



wwPDB EM Validation Summary Report ⓘ

Feb 12, 2024 – 09:44 AM EST

PDB ID : 3JBO
EMDB ID : EMD-6452
Title : Cryo-electron microscopy reconstruction of the Plasmodium falciparum 80S ribosome bound to P/E-tRNA
Authors : Sun, M.; Li, W.; Blomqvist, K.; Das, S.; Hashem, Y.; Dvorin, J.D.; Frank, J.
Deposited on : 2015-09-16
Resolution : 5.80 Å (reported)
Based on initial models : 3J7A, 3J79

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

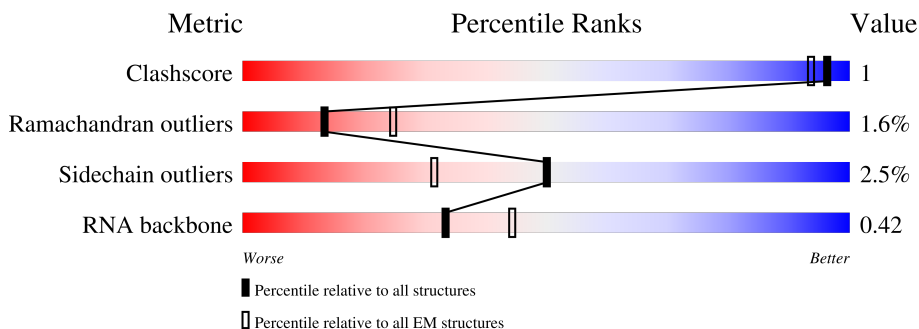
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	1608	32% 45% 20% .
2	7	75	17% 49% 32% .
3	Q	144	86% 12% .
4	S	128	85% 12% .
5	T	48	90% 8% .
6	M	138	90% 9% .
7	U	149	92% 7% ..


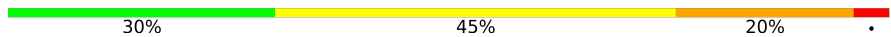
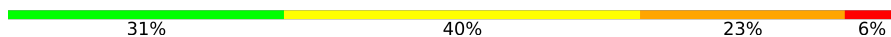


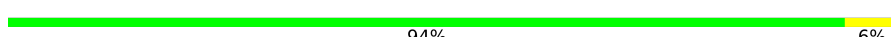




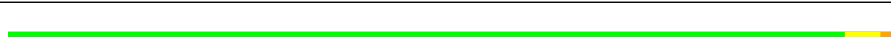


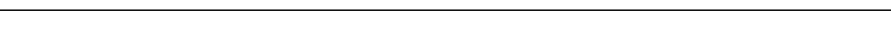
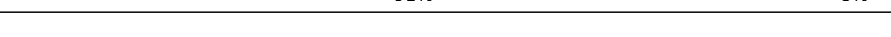
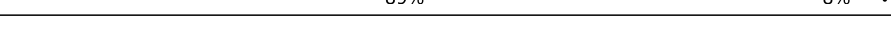

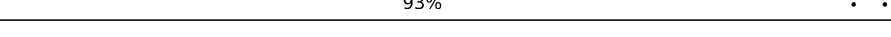

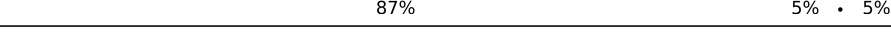

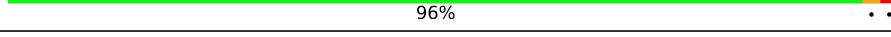

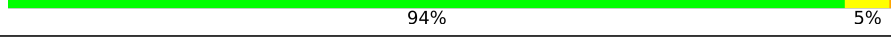
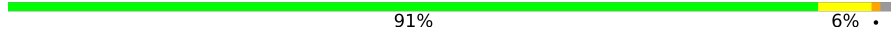
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	V	156	83% 9% 6%
9	E	185	91% 8%
10	X	103	83% 9% 7%
11	G	224	95%
12	W	108	81% 7% 12%
13	R	114	82% 14%
14	I	189	87% 7% 5%
15	O	79	87% 13%
16	Y	154	86% 14%
17	Z	72	97%
18	1	120	88% 12%
19	2	68	54% 6% 40%
20	C	195	95% 5%
21	3	95	87% 12%
22	4	76	92% 7%
23	5	65	77% 12% 11%
24	6	43	86% 9% 5%
25	B	210	93% 5% 2%
26	D	209	70% 25%
27	F	257	92% 6%
28	H	214	88% 7% 5%
29	K	129	90% 9%
30	J	188	91% 9%
31	N	98	97%
32	P	127	89% 9%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
33	L	214	 71% 8% 20%
34	AA	3192	 30% 45% 20% .
35	AC	151	 31% 40% 23% 6%
36	AB	118	 30% 53% 16% .
37	AL	211	 87% 13%
38	A0	62	 94% 6%
39	AO	147	 90% 10% .
40	Ai	95	 88% 8% .
41	A2	118	 81% 8% 12%
42	A4	66	 94% . . .
43	A6	98	 94% . .
44	A7	102	 87% 6% . 6%
45	A1	145	 92% . . .
46	AN	146	 91% 8% .
47	A8	125	 89% 8% .
48	A9	103	 83% 14% . .
49	Aa	106	 93% . .
50	Ab	105	 83% 7% . 10%
51	Ad	76	 87% 5% . 5%
52	Ae	50	 70% 12% . 14%
53	Af	51	 96% . .
54	AP	204	 82% 16% .
55	Ah	85	 94% 5% .
56	AI	213	 91% 6% . .
57	Ac	89	 84% 11% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
58	AK	201	90% 8% .
59	AM	132	95% 5% .
60	AS	186	87% 8% 5%
61	AQ	205	79% 10% . 8%
62	AR	289	79% 6% . 13%
63	AW	170	91% 8% ..
64	AY	101	96% . .
65	AT	181	89% 9% .
66	AZ	121	88% 11% .
67	A3	119	88% 9% ..
68	A5	223	89% 9% .
69	AD	247	89% 9% .
70	AE	380	92% 7% .
71	AF	390	89% 10% .
72	AG	159	68% 9% . 22%
73	AU	180	88% 10% .
74	AH	185	95% . .
75	AV	155	90% 9% .
76	Ag	37	76% 19% 5%
77	AX	97	92% 7% .
78	AJ	244	86% . . 9%

2 Entry composition [i](#)

There are 78 unique types of molecules in this entry. The entry contains 193017 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1608	34207	15346	6106	11169	1586	0	0

- Molecule 2 is a RNA chain called P/E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	7	75	1598	713	290	521	74	0	0

- Molecule 3 is a protein called 40S ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	Q	144	1129	712	222	193	2	0	0

- Molecule 4 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	S	128	1047	657	205	181	4	0	0

- Molecule 5 is a protein called 40S ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	T	48	405	252	85	64	4	0	0

- Molecule 6 is a protein called 40S ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	M	138	1099	704	200	194	1	0	0

- Molecule 7 is a protein called 40S ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	U	149	1202	769	220	210	3	0	0

- Molecule 8 is a protein called 40S ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	V	146	1206	772	227	200	7	0	0

- Molecule 9 is a protein called 40S ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	E	185	1515	962	290	261	2	0	0

- Molecule 10 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	X	96	777	497	137	139	4	0	0

- Molecule 11 is a protein called 40S ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	G	224	1758	1132	307	310	9	0	0

- Molecule 12 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	W	95	786	498	149	136	3	0	0

- Molecule 13 is a protein called 40S ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	R	98	747	474	123	146	4	0	0

- Molecule 14 is a protein called 40S ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	I	180	1424	893	263	258	10	0	0

- Molecule 15 is a protein called 40S ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	O	79	687	450	116	119	2	0	0

- Molecule 16 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	Y	154	1267	811	239	215	2	0	0

- Molecule 17 is a protein called 40S ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	Z	72	557	346	102	105	4	0	0

- Molecule 18 is a protein called 40S ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	1	120	986	632	189	163	2	0	0

- Molecule 19 is a protein called 40S ribosomal protein eS25.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
19	2	41	321	208	56	57	0	0

- Molecule 20 is a protein called 40S ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	C	195	1539	990	266	274	9	0	0

- Molecule 21 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	3	95	Total	C	N	O	S	0	0
			782	478	169	129	6		

- Molecule 22 is a protein called 40S ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	4	76	Total	C	N	O	S	0	0
			586	368	102	107	9		

- Molecule 23 is a protein called 40S ribosomal protein eS28.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	5	58	Total	C	N	O	0	0
			458	285	93	80		

- Molecule 24 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	6	43	Total	C	N	O	0	0
			346	213	75	58		

- Molecule 25 is a protein called 40S ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B	210	Total	C	N	O	S	0	0
			1714	1097	301	304	12		

- Molecule 26 is a protein called 40S ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D	157	Total	C	N	O	S	0	0
			1229	782	225	215	7		

- Molecule 27 is a protein called 40S ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	257	Total	C	N	O	S	0	0
			2062	1320	377	357	8		

- Molecule 28 is a protein called 40S ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	H	204	1648	1045	313	284	6	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	158	ILE	-	insertion	UNP Q8IDR9
H	195	ASP	GLU	conflict	UNP Q8IDR9

