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Supplementary Information (16 pages) for:

Schut, G. J., Zhou, J. and Adams, M. W. W. (2001) "DNA microarray analysis of the hyperthermophilic archaeon *Pyrococcus furiosus*: evidence for a new type of sulfur-reducing enzyme" *J. Bacteriol.* (accepted for publication)

This file contains the complete list of 275 ORFs (Tables 1-8) that were used for the DNA microarray experiments described in the article. Tables 1-4 are taken from the article while the additional ORFs that were studied are given in Tables 5-8.

Table 1. ORFs whose expression is dramatically (> 5-fold) down-regulated by S⁰.

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Table 8. ORFs that did not yield PCR products.

Table 1. ORFs whose expression is dramatically (> 5-fold) down-regulated by S°.

ORF ^a	ORF Description ^b	Intensity Ratio (log ₂ ± SD) ^c	Change in expression (-fold) ^c
577932	[hydrogenase expression/formation regulatory protein, <i>hypF</i>]	5.28 ± 0.89	39.0
1337916	membrane bound hydrogenase ORF 1, <i>mbh1</i> ^d	4.14 ± 0.80	17.6
1251888	hydrogenase II gamma, <i>hydG2</i>	3.78 ± 1.47	13.7
1338167	membrane bound hydrogenase ORF 2, <i>mbh2</i> ^d	3.77 ± 1.29	13.6
1339081	membrane bound hydrogenase ORF 5, <i>mbh5</i> ^d	3.68 ± 1.30	12.8
1339520	membrane bound hydrogenase ORF 6, <i>mbh6</i> ^d	3.65 ± 0.77	12.6
1253842	hydrogenase II alpha, <i>hydL2</i>	3.57 ± 1.45	11.8
1341399	membrane bound hydrogenase ORF 8 (like <i>cooM</i> , <i>mbh8</i>) ^d	3.49 ± 0.79	11.2
1338538	membrane bound hydrogenase ORF 3, <i>mbh3</i> ^d	3.31 ± 1.66	9.9
1252601	hydrogenase II delta, <i>hydS2</i>	3.25 ± 1.43	9.5
1342770	membrane bound hydrogenase ORF 11, <i>mbh11</i> ^d	3.06 ± 1.22	8.3
866528	hydrogenase I delta, <i>hydS1</i>	2.95 ± 0.66	7.7
1345018	membrane bound hydrogenase ORF 13 (like <i>hydC</i> , <i>cooK</i> , <i>echB</i> , <i>mbh13</i>) ^d	2.77 ± 0.85	6.8
1345434	membrane bound hydrogenase ORF 14 (like <i>hycF</i> , <i>echF</i> , <i>cooX</i> , <i>mbh14</i>) ^d	2.73 ± 1.40	6.6
1344050	membrane bound hydrogenase ORF 12, catalytic NiFe subunit, <i>mbh12</i>	2.68 ± 0.59	6.4
864857	hydrogenase I beta, <i>hydB1</i>	2.66 ± 1.08	6.3
1251025	hydrogenase II beta, <i>hydB2</i>	2.65 ± 1.04	6.3
1342256	membrane bound hydrogenase ORF 10, small subunit homolog, <i>mbh10</i> ^d	2.59 ± 0.87	6.0

51760	[conserved hypothetical protein]	2.59 ± 1.14	6.0
1338785	membrane bound hydrogenase ORF 4, <i>mbh4</i> ^d	2.54 ± 2.16	5.8
615154	ornithine carbamoyltransferase, <i>argF</i>	2.43 ± 0.49	5.4

^aORF designation is the end nucleotide number (<http://comb5-156.umbi.umd.edu/>).

^bThe ORF description is derived either from annotation by homology (given within brackets) or where there is experimental data to support the ORF assignment specifically in *P. furiosus* (given without brackets).

^cThe intensity ratio is expressed as a \log_2 value so that the standard deviation can be given. For ease of comparison between ORFs, the apparent change in the expression level of a given ORF is also indicated.

^dThis work, see text for details.

Table 2. ORFs whose expression is dramatically up-regulated by S°.

