi|121588138|ref|ZP_01677885.1| conserved hypothetical protein [Vibrio cholerae 2740-80]

MNRLKNMSKYSDAKELASLTGKKTAYANQYDPSLLQPVPRSLNRNDLHLSATLPFQGCIDIWTLYELSWL
NQKGLPQVAIGEVSIPATSANLIESKSFKLYLNSYNQTRFASWDEVQTRLVHDLACAGETVTVNVKSLN
EYTAEPVITMQGECIDDQDIEIANYEFDDALLQGAAQGEVSEVLHSHLLKSNCLITNQPDWGSVEIAYH
GAKMNREALRLYLVSFRHNEFHEQCVERIFTDIMRYCQPQSLTVYARYTRRGGLDINPFRSSHQSAPNH
NQRMARQ

>gi|24114078|ref|NP_708588.1| 7-cyano-7-deazaguanine reductase [Shigella flexneri 2a str. 301]

MSSYANHQALAGLTGKSTDYRDTYDASLLQGVPRSLNRDPLGLKADNLPFHGTDIWTLYELSWLNAKGL
PQVAVGHVELDYTSVNLIIESKSFKLYLNSFNQTRFNWDEVQRQTLERDLSTCAQGGKISVALYRLDELEGQ
PIGHFNQTCIDDQDITIDNYEFTTDYLENATSGEKVVEETLVSHLLKSNCLITHQPDWGSIQIQYRGRQI
DREKLLRYLVSFRHNEFHEQCVERIFNDLLRFCQPEKLSVYARYTRRGGLDINPWRNSNSDFVPSTTRLV
RQ

>gi|16078439|ref|NP_389258.1| 7-cyano-7-deazaguanine reductase [Bacillus subtilis subsp. subtilis str. 168]

MTTRKESELEGVTLGNQGTNYLFEYAPDVLESFPNKHVNRDYFVKFNCPEFTSLCPKTGQPDFATIYIS
YIPDEKMVESKSLKLYLFSFRNHGDFHEDCMNIIMNDLIELMDPRYIEVWGKFTPRGGISIDPYTNYGKP
GTKYEKMAEYRMMNHDLYPEIDNR

>gi|15923718|ref|NP_371252.1| 7-cyano-7-deazaguanine reductase [Staphylococcus aureus subsp. aureus Mu50]

MAHGRQQDELQDITLLGNQDNTYNFDYRDPDVLESFDNKHQGRDYFVKFNCPEFTSLCPITGQPDFATIYI
SYIPNVKMVESKSLKLYLFSFRNHGDFHEDCMNIIMNDLIELMDPHYIEVWGKFTPRGGISIDPYTNYGR
PNSKYEKMAEHRMLMNHDLYPEKIDNR

>gi|15606257|ref|NP_213635.1| hypothetical protein aq_931 [Aquifex aeolicus VF5]

MEAKEKKYGEIEIEKAQLEAWPNPNPERDYMIEITFPEFTCLCPRSGYPDFATIKIRYIPDKYIVELKSL
KLWLNKFRNRYISHEAATNEIYQALYDLLKPRFLEVVGDFHPRGNVHTVVRVRSDENYG

>gi|30250215|ref|NP_842285.1| 7-cyano-7-deazaguanine reductase [Nitrosomonas europaea ATCC 19718]

MTTQPSKQLETFFENPVQTRDYRIHMEIPEFTCLCPKTGQPDFARLTLDYIPDKKCIELKSLKLYIWSYRD
EGAFHEAVTNRILDDLVAAMKPRFIRLTSKFYVRRGGIFTNVVAEHRKKGWQPPVLLLEVFEQQFNTHG

>gi|57236909|ref|YP_179862.1| 7-cyano-7-deazaguanine reductase [Campylobacter jejuni RM1221]

MRYGEKEIKEFDVENMEIWPNDKNDYIIKITLPEFMCCCPRSGYPDFATIYLEYMPNKFVVELKAIKLY
INTFMYRNVSHEASINEIYNTLKDKLKPKWIKVVGDFNPRGNVHTVIECRSDMVVVK

>gi|291276630|ref|YP_003516402.1| NADPH-dependent 7-cyano-7-deazaguanine reductase QueF [Helicobacter mustelae 12198]

MKDLSLLGKQDVEYAFHYNPKILETFENRHKENDYFVKFNCPEFTSLCPMTGQPDFATIYINYIPQHKMV
ESKSLKLYLFSFRNHGDFHENCNVNIMKDLIGVMEPKFIEVWGKFLPRGGISIDPYANYGLPNTKYEEMA
HYRLLHHDLSFEKIDNR

3. Supplemental data 2

gi|14521321|ref|NP_126796.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Pyrococcus abyssi GE5]

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MSRGDKMLKFEVKARDGAGRIGKLEVNGKKIETPAIMPVVNPKQLIVEPKELEKMGFDIIITNSYIIYKD  
RELREKALEVGIHKLLGYDGIIEVDSGSFQLMRYGNVDVSNREIVEFQHRIGVDIGTFLDIPTPPDAPKE  
KAMEDLKITLERAREAEIEKEIAMNAAIQGSTYTDLRRYAARRLSSMNFEIHPIGGVVPLLEAYRFREVV  
DIVISSKMALRPDRPVHLFGAGHPMVFALAVAMGVDLFDSASYALYAKDDRYLTPEGTKRLEDELEYFPCS  
CPVCSRYTPQELREMPKEERARLLAIHNLWVIKKEIERIKQAIREGELWRLVDERARSHPKLYSAYKRLL  
DHYTFLEEFEPVTKKSAVFKISHESLRWPLVRRARERAERVNSKFGDLVEHPIFGKVTKYLTLYPFAQS  
EAEDFSIEKPTRENAIRYVMAIAEYQFGENASKAFEGAEVELARTGMQRQVKLNGKRLATVRAEDGFLT  
LGIEGAKRLHKVLEYPRMRVVVSEEAEPFARKGKDVFAKFVLFADPGIRPYDEVLVVNEKDELLATGQAL  
MSGREMIVFQYGRAVKVRRGISGG
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>gi|14590946|ref|NP_143020.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Pyrococcus horikoshii OT3]

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MSRGDKMLKFEIKARDGAGRIGKLEVNGKKIETPAIMPVVNPKQMVVEPKELEKMGFEIIIITNSYIIYKD  
EELRRKALELGIHRMLDYNGIIEVDSGSFQLMKYGSIEVSNREIEFQHRIGVDIGTFLDIPTPPDAPRE  
QAVKELEITLSRAREAEIEKEIPMNATIQQSTYTDLRRYAARRLSSMNFEIHPIGGVVPLLESYRFRDVV  
DIVISSKMALRPDRPVHLFGAGHPIVFALAVAMGVDLFDSASYALYAKDDRYMTPEGTKRLELDYFPCS  
CPVCSKYTPQELREMPKEERTRLALHNLWVIKKEIKRVKQAIKEGELWRLVDERARSHPKLYSAYKRLL  
EHYTFLEEFEPITKKSALFKISNESLRWPVVRRAKERAKSINERFGELVEHPIFGRVSRYSLSLYPFAQS  
EAEDDFKIEKPTKEDAIKYVMAIAEYQFGEASRAFDDAKVELSKTGMQRQVKVNGKRLATVRADDGLLT  
LGIEGAKRLHRVLPYPRMRVVVNKEAEPFARKGKDVFAKFVIFADPGIRPYDEVLVVNEDELLATGQAL  
LSGREMIVFQYGRAVKVRKQVE
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>gi|18977418|ref|NP_578775.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Pyrococcus furiosus DSM 3638]

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MSRGDSMLRFEIKDRDAAGRIGKLEVNGKKIETPAIMPVVNPKQLIVEPKELKRMGFDIIITNSYIIYKD  
KKLREKALEKGIHRLLDYDGIIEVDSGSFQLMRYGKVEVTNREIVEFQHKIGVDIGTFLDIPTPPDAPRE  
KAEQDLKITLERAKEAESIKQIPMNATVQGSTYLDLRKLAARKLSEMNFIEHPIGAVVPLLESYRFKDVV  
DIVIASKMGLRPDRPVHLFGAGHPMVFALAVAMGVDLFDSASYALYAKDDRYLTPQGTRKLEELEYFSCS  
CPVCSKYTPQELREMPKEEREKLLALHNLWVIREEINRVKQAIKEGELWRLVDERARAHPKLYAAYKRLL  
EYYHYLEEYEPITKKSALFKISEESLKWPIARRAKERAEKVKAKFPESIPHPIFGEIPKYLSTLYPFAQS  
ESEEDFQIEKPTRENAIYMAIAEYQFGEAGEAFRDAEVEIAKTGMQRQVKKNGKRLATVRAEDGLLT  
LGIEGAKRLHELLPYPMRVVVVNKEAEPFARKGKDVFAKFVEFADPKIRPYDEVLI VNEDELLATGQAL  
LSGREMVLFSGRAVKTRRGVEEKK
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>gi|57640695|ref|YP_183173.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Thermococcus kodakarensis KOD1]

MVDFRFEVKARDASGRIGKLTVNGKTIVETPAIMPVINPKQLIVTPKELKEMGFGMIITNSYIIYKTPELR
EKALEVGIHKLLDYDGIIEVDSGSFQLMRYGGVEVTNREIVEFQHEIGVDIGTFLDIPTPPDAPREKAEE
DLRITLERAKEAEEIKEIAMNAAVQGSTYDLRTYAARELSRMNFEIHPIGAVVPLMESYRYRDLVDVVI
ASKVGLRPDRPVHLFGAGHPMIFALAVAMGIDLFDSASYALYAKDDRYMTPEGTKRLEELEYFPCSCPVC
SRYTPQELREMPKEERTLLAIHNLWVIREELNRVKQAIKEGELWRLVDERARSHPKLYAAYKRLLEYRE
YLEKNEPVTKASAFFKVSEELRWPIVERARERAERVRSKFPETISHPIFGEIPKYLSLSYPFAQSEGEE
DFTVEKPEKGEARKYVMAVAEYQFGEGAGEAFKDAFVELSRKTGMPRQIKAKGKHLATFRAEDGLLTLGI
EGAKRLHEVLFPFRMRVVVDEDAEPFARRGKNVFAKFVVDADLNIRPYDEVLVVNRNDELLATGQTLNNG
EELKIFQQGLAVKVRGVEK

>gi|15678204|ref|NP_275319.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Methanothermobacter thermautotrophicus str. Delta H]

MISLISRGNTLLMTLWEDFMFEIKSKDGLGRTGILKTEHGTVRTPALMPVIHPGKQOTIDVKGPGAEIVIT
NAYIIYRNPELRERALS DGVHRLIDFDGPIMTDSGSFQLSEYGDIEVENPEIIRFQDEIGTDIGTSLDIP
TPPGVSHRRAIEEVEVTLERARESIEYRERMMLNAVVGSTHPDLRRYCASRLAELPVELHPIGAVVPLM
ESYRYRELVDVAVLSSVSELPPSRPRHLMGAGHPMLFALAVSMGCDLFD SAAYILYAEDDRLLSTEGTYKL
ENLQEMPCSCSVCTDYTPSELGMGDREERNLIAEHNHLSVFAEIRKVRQAIHDGNLMELVEERCRAHPR
LLEGYRRMSEYLDLIEKFEPKRSKSAFFYTGPESLGRVEVHRHLKRVKEHLGERLALVAPSRPYSSSLP
ARIGGFSSLRPQSGGPWRVVVDLPFGIIPLELDQVYPLAQSDAPGIMDLDGEEFLRGLVRDLMDGDAIV
DDALCSELGIELPYKYMGEVETTVDLDRVMVADYQFGMGAGELLFTDDVRIERSRNTGKIRHIYAGDE
LICTMRASDGLLVGAEGAVRLHKGTDYPAWRVAVNEESEPFARKGKSVFAKFIIDCDNNIRANDEVLIV
NADDELLATGKALLCAEEMMDLNHGQAVKTRKGGF

>gi|45358173|ref|NP_987730.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Methanococcus maripaludis S2]

MFEIKARDAMGRG SITINGKKIETPTIMPVIHPNPKKQTVSMDLINKMADVITNSYITYTTPELREIA
ETKGIHELIDFKNVVVTDSGSFQLSVYGDVNVGPMEIIDFQEKIGVDVGTILDIP TGPDSREKAESDLI
ETFKRAEDSIKRRKEMGYKLALNGTIQGSKYLDLRQKSAEVMGKMDFDIYPIGAVVPLMEDYRYREVAEV
ILNSKMHLPTNKPVHLFGCGHPMLFALSVALGCDLFD SAAYALYAKNGRYLTADGTLHLKMDKDLKSFPC
TCKVCSEYTPKQLYNLEEKEKTRLLAEHNLYVTFEEDRIKNAIKEGNLWELVEERCRSHPKLLNGLRVI
SKYMDFIEKHDPVSKKSGFFYTGYESMNRPEIYRHKQRLDRIQYDKIYVTSVSENTSKPYSENLSNVPCD
VDVLVKDSVFGVPLNIDTMYPLAQNEVPDLYDFEKYNNFVSEFNEKHAEKILDISTYNYIINHYGKK
KECDKINPDIFRIGKMLEYQYGA KILDEELMEKVKSRRSKNTGRIRNLLLEKEVLF TLRANDNFLIPAKS
GAELLHEKLEFPKYRIVIDSSVEEFARAGKSVYSKFKDCPELRPFEEVLIVNSDDELLAYGTTILNGR
ELMEFDYGVAATLRGGLKK

>gi|159904673|ref|YP_001548335.1| 7-cyano-7-deazaguanine tRNA-
ribosyltransferase [Methanococcus maripaludis C6]