- Molecule 29 is a protein called 40S ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	K	129	1037	665	189	178	5	0	0

- Molecule 30 is a protein called 40S ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	J	188	1529	982	264	279	4	0	0

- Molecule 31 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	N	98	772	484	135	148	5	0	0

- Molecule 32 is a protein called 40S ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	P	127	954	591	184	176	3	0	0

- Molecule 33 is a protein called 40S ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	L	171	1383	872	264	243	4	0	0

- Molecule 34 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
34	AA	3192	67862	30436	12049	22217	3160	0	0

- Molecule 35 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
35	AC	151	3215	1444	589	1034	148	0	0

- Molecule 36 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
36	AB	118	2522	1128	461	816	117	0	0

- Molecule 37 is a protein called 60S ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	AL	211	1757	1116	346	291	4	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AL	19	HIS	ARG	conflict	UNP Q8IAX6
AL	20	ARG	HIS	conflict	UNP Q8IAX6
AL	201	CYS	ARG	conflict	UNP Q8IAX6

- Molecule 38 is a protein called 60S ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	A0	62	522	336	97	88	1	0	0

- Molecule 39 is a protein called 60S ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	AO	147	1172	747	232	189	4	0	0

- Molecule 40 is a protein called 60S ribosomal protein eL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ai	95	Total	C	N	O	S	0	0
			779	490	152	128	9		

- Molecule 41 is a protein called 60S ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A2	104	Total	C	N	O	S	0	0
			831	529	151	148	3		

- Molecule 42 is a protein called 60S ribosomal protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	A4	66	Total	C	N	O	S	0	0
			555	347	116	90	2		

- Molecule 43 is a protein called 60S ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	A6	98	Total	C	N	O	S	0	0
			741	462	132	140	7		

- Molecule 44 is a protein called 60S ribosomal protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	A7	96	Total	C	N	O	S	0	0
			794	508	151	130	5		

- Molecule 45 is a protein called 60S ribosomal protein eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	A1	140	Total	C	N	O	S	0	0
			1134	736	204	191	3		

- Molecule 46 is a protein called 60S ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AN	146	Total	C	N	O	S	0	0
			1202	781	210	205	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AN	?	-	LYS	deletion	UNP Q8ILE8

- Molecule 47 is a protein called 60S ribosomal protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	A8	125	1037	660	206	164	7	0	0

- Molecule 48 is a protein called 60S ribosomal protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	A9	103	845	543	163	136	3	0	0

- Molecule 49 is a protein called 60S ribosomal protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	Aa	106	859	530	184	139	6	0	0

- Molecule 50 is a protein called 60S ribosomal protein eL36.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
50	Ab	95	757	477	150	130	0	0

- Molecule 51 is a protein called 60S ribosomal protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	Ad	72	604	395	107	100	2	0	0

- Molecule 52 is a protein called 60S ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	Ae	43	388	243	92	52	1	0	0

- Molecule 53 is a protein called 60S ribosomal protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Af	51	Total	C	N	O	S	0	0
			414	255	87	67	5		

- Molecule 54 is a protein called 60S ribosomal protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AP	204	Total	C	N	O	S	0	0
			1697	1075	351	267	4		

- Molecule 55 is a protein called 60S ribosomal protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Ah	85	Total	C	N	O	S	0	0
			659	417	127	108	7		

- Molecule 56 is a protein called 60S ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AI	207	Total	C	N	O	S	0	0
			1685	1096	298	286	5		

- Molecule 57 is a protein called 60S ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Ac	89	Total	C	N	O	S	0	0
			710	441	150	114	5		

- Molecule 58 is a protein called 60S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AK	201	Total	C	N	O	S	0	0
			1660	1064	311	277	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AK	109	ALA	TYR	conflict	UNP Q8IJZ7

- Molecule 59 is a protein called 60S ribosomal protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	AM	132	996	631	179	178	8	0	0

- Molecule 60 is a protein called 60S ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	AS	186	1503	958	299	241	5	0	0

- Molecule 61 is a protein called 60S ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	AQ	189	1545	984	291	262	8	0	0

- Molecule 62 is a protein called 60S ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	AR	252	2050	1300	385	359	6	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AR	?	-	LYS	deletion	UNP Q8ILL3

- Molecule 63 is a protein called 60S ribosomal protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	AW	170	1319	824	266	222	7	0	0

- Molecule 64 is a protein called 60S ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	AY	101	797	502	144	145	6	0	0

- Molecule 65 is a protein called 60S ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	AT	181	Total	C	N	O	S	0	0
			1509	952	309	244	4		

- Molecule 66 is a protein called 60S ribosomal protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	AZ	121	Total	C	N	O	S	0	0
			1001	626	206	166	3		

- Molecule 67 is a protein called 60S ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	A3	119	Total	C	N	O	S	0	0
			995	635	194	164	2		

- Molecule 68 is a protein called 60S ribosomal protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	A5	223	Total	C	N	O	S	0	0
			1879	1211	357	306	5		

- Molecule 69 is a protein called 60S ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	AD	247	Total	C	N	O	S	0	0
			1867	1166	374	318	9		

- Molecule 70 is a protein called 60S ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	AE	380	Total	C	N	O	S	0	0
			3062	1948	575	522	17		

- Molecule 71 is a protein called 60S ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	AF	390	Total	C	N	O	S	0	0
			3095	1962	594	528	11		

- Molecule 72 is a protein called 60S ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	AG	124	1011	636	197	172	6	0	0

- Molecule 73 is a protein called 60S ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	AU	180	1497	946	289	255	7	0	0

- Molecule 74 is a protein called 60S ribosomal protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	AH	185	1476	950	264	256	6	0	0

- Molecule 75 is a protein called 60S ribosomal protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	AV	155	1276	814	241	215	6	0	0

- Molecule 76 is a protein called 60S ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	Ag	37	343	210	86	45	2	0	0

- Molecule 77 is a protein called 60S ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	AX	97	825	548	135	140	2	0	0

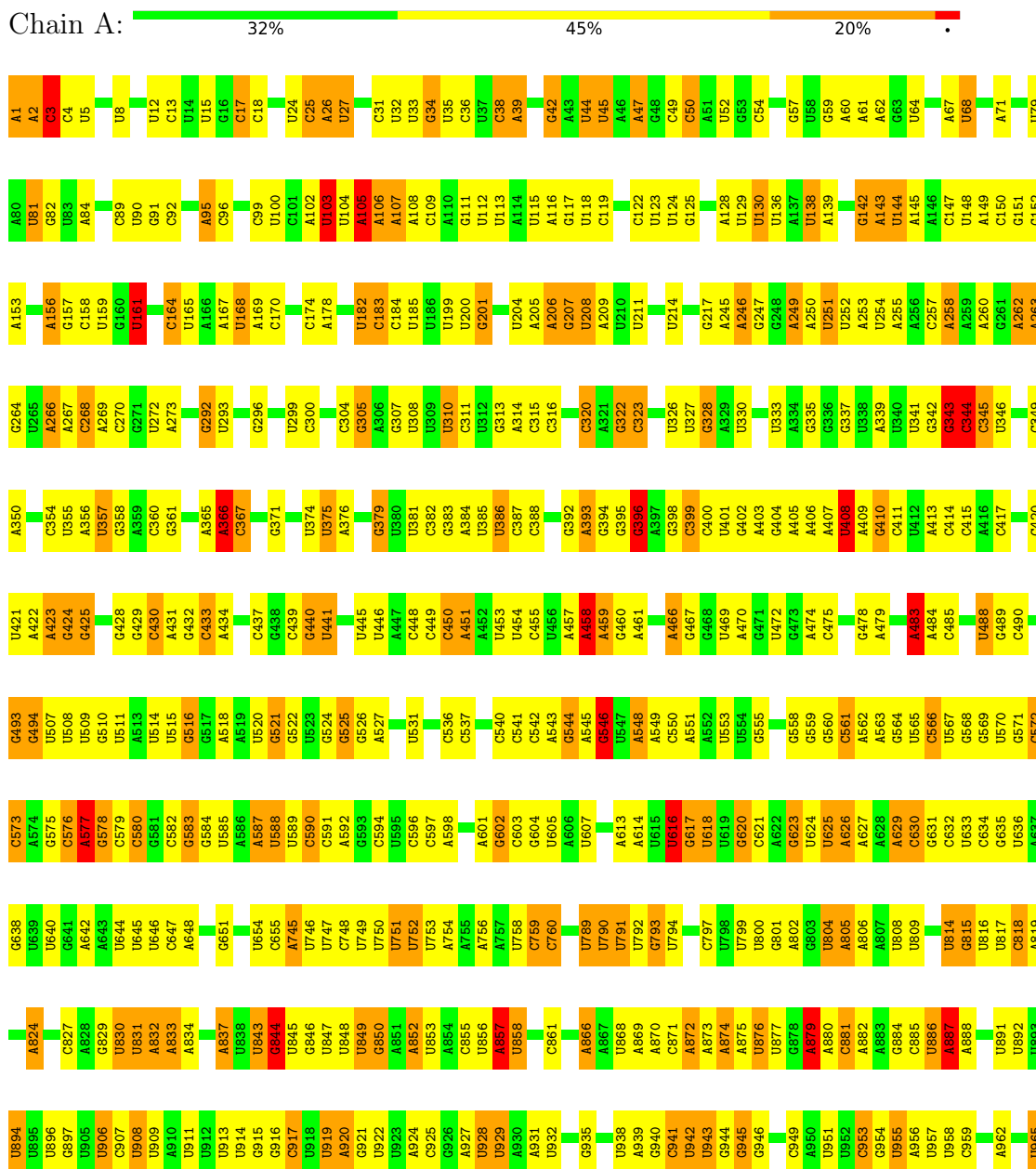
- Molecule 78 is a protein called 60S ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	AJ	222	1813	1174	323	309	7	0	0

