Neuron-Like Networks Between Ribosomal Proteins Within the Ribosome

Olivier Poirot & Youri Timsit

Supplementary Information

Table S1
Properties of the extensions of the eukaryotic ribosomes (from the pdb structure 4v88)

Segment	Length (aas)	Mix.	Lenth (aas)	α–helix tot	α–helix prop	Loop	Length (aas)	Helix	Length (aas)	β-HP	Length (aas)
60S eukaryotes											
uL3	20	**uL3**	14	7	0,50	**uL3**	54	**eL14**	49	**uL22**	21
eL6_1	28	**uL4**	100	34	0,34	**uL4_1**	71	**uL13**	54		
eL6_2	16	**uL18_1**	29	11	0,38	**uL4_2**	19	**eL34**	33		
eL14	10	**uL18_2**	43	23	0,53	**uL16**	22	**eL40**	15		
eL15	32	**uL30**	60	43	0,72	**uL5_1**	18	**eL43_1**	32		
eL18	18	**eL8_1**	50	14	0,28	**uL5_2**	25	**eL43_2**	18		
eL20	28	**eL8_2**	25	13	0,52	**eL15**	31	**av**	33,5		
eL21	25	**uL16**	22	5	0,23	**uL13**	18	**max**	54		
uL23	37	**eL13_1**	47	18	0,38	**eL20**	14				
eL33	6	**eL13_2**	71	26	0,37	**uL14**	12				
eL34	37	**uL22**	32	12	0,38	**uL23**	6				
eL42	11	**eL18**	10	5	0,50	**eL27**	16				
av.	22,3	**eL19**	136	98	0,72	**eL32**	69				
max	37	**eL21**	60	23	0,38	**eL33_1**	12				
		eL24	39	6	0,15	**eL33_2**	10				
		uL24	22	8	0,36	**eL42**	42				
		uL15	70	7	0,10	**av**	27,4				
		eL29	57	29	0,51	**max**	71				
		uL29	50	16	0,32						
		eL36	47	14	0,30						
		eL37	86	26	0,30						
		eL39	49	12	0,24						
		av.	50,9	20,5	0,4						
		max	136								
40S eukaryotes											
uS3	30	**uS5**	25	9	0,36	**eS4**	14			**uS5**	25
eS4	35	**eS4**	19	9	0,47	**eS7**	19			**uS17**	27
uS4	18	**uS7**	61	9	0,15	**eS8**	27			**eS19**	10
eS10	16	**eS6**	108	59	0,55	**uS17**	43			**uS10**	21
uS15	26	**uS4**	20	17	0,85	**eS12**	20			**av**	20,8
uS11	20	**uS17**	14	4	0,29	**eS21**	13			**max**	27
uS19_1	13	**eS17**	55	20	0,36	**eS26**	25				
uS19_2	11	**uS13**	70	30	0,43	**av**	23				
uS9	30	**uS12**	38	29	0,76	**max**	43				
uS13	29	**eS24**	40	27	0,68						
eS21_1	17	**eS27**	30	7	0,23						
eS21_2	12	**uS14**	52	16	0,31						
eS31	24	**eS30**	59	20	0,34						
av.	21,6	**av.**	45,5	19,7	0,44						
max	35	**max**	108								

Table S2
Properties of the extensions of the eubacterial and archaeal ribosomes (from the pdb structure 4v8i and 1s72, respectively)

Segment	Length (aas)	**Mix**	Length (aas)	**α–helix tot.**	**α–helix prop.**	**Loop**	Length (aas)	**Helix**	Length (aas)	**β-HP**	size
50S eubact.											
uL13	11	**uL2**	52	8	0,15	**uL3**	53	**bL9**	37	**bL21**	17
uL15	78	**bL19**	19	9	0,47	**uL4**	59	**bL19**	13	**uL22**	16
uL16	30	**bL20**	71	54	0,76	**uL13_1**	16	**av.**	**25**	**uL23**	17
bL17	13	**bL25**	25	8	0,32	**uL13_2**	15		37	**bL28**	29
bL27	26	**bL32**	29	11	0,38	**uL16**	13			**av.**	**19,8**
bL31_1	9	**av.**	**39,2**		**0,42**	**bL17**	12			**max**	29
bL31_2	13	**max**	71			**bL35**	21				
bL34	6					**av.**	**27**				
av.	**23,3**					**max**	59				
max	78										
30S eubact											
bS6	8	**uS12**	27	8	0,30	**uS8**	19	**uS5**	8	**uS5**	13
uS7	18	**uS13**	50	29	0,58					**uS7**	10
uS9	29	**uS14**	59	21	0,36					**uS10**	24
uS11	16	**av.**	**45,3**		**0,41**					**uS17**	17
bS18	10	**max**	59							**av.**	**16**
uS19	9									**max**	24
av.	**15**										
max	29										
50S archae											
uL3	15	**eL19**	39	22	0,56	**uL3**	56	**uL24**	22	**eL22**	16
uL15	60	**eL37**	55	4	0,07	**uL4_1**	62	**eL43**	11		
eL15	24	**eL39**	48	18	0,38	**uL4_2**	12	av.	**16,5**		
uL18	19	**av.**	**47,3**		**0,34**	**uL5_1**	20	**max**	22		
eL21	25	**max**	55			**uL5_2**	11				
av.	**28,6**					**uL16**	22				
max	60					**uL13_1**	12				
						uL13_2	9				
						uL14	12				
						eL15	29				
						eL32	45				
						eL42	43				
						av.	**27,.8**				
						max	62				

Table S3

List of the intermolecular interactions between the ribosomal proteins within the 60S subunit of the eukaryotic ribosome (from the pdb structure 4v88). Colour code: light pink: 3 extensions; light blue: 2 extensions; light green: 1 extension; white: without extension.

Name	Ch.		1	2	3	4	5	6	7	8
uL2	A	glob. domain	eL8 ***GS***	eL15 ***GL***	eL43 ***GG/GH***					
uL3	B	glob. dom.	uL13 ***GG***	uL14 ***GG***	eL24 ***GG***	eS6 (40S) ***GG***				
		seg-N 1-21		uL14 ***SL***						
		loop 220-274	uL13 ***LL***							
		mix-C 373-387			eL24 ***HG***					
uL4	C	glob. dom.						eL18 ***GG***		
		loop 44-115	eL13 ***LH***	eL15 ***LS***	eL37 ***LH***					
		loop 183-202				uL24 ***LH***				
		mix-C 262-362					uL30 ***HH/HG***	eL18 ***HG***	eL20 ***HG***	eL21 ***HS***
uL5	J	glob. dom.								
		loop 48-66		eL42 ***LS***						
		loop 131-156	uL18 ***LS/LG***							
uL6	H	glob. dom.	eL14 ***GS***	uL13 ***GG***	eL20 ***GS***	eL40 ***GH***				
eL6	E	glob. dom.		eL14 ***GH***	eL33 ***GG/GS***					
		seg-N 2-30	eL32 ***SG***							
		seg-C 160-176			eL33 ***SS/SG***					
eL8	G	glob. dom.		eL15 ***GG***			eL36 ***GG***			
		mix-N 24-73	uL2 ***SG***	eL15 ***HG***	uL23 ***SS***	eL27 ***SL***				
		mix-C 231-256	-							
uL13	O	glob. dom.	uL3 ***GG***	uL6 ***GG***		eL20 ***GS***	eL33 ***GG***			
		loop 58-76	uL3 ***LL***							
		helix 145-199			eL14 ***HH***					
eL13	L	glob. dom.					uL29 ***GS***	eL36 ***GS***		
		mix-N 2-49	uL4 ***HL***	eL15 ***SS***	eL18 ***SG***	uL15 ***SH***				
		mix-C 123-194				uL15 ***SG***		eL36 ***HS***		
uL14	V	glob. dom.	uL3 ***GG***	eL24 ***GG***						
		loop 39-51	uL3 ***LS***							
eL14	M	glob. dom.				eL20 ***GG /GS***				
		seg-N 3-13		uL6 ***SG***		eL20 ***SS***				
		helix 89-138	eL6 ***HG***		uL13 ***HH***					
uL15	a	glob. dom.	eL13 ***GS***	eL18 ***GG***		eL36 ***GS***				
		mix-N 2-72	eL13 ***HS***	eL18 ***SG***	eL32 ***SL***		eL42 ***SH***			
eL15	N	glob. dom.			eL8 ***GG***		uL29 ***GS***	eL36 ***GH***		
		loop 67-98	uL2 ***LG***						eL42 ***LL***	
		seg-C 172-204		uL4 ***SL***		eL13 ***SS***				

uL16	I	glob. dom.		eL20 ***GG***	eL21 ***GS***					
		loop 99-121	-							
		mix-C 199-221	uL18 ***HH***							
uL18	D	glob. dom.	uL5 ***GL***	eL21 ***GG***						
		mix-N 1-30	uL5 ***SL***	eL21 ***SS***						
		mix-C 254-297			uL16 ***HH***					
eL18	Q	glob. dom. 1	uL4 ***GH***			uL15 ***GG***				
		seg-N 2-20		uL30 ***SG***						
		mix 144-154								
		glob. dom. 2			eL13 ***GS***	uL15 ***GS***				
eL19	R	glob. dom.	-							
		mix 53-189	eS7 (40S)							
eL20	S	glob. dom.	uL4 ***GH***	uL30 ***GG***		eL14 ***GG***		eL21 ***GS***		
		loop 11-25						eL21 ***LS***		
		seg-C 144-172			uL6 ***SG***	eL14 ***SG/SS***	uL13 ***SG***			
eL21	T	glob. dom.		uL18 ***GG***				eL29 ***GS***		
		seg-N 2-27		uL18 ***SS***						
		mix-C 100-160	uL4 ***SH***		uL30 ***SS***	uL16 ***SG***	eL20 ***SG***			
uL22	P	glob. dom.	-							
		β-hairpin 122-143	-							
		mix-C 152-184	eL33 ***SL***							
eL22	U	glob. dom.	-							
uL23	X	glob. dom.		uL29 ***GG***						
		seg-N 22-59	eL8 ***SS***	uL29 ***SS***						
		loop 114-120			eL39 ***LH***					
uL24	Y	glob. dom.		eL39 ***GL***						
		mix-N 2-24	uL4 ***HL***							
eL24	W	glob. dom.	uL3 ***GS***	uL14 ***GG***						
		mix-C 59-98			eS6 (40S) ***HG***					
eL27	Z	glob. dom.		eL30 ***GG***	eL34 ***GH***					
		loop 51-67	eL8 ***LS***							
uL29	h	glob. dom.			uL23 ***GG***					
		mix-C 70-120	eL13 ***SG***	eL15 ***SG***	uL23 ***SS***	eL37 ***SH***				
eL29	b	mix-N 2-59	eL21 ***SG***							
uL30	F	glob. dom.	uL4 ***GH***	eL18 ***GS***	eL20 ***GG***					
		mix-N 23-83 (helix maj)	uL4 ***HH***			eL21 ***SS***				
eL30	c	glob. dom.	eL27 ***GG***	eL34 ***GH***	eL43 ***GG***					
eL31	d	glob. dom.	-							
eL32	e	glob. dom.	eL6 ***GS***							
		loop 3-72		uL15 ***LS***	eL33 ***LL***					

eL33	f	glob. dom.	eL6 ***GG***	uL13 ***GG***						
		seg-N 2-8	eL6 ***SG***							
		loop 16-28				eL32 ***LL***				
		loop 54-64			uL22 ***LS***					
eL34	g	glob. dom.	-							
		seg-N 2-39			eL39 ***SS***					
		helix 80-113	eL27 ***HG***	eL30 ***HG***						
eL36	i	glob. dom.	eL8 ***GG***							
		mix-N 2-49		eL13 ***SG/SH***	eL15 ***HG***	uL15 ***SG***				
eL37	j	mix-N 2-88	uL4 ***HL***	uL29 ***HS***	eL39 ***SS***					
eL38	k	glob. dom.	-							
eL39	l	mix-N 2-51	uL23 ***HL***	uL24 ***LG***	eL34 ***SS***	eL37 ***SS***				
eL40	m	glob. dom.	-							
		helix 77-92	uL6 ***HG***							
eL41	N	glob. dom.	-							
eL42	o	glob. dom.	-							
		loop 27-69		eL15 ***LL***	uL15 ***HS***					
		seg-C 95-106	uL5 ***SL***							
eL43	p	glob. dom.	uL2 ***GG***	eL30 ***GG***						
		helix 2-34	uL2 ***HG***							
		helix 74-92	uL2 ***HG***							

Table S4

List of the intermolecular interactions between the ribosomal proteins within the 40S subunit of the eukaryotic ribosome (from the pdb structure 4v88). Colour code as in Table S3.

Name	Ch.		1	2	3	4	5	6	7	8
eS1	B	glob. dom.	uS11 ***GG***	eS26 ***GL***						
uS2	A	glob. dom.	uS5 ***GG/GH***	eS17 ***GS/GH***	eS21 ***GG/GL***					
uS3	D	glob. dom.	uS5 ***GG***	eS10 ***GG/GS***		uS10 ***GG***	uS14 ***GH***		Stm1 ***GH***	
		seg-C 195-225			eS17 ***SG***			GBP ***SG***		
uS4	J	glob. dom.	uS5 ***GG***		uS8 ***GG***	eS24 ***GG***	eS30 ***GH***			
		seg-N 2-20		eS4 ***SG***						
		mix-C 166-186	-							
eS4	E	glob. dom.	eS6 ***GH***	uS4 ***GS***		eS24 ***GG***				
		seg-N 2-37	-							
		loop 197-211			uS17 ***LG***					
		mix-C 242-261		uS4 ***HG***						
uS5	C	glob. dom.	uS2 ***GG***	uS3 ***GG***	uS4 ***GG***	eS21 ***GG/GS***	uS8 ***GG***	Stm1 ***GS***		
		β-hairpin 80-105	-							
		mix-C 225-250	uS2 ***HG***			eS21 ***SS***				
eS6	G	glob. dom.		eS24 ***GH***	eL24 (60S)	uL3 (60S)				
		mix-C 118-226	eS4 ***HG***							
uS7	F	glob. dom.		eS25 ***GG***	eS28 ***GG***					
		mix-N 20-81	uS9 ***HG/SG***							
eS7	H	glob. dom.	uS15 ***GS***	uS8 ***GG***						
		loop 94-113	-							
uS8	W	glob. dom.	uS5 ***GG***	eS7 ***GG***	uS4 ***GG***	uS17 ***GB***	uS15 ***GS***	eS21 ***GG***	uS12 ***GS***	eS27 ***GS***
eS8	I	glob. dom.	uS17 ***GL***							
		loop 3-30	uS17 ***LG***							
uS9	Q	glob. dom.	uS7 ***GH/GS***	eS19 ***GG***		GBP ***GG***				
		seg-C 113-143			uS10 ***SB***					
uS10	U	glob. dom.	uS3 ***GG***							
		β-hairpin 63-84		uS9 ***BS***	uS14 ***BH***					
eS10	K	glob. dom.	uS3 ***GG***	eS12 ***GG***	S29 ***GS***	STM1 ***GH***				
		seg-C 80-96	uS3 ***SG***							
uS11	O	glob. dom.	eS1 ***GG***	eS26 ***GL***						
		seg-C 117-137		eS26 ***SG***						
uS12	X	glob. dom.			eS30 ***GS***	STM1 ***GS***				
		mix 2-40	uS17 ***HB***	uS8 ***SG***						
eS12	M	glob. dom.	eS10 ***GG***	eS31 ***GS***						
		loop 101-121	-							

uS13	S	glob. dom.		eS19 ***GG***						
		seg-N 2-31			eS25 ***SG***	STM1 *SS*				
		mix-C 76-146	uS19 ***HG/SS***							
uS14	d	mix 4-56	uS3 ***HG***	eS10 ***SG***	uS10 ***HB***					
uS15	N	glob. dom.		uS17 ***GH***		eS27 ***GG***				
		seg-N 2-28	eS7 ***SG***		uS8 ***SG***	eS27 ***SS***				
uS17	L	glob. dom.	eS4 ***GL***	eS8 ***GL***						
		loop 2-45		eS8 ***LG***						
		β-hairpin 83-110				uS8 ***BG***	uS12 ***BH***			
		mix-C 142-156			uS15 ***HG***					
eS17	R	glob. dom.		uS3 ***GS***	GBP *GG*					
		mix-C 71-126	uS2 ***SG/HG***							
uS19	P	glob. dom.	uS13 ***GH***							
		seg-N 8-21	uS13 ***SS***							
		seg-C 120-131		STM1 *SS*						
eS19	T	glob. dom.	uS9 ***GG***	uS13 ***GG***						
		β-hairpin 83-93	-							
eS21	V	glob. dom.	uS2 ***GG***	uS5 ***GG***	uS8 ***GG***					
		seg-N 1-18		uS5 ***SG/SS***						
		loop 37-50	uS2 ***LG***							
		seg-C 75-87				eS27 ***SS***				
eS24	Y	glob. dom.	eS4 ***GG***		uS4 ***GG***					
		mix-C 95-135		eS6 ***HG***						
eS25	Z	glob. dom.	uS7 ***GG***	uS9	uS13 ***GS***					
eS26	a	glob. dom.		uS11 ***GS***						
		loop 42-67	eS1 ***LG***	uS11 ***LG***						
eS27	b	glob. dom.	uS15 ***GG***							
		mix-N 2-32	uS15 ***SS***	eS21 ***SS***	uS8 ***SG***					
eS28	c	glob. dom.	uS7 ***GG***							
eS30	e	mix 2-61	uS4 ***HG***	uS12 ***SG***	STM1 *SH*					
eS31	f	glob. dom.	-							
		seg-C 83-107	eS12 ***SG***							

Table S5

List of the intermolecular interactions between the ribosomal proteins within the 50S subunit of the archaeal ribosome (from the pdb structure 1s72). Colour code as in Table S3.

Name	Ch.		1	2	3
uL2	A	glob. dom.	eL43 ***GH***		
uL3	B	glob. dom.	uL13 ***GG***	uL14 ***GG***	eL24 ***GG***
		seg-N 1-16		uL14 ***SL***	
		loop 205-261	uL13 ***LL***		
uL4	C	glob. dom.	eL18 ***GG***		
		loop 42-104			eL37 ***LS***
		loop 174-186		uL24 ***LH***	
uL5	D	glob. dom.			
		loop 51-71	-		
		loop 135-146	uL18 ***LS/LG***		
uL6	E	glob. dom.	uL13 ***GL***		
eL8	F	glob. dom.	eL15 ***GG***		
uL10	G	glob. dom.	-		
uL11	I	glob. dom.	-		
uL13	J	glob. dom.	uL3 ***GG***		
		loop 63-75	uL3 ***LL***		
		loop 120-129		uL6 ***LG***	
uL14	K	glob. dom.	uL3 ***GG***	eL24 ***GG***	
		loop 34-46	uL3 ***LS***		
uL15	L	glob. dom.	eL18 ***GG***		
		seg-N 1-61		eL32 ***SL***	eL42 ***SL***
eL15	M	glob. dom.	eL8 ***GG***		
		loop 68-97		eL42 ***LL***	
		seg-C 170-194	-		
uL16	H	glob. dom.	-		
		loop 97-119	-		
uL18	N	glob. dom.		eL21 ***GG***	
		seg-N 1-20	uL5 ***SL***	eL21 ***SS***	
eL18	O	glob. dom.	uL4 ***GG***	uL15 ***GG***	
eL19	P	glob. dom.	-		
		mix-C 51-90	> 30-S ?		
eL21	Q	glob. dom.	uL18 ***GG***		
		seg-N 1-26	uL18 ***SS***		
uL22	R	glob. dom.	-		
		β-hairpin 122-138	-		
uL23	S	glob. dom.	uL29 ***GG***	eL39 ***GH***	
uL24	T	glob. dom.	-		
		helix 1-23	uL4 ***HL***		

eL24	U	glob. dom.	uL3 ***GG***	uL14 ***GG***	
uL29	V	glob. dom.	uL23 ***GG***		
uL30	W	glob. dom.	-		
eL31	X	glob. dom.	-		
eL32	Y	glob. dom.	-		
		loop 124-169	uL15 ***LS***		
eL37	1	mix 1-56	uL4 ***SL***	eL39 ***SS***	
eL39	2	Mix 1_49	uL23 ***HG***	eL37 ***SS***	
eL42	3	glob. dom.	-		
		loop 24-67	uL15 ***LS***	eL15 ***LL***	
eL43	Z	glob. dom.	-		
		helix 71-82	uL2 ***HG***		

Table S6

List of the intermolecular interactions between the ribosomal proteins within the 50S subunit of the eubacterial ribosome (from the pdb structure 4v8i). Colour code as in Table S3.