ORF ^a	ORF Description ^a	Intensity Ratio (log ₂ ± SD) ^a	Change in expression (-fold) ^a
1871822	[conserved hypothetical protein, <i>sipA</i> ^b]	5.94 ± 1.43	61.4
1872873	[putative polyferredoxin, <i>sipB</i> ^b]	4.65 ± 1.90	25.1
1487371	[tryptophan synthase, subunit beta, <i>trpB-I</i>]	2.98 ± 0.69	7.9
1805557	[conserved hypothetical protein]	2.93 ± 1.29	7.6
1008251	[aspartokinase II alpha subunit]	2.92 ± 0.89	7.6
1131551	[NADH oxidase, <i>noxA-2</i>]	2.88 ± 0.39	7.4
1825269	[thermosome, single subunit]	2.83 ± 1.69	7.1
900019	[acetolacetate synthase]	2.78 ± 1.02	6.9
65527	[fibrillar-like pre-rRNA processing protein]	2.70 ± 0.80	6.5
204761	[oligopeptide transport system permease protein]	2.68 ± 0.45	6.4
102519	[glutaredoxin-like protein]	2.61 ± 1.72	6.1
1352206	[NADH dehydrogenase subunit]	2.59 ± 0.59	6.0

^aSee Table 1 for details.

^bSee text for details.

Table 3. Highly-expressed^a S^o-independent ORFs.

ORF ^b	ORF description ^b
49183	phosphoenolpyruvate synthetase, <i>ppsA</i>
143318	[conserved hypothetical protein]
232621	enolase (2-phosphoglycerate dehydratase)
236793	[hexulose-6-phosphate synthase]
358419	aldehyde ferredoxin oxidoreductase, <i>aor</i>
478142	glyceraldehyde-3-phosphate ferredoxin oxidoreductase, <i>gor</i>
683389	[methylmalonyl-CoA decarboxylase, subunit alpha, <i>mmdA</i>]
720985	[alkyl hydroperoxide reductase subunit C]
925374	pyruvate ferredoxin oxidoreductase beta, <i>porB</i>
926380	pyruvate ferredoxin oxidoreductase alpha, <i>porA</i>
927947	2-ketoisovalerate ferredoxin oxidoreductase beta, <i>vorB</i>
928888	2-ketoisovalerate ferredoxin oxidoreductase subunit alpha, <i>vorA</i>
1145403	formaldehyde ferredoxin oxidoreductase, <i>for</i>
1208774	[LSU ribosomal protein L10]
1210188	superoxide reductase, <i>sor</i>
1210814	[rubrerythrin]
1425928	[ethylene-inducible protein homolog]
1493675	glutamate dehydrogenase, <i>gdh</i>
1599202	intracellular protease, <i>pfpI</i>
1619038	[putative trehalose synthase]

^aORFs displaying average fluorescent intensities >20,000, see Fig. 1B.

^bSee Table 1 for details

Table 4. Poorly-expressed S^o-independent ORFs^a

ORF ^b	ORF description ^b
53135	[conserved hypothetical protein]
349245	[flagella-related protein D, putative]
350457	[conserved hypothetical protein]
350944	[flagellin B2 precursor]
351748	[flagellin B2 precursor]
373060	[ABC transporter, OppBC family]
379218	[beta-galactosidase precursor]
488057	[DNA mismatch repair protein, <i>MutS</i>]
562899	[molybdopterin converting factor, subunit 1, <i>moaD</i>]
575520	[NADH oxidase, <i>noxA-4</i> /nitrite reductase]
637268	[molybdopterin-guanine dinucleotide biosynthesis protein, <i>mobA</i>]
637303	[hydrogenase maturation protease, <i>hycI</i>]
722839	[conserved hypothetical protein]
738742	[conserved hypothetical protein]
743892	[putative proline depeptidase]
834030	[conserved hypothetical protein]
838710	[conserved hypothetical protein]
880926	[ferric enterobactin transport ATP-binding protein homolog]
881669	[iron (III) ABC transporter, permease protein, <i>hemU-1</i>]
882732	[iron (III) ABC transporter ATP-binding protein, <i>hemV-2</i>]
962748	[alkaline phosphatase IV precursor]
1012695	[phosphoglycerate kinase]
1138558	[transcriptional regulator (FurR family)]
1158892	[dissimilatory sulfate adenylyl transferase]
1165967	[4-aminobutyrate aminotransferase]
1197174	[putative nucleolar protein II, Noll-Nop2-sun family]
1208389	[conserved hypothetical protein]