3 Residue-property plots [i](#)

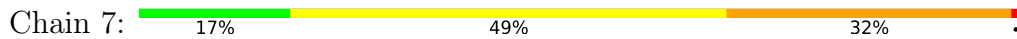
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 18S ribosomal RNA



C966	U1008	U1100	C1206	U1275	A1376	A1450	U1661	A1730	U1829	U1891	U1954	G2052	C2078	U2090
A967	U1029	G1101	U1207	C1278	U1377	G1451	G1664	C1731	C1850	U1892	G1955	U2063	C2079	A35
G968	G1209	C1102	G1208	G1279	C1380	A1452	G1665	A1732	U1831	C1893	G1956	A2053	G2084	A36
A969	C1030	C1103	G1209	G1279	C1380	G1453	G1666	A1733	U1832	C1893	G1959	A2054	G2085	A37
G970	C1031	C1104	G1210	G1280	C1381	A1454	C1667	A1734	U1833	C1894	G1960	A2055	G2086	A38
G971	A1035	A1105	G1211	G1281	C1382	A1455	C1667	A1735	U1834	C1895	G1961	A2056	G2087	A39
U972	A1038	C1106	C1212	U1282	U1383	A1456	A1668	A1741	U1835	C1896	U1961	A2057	U2087	C40
G973	G1041	U1107	G1215	U1283	U1384	A1457	C1669	A1742	G1836	U1897	U1962	A2058	U2087	C41
A974	G1041	A1108	G1215	U1284	U1385	G1458	C1670	U1745	G1837	U1898	G1964	G2059	U2087	C42
A975	G1041	A1109	U1219	A1285	A1388	A1460	C1672	U1746	G1838	U1900	U1965	G2060	G2089	C43
A976	G1044	G1110	G1220	U1287	U1389	A1461	G1673	U1747	U1839	U1901	U1966	U2061	G2090	C44
U977	G1044	U1111	G1221	U1288	U1390	A1462	G1674	U1748	U1840	G1902	U1967	U2062	G2091	C45
U978	U1061	G1112	G1222	G1289	U1391	C1463	U1676	C1749	A1842	U1903	G1972	C2064	G2092	C46
C979	U1062	G1116	C1223	A1290	C1392	U1464	U1677	C1781	U1843	U1904	U1973	C2065	G2093	C47
U980	A1063	G1117	C1224	C1291	C1403	A1604	U1678	C1782	U1844	U1905	U1974	A2068	G2094	C48
U981	G1054	U1118	G1225	C1292	U1404	A1605	G1679	U1783	U1845	A1907	G1975	G2069	G2095	C49
A982	G1055	G1119	A1226	C1293	U1405	A1606	U1680	U1783	U1846	A1908	G1976	G1976	G2096	C50
A983	G1056	G1120	G1227	A1294	U1406	U1607	G1681	A1784	A1847	C1909	G1977	G2070	G2097	C51
U984	A1057	G1121	C1228	A1295	G1408	U1608	A1882	C1785	U1848	U1910	C1978	G2071	G2098	C52
U985	G1058	U1122	G1229	C1296	U1407	C1609	U1683	U1786	U1849	U1911	U2004	G2072	U2087	C53
U986	U1059	U1123	G1229	C1297	U1408	C1609	U1684	U1787	U1850	A1912	U2005	A2073	U2087	C54
U987	G1060	C1166	G1231	C1298	U1409	C1609	U1685	U1788	C1851	G1913	U2006	A2074	U2087	C55
U988	A1061	C1166	G1231	C1298	U1409	C1609	U1686	U1789	A1852	G1914	U2007	C2075	U2087	C56
C989	A1062	C1169	A1232	G1299	G1411	C1622	C1687	U1790	A1853	C1915	U2008	C2076	U2087	C57
U990	G1063	C1170	A1233	C1300	U1412	U1624	C1687	C1791	U1854	C1916	U2009	C2077	U2087	C58
G991	A1064	U1171	U1236	G1302	U1413	C1625	G1691	C1792	U1855	C1917	U2010	C2078	U2087	C59
A993	G1065	U1172	G1239	A1303	U1414	U1626	A1692	C1793	A1856	C1918	U2011	G2084	U2087	C60
G994	G1066	C1173	A1239	A1304	U1415	U1627	A1693	C1794	U1857	G1919	U2012	G2085	U2087	C61
A995	A1067	A1174	A1240	A1305	U1416	A1628	U1694	G1795	U1858	G1920	C2009	A2086	U2087	C62
C996	U1068	G1175	A1241	A1306	U1417	G1629	C1697	C1796	A1859	C1921	U2010	U2087	U2087	C63
	C1069	U1176	G1242	U1307	U1418	A1630	U1698	C1797	A1860	C1922	G2011	U2087	U2087	C64
C1000	A1070	A1177	G1242	C1308	U1419	G1631	U1699	G1798	U1861	U1923	G2012	U2087	U2087	C65
A1001	G1071	C1178	G1247	A1309	U1420	C1635	G1701	A1799	C1862	U1924	A2013	U2087	U2087	C66
U1002	A1072	C1179	G1249	C1310	U1421	C1636	U1702	A1800	U1863	U1925	A2014	U2087	U2087	C67
C1003	U1073	U1180	C1249	U1311	U1422	A1637	U1703	A1801	U1864	U1926	A2015	U2087	U2087	C68
U1004	A1074	U1181	G1250	A1312	U1423	U1638	G1704	G1802	G1865	A1927	C2018	U2087	U2087	C69
G1005	C1075	A1182	G1251	G1313	U1424	U1639	C1705	G1803	A1866	C1929	C2019	U2087	U2087	C70
C1006	C1076	U1183	G1251	U1314	U1425	G1639	A1706	C1804	A1867	A1930	G2020	U2087	U2087	C71
G1007	G1077	G1184	G1254	U1315	U1426	G1640	C1707	G1809	C1868	C1931	U2021	U2087	U2087	C72
A1008	U1078	A1185	G1255	U1316	U1427	G1641	U1708	U1810	G1869	A1932	A2022	U2087	U2087	C73
A1009	C1079	G1186	G1256	U1317	U1428	G1642	C1709	U1811	A1870	C1933	U2023	U2087	U2087	C74
A1010	G1080	A1187	C1257	A1318	U1429	G1643	C1713	A1812	G1871	G1934	U2024	U2087	U2087	C75
A1011	U1081	A1188	C1257	A1319	U1430	G1644	U1714	U1813	A1872	C1935	C2026	U2087	U2087	C76
A1012	A1082	A1189	C1259	A1320	U1432	C1645	U1715	U1814	A1873	C1936	C2027	U2087	U2087	C77
A1013	U1086	U1190	G1260	C1321	U1433	U1646	U1716	C1815	G1876	C1937	U2028	U2087	U2087	C78
U1014	U1087	C1191	A1261	A1322	U1434	A1647	G1715	U1816	C1877	C1938	A2029	U2087	U2087	C79
U1015	A1088	A1192	C1262	U1362	U1435	A1648	A1717	U1817	C1878	G1939	U2030	U2087	U2087	C80
U1016	U1088	A1193	C1263	U1363	U1436	C1649	C1718	U1818	C1879	U1940	C2031	U2087	U2087	C81
G1017	A1089	A1194	A1264	G1364	U1437	A1650	U1719	U1819	G1881	C1941	U2032	U2087	U2087	C82
U1018	C1090	G1195	G1265	G1365	U1440	C1651	G1720	U1819	G1882	U1944	U2033	U2087	U2087	C83
U1019	C1091	U1196	G1266	A1366	C1441	A1652	A1721	U1820	U1882	C1945	U2034	U2087	U2087	C84
U1020	A1092	U1197	G1267	U1367	C1442	A1653	U1722	A1821	U1883	C1946	A2042	U2087	U2087	C85
A1021	U1093	U1198	G1268	U1368	U1442	G1654	U1723	A1822	A1884	C1947	U2043	U2087	U2087	C86
A1022	A1094	U1199	G1269	U1369	G1443	G1655	U1724	U1823	G1885	U1948	U2044	U2087	U2087	C87
A1023	A1095	U1200	G1270	U1370	G1444	A1656	A1725	A1824	C1886	C1949	A2047	U2087	U2087	C88
A1024	A1096	G1201	G1271	U1371	U1445	A1657	U1726	U1825	U1887	C1950	A2048	U2087	U2087	C89
A1025	C1097	U1204	A1272	U1373	U1446	G1658	U1727	U1826	U1888	U1953	A2049	U2087	U2087	C90
A1026	U1098	U1204	G1273	G1374	U1449	G1659	U1728	U1827	G1889	U1954	G2051	U2087	U2087	C91
C1027	A1099	U1205	C1274	C1375	U1449	U1660	A1729	A1828	A1890	U1955	U2051	U2087	U2087	C92