MFEIKARDAMGRG VITINGKKIETPTIMPVIHPNPKKQTVSMDLINKMADVITNSYITYTTPELREIA
ETKGIHELIDFKNVVVTDSGSFQLSVYGDVNVGPMEIIDFQEKIGVDVGTILDIP TGPDSREKAESDLL
ETFKRAEDSIKRRKEMGYKLALNGTIQGSKYLDLRQKSA DVMGKMDFDIYPIGAVVPLMEDYRYREVAEV
ILNSKMHLPTNKPVHLFGCGHPMLFALSVALGCDLFD SAAYALYAKNGRYLTADGTLHLEDMDKDLKNFPC

TCKVCSEYTPKQLFNLEEKEKTRLLAEHNLYVTFEEIDRIKNAIKEGNLWELVEERCERSHPKLLNGLRVI
SKYMDFIEKHDPVSKKSGFFYTGYESMNRPEIYRHKQRLERIQYDKIYVTTVSENTSKPYHENLDNVPCD
VDVLIKDSVFGVPLNIDTMYPLAQNEVPDLYDFEKKYNNEFVSNFMEKNSEKILDISTYNYIINHGYTK
KECDKINPDVFRVGMLEYQYGAKILDDELMEKVKTRRSKNTGRIRNLLLEKEVLFTRANDNFLIPAKS
GAELLHEKLEFPKYRIVIDSSVEEYARAGKSVYSKFKDCPELRPFEEVLIVNSDDELLAYGTTILNGL
ELMEFDYGVAATLRGGLKK

>gi|134046031|ref|YP_001097517.1| 7-cyano-7-deazaguanine tRNA-
ribosyltransferase [Methanococcus maripaludis C5]

MFEIKARDAMGRLGVITINGKKIETPTIMPVIHPNPKKQTVSMDL INKLADVITNSYITYTTPELREIA
ETKGIHELIDFKNVVVTDSGSFQLSVYGDVNVGPMEIIDFQEKIGVDVGTILDIPDTPGVSREKAESDLL
ETFKRAKDSIKRRKEMGYKLALNGTIQGSKYLDLRQKSAEVMGKMDFDIYPIGAVVPLMEDYRYREVAEV
ILNSKMHLPTNKPVHLFGCGHPMLFALSVALGCDLFD SAAYALYAKNGRYLTAEGTLHLEDMDKLSFPC
TCKVCSEYTPKQLFNLEEKEKTRLLAEHNLYVTFEEIDRIKNAIKEGNLWELVEERCERSHPKLLNGLRVI
SKYMDFIEKHDPVSKKSGFFYTGYESMDRPEIYRHKQRLERIQYDKIYVTSVSENTSKPYHENLSNVPCD
VDVLIKDSVFGVPLNIDTMYPLAQNEVPDLYDFEKKYNNEFVSEFREKHTEKILDISTYNYIINHGYTK
KDCDKINPDIFRIGKMLEYQYGAKILDDELMDGKVKSRRSKNTGRIRNLLLEKEVLFTRANDNFLIPAKY
GAELLHEKLEFPNYRIVIDSSVEEFARAGKSVYSKFKDCDHELPRPFEEVLIVNSDDDLLAYGTTILNGQ
ELMEFDYGVAATLRGGIKK

>gi|15668612|ref|NP_247410.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Methanocaldococcus jannaschii DSM 2661]

MEIIEFQERIGVDVGTILDIPDTPDVRERAEKELEETLKRAKASIELKEERGFKLLLNGTVQGSTYLDL
RQKSAKEMAKLGFDIYPIGAVVPLMEQYRYRDAEII INSKMYLPTNKPVHLFGCGHPMFFALAVAGCD
LFDSAAYALYAKDDRYLTERGTLHLEEIKDLKAFPCSCPVCSSYTPKELASLNKKERERLLAEHNLYVTF
EEINRIKQAIRDGLWELVEERVCHPKLLEAYRVVRKYIDYIEKFDPVTKKSAFFYTGIESMFRPEVLR
HKKRLKRLRYEKVYITTVSSIEKPYHEHLNVVETDVIDILIKDPVFGFIPYYIDTVYPLSQHEIPELFDY
EKEINKRFVDEFIDWLKKGIGEDNILDIMTYNYIYNYFSANKKINADALRIRKMLQYQYGFDIIDDEL MN
KIKVVRSKTTGRLRQVLDENGEILFSVRSNDNLLIPSEKGA LLWKKIPFPKYRVVVNKEAEFAREGRN
VFAKFVIDCDEELRPYEEVLVNVNEDDELLAYGTTILNGIELREFNYGLAVKVRGGLKINK

>gi|170290974|ref|YP_001737790.1| tRNA-guanine transglycosylase [Candidatus
Korarchaeum cryptofilum OPF8]

MGLYFRVRKSDASARLSELKTKSGTLILPEFFPVYNPNKPVITPREMSEMGIKAIITNSYLIYRSPELRE
AAIERGIHSLGFDGVVMTDSGAYQIYRYGRVDVTNSEILRFQHSIGSDIGSILDVPMSSIEGREEAESG
VERTIRNAEEWASMREELSNTLWVGTPQGSYRDLVIKCSERIRELDFDYNVGSIKVALEKYDFVTQVD
HFMSIRSILRAGKPFHFWGIGHPSTFAFFAAIGADSFDSASYSLYAEQGRYMPHGTL LLLDEIEEFPCSC
PVCSSHDPKEVKAMSKEERTKLLAKHNLYISISEIKKVREAIRGEWLWELVQERSRFHPNLYFALMHLR
RYSSLLEAREPLFKSSGLQCSGPESFLRPEVVRARNRLKYIHYNGKFRRVLYGDVPLGLKYLYPFGQTIC
PYDEEVQDEPEDDEIITCVLSYQYEFPPKLP AIMRRSKSTGT LREVSLEGKVI GHFRPN DGAFIPTLDG
ASLILSHLPYPKGRVVVKGLFSDTVARGTTVFVKFVKEADPSIRPKSEVIVVNESDELLATGKAVLSGVE

YHQYHPDHPFIIIRRHVKPRSEEKPEVDS

>gi|20093628|ref|NP_613475.1| queuine/archaeosine tRNA-ribosyltransferase
[Methanopyrus kandleri AV19]

MNVAFEVKDRDVAGRLGRLEVNGRRLKTPALLPVVNPKNPTLDPREISKLGFDGVITNAYIIRKHEHLRE
QALEEGVHGLLGFDFVMTDSGSFQLAEYGDVEVSNEEIVRFQAKIGSDVGTILDVPTPPDAPRSRVERD
LETTLKRAREAVELDEHPPLALTVQGSTYEDLRRLCAEKLAELPAAVYPVGGVVPLLEEYRFVDVVRVVL
AAKSSLPHPRPVHLFGCGHPLAIPLAVAMGCDLFDASAYAIYARSDRYMSILGTLKLEELTFPCSCPAC
TRHDPDDVREMEPRERTRVLATHNLYELRRVIETTRQAIIVSGELWELAESVCRAHPRAWAGMVVELARRGG
ELERWCPAVKRSVFCDEVSFKRPELRRLYRRRLRDRFGELSGRKVVKGISRPYAEIVEWLEPWELAFADE
WLGVVPGELSWSYPCHCLVEPSGDDEGEDRRRGEEGRRR

>gi|16082455|ref|NP_394944.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Thermoplasma acidophilum DSM 1728]

MKIEERDGLARIAKFETPHGPIETPTVLPVINPNIMNITPQEMKPLGLQGIITNSYIILRTPELRERLR
EGLHSLIGYDGPIMTDSGTFQSYVYGSIEFNNREVVDFQRRIGSDISTILDVFTTPGTPKPEAEKAVIET
YNRMLEVNDEEGI IAGPVQGGVYDPLRQKSAELMNSTNAGYHP IGGVVPLLETYDYSTLVDII INSKINL
SFKPKVHLFGGGHPMFFAFSVYLGVDLFDASAYIKYAKDDRLIYDPGTRDLARITELPQWSPLYDRYTVK
EIRDLDKERRSLEIARHNLKAI FMEI SEIKERIYEEGLAQYVAQKARSHPSLMKAYSRIMSYSNILEKYE
DLSKKTAYFFYDSFSTRNPYVSRINRFTE SYLSSNKD TYAFTYRAWNPGYTNSEFVRDVYQKIDCNALI
SWSGTFVPAELENTYPIEQTVSSGFEPDPDF SRAKDLIAPFRVDMYKGEKFEQEQRVSNLNKIRMVADY
QFGSGVGRMIFRDDVRINVSKTGRIRGILSKEGRQIATMRNDGFFTLTYYGASLIHSQLKPPAMRVTVSK
ESAEYNAKGYSVFFKFILGSDENIIAKNDVLVDEDDVLA AVGKAMVSGRELREYTEGIAVKVHEGRDQS
EK

>gi|13542328|ref|NP_112016.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Thermoplasma volcanium GSS1]

MEIRERDGLARIARFDTPHGTIETPTVLPVINPNIMDITPEEMKKYGVHGVITNSYIILRNDRLREEAEK
YGVHSLIGYDGPVMTDSGTFQSYVYGSVEFNNRQVVEFQKTIGSDILTILDIFTTPSSSRQEVENAITET
YRRMLEVNDAGGMIAGPIQGGIYDPLRKRSAELMNSTNASYLP IGGVVPLLESY EYDKLVDIILNSKLN
SFGKPIHLFGGGHPMFFAFAVYLGVDLFDASAYVYKAKDDRLIYDPGTRDLARIEIPEWSPLFDKYTVK
ELKELPKEQRSVELSRHNLKAI FMEI SEIRERIYEE SMDQYLAQKAKSHPSLLKAYVKVMQYSKMLEKYQ
DLFKKAAYFFYDSFSTKNYVARLEKFTSKYLTSKKKETYVFSRKDWLPGYTNLNFVRDVYERTECNALI
PWSGIMVPAELENTYPIEQTVSSGLEPDPDVSAISESISPFDIRVYKGESVDSKIRSFDFLEKIRTIADY
QFGYGIGKDFKDDVRIFKSKTGRIRGVFDKGNKLIATLRNDGFFTLTFHGATLLYNVSKSPNLRVFKV
ESAEYNAKGYSVFFKFILDADPDI IAKNETLVVNENGELVAVGKATVSGKELREYSDGIAVKIHEGRDQS
AK

>gi|48477526|ref|YP_023232.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Picrophilus torridus DSM 9790]

MEILFRENLARIARFKTPHGEIETPTVMPVINPNLNFLDESTLRSYGVQAVITNSYI IKNRQRLNEDALR
HGLHSLIKFSGPIMTDSGTFQSHVYGDIEYSNKEIVDFQKAIGSDIITILDVFTPEDESYSNARSKVIET

YKRLKEIDFEDKIIAGPVQGSIIYDPLRRLSAYLMSDALYLP IGGVVPLLESYRYSDLVKIIFNSKVSSDF
SRPVHLFGGGHPMFFAFVAVMLGVDLFDSASYIKYAKDNRLLYSEGTRALNDIREFPEWSPHKGKYPQEL
LHEESEKRTRMLALHNLKSI FIEINEIKERIYENTLYNYVEEKARSHPALFKAFMSMINYDTSYSPLSY
KSPFFYYDKTSLNHPIIKRIMKFTENYISNSRHTLIIS SKYWRPGVKNENVIKNIVECTDFNLLVSWNGI
YIPLFLEDSPVQQLVSSGLNDKLEEDYLKRLK SINNDIEFYEGEHYDKRLRDYDTEKINTIAMFQFNI
NERFFDKSNIKSKSTGHIRNI IEDNNIIATMRNDGYLTLSIKGAYRLLSMKPWPGLRVVVDDESGRFNA
NGYNVFFKFIKSFDTGIIPGNETLVVSEDDDLAVGKAAVSGIEMYYYYKSGVAVKVHEGVNKKAA

>gi|257076281|ref|ZP_05570642.1| 7-cyano-7-deazaguanine tRNA-
ribosyltransferase [*Ferroplasma acidarmanus fer1*]
MFFREGLARIGKFSTPHGDIETPTVMPVINPNLFLTKEELK SIGVQAVITNSYIIKRTASLEQDALKHG
VHRLINFDGPIMTDSGTFQSYVYGDIEYGNKEIVQFQKDIGSDIITILDIFTK PQDSYEQAKAAVYETSR
RLQEVNTPDSIIAGPIQGSIIYDPLRRESARLMSEASYLPIGGVVPLLESYRYSDLVNI IINSKLNSDFSK
PVHLFGGGHPMFFAFVSVLLGVDFDSASYIKYAKDNRLVLYTEGTRNLKEIRDFPEWSPLFNKYSPVELIK
ADEKTRLKLLSLHNLKAI FNEITEIKERIYENTLYQYVEEK SMAHPALYRAYLEMLDHNLEPFWNISLKS
PLYFFNSSTYKNTFIKRLVKFTEDYISNGKKT VLVSYRQWRHGFVSDDILRSYETTDYNFLIEWNDIFI
PMELENTY PVSQMVPSGVLDKIYRDDYIAWLK SINNDISFYDPSITGSEKIRNYSHSKINEVFHLQFKAR
KNL FVNSDKIIKSKATGHIRNIKRGEKIIATMRNDGFLTLSIYGGKLLNDMLDFPASRVIVTDDSGEFNS
QGYNVFFKFVEDCDREIIAGNDVMVTSASGDLYAVGHATVSGKEMGFYRNGI AVKVHEGINKL

