

Archaea/eukaryote-specific ribosomal proteins - guardians of a complex structure

Ivan Kisly and Tiina Tamm

SUPPLEMENTARY MATERIAL

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Supplementary Table S1. Characteristics of archaea/eukaryote-specific r-proteins.

Protein ³	<i>Euryarchaeota</i>		Lower eukaryotes		Higher eukaryotes	
	<i>P. furiosus</i> ¹		<i>S. cerevisiae</i> ²		<i>H. sapiens</i> ¹	
	Length (aa)	pI	Length (aa)	pI	Length (aa)	pI
eS1	198	9.97	255	10.75	264	9.75
eS4	243	9.89	261	10.73	263	10.16
eS6	125	9.88	236	11.14	249	10.85
eS8	127	11.52	200	11.33	208	10.32
eS17	67	10.49	136	11.15	135	9.85
eS19	150	9.72	144	10.12	145	10.31
eS24	99	7.84	135	11.20	133	10.79
eS25	-	-	108	11.02	125	10.12
eS27	63	9.38	82	9.51	84	9.57
eS28	71	9.95	67	11.42	69	10.70
eS30	-	-	63	12.22	57	12.15
eS31	50	9.55	76	10.13	80	9.86
eL8	123	5.35	256	10.72	266	10.61
eL13	-	-	199	11.76	211	11.65
eL14	83	10.35	138	11.62	215	10.94
eL15	194	11.02	204	11.91	204	11.62
eL18	120	10.35	186	12.23	188	11.73
eL19	150	10.93	189	11.91	196	11.48
eL20	77	9.73	172	10.92	176	10.72
eL21	97	11.42	160	11.00	160	10.49
eL24	66	9.97	155	11.90	157	11.26
eL30	99	7.89	105	10.35	115	9.65
eL31	95	10.10	113	10.66	125	10.54
eL32	130	11.19	130	11.79	135	11.32
eL33	87	10.62	107	11.63	110	11.07
eL34	89	11.69	121	11.51	117	11.48
eL37	62	11.50	88	12.17	97	11.74
eL38	-	-	78	11.63	70	10.10
eL39	51	12.38	51	13.06	51	12.55
eL40	51	10.56	52	10.32	52	10.32
eL41	37	12.66	25	13.46	25	12.96
eL42	94	10.89	106	11.32	106	10.59
eL43	83	11.27	92	11.05	92	10.44
P1	107	4.29	106	3.53	114	4.21
P2	-	-	106	3.68	115	4.38

¹ Data source: UniProt [1]