• Molecule 2: P/E-tRNA



C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16	C17	C18	C19	C20	C21	C22	C23	C24	C25	C26	C27	C28	C29	C30	C31	C32	C33	C34	C35	C36	C37	C38	C39	C40	C41	C42	C43	C44	C45	C46	C47	C48	C49	C50	C51	C52	C53	C54	C55	C56	A59	U60	C61	C62
----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



- Molecule 3: 40S ribosomal protein uS12

Chain Q: 86% 12%



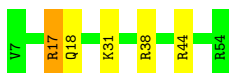
- Molecule 4: 40S ribosomal protein uS13

Chain S: 85% 12%



- Molecule 5: 40S ribosomal protein uS14

Chain T: 90% 8%



- Molecule 6: 40S ribosomal protein uS9

Chain M: 90% 9%



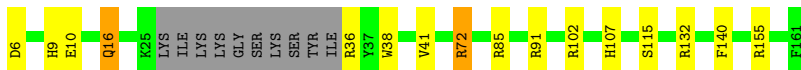
- Molecule 7: 40S ribosomal protein uS15

Chain U: 92% 7%



- Molecule 8: 40S ribosomal protein uS17

Chain V: 83% 9% 6%



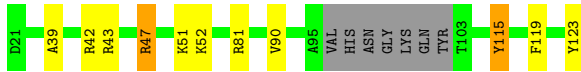
- Molecule 9: 40S ribosomal protein uS4

Chain E: 91% 8%



- Molecule 10: 40S ribosomal protein uS19

Chain X: 83% 9% 7%



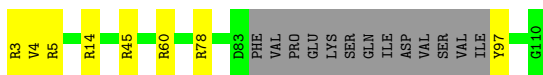
- Molecule 11: 40S ribosomal protein uS5

Chain G: 95%



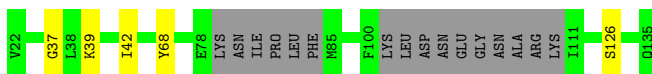
- Molecule 12: 40S ribosomal protein eS17

Chain W: 81% 7% 12%



- Molecule 13: 40S ribosomal protein eS12

Chain R: 82% 14%



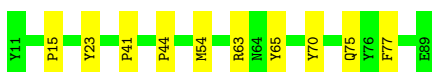
- Molecule 14: 40S ribosomal protein uS7

Chain I: 87% 7% 5%



- Molecule 15: 40S ribosomal protein eS10

Chain O: 87% 13%



- Molecule 16: 40S ribosomal protein eS19

Chain Y: 86% 14%



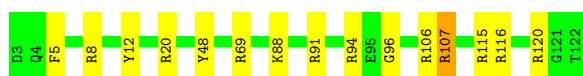
- Molecule 17: 40S ribosomal protein eS21

Chain Z: 97%



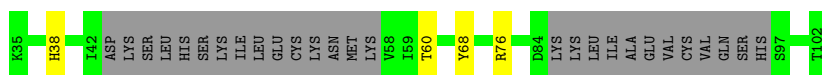
- Molecule 18: 40S ribosomal protein eS24

Chain 1: 88%



- Molecule 19: 40S ribosomal protein eS25

Chain 2: 54%



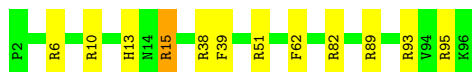
- Molecule 20: 40S ribosomal protein uS2

Chain C: 95%



- Molecule 21: 40S ribosomal protein eS26

Chain 3: 87%



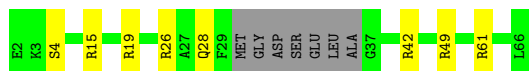
- Molecule 22: 40S ribosomal protein eS27

Chain 4: 92%

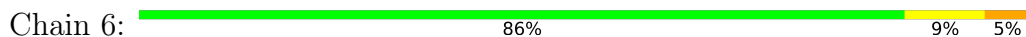


- Molecule 23: 40S ribosomal protein eS28

Chain 5: 77%



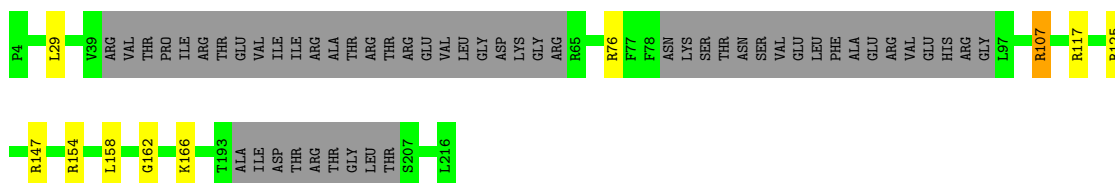
- Molecule 24: 40S ribosomal protein eS30



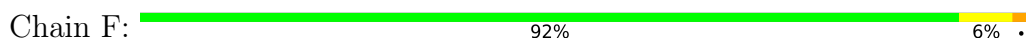
- Molecule 25: 40S ribosomal protein eS1



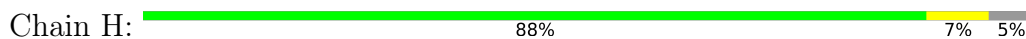
- Molecule 26: 40S ribosomal protein uS3



- Molecule 27: 40S ribosomal protein eS4



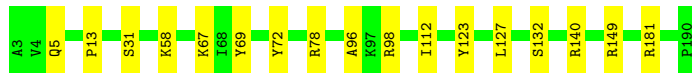
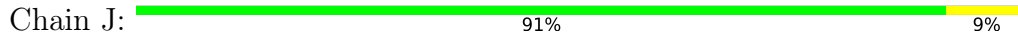
- Molecule 28: 40S ribosomal protein eS6



- Molecule 29: 40S ribosomal protein uS8



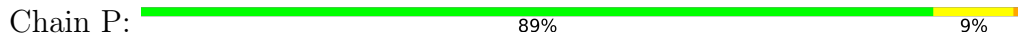
- Molecule 30: 40S ribosomal protein eS7



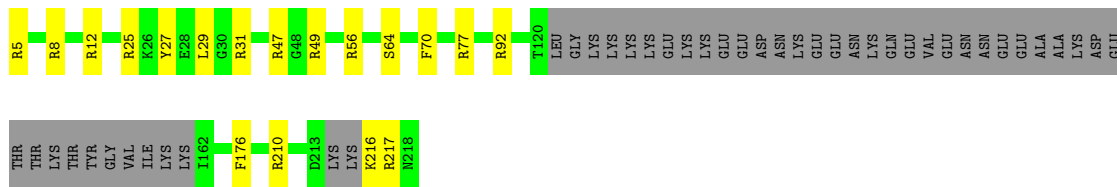
- Molecule 31: 40S ribosomal protein uS10



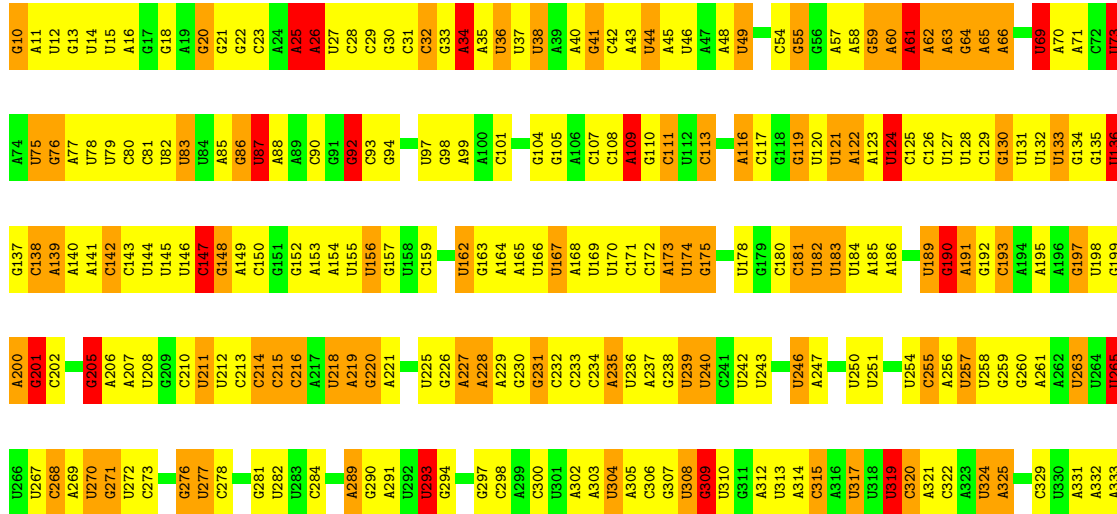
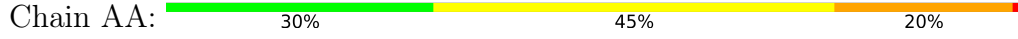
- Molecule 32: 40S ribosomal protein uS11