>gi|84489330|ref|YP_447562.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[*Methanospaera stadtmanae DSM 3091*]
MVDIIVDFEIKYKDAMARVGKFKTPHGTVTTPALMPVVHPGKQTL DVKKLGAQIVITNSYIIYKNEELKK
KALEEGVHSLIDFPNTIETDSGSFQLSVYGDIDITNEEVIKFQEAIKTDIGTSLDIPTAPYVKREEAEND
LEITIERAKEAANVKS DLLLLNSVVQGSTFPDLREKCAKEISKYDADIYPIGAVVPLMEMYRYADLVDAVM
YSMRGLPENKPRHLMGAGHPMV FALATAMGCDLFD SAAYILYANKDRFMMPDGTLRLEDLIEMPCSCRVC
CEYTVDELKQMDQKKRAKLI AEHNLHISFAEIRRIRQAIVDGELMKLVELRCRSHPFLLDGLRRLMEYKE
DMERLNPSSKKS AFFYTGYESLARSEVPKHLKQLENIKPKNKNLVILPHTRKPYTKYVNREYIKKYTPKI
PTYYSNTTNTDYSNSDVV VADIPFGI IPLGLDEFYPLAQNESPSI HDLDSKRFIRDI INNYSKKYDNVLI
HRKVIEKFDITNFNLI EDELQLPEAKISDFNRLNDIADYQFGCGAGNALFGGDEDKITIEKSRKTKKIRH
VFEDNENIVNMRANDGFLILSDLGAKRLHKFLEYPHNRV VVSEDSEPFALKGKSVFNK FVLDCDENIRRN
DEVLIVNKDDKLLAFGKALLSSYEIKDFNTGQA I KTRKWKKEIE

>gi|240103198|ref|YP_002959507.1| 7-cyano-7-deazaguanine tRNA-
ribosyltransferase [*Thermococcus gammatolerans EJ3*]
MRGESMEFRFEVKARDAAGRIGKLT VNGKSIETPAIMPVINPKQLIVTPKELEEMGFGMIITNSYIIYKT
PELKEKALELGIHRLLDYDGIIEVDSGSFQLMRYGEVEVTNREIIEFQEKIGVDIGTFLDIPTPPDAPRE
KAEEDLRITLERAKEAES IKNIAMNAAVQGSTYPDLRTHAAQELSKMNFEIHP I GAVVPLMESYRYRDLV
DVVVASKLGLRPDRPVHLFGAGHPMIFALAVAMGVDLFDSASYALYAKDDRYLTPEGTKRLEELEYFPCS
CPVCSRYTPQELREMPKEERTRL LAIHNLWVIREELNRVKQAIKEGELWRLVDERARSHPKLYSAYKRL
EYRDYLEKNEPITKASAFFKVSEEAMRWP IVYRAKERAERVAKKFPERIRHPIFGEIPKYL SLSYPFAQS
EGEEDFTIEKPRKG EARKYVMAVAEYQFGEGAGEAFKDAFVELSRKTGMPRQVKAKGKHLATFRAEDGLL

TLGIEGAKRLHALLPFPKMRVVVNEDAEPFAKRGKNVFAKFVVDADPSIRPYDEVLVVNEKDELLATGQT
LLNGEELKVFQSGLAVKVRGIEKG

>gi|91772941|ref|YP_565633.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Methanococcoides burtonii DSM 6242]

MSSIFEITHKDAAGRIGKLRTPHGTVETPTVMPVINPNLQVIKPSMRDFGAQMLITNSYIISRDKLRE
KALKDGLHSLLDGDFGIMTDSGSFQLSVYGDIEVTNEQIIEFQKTIGSDVGVPLDIPTPPDVPRSRAESE
METTIERLIEARSMVNDEMLLAGPVQGSTYTDLREKCASTISEHKFDVYPLGAVVPLMESYRYAELVDVI
VSSKKGLDPTVPVHLFGAGHPMMFALAVALGCDLFD SAAYALYAKDRRYITSKGTYHIDNLSYLPCSCPI
CVSHTAEVVKADNCSDLLARHNLVYTFEELIRLIKQSIKEGNLLELVEMRCRSHPRMLEALKRMYSYSDW
IEKYDPASKSTFFYCGPESSQRPEVLRFSKRLERFTIKGTAVIRPF SMRTYPESDNDLMFKPPFGTFPAE
LSEVYPFNAEVIEDTDIESLGKALENTIRLIELNPDAEFTFIKGKELEHPLFEKLEKIADVKE

>gi|21227203|ref|NP_633125.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Methanosarcina mazei Gol]

MSAIFEILDKDAGGRIGKLRTPHGVVETPTVMPVINPNIQLISPKEMRSFGAEILITNSYIIRKEELRT
VALEKGLHELLGDFGIMTDSGSFQLSVYGSVEVTNEEILGFQEKIGSDIIVPLDIPTPPDVHFRRAEEEE
LATTAERLEAARKFIQSKQLLAGPVQGSTYPELREKAASHLKDNLNFEVYPLGAVVPLMESYRYAELVDVI
AASKKGLSPTSPVHLFGAGHPMMFALAVALGCDLFD SAAYALYAKDGRYITSNGTYHLEKLNLYPCSCP
CSRYTAEELRKAKNKEELLGRHNLATFAEIRLIKQSIKDGKLELVEQRCRAHPKLLDGLKRLYTHSAW
LEQFDPATKGTFFYCGPESASRPEVLRFGKRLERFSIEGSAIIRTSPVKGEKDYDRILTFKAPFGTFPAE
MEEVYPFNAEVPKFPDYEALSTSLNNTIKLMDLNPGAFTFICEKEFQHPLIEEIGKKAKLVYREAWKKE

>gi|20093206|ref|NP_619281.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Methanosarcina acetivorans C2A]

MSAIFEILDKDAGGRIGKLRTPHGIVETPTVMPVINPNIQLISPKEMKSFGAEILITNSYIIRKEELRT
VALEKGLHGLLDFGDFGIMTDSGSFQLSVYGSVEVTNEEILGFQKIGSDIIVPLDIPTPPDVHFRRAEEEE
LAVTAERLEAARKFIQGEQLLAGPVQGSTYPELREKAASRLRDLNFEVYPLGAVVPLMEAYRYAELVDVI
AASKKGLSPTSPVHLFGAGHPMMFALAVSLGCDLFD SAAYALYAKDGRYITANGTYHLEKLNLYPCSCP
CSKYTAEELRKAKNKEELLGKHNLYATFAEIRLIKQSIKDGKLELVEQRCRAHPKLLDGLKRLYTHSAW
LEQFDPATKGTFFYCGPESSFRPEVLRFEKRLDRFSLEGSAIIRTAPVKGEKDYDRVLTFFKAPFGSFP
MEEVYPFNAEVPKFPDYETLSTALSNTLKLMELNPGAFTFICEKEFEHPLIEEIGKKAKLVYRAAWKKE

>gi|73668621|ref|YP_304636.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Methanosarcina barkeri str. Fusaro]

MSAIFEILDKDAGGRIGRLRTPHGTVETPTVMPVINPNIQLIPPKEMRNFGAEILITNSYIIRKEELKS
VALEKGLHGLLDFGDFGIMTDSGSFQLSVYGSVEVTNEEILGFQKIGSDIIVPLDIPTPPDVHYRRAEEEE
LAITAERLEAARKFIQSEQLLAGPVQGSTYPELREKAASHLKDNLNFEVYPLGAVVPLMEAYRYAELVDVI
AASKKGLSPASPVHLFGAGHPMMFALAVAMGCDLFD SAAYALYAKDGRYITVNGTYHVEKLNLYPCSCP
CSKYTAEELKADNREELLGKHNLYATFAEIRLIKQCIKDGKLELVEQRCRAHPKLLDGLKLYTHSSW
LEQLDPATKGTFFYCGPESSSRPEILRFKRLDRFSLQGSVIIRTGSKVGEKDYDQILTFKAPFGAFPVE

MEEVYPFNAEVPKFPDYESLNTALSNTLKLIDLNPEAEFTFICEEEFKHPLIEEIRKRAKLVYRKDWKKE

>gi|73671775|gb|AAZ80293.1| archaeosine tRNA-guanine transglycosylase catalytic subunit [Methanosarcina barkeri]

MSAIFEILDKDGGRIGRLRTPHGTVETPTVMPVINPNIQLIPPKEMRNFGAEILITNSYIIYRKEELKS
VALEKGLHGLLGFDPIMTDSGSFQLSVYGSVEVTNEEILGFQQKIGSDIIVPLDIPTPPDVHYRRAEEE
LAITAERLEAARKFIQGEQLLAGPVQGSTYPELREKAASHLKDNLNFVYPLGAVVPLMEAYRYAELVDVI
AASKKGLSPASPVHLFGAGHPMMFALAVAMGCDLFD SAAYALYAKDGRYITVNGTYHIEKLNLYPCSCPV
CSRYTAEELKKADNREELLGKHNLYATFAEIRLVKQCIKDGKLELVEQRCRAHPKLLDGLKKLYTHSSW
LEQLDPATKGTFFYCGPESSSRPEVLRFGKRLDRFSLQGSVIIRTGPVKGEKDYDQILTFKAPFGAFPVE
MEEVYPFNAEVPKFPDYESLNSALSNTLKLIDLNPEAEFTFICEEEFKHPLIEEIRKRAKLVYRKDWKKE

>gi|116754948|ref|YP_844066.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase [Methanosaeta thermophila PT]

MQGCFEILHKDLAGRIGRLHTPHGIVETPALMPVVNPHVLLLSPQELADLGAEMIITNSYIIHQDPVLRD
TALERGVHGLLNFDGPMVMTDSGAFQLSVYGSVDIEPLEILKFQQKIRSDVSVPLDIPTAPDAPREQAERE
LAETERRLREAVDHRSESLLLAGPVQGGIYPDRESSARRLRDLGFDLYPIGAVVPLMESYRFRELVDVV
VASKTGLGPGVPVHLFGAGHPMVFALAAALGCDLFD SAAYALYARDGRYLTPRGTYRLSEMKYLPSCSDV
CRKHTPESLNEDPKRVELLARHNLAVSFQEI RAVRQSIHEGSLWEHLERRCRSHPRMYQAFKHL SRYVEY
FERLDRVSKSTLFYLS TESARRPEVLR YRKRICRLELRGRVLTDRRPAEEDRSKYDHILGFLPPFGPYP
LGLEEMYPLNAELPDEM DENAMKEALDTLRL LIRENPDAEFHFEIRCLEGHRDAVL

>gi|55379810|ref|YP_137660.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase [Haloarcula marismortui ATCC 43049]

MTNFEVRQYDAAGRLGELTVPRAGVTVETPTILPVVNPVHVQTVAPATLASEFGAEILITNSYILHGSDDL
REPVLEQGLHDLLGFDGAIMTDSGSFQLAEYGDIDVTTEEIILEFQHEIGSDIGTPVDIPTPPDVDRERAT
EELKTTQERLEHAATVDTGEMLV SAPVQGATYPDLRERAAADAVSTGLDVFPLGAVVPLMNEYRYADLAD
VVAACKRGLGEVGPVHLFGAGHPMMFAMAAALGCDLFD SAAYALYARDDRYLTVQGTELLDELSYFPCHC
PVCTDHTPAELDAMDADAREELLARHNLHVTYGEIRTVKQAIRSGNLMELVDSRARGHPEMLDGYRALLD
HSEQLERTDPVSKDAFFYTSTESARRPEVRRHQDRLERLPVEGEEVLLTEGSSSAQYDESWGVLPPFGPY
PRELADTYPLTAETPDRTDRAAYEAAATGVRRLVELHPDVSFTLVHDDWPATALDRVPEGVRLRDLHARD

>gi|88602410|ref|YP_502588.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase [Methanospirillum hungatei JF-1]

MTLSFEILEKDIAGRIGKLSGQKIVKTPTLLPVINPHLNLIPPKEMQEMGVEAVITNAYIFSRSEEYRE
RALTDGLAKTLDFDGVIMTDSGSFQLSVYGEVEITNAQTIAFQQAIKSDIIVPLDIPTHSPREQVEQE
LSVTMDRIMEAKDIADHEHHTLAGPVQGGFLPDLREETGRRLSEAGFRFCPIGAVVPLMESYRYAELVKV
VMAAKRGLSPAVCVHLFGAGHP SMFALAVAMGCDLFD SAAYALYAKDGRYMTTHGSYHLNELSYLPCPCP
VCVGHTAKELNESPDRELLAMHNLRVSLAEINRVRQAIRDGVLWELVDERC SRSHPALLRGYRTLLGYNE
ELTALDRETKRRFFYRGDESKRTEVVRYHQMVGRLTAGERTLISFSRHIKKKQTEEYDSVFYFKPPFGP
FPAELTETFPIGQSEIPDFDEEMIKTGCIGIARLMETNPDSHFTIRCRPVWKDLITQILPTVEVQDEGS

>gi|76801897|ref|YP_326905.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Natronomonas pharaonis DSM 2160]

MRDIFERRDGDAAGRIGELSVPRAGTTVETPALLPVVNPHERTIAPAELESTFGAQILITNGYILYGSDE
YRERALADGLHDLDFDMSGAIMTDSGSFQLSEYGEISVTNEEILRFQRDIGSDIGTPVDIPTPPEASREQT
AADLETTKARLEAAETVDTGEMLVNAPVQGGTYPDLREEAAEHAYGTTLDVFPVGAVVPLMNSYRYGDMI
EAILGAKRGLGADAPVHLFGAGHPMMFALAVAAGCDLFDAAAYALYARDDRYLTVAGTDHLLDLEYLPCS
CPVCADHTPAELQAEDDTERERLLARHNLHVSFQELRTIKQAIKKGNNLELVERRARGHPAMVDGYRALL
EADQLERDDPVSKGSFFYLSGESARRPEVKRHHDRLSRLSVDGDRVLLSEGGDNSRFDETWRLQPPFGP
FPPALSDSYPLTAELPERLDDRAYEAAAAGVRRLLVDDHPETEFVAHVHGWPDAAALDSLDPDGVELLRLGAD
SDHPPERDSAQSDMDGDEPKEDYPPGEDENA