Name	Ch.		1	2	3	4
uL2	D	glob. dom.	uL2 ***GS***	bS6 (30S) ***GG***		
		mix-C 220-272	uL2 ***SG***			
uL3	E	glob. dom.		uL14 ***GG***		bL19 ***GH***
		loop 109-162	uL13 ***LL***		bL17 ***LS***	
uL4	F	glob. dom.	uL15 ***GS***			
		loop 44-103		bL20 ***LS***		
uL5	G	glob. dom.	bL31 ***GG/GS***	uS13 (30S) ***GG***		
uL6	H	glob. dom.	-			
bL9	I	glob. dom.	bL28 ***GG***			
		helix 41-78				
uL13	N	glob. dom.	-			
		seg-N 1-12			bL21 ***SG***	
		loop 35-51		bL20 ***LH***		
		loop 71-86	uL3 ***LL***			
uL14	O	glob. dom.	uL3 ***GG***	bL19 ***GG***		
uL15	P	glob. dom.	-			
		seg-N 1-79	uL4 ***SG***	bL21 ***SB***	bL35 ***SG***	
uL16	Q	glob. dom.	bL25 ***GG***			
		seg-N 1-31	bL25 ***SG***			
		loop 76-89		bL27 ***LS***		
bL17	R	glob. dom.	-			
		seg-N 1-14	uL3 ***SL***			
		loop 99-111		uL22 ***LG***	bL32 ***LG***	
uL18	S	glob. dom.	bL27 ? ***GG***			
bL19	T	glob. dom.	uL3 ***GG***	uL14 ***GG***		
		helix 1-14	uL3 ***HG***			
		mix-C 116-135	-			
bL20	U	glob. dom.			bL21 ***GG***	
		mix-N 1-72	uL4 ***SL***	uL13 ***HL***	bL21 ***HB***	bL32 ***SH***
bL21	V	glob. dom.	uL13 ***GS***		bL20 ***GG***	
		β-hairpin 70-87		uL15 ***BS***	bL20 ***BH***	
uL22	W	glob. dom.	bL17 ***GL***	bL32 ***GS***		
		β-hairpin 82-98	-			
uL23	X	glob. dom.	uL29 ***GG***			
		β-hairpin 59-76		bL34 ? ***BS***		
uL24	Y	glob. dom.	-			

bL25	Z	glob. dom.	uL16 ***GG***			
		mix-C 177-202	uL16 ***SG***			
bL27	0	glob. dom.		uL18 ***GG***		
		seg-N 2-28	uL16 ***SL***			
bL28	1	glob. dom.	bL9 ***GG***			
		β-hairpin 13-42	-			
uL29	2	glob. dom.	uL23 ***GG***			
uL30	3	glob. dom.	-			
bL31	4	glob. dom.	uL5 ***GG***	uS13 (30S) ***GG***		
		seg-N 1-10	uL5 ***SG***			
		seg-C 33-46	uL5 ***SG***			
bL32	5	glob. dom.	bL17 ***GL***			
		mix-N 2-31		bL20 ***HS***	uL22 ***SG***	
bL33	6	glob. dom.	bL35 ***GL***			
bL34	7	glob. dom.	-			
		seg-N 1-7	uL23 ***SB***			
bL35	8	glob. dom.	uL15 ***GS***			
		loop 25-46		bL33 ***LG***		
bL36	9	glob. dom.	-			

Table S7

List of the intermolecular interactions between the ribosomal proteins within the 30S subunit of the eubacterial ribosome (from the pdb structure 4v8i). Colour code as in Table S3.

Name	Ch.		1	2	3	4
uS2	B	glob. dom.	uS8 ***GL***			
uS3	C	glob. dom.	uS5 ***GG***	uS10 ***GG/GB***	uS14 ***GH***	
uS4	D	glob. dom.	uS5 ***GG***			
uS5	E	glob. dom.	uS3 ***GG***	uS4 ***GG***		
		β-hairpin 15-28	-			
		helix 144-152			uS8 ***HG***	
bS6	F	glob. dom.	uS15 ***GG***	bS18 ***GG***	uL2 (50S) ***GG***	
		seg 92-100		bS18 ***SG***		
uS7	G	glob. dom.	uS9 ***GG***	uS11 ***GG***		
		seg-N 2-20	-			
		β-hairpin 77-87			Inh ***BH***	
uS8	H	glob. dom.		uS5 ***GH***	uS17 ***GB***	
		loop 63-82	uS2 ***LG***			
uS9	I	glob. dom.	uS7 ***GG***			
		seg-C 97-126		uS10 ***SB***	uS14 ***SS***	
uS10	J	glob. dom.	uS3 ***GG***			
		β-hairpin 43-67	uS3 ***BG***	uS9 ***BS***	uS14 ***BH***	
uS11	K	glob. dom.	uS7 ***GG***	bS18 ***GS***		
		seg-C 110-126	-			
uS12	L	glob. dom.	-			
		mix 5-32	uS17 ***HB***			
uS13	M	glob. dom.	-			
		mix-C 65-115	uS19 ***HG/HS***	uL5(50S) ***GG***	bL31(50S) ***GG***	
uS14	N	mix-N 2-61	uS3 ***HG***	uS9 ***SS***	uS10 ***HB***	
uS15	O	glob. dom.	bS6 ***GG***			
bS16	P	glob. dom.	-			
uS17	Q	glob. dom.	-			
		β-hairpin 23-40	uS8 ***BG***	uS12 ***BH***		
bS18	R	glob. dom.	bS6 ***GG/GS***			
		seg-C 77-87		uS11 ***SG***		
uS19	S	glob. dom.	uS13 ***GH***			
		seg-C 75-84	uS13 ***SH***			
S20	T	-				

Table S8

Numbers of interacting partners within the networks of ribosomal proteins. Proteins are listed in function of their number of interacting partners. Colour code as in Table S3.

Number of interacting partners	Number and names of the proteins found in each category												
60S Euk.	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**
0	eL22	eL31	eL38	eL41									
1	uL22	eL19	eL29	eL40									
2	uL5	uL14	uL24	eL43									
3	uL2	uL18	eL6	uL16	eL24	uL23	eL27	eL30	eL32	eL34	eL37	eL42	
4	uL3	uL30	uL6	eL14	eL18	eL33	uL29	eL36	eL39				
5	eL8	uL13	uL15										
6	eL13	eL20	eL21										
7	eL15												
8	uL4												
40S													
0													
1	eS8	uS19	eS28	eS31									
2	eS1	eS7	eS12	uS11	eS17	eS19	eS26	eS30					
3	uS2	uS7	eS10	uS9	uS13	uS10	uS12	eS24	eS25	eS27	uS14		
4	eS4	eS6	uS15	eS21									
5	uS5	uS3	uS4	uS17									
6													
7													
8	uS8												
50S eubact													
0	uL6	uL24	uL30	bL36									
1	uL2	bL9	uL18	bL25	bL28	uL29	bL33	bL34					
2	uL4	uL5	uL14	uL16	bL19	uL22	uL23	bL27	bL31				
3	uL13	uL15	bL17	bL21	bL32								
4	uL3	bL20											
30S													
0	bS16	bS20											
1	uS2	uS4	uS12	uS15	uS19								
2	bS6	uS7	uS11	uS17	bS18								
3	uS3	uS5	uS8	uS9	uS10	uS13	uS14						
50S archaea													
0	uL10	uL16	uL11	uL22	uL30	eL31							
1	uL2	uL5	uL6	eL8	eL19	eL21	uL24	uL29	eL32	eL43			
2	uL13	uL14	eL15	uL18	eL18	eL24	eL37	eL39	eL42				
3	uL3	uL4	uL15										

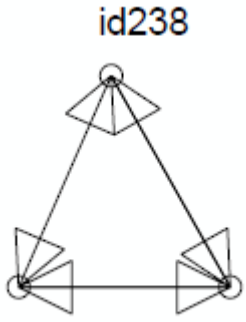
Table S9
Properties of the ribosomal protein networks according to Barabasi et al. (2004) (reference 4 in Methods)

network	mean degree	avg clustering coef.	assortativity	gamma	beta	avg. shortest path	log(n)
60S euk.	3,66	0,31	0,18	2,52	0,25	3,3	3,56
40S euk.	2,81	0,31	0,15	2,64	1,05	3,54	3,26
50S eub.	2,62	0,36	-0,02	1,23	1,86	2,73	2,56
30S eub.	2,13	0,13	0,24	n/a	n/a	4,26	2,71
50S arc.	1,71	0	-0,16	n/a	n/a	2,66	2,64

Table S10
Motifs found in the protein ribosomal networks according to Alon et al. (2007) (reference 5 in Methods)

60S eukarya
size 3:
238 22 7.2+-2.2 6.67 0.000 7 125.71
size 4:
4958 123 53.0+-15.4 4.55 0.000 5 226.94
size 5:

40S eukarya
size 3:
238 14 3.6+-1.7 6.26 0.000 6 135.92



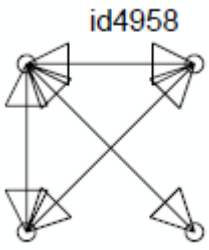


Table S11

List of the pdb structures of eubacterial 70S ribosomes and 50S subunits analysed.
A brief summary about each structure is indicated: year of publication, resolution, space group, translation step, occupancy of tRNA sites and mRNA, translation factor and antibiotics.

					tRNA					
PDB_ID	**Year**	**Resol.**	**Sp. Gr.**	**Functional state**	**A**	**P**	**E**	**mRNA**	**factor**	**Antibiotic**
T. Thermophilus										
4V6F	2010	3.1	$P2_12_12_1$	Elongation	phe	phe	phe	30		
4V6G	2010	3.5	$P2_12_12_1$	Initiation		met	met	25		
4V87	2012	3.1	$P2_12_12_1$	Elongation decoding	leu	met	met	10		
4V8B	2012	3.0	$P2_12_12_1$	Elongation decoding	leu NC	met	met	10		
4V8C	2012	3.3	$P2_12_12_1$	Elongation decoding	leu NC	met	met	10		paromomycin
4V8D	2012	3.3	$P2_12_12_1$	Elongation decoding	tyr	met	tyr	16		
4V8E	2012	3.3	$P2_12_12_1$	Elongation decoding	tyr NC	met	tyr	16		
4V8F	2012	3.3	$P2_12_12_1$	Elongation decoding	tyr NC	met	tyr	16		paromomycin
4V9A	2013	3.3	$P2_12_12_1$	Initiation		met		4		tetracyclin
4V9B	2013	3.1	$P2_12_12_1$	Initiation		met		6		tigecyclin
4WQ1	2015	3.1	$P2_12_12_1$	Elongation decoding	tyr NC	met	tyr	30		
4WQR	2015	3.1	$P2_12_12_1$	Elongation decoding	phe NC	met	phe	30		
4WR6	2015	3.05	$P2_12_12_1$	Elongation decoding	tyr NC	met	tyr	27		
4WRA	2015	3.05	$P2_12_12_1$	Elongation decoding	tyr NC	met	tyr	30		paromomycin
4WRO	2015	3.05	$P2_12_12_1$	Elongation decoding	phe NC	met	phe	30		
4WSD	2015	2.95	$P2_12_12_1$	Elongation decoding	phe NC	met	phe	30		paromomycin
4WSM	2015	3.3	$P2_12_12_1$	Elongation decoding	leu NC	leu	leu	60		
4WT1	2015	3.05	$P2_12_12_1$	Elongation decoding	phe NC	met	phe	27		
4WU1	2015	3.2	$P2_12_12_1$	Elongation decoding		tyr NC	tyr	27		
4WZD	2015	3.1	$P2_12_12_1$	Elongation decoding		tyr	tyr	30		
4WZO	2015	3.3	$P2_12_12_1$	Elongation decoding	met	met	phe	27		
4V51	2006	2.8	$P2_12_12_1$	Elongation Pre1transloc	asl phe	met	phe	24		paromomycin
4V5A	2007	3.5	$P2_12_12_1$	termination		asl phe	met	31	RRF	
4V5E	2008	3.45	$P2_12_12_1$	Termination		phe	phe	8	RF2	
4V5C	2009	3. 3	$P2_12_12_1$	Elongation Post1pept transfer	phe	met	phe	10		paromomycin
4V5D	2009	3.5	$P2_12_12_1$	Elongation Pre1pept transf	phe	phe	phe	11		paromomycin
4V7J	2009	3.3	$P2_12_12_1$	Pre1mRNA cleavage		met	met	25	relE	
4V5J	2010	3.1	$P2_12_12_1$	Termination		phe	phe	8	RF2	
4V5L	2010	3.1	$P12_11$	Elongation decoding	trp	phe	phe	14	EF1Tu GCP	paromomycin
4V5P	2011	3.1	$P12_11$	Elongation decoding	trp NC	phe	phe	27	EF1Tu GDP	kirromycin
4V5Q	2011	3.1	$P12_11$	Elongation decoding	trp NC	phe	phe	27	EF1Tu GDP	kirromycin
4V5S	2011	3.1	$P12_11$	Elongation decoding	Trp NC	phe	phe	27	EF1Tu GDP	kirromycin
4V5R	2011	3.1	$P12_11$	Elongation decoding	trp	phe	phe	27	EF1Tu GDP	kirromycin
4V8Q	2012	3.1	$P12_11$	elongation	tm	met	met	19	EF1Tu GDP	Kirromycin
4V8N	2013	3.1	$P2_12_12_1$	Elongation	ile	ile	ile	24		
4V9H	2013	2.86	$P12_11$	elongation P/E intermediate		P/E hyb		25	EF1G GCP	
4V9I	2013	3.3	$P2_12_12_1$	elongation decoding	ser	ser	ser	7		paromomycin
4V63	2008	3.2	$P2_12_12_1$	Termination		met	met	27	RF1	
4V67	2008	3.0	$P2_12_12_1$	Termination		met	met	27	RF2	
4V83	2011	3.5	$P2_12_12_1$			IRES				
4V84	2011	3.4	$P2_12_12_1$			IRES				
4V9N	2013	3.4	$P2_12_12_1$	termination		met		10	RF2	
4V9Q	2013	3.4	$P2_12_12_1$	Translation inhibition		met	met	5		Blasticidin
4V90	2013	2.95	$P12_11$	Pre1translocation		P/E hyb			EF1G GCP	
4V8X	2013	3.35	$P2_12_12_1$	Pre1 mRNA cleavage		met	met	25	YOEB	
4V9K	2013	3.5	C121	Intermdediate state of translocation		P/E hyb		23	EF1G GDPNP	viomycin

4V9L	2013	3.5	$P2_12_12_1$	Pe*/E state		P/E hyb		23	EF1G GDP	Fusidic acid
1VVJ	2014	3.44	$P2_12_12_1$	+1 frame shift decoding	ASL SufA6	met		18		paromomycin
4L47	2014	3.22	$P2_12_12_1$	+1 frame shift decoding	ASL SufA6	met		18		paromomycin
4LNT	2014	2.94	$P2_12_12_1$	+1 frame shift decoding	ASL SufA6	met		18		paromomycin
4LSK	2014	3.48	$P2_12_12_1$	+1 frame shift decoding	ASL SufA6	met		17		
4TUE	2014	3.5		+1 frame shift decoding	ASL SufJ	met		25		Paromomycin PPU
4ZER	2015	3.1	$P2_12_12_1$	Translation inhibition		met		27	Onc1112	
4V6A	2009	3.1	$P2_12_12_1$	1st peptide bond		met		5	EF1P	
4V7L	2010	3.0	$P2_12_12_1$	Translocation Inhibition	gln	met	gln	30		viomycin
4V7W	2010	3.0	$P2_12_12_1$							chloramphenicol
4V7X	2010	3.0	$P2_12_12_1$							erythromycin
4V7Y	2010	3.0	$P2_12_12_1$							azythromycin
4V7Z	2010	3.1	$P2_12_12_1$							telithromycin
4V8A	2012	3.2	$P2_12_12_1$							thermorubin
4V8G	2012	3.0	$P2_12_12_1$	stationary					RMF	
4V8H	2012	3.1	$P2_12_12_1$	stationary					HPF	
4V8I	2012	2.7	$P2_12_12_1$	stationary					YfiA	
4V95	2012	3.2	$P2_12_12_1$	stationary		met		16	YaeJ	
1VY4	2014	2.6	$P2_12_12_1$	Pre1attack	phe	met	phe	24		
1VY5	2014	2.55	$P2_12_12_1$	Post1catalysis	phe	met	phe	24		
1VY6	2014	2.9	$P2_12_12_1$	Pre1attack	Mimic	met		24		
1VY7	2014	2.8	$P2_12_12_1$	Pre1attack	Mimic	met		24		
4V9R	2014	3.0	$P2_12_12_1$			met		24		dityromycin
4V9S	2014	3.1	$P2_12_12_1$			met		24		GE82832
4W2E	2014	2.9	$P2_12_12_1$	Back translocation		phe	phe	18	EF14 GDP	
4W2F	2014	2.4	$P2_12_12_1$		phe	met	phe	24		amicoumacin
4W2G	2014	2.55	$P2_12_12_1$		phe	met	phe	24		pactamycin
4W2H	2014	2.7	$P2_12_12_1$			met	Phe aS	24		pactamycin
4W2I	2014	2.7	$P2_12_12_1$		phe	met	phe	24		negamycin
4WPO	2015	2.8	$P2_12_12_1$	Pre-translocation	phe	met	phe	24	EF1G GDP	
4WQF	2015	2.8	$P2_12_12_1$	Post-translocation		met	phe	18	EF1G GDP	Fusidic acid
4WQU	2015	2.8	$P2_12_12_1$	Post-translocation		phe	phe	18	EF1G GDP	ditromycin
4Y4O	2015	2.3	$P2_12_12_1$						YfiA	
4Y4P	2015	2.5	$P2_12_12_1$		phe	met	phe	24		
4Z3Q	2015	2.6	$P2_12_12_1$		phe	met	phe	24		hygromycin
4Z3R	2015	3.1	$P2_12_12_1$							hygromycin
4Z3S	2015	2.6	$P2_12_12_1$		phe	met	phe	27		4M2
4Z8C	2015	2.5	$P2_12_12_1$			met		24		oncocin
D. radiodurans										
2ZJR	2008	2.9	I222	50S						
2ZJQ	2008	3.3	I222	50S						micrococin
3CF5	2008	3.3	I222	50S						thiostrepton
3PIO	2011	3.25	I222	50S						Lankamycin lankacidin
4IO9	2013	3.2	I222	50S						erythromycin
4IOA	2013	3.2	I222	50S						4e
5DM6	2015	2.9	I222	50S						
E. coli										
4V52	2007	3.2	$P2_12_12_1$							neomycin
4V54	2007	3.3	$P2_12_12_1$	termination					RRF	
4V57	2007	3.5	$P2_12_12_1$							neomycin spectinomycin
4V64	2008	3.5	$P2_12_12_1$							Hygromycin B
4V6C	2009	3.19	$P2_12_12_1$	intermediate ratcheting						
4V7U	2010	3.1	$P2_12_12_1$							erythromycin
4V7S	2010	3.25	$P2_12_12_1$							telithromycin
4V7V	2010	3.29	$P2_12_12_1$							clindamycin
4V7T	2010	3.19	$P2_12_12_1$							chloramphenicol
4WWW	2010	3.1	$P2_12_12_1$							CEM1101
4V9D	2011	3.0	$P2_12_12_1$	termination		phe		16	RRF	
4V85	2012	3.2	$P2_12_12_1$	termination				27	RF3 GDPNP	viomycin
4V9C	2012	3.3	$P2_12_12_1$	termination		phe		24	RRF	neomycin
4V9O	2013	2.9	$P12_11$	Subunit rotation					EF1G GCP	viomycin
4U1U	2014	2.95	$P2_12_12_1$							quinupristin
4U1V	2014	3.0	$P2_12_12_1$							linopristin
4U20	2014	2.9	$P2_12_12_1$							flopristin
4U24	2014	2.9	$P2_12_12_1$							daflopristin
4U25	2014	2.9	$P2_12_12_1$							virginamycin
4U26	2014	2.8	$P2_12_12_1$							daflopristin quinupristin
4U27	2014	2.8	$P2_12_12_1$							Flopristin linopristin
4WF1	2014	3.1	$P2_12_12_1$							negamycin
4WOI	2015	3.0	$P2_12_12_1$	termination		phe		16	RRF	paromycin
4YBB	2015	2.1	$P2_12_12_1$							

Table S12

Conserved residues at the interfaces of the interacting proteins within the 50S eubacterial subunit. Left column: residues found in the interface. Right column: conserved interface residues. Residues whose properties conserved are underlined and strictly conserved residues are written in bold. AR: conserved aromatic residues; BA: conserved basic residues; AC: conserved acid residues; HP: conserved hydrophobic residues; PO: conserved polar residues; SM: conserved small chain residues. See also figure uS5 that displays the consensus sequence from sequence alignments (reference 6 in Methods).