- Molecule 33: 40S ribosomal protein eS8

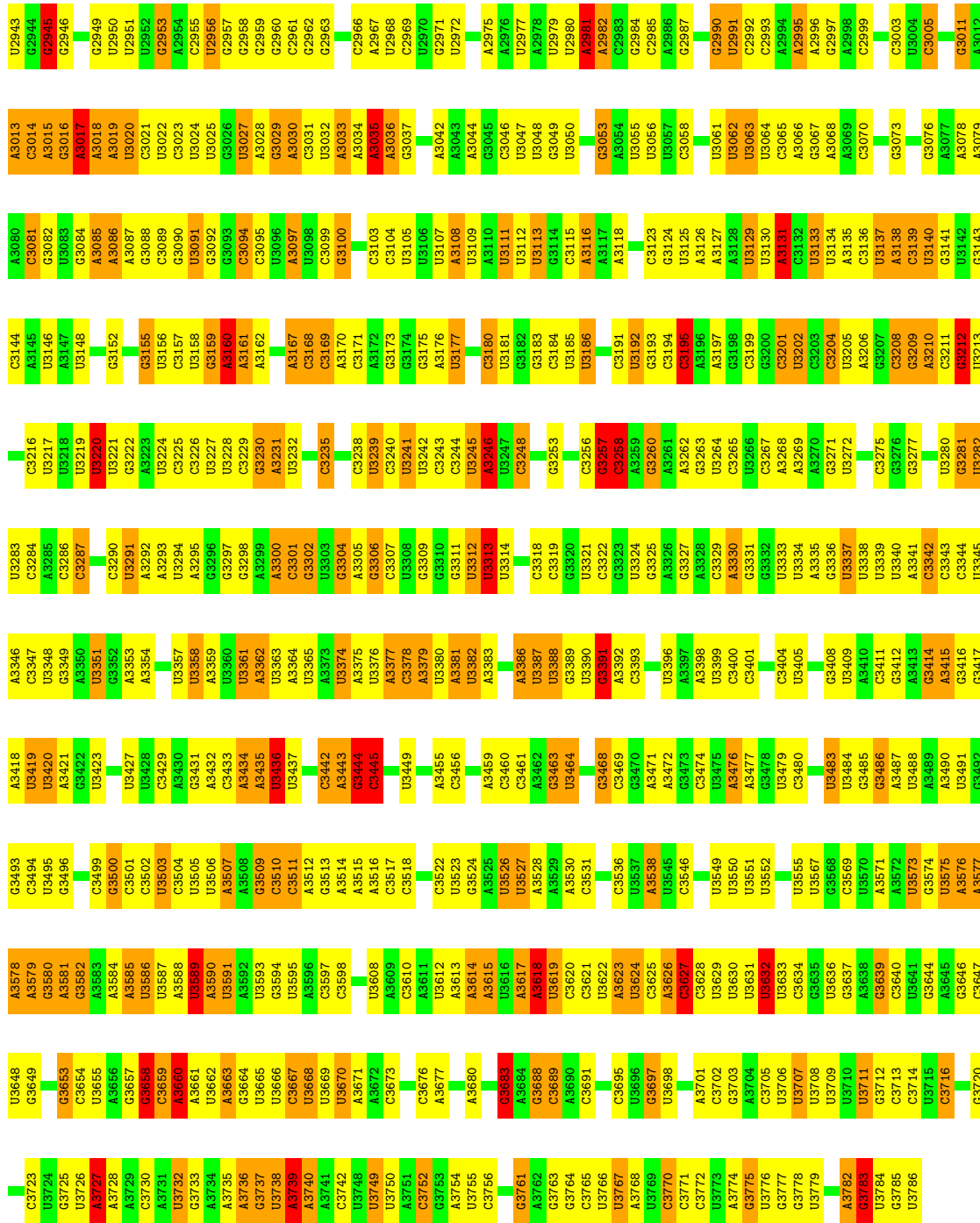


- Molecule 34: 28S ribosomal RNA

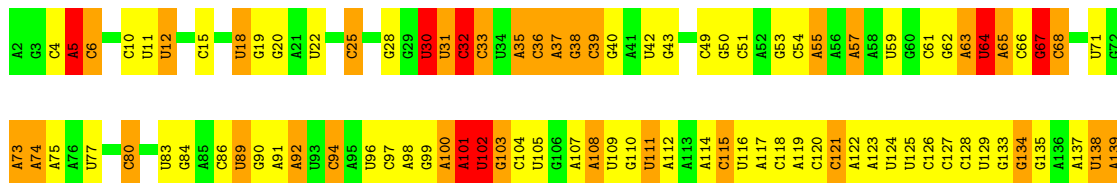


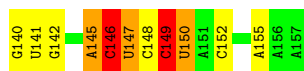
U1343	U1344	A1345	A1346	A1415	A1416	G1417	A1418	A1419	C1420	A1421	A1422	G1423	C1424	C1425	A1426	A1427	A1428	A1429	A1430	A1431	A1432	A1433	G1434	A1435	A1436	A1437	C1440	C1441	C1442	A1443	A1444	A1445	A1446	G1447	A1448	G1449	A1450	A1451	A1452	A1453	A1454	C1455	C1456	A1457	A1458	A1459	A1460	C1461	A1462	C1466	C1467	A1468	A1469	A1470	A1473	A1474																																																																																																																																									
C1281	U1282	C1283	C1284	U1285	A1286	A1287	C1288	A1289	C1290	U1291	U1292	G1293	G1294	A1295	A1296	A1297	A1298	C1299	G1300	U1301	G1302	C1303	C1304	U1305	A1306	A1307	A1308	U1309	A1310	U1311	U1312	C1313	G1314	C1315	A1316	C1317	A1318	U1319	G1320	A1321	U1324	C1325	C1326	C1327	A1328	U1329	A1330	A1331	A1332	A1333	G1334	U1335	U1336	G1337	U1338	U1339	G1340	U1341	U1342																																																																																																																																						
A1215	C1216	C1217	C1218	A1219	U1220	U1221	A1222	A1223	C1224	U1225	A1226	A1227	A1228	A1229	A1230	A1231	A1232	A1233	A1234	C1235	U1236	C1237	C1238	C1239	A1240	C1243	G1244	G1245	G1246	C1247	U1251	U1252	U1253	G1254	G1255	A1256	A1257	A1258	G1259	C1260	A1261	A1262	A1263	A1264	C1265	U1266	C1269	G1270	A1271	U1272	G1273	A1274	G1275	A1278	U1279	C1280																																																																																																																																									
G1141	C1154	C1155	U1156	U1157	G1158	A1159	C1160	U1161	A1162	A1163	U1164	U1165	C1166	A1167	A1168	C1169	A1170	A1171	C1172	U1173	C1174	C1175	C1176	U1179	U1183	U1184	A1185	A1186	A1187	A1188	G1189	U1190	G1191	C1192	G1193	A1194	A1195	A1196	U1197	A1198	A1199	U1200	C1201	C1202	A1203	A1204	U1205	U1206	U1207	U1208	U1209	A1210	U1211	U1212	U1213	C1214																																																																																																																																									
U1075	C1076	U1077	C1078	U1079	G1082	C1086	C1087	C1088	U1089	A1092	C1093	U1094	U1095	C1096	A1097	U1098	A1100	A1101	A1102	A1103	U1104	A1105	A1106	U1107	A1108	A1109	U1110	A1111	C1112	A1113	A1114	U1115	G1116	U1117	A1118	A1119	A1120	G1121	A1122	U1123	A1124	A1125	U1126	A1127	A1128	U1129	U1130	A1131	G1132	A1133	U1134	G1135	A1136	C1139	A1140																																																																																																																																										
U1012	U1013	C1014	A1015	A1016	U1017	C1018	A1019	G1020	G1021	U1022	U1023	U1024	A1025	A1026	G1027	G1028	C1029	A1030	A1031	A1032	A1033	A1034	G1035	A1036	C1037	U1038	A1039	A1040	U1041	G1042	G1043	G1048	A1049	U1051	G1052	G1053	U1056	C1057	U1058	G1059	G1060	U1061	U1062	A1063	U1064	U1065	U1066	U1067	C1068	G1069	A1070	A1071	A1072	G1073	A1074																																																																																																																																										
C875	C876	U879	A880	A881	G882	A883	A884	A885	A886	U889	A890	C891	U892	U893	U894	A895	C895	A896	A899	G900	U901	G904	A905	G906	C907	A908	U909	A910	U911	U912	U913	G914	C915	U916	A917	U918	G919	A920	C921	C922	C923	G924	A925	G926	A927	C930	U931	U932	U933	G934	A935	U936	C937	U938	A939	A940																																																																																																																																									
G941	C942	G943	U944	A945	A946	U947	G948	A949	G950	A951	U952	U953	G954	A955	A956	G1027	C959	A960	C963	A964	A965	A966	A967	G968	U969	C970	G971	G972	G973	G974	G979	A980	U981	C982	G983	A984	G985	U986	U987	C988	A989	U990	A991	C992	U993	C996	G997	U998	G999	C1000	A1005	G1006	U1007	U1008	A1009	C1009																																																																																																																																									
A774	C775	U779	U792	A793	U794	C795	A796	U797	A798	A799	A800	U801	U802	A803	A804	U805	G806	U807	A808	A809	U810	A811	U812	G813	U817	C818	A822	A823	U824	G825	G828	A829	U830	U831	U832	A833	U834	U835	U836	A837	A838	A839	A840	A841	A842	A843	A844	A845	A846	A847	A848	A849	A850	A851	A852	A853	A854	A855	A856	A857	A858	A859	A860	A861	A862	U865	U866	U867	U868	U869	U870	A871	A872	A873	A874																																																																																																																						
U495	C496	U497	U498	U499	A500	U501	U502	A503	A504	A505	A506	G507	A508	A509	A510	C511	U512	U513	C514	U517	U521	U522	A523	U524	U525	U526	A527	A528	U529	U530	U531	C532	A533	A534	U535	A536	A537	A538	C451	A542	A543	A544	A545	A546	C547	U548	A550	A551	A552	A553	A554	A555	A556	A557	A558	A559	A560	A561	A562	A563	A564	A565	A566	A567	A568	A569	A570	A571	A572	A573	A574	A575	A576	A577	A578	A579	A580	A581	A582	A583	A584	A585	A586	A587	A588	A589	A590	A591	A592	A593	A594	A595	A596	A597	A598	A599	A600	G601	G604	A605	A606	A607	A608	C609	U610	C613	U614	U615	A616	A617	U618	A619	A620	A621	U622	C540	A623	C624	A627	U628	C544	C545	C546	C547	U631	U632	U633	U634	U635	U636	U637	U638	U639	U640	U641	U642	U643	U644	U645	U646	U647	U648	U649	U650	U651	U652	U653	U654	U655	U656	U657	U658	U659	U660	U661	U662	U663	U664	U665	U666	U667	U668	U669	U670	U671	U672	U673	U674	U675	U676	U677	U678	U679	U680	U681	U682	U683	U684	U685	U686	U687	U688	C691	U694	A695	A697	U698	U699	U700	U701	U702	U703	U704
U334	A335	U336	A337	U338	G339	U340	A341	G342	G343	A344	G345	A346	C347	C348	G349	A350	U351	A352	C353	C354	A355	A356	A357	C358	A359	A360	G361	A362	A363	A364	C365	G366	U367	G372	U378	G379	A380	A381	A382	A383	G385	A387	U388	A389	C390	A391	G392	G393	A394	A395	U396	C400	A401																																																																																																																																												
A402	U403	U404	A405	U408	A409	G410	U411	G412	A413	A414	C415	A416	U417	G418	U419	A420	C421	G422	U423	U424	G431	A432	A433	C434	G435	G436	A437	U438	U439	A440	A441	G442	A443	G444	A445	G446	A447	A448	A449	A450	C451	A452	A453	A458	G459	G462	G463	G464	U467	A488	A489	U490	C491	U492	C493	U494																																																																																																																																									