>gi|126179234|ref|YP_001047199.1| 7-cyano-7-deazaguanine tRNA-
ribosyltransferase [Methanoculleus marisnigri JR1]

MAITFEVIHKDIAGRVGKLRVNDKTVRTPALLPVVNPPLVTPREMREMGVEALITNAYIFRRSTEFHD
RALAEGLHGVLDLFDGVIIMTDSGSFQLSVYGEVEVSNRDTLEFQQAIKSDIVVPLDLPTPPDAGPGRARE
LAVTMERIREAQALFPDANLAAPVQGGIFTDLREEAGRAVRDLDFTFAPIGAVVPLMESYRYKELVQVVL
AAKRGLSPGTAVHLFGAGHPSMFALAVAMGCDLFDAAAYALFAREGRYITPHGSLKIDELAEALPCACRVC
RSMTADELRKSEDRERLLALHNLHVTLAEIARIRQAIQDGTLLWELVDERCRSHPRLLDGYRELLAHVAEL
ERDDPVSKRRFFYRGSETCRRETVLRFHEVIPRIPLGERVLVSFDGQGAPGFDTVLNFKPPFGPYVELA
ETFPVQSEVPEWDDDMVRS GCAGIRSLMEAHPE SRFTVQCGEVWTRLVLEEVPAEVLHEQV

>gi|124486027|ref|YP_001030643.1| 7-cyano-7-deazaguanine tRNA-
ribosyltransferase [Methanocorpusculum labreanum Z]

MAITFEVIHKDIAGRVGKLGKAGDKAIRTPALLPVVNPPLQIIPPSEMKKMGVEGIITNAYIFSKSEEFRG
PALEKGLHEVLDFDGLIMTDSGSFQMSVYGSVDITNEQTLFSQRDIGSDI WVPLDIPHPDTERDEVIAQ
MEITMARMKEAKELFGDDAPISGPVQGVAFEDLREYAGKTVSDMGFAYCPVGAVVPLMESYRYRELVDVI
LAAKGLNPGACVHLFGAGHPSMFALAAALGCDVFDAAAYALYAKEGRYITTYGTLKLDENSELPCACPV
CRSHTVEELKKS PDKQKLLAYHNLAVTMAEISRIIRAAIQDGTLLWELVDERCRAHPKLLDGYRLLERVEE
IEHLDRASKRRFFYRGSESCRREVTNYHAMIPRVKLSDVSLIAAGGPVPSRFEEVIEFKPPFGPLPYEL
AETFPAGPAEVPTWDEEMMKYGIKGLKGLLATNPDTKVTISTTAKWADLFRAEFPAAEVIT

>gi|15790835|ref|NP_280659.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Halobacterium sp. NRC-1]

MRDVFEVGAQDGLARIGELDVPRAGVTVETPTLMPVVNPNLITVEPSRFVDFGAELLITNSYIINSDDD
LRERALDEGLHEMLGFDGAIMTDSGSFQLAEYGEIDTDTEAILRFQHDIGSDIGTPVDIPTPPDADREQA
AAELETQQRLELAETVDVGDMLVNAPVQGATQPDRLREQAGAHAYGTALDLFPVGAVVPLMNQYRYDDMT
EAVLAAKRGLGRDAPVHLFGAGHPMMFALAAALGCDLFDAAAYAIYARDDRYLTVSGTEHLDDLHYFPCD
CPVCAEHSPQAVRGMAAGDRERLLAEHNLHVSFGEIRRVKQAIKSGTLMELVAARAHHPSTLDGYRALL
DHSDQLEASDPASKDAFFYTGAGSARRPEVHRHHQRLDRLDVDGDDVLLTEGDSNHRYDESWNVLPFGP
YPSALATTYPLTAETPARMDRAGYAAAEGVCRLAEANPDFTAFTLAHDDWPESALEAVPQRVSLYNAVRG
E

>gi|11498196|ref|NP_069422.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase [Archaeoglobus fulgidus DSM 4304]

MQRFEILDKAMDGRICRIETPHGRIETPTILPVINPNIPFIRAEEMKKFGAQAVITNSYIIYRSMREEAL
EKGVHGILETDMPVMTDSGSYQLMVYGDVEIKNAEIVEFQRHIGSDIIVPLDIPTPPDADYATAESDLRI
TLEREREAKELLKGAENLLAVPVQGSTHPDLRRFAAGEARKIGGDIYPIGAVVPLMDAYRFRDLARVILE
VRSALPVEPIHFLGCGHPMLFAMAVALGCDLFDSDAAYALYAKDDRYLTVYGTKKLSELYNFPCKCPVCSN
HDPEELRRMEKNERERLIAEHNLYVSFQEIETIKQAIKENSLELVEKRVRAHPNMLAGWRQVKHYWELL
EKADPKMKRKFLYTGIDSLYRPAVRRHVKAIKNVELPEEVLVSTDFGIYANIYLRPVFGPVAEMLETYP
AGHAEIPEEDVVEEALKAASEALMELMNSHPEKRFKVYVSKVWVKHLQNLPPNGELNVL

>gi|154150856|ref|YP_001404474.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase [Candidatus Methanoregula boonei 6A8]

MAITFESLDSDIAGRTGKLGAGKRIIKTPALLPVINPHLMLVTPKELRAMGVEALITNAYIFSQSRQYSE
RVKEEGLHKLDFDGLIMTDSGSFQLSVYGVQVSFTNKQTLQYQDIDIGSDIIVPLDIPTSPDADRPTTERE
LAITMERLREAKELFGNDAPLAGPVQGGIFPDLRERAGKEVGDGFSFCPIGAVVPLMESYRYRELVDVV
MAAKSTIPRSACVHLFGAGHPAMFALAAAMGCDLFDSDAAYALYAKDGRYLTTGHSFRIDELTDLPCACAV
CRSHTAEELCTAKDRTRLLALHNLAVTLAEISRIRQAIADGTLWELVDERCRTHPQLLSGYRRLLSHAAD
LELYDRASKRRFFYRGDESCARTEVLRVYQRQLDRLRLGKTVLVACDGKEREYDDVLFKPPFGPYPPAL
KETFPIGPAEIPWDEAMVRQGCGRGIRMLAESHKESRIMVSGLLNWEEIFTQEAGDAAELVR

>gi|119719273|ref|YP_919768.1| tRNA-guanine transglycosylases, various specificities [Thermofilum pendens Hrk 5]

MVWSEVFEIKEVDLLGRIGSISTRGNVETPTLTPVINPSKPVLEPREIQQMGNLIMTNSYIIKRQYGD
LAKEVKVHQLLGVDTPVMTDSGAYQLMVYGRVEVDPLEIVRFQVEIGSDIGVILDIPTKKGVPRGQVLAE
VEETLRRAEASLAVERDGMMLLVGPVQGGLYTDIVATAARRLGEMPFVYAVGGPTQLMEEYDFSELVKLV
MTARLNLWPWEAPLHLFGAGHPVMLPLAVAMGVDTFDSASYVLYARDRVFTSRGTLRLGEVEELPCNCPV
CSKYSARELRELPKQERVVLLARHNLVYIQKELKEIREAIEHGRWLWELLEERSMTHPSLRDALRVFARYA
EYIAKRHPVTRSPVQGLFFYSGLSRYRPEVVRHVNRLAQRYKRARDTLVVFEEETPQKPFTRAGLVKEILG
ADPMLPVDVDVAVLSGAFSVIPLELDGFYPLSQYEASGEVFREAVDEVLADLAWFVLSKGYRRVVLVYHS
LPKVFLDKLKERLSLEGVLLAYVEVENYDEALLNPSAVAGRIRSMISFLESIA

>gi|15920526|ref|NP_376195.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase [Sulfolobus tokodaii str. 7]

MVGEFEIKDEDLAGRIGIIEKSGKLETPVFFPVINPFKSEISIKDIENLGFKNLITNAYLIKKITNTKI
QDIHSFLQFNGVIMTDSGAYQILQYGNIEVTNREIVEYERDINTDIAVYLDLPTGDTNSRDEAINSVKIT
LERAKEIEDIVKNDSEIRIWHPIQGGRFDLVEYSAIEADKNEAFKMLALGSPTVVMKEYDYSLIDMVF
IAKSNVSRGKPFHLFGGGLPHIMPLVIALGVDSFDSASYILYARDNRYITRSRVYRLEELEYFPCSCPIC
LKYPKELLELPKEERTKLLALHNLVYIKEELNAIKQAIREGRLFYIIEKAYSHPAVYSFAFKKILKYKD
YLEKYDPRVKGNIRGIFLFDLKSINRPEIVRHYNFLDRINKNNDKAIIECEKRENILKKVKNNEVDIYL
FNPFGYGLIPINLIEVYPYFQTEYPEEIDEDVLRVIESKIVEFVRSKGYTKIDFIGCEKYLSHINSIGAFF

S

>gi|70606466|ref|YP_255336.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Sulfolobus acidocaldarius DSM 639]

MIGDFEIKDEDLGRIGILETKHGKLETPAFFPVINPVKNEITIQDILSVGFESIITNAFLIKKYIGKEE
DLHSILNYNKILMTDSGAYQILQYGDIDVSNVDIVNYETKLPDIAVILDIPTGLTEDKKEAEKSVESTI
SRAKEASKFVELSKDEI IWVHPIQGGMYLDLIEYSARIADMNQDYKMLALGSPTVLMQRYEYAPLIDMIY
KSKSNVSRGKPFHFLFGGGHPHIFAFVAVALGVDTFDSASYILYARDHRYMTRERVYRLEELDYPFCSCPIC
SRYSKPKDVMEMPEEQKVR LIALHNLVIKKEEINYIKQSLKEGRLFEYIQQKAYSHPSTFEAFRRILNYSK
YLEKYDPRVKGEVKGVFLFDNSSLHRPEVIRHAYTLSKIKQRSKALVLYCSDSKDNPLKNTEDMKNADVY
IVLPFYGCVPYNVFFTYPYFQSEMPSTIDKDVIIYDLKNKLKEFLSQRSYETVSIIGCEKILHVDSIRGAP
VNLLLNLK

>gi|124027358|ref|YP_001012678.1| 7-cyano-7-deazaguanine tRNA-
ribosyltransferase [Hyperthermus butylicus DSM 5456]

MKREIGVFEIREKDLGRIARLYTPHGVLETPALLPVIDPVRQEVPLVEIKRLGFNAVITNAYLLWKRLG
EQAAEKGVHGVLFEGIVMTDSGAYQLLEYGHVEVEPREIVEYEKIGSDIAVILDVPTGNTRDRKQAE
SVRETLRRAEEAQSYIDPDKRIWTLPIQGGPFIDLVRESAEKARKLKDYKLYALGSPTVLLERYEYSTLL
DMVFTARFSLPVTRPLHLFGAGHPMIIPFAVALGVMDFDSASYILYARDNRYMTLTKTYRLENLEYFPCS
CPVCSRYTPQELREMPRDERVKLLALHNLVLRQAINEVKTAIREGRLWELLEERSRAHPSLATAFAKFR
QYIEKIEQLAPRVKTGFVRGLLLYGSSELYNPRVVAYRRSIRINYKPRIRGELKLIPVSPFEKPFSTSSKL
YRSIKKGRDIHVVGMYLYLGP IPEELAETYPGSQFEVNLTPYWEVVEETARSIAEYVEANKANYTSIEI
YYCQGDGLKWSRPVAEKTTELLRKRGVKLAELGEC

>gi|161529044|ref|YP_001582870.1| tRNA-guanine transglycosylase
[Nitrosopumilus maritimus SCM1]

MKIYLF EISKTDLAGRIGTIDTNHGKIETPAYVPVIHPVKQTIPSKKIKEIGFDLVITNAYITRNNYGDK
AVKKGIIHKIIDYDRGIMTDSGGYQVLEYGDPVPAPTEMA EFEQGIMTDFAIPLDKPTGFGLPIKKA EAYV
KHTLVCKQTIEDSKDNGQIWIWPIQGGHEFDLVAKSTKGLIKMGYKMLALGSPVEFMESYEYRLLAQMI
IAAKKQIPHNIPLHLFGAGHPLTIPFAVALGCDTFDSASYMLYAKQNR YITEDGTRDLSDIVVFPCNCEI
CTKYTPDEL RQLESIEKINQIAIHNLHAIKLEVDKVKQAIHEGRLWEYVIKKARAHPKLFEMVEVMTENS
EFLKIGTPKFKERAIFLFDKEDQFRPEVQVFHEIVRGFKSKKEKILITNESSTKPGYLSHQFVNLSKLLK
DFEEVQICQYNPQLGLPIEISDIFPAAHHETSRMNFDPKEFTEFEKTWKIFFENK FSEIRYNKDDEFL
KYFVKTLPKNIKKKSFL

>gi|41614920|ref|NP_963418.1| hypothetical protein NEQ124 [Nanoarchaeum
equitans Kin4-M]

MFLYMKIKFEIKYKDAAGKVGKIKLNGKTIETPYLFPVINPQELPIKEIKKMGFNAIITNAYILFKRK
EEVMEKGIHNLFGFDGIIETDSGAYQLLQYGDIDIENEDIYFQNEIGVDIGNILDIPSYGKTYEEAKKD
LEITLERLQAIEMANFAINGPIQGDKYLDLRYKALEEVSKLDDIDIYAIGGIVPYMNQYKIESLAKIIGP
LLLDIPRDRPVHLFGLGHPLIMPLFVALGADLFDASYSLFAKEERILTPFRTRFLEDLTD SYILDYKAS
ELKGMENKTYIIAKHNLLVLRNEINFIRDLIRQNRLWDYVIIKAHAHPSIYFATKYVLENLYEKLKEHEP

