SUPPLEMENTARY INFORMATION

Plasmids and strain construction

Plasmids for the production of N-terminally tagged intein fusion derivatives of LeuRS, ProRS and EF1A (TK1461, TK0550 and TK 0308, respectively) were constructed by inserting the corresponding PCR amplified genes into pTYB11 between *Sap*I and *Xho*I. For the intein tagged LeuRS, ProRS and EF1A constructs the forward primer used were 5 'GTTGTTGTACAGAAC ATGGCTGAGCTTAACTTTAAG 3', 5' GTTGTTGTACAGAACATGGCGGTTGAGAGA AAGAA 3' and 5' GTTGTTGTACAGAACATGGCTAAGGAGAAG 3' and the reverse primers were 5 'CTGCAGTCACCCGGGTCACTCCACAAACACCGCGGG 3', 5' CTGCAGTCACCCGGGTCAGTCAGTCAGC 3' and 5' CTGCAGTCACCCGGGTCAGTCAGTCGGCCTTCTG 3', respectively. A clone containing an N-terminally His₆ tagged TyrRS (TK0568) was construced by amplifying the gene from the *T. kodakarensis* DNA and ligating the purified amplicon into the *Bam*HI and *Hind*III digested pQE31 plasmid. The primers used were 5' CATACGGATCCG 3' flanked by *BamH*I and *Hind*III sites.

The plasmid to express the gene encoding the LeuRS-derived bait for interactome analysis was constructed as follows. The gene encoding LeuRS (*leuS*) was PCR amplified from *T. kodakarensis* DNA and the coding sequence was extended in frame by ligation of an oligonucleotide sequence that added the constitutive promoter from the *M. thermoautotrophicum* archaeal histone-encoding (hmtB) gene, a mutant RBS (AAGTGG), and also encoded a hemagglutinin (HA) epitope and six histidine residues (His₆) at the N terminus of LeuRS (Supplementary Fig. 1). This gene was then ligated into plasmid pLC70 between *Sal*I and *Not*I sites. Plasmid MR3 was similar to MR4 except that the RBS site was WT(AGGTGG). The mutant RBS was used to limit synthesis and thus mimic native expression of LeuRS in the cell (Supplementary Fig. 2).



Supplementary Figure 1. Map of plasmid pHis₆-HA-LeuRS (pMR4).



Supplementary Figure 2. Production of LeuRS in *T. kodakarensis* assessed by the aminoacylation activity of LeuRS . Aminoacylation activities of cell free extracts of *T. kodakarensis* strain KW128 transformed with pLC70 plasmid (a parent vector lacking a LeuRS coding sequence, open circle), pMR3 (open square) and pMR4 (open triangle) were measured with 5 μ M tRNA^{Leu} after dialyzing the extracts against 25 Mm Tris-HCl pH7.5, 100 mM KCl and 10 mM beta-mercaptoethanol.

Supplementary Table 1

Function	ORF	Description	Mascot
			Score
Translation	TK0568	tyrosyl-tRNA synthetase	953
	TK0978	glycyl-tRNA synthetase	435
	TK0550	prolyl-tRNA synthetase	291
	TK1461	leucyl-tRNA synthetase	117
	TK0444	cysteinyl-tRNA synthetase	110
	TK1049	methionyl-tRNA synthetase	102
	TK0308	elongation factor 1-alpha	13099
	TK0556	translation initiation factor IF-2B subunit beta	618
	TK1305	translation initiation factor IF-2	120
	TK0309	elongation factor EF-2	214
	TK0506	translation-associated GTPase	151
	TK1254	30S ribosomal protein S3Ae	369
	TK1529	30S ribosomal protein S4e	364
	TK1538	30S ribosomal protein S19P	336
	TK1276	30S ribosomal protein S19e	326
	TK1504	30S ribosomal protein S11P	319
	TK1505	30S ribosomal protein S4	299
	TK1496	30S ribosomal protein S2	294
	TK0307	30S ribosomal protein S10P	248
	TK1521	30S ribosomal protein S5P	212
	TK1526	30S ribosomal protein S8P	180
	TK1099	30S ribosomal protein S27e	178
	TK1500	30S ribosomal protein S9P	171
	TK1078	30S ribosomal protein S12P	161
	TK1251	30S ribosomal protein S15P	143
	TK1532	30S ribosomal protein S17P	131
	TK1951	30S ribosomal protein S6e	106
	TK1239	pentide chain release factor 1	331
	TK1671	tRNA-modifying enzyme	172
	TK0981	N2 N2-dimethylguanosine tRNA methyltransferase	170
	TK0970	N(2) N(2)-dimethylguanosine tRNA methyltransferase	145
	TK0704	SAM-dependent methyltransferase	144
	TK1114	ribonuclease Z	122
Proteasome	TK2252	proteasome-activating nucleotidase	474
1100000000000	TK1637	proteasome subunit alpha	174
Protein binding and	TK2303	chaperonin beta subunit	460
modification	TK1473	amino acid kinase	203
	TK1085	protein disulfide oxidoreductase	139
	TK1022	D-aminopeptidase	540
Metabolic enzymes	TK0914	3-hydroxy-3-methylglutaryl-CoA reductase (meyanolate	7866
	1120711	Pathway)	,
	TK1470	isopentenyl pyrophosphate isomerase (mevanolate Pathway)	500
	TK0180	acetyl-CoA acetyltransferase (mevanolate Pathway)	110
	TK0828	NAD(P)H:rubredoxin oxidoreductase (Fatty acid metabolism)	120
	TK0187	glutamine amidotransferase, class I	437
	TK1404	phosphomannomutase-related protein	321
	TK0217	pyridoxine biosynthesis protein	1183