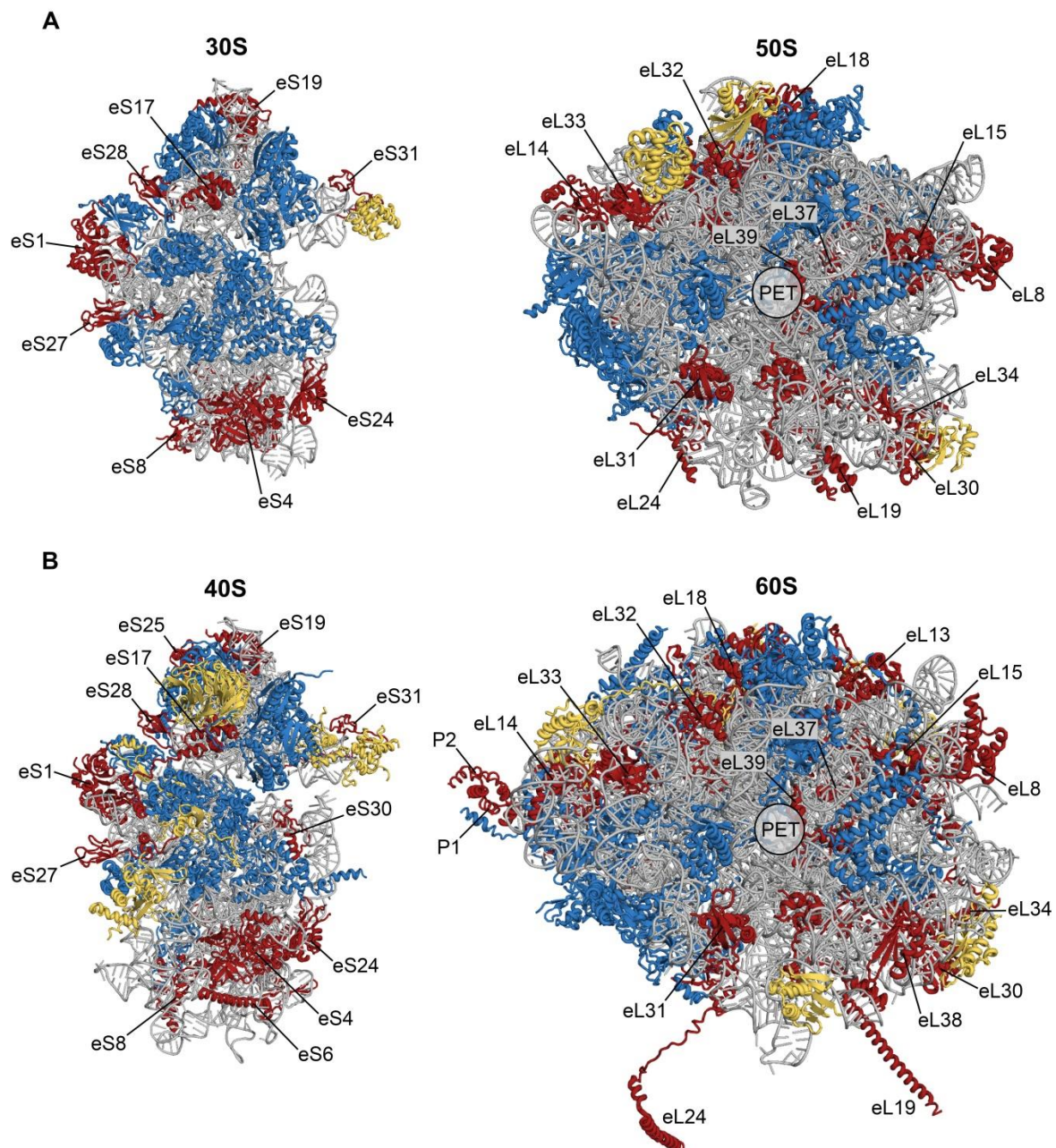
² Data source: Saccharomyces Genome Database [2]. Where the r-protein is encoded by paralogous genes, the data are given for the r-protein encoded by paralog A.

³ Protein names are according to the nomenclature from [3]

Supplementary Table S2. Positional homology of bacteria-specific and archaea/eukaryote-specific r-proteins. To analyse positional homology, PDB coordinates 6BU8 for *E. coli* [4], 4V6U for *P. furiosus* [5], and 4V88 for *S. cerevisiae* [6] were rendered in PyMol. R-proteins that interact with rRNA are included. Conserved interactions are indicated in bold.