ITKRVGILYQGELTELRSDLRYAIEQLKKLDKSQINDILDYAWPFGQFEIGEKKKLFQRFK
>gi|156937272|ref|YP_001435068.1| tRNA-guanine transglycosylase, various
specificities [*Ignicoccus hospitalis* KIN4/I]

MIWEPEARDDGPARAGKLVGAYEVETPALLAVVDPDPKKQLVPLDEMRRAGVQVIMTSAFIAKKKVGPTN
LKERLGWEGLLYTDSGTFQAYSRGVRVDPEESVRYQISAGSDIITPVDLFSLPTDSKEVAAKKAEVSFRR
WLRARELKEEVSAPVQGGLYPDVRAAVARRYSEAGARLLAVGGIVPLMEEYKFKELVNAVLPVLASRPPE
AAVHAFGAGHPLAFPLLAFLGVDLFDSDAMYAIAAREGRYLTFFGTFRLEELVMMREFPCDCPACSSLSR
DLLSMSEEERTKFLALHNLAAIKMVKEIRERIVYGTFFHKWAIATAHSHPRLYEAFAEALGKWRGYFERE
RNALPKSPVPEGCELCDSSEPERDPVGEPTYGTRELFNVIKRAYGKGLSSEEPLEALRPPRASFSRPRALR
ELCSVTLNSPKGRAIRKKDLKEVNCLLRPNHEVLVLWEGGEAKAVSLVSFAELSLASEEAVALLLPEP
LHGKVLGGLVGRVEAGDHGG

>gi|292656129|ref|YP_003536026.1| queuine/archaeosine tRNA-ribosyltransferase
[*Haloferax volcanii* DS2]

MRDHFELRDGDLGRIGRLSVPRAGVTVETPALLPVVNPNIIDTISPARLESEFGAEILITNSYIIKTNDH
LREEALDVGLHEMLDFDGAIMTDSGSFQLAEYGEIDTTTEEILQFQRDIGTDIATPVDIPTPPDVAREQA
EADLEITRQALADAEAAADTGEMLVNAPVQGSTYPLDREEAGRHADATDLDFVPVGAVVPMNAYRYDDMV
DAVAAAKRGLGVDAPVHLFGAGHPMMLALAVALGCDLFDSDAAYALYARDGRYLTVRGTEHLEDLDYLPCT
CPICTEYSPDDLREKGSKRQEQLLAEHNLHVTFEALRRIKQAIRDGDLMELVEERARSHPAMLDGYRALL
AHVDQLEREDPASKGAFFYASNESAHRPEVARHHARMRLTAEGHVLLTEGGVPSGDDFDATWRVPPFG
PFPRSLSETYPLTAEVPERLDRDAYEQAARGVSRLVEENPDAAFTLAHDDWPESALARVPESVELESLSA
VSERLGDEASVGGDDGDDGGSASSAE

>gi|118576825|ref|YP_876568.1| queuine/archaeosine tRNA-ribosyltransferase
[*Cenarchaeum symbiosum* A]

MTFEIFKCDLGGRIGSIQTSRGTVETPAFVPIHPVRQGI PAAKIQDMGFNLVITNAYIAMKNHGEEAVR
RGIHGIIGFDGPMVMTDSGGYQVLEYGDVDTDPAAMARFEEGIGSDIAVPLDRPTGIGLSRKRAGELVRHT
LRVSKETLENSSSGGPLWAGPIQGSEHLDLVRSSAKALTGYGFRMMALGSPVEFMESYEYGPLAGMIAAAR
ESIPDSVPLHLFGAGHPLTIPLAISLGCDFDSASYILYARQGRYITEDGTRRIKEMGYLSCSCEVCSKY
TAPELAGAKDKERIDGIALHNLHAIKSEVDRVKEAIEHGRLEWYTMKKMRAHPRLFESARILEQNGARFI
RTTPRFKSRVFLFGPEDQYRPEVISYHNMAREYTTTRKKILCITRDAQIKPAYLSPQYSTLKARFIDPGK
VQFCQYNPVLGIIIPVEISDIFPAAHYVYGGRAEPGDFAEFAITWDAFLARNKFAEIHYEKTDPFISHFIK
RAKGARRLALKSRKRKNT

ArcTGT from crenarcheota that don't have ArcS:

>gi|14601784|ref|NP_148325.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[*Aeropyrum pernix* K1]

MFEIRDVDLAGRIGRIYTOHGVVETPAFFPVIDVYRQEVSVDEVRAAGFGQVITNAYLLWKRFGWEEAAEK
GVHRILGFPVMTDSGAYQILEYGGVELSQGEVVEYQKRLGSDIAVILDIPTGDVGRREAEESVRETIR
RALEARVMIEGDERIWIYPVQGGRYFDLVEESARVGGRLGFYRMYGIGSPTVFLERYMYHVVEAVYRAK

KHLPWGRPVHLFGAGHPLIFPYAVALGVDTFDSASYILYAREGRYITEYGVYRIEDLDYLPCSCPVCSRY
TPQELREMDRVERTRLLALHNLYVISASMRRVKQAIREGRLWELLEETSARKHPSTARVMARMRYIDALE
KGSARGRGVVRGVRAYGLESLSNPRLSRFSSDAARLVEAMAEEKWGGGKAVLKPLDPKPEPGQCESMVG
EWILFYQPFLGVFPVEACGAYPSLQIDYPQEGLPAEVIIGDLASKIASTVSI LRGRGFTVRLEYCGKVEWQ
ARAVEALKTAAAGDLPTVEACG

>gi|70606466|ref|YP_255336.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Sulfolobus acidocaldarius DSM 639]

MIGDFEIKDEDLAGRIGILETKHGKLETPAFFPVINPVKNEITI QDILSVGFESIITNAFLIKKYIGKEE
DLHSILNYNKILMTDSGAYQILQYGDIDVSNVDIVNYETKLPDIAVILDIPTGLTEDKKEAEKSVESTI
SRAKEASKFVELSKDEI IWVHPIQGGMYLDLIEYSARIADMNQDYKMLALGSPTVLMQRYEYAPLIDMIY
KSKSNVSRGKPFHFLGGGHPHIFAFVAVALGVDTFDSASYILYARDHRYMTRERVYRLEELDYPFCSCPIC
SRYSKPKDVMEMPEEQVRLIALHNLYVIKKEEINYIKQSLKEGRLFEYIQQKAYSHPSTFEAFRRILNYSK
YLEKYDPRVKGEVKGVFLFDNSSLHRPEVIRHAYTSLKIKQRSKALVLYCSDSKDNPLKNTEDMKNADV
IVLPFYGCVPYNVFFTYPFYQSEMPSTIDKDVYDLKKNLKEFLSQRSYETVSIIGCEKILHVDSIRGAP
VNLLLNKL

>gi|227828119|ref|YP_002829899.1| 7-cyano-7-deazaguanine tRNA-
ribosyltransferase [Sulfolobus islandicus M.14.25]

MTVFEVKYEDLAGRIGILKTRSGNLETPVFFPVINILKDEISIDEIKNMGFKNFITNSYILYKNKYIKDD
IHKELNSEDMIIMTDSGAYQILEYGDIGITNYEIVNYQLKIKPDIGVILDLPTGNTNDYENAKITVYETL
KRIEEEASKIIVKNQDNNI IWVYPIQGGKYL DLVKTSAEGLSKFEDIYNMVALGSPTVLLERYMYDTVIDM
IYTAKSNIKRGIPFHLFGGGLPHIIPFAVALGVDSFDSASYI IYARDNRYITRTRVYKLEDLEYFPCSCP
ICSKYTPKDLLEMNEEERTRALAIHNLYTILEEFKATKQAIKEGRLFEYLQEKAYSHPAVYSAFKRLIKY
KDYLEKYDPRIRGDPKGLFLFDNSSLHRPEIIRHSRFLERYVQKKDKVAICYDKAISDTAYDYIKSIKE
RITDHNSSDIFIAIPFFGLIPLEVSDSYPLSQFEIPNEIDEDVIADMKTKIVSFLRCKNYQKVELVNCEK
LGLHIDSISTSS

>gi|126465809|ref|YP_001040918.1| 7-cyano-7-deazaguanine tRNA-
ribosyltransferase [Staphylothermus marinus F1]

MEYYDPRDYDLAGRIARLKTRHGVIETPYLFPVNVPLRQQPSIEKLYELGFNAFITNAYLFYRRNKGEIR
NIHEALGWNHVMITDSGGYQILVYGSVEIDNKTIVEYEKIGVDIGVILDIPTGTRMSWGEAREAVFETY
KRAVEALPLIMSDQLWVLP IQGSPYKDLLIYSSIKAWTLPYHIHALGSPTVLLKDYDYEKIVELTAIAR
IHLPPHKPLHVFVGHPMIIPFLVALGADLFDASASYILYARDNRYMTETGTRLEELQYLPCNCPVCSRY
SVKELLEMPRYKRIELLALHNLYMLKKELNNTKQAIKEGRLWEYLEYKSKAHPSLRKAFNILKKYLEYIK
KYNPATKGTTLALLLNDSDSLINPRLSLTKENTKEYILKKYRGKQILLPAIEKPFNQEKTYLRTKKQYK
GYEILFYHPFLGVFPQLSNTYPPFQHEVGVINENVIENLVNELKKVILEINPEKIVLVKIGMKPYDDII
DELLKDKNLVSTYTL DVLSLSA

>gi|146305018|ref|YP_001192334.1| 7-cyano-7-deazaguanine tRNA-
ribosyltransferase [Metallosphaera sedula DSM 5348]

MIGDFEVKDEDLAGRIGILETKHGKLETPVFFPVINPLKQEVFLEELKAVGFNNFITNSFILKKNNILQG
TIHEKFGDNFVIMTDSGAYQILEYGEIEQTNRDIVSFEAKIRPDIAVFLDIPTGNTDDREEAKFSVEMTL
ERGKEIADIVDQNEIDIWVHPIQGGQFLDLVEYSAREANKRTNYKMLALGSPTVFMKEYKYDTLVDMIYT
AKSSVSRGVPFHLFGGGVPHIIPFAVALGVDSFDSASYAIFARDNRYLTSERTYRLEDLEYFPCSCPVCS
RYDPSELLEMKSEERYKLLAIHNLWKIREEVNRVKQAIKEGRLFYEQKAYSHPALYSAFKSILKYSSY
LEKYDPRVKGNVKGLLLFHDHNSMNRPELLRHSEFMANLKPKNKVIICGDKLGSPPFISDPKVKSIQGRN
RDYDTFVALPFYGLVPMASEAFPLSQFEIPDIIIDDTTLNETILKIKETLRNKNYAEIKFMECEKSVLSH
IMSINPTL

>gi|307595970|ref|YP_003902287.1| tRNA-guanine transglycosylase, various
specificities [Vulcanisaeta distributa DSM 14429]

MSFEILDKDLAGRIGRLRTRSGVIETPALFPVINPVKQVVPLSDIADIGFNQVITNAYLLKRHYGDLVRE
VGVHKLNLNWDKPIMTDSGAYQLLMYGRVEVSPDEILKYEIDIGTDIGVILDIPTQWGRPKEAVVLEVEET
LRRARAALTKARIWDPEHRMLIVGPVQGGDKLDILSYSATKMSELNFDIYAIGSPTTLLEEYEFSTIMRM
IAVVKEKLPKPVHLFGAGHPLILPFVAMGIDLFDSASYVLYARDDRLILRDRTVRLSEVKVDKIPCN
CPVCRKYTVKELMSMKAERERLLAIHNLVYLWEEIQEIKARIKEGTLWEYLEEKAGGDARVKSALLALR
RGLRALLKVIPDESGRVRLHITSVESLHRPEVIRHVERLLNNYEPQGCVVMVLPGELLDRPYIRDSL
YWLIDQLSTSNLLGKVHVVINNPVLGPIPYEISEIYPLSQHEYPEPTPNHMRSLSHYLLRKYLSKLRNRG
FTDIIIVKESRGKIMNELVNLGFRGVTVLEAGSRQELYSLMPWVIKEVSGIQCGNQM

>gi|119872581|ref|YP_930588.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Pyrobaculum islandicum DSM 4184]

MSFEIVAKDIAGRIGLLYTKSGVVETPALFPVVDPRRQEVPLEVVEKYFNQVITNAYFLYRLTGKKAVDI
KKLLGWRGVVMTDSGAYQILRYGTVEVDPDEILYFQQKIGSDIGVILDLPFDYEEPYESALLKVEETIRR
AKRAAVLKDLDMLVVAPIQGALYTDLLIRSAKELSKLGFHIYAIGSPTTLLEEYKFDLILKIVLDVKLN
MMREAPLHLFGAGHPLVLPFAVALGVDLFDSASYILYARDDRIILRDRTLRLDDVKTEYLPCSTKLCYTP
VKELREMPKQERMMLIAEHNLAVLREELLEIKQRIYEGTLWEYLEIKARAHPALYRFLKNLHRYRRLLEE
YDPETHPDPHGLFFFADTASSRPEPMRHWRMSHVSALSCKKAVVIRVNEKPYNRSWEYIYLKGIIGDRAH
ILFYDPIFGIPEELAEIYPLSQNESEGEDEAARARAYEWLDRYDVIIITYNVDIPLVNKSVIKASSLEEI
ALYV

>gi|18312172|ref|NP_558839.1| 7-cyano-7-deazaguanine tRNA-ribosyltransferase
[Pyrobaculum aerophilum str. IM2]