	Interface residues						**Conserved residues**			
bL20-uL4										
bL20	pro						pro/ala			
	2						2			
uL4	**arg**	ala	pro				**arg**	pro/ala		
	45	49	92				45	92		
bL32-bL20										
bL32	**lys**	**ser**	**lys**	ala			**BA**	**ser**	**BA**	SM
	10	12	13	14			10	12	13	14
bL20	trp	**gly**	leu	lys			AR/arg	BA/asn		
	25	26	27	30			25	30		
uL13-bL21										
uL13	**met**						**met**			
	1						1			
bL21	**gln**	**tyr**	**arg**	**leu**			**gln**	**AR**	**BA**	**HP**
	11	12	13	20			11	12	13	20
uL15-bL21										
uL15	pro	**gly**	**lys**				**gly**	**lys**		
	23	24	29				24	29		
bL21	gln	**arg**	**arg**				PO	**BA**	**BA**	
	80	82	83				80	82	83	
uL3-bL17										
uL3	**lys**	**gly**	**arg**	**lys**			**lys**	**gly**	**BA**	**lys**
	109	110	111	118			109	110	111	118
bL17	**met**	**his**					met	**his**		
	1	3					1	3		
bL17-uL22										
bL17	ala	glu	arg	**arg**	arg	**gly**	**gly**	**arg**	**gly**	
	101	102	103	104	105	106	101	104	106	
uL22	arg	**tyr**	asn	**arg**			PO	**AR**	PO	**BA**
	37	38	40	42			37	38	40	42
uL3-uL14										
uL3	arg	**phe**	asp	arg	ala		arg/gln	**AR**	AC/PO	PO
	13	15	18	19	20		13	15	18	19
uL14	pro	**asp**	**gly**				**asp**	**gly**		
	72	73	74				73	74		
uL3-uL13										
uL13	**tyr**	gly	**tyr**	pro			**AR**	**AR**	*pro*/HP	
	75	77	78	79			75	78	79	
uL3	**arg**	**tyr**	**lys**	**gly**			**BA**	**AR**	**lys**	**gly**
	149	151	152	153			149	151	152	153

bL35-bL33

bL35	leu	trp	gln					HP	PO	PO			
	32	34	35					32	34	35			
bL33	ala	lys	ala	**thr**	glu	**ile**		**thre**	PO	**HP**			
	2	8	22	23	24	54		23	24	54			

bL28-bL9

bL28	ile	pro	tyr	glu	glu								
	67	68	71	72	75								
bL9	**met**	**arg**	**asn**	**leu**	val	leu	**thr**	**arg**	**asn**	**leu**	**thr**		
	1	27	28	31	37	38	40	27	28	31	40		
	ser	asn						asn/HP					
	42	43						43					

uL16-bL27

uL16	**lys**	**leu**	**glu**	val	**arg**	**gly**	lys	**lys**	**HP**	**glu**	val/thr	**arg**	**gly**	Lys /ser
	11	79	80	81	82	84	85	11	79	80	81	82	84	85
	gly	**lys**						**gly**	**lys**					
	86	87						86	87					
bL27	**ala**	**his**	**lys**	**lys**	gly	leu	**gly**	**ala**	**his**	**lys**	**lys**	gly/a la	**gly**	
	2	3	4	5	6	7	8	2	3	4	5	6	8	
	ser	thr	**asn**					**ser**	thr/ser	**asn**				
	9	10	11					9	10	11				

bL17-bL32

bL17	arg	**arg**	**leu**	**lys**	leu	ala	gln	**arg**	**HP**	**lys**	SM		
	33	96	98	99	100	101	102	96	98	99	101		
	leu	**glu**	gln					**glu**					
	113	115	118					**115**					
bL32	pro	**his**	thr	**val**	pro	glu	**tyr**	**his**	**BA**	**HP**	PO	**tyr**	
	41	43	44	45	47	48	52	43	44	45	48	52	
	arg	**val**	**leu**					**val**	**HP**				
	55	57	58					57	58				

uL22-bL32

uL22	arg	**leu**	**asp**	leu	asn	**ile**	arg	arg/gln	**leu**	**asp**	HP /gln	**HP**	PO
	15	19	22	23	34	35	37	15	19	22	23	35	37
	tyr	thr	lys					**AR**	thr/ser	lys/PO			
	38	39	41					38	39	41			
bL32	**arg**	his	**ala**	**leu**	thr	pro	pro	**arg**	AR/asp	ala/lys	T/K/S	pro/ HP	
	20	23	24	25	26	27	28	20	23	24	26	28	
	leu	met	**lys**	pro	pro	glu		**HP**	BA	PO			
	30	39	40	41	47	48		30	40	48			

uL15-uL4

uL15	**met**	lys	**leu**	asp	**leu**	arg	**pro**	**met**	PO	**leu**	PO	**leu**	PO	**pro**
	1	2	3	5	6	7	8	1		3	5	6	7	8
	asn	ala	asn	arg				SM	PO					
	9	12	13	16				12	16					
uL4	ile	asn	pro	his	**leu**	**trp**	**val**	asn/PO	**HP**	**AR**	**val**			
	28	29	30	31	33	34	37	29	33	34	37			
	arg	arg	asp	arg	glu	tyr	val	PO	PO	PO				
	38	95	116	117	120	184	187	95	116	120				
	arg													
	188													

uL23-uL29

uL23	met	thr	tyr	asp	**ile**	leu	ala	**pro**	PO	**ile**	**pro**				
	1	3	5	6	8	9	10	11	6	8	11				
	leu	**phe**	ala	**phe**	lys	ala	leu	leu	**HP**	**phe**	HP	HP	HP		
	13	28	46	47	48	91	92	95	13	28	46	92	95		
uL29	glu	**val**	arg	**lys**	arg	leu	met	**arg**	PO	**HP**	lys/leu	PO	**AR**	**arg**	
	22	25	26	29	30	32	33	36	22	25	29	30	33	36	
	phe	ser	ile	leu	leu	arg			**HP**						
	37	40	41	61	64	68			37						

uL13-bL20

uL13	met	lys	**thr**	**tyr**	val				*lys/thr*	**thr**	**AR**				
	1	2	3	4	5				2	3	4				
	lys	his	**arg**	pro	asp	**trp**	**thr**	**pro**	**lys**	*his/asn*	*pro/ala*	**BA**	**AR**	**thr**	**pro**
	37	38	39	40	41	42	43	44	37	38	40	39	42	43	44
bL20	**phe**	**leu**	**trp**	val	**arg**	**ala**	ala	gln	**phe**	**leu**	**trp**	**arg**	**ala**	**ala**	
	57	60	61	63	64	67	68	71	57	60	61	64	67	68	
	lys	asn	ala	**asp**	**ala**	**val**	arg		**lys**	**AC**	**ala**	**HP**			
	93	94	96	97	99	100	101		93	97	99	100			

uL3-bL19

uL3	val	**lys**	**val**	**gly**	**met**	**thr**	arg	**ile**	**lys**	**HP**	**gly**	**met**	**thr**	arg/ gln	**HP**
	7	8	9	10	11	12	13	14	8	9	10	11	12	13	14
	phe	asp	asp	arg	**val**	leu	leu	asp	**AR**	PO	PO	**HP**	PO		
	15	17	18	19	25	27	52	174	15	17	18	25	174		
	ile	glu	**leu**	**leu**	asn	gly			**HP**	**HP**	PO	gly/PO			
	176	179	181	183	192	193			181	183	192	193			
bL19	met	arg	**leu**	**ile**	leu	**val**	gln	arg	**HP**	**ile**	**HP**	glu/PO	PO		
	1	3	6	7	9	10	11	13	6	7	10	11	13		
	tyr	**lys**	lys	thr	**phe**	asn	thr	pro	**BA**/AR	PO	**HP**	PO	SM		
	14	33	35	40	57	58	60	77	33	40	57	58	60		
	his	**ser**	**pro**	leu					**AR**/PO	**ser**/thr	**pro**				
	79	80	81	82					79	80	81				

uL15-bL35

uL15	pro	arg	arg	**phe**	**glu**	arg	**thr**	leu	**gly**	**phe**	**glu**	**gln**			
	48	49	50	51	52	55	58	59	50	51	52	55			
	met	**arg**	**leu**	**pro**	**lys**	**arg**	gln		**arg**	**leu**	**pro**	**lys**			
	60	61	62	63	64	65	68		61	62	63	64			
bL35	**met**	**lys**	**his**	gly	ala	lys	**lys**	**arg**	**HP**	**lys**	**BA**	SM	SM	**lys**	**arg**
	4	5	7	9	10	11	12	13	4	5	7	9	10	12	13
	val	ala	met	lys	thr	arg	lys	phe	**phe**	PO	SM	arg/ser			
	14	24	25	26	27	30	47	48	14	26	27	30			
	leu	**glu**	arg	**ile**	leu	**leu**			**HP**	**glu**	**HP**	**HP**			
	50	54	57	58	60	61			50	54	58	61			

bL20-bL21

bL20	**lys**	leu	arg	**leu**	phe	gly	**ala**	**tyr**	**lys**	leu/gln	arg/asn	HP	**ala**	**AR**	
	16	20	36	39	40	43	46	47	16	20	36	39	46	47	
	arg	**ala**	gly	**ile**	**glu**	**val**	asp	**lys**	**arg**	**ala**	**HP**	**AC**	**HP**	**lys**	
	50	86	87	88	89	90	91	93	50	86	88	89	90	93	
	asn	**asp**	**leu**	arg	**glu**	gln	val	glu	**AC**	**HP**	**AC**				
	94	97	98	101	102	104	105	108	97	98	102				
	leu	arg							**HP**						
	109	112							109						
bL21	**phe**	**ile**	lys	**gly**	**lys**	**gln**	**tyr**	**arg**	**AR**	**HP**	PO	**gly**	**lys**	**gln**	**AR**
	2	4	6	9	10	11	12	13	2	4	6	9	10	11	12
	leu	**leu**	**leu**	gly	gly	thr	**val**	**gly**	**HP**	**leu**	**HP**	**HP**	**gly**		
	38	39	40	41	42	45	47	48	38	39	40	47	48		
	thr	**pro**	**ile**	leu	**val**	ser	**lys**	phe	**pro**	**HP**	**HP**	**lys**			
	49	50	70	71	72	73	74	75	50	70	72	74			
	arg	**lys**							**BA**	**BA**					
	82	84							82	84					

bL25-uL16

bL25	leu	phe	asp	phe	arg	ser	ile	his							
	41	44	45	48	49	52	53	54							
	arg	**gln**	val	leu	asp	lys	arg	arg	**gln**	BA/thr					
	72	73	74	76	77	78	79	80	73	78					
	arg	pro	ala	gly	val	leu	gln	phe							
	81	83	113	114	116	117	118	119							
	arg	asp	ile	val	pro	pro	glu	asp							
	122	123	146	175	176	178	179	180							
	val	lys	leu	glu	ala	ala	glu	val							
	181	182	183	186	187	189	190	191							
	ala	glu	pro	glu	val	lys									
	192	193	194	195	196	198									
uL16	**met**	met	**pro**	**arg**	**arg**	met	**lys**	**tyr**	**met**	**pro**	**BA**	**arg**	**lys**	**AR**	**AR**
	1	3	4	5	6	7	8	9	1	4	5	6	8	9	9
	arg	**gly**	ala	thr	lys	gly	asp	tyr	**arg**	**gly**					
	10	19	20	21	22	23	25	26	10	19					
	val	**phe**	**asp**	val	**glu**	**arg**	val	val	**HP**	**phe**	**AC**	**glu**	**arg**	thr/ asn	thr/ asn
	27	29	31	35	48	51	52	55	27	29	31	48	51	55	55
	arg	phe	**arg**	**arg**	gly	**gly**	lys	**ile**	**arg**	AR	**lys**	**arg**	gly/gl n	**gly**	
	56	58	59	60	61	62	63	64	56	58	59	60	61	62	
	phe	**tyr**	**pro**	**gly**	ala	**gly**	lys	**val**	**AR**	**tyr**	**AR**	**pro**	**gly**	**HP**	
	65	93	99	100	107	108	130	132	65	93	93	99	100	132	
	arg	**arg**	asp	ala	tyr	asp	gln	ala	**BA**						
	133	134	135	136	137	138	139	140	134						
	glu														
	141														

Table S13
New nomenclature for proteins of the small subunit (adapted from reference 35)

New Name	Taxonomic Range	Bacteria	Yeast	Human
bS1	B	S1	-	-
eS1	A E	-	S1	S3A
uS2	B A E	S2	S0	SA
uS3	B A E	S3	S3	S3
uS4	B A E	S4	S9	S9
eS4	A E	-	S4	S4
uS5	B A E	S5	S2	S2
bS6	B	S6	-	-
eS6	A E	-	S6	S6
uS7	B A E	S7	S5	S5
eS7	E	-	S7	S7
uS8	B A E	S8	S22	S15A
eS8	A E	-	S8	S8
uS9	B A E	S9	S16	S16
uS10	B A E	S10	S20	S20
eS10	E	-	S10	S10
uS11	B A E	S11	S14	S14
uS12	B A E	S12	S23	S23
eS12	E	-	S12	S12
uS13	B A E	S13	S18	S18
uS14	B A E	S14	S29	S29
uS15	B A E	S15	S13	S13
bS16	B	S16	-	-
uS17	B A E	S17	S11	S11
eS17	A E	-	S17	S17
bS18	B	S18	-	-
uS19	B A E	S19	S15	S15
eS19	A E	-	S19	S19
bS20	B	S20	-	-
bS21	B	S21	-	-
bTHX	B	THX	-	-
eS21	E	-	S21	S21
eS24	A E	-	S24	S24
eS25	A E	-	S25	S25
eS26	E	-	S26	S26
eS27	A E	-	S27	S27
eS28	A E	-	S28	S28
eS30	A E	-	S30	S30
eS31	A E	-	S31	S27A
RACK1	E	-	Asc1	RACK1

Table S14
New nomenclature for proteins of the large subunit (adapted from reference 35)

New name	Taxonomic range	Bacteria	Yeast	Human
uL1	B A E	L1	L1	L10A
uL2	B A E	L2	L2	L8
uL3	B A E	L3	L3	L3
uL4	B A E	L4	L4	L4
uL5	B A E	L5	L11	L11
uL6	B A E	L6	L9	L9
eL6	E	-	L6	L6
eL8	A E	-	L8	L7A
bL9	B	L9	-	-
ul10	B A E	L10	P0	P0
uL11	B A E	L11	L12	L12
bL12	B	L7/L12	-	-
uL13	B A E	L13	L16	L13A
eL13	A E	-	L13	L13
uL14	B A E	L14	L23	L23
eL14	A E	-	L14	L14
uL15	B A E	L15	L28	L27A
eL15	A E	-	L15	L15
uL16	B A E	L16	L10	L10
bL17	B	L17	-	-
uL18	B A E	L18	L5	L5
eL18	A E	-	L18	L18
bL19	B	L19	-	-
eL19	A E	-	L19	L19
bL20	B	L20	-	-
eL20	A E	-	L20	L18A
bL21	B	L21	-	-
eL21	A E	-	L21	L21
uL22	B A E	L22	L17	L17
eL22	E	-	L22	L22
uL23	B A E	L23	L25	L23A
uL24	B A E	L24	L26	L26
eL24	A E	-	L24	L24
bL25	B	L25	-	-
bL27	B	L27	-	-
eL27	E	-	L27	L27
bL28	B	L28	-	-
eL28	E	-	-	L28
uL29	B A E	L29	L35	L35
eL29	E	-	L29	L29
uL30	B A E	L30	L7	L7
eL30	A E	-	L30	L30
bL31	B	L31	-	-
eL31	A E	-	L31	L31
bL32	B	L32	-	-
eL32	A E	-	L32	L32
bL33	B	L33	-	-
eL33	A E	-	L33	L35A
bL34	B	L34	-	-
eL34	A E	-	L34	L34
bL35	B	L35	-	-
bL36	B	L36	-	-
eL36	E	-	L36	L36
eL37	A E	-	L37	L37
eL38	A E	-	L38	L38
eL39	A E	-	L39	L39
eL40	A E	-	L40	L40
eL41	A E	-	L41	L41
eL42	A E	-	L42	L36A
eL43	A E	-	L43	L37A
P1/P2	A E	-	P1/P2 (A/B)	P1/P2 (α/β)

Table S15

Status of the pdb models when different conformations are observed at protein-protein interfaces of 50S subunits and 70S eubacterial ribosomes.

For each protein-pairs where different conformations have been observed, the status of the models is noted as follow: white: correct model; "?" and green: the map is not incompatible with the different model built in the map; "-" and yellow: non-interpretable electron density map in the corresponding region; "x" and red: incorrect model, the model is not correctly fitted into its density map. For uL16-bL27, the "S" indicates that bL27 is fully structured at the interface (see also Supplementary fig. S10 that display the correct and incorrect (x) model found in the twelve protein-protein contact regions that display different conformation

				tRNA			1	2	3	4	5	6	7	8	9	10	11	12
PDB_ID	**Year**	**Res.**	**Sp. Gr**	**A**	**P**	**E**	**uL3 uL13**	**uL13 bL20**	**uL13 bL21**	**uL15 bL21**	**uL15 bL35**	**bL35 bL33**	**bL17 uL3**	**uL3 uL14**	**bL17 bL32**	**bL20 uL4**	**uL16 bL27**	**uL23 uL29**
T.Thermophilus																		
4V6F_1	2010	3.1	$P2_12_12_1$	phe	phe	phe				?		-			x		x	x
4V6F_2											x	-			x		x	x
4V6G_1	2010	3.5	$P2_12_12_1$		met	met				?		-			x		x	x
4V6G_2											x	-			x		x	x
4V87_1	2012	3.1	$P2_12_12_1$	leu	met	met					x	-			x			x
4V87_2										?		-			x			x
4V8B_1	2012	3. 0	$P2_12_12_1$	leu	met	met					x	-			x		x	x
4V8B_2				NC						?		-			x		x	x
4V8C_1	2012	3.3	$P2_12_12_1$	leu	met	met			-		x	-			x			x
4V8C_2				NC					-	?		-			x			x
4V8D_1	2012	3.3	$P2_12_12_1$	tyr	met	tyr					x	-			x			x
4V8D_2										?		-			x			x
4V8E_1	2012	3.3	$P2_12_12_1$	tyr	met	tyr					x	-			x			x
4V8E_2				NC						?	x	-			x			x
4V8F_1	2012	3.3	$P2_12_12_1$	tyr	met	tyr					x	-			x			x
4V8F_2				NC								-			x			x
4V9A_1	2013	3.3	$P2_12_12_1$		met				-		x	-			x			x
4V9A_2									-	?		-			x			x
4V9B_1	2013	3.1	$P2_12_12_1$		met						x	-			x			x
4V9B_2										?		-			x			x
4WQ1_1	2015	3.1	$P2_12_12_1$	tyr	met	tyr					x	-			x			x
4WQ1_2				NC						?	x	-			x		x	x
4WQR_1	2015	3.1	$P2_12_12_1$	phe	met	phe					x	-			x		x	x
4WQR_2				NC						?	x	-			x		x	x
4WR6_1	2015	3.05	$P2_12_12_1$	tyr	met	tyr					x	-			x			x
4WR6_2				NC						?	x	-			x		x	x
4WRA_1	2015	3.05	$P2_12_12_1$	tyr	met	tyr					x	-			x		x	x
4WRA_2				NC						?		-			x		x	x
4WRO	2015	3.05	$P2_12_12_1$	phe	met	phe						-			x		x	x
				NC														
4WSD_1	2015	2.95	$P2_12_12_1$	phe	met	phe					x	-			x		x	x
4WSD_2				NC						?		-			x		x	x
4WSM_1	2015	3.3	$P2_12_12_1$	leu	leu	leu					x	-			x			x
4WSM_2				NC					-	?		-			x			x
4WT1_1	2015	3.05	$P2_12_12_1$	phe	met	phe					x	-			x		l	x
4WT1_2				NC						?	x	-			x		l	x
4WU1_1	2015	3.2	$P2_12_12_1$		tyr	tyr						-			x			x
4WU1_2					NC				-	?		-			x			x
4WZD_1	2015	3.1	$P2_12_12_1$		tyr	tyr						-			x		S	x
4WZD_2									-	?		-			x			x
4WZO_1	2015	3.3	$P2_12_12_1$	met	met	phe						-			x		l	x
4WZO_2										?		-			x		l	x
4V51	2006	2.8	$P2_12_12_1$	asl	met	phe			x	-	x	-	x		x		-	-
				phe														
4V5A	2007	3.5	$P2_12_12_1$		asl	met			x	-	x	-	x		x		-	-
					phe													
4V5E	2008	3.45	$P2_12_12_1$		phe	phe					x	-	x		x			x
4V5C	2009	3. 3	$P2_12_12_1$	phe	met	phe			x		x	-	x		x		S	x
4V5D	2009	3.5	$P2_12_12_1$	phe	phe	phe			x		x	-	x		x		S	x
4V7J	2009	3.3	$P2_12_12_1$		met	met			x		x	-	x		x		S	
4V5J	2010	3.1	$P2_12_12_1$		phe	phe			x		x	-	x		x		S	x
4V5L	2010	3.1	$P12_11$	trp	phe	phe			x		x	-	x		x		S	x
4V5P	2011	3.1	$P12_11$	trp	phe	phe			x		x	-	x		x		S	x
				NC														
4V5Q	2011	3.1	$P12_11$	trp	phe	phe			x		x	-	x		x		S	x
				NC														
4V5S	2011	3.1	$P12_11$	Trp	phe	phe			x		x	-	x		x		S	x
				NC														
4V5R	2011	3.1	$P12_11$	trp	phe	phe			x		x	-	x		x		S	x
4V8Q	2012	3.1	$P12_11$	tm	met	met			x		x	-	x		x		S	x
4V8N	2013	3.1	$P2_12_12_1$	ile	ile	ile			x		x	-	x		x		S	x
4V9H	2013	2.86	$P12_11$		P/E				x		x	-	x		x		S	x
					hyb													
4V9I	2013	3.3	$P2_12_12_1$	ser	ser	ser			x		x	-	x		x		S	x
4V63	2008	3.2	$P2_12_12_1$		met	met					x		x		x		x	x
4V67	2008	3.	$P2_12_12_1$		met	met					x		x		x		x	x
4V83	2011	3.5	$P2_12_12_1$		IRES						x		x		x		x	x