Bacteria		<i>Euryarchaeota</i>		Lower eukaryotes	
<i>E. coli</i>		<i>P. furiosus</i>		<i>S. cerevisiae</i>	
Protein ¹	rRNA	Protein ¹	rRNA	Protein ¹	rRNA
bS6	h22, h23	eS1	h22, h23 , h26	eS1	h22, h23 , h23a, h26, ES7, h45
bS16	h4, h6a, h7, h15 , h17, h21	eS4	h7 , h9, h12, h15 , h21	eS4	h7 , h9, h12, h13, h15 , h21
bS18	h23, h26	eS1	h22, h23, h26	eS1	h22, h23 , h23a, h26 , ES7, h45
bS20	h6, h8, h9, h11 , h13 , h14, h44	eS8	h6a, h7, h9, h11 , h13, h44	eS8	h6a, h7, h9 , ES3a, ES3b, h11, h13, h44
bL17	H47 , H57, H61 , H96 , H100, H101	eL31	H47 , H48, H61 , H96 , H100, H101	eL31	H47 , H48, H61 , H96 , H101
bL19	H64, H96 , H101	eL24	H64, H96 , H101	eL24	H63a, H96 , ES41
bL20	H2, H4, H25 , H25a, H41 , H46	eL33	H25 , H40, H41	eL33	H25 , ES7b, H40, H41 , ES39