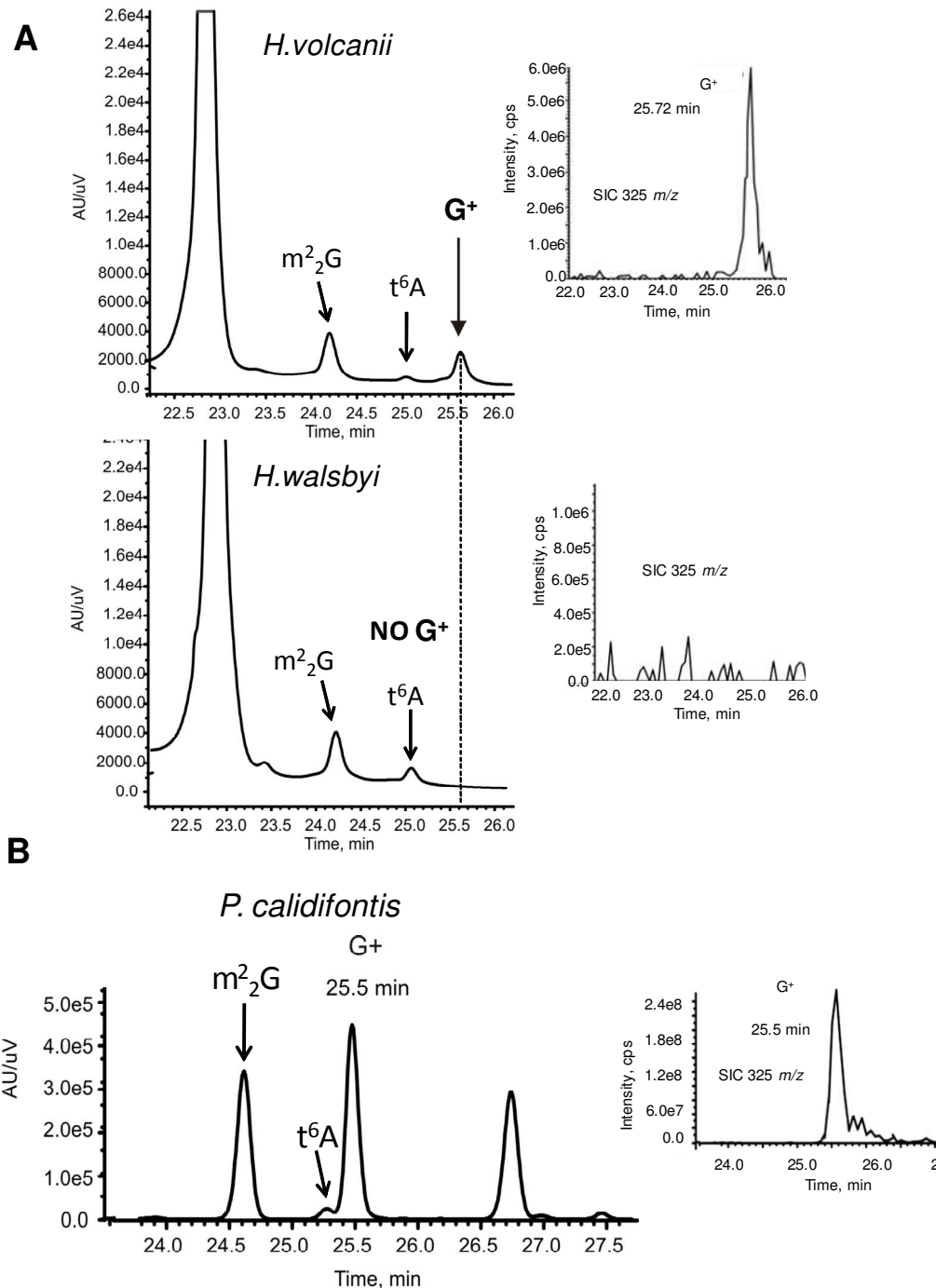
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AKRASAMLDKLEDMLVVGPIQGGLYLDLLATSAREISKLGFHIFAVGSPTTLLEEYRFDLLELVILHVKA
NILREAPLHLFGAGHPLVLPFAVALGVDLFDSASYILYARDDRIMLRDRTLRLLEDVKTDYLPSTKLCCHK
PVKELREMPHEERIQLIAEHNLAAILREELLEIKQRIHEGTLWEYLEIKARAHPTLYRFLRSLGRYKRLIE
EYDPETHPETHGLFFYQDTAESRPEPHRHSRTANLYTPSKVAIVIRAGEKPYNKSWEYRYLKSIVGDRA
HVLFYDPVFGVLPVEEVAEIYPLSQNEAEGESEAAARAFAYEWLNNDVILLYRVDLPMLSKKVIPLRSLDD
VLHYI

>gi|171184515|ref|YP_001793434.1| 7-cyano-7-deazaguanine tRNA-
ribosyltransferase [Thermoproteus neutrophilus V24Sta]
MSFEIVAKDLAGRVGLLHTKSGVVETPALFPVVDPRKQEVPLEAVQRYFGQVITNSYFIYRLTGGRAVDV
KKMLGWGGVMTDSGAYQILRYGTVEVDPDEILRFQOKIGSDIGVILDLPFDYEEPYGSALLKVEETIRR
AKRAAYLKEMDMLVVAPIQGALYADLLARSARELSRLGFHIFAIGSPTTLLEEYRFDLILRVVLEVKAN
IAREAPIHLFGAGHPLVLPFAVALGVDLFDSASYILYARDDRIILRDRTLRLDDVKTDYLPKSTKLCYTP
VKELREMPKQERTLLIAEHNLAVLREELLEIRQRIHEGTLWEYLEIKARAHPTLYRFLKSIDRRLLLEEYD
PETHDPHGLFFYSDTAPRRPEPARHRERLNNVEPLSRRRAVVIKVEEKPYNRNWQYLYLKKTLGDRAHIL
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YIQP

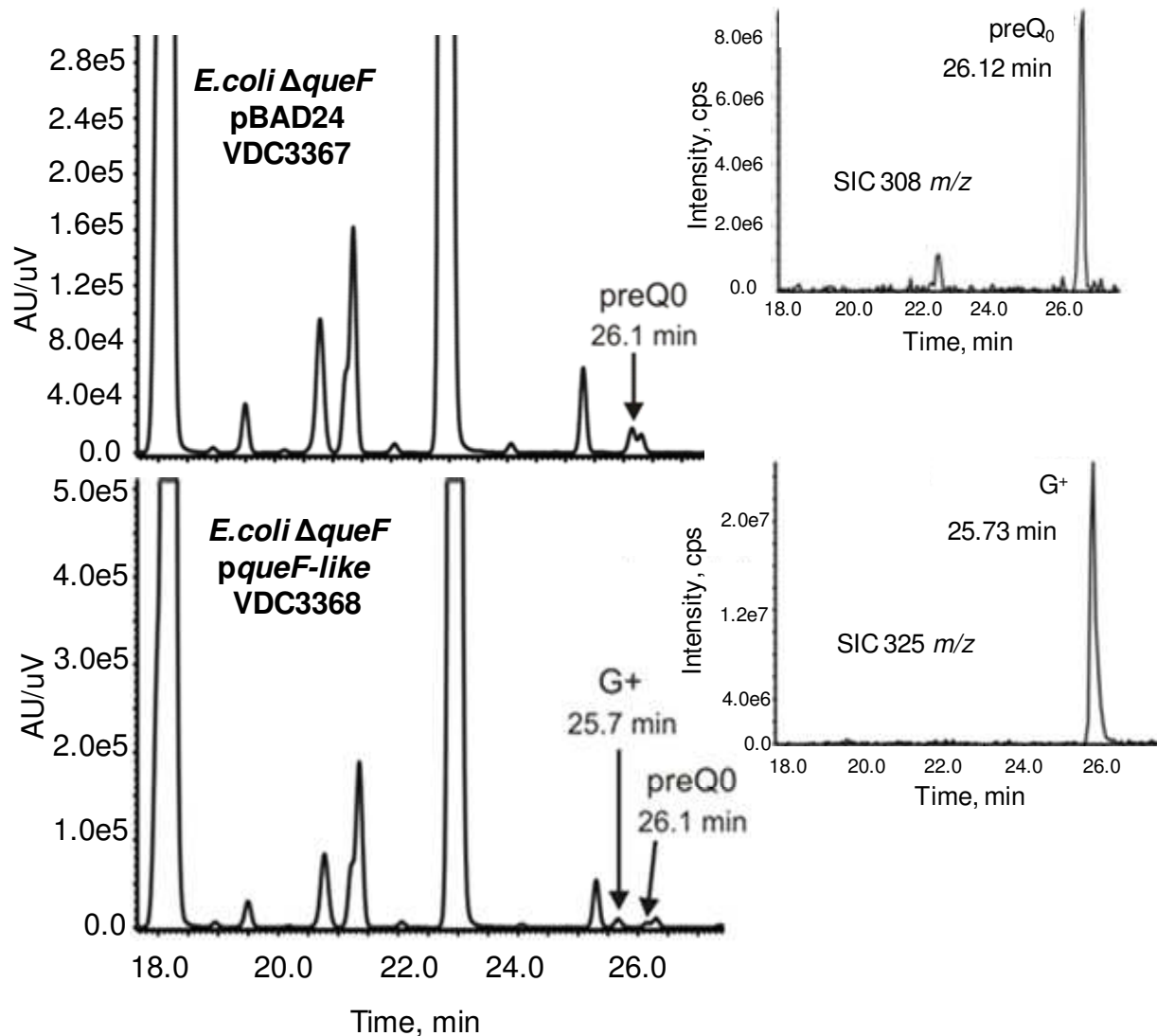
>gi|126460752|ref|YP_001057030.1| 7-cyano-7-deazaguanine tRNA-
ribosyltransferase [Pyrobaculum calidifontis JCM 11548]
MGVFEIVAKDLGGRIGRLYTKSGVVETPALFPVVDPRKQEVSEVLKRYFGQVITNSYFIYRLAKGGDVN
VKRLKWDGVMVMTDSGAYQILRYGTVDVDPDEILLYQHKGISDIGVILDLPFDYEEPYHSALLKVEETLR
RARRATRLKDLMLVVAPIQGATYLDLLRRSARELSQMGFPIYAVGSPTTLLEEYRFDTILEIVLEAKM
AMVRDAPLHLFGAGHPLILPFAVALGVDLFDSASYILYARDGRIMLRDRTLRLDDAKSEYLPCSTKLCQT
PVKELREMPREERTLLIAEHNLAVLREELMEIRQRIHEGTLWEYLEAKARAHPSLYRFLKLSKFRYYIE
ALDPETHPKPHGLFFYHDTSPSRPEPLRHFTRELVNDPPSKKALVVKASTKPYNRSWEYRYLKVGERV
HIIFYDPVFGAVPEELADEVYPLSQNEAEGESEEARARLYEWLNRYDEIYTYGVDIPLVGKAVRRLSSIED
ARYIA

>gi|159040616|ref|YP_001539868.1| tRNA-guanine transglycosylase [Caldivirga
maquilingensis IC-167]
MFEVIEKDEIARIGKLYTRHGVETPALFPVINPSKQYVDLSRIKELGFNQIITNAYIIRKTYGDAAREV
GLHEIIGWDGPLMTDSGAYQILQYGNIEVSPDEALRYQVEIGSDIGVILDIPTSYPRPRELVEVEVNETI
RRARRAILQLKELDPEHRMLIVGPTQGGVYRDLLAYSARMVSELPFDIYAIGSPTTLQAYNFTGIIKMI
LTVKSIIPPGKPVHLFGVGHPLILPLAVALGIDLFDASASYMLYANDDRIILSSRTVRLSELDKDYVLDGC
GKRAGELMEMSKEERIRLIAQHNLWTLRELMEIKQRIKEHDIWSYVAQKARQHPSVYRAYLTLSSSLF
RKLTIKLASGLKVNATQLSILDNSDLARPEVQWARRRLRLIKGMGVLTNVLIIGDYEEPFIRTQIANE
VTRLGVRVFTYNEVYGLIPIELSDVYPFSTVVRVNVKPRPIKYEIRDSVILVEDKYRDLVKFIKCSGECF
IIYVDSLKNIKAYEKYVGLALMKRVNEGSGIK

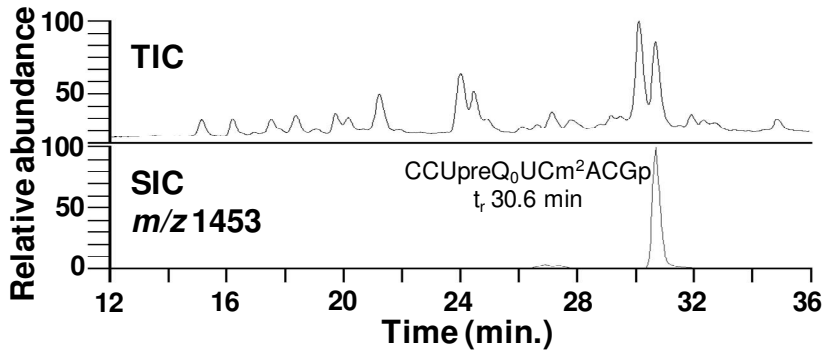
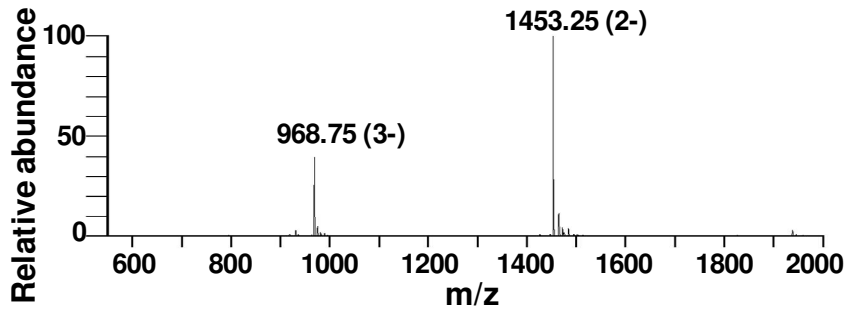
4. Supplemental Figures