Complete list of proteins that co-purified with His₆-HA tagged LeuRS

TK0890	thiamine monophosphate kinase	179
TK1990	cysteine desulfurase	521
TK1796	glutamine synthetase	120
TK0193	GMP synthase subunit B	184
TK0504	aspartate racemase	166
TK0297	L-aspartate oxidase	322
TK1548	serineglyoxylate aminotransferase, class V (transferase-	258
	transaminase)	
TK1379	glycine dehydrogenase subunit 2	255
TK0149	Pyruvoyl-dependent arginine decarboxylase	154
TK2257	deoxycytidylate deaminase	163
TK0305	uridylate kinase	164
TK1517	adenylate kinase	109
TK1514	cytidylate kinase	305
TK2196	aspartate carbamoyltransferase catalytic subunit	158
TK1895	5'-methylthioadenosine phosphorylase II	280
TK1482	5'-methylthioadenosine phosphorylase	158
TK1193	CTP synthetase	105
TK2042	ATPase	260
TK1326	NAD(P)H-flavin oxidoreductase	471
TK1299	NADH oxidase	432
TK1056	rubrervthrin-related protein	317
TK0814	Type A Flavoprotein	911
TK2290	ribulose bisophosphate carboxylase	1767
TK1426	ribose-5-phosphate isomerase A	107
TK2164	fructose-1.6-bisphosphatase	140
TK0866	cofactor-independent phosphoglycerate mutase	909
TK2106	phosphopyruvate hydratase	650
TK1396	glycerol kinase	257
TK1125	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	407
TK1123	2-oxoglutarate ferredoxin oxidoreductase subunit gamma	352
TK1009	putative 5-methylcytosine restriction system. GTPase subunit	947
TK1325	Putative oxidoreductase	538
TK1326	ferredoxinNADP(+) reductase subunit alpha	471
TK0793	GTP cyclohydrolase	398
TK0795	nyruvate formate lyase family activating protein	298
TK 1093	pyruvate ferredovin ovidoreductase subunit beta	290
TK 1204	PBP family phospholinid-hinding protein	202
TK 2077	4Fe-4S cluster-binding protein	254
TK1611	metal_dependent hydrolase	253
TK 1007	hydrogenase maturation protein HypE	235
TK177/	lineate-protein ligase A C terminal section	233
TK1234	hifunctional carboxynentidase/aminoacylase	234
TK0494	auinolinate synthetase	206
TK0290	his(5'-adenosyl)-trinhosphatase	205
TK15/0	nredicetd ATPase	203
TK1/91	NADH:polyculfide ovidoreductase	207
TK 1962	N6_adenine_specific DNA methylasa	194
TK 1457	no-auchine-specific DIVA incluyiase	103
TK 2016	iron-molyhdenum cofactor hinding protein	193
TK2010	molybdenum cofactor biosynthesis protein	192
TK2223	acetylnolyamine aminohydrolace	102
TK11/0	methylmalonyl_CoA mutase N terminus of large subunit	172
111147	memymatonyi-Cor mutase, in-terminus of large subuille	1/2

	TK1605	metallo-beta-lactamase superfamily hydrolase	134
	TK1716	cytidylyltransferase	128
	TK0354	putative molybdenum cofactor biosynthesis protein C	127
	TK0828	NAD(P)H:rubredoxin oxidoreductase	120
	TK1711	sugar-phosphate nucleotydyltransferase	108
Cell Division	TK2271	cell division protein FtsZ	821
Transcription	TK1331	Lrp/AsnC family transcriptional regulator	378
	TK1881	ArsR family transcriptional regulator	113
	TK1083	DNA-directed RNA polymerase subunit beta	373
	TK1503	DNA-directed RNA polymerase subunit D	302
	TK1769	transcriptional regulator	364
DNA repair	TK2213	Binolar DNA helicase	448
Difficient	TK1899	DNA repair and recombination protein RadA	323
	TK0155	RecI-like exonuclease	476
	TK1165	AP endonuclease (base excision repair pathway)	365
Ribosome	TK0566	DEAD/DEAH box RNA belicase	175
Riogenesis	TK0679	serine/threenine protein kinase	111
Diogenesis	TK1636	putative RNA associated protain	167
Quorum sensing	TK1605	metallo bata lagtamasa superfamily hydrolasa	107
Miscellaneous	TK1003	N agetulghitghigge deagetulase	134
winscentarieous	TK1/04	flagellin	124
	TK1036	Indgelilli	110
	TK1057	DNA methylase	116
	TK0008	DNA incluyedse	200
	TK0790	DNA topoisomerase VI subunit P	209
	TK0/99	binder DNA heliesee	192
I I an ath ati a al	TK1402	bipolar DNA helicase	448
Drotoina	TK1492		921
Proteins	TK2200		813
	1K0433		08/
	TK06/5		620 502
	TK1430		392
	1K2148 TK0022		4/4
	TK0033		349
	TK0205		324
	TK1196		268
	1K1424		261
	TK0027		259
	1K0013		240
	TK1497		205
	1K01/5		200
	TK0897		193
	1K1996		198
	TK0593		176
	1K0361		152
	TK0109		147
	TK0515		140
	TK1626		140
	TK0335		140
	TK0733		135
	TK0318		135
	TK0206		124
	TK0438		123
	TK0790		111

TK2038	111
TK2294	107
TK1882	105