4V84	2011	3.4	$P2_12_12_1$		IRES						x		x		x		x	x
4V9N	2013	3.4	$P2_12_12_1$		met						x		x		x		x	x
4V9Q	2013	3.4	$P2_12_12_1$		met	met					x		x		x		x	x
4V90	2013	2.95	$P12_11$		P/E hyb				x				x		x		S	
4V8X	2013	3.35	$P2_12_12_1$		met	met			x		x		x		x		S	x
4V9K	2013	3.5	C121		P/E hyb						x		x				S	x
4V9L	2013	3.5	$P2_12_12_1$		P/E hyb						x		x		x		S	x
1VVJ	2014	3.44	$P2_12_12_1$	ASL SufA6	met						x				x		S	x
4L47	2014	3.22	$P2_12_12_1$	ASL SufA6	met						x				x		x	x
4LNT	2014	2.94	$P2_12_12_1$	ASL SufA6	met										x		x	x
4LSK	2014	3.48	$P2_12_12_1$	ASL SufA6	met										x		x	x
4TUE	2014	3.5		ASL SufJ	met						x				x		x	x
4ZER	2015	3.1	$P2_12_12_1$		met													
4V6A_1	2009	3.1	$P2_12_12_1$		met								x		x			
4V6A_2									x		x		x		x			x
4V7L	2010	3.	$P2_12_12_1$	gln	met	gln			x				x		x		S	x
4V7W	2010	3.	$P2_12_12_1$						x	x	x	x	x		x		x	x
4V7X	2010	3.	$P2_12_12_1$						x	x	x	x	x		x		x	x
4V7Y	2010	3.	$P2_12_12_1$						x	x	x	x	x		x		x	x
4V7Z	2010	3.1	$P2_12_12_1$						x	x	x	x	x		x		x	x
4V8A	2012	3.2	$P2_12_12_1$															
4V8G	2012	3.	$P2_12_12_1$															
4V8H	2012	3.1	$P2_12_12_1$															
4V8I	2012	2.7	$P2_12_12_1$															
4V95	2012	3.2	$P2_12_12_1$		met													
1VY4	2014	2.6	$P2_12_12_1$	phe	met	phe											S	
1VY5	2014	2.55	$P2_12_12_1$	phe	met	phe											S	
1VY6	2014	2.9	$P2_12_12_1$	Mimic	met												S	
1VY7	2014	2.8	$P2_12_12_1$	Mimic	met												S	
4V9R	2014	3.	$P2_12_12_1$		met												S	
4V9S	2014	3.1	$P2_12_12_1$		met												S	
4W2E	2014	2.9	$P2_12_12_1$		phe	phe												
4W2F	2014	2.4	$P2_12_12_1$	phe	met	phe											S	
4W2G	2014	2.55	$P2_12_12_1$	phe	met	phe											S	
4W2H	2014	2.7	$P2_12_12_1$		met	Phe aS											S	
4W2I	2014	2.7	$P2_12_12_1$	phe	met	phe											S	
4WPO	2015	2.8	$P2_12_12_1$	phe	met	phe											S	
4WQF	2015	2.8	$P2_12_12_1$		met	phe											S	
4WQU	2015	2.8	$P2_12_12_1$		phe	phe												
4Y4O	2015	2.3	$P2_12_12_1$															
4Y4P	2015	2.5	$P2_12_12_1$	phe	met	phe											S	
4Z3Q	2015	2.6	$P2_12_12_1$	phe	met	phe											S	
4Z3R	2015	3.1	$P2_12_12_1$															
4Z3S	2015	2.6	$P2_12_12_1$	phe	met	phe											S	
4Z8C	2015	2.5	$P2_12_12_1$		met													
D. Radiodurans																		
2ZJR	2008	2.9	I222				x	x			-	-	x	x	x	x	x	
2ZJQ	2008	3.3	I222				x	x			-	-	x	x	x	x	x	
3CF5	2008	3.3	I222				x	x			-	-	x	x	x	x	x	
3PIO	2011	3.25	I222				x	x			-	-	x	x	x	x	x	
4IO9	2013	3.2	I222				x	x			-	-	x	x	x	x	x	
4IOA	2013	3.2	I222				x	x			-	-	x	x	x	x	x	
5DM6	2015	2.9	I222								-	-	x	x	x	x	S	
E. Coli																		
4V52	2007	3.2	$P2_12_12_1$					x						x				
4V54	2007	3.3	$P2_12_12_1$					x						x				
4V57	2007	3.5	$P2_12_12_1$					x						x				
4V64	2008	3.5	$P2_12_12_1$					x						x				
4V6C_1	2009	3.19	$P2_12_12_1$					x						x				
4V6C_2								x						x				x
4V7U_1	2010	3.1	$P2_12_12_1$					x						x				
4V7U_2								x						x				x
4V7S_1	2010	3.25	$P2_12_12_1$					x						x				
4V7S_2								x						x				x
4V7V_1	2010	3.29	$P2_12_12_1$					x						x				
4V7V_2								x						x				x
4V7T_1	2010	3.19	$P2_12_12_1$					x						x				
4V7T_2								x						x				x
4WWW_1	2010	3.1	$P2_12_12_1$					x						x				
4WWW_2								x						x				x
4V9D	2011	3.	$P2_12_12_1$		phe													
4V85	2012	3.2	$P2_12_12_1$					x						x				
4V9C	2012	3.3	$P2_12_12_1$		phe													
4V9O_1,2	2013	2.9	$P12_11$					x						x				
4V9O_3,4								x										
4U1U	2014	2.95	$P2_12_12_1$															
4U1V	2014	3. 0	$P2_12_12_1$															
4U20	2014	2.9	$P2_12_12_1$															
4U24	2014	2.9	$P2_12_12_1$															
4U25	2014	2.9	$P2_12_12_1$															
4U26	2014	2.8	$P2_12_12_1$															
4U27	2014	2.8	$P2_12_12_1$															
4WF1	2014	3.1	$P2_12_12_1$															
4WOI	2015	3. 0	$P2_12_12_1$		phe													
4YBB	2015	2.1	$P2_12_12_1$															

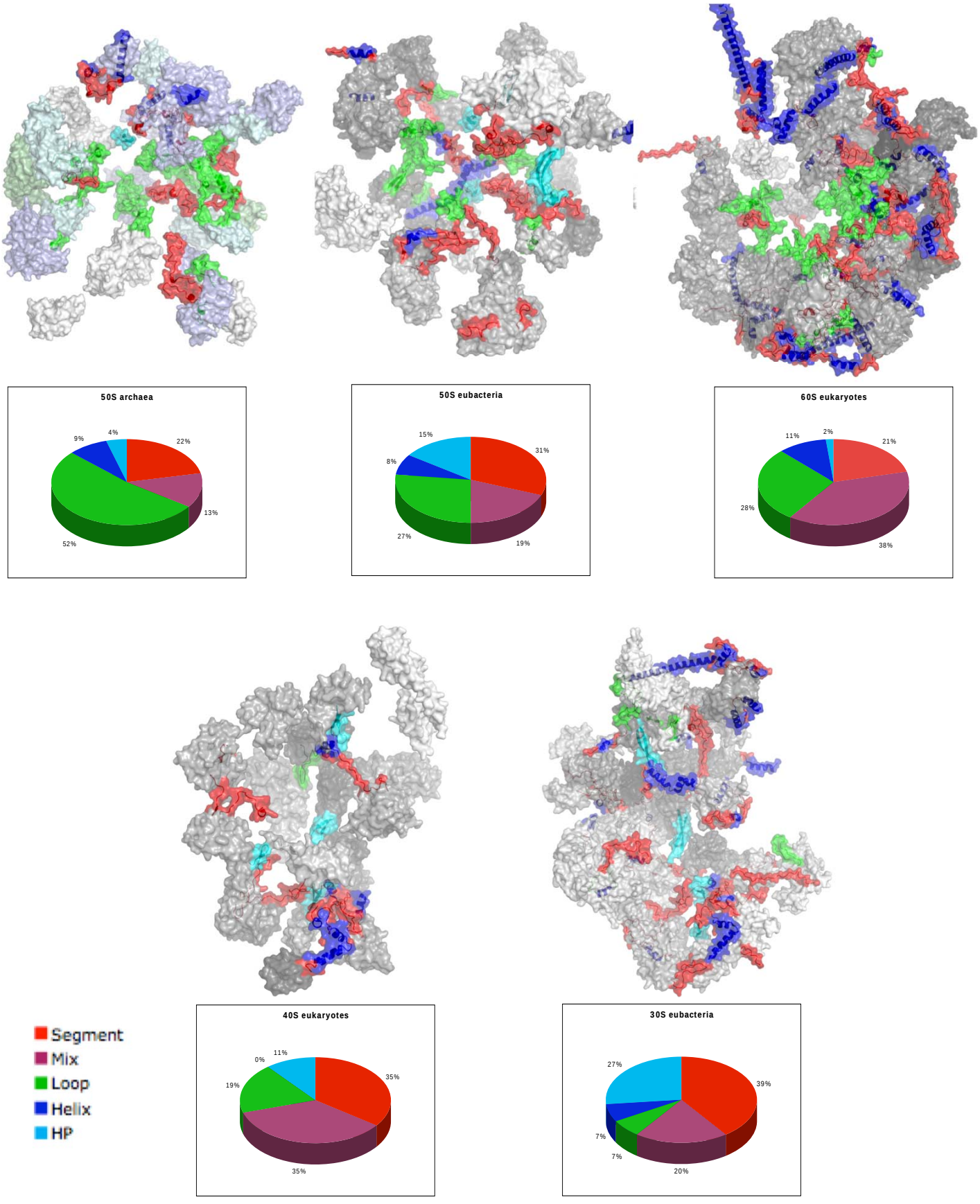
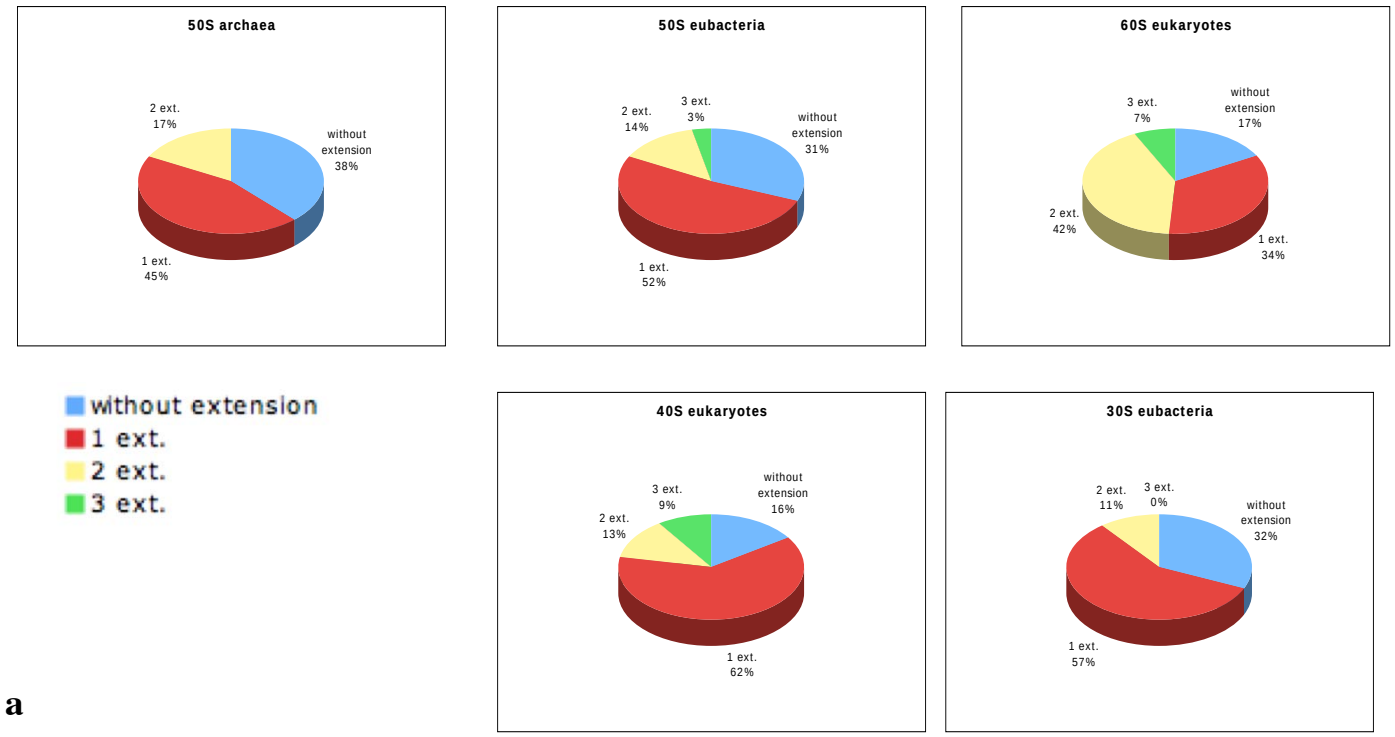
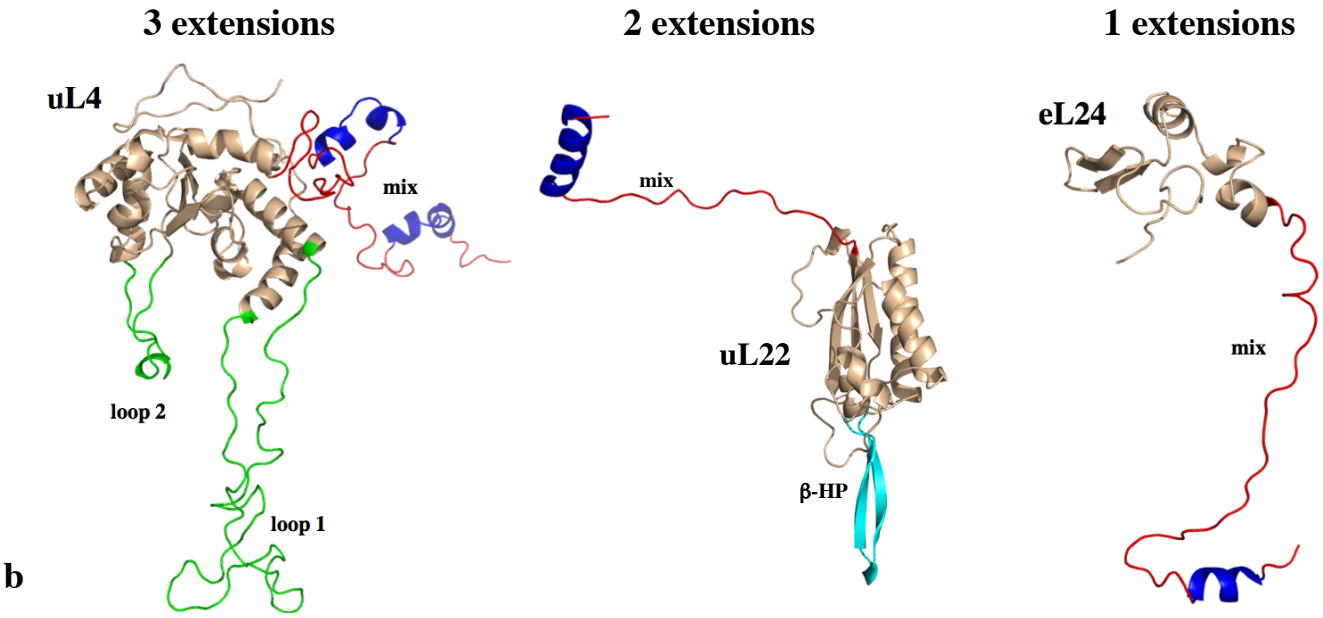


Figure S1
Statistic of the types of extensions of the archaeal (pdb_id: 1s72), eubacterial (pdb_id: 4v8i) and eukaryotic (pdb_id: 4v88) ribosomes



a



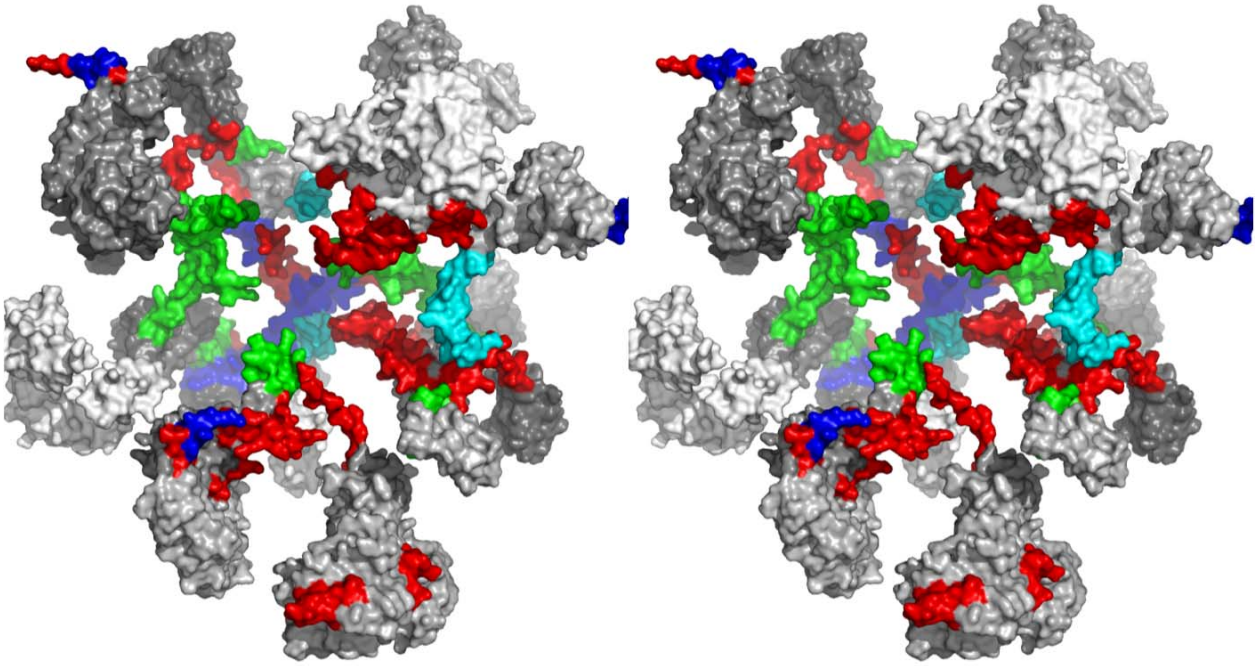
b

Figure S2

a. Statistic of number of extensions per protein within the archaeal (pdb_id: 1s72), eubacterial (pdb_id: 4v8i) and eukaryotic (pdb_id: 4v88) ribosomes

b. Examples of proteins with multiple extensions

Eubacteria 50S



Eukarya 60S

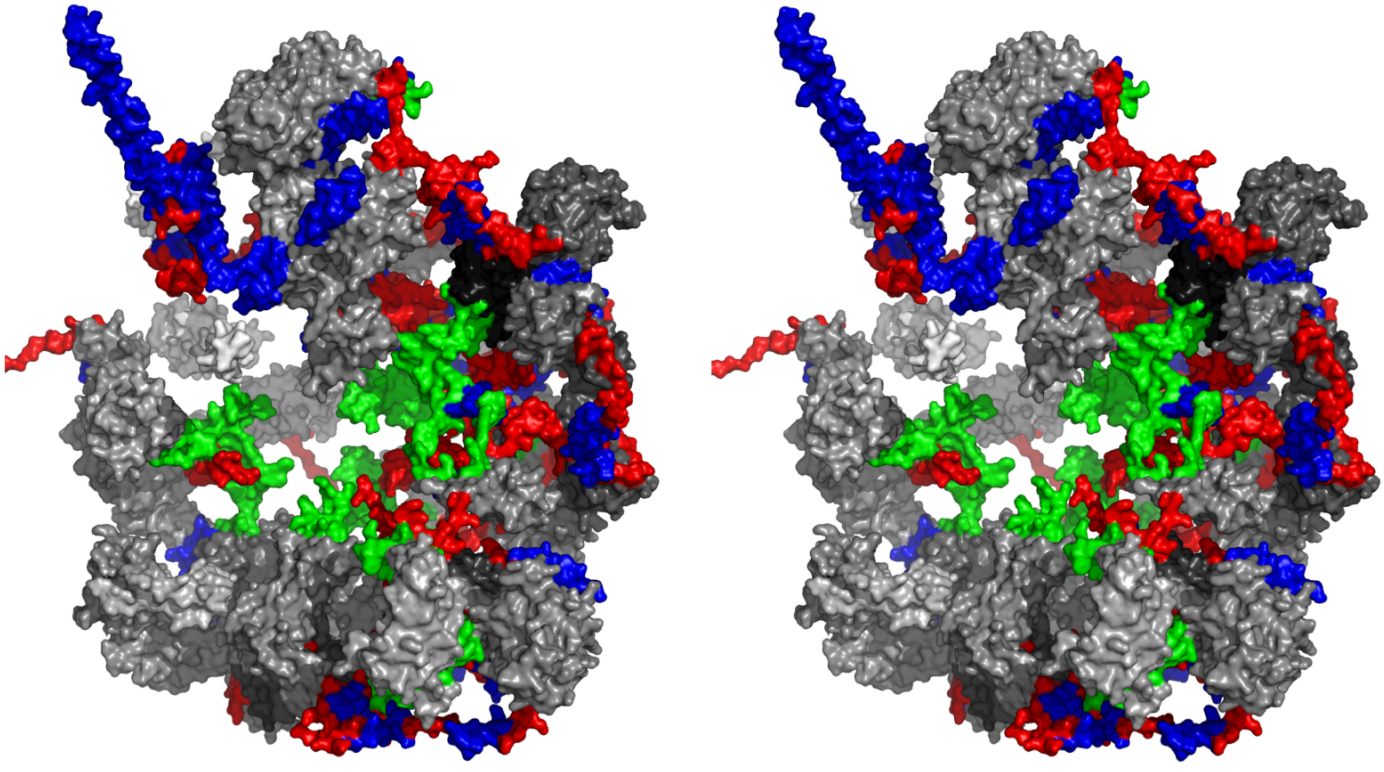


Figure S3 a: stereo views of the large subunits
(up) eubacteria (pdb_id: 4v8i)
(down) eukarya (pdb_id: 4v88)
Extensions are coloured according to their secondary structures
Green: loops, Red: segments, Blue: α-helices, Cyan: β-hairpins