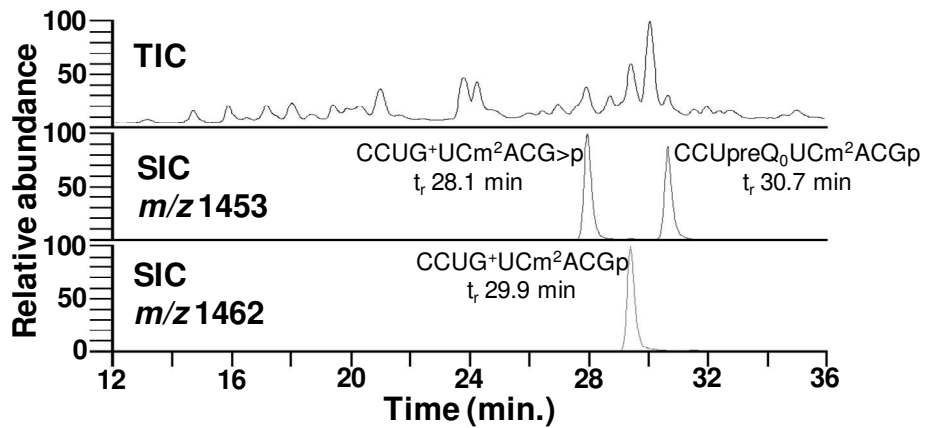
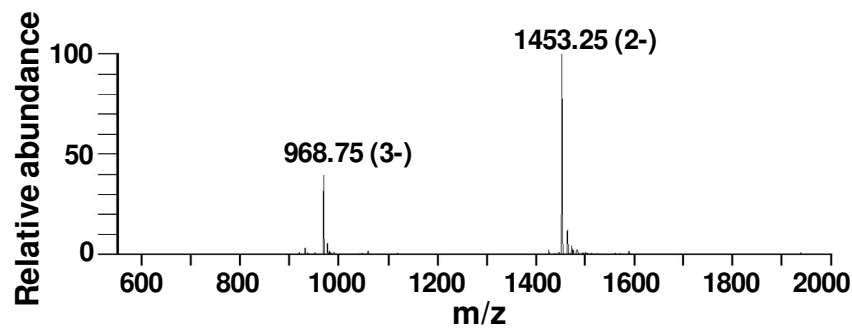
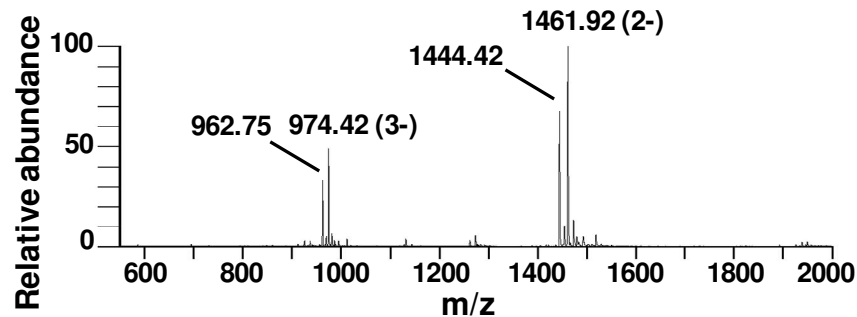
Supplemental Figure 1. LC-MS/MS analysis of bulk tRNA extracted from (A) *H. walsbyi* compared to *H. volcanii*; the G^+ peak eluted at 25.7 min in the UV chromatogram (254 nm) of the tRNA extracted from *H. volcanii* was not detected in the UV chromatogram (254 nm) of the bulk tRNA extracted from *H. walsbyi*. The extraction ion chromatograms for 325 m/z are shown in the insets. (B) *P. calidifontis*. The UV traces at 254 nm and the extraction ion chromatograms (insets) for 325 m/z are shown. The G^+ peak elutes at 25.5 minutes. As internal standards, the m^2_2G and t^6A peaks are shown.



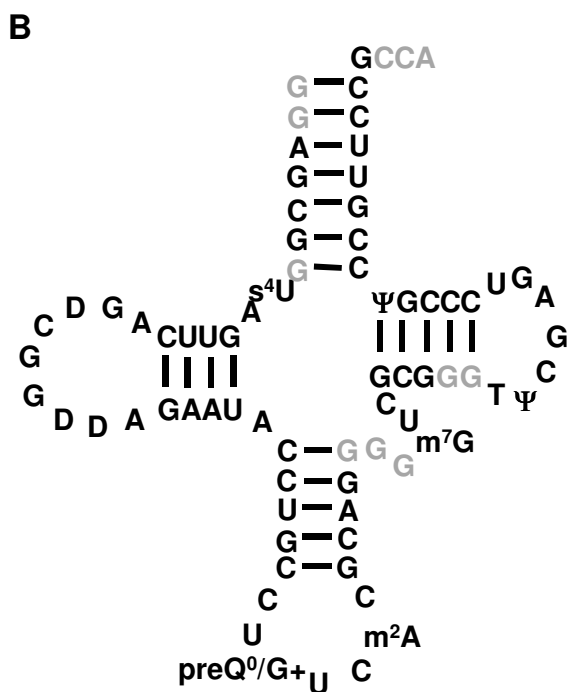
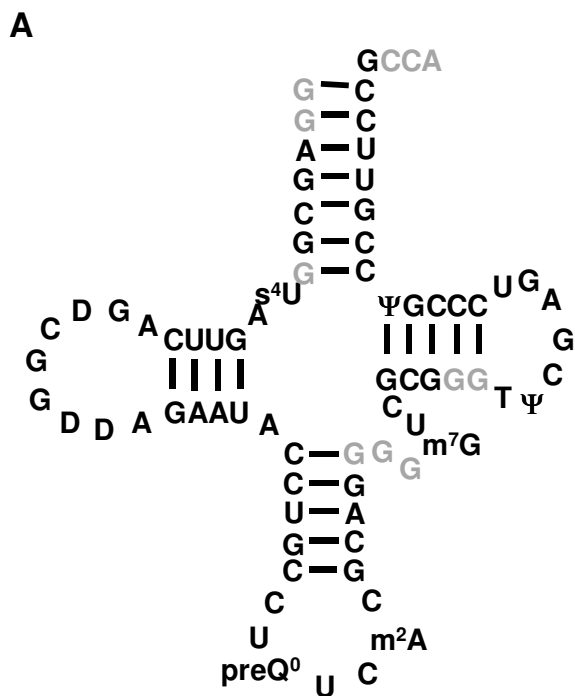
Supplemental Figure 2. LC-MS/MS analysis of bulk tRNA extracted from *E. coli* $\Delta queF$ derivative strains. The UV traces at 254 nm and the extraction ion chromatograms (insets) for 325 m/z are shown. The UV chromatogram of the bulk tRNA extracted from VDC3368 showed the G^+ peak eluted at 25.7 min and preQ₀ peak eluted at 26.1 min. The UV chromatogram of the bulk tRNA extracted from VDC3367 (the negative control) showed only the preQ₀ peak eluted at 26.1 min.

A**B**

Supplemental Figure 3. LC-MS of strain VDC3367 tRNA^{Asp} resulted in the identification of one RNase T1 digestion product not expected in wild type tRNA^{Asp}. (A) TIC of RNase T1 digested tRNA^{Asp} and the SIC for m/z 1453 (2-). (B) Mass spectrum corresponding to the m/z 1453 SIC peak eluting at 30.6 min. These two ions, m/z 1453.25 (2-) and m/z 968.75 (3-), correspond to a molecular ion mass of 2908 Da, which is consistent with an RNase T1 digestion product with the sequence CCUp_{re}Q₀UCm²ACGp. The sequence of this RNase T1 product was confirmed by collision-induced dissociation (CID) tandem mass spectrometry (Figure 3D, top).

A**B****C**

Supplemental Figure 4. LC-MS of strain VDC3368 tRNA^{Asp} resulted in the identification of three RNase T1 digestion products not found in wild type tRNA^{Asp}. (A) TIC of RNase T1 digested tRNA^{Asp} and the SICs for *m/z* 1453 (2-) and 1462 (2-). (B) Mass spectrum corresponding to the *m/z* 1453 SIC peak eluting at 30.7 min. The two ions correspond to a molecular ion mass of 2908 Da, which is consistent with an RNase T1 digestion product with the sequence CCUpreQ₀UCm²AGp, as in Supplemental Figure 3. (C) Mass spectrum corresponding to the *m/z* 1462 SIC peak eluting at 29.9 min. The two ions, *m/z* 1461.92 (2-) and *m/z* 974.4 (3-), correspond to a molecular ion mass of 2926 Da, which is consistent with an RNase T1 digestion product with the sequence CCUG⁺UCm²AGp. The sequence of this RNase T1 product was confirmed by CID tandem mass spectrometry (Figure 3D, bottom). The peak eluting at 28.1 min in the *m/z* 1453 SIC trace in (A) corresponds to the cyclic phosphate RNase T1 digestion product, CCUG⁺UCm²AG>p.



Supplemental Figure 5. tRNA sequences of tRNA^{Asp} determined by LC-MS/MS from strain (A) VDC3367 and (B) VDC3368. Identified RNase T1 digestion products, including modified nucleosides found in wild type tRNA^{Asp}, are depicted in bold type. Regions of the tRNA that could not be sequenced by LC-MS/MS, primarily single Gp residues, are in gray. In strain VDC3367 only preQ₀ was found at the wobble position whereas in VDC3368 digestion products with both preQ₀ and G⁺ at the wobble position were found.

P. horikoshii-ArcTGT

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10   20   30   40       50       60       70
beta1  beta2  beta3  beta4  alpha1  beta5  alpha2
P.horikoshii-ArcTGT KMLKFEIKARDGAGRIGKLEEVNGGKKIETTPAIMVVVNPKQMVVEPKELEKMGFEITITNSSYITYKDEELRR
A.pernix-ArcTGT . . . EIRDVDLAGRIGRIYTQHGVVETPAFPVVIDVYRQEVSDVEVRAAGFGQVIITNAYLLWKRFGWEA
C.maquilingensis-ArcTGT . . . FEVIEKDEIARIGKLYTRHGVIETTPLPFPVD.PRKQEIPLSIIKQYFGQVIITNAYLLWKRFGWEA
M.sedula-ArcTGT . . . IGDFEVKDEDLAGRIGILETKHGKEETPVFFPVINPLKQEVFLEELKAVGFNNITFSFILKNNILQG
P.aerophilum-ArcTGT . . . MSFEIIAKDLAGRVGKLYTKSGVITPTLPFPVD.PRKQEIPLSIIKQYFGQVIITNAYLLWKRFGWEA
P.arenaticum-ArcTGT . . . MAFEIIAKDLAGRVGKLYTKSGVITPTLPFPVD.PRKQEIPLSIIKQYFGQVIITNAYLLWKRFGWEA
P.calidifontis-ArcTGT DMGVFEIVAKDLAGRIGRLYTKSGVETPALFPVPD.PRKQEVPSEVLKRYFGQVIITNAYLLWKRFGWEA
P.islandicum-ArcTGT . . . MSFEIIVAKDLAGRIGLLYTKSGVETPALPFPVDP.RRQEVPLEVVEKYFFNQVITNAYFLYRLTGGKA
S.marinus-ArcTGT .MEYYDPRDYDLAGRIARLTRHGVIETPTYLFPVVNPLRQQPSIEKLYELGFNAFITNAYFLYRRNKGEI
S.acidocaldarius-ArcTGT .IGDFEIKDEDLAGRIGILETKHGKEETPAFPFPVINPKVEITIQDLSVGFESIITNAFLIKYY.IGK
S.islandicum-ArcTGT .MTVFEVKYEDLAGRIGILTRSGNIETPVPFPVINILKDEISIEIKNMGFKNFITSYFLYKNIKYIKD
T.neutrophilus-ArcTGT .MSFEIIVAKDLAGRVGLLHTKSGVIETPALFPVPDPRKQ.EVLEAVQRYFGQVIITNAYLLWKRFGWEA
V.distributa-ArcTGT .MSFEIILDKDLAGRIGRLTRSGVETPALFPVPVINPKQVVPLSDIADIGFNQVIITNAYLLWKRFGWEA
T.pendens-ArcTGT WSEVFEIKEVDLLGRIGSISTRRGNVETPTLTPVINPSKPVLEPREIQMGFNLIMTNSYILKRQYGDLA