1417217 [sugar-binding transport ATP-binding protein]
1647980 2-keto acid:ferredoxin oxidoreductase subunit alpha]
1668574 [sarcosine oxidase, alpha subunit, *SoxA*]
1669077 [putative polyferredoxin, *muhB*]
1711295 [molybdenum cofactor biosynthesis protein, *moaC*]
1873595 [nitrogen reductase, N-terminus]
1873914 [ferredoxin-family protein]

^aORFs displaying average fluorescent intensities below 2,000, see Fig. 1B.
^bSee Table 1 for details.

Table 5. ORFs whose expression is moderately (2 to 5-fold) down-regulated by S^o.

ORF ^a	ORF Description ^a	Intensity Ratio (log ₂ ± SD) ^a	Change in expression (-fold) ^a
224077	[arginosuccinate synthetase, <i>argG</i>]	-1.63 ± 1.51	3.10
521928	[probable iron (FeIII) ABC transporter]	-1.47 ± 0.47	2.78
566869	[hydrogenase expression/formation protein, <i>hypC</i>]	-1.17 ± 0.89	2.24
567973	[hydrogenase expression/formation protein, <i>hypD</i>]	-1.32 ± 0.50	2.50
636092	[hydrogenase expression/formation protein, <i>hypA</i>]	-1.37 ± 0.88	2.58
685707	carbamate kinase-like carbamoylphosphate synthetase, <i>cpkA</i>	-1.72 ± 1.00	3.29
700151	not annotated	-2.02 ± 1.29	4.05
702081	[prismane protein homolog]	-1.45 ± 1.33	2.74
714814	[conserved hypothetical protein]	-2.11 ± 0.83	4.32
739367	[probable ferritin, <i>rsgA</i>]	-1.69 ± 0.39	3.22
825121	[iron-dependent repressor]	-1.65 ± 1.24	3.13
865732	hydrogenase I, gamma, <i>hydG1</i>	-2.28 ± 3.91	4.87
867811	hydrogenase I, alpha, <i>hydL1</i>	-1.17 ± 1.06	2.25
1092336	[conserved hypothetical protein]	-1.24 ± 0.98	2.36
1148005	beta-mannosidase, <i>BmnA</i>	-1.16 ± 0.80	2.23
1341748	membrane bound hydrogenase ORF 9, <i>mbh9</i> ^d	-2.07 ± 0.72	4.20
1418206	[ABC transporter integral membrane protein]	-1.20 ± 0.97	2.30
1591790	[carbamoyl-phosphate synthase, small subunit, <i>carA</i>]	-1.49 ± 1.55	2.80
1626630	[probable sulfate transport system permease protein ABC transporter]	-1.33 ± 0.41	2.51
1689568	[archaeal histone A1, <i>hpyAI-2</i>]	-1.47 ± 1.02	2.77
1760272	ferredoxin	-2.00 ± 1.23	4.00

^asee Table 1 for details

Table 6. ORFs whose expression is moderately (2 to 5-fold) up-regulated by S°.