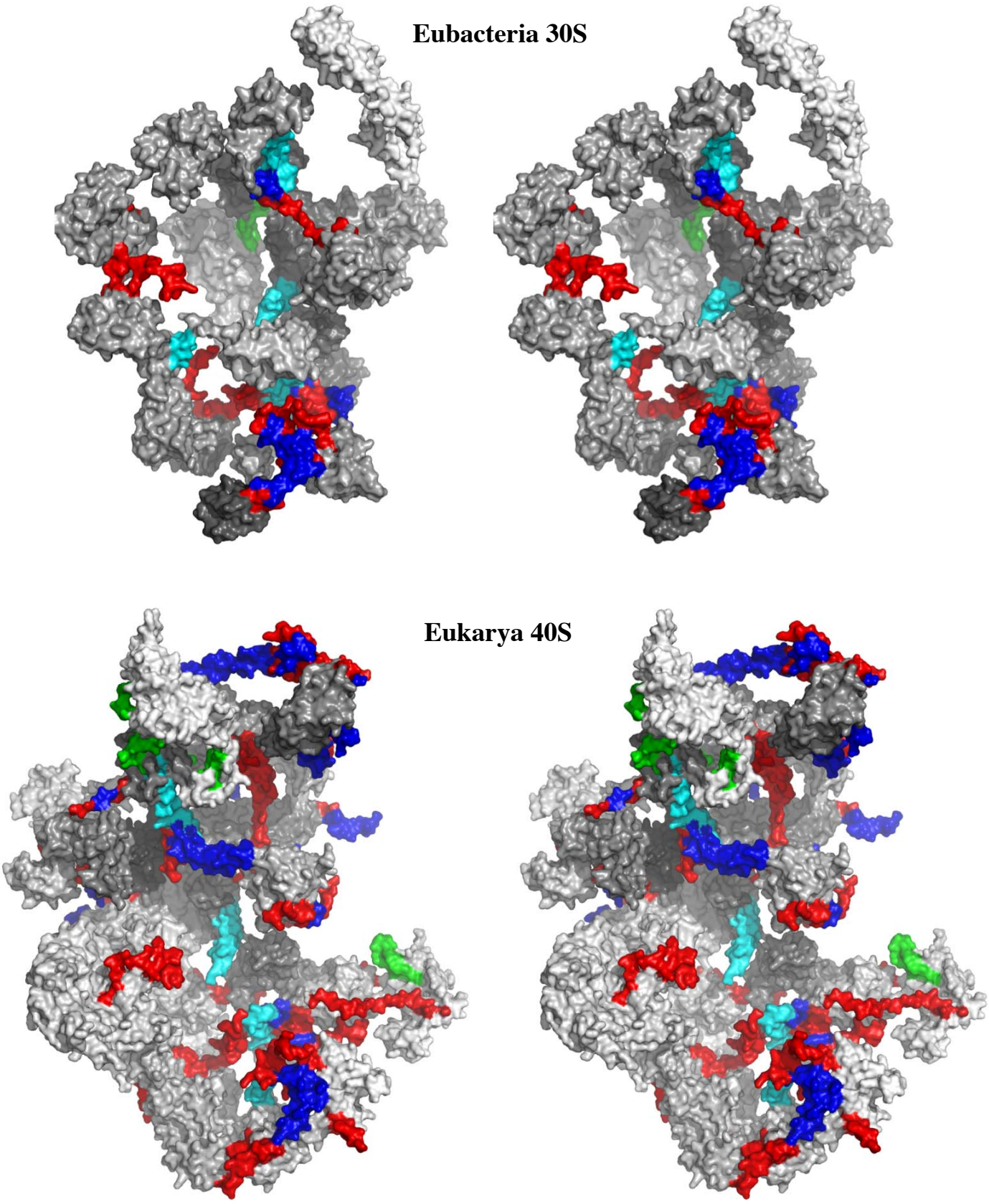


Figure S3 b: stereo views of the small subunits
(up) eubacteria (pdb_id: 4v8i); (down) eukaryotic ribosomes (pdb_id: 4v88)
Extensions are coloured according to their secondary structures
Green: loops, Red: segments, Blue: α-helices, Cyan: β-hairpins

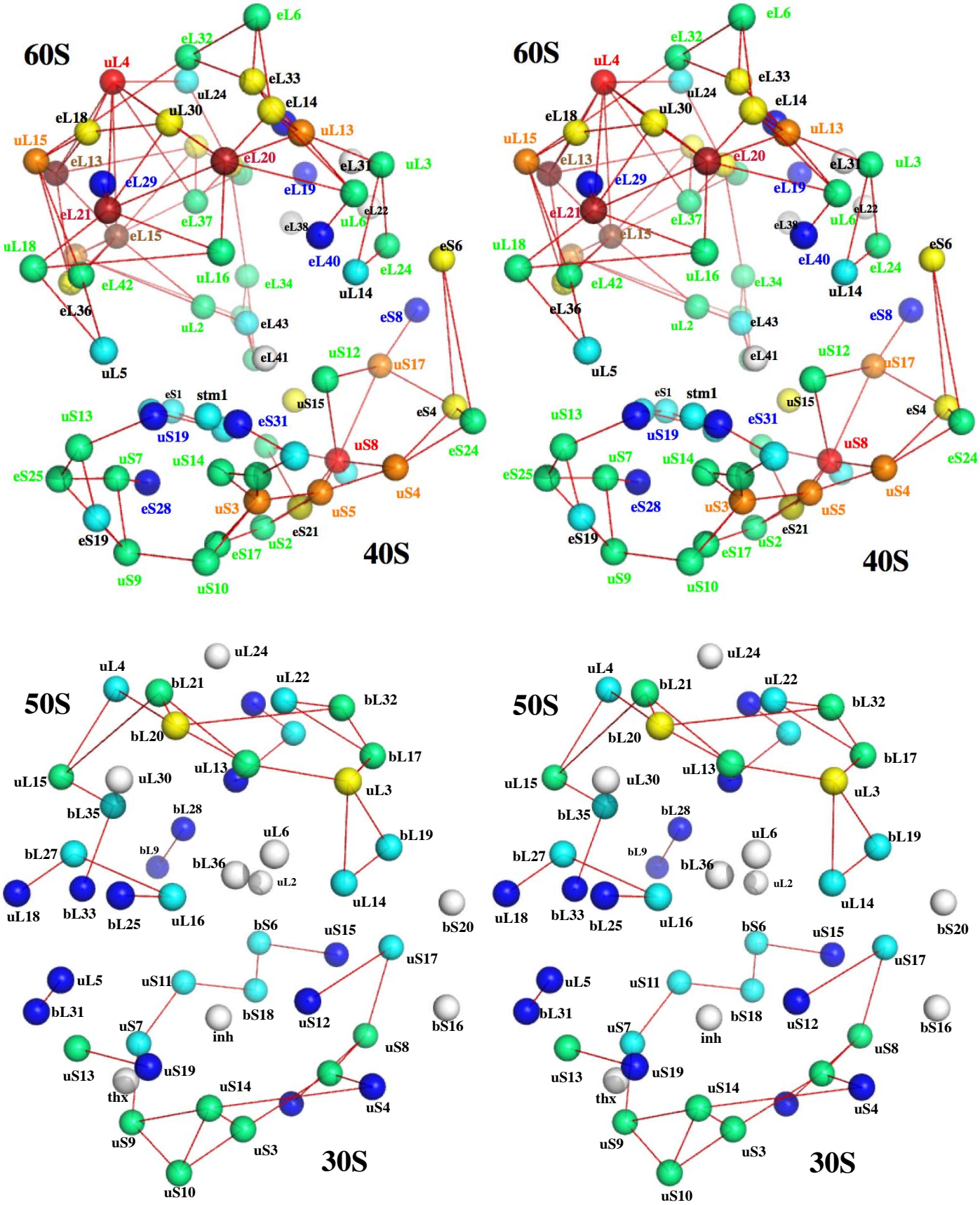
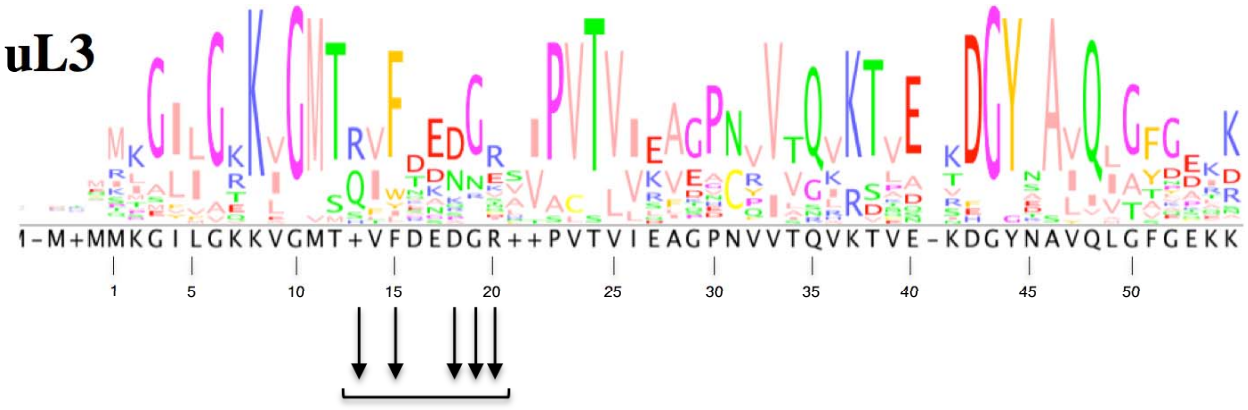
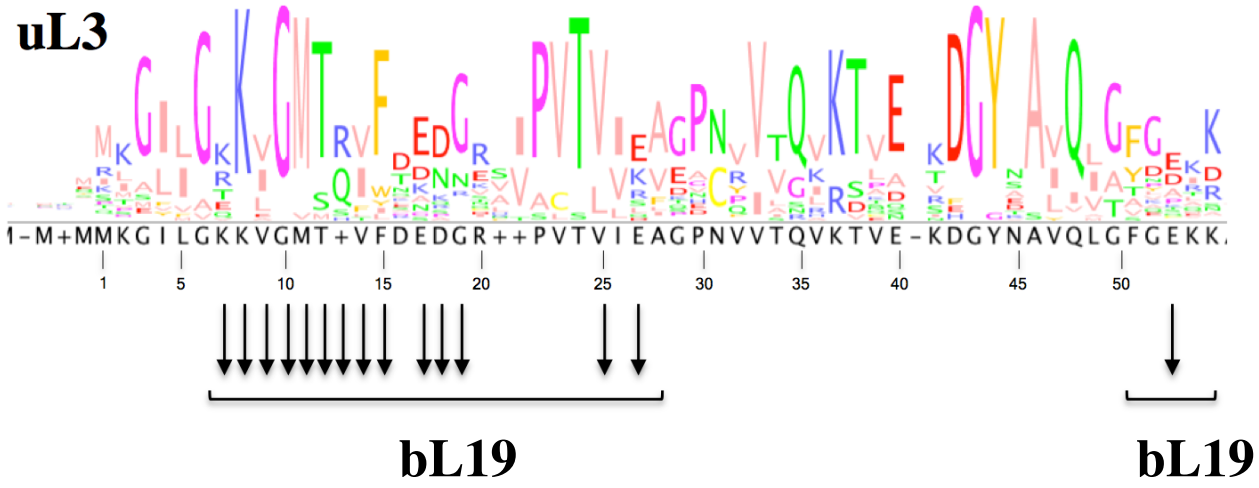


Figure S4: stereo views of the ribosomal protein interaction networks
(up) eukarya (pdb_id: 4v88) (down) eubacteria (pdb_id: 4v8i).The coloured spheres correspond to the centre of mass of the ribosomal proteins. Red lines indicate their connection within the ribosome structures. The proteins are coloured in function of their number of interacting partners following the same colour codes as in Figure 2 (main text).





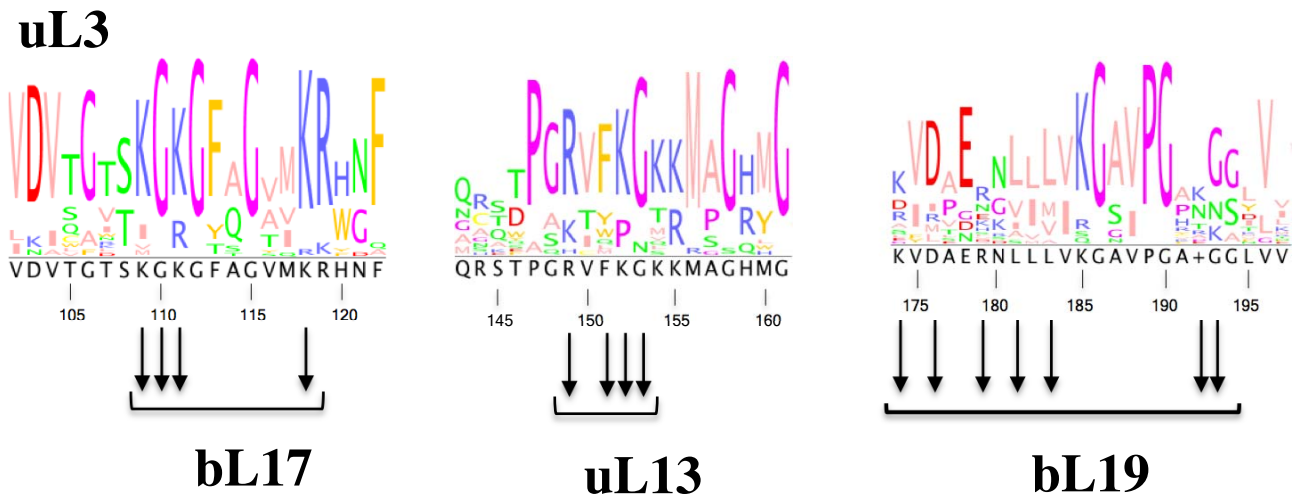
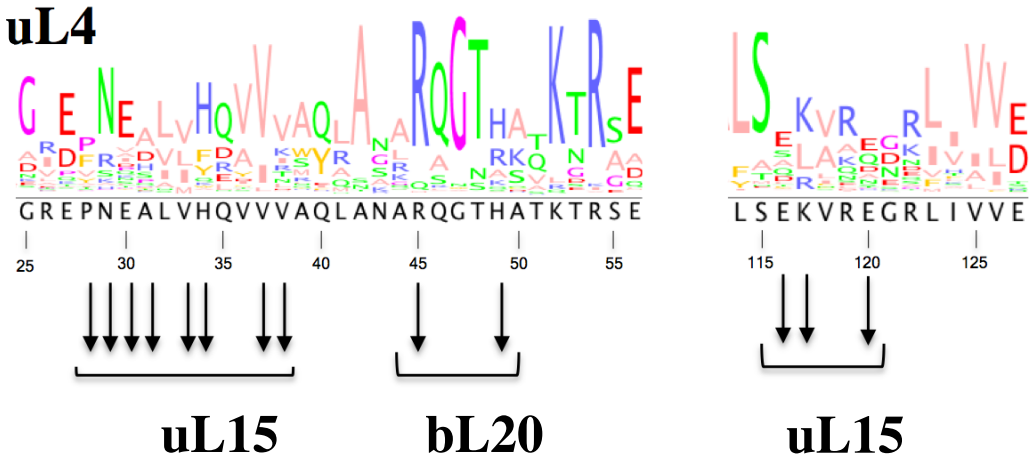
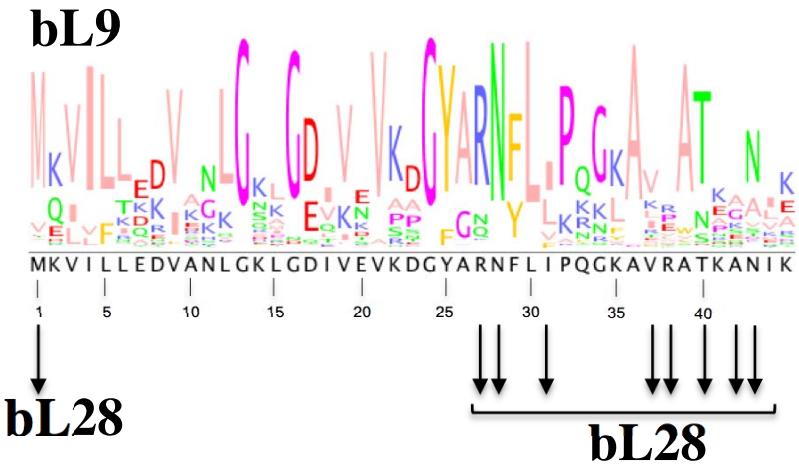


Figure S5: amino acids conservation at the protein interfaces





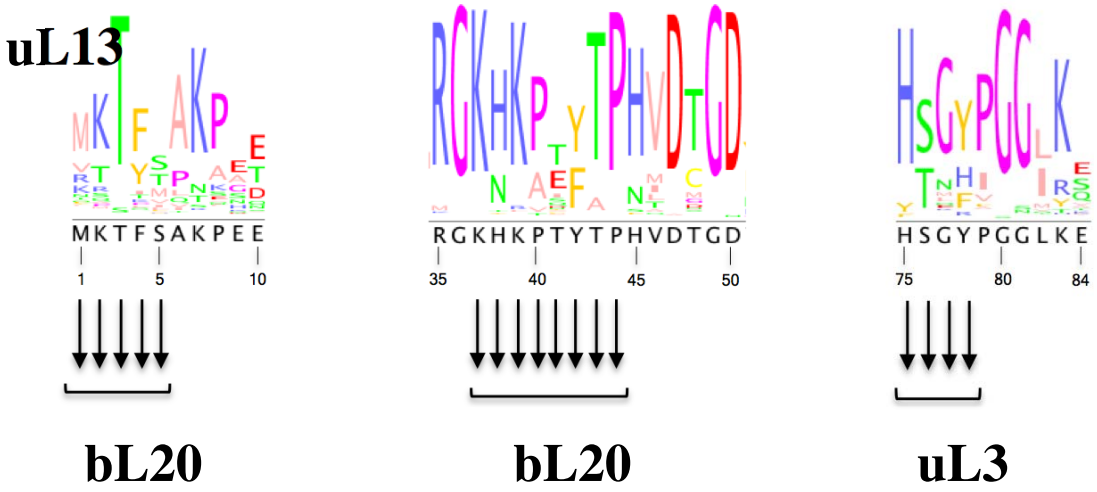
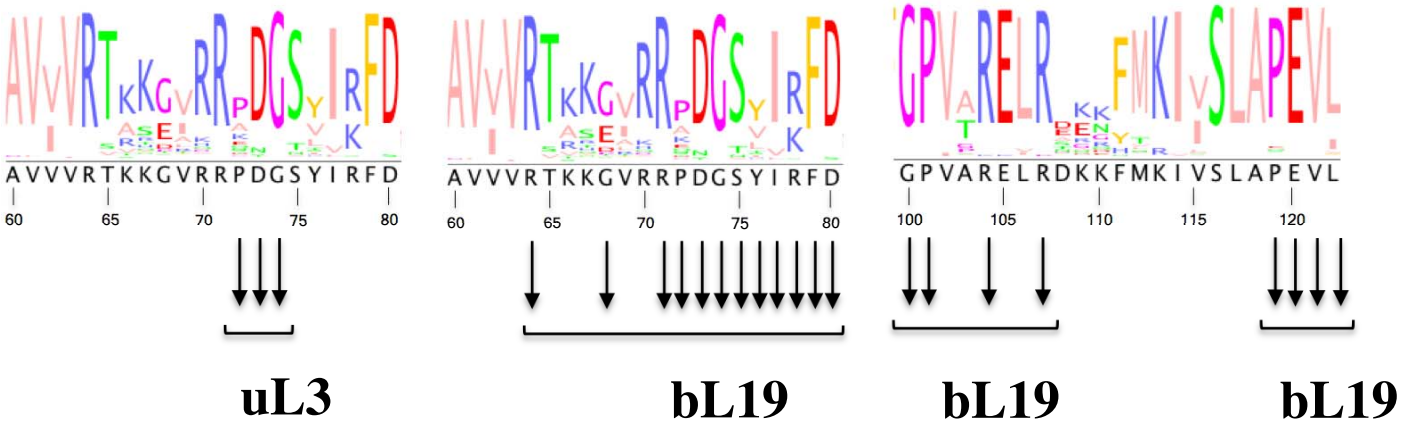


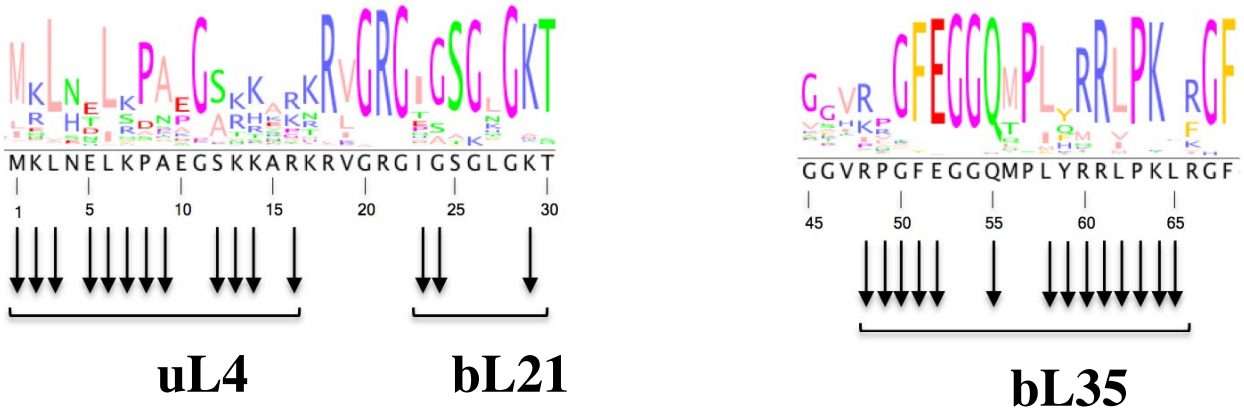
Figure S5 (continued)

uL14



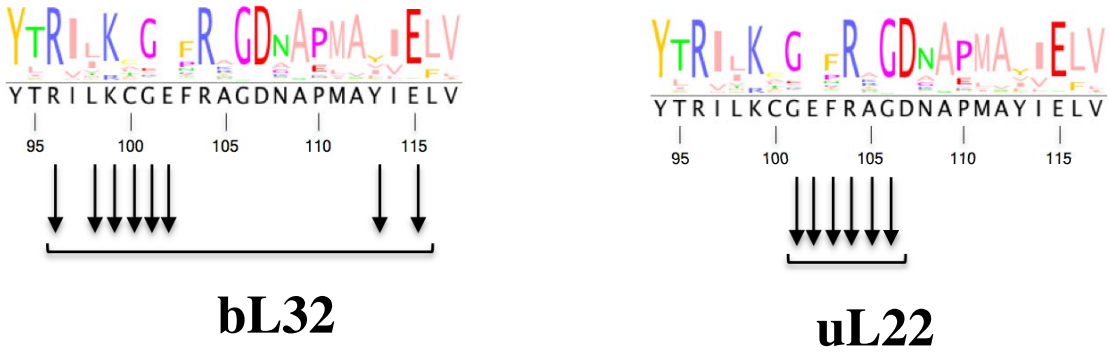
uL3 bL19 bL19 bL19

uL15



uL4 bL21 bL35

bL17



bL32 uL22

Figure S5 (continued)