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P. horikoshii-ArcTGT

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80   90   100   110   120   130
alpha3 beta6 alpha4 alpha5 beta7 TT
P.horikoshii-ArcTGT KALELGIHRMLDYNGITEVDSGFOLMKYGSTEVSNREIIEFQHRIIGVDITGFLDITPPPDA. . . . P
A.pernix-ArcTGT AEK.GVHRILGFPGVVMTDSGAYQLLEYGETELVSQGEVVEYQKRLGSDIAVILDITPTGD. . . . .G
C.maquilingensis-ArcTGT AAREVGLHEIIGWDGPLMTDSGAYQLLEYGETELVSPDEALRYQVEIGSDIAVILDITPTSYPR. . . . .P
M.sedula-ArcTGT TI. . . . .HEKFGDNFPVIMTDSGAYQLLEYGETELVSQTRNDIVSFEAKIRPDAVILDITPTGNTD. . . . .D
P.aerophilum-ArcTGT V. . . . .DIKKVLSWNAVLMTDSGAYQLLEYGETELVSDPDELLQFOARIGSDIGVILDITPFDYEE. . . . .P
P.arenaticum-ArcTGT V. . . . .DVKKLLGWDGIIMTDSGAYQLLEYGETELVSDPDELLVYQDKIGTDIGVILDITPFDYEE. . . . .P
P.calidifontis-ArcTGT V. . . . .NVKRLLKWDGVVMTDSGAYQLLEYGETELVSDPDELLYQHKIGSDIGVILDITPFDYEE. . . . .P
P.islandicum-ArcTGT V. . . . .DIKKLLGWRGVVMTDSGAYQLLEYGETELVSDPDELLYFOQKIGSDIGVILDITPFDYEE. . . . .P
S.marinus-ArcTGT R. . . . .NIHEALGWNHVIMTDSGAYQLLEYGETELVSDPINDKTIVEYEKKIGVDIGVILDITPBTGRM. . . . .S
S.acidocaldarius-ArcTGT E. . . . .EDLHSILNYNKILIMTDSGAYQLLEYGETELVSDPNSVDIVNYETKLKPDAVILDITPTGLTE. . . . .D
S.islandicum-ArcTGT . . . . .DIHK. . . . .DMIIMTDSGAYQLLEYGETELVSDPINYQLKIKPDIGVILDITPBTGN. . . . .D
T.neutrophilus-ArcTGT V. . . . .DVKKMLGWGGVVMTDSGAYQLLEYGETELVSDPDELLRFQKIGSDIGVILDITPFDYEE. . . . .P
V.distributa-ArcTGT R. . . . .EVGVHKLLNWDKPIMTDSGAYQLLEYGETELVSDPDELLKYEIDIGTDIGVILDITPBTQWGRPKEAVVLE
T.pendens-ArcTGT KEV.KVHQLLGVDTPVMTDSGAYQLLEYGETELVSDPDELVRFQVEIGSDIGVILDITPBTKKGV. . . . .P

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P. horikoshii-ArcTGT

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140  150  160  170  180  190
alpha6 beta8 alpha7 beta9
P.horikoshii-ArcTGT REQAVKELEITLSRAREAE. . . . .EIK. . . . .EIPMNATIOGSTYTDLRRYAARRLSSM.NF.EIHPITG
A.pernix-ArcTGT RREAEESVRETIRRALEAR. . . . .VIEBGD. . . . .ERIWVYVPQGRYFDLVESARVGGRLGFY. . . . .RMYGITG
C.maquilingensis-ArcTGT RELVEVENTIRARRAI. . . . .LQLEDPEHRMLIVGPTOGGVYRDLLAYSARMVSELPF. . . . .DIYAITG
M.sedula-ArcTGT REEAKFSVEMTLERGKEIA. . . . .DIVQNE. . . . .DIWVHIOGGQLLVEYSAREANKRTNY. . . . .KMLALG
P.aerophilum-ArcTGT YSALLKVEETIRRAKRAS. . . . .AMLDKLE. . . . .DMLVVGPIGGGLVLLDLLARSAREISKLGF. . . . .HIFAVG
P.arenaticum-ArcTGT YSALLKVEETIRRAKRAA. . . . .ATLLDKL. . . . .SMLVVGPIGGGLVLLDLLARSAREISRLGF. . . . .PILAITG
P.calidifontis-ArcTGT YHSALLKVEETLRRARRAT. . . . .RLLKDL. . . . .DMLVVAPIOGGATYLLDLRRSARELSQMGF. . . . .PIYAVG
P.islandicum-ArcTGT YSALLKVEETIRRAKRAA. . . . .AVLKDL. . . . .DMLVVAPIOGGALYTLDLLRSAKELSKLGF. . . . .HIYAITG
S.marinus-ArcTGT WGEAREAVFEYKRAVEAL. . . . .PLIMDS. . . . .DQLWVLPIOGSPKDLLIYSSIKAWTLPY. . . . .HIHALG
S.acidocaldarius-ArcTGT KKEAKESVESTISRAKEAS. . . . .KFVELSKD. . . . .EIWVHPIOGGMYLDLLIEBYSARIADMQNY. . . . .KMLALG
S.islandicum-ArcTGT YENAKITYVETLKRIEAS. . . . .KIIVKQDN. . . . .NIWVYPIGGGKVLDLVKTSABESKFP. . . . .EDINYMVAITG
T.neutrophilus-ArcTGT YSALLKVEETIRRAKRAAYLKEM. . . . .RMLVVAPIOGGALYDLDLLARSARELSRLGF. . . . .HIFAVG
V.distributa-ArcTGT VEETLRRARAALTKARIWD. . . . .PEH. . . . .RMLIVGPIGGGDKLDLSYSATKMSELNF. . . . .DIYAITG
T.pendens-ArcTGT RGQVLAEVETTLRRAEASL. . . . .AVE. . . . .RDGMLLVGPIGGGLVTLDIVATAARRLGEMPF. . . . .DVYAVG

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P. horikoshii-ArcTGT

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200  210  220  230  240  250  260
alpha8 alpha9 beta10 eta1 alpha10 beta11 alpha11 beta12
P.horikoshii-ArcTGT GVVPLLESYRFRDVVDIVISSKMALRPDRPVPHFFGAGHIVFALAVAMGVDIFDSASYALYAKDDRYMTFP
A.pernix-ArcTGT SPTVFLERYMYHVVAVYRAKKHLPWGRVPHFFGAGHLIFFPYAVALVGVDIFDSASYILYAREGRYITE
C.maquilingensis-ArcTGT SPTTLLQANFTGIKMLITVKSIIPPKPHFGVGHLLPLAVALGVDIFDSASYVMLYAMDDRILS
M.sedula-ArcTGT SPTVFMEKKYDTLVDMIYTAKSSVSRGVPHFFGCVPHIIPFAVALGVDIFDSASYAIFARDNRYLTS
P.aerophilum-ArcTGT SPTTLLEBYRFDLLLEVILHVKNILREAPLHFFGAGHLVLFPAVALGVDIFDSASYILYARDNRIMLR
P.arenaticum-ArcTGT SPTTLLEBYRFDLLLEAVLVHVKNIAREAPLHFFGAGHLLFPAVALGVDIFDSASYILYARDNRIMLR
P.calidifontis-ArcTGT SPTTLLEBYRFDTLLEIVLBAKMAVRDAPLHFFGAGHLLLFPAVALGVDIFDSASYILYARDNRIMLR
P.islandicum-ArcTGT SPTTLLEBYRKFDLLKIVLVDVKLNMREAPLHFFGAGHLVLFPAVALGVDIFDSASYILYARDNRIMLR
S.marinus-ArcTGT SPTVLLEKYDYEKIVELTAIARLNPHPKPLHVFGVGHEMIIPFLVALGADIFDSASYILYARDNRYMTE
S.acidocaldarius-ArcTGT SPTVLMQRYEYAPLDMIYKSNSVSRGKFPPHFGGGHHIFAVAVALGVDIFDSASYILYARDHRYMTE
S.islandicum-ArcTGT SPTVLLERYMYDTVIDMIYTAKSNIKRGIPKPLHVFGVGHEMIIPFLVALGADIFDSASYILYARDNRYITR
T.neutrophilus-ArcTGT SPTTLLEBYRFDLLRRVVLVEVKNIAREAPLHFFGAGHLVLFPAVALGVDIFDSASYILYARDDRILR
V.distributa-ArcTGT SPTTLLEBYREFSTLRMIAVVKELPPGKPVHFGAGHLLFPAVAMGDIFDSASYVLYARDDRLILR
T.pendens-ArcTGT GPTQLMEBYDFSELVLKLVMTARLNLPWEAPLHFFGAGHEVMLPLAVAMGVDIFDSASYVLYARDDRYFTS

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P. horikoshii-ArcTGT

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270  280  290  300  310  320
beta13 eta2 alpha12 alpha13
P.horikoshii-ArcTGT . . . GTKRLDEL. . . . .DYFPCSCPVCSKYTPQBLREMPKE. . . . .ERTRLLABHNLVWIKEEIKRVKQAIKEG
A.pernix-ArcTGT . . . GVYRIEDL. . . . .DYLPCSCPVCSRYTPQBLREMDRV. . . . .ERTRLLABHNLVIVSASMRRVKQAIKEG
C.maquilingensis-ArcTGT . . . RTVRLSEL. . . . .DKDYVLD.GCGK.RAGELMEMSKE. . . . .ERTRLLABHNLWTLSREMBEIKRQAIKEG
M.sedula-ArcTGT . . . RTVRLEDL. . . . .EYFPCSCPVCSRYTPSELLEMKSE. . . . .ERYKLLABHNLWKIREELNRVKQAIKEG
P.aerophilum-ArcTGT . . . RTLRLEDVKTDYLPCSTKL. . . . .CHKPLVKELREMPHEERIQLIABHNLAILREELLEIKRQAIKEG
P.arenaticum-ArcTGT . . . RTLRLDDVKTEHLPCSTKL. . . . .CYKTPVKELREM. . . . .TQELLLIABHNLAVLREELLEIRQRIHEG
P.calidifontis-ArcTGT . . . RTLRLDDAKSEYLPCSTKLCTPV.KELREMPRE. . . . .ERTLLIABHNLAVLREELLEBEIRQRIHEG
P.islandicum-ArcTGT DRT. . . . .LRLDDVKT. . . . .EYLPCSTKLCTPV.KELREMPKQ. . . . .ERMMLIABHNLAVLREELLEBEIKRQAIKEG
S.marinus-ArcTGT . . . GTKRLEEL. . . . .QYLPCNCPVCSRYSVKELLEMPRY. . . . .KRIELLABHNLYMLKELLNTKQAIKEG
S.acidocaldarius-ArcTGT . . . RVYRLEEL. . . . .DYFPCSCPVCSRYSPKVEMPEE. . . . .QVVRLEABHNLVIKEINYIKQSLEG
S.islandicum-ArcTGT . . . RVYKLED. . . . .EYFPCSCPVCSKYTPKDLLEMNE. . . . .ERTRLLABHNLYTILEFKATKQIKEG
T.neutrophilus-ArcTGT . . . DRTLLRLDDDVKT. . . . .DYLPCSTKLCTPV.KELREMPKQ. . . . .ERTLLIABHNLAVLREELLEBEIRQRIHEG
V.distributa-ArcTGT . . . RTVRLSEVKVDKIPCNCPVCSKYTVKELLSMNKA. . . . .ERERLLIABHNLVLVWEEIQBEIKARIHEG
T.pendens-ArcTGT . . . R. . . . .GTLRLGEV. . . . .EELPCNCPVCSKYSARELRELPKQ. . . . .ERVVLLARNLYVIQKELKEIREAIHEG

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Supplemental Figure 6. Differences in the substrate binding pocket between the canonical (euryarchaeal) arcTGT and crenarcheal arcTGT. a) Structure based multisequence alignment of the crenarcheal arcTGT and the canonical arcTGT in the catalytic domain. Of the canonical arcTGTs, only the *Pyrococcus horikoshii* sequence is shown. Secondary structure elements from *P. horikoshii* arcTGT crystal structure (PDB ID 1IQ8, (10)) are shown on top. Blue arrows indicate substrate recognition determinants in the canonical arcTGT that are conserved in crenarcheal arcTGT. Double arrows indicate substrate binding determinants that are absent in crenarcheal sequences. The recognition features for the preQ₀ cyano group are not conserved in crenarcheal arcTGT. These include Met102 (Leu in all crenarcheal arcTGT), and Val198 (Thr in crenarcheal arcTGT) located in the preQ₀ selection helix that harbors the major antideterminants against recognition of preQ₁.

5. Supplemental References

1. Sambrook, J. E., Fritsch, F., and Maniatis, T. (1989) *Molecular cloning : A laboratory manual, 2nd edn.*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor.
2. Burns, D. G., Janssen, P. H., Itoh, T., Kamekura, M., Li, Z., Jensen, G., Rodriguez-Valera, F., Bolhuis, H., and Dyall-Smith, M. L. (2007) *Haloquadratum walsbyi* gen. nov., sp. nov., the square haloarchaeon of Walsby, isolated from saltern crystallizers in Australia and Spain, *Int J Syst Evol Microbiol* 57, 387-392.
3. Dyall-Smith, M. L. (2009) The Halohandbook: Protocols for haloarchaeal genetics.
4. Allers, T., Ngo, H., Mevarech, M., and Lloyd, R. G. (2004) Development of additional selectable markers for the halophilic archaeon *Haloferax volcanii* based on the *leuB* and *trpA* genes, *Appl. Environ. Microbiol.* 70, 943-953.
5. Rinehart, J., Krett, B., Rubio, M. A. T., Alfonzo, J. D., and Söll, D. (2005) *Saccharomyces cerevisiae* imports the cytosolic pathway for Gln-tRNA synthesis into the mitochondrion, *Genes Dev.* 19, 583-592.
6. Miller, J. H. (1972) *Experiments in Molecular Genetics*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.
7. Baba, T., Ara, T., Hasegawa, M., Takai, Y., Okumura, Y., Baba, M., Datsenko, K. A., Tomita, M., Wanner, B. L., and Mori, H. (2006) Construction of *Escherichia coli* K-12 in-frame, single-gene knockout mutants: the Keio collection, *Mol. Syst. Biol.* 2, 2006.0008.
8. Datsenko, K. A., and Wanner, B. L. (2000) One-step inactivation of chromosomal genes in *Escherichia coli* K-12 using PCR products, *Proc. Natl. Acad. Sci. U. S. A.* 97, 6640-6645.
9. Guzman, L. M., Belin, D., Carson, M. J., and Beckwith, J. (1995) Tight regulation, modulation, and high-level expression by vectors containing the arabinose P_{BAD} promoter, *J. Bacteriol.* 177, 4121-4130.
10. Ishitani, R., Nureki, O., Fukai, S., Kijimoto, T., Nameki, N., Watanabe, M., Kondo, H., Sekine, M., Okada, N., Nishimura, S., and Yokoyama, S. (2002) Crystal structure of archaeosine tRNA-guanine transglycosylase, *J. Mol. Biol.* 318, 665-677.