bL27	H38, H81 , H82, H86 ; 5S rRNA H1	eL21	H38, H80, H81 , H85, H86 , H87; 5S rRNA H1	eL21	H38a, ES12, H80, H81 , H83, H86 , H87; 5S rRNA H1
bL28	H11, H21, H52 , H75, H79	eL15	H10, H11 , H14, H15, H21 , H32, H52 , H66, H75 , H79	eL15	ES4, H11 , H13, H14, H15, H21 , H22, H28, ES8, H35a, H52 , H66, H75, H79 ; 5.8S rRNA H10
bL33	H83, H86, H88	eL42	H11, H21, H68, H75, H82, H83 , H86, H88	eL42	H11, H21, ES9, H74, H82, H83, H86, H88
bL34	H11, H23, H33 , H35 , H52	eL37	H4, H5, H6, H8, H11, H23, H33 , H35 , H35a, H49a, H52, H65	eL37	H11, H23 , H32, H33 , H35 , H35a, H65; 5.8S rRNA: H4, H5, H6, H7
bL36	H42, H89, H91 , H97	eL40	H42 , H44, H89 , H91, H97	eL40	H42, H89, H91, H97

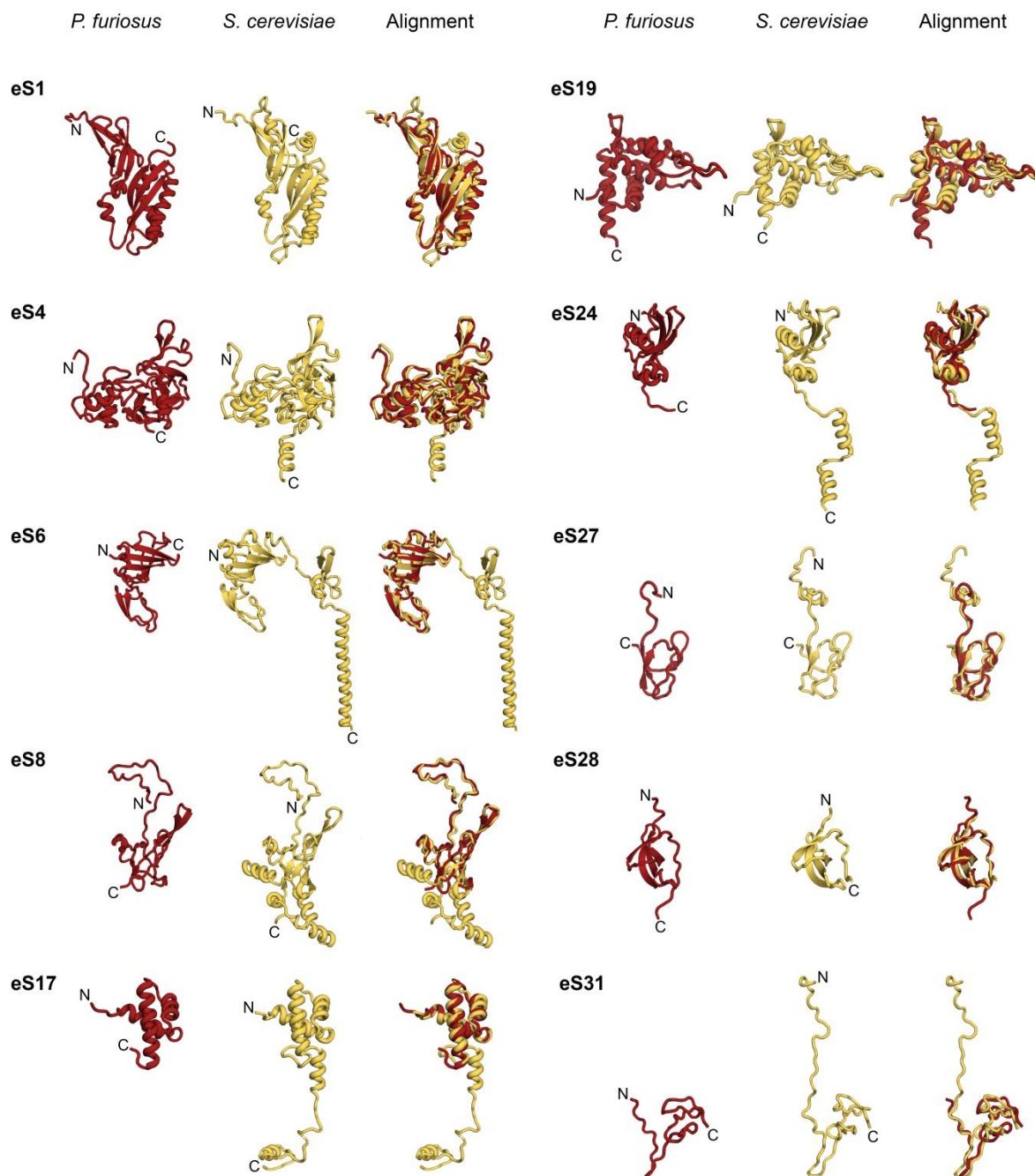
¹ Protein names are according to the nomenclature from [3]