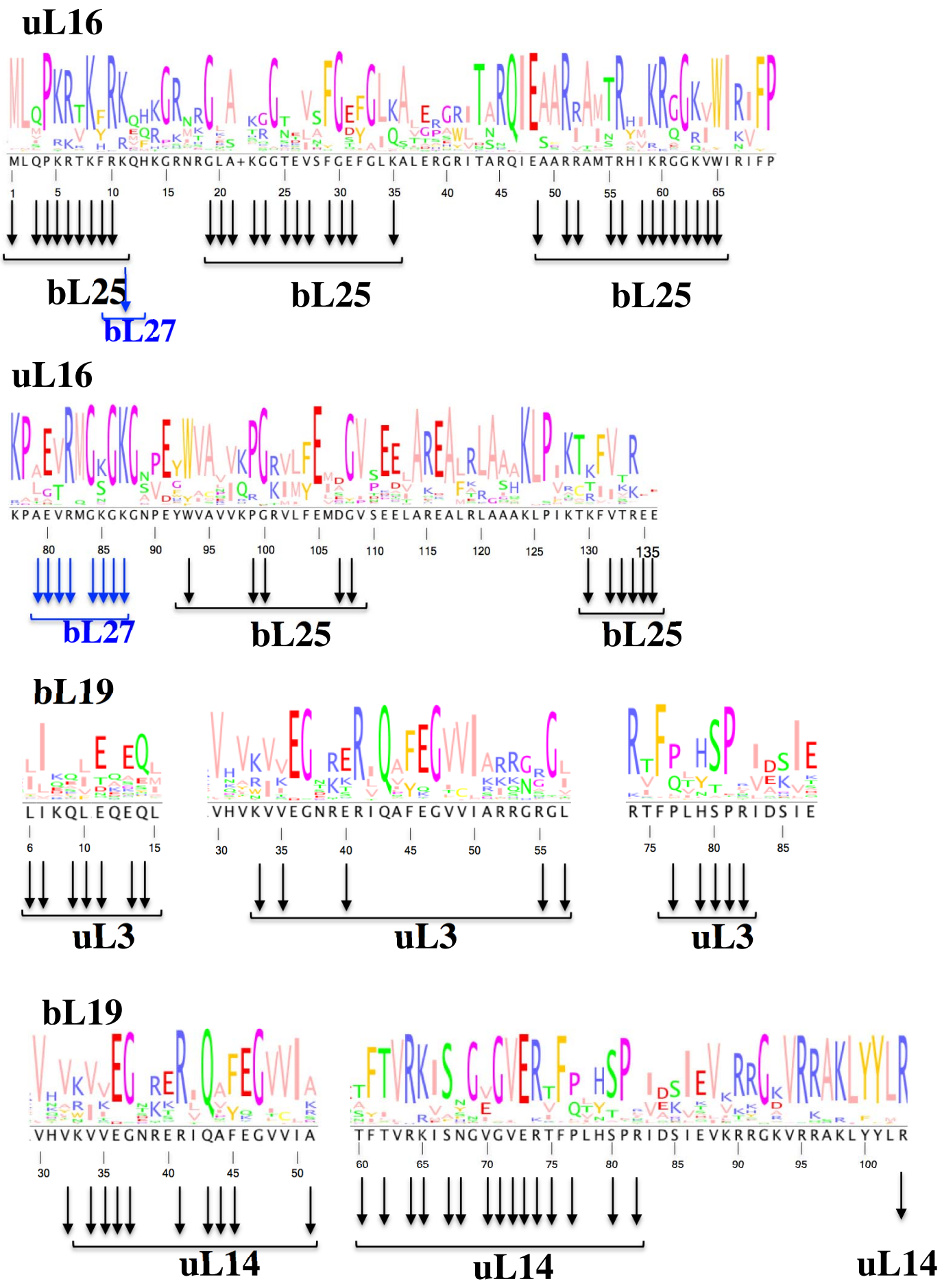
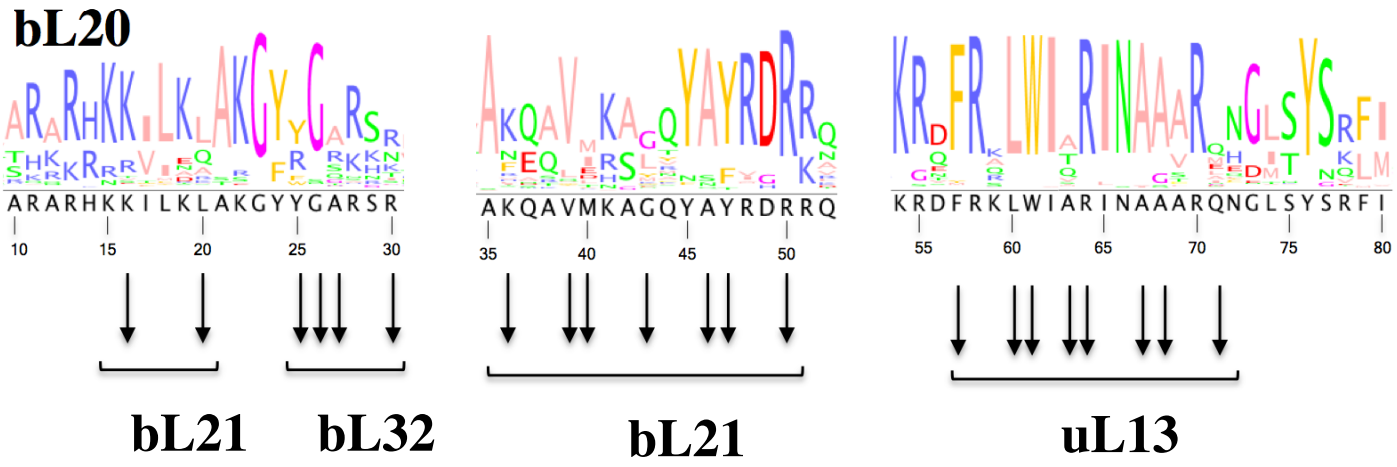
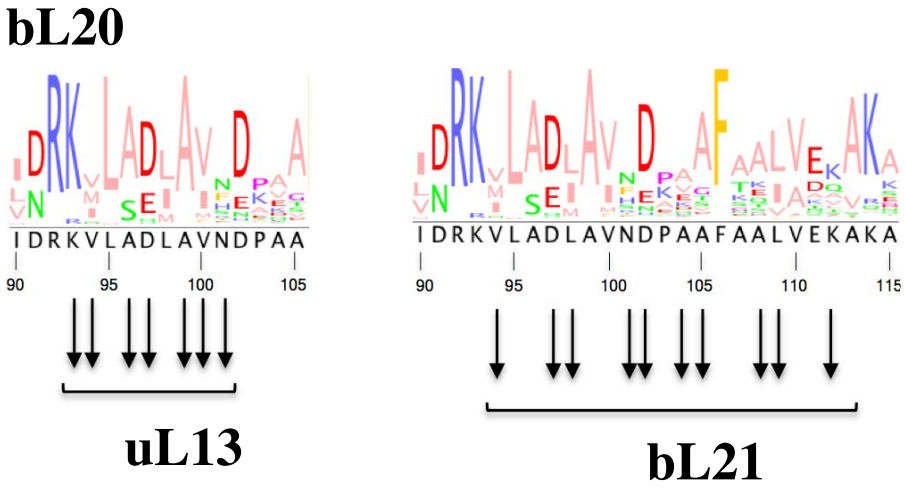


Figure S5 (continued)





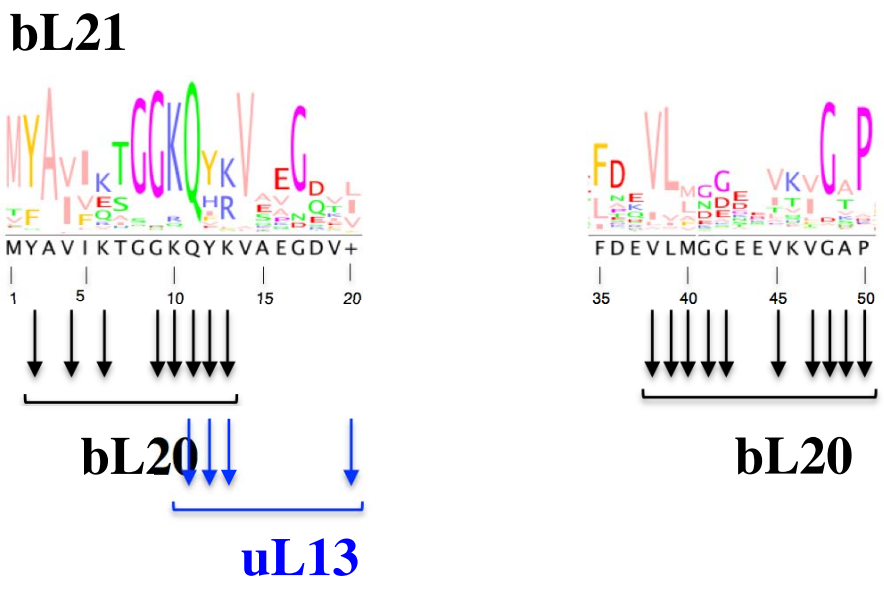
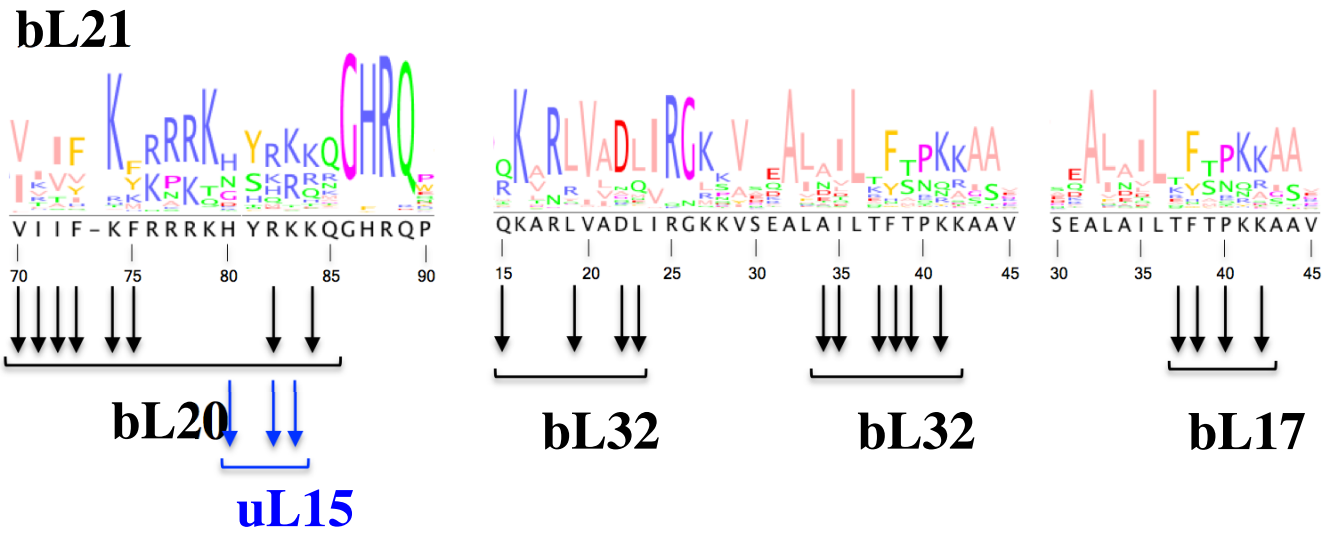
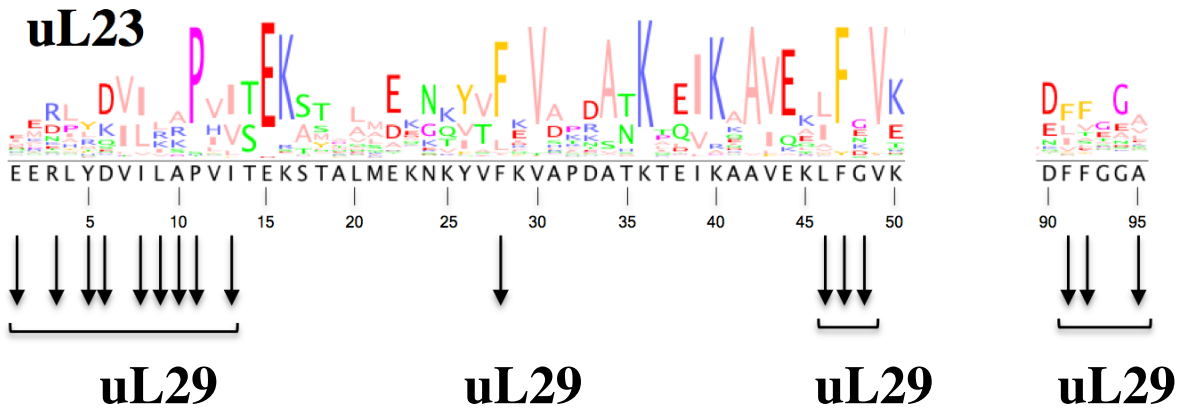


Figure S5 (continued)





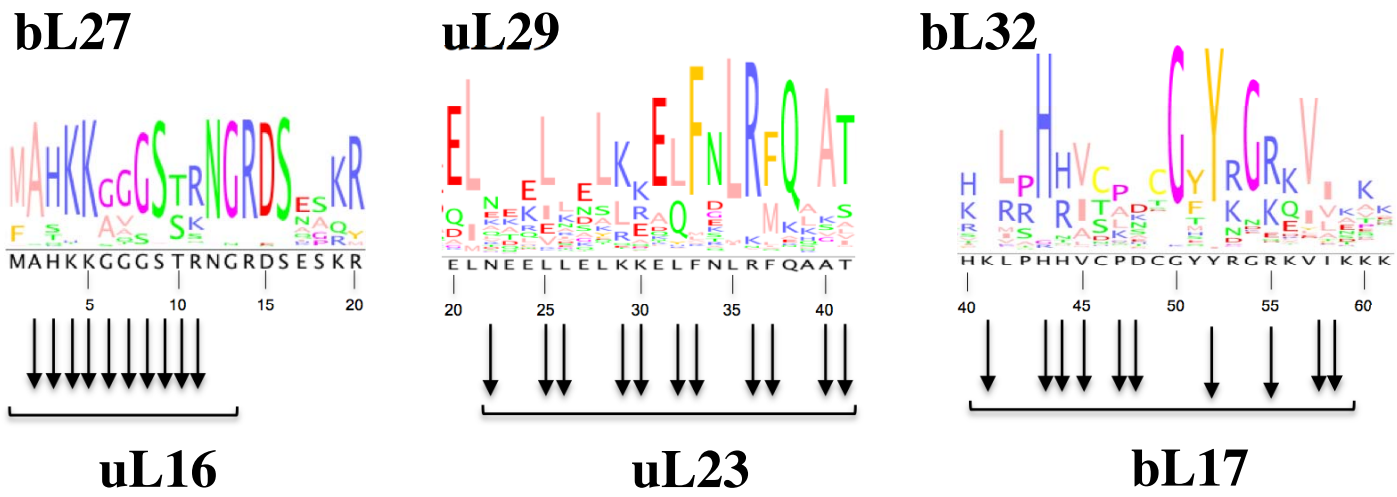


Figure S5 (continued)

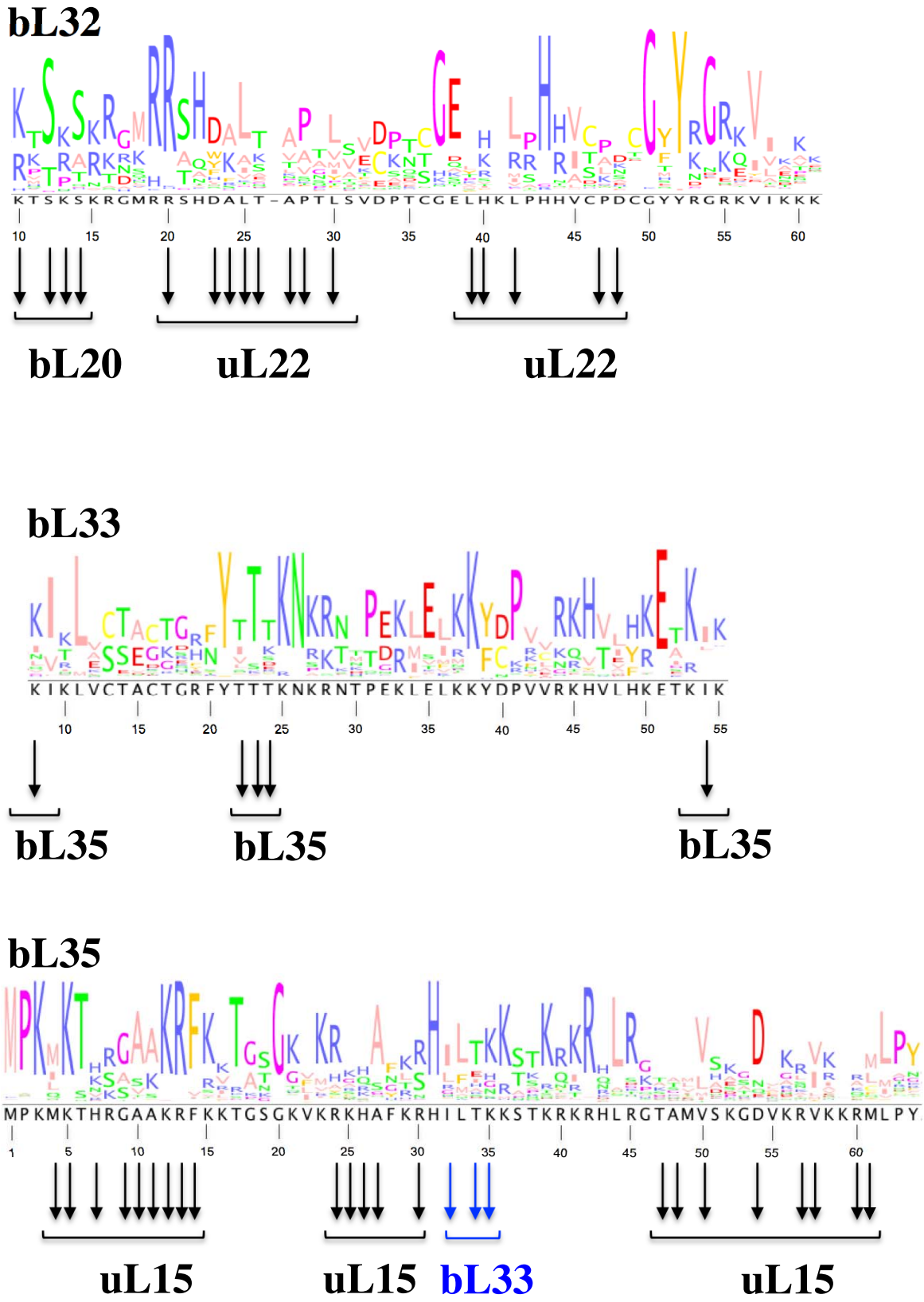
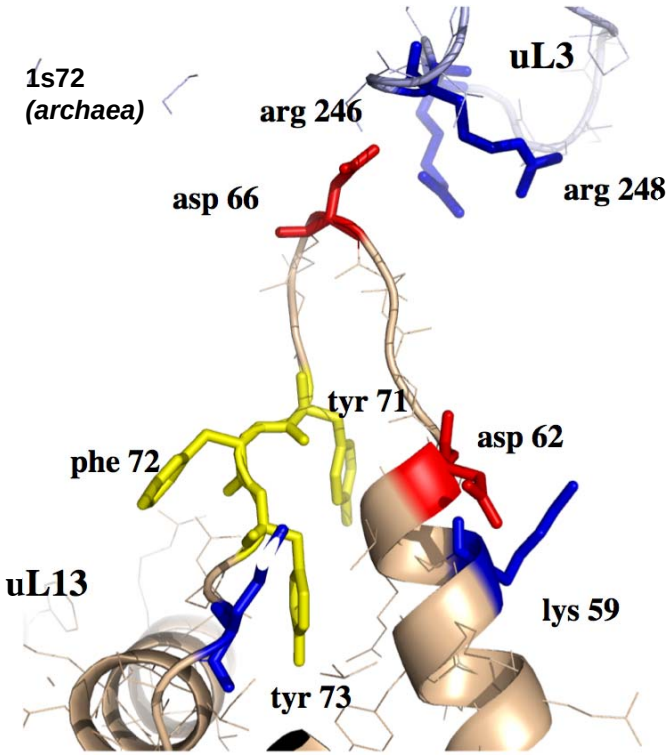


Figure S5: sequence conservation in the protein contact regions of ribosomal proteins of the 50S eubacterial subunit. The logo of the consensus sequences have been generated with *jalview* using the aligned eubacterial ribosomal protein sequences provided by U. Wolf and N. Yutin (see reference 15 and Supplementary Table S12). The arrows indicate the residues in contact with another protein.

a



b

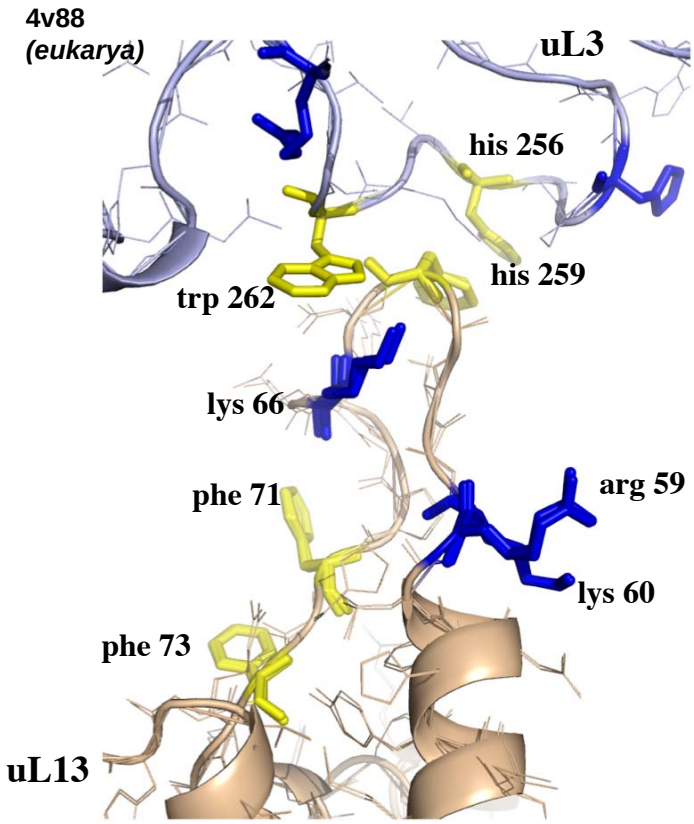


Figure S6: universal uL13-uL3 interaction
a: archaea (in which the cation-π interaction is replaced by a ionic one) and b: eukarya. Equivalent key residues are represented by coloured sticks.