G747	G2801	A2602	G2540	C2462	G2389	U2144	G2068	U1963	C1852	A1787	C1720	A1636	G1562	G1475
C2801	G2603	U2603	C2541	U2463	U2390	A2145	C2069	G1964	C1853	C1788	C1721	G1637	U1563	A1476
A2802	G2604	G2605	G2542	G2464	A2391	A2146	U2070	U1965	U1854	U1789	C1722	G1641	G1564	A1479
G2804	A2606	A2607	G2543	G2465	A2392	A2147	U2071	U1966	U1855	U1790	C1723	G1642	G1565	G1480
U2805	U2607	U2608	A2544	C2472	C2394	A2148	G2073	G1967	U1856	A1791	U1725	U1643	A1567	A1481
U2806	G2608	A2473	G2546	A2473	U2395	U2149	G2074	C1968	A1857	U1792	U1726	U1644	C1568	A1486
U2807	U2611	C2474	U2547	C2474	C2396	A2153	C2080	A1969	C1861	A1793	U1727	U1645	A1869	A1487
U2808	U2611	U2548	A2548	A2548	U1971	A2154	U2080	U1970	U1861	U1794	U1728	U1646	U1570	U1493
A2809	U2611	U2549	U2477	U2477	C2401	G2157	U2081	U1974	C1865	A1797	U1729	U1647	C1571	U1496
A2810	A2614	G2478	U2478	U2478	U2402	G2157	C2082	U1974	C1866	A1798	U1730	U1648	U1572	U1497
G2811	C2615	U2479	G2480	G2480	G2403	U2158	U2083	A1975	U1867	A1799	U1731	U1649	C1573	U1498
G2812	A2481	A2481	A2481	A2481	A2404	A2159	U2084	U1976	U1868	U1800	A1732	U1650	C1574	U1499
U2813	U2553	U2553	U2553	U2553	U1977	G2160	G1869	U1801	G1869	G1801	C1651	C1651	C1575	U1499
U2814	G2554	G2554	G2554	G2554	U1978	G2161	C2089	U1879	C1870	G1804	G1735	C1652	U1576	U1502
U2815	A2555	A2555	U2484	U2484	G2408	U2089	U2090	U1871	C1804	C1804	A1736	C1654	G1583	G1502
U2816	C2556	C2556	C2485	C2485	G2409	U2090	U2091	A1871	U1805	U1805	A1737	C1654	A1503	A1503
U2817	C2557	C2557	U2486	U2486	A2410	G2166	U2092	U1872	U1806	U1806	A1738	G1656	A1504	A1504
U2818	C2558	C2558	G2487	G2487	C2411	G2167	G2093	U1873	C1807	C1807	A1739	G1657	U1505	U1505
U2819	A2559	A2559	G2488	G2488	G2415	A2168	U2094	A1989	C1874	C1874	C1740	G1658	C1566	C1566
U2820	C2560	C2560	C2489	C2489	G2415	A2169	U2095	A1990	U1879	U1809	G1741	A1659	C1567	U1507
C2821	U2561	U2561	U2627	U2627	U2415	U2171	U2096	U1991	U1879	U1809	G1742	U1660	U1588	U1510
U2822	G2562	G2562	C2495	C2495	A2419	C2172	G2096	U1994	A1880	U1810	U1743	U1661	G1592	U1511
U2823	A2563	A2563	U2496	U2496	U2420	G2173	A2097	U1994	C1881	A1811	U1744	C1665	G1593	A1512
A2824	A2564	A2564	U2497	U2497	U2421	G2174	G2098	U1994	C1882	C1812	U1745	C1666	A1594	U1513
U2825	G2565	G2565	U2498	U2498	C2422	C2175	C2099	G1996	U1883	A1813	G1745	A1666	A1595	U1514
C2826	G2566	G2566	G2499	G2499	C2423	A2176	A2102	G1998	C1884	U1814	A1748	C1667	A1596	U1515
C2827	U2567	U2567	A2424	A2424	A2424	G2182	C2103	U1999	A1886	A1816	U1749	C1668	U1597	U1516
A2832	C2570	C2570	U2500	U2500	U2425	G2183	C2104	G2000	U1887	G1817	U1750	C1672	U1598	U1517
U2833	G2571	G2571	U2501	U2501	A2105	G2184	A2105	U2001	A1888	C1818	C1751	U1672	U1599	A1518
U2834	C2572	C2572	U2502	U2502	G2427	C2185	A2106	G2002	A1888	U1819	C1752	A1673	G1599	U1519
G2835	C2573	C2573	C2505	C2505	U2428	C2186	C2107	G2003	G1892	U1820	U1753	C1674	C1600	U1520
G2836	A2506	A2506	U2506	U2506	U2429	C2187	A2108	G2004	G1893	U1821	U1753	C1675	A1601	U1521
G2837	G2507	G2507	A2507	A2507	U2433	U2188	A2109	G2008	U1894	A1892	G1756	A1676	A1602	U1522
A2838	U2508	U2508	U2508	U2508	U2433	U2189	A2109	G2008	U1895	A1893	C1757	C1677	C1603	C1525
U2839	G2509	G2509	U2509	U2509	U2434	A2190	A2110	A2009	C1896	A1823	C1758	C1678	C1604	G1526
U2840	U2510	U2510	U2510	U2510	A2435	C2191	G2112	G2010	C1897	U1825	A1759	U1679	A1605	U1527
A2850	G2514	G2514	U2514	U2514	A2436	U2192	C2113	G2011	U1898	U1826	A1760	C1680	U1606	U1528
A2851	A2515	A2515	A2515	A2515	A2437	U2193	A2114	U2013	U1899	U1827	U1761	C1681	U1607	U1533
G2852	U2516	U2516	U2516	U2516	A2438	U2194	U2115	C2014	G1900	U1827	A1762	U1682	C1608	U1534
G2853	C2517	C2517	U2517	U2517	A2439	G2202	C2116	C2015	A1901	U1892	G1763	A1683	G1536	U1535
G2854	U2518	U2518	U2518	U2518	U2440	G2203	C2117	C2016	A1902	G1833	U1764	A1684	U1537	U1536
G2855	C2519	C2519	U2519	U2519	U2441	A2204	G2118	U2017	C1903	C1834	U1765	G1685	G1538	G1537
G2856	G2520	G2520	U2520	U2520	U2441	U2205	G2118	G2018	U1904	G1835	U1766	G1686	U1539	U1538
G2857	A2521	A2521	U2521	U2521	C2444	U2206	C2121	A2019	C1906	U1836	U1767	A1688	U1539	U1539
G2858	A2522	A2522	U2522	U2522	A2445	G2207	U2122	A2020	A1906	U1837	A1768	A1689	C1618	G1540
G2859	C2523	C2523	U2523	U2523	U2446	G2208	C2123	A2021	A1907	U1838	U1769	A1690	C1619	C1544
G2860	A2524	A2524	U2524	U2524	C2209	G2209	C2124	A2022	U1908	U1839	G1770	C1692	A1624	U1549
G2861	A2525	A2525	U2525	U2525	U2449	U2210	A2125	U1909	U1909	C1840	A1771	C1693	A1625	U1550
G2862	G2526	G2526	U2526	U2526	G2450	C2211	A2132	G2030	C1910	U1841	G1772	G1694	G1626	U1552
G2863	C2528	C2528	U2528	U2528	A2451	G2215	A2133	C2033	A1913	U1842	U1773	G1695	A1627	U1553
G2864	G2529	G2529	U2529	U2529	A2452	G2216	C2136	G2034	A1914	U1843	U1774	G1696	A1628	U1554
G2865	C2530	C2530	U2530	U2530	A2453	A2217	C2137	G2035	A1914	G1844	U1775	G1697	A1629	U1555
G2866	G2533	G2533	U2533	U2533	C2456	C2218	C2138	C2036	U1957	C1845	G1780	U1703	G1629	G1629
G2867	A2536	A2536	U2536	U2536	C2457	A2219	U2138	C2037	U1958	C1846	A1781	A1704	A1630	G1630
G2868	C2537	C2537	U2537	U2537	A2458	U2220	C2139	U2038	G1959	C1847	U1782	A1705	A1631	G1631
G2869	U2538	U2538	U2538	U2538	A2459	U2221	C2140	U2039	U1960	U1848	G1783	A1706	G1632	G1632
G2870	C2539	C2539	U2539	U2539	A2460	U2222	U2140	G2040	U1961	U1849	U1784	A1706	U1633	U1633
G2871	U2540	U2540	U2540	U2540	A2461	A2381	U2141	G2041	U1962	U1851	U1785	G1712	G1634	U1660
G2872	C2601	C2601	U2541	U2541	A2461	U2388	U2143	U2041	U1962	A1851	A1786	G1712	G1635	U1661