Supplementary Figure S1. Comparison of the location of archaea/eukaryote-specific r-proteins in archaeal and eukaryotic ribosomes.

Solvent view of individual subunits of *Pyrococcus furiosus* (A) and *Saccharomyces cerevisiae* (B) (left – SSU (30S, 40S), right – LSU (50S, 60S)) are shown. rRNA and universally conserved r-proteins are highlighted in grey and dark blue, respectively. Archaea/eukaryote-specific proteins are colored red and labelled. Domain-specific proteins are yellow. Approximate position of the peptide exit tunnel (PET) is indicated.

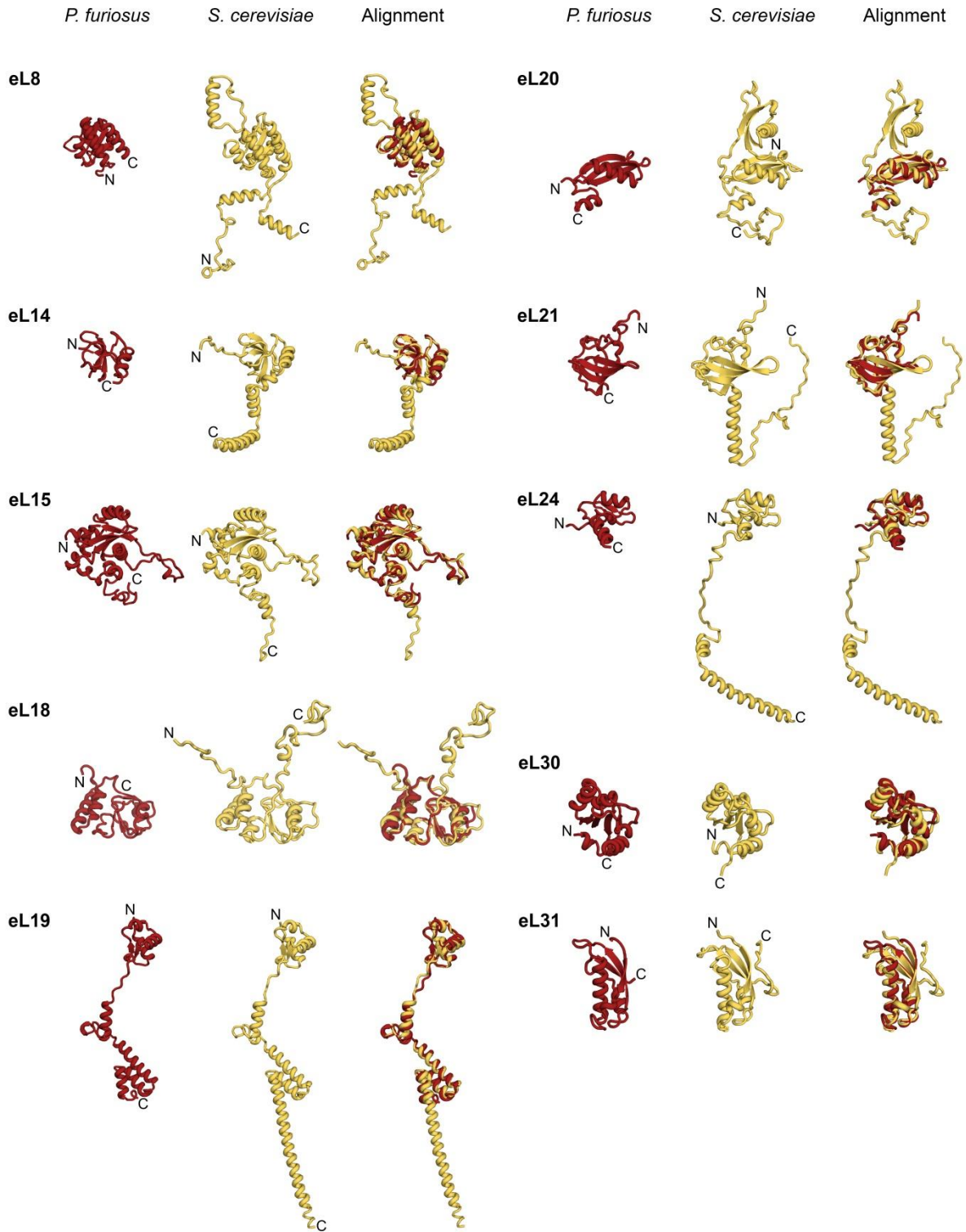
Protein groups and nomenclature are according to [3]. PDB coordinates 4V6U for *P. furiosus* [5] and 4V88 for *S. cerevisiae* [6] were rendered in PyMol.



