

Supplemental Table 3. Proteins conserved in three *Pyrococcus* spp. but not in *T. kodakaraensis* in comparison among the order Thermococcales

DNA metabolism			
PAB0067	PF0085	PH0109	DNA replication helicase, Dna2 homolog
PAB1312	PF1902	PH0450	ERCC3/XPB TFIIH basal transcription factor complex helicase, XPB subunit homolog
PAB0058	PF0042	PH0093	Putative deoxyribonuclease TatD, related
PAB0588	PF0567	PH0905	Predicted DNA methylase
PAB0704	PF1298	PH1212	Thermonuclease precursor
Translation			
PAB0825	PF0668	PH0854	Translation initiation inhibitor
PAB0591	PF0564	PH0900	Putative DEAH ATP-dependent helicase
Protein fate			
PAB2178	PF0747	PH1902	Xaa-pro dipeptidase
PAB2375	PF0369	PH0519	Aminopeptidase from family M42
PAB0742	PF1049	PH1113	Pyruvate formate-lyase activating enzyme homolog
PAB2001	PF1481	PH1621	Hypothetical protein [COG1765: Predicted redox protein, regulator of disulfide bond formation]
Regulatory functions			
PAB1641	PF1338	PH1161	Hypothetical protein, containing TENA/THI-4 domain [COG0819: Putative transcription activator]
PAB1642	PF1337	PH1160	Transcription activator, putative
PAB1089	PF0284	PH0306	Hypothetical protein [COG2150: Predicted regulator of amino acid metabolism, contains ACT domain]
PAB1657	PF0846	PH1139	Exoenzymes regulatory protein AepA precursor
Cell envelope			
PAB0056	PF0044	PH0090	Glycosyl transferase, family 39
PAB1210	PF1916	PH1879	Probable glycosyltransferase
PAB1586	PF0411	PH1271	Oligosaccharyl transferase, STT3 subunit
PAB1622	PF1747	PH1107	Hypothetical protein [COG2152: Predicted glycosylase]
PAB1900	PF1459	PH1462	Conserved hypothetical protein (C-terminal part) [COG2407: L-fucose isomerase and related proteins]
PAB1971	PF1594	PH1585	Glycosyltransferase
PAB0336	PF1761	PH1674	Hypothetical protein, containing putative cell wall-binding domain
PAB0337	PF1762	PH1673	Hypothetical protein, containing putative cell wall-binding domain
PAB1102	PF0261	PH0286	Hypothetical protein [COG1361: S-layer domain]
Central intermediary metabolism			
PAB0689	PF1746	PH1222	Hypothetical protein [COG3408: Glycogen debranching enzyme]
Amino acid metabolism			
PAB1674	PF1052	PH1086	LysC-like aspartate kinase related
PAB1677	PF1055	PH0857	Threonine synthase
PAB2303	PF0010	PH0054	Putative 1-aminocyclopropane-1-carboxylate deaminase
Cofactor and prosthetic group metabolism			
PAB1645	PF1334	PH1156	Thiamine phosphate pyrophosphorylase
PAB2432	PF1335	PH1157	Hydroxyethylthiazole kinase
Energy metabolism			
PAB0943	PF1066	PH0626	Aminotransferase, class-V
PAB2386	PF0513	PH0782	Pyridoxal phosphate-dependent aminotransferase
PAB2342	PF1975	PH0016	Archaeal phosphoenolpyruvate carboxylase
PAB0712	PF0849	PH1166	Hypothetical protein [COG1625: Fe-S oxidoreductase, related to NifB/MoaA family]
PAB0798	PF1203	PH1274	Formaldehyde:ferredoxin oxidoreductase
PAB1021	PF0024	PH0495	Putative hydroxypyruvate reductase
PAB1138	PF1917	PH1881	NADH dependent dyhydrogenase related protein
PAB1139	PF1919	PH1882	Oxidoreductase, substrate unknown
Transport and binding proteins			
PAB0804	PF1150	PH0943	Multisubunit Na ⁺ /H ⁺ antiporter MnhB subunit, putative
PAB1527	PF0514	PH0781	Probable Na ⁺ /alanine transport protein
PAB1643	PF1336	PH1159	CodB-like purine-cytosine permease related
PAB2230	PF0118	PH0205	Sugar transport binding protein dependent membrane protein (MALFG subfamily)
PAB2231	PF0117	PH0204	Sugar transport binding protein dependent protein (inner membrane) (MALFG subfamily)
PAB2232	PF0116	PH0203	Sugar transport, ABC transporter ATP-binding protein
PAB2334	PF1968	PH0024	MalF-like probable sugar ABC transporter, permease protein
PAB2335	PF1969	PH0023	Sugar permease
PAB2336	PF1970	PH0022	ATP hydrolyzing subunit of the trehalose/maltose transport system
PAB1871	PF1408	PH1409	ABC-type periplasmic dipeptide transport protein
PAB1872	PF1409	PH1410	Dipeptide ABC transporter, permease protein
PAB1873	PF1410	PH1411	Dipeptide ABC transporter, permease protein
PAB1874	PF1411	PH1412	Dipeptide ABC transporter, ATP-binding protein
PAB1875	PF1412	PH1413	Dipeptide ABC transporter, ATP-binding protein
PAB0285	PF1671	PH1729	Predicted permease
PAB2147	PF1654	PH1736	ABC-type transport system, ATPase component, substrate unknown
PAB2333	PF1967	PH0025	Bacterial type extracellular binding protein, substrate unknown
PAB2439	PF0119	PH0206	Extracellular solute binding protein, substrate unknown
General function prediction only			
PAB0589	PF0566	PH0902	Hypothetical protein [COG1483:Predicted ATPase (AAA+ superfamily)]
PAB1276	PF0418	PH0329	MoxR-like methanol dehydrogenase regulatory protein
PAB1355	PF0585	PH0922	Hypothetical protein, contains ATP/GTP-binding site [COG1373: Predicted ATPase (AAA+ superfamily)]

PAB1598	PF0634	PH0830m	Hypothetical protein, containing DUF238 and DUF234 domains [COG1672: Predicted ATPase (AAA+ superfamily)]
PAB2304	PF1097	PH1067	Hypothetical protein, containing ATP/GTP-binding site motif A [COG1672: Predicted ATPase (AAA+ superfamily)]
PAB1741	PF1206	PH0708	Predicted nucleic acid-binding protein, contains PIN domain
PAB0023	PF0038	PH0096	Metallo-beta-lactamase superfamily protein
PAB0817	PF0590	PH0926	Hypothetical protein [COG3769: Predicted hydrolase (HAD superfamily)]
PAB0317	PF1728	PH1697	Nucleotidyltransferase
PAB1869	PF1406	PH1406	Pyridoxal phosphate dependent enzyme

Unknown function

PAB0054	PF0046	PH0088	Predicted archaeal membrane protein, DUF70 family
PAB0302	PF1695	PH1714	Membrane lipoprotein
PAB1274	PF0420	PH0326	Hypothetical protein, containing transglutaminase-like core domain
PAB1440	PF0428	PH0574	AlaRS-like alanyl-tRNA synthetase related protein (fragment)

Hypothetical proteins, conserved

55 proteins	Hypothetical protein, conserved
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Frame shift, truncation, or fusion with unknown region in *T. kodakaraensis* counterpart

5 proteins