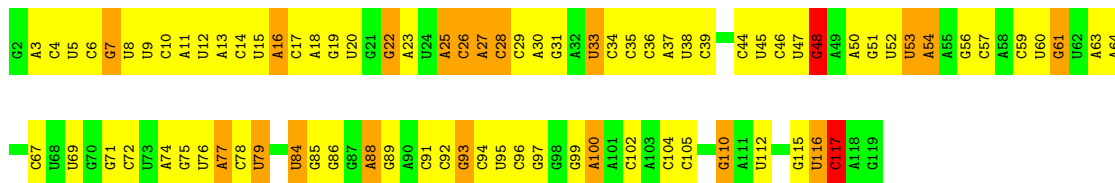
• Molecule 35: 5.8S ribosomal RNA





- Molecule 36: 5S ribosomal RNA

Chain AB: 30% 53% 16%



- Molecule 37: 60S ribosomal protein eL13

Chain AL: 87% 13%



- Molecule 38: 60S ribosomal protein eL24

Chain A0: 94% 6%



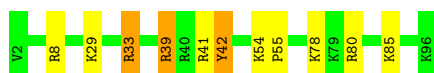
- Molecule 39: 60S ribosomal protein uL15

Chain AO: 90% 10%



- Molecule 40: 60S ribosomal protein eL44

Chain Ai: 88% 8%



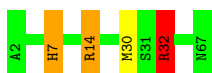
- Molecule 41: 60S ribosomal protein eL28

Chain A2: 81% 8% 12%



- Molecule 42: 60S ribosomal protein eL29

Chain A4:  94% . . .




- Molecule 43: 60S ribosomal protein eL30

Chain A6:  94% . . .



- Molecule 44: 60S ribosomal protein eL31

Chain A7:  87% 6% • 6%



- Molecule 45: 60S ribosomal protein eL27

Chain A1:  92% . . .




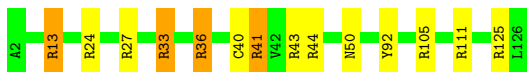
- Molecule 46: 60S ribosomal protein eL14

Chain AN:  91% 8% . . .




- Molecule 47: 60S ribosomal protein eL32

Chain A8:  89% 8% . . .



- Molecule 48: 60S ribosomal protein eL33

Chain A9:  83% 14% . . .




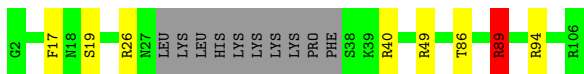
- Molecule 49: 60S ribosomal protein eL34

Chain Aa:  93%




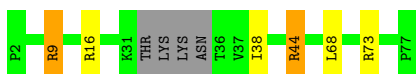
- Molecule 50: 60S ribosomal protein eL36

Chain Ab:  83%



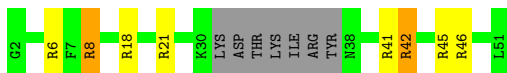
- Molecule 51: 60S ribosomal protein eL38

Chain Ad:  87%



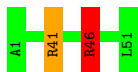
- Molecule 52: 60S ribosomal protein eL39

Chain Ae:  70%




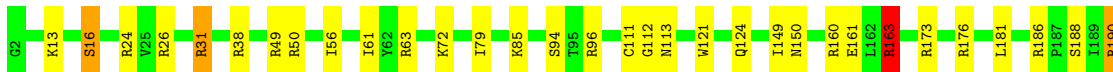
- Molecule 53: 60S ribosomal protein eL40

Chain Af:  96%



- Molecule 54: 60S ribosomal protein eL15

Chain AP:  82%



- Molecule 55: 60S ribosomal protein eL43

Chain Ah:  94%




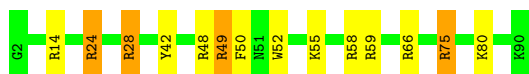
- Molecule 56: 60S ribosomal protein eL6

Chain AI:  91% 6% ..



- Molecule 57: 60S ribosomal protein eL37

Chain Ac:  84% 11% .



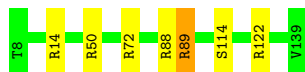
- Molecule 58: 60S ribosomal protein uL13

Chain AK:  90% 8% .




- Molecule 59: 60S ribosomal protein uL14

Chain AM:  95% 5% .




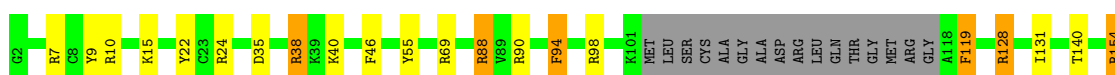
- Molecule 60: 60S ribosomal protein eL18

Chain AS:  87% 8% 5%




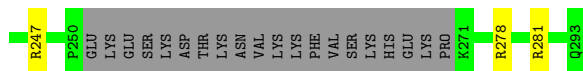
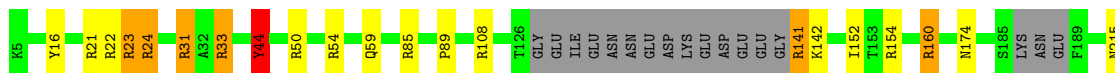
- Molecule 61: 60S ribosomal protein uL16

Chain AQ:  79% 10% . 8%



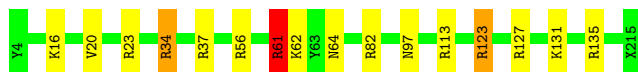
- Molecule 62: 60S ribosomal protein uL18

Chain AR:  79% 6% . 13%



- Molecule 63: 60S ribosomal protein uL22

Chain AW: 91% 8% ..



- Molecule 64: 60S ribosomal protein uL23

Chain AY: 96% ..



- Molecule 65: 60S ribosomal protein eL19

Chain AT: 89% 9% .



- Molecule 66: 60S ribosomal protein uL24

Chain AZ: 88% 11% .



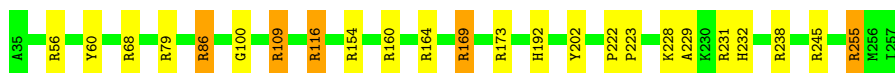
- Molecule 67: 60S ribosomal protein uL29

Chain A3: 88% 9% ..



- Molecule 68: 60S ribosomal protein uL30

Chain A5: 89% 9% .