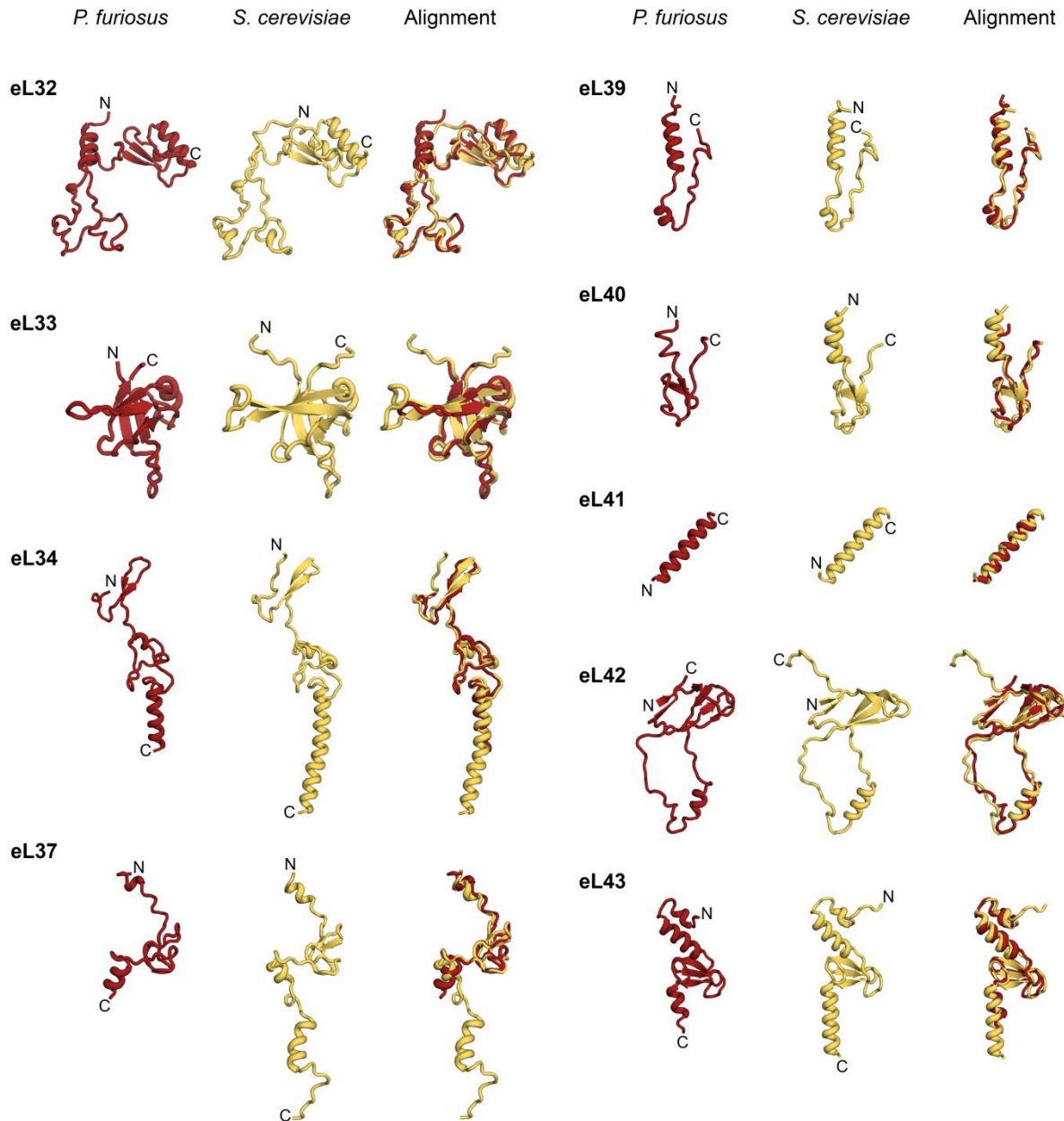
Supplementary Figure S2. Comparison of the architecture of archaea/eukaryote-specific r-proteins of small ribosomal subunit.

R-proteins from archaeal ribosome (*P. furiosus*) are colored red. R-proteins from eukaryotic ribosome (*S. cerevisiae*) are shown in yellow. The positions of the N and C termini are indicated. Structural alignments reveal the structurally conserved core and domain specific extensions.

PDB coordinates 4V6U for *P. furiosus* [5] and 4V88 for *S. cerevisiae* [6] were rendered in PyMol.



Supplementary Figure S3 continues



Supplementary Figure S3. Comparison of the architecture of archaea/eukaryote-specific r-proteins of large ribosomal subunit.

R-proteins from archaeal ribosome (*P. furiosus*) are colored red. R-proteins from eukaryotic ribosome (*S. cerevisiae*) are shown in yellow. The positions of the N and C termini are indicated. Structural alignments reveal the structurally conserved core and domain specific extensions.

PDB coordinates 4V6U for *P. furiosus* [5] and 4V88 for *S. cerevisiae* [6] were rendered in PyMol.

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