ORF ^a	ORF description ^a	Intensity Ratio (log ₂ ± SD) ^a	Change in expression (-fold) ^a
9230	[thiamine biosynthesis protein, <i>thiF</i>]	1.02 ± 0.58	2.02
66216	[Nop58/Nop56 related protein]	2.02 ± 0.75	4.05
80317	[alcohol dehydrogenase, short chain]	1.43 ± 1.59	2.70
81500	[alcohol dehydrogenase]	1.69 ± 1.81	3.22
83139	not annotated	1.00 ± 1.09	2.00
97550	[molybdenum cofactor biosynthesis protein, <i>moaA</i>]	2.16 ± 0.84	4.46
105386	[bacteriochlorophyll synthase, 43 kDa subunit, <i>chlP-1</i>]	2.13 ± 0.52	4.38
120590	[probable multiple sugar transport protein]	1.05 ± 0.74	2.07
126676	[probable aspartate aminotransferase]	1.27 ± 0.26	2.41
221932	[glutamate synthase (NADPH) subunit alpha]	1.31 ± 0.69	2.49
228606	DNA-directed DNA polymerase	1.35 ± 0.40	2.55
245558	[conserved hypothetical protein]	1.52 ± 1.24	2.87
334012	[similar to acylaminoacyl-peptidase]	2.08 ± 0.94	4.22
471039	[carboxypeptidase 1]	1.84 ± 0.63	3.58
517476	[reverse gyrase, <i>rgy</i>]	1.37 ± 0.67	2.58
518483	[conserved hypothetical protein]	1.36 ± 1.06	2.56
636814	[nucleotide-binding protein, Mrp/Nbp35 family]	1.51 ± 0.61	2.85
747589	[thioredoxin peroxidase]	1.18 ± 1.94	2.27
757388	[NDP-sugar dehydrogenase]	1.31 ± 0.58	2.49
863522	[leucyl-tRNA synthetase]	1.51 ± 0.56	2.85
903832	[3-isopropylmalate dehydratase large subunit, <i>leuC</i>]	2.05 ± 1.34	4.15
930439	pyruvate ferredoxin oxidoreductase, gamma,	1.29 ± 0.60	2.45

<i>porG</i>			
973527	[conserved hypothetical protein]	1.30 ± 0.56	2.46
977368	[transcriptional regulatory protein, AsnC family]	1.32 ± 1.63	2.49
1050569	[bifunctional short chain isoprenyl diphosphate synthase]	1.03 ± 0.27	2.04
1175771	[dehydrogenase subunit alpha]	1.12 ± 0.71	2.17
1187250	[aspartate transaminase]	1.52 ± 1.07	2.87
1262501	[XAA-PRO dipeptidase (proline dipeptidase)]	1.21 ± 0.72	2.31
1285543	[LSU ribosomal protein L7AE, <i>rpl7AE</i>]	1.03 ± 0.55	2.04
1325941	[dipeptide transport system permease protein, <i>dppB</i>]	1.92 ± 0.70	3.79
1334722	[hypothetical 4-aminobutyrate aminotransferase]	1.41 ± 1.29	2.65
1336194	[thioredoxin reductase, <i>trxB</i>]	1.30 ± 0.57	2.46
1350388	[NADH dehydrogenase subunit]	2.15 ± 0.90	4.43
1359534	[NADH dehydrogenase subunit]	1.72 ± 0.59	3.30
1368790	[L-asparaginase (L-asparagine amidohydrolase)]	1.11 ± 1.32	2.15
1383440	[putative oxidoreductase Fe-S subunit]	1.12 ± 1.86	2.17
1385199	[formaldehyde:ferredoxin oxidoreductase, <i>wor5</i>]	1.66 ± 0.38	3.16
1397077	[putative transaminase]	1.65 ± 0.60	3.14
1430634	[NADH oxidase, <i>noxA-3</i>]	2.00 ± 0.64	4.00
1432910	[alpha-glucan phosphorylase]	1.29 ± 0.56	2.44
1440640	[conserved hypothetical protein]	2.15 ± 0.55	4.45
1459639	[DNA directed RNA polymerase subunit B]	1.31 ± 0.44	2.48
1581651	[chorismate synthase, <i>aroC</i>]	1.14 ± 2.21	2.21
1590580	[hypothetical protein]	1.68 ± 1.00	3.20
1594946	[pyrroline-5-carboxylate reductase, <i>proC</i>]	1.69 ± 0.94	3.22