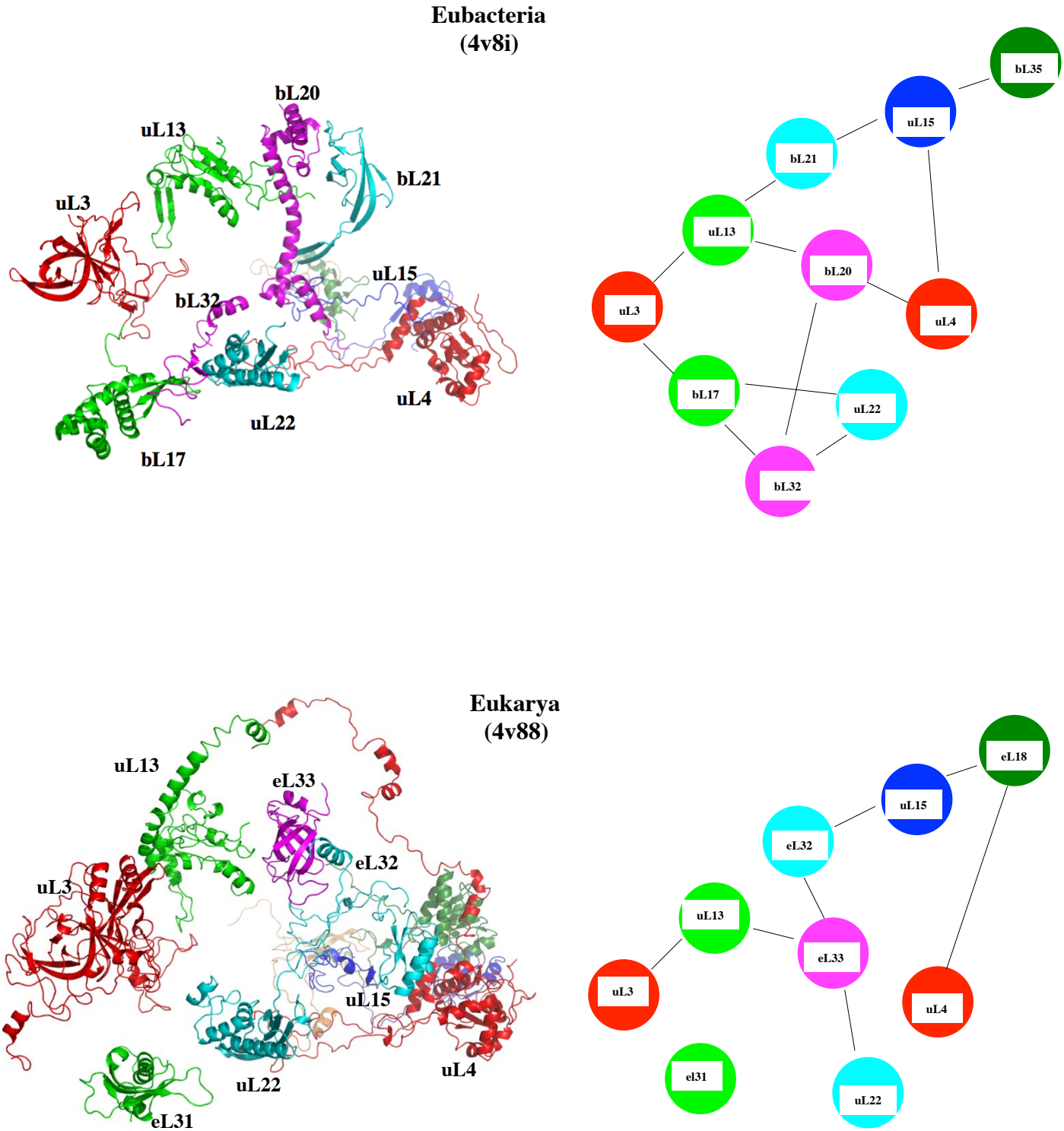


Figure S7: homologies and analogies in protein circuits
(up) 50S (pdb_id: 4v8i); (down) 60S (pdb_id: 4v88).
Equivalent protein are represented with the same colour.

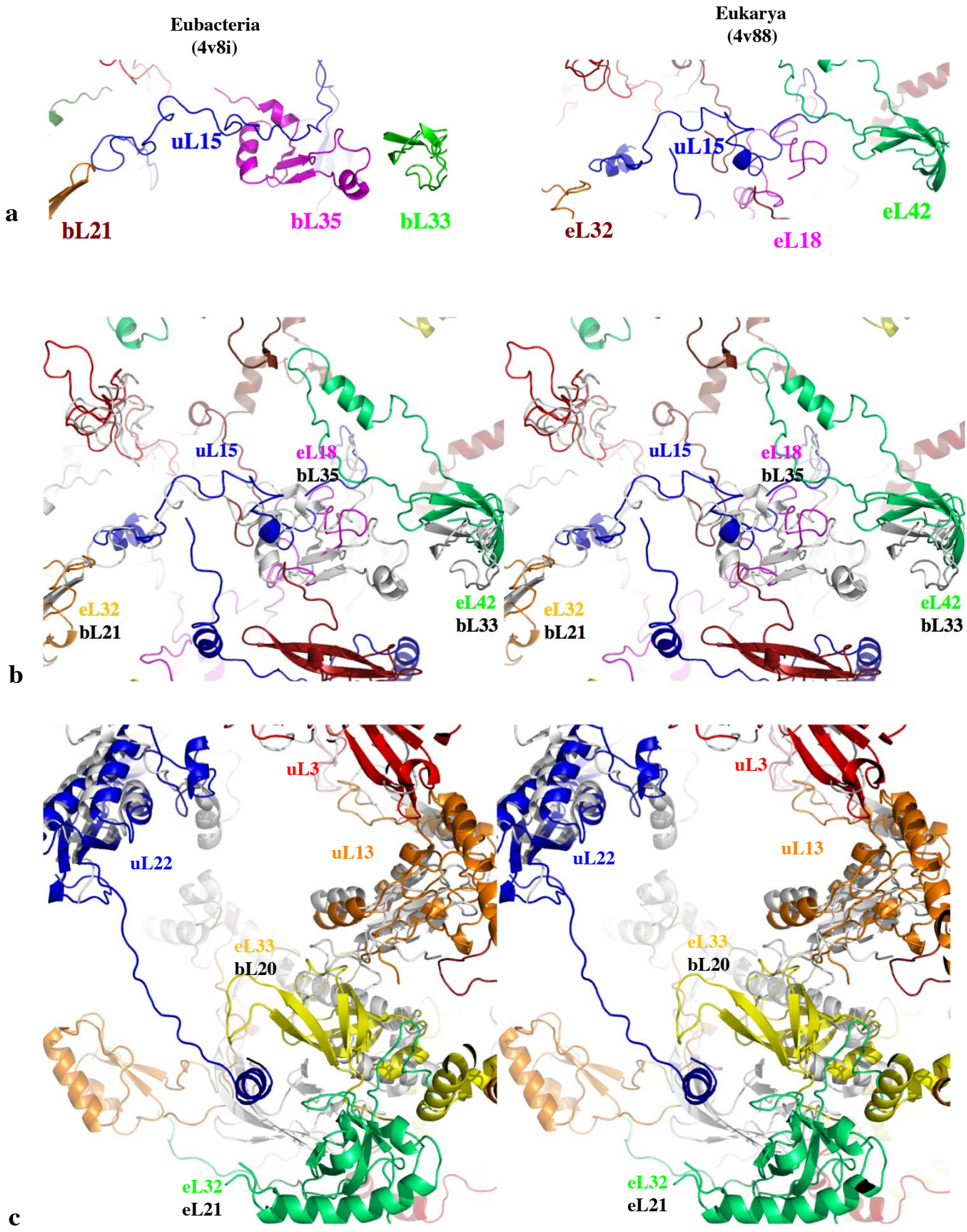


Figure S8: equivalent and alternative pathways in networks of the 50S and 60S subunits
a: Eubacterial (pdb_id: 4v8i) and eukaryotic (pdb_id: 4v88) circuits connecting the E-site
b: Stereo views of the superimposition of the equivalent proteins around the E-sites
c: Stereo views of the superimposition of the equivalent proteins around the exit tunnel
The bacterial proteins are represented in grey and the eukaryotic protein are coloured.

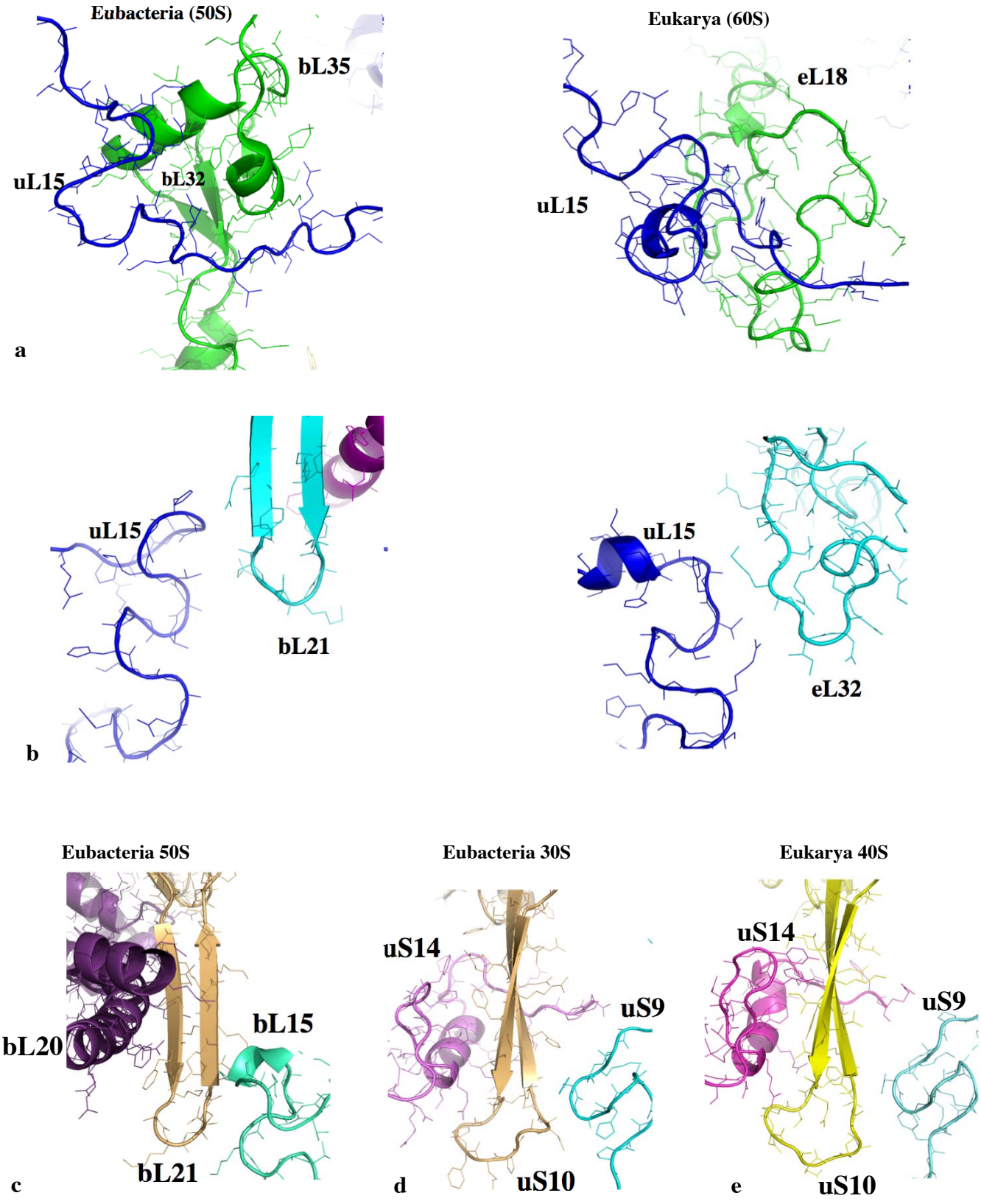


Figure S9 :recurrent interacting motifs in ribosomal subunits across the evolution
a: Comparison of uL15 - bL35 interaction in bacteria (pdb_id: 4v8i) and eukarya (pdb_id: 4v88).
b: Comparison of uL15 - bL21 interaction in bacteria (pdb_id: 4v8i) and eukarya (pdb_id: 4v88).
Recurrent triplet motif formed by a α-helix, a β-hairpin and a locally unstructured chain.
c: bL20-bL21-uL15 in eubacterial 50S subunit (pdb_id: 4v8i)
d: uS14-uS10-uS9 in eubacterial 30S subunit (pdb_id: 4v8i)
e: uS14-uS10-uS9 in eukaryotic 40S subunit (pdb_id: 4v88)

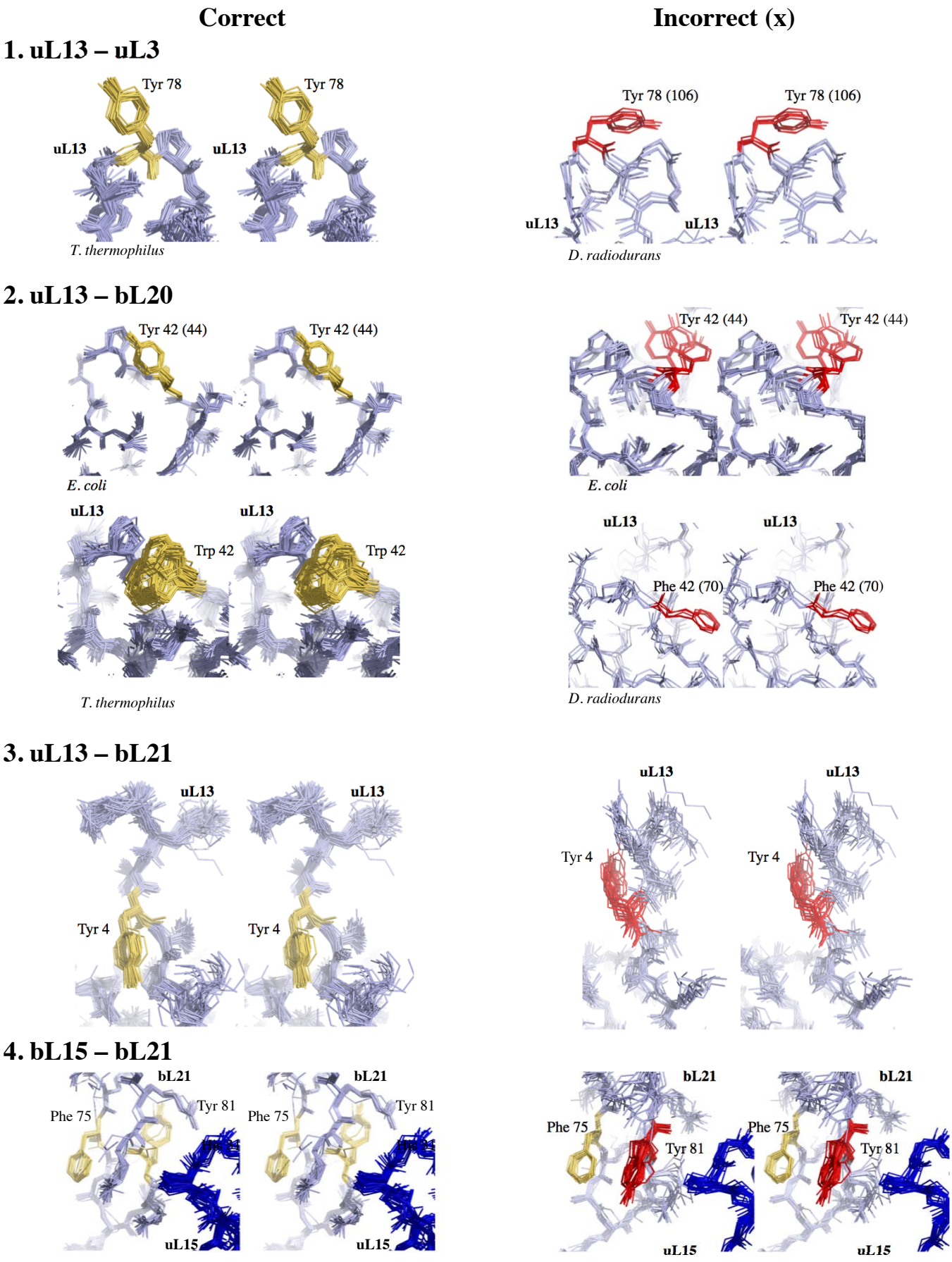
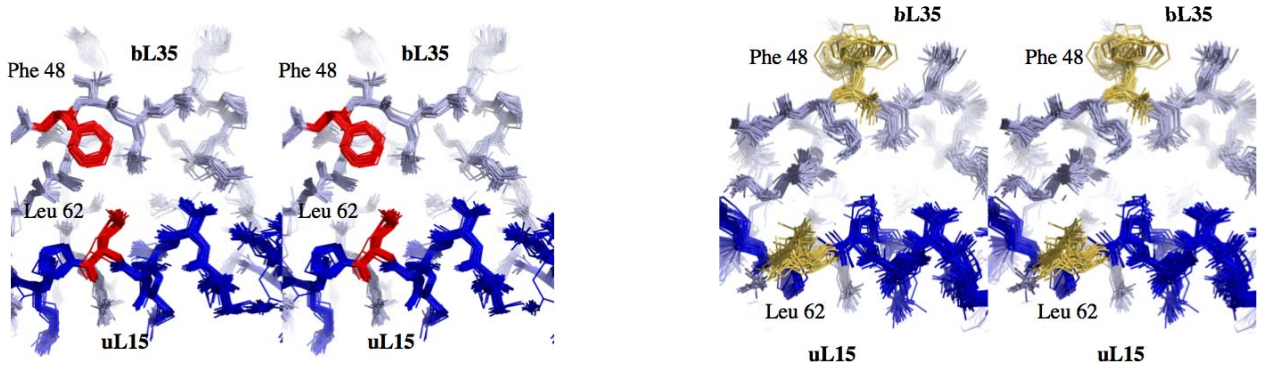


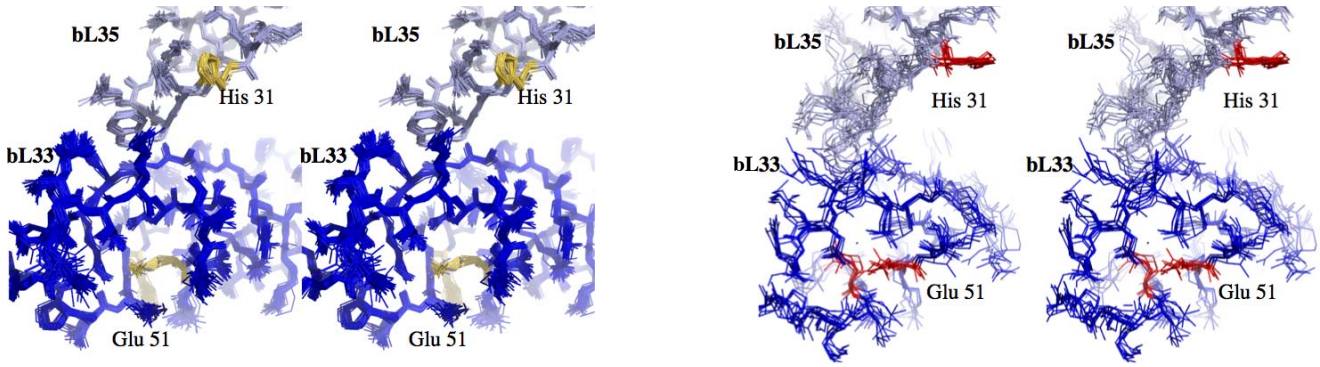
Figure S10: Correct and incorrect (x) models at the protein-protein interfaces of 50S and 70S pdb structures listed in table S15