1609923	[transcriptional regulatory protein, AsnC family]	1.01 ± 1.64	2.01
1632493	[possible fumarate hydratase (fumarase) alpha subunit]	1.18 ± 0.79	2.26
1650532	[iron (III) ABC transporter, ATP-binding protein, <i>hemV-2</i>]	1.81 ± 1.15	3.50
1661667	[conserved hypothetical protein]	1.37 ± 0.41	2.59
1692502	[conserved hypothetical protein]	1.59 ± 0.32	3.01
1709262	[glutamate synthase small subunit]	1.73 ± 0.67	3.33
1729232	[glyceraldehyde-3-phosphate dehydrogenase]	1.56 ± 0.57	2.94
1736497	[small heat shock protein (class I)]	2.01 ± 1.05	4.02
1776415	[recombinase, <i>radA</i>]	1.71 ± 0.75	3.26
1802989	[iron-sulfur protein]	2.00 ± 0.72	3.99
1811080	[aldose reductase]	1.97 ± 0.69	3.92
1812948	[tungsten-containing formaldehyde ferredoxin oxidoreductase, <i>wor4</i>]	1.49 ± 0.64	2.81
1829226	[quinolinate synthetase, <i>nadA</i>]	2.03 ± 0.50	4.09
1830066	[nicotinate-nucleotide pyrophosphorylase, <i>nadC</i>]	1.68 ± 0.44	3.21
1849443	[glycine dehydrogenase (decarboxylating) subunit 2]	1.11 ± 0.69	2.16
1862794	[extragenic suppressor, <i>suhB</i>]	1.52 ± 0.63	2.87
1865094	[ATP-dependent RNA helicase, putative]	1.37 ± 1.31	2.59
1873389	[nitrogen reductase (C-terminus of 1873592)]	1.95 ± 1.65	3.85

^aSee Table 1 for details.

Table 7. Moderately-expressed S^o-independent ORFs^a

ORF ^b	ORF description ^b
24502	[recombinase called <i>RadB</i>]
55124	[conserved hypothetical protein]
78019	beta-glucosidase, <i>celB</i>
84211	[cyclic 2,3-diphosphoglycerate-synthetase]
88335	[conserved hypothetical membrane protein]
107582	[molybdopterin converting factor (subunit 2)]
132382	[spermidine synthase, <i>speE</i>]
149451	[2-keto acid:ferredoxin oxidoreductase subunit gamma]
156299	[putative 3-isopropylmalate dehydratase large subunit]
157236	[putative alcohol dehydrogenase/reductase]
175761	[<i>nifS</i> protein]
179810	[putative nucleolar protein III (Nol1-Nop2-sun family)]
183489	[protein-export membrane protein, <i>SecF</i>]
186105	[ATP synthase subunit B]
188098	[ATPase subunit I]
214120	[aconitate hydratase (aconitase)]
245544	[conserved hypothetical protein]
304310	[phosphoenolpyruvate carboxykinase (GTP)]
327695	ADP-dependent glucokinase, <i>glkA</i>
356987	[tungsten-containing AOR cofactor modifying protein]
358122	[molybdopterin converting cofactor, subunit 1 (<i>moaD</i>)]
368506	[beta-galactosidase]
387554	[molybdenum cofactor biosynthesis protein (<i>moaB</i>)]
438413	[phosphoribosylglycinamide formyltransferase 2]
459493	[beta-glucosidase]
465719	[glutamine synthetase I]
477397	[hydrolase rel. to 2-haloalkanoic acid dehalogenase]