Correct **Incorrect (x)**

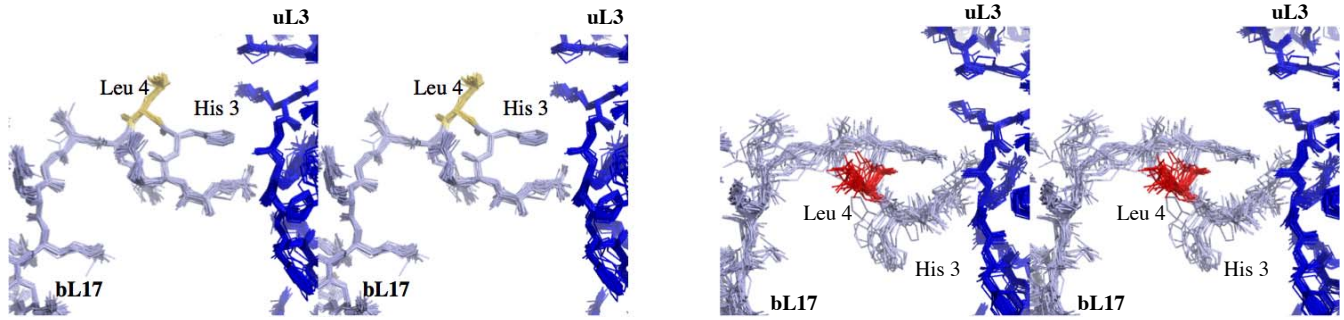
5. uL15-bL35



6. bL35 – bL33



7. uL3 - bL17



8. uL3–uL14

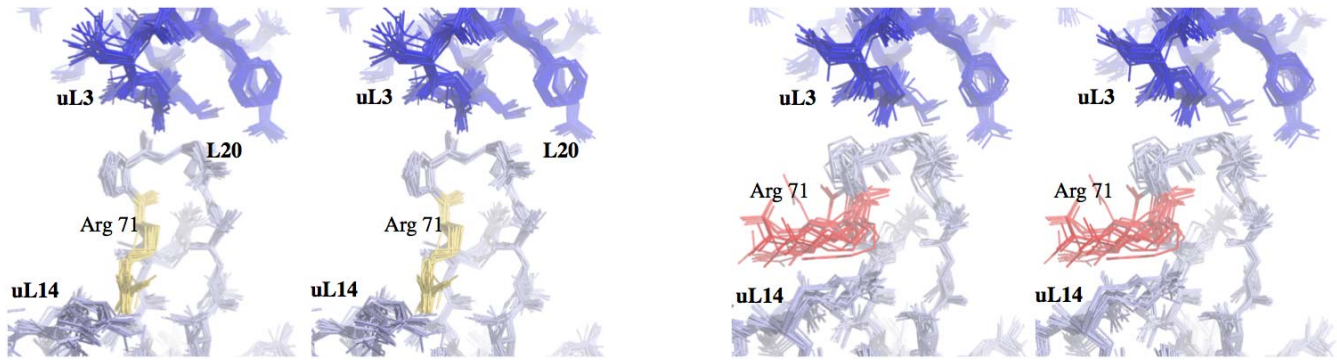
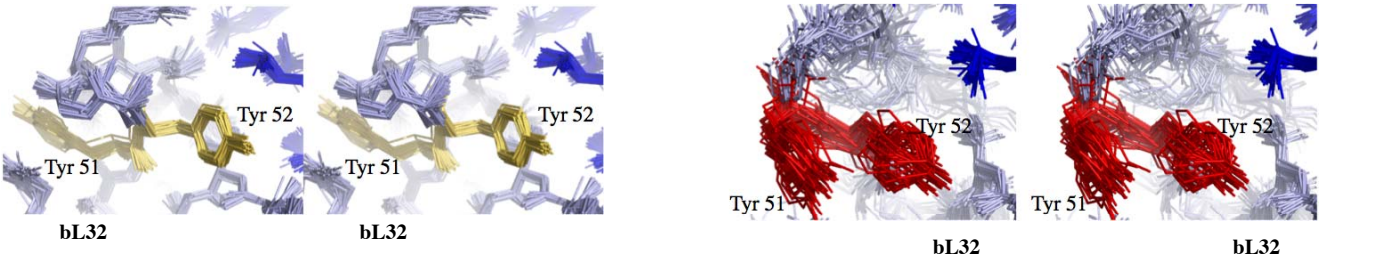


Figure S10: Correct and incorrect (x) models at the protein-protein interfaces of 50S and 70S pdb structures listed in table S15 (continued)

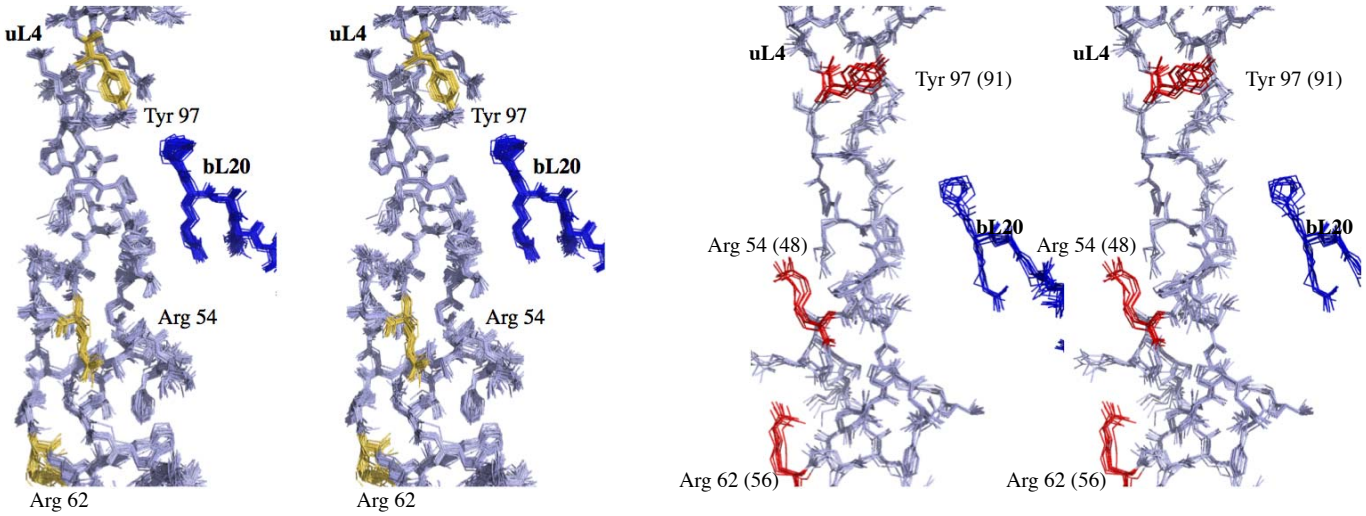
Correct

Incorrect (x)

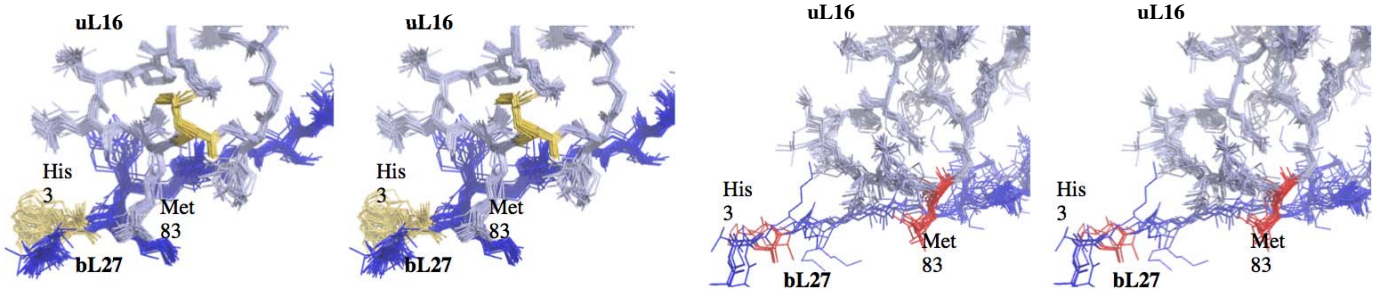
9. bL17 - bL32



10. bL20 - uL4



11. uL16 - bL27



12. uL23 - uL29

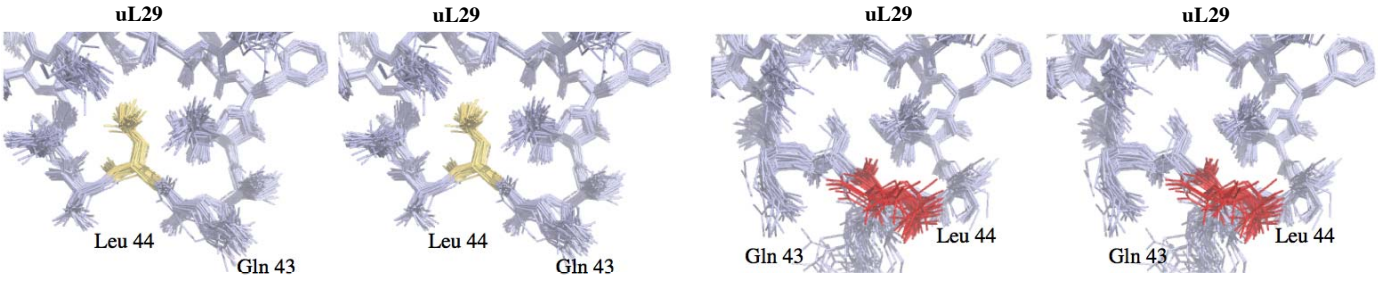


Figure S10: Correct and incorrect (x) models at the protein-protein interfaces of 50S and 70S pdb structures listed in table S15. Our careful inspection of electron density maps of each structure has revealed that except ul15-bL21 (that has been marked "?" in table S15), most of the models "x" are probably the results of a misinterpretation of a not well-resolved electron density map in the region.

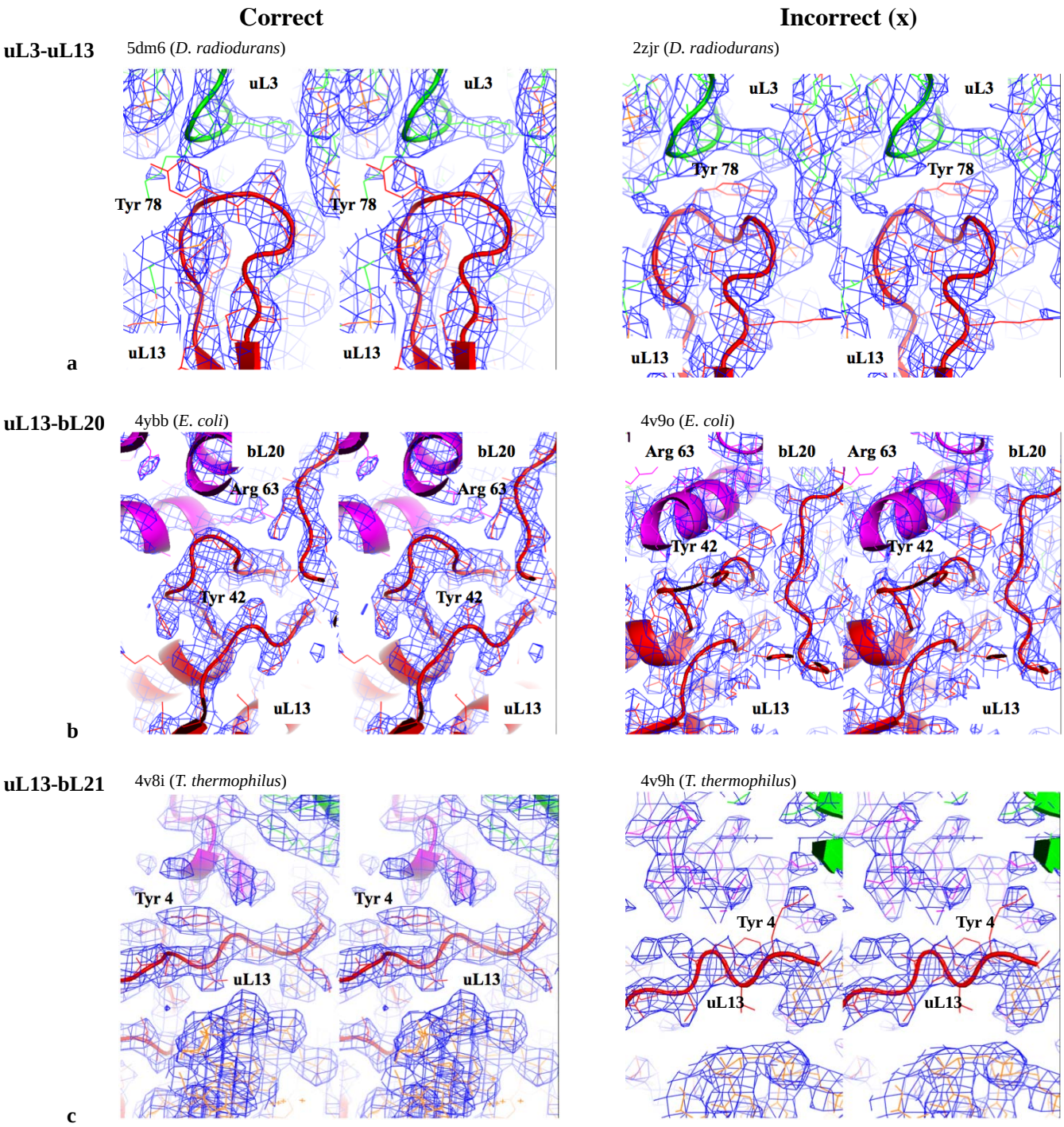


Figure S11: Comparison of the electron density maps of the alternative models at the protein-protein interfaces reported in table S15. Left: correct models; right: incorrect (x) models.

a: uL13-uL3 interface in the *D. radiodurans* 50S subunit
left: correct model (5dm6)
right: incorrect model (2zjr): tyr 106 (uL13) (78 in *T. thermophilus*) has been fitted into the density peak of gln 107 (uL13).
b: uL13-bL20 interface in the 70S *E. coli* 70S ribosome
left: correct model observed in the high resolution *E. coli* 70S ribosome 4ybb
right: incorrect model : in which tyr 42 (uL13) has been fitted into the density peak of arg 63 (bL20).
c: uL13-bL21 interface in the *T. thermophilus* 70S ribosome
left: correct model (4v8i)
right: incorrect model "1" in which tyr 4 (uL13) has been been erroneously fitted into the density of thr 3 (uL13).

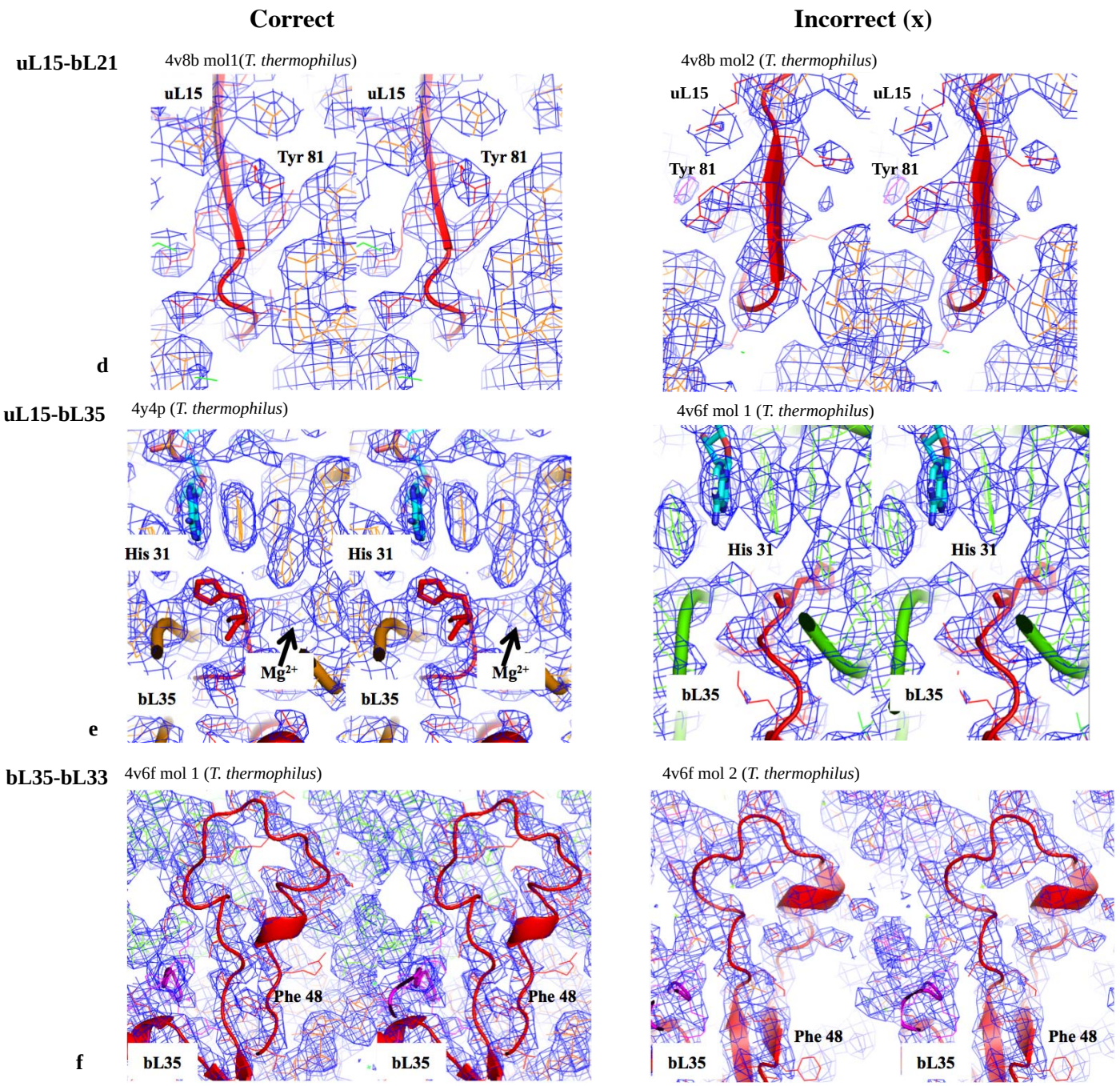


Figure S11 (continued)

d: uL15-bL21 interface in the *T. thermophilus* 70S ribosome

left: correct model observed in the first molecule of the asymmetric unit of 4v8b. The two aromatic residues of bL21 phe 75 and tyr 81 are on the opposite sides of the b-sheet.

right: alternative model "?" observed in the second molecule of the asymmetric unit of 4v8b. The two aromatic residues of bL21 phe 75 and tyr 81 are on the same side of the b-sheet. This alternative structure is compatible with the corresponding electron density map. However this structure only observed in a set of pdb entry marked "?" in table S15.

e: uL33-bL35 interface in the *T. thermophilus* 70S ribosome

left: correct model found in the 2.5 Å resolution 4y4p structure

right: incorrect model found in the molecule 2 of 4v6f structure. His 31 has been fitted into a peak that correspond to a Mg^{2+} ion in the high resolution structure.

f: uL15-bL35 interface in the *T. thermophilus* 70S ribosome (continued)

left: correct model found in the molecule 1 of 4v6f and other high-resolution structures of the *T. thermophilus* 70S ribosome.

right: incorrect model found in the molecule 2 of the 4v6f structure. Lys 47 has been fitted into the density peak of phe 48 that becomes extruded out of density.

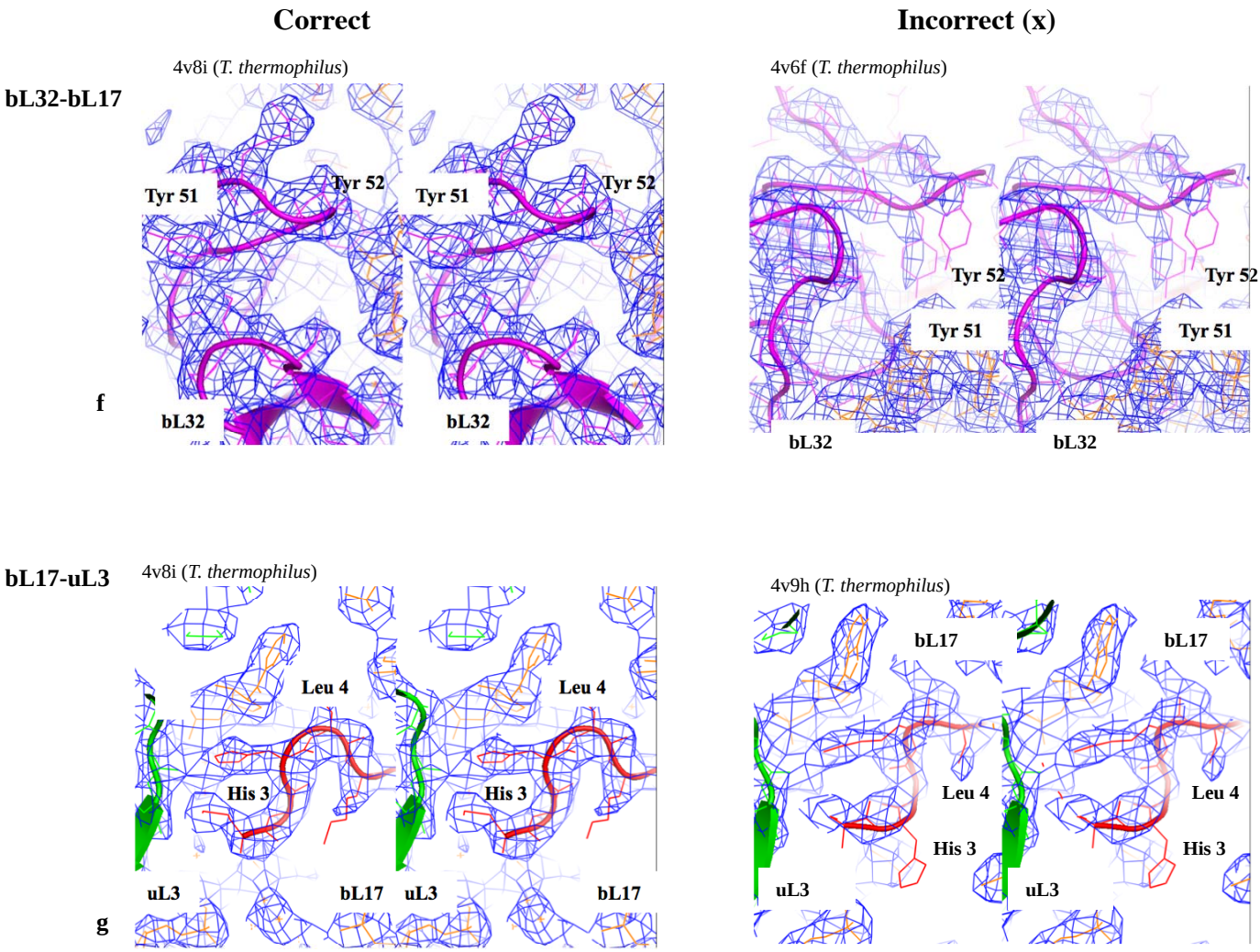


Figure S11 (continued)
g: bL17-bL32 interface in the *T. thermophilus* 70S ribosome
left: correct model found in 4v8i
right: incorrect model found in the structure of 4v6f. The tyrosines 51 and 52 of bL32 have been incorrectly fitted due to an interpretable map in this region.

h: bL17-uL3 interface in the *T. thermophilus* 70S ribosome
left: correct model found in 4v8i and other high-resolution structures of the *T. thermophilus* 70S ribosome.
right: incorrect model found in the structure of 4v9h. His 3 and leu 4 of bL17 have been incorrectly fitted due to an interpretable map in this region.