532443 [probable glutamate aminotransferase]
 540820 [aspartate transaminase]
 549216 [conserved hypothetical protein]
 551149 indolepyruvate ferredoxin oxidoreductase alpha, *iorA*
 551790 indolepyruvate ferredoxin oxidoreductase beta, *iorB*
 561253 methionine aminopeptidase, MAP, Peptidase M
 562615 [molybdenum cofactor biosynthesis protein, *moeA-1*]
 619035 [IAA-amino acid hydrolase homolog 1 precursor]
 619484 [aspartate carbamoyltransferase, catalytic subunit, *pyrB*]
 621560 [conserved hypothetical protein]
 626147 [hydrogenase expression/formation protein, *hypE*]
 631178 [alcohol dehydrogenase]
 674979 [putative nucleolar protein IV (Nol1-Nop2-sun family)]
 699847 [conserved hypothetical protein, possible thioredoxin/glutaredoxin]
 748043 [2-keto acid:ferredoxin oxidoreductase subunit beta]
 748906 [2-keto acid:ferredoxin oxidoreductase subunit alpha]
 750669 [non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase]
 796206 [conserved hypothetical protein]
 817300 [2-keto acid:ferredoxin oxidoreductase subunit alpha]
 927581 pyruvate ferredoxin oxidoreductase, delta, *porD*
 930085 2-ketovalerate ferredoxin oxidoreductase, delta, *vorD*
 981072 [malate oxidoreductase (malic enzyme)]
 988026 [conserved hypothetical protein]
 989258 [alkyl hydroperoxide reductase]
 991757 [conserved hypothetical protein]
 998565 [adenylate kinase, *adk*]
 1019818 [putative aminotransferase]
 1020852 [SSU ribosomal protein S8E]
 1035285 [conserved hypothetical protein]
 1093579 [conserved hypothetical protein]
 1104585 [ribulose-1,5-bisphosphate carboxylase (RUBISCO)]

1131554 [acetylornithine deacetylase, *argE*]
1135494 [pyruvate kinase]
1140762 [sugar fermentation stimulation protein]
1140779 [cation efflux system protein CZCD]
1152634 [dipeptide ABC transporter, permease protein, *dppB*]
1164067 [transcriptional regulatory protein, AsnC family]
1191037 [putative nucleolar protein III (Nol1-Nop2-sun family)]
1191040 [conserved hypothetical protein]
1210573 rubredoxin
1249026 ferredoxin NADPH oxidoreductase, beta
1260646 [aminomethyl transferase]
1282720 [conserved hypothetical protein]
1296839 [sn-glycerol-1-phosphate dehydrogenase]
1330601 [endo/exonuclease, *fen-1*]
1363259 [glutaredoxin/thioredoxin-like protein]
1419794 [formate dehydrogenase alpha chain]
1441788 [transcriptional regulatory protein, AsnC family]
1492512 [ferripyochelin binding protein]
1493159 leucine response protein, *lrpA*
1548241 [imidazoleglycerol-phosphate synthase, cyclase subunit, *hisF*]
1567563 [acetylornithine aminotransferase, *argD-1*]
1584456 [tryptophane synthase, subunit beta, *trpB-2*]
1594957 [carbamoyl-phosphate synthase large chain, *carB*]
1610863 [transcriptional regulatory protein, AsnC family]
1628301 [probable sugar-binding transport ATP-binding protein]
1632002 [possible fumarate hydratase (fumarase) beta subunit]
1645457 [2-keto acid:ferredoxin oxidoreductase subunit alpha]
1657500 [molybdenum cofactor biosynthesis protein, *moeA-2*]
1658728 ADP-dependent phosphofructokinase, *pfk*
1661227 [centromere binding protein homolog/pseudouridine synthase]
1670984 [adenylate kinase (ATP-AMP transphosphorylase)]

1671649	[preproteintranslocase, <i>secY</i>]
1693216	[conserved hypothetical protein]
1716363	[conserved hypothetical protein]
1751962	[DNA repair helicase putative]
1782299	[putative sugar transport ATP-hydrolyzing]
1783837	amylopullulanase
1808382	[agmatinase, <i>speB</i>]
1813313	[4-hydroxybenzoate octaprenyltransferase, putative]
1819997	[probable multiple sugar-binding transport ATP-binding protein]
1828270	[L-aspartate oxidase (quinolinate synthetase)]
1889236	[L-asparaginase]

^aORFs displaying average fluorescent intensities between 2,000 and 20,000, see Fig. 1B.

^bSee Table 1 for details.

Table 8. ORFs that did not yield PCR products.

ORF	ORF description ^a
348225	[putative flagella-related protein G]
348707	[putative flagella-related protein]
1351020	[NADH dehydrogenase subunit]
1862027	[conserved hypothetical protein]

^aSee Table 1 for details.