- Molecule 69: 60S ribosomal protein uL2

Chain AD:  89% 9%



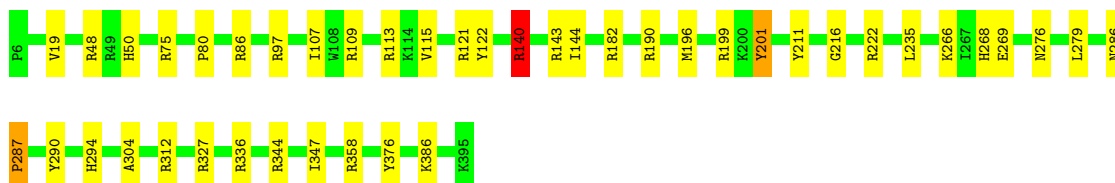
- Molecule 70: 60S ribosomal protein uL3

Chain AE:  92% 7%



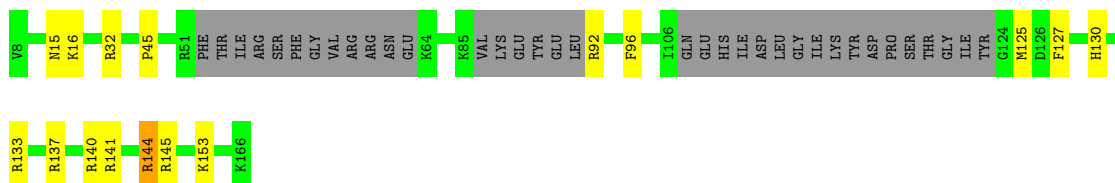
- Molecule 71: 60S ribosomal protein uL4

Chain AF:  89% 10%




- Molecule 72: 60S ribosomal protein uL5

Chain AG:  68% 9% 22%



- Molecule 73: 60S ribosomal protein eL20

Chain AU:  88% 10%



- Molecule 74: 60S ribosomal protein uL6

Chain AH:  95%

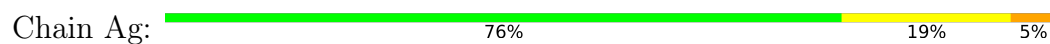


- Molecule 75: 60S ribosomal protein eL21

Chain AV:  90% 9%



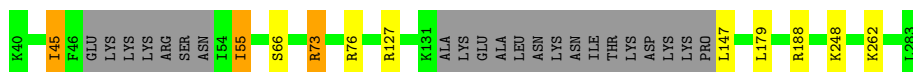
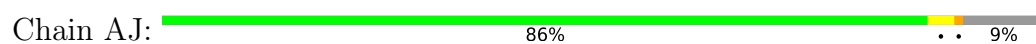
- Molecule 76: 60S ribosomal protein eL41



- Molecule 77: 60S ribosomal protein eL22



- Molecule 78: 60S ribosomal protein eL8



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	22793	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each micrograph	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	30120	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor

5 Model quality i

5.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.10	7/38275 (0.0%)	1.52	877/59596 (1.5%)
2	7	1.15	0/1785	1.70	63/2782 (2.3%)
3	Q	0.72	0/1149	1.13	11/1532 (0.7%)
4	S	0.65	0/1063	1.17	10/1425 (0.7%)
5	T	0.79	0/412	1.14	5/544 (0.9%)
6	M	0.71	0/1114	1.14	9/1487 (0.6%)
7	U	0.68	0/1223	1.10	10/1634 (0.6%)
8	V	0.73	0/1233	1.12	10/1645 (0.6%)
9	E	0.71	0/1539	1.12	14/2055 (0.7%)
10	X	0.70	0/788	1.18	7/1050 (0.7%)
11	G	0.69	0/1800	1.00	5/2429 (0.2%)
12	W	0.71	0/793	1.13	4/1053 (0.4%)
13	R	0.73	0/755	1.02	2/1013 (0.2%)
14	I	0.71	0/1443	1.06	7/1936 (0.4%)
15	O	0.74	0/706	1.08	8/950 (0.8%)
16	Y	0.70	0/1295	1.17	15/1742 (0.9%)
17	Z	0.70	0/565	0.97	1/758 (0.1%)
18	1	0.73	0/999	1.26	13/1321 (1.0%)
19	2	0.78	0/324	0.92	0/435
20	C	0.68	0/1570	1.06	7/2129 (0.3%)
21	3	0.73	0/794	1.26	13/1055 (1.2%)
22	4	0.67	0/597	0.98	0/801
23	5	0.76	0/459	1.20	6/606 (1.0%)
24	6	0.75	0/349	1.23	4/458 (0.9%)
25	B	0.67	0/1738	1.05	8/2321 (0.3%)
26	D	0.76	0/1241	1.09	6/1652 (0.4%)
27	F	0.68	0/2098	1.11	12/2819 (0.4%)
28	H	0.69	0/1665	1.08	9/2210 (0.4%)
29	K	0.71	0/1054	1.12	8/1411 (0.6%)
30	J	0.69	0/1545	1.03	5/2064 (0.2%)
31	N	0.69	0/780	1.10	2/1053 (0.2%)
32	P	0.69	0/966	1.21	12/1295 (0.9%)
33	L	0.72	0/1407	1.12	15/1879 (0.8%)
34	AA	1.23	16/75922 (0.0%)	1.52	1781/118216 (1.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AC	1.12	0/3599	1.55	91/5603 (1.6%)
36	AB	1.13	2/2823 (0.1%)	1.48	71/4400 (1.6%)
37	AL	0.69	0/1789	1.15	13/2381 (0.5%)
38	A0	0.76	0/534	1.16	3/711 (0.4%)
39	AO	0.68	0/1199	1.17	10/1597 (0.6%)
40	Ai	0.69	0/789	1.17	9/1032 (0.9%)
41	A2	0.74	0/840	0.98	4/1114 (0.4%)
42	A4	0.68	0/564	1.00	2/737 (0.3%)
43	A6	0.70	0/749	1.06	4/1001 (0.4%)
44	A7	0.71	0/806	1.20	8/1073 (0.7%)
45	A1	0.69	0/1151	1.00	5/1531 (0.3%)
46	AN	0.71	0/1218	1.11	7/1621 (0.4%)
47	A8	0.72	0/1054	1.28	15/1399 (1.1%)
48	A9	0.71	0/865	1.22	12/1160 (1.0%)
49	Aa	0.68	0/872	1.20	7/1161 (0.6%)
50	Ab	0.72	0/763	1.06	3/1008 (0.3%)
51	Ad	0.72	0/612	1.15	5/812 (0.6%)
52	Ae	0.77	0/396	1.45	8/521 (1.5%)
53	Af	0.68	0/419	1.19	4/556 (0.7%)
54	AP	0.72	0/1735	1.22	16/2320 (0.7%)
55	Ah	0.68	0/668	1.16	6/887 (0.7%)
56	AI	0.67	0/1708	1.03	7/2274 (0.3%)
57	Ac	0.74	0/723	1.24	10/951 (1.1%)
58	AK	0.70	0/1690	1.08	9/2260 (0.4%)
59	AM	0.68	0/1012	1.10	9/1363 (0.7%)
60	AS	0.71	0/1531	1.22	18/2040 (0.9%)
61	AQ	0.74	0/1580	1.21	21/2113 (1.0%)
62	AR	0.71	0/2079	1.17	18/2777 (0.6%)
63	AW	0.71	0/1244	1.15	10/1663 (0.6%)
64	AY	0.67	0/806	0.97	2/1074 (0.2%)
65	AT	0.69	0/1525	1.18	20/2016 (1.0%)
66	AZ	0.70	0/1013	1.24	14/1339 (1.0%)
67	A3	0.69	0/1005	1.18	11/1329 (0.8%)
68	A5	0.71	0/1917	1.18	22/2562 (0.9%)
69	AD	0.68	0/1902	1.16	17/2544 (0.7%)
70	AE	0.68	0/3130	1.12	21/4195 (0.5%)
71	AF	0.70	0/3145	1.10	19/4205 (0.5%)
72	AG	0.75	0/1021	1.16	7/1349 (0.5%)
73	AU	0.71	0/1527	1.18	15/2043 (0.7%)
74	AH	0.67	0/1501	1.08	6/2025 (0.3%)
75	AV	0.69	0/1301	1.10	9/1732 (0.5%)
76	Ag	0.82	0/348	1.50	10/448 (2.2%)
77	AX	0.72	0/842	1.14	8/1125 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	AJ	0.84	1/1840 (0.1%)	0.99	5/2456 (0.2%)
All	All	1.01	26/207281 (0.0%)	1.39	3550/303864 (1.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	141
2	7	1	5
3	Q	0	4
5	T	0	1
6	M	0	2
7	U	0	1
8	V	0	3
9	E	0	3
10	X	0	2
12	W	0	3
14	I	0	3
16	Y	0	2
18	1	0	3
19	2	0	1
21	3	0	2
23	5	0	1
24	6	0	4
25	B	1	4
27	F	0	4
28	H	0	4
29	K	0	1
32	P	0	5
33	L	0	2
34	AA	1	328
35	AC	0	13
36	AB	0	8
37	AL	0	7
38	A0	0	1
39	AO	0	1
40	Ai	0	3
41	A2	2	0
42	A4	0	5
43	A6	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
44	A7	0	1
46	AN	0	3
47	A8	0	3
48	A9	0	3
49	Aa	0	2
50	Ab	0	3
51	Ad	0	2
52	Ae	0	2
53	Af	0	2
54	AP	0	7
55	Ah	0	1
56	AI	0	2
57	Ac	0	3
58	AK	0	8
60	AS	0	9
61	AQ	0	6
62	AR	0	7
63	AW	0	4
64	AY	0	1
65	AT	0	3
66	AZ	0	4
67	A3	0	1
68	A5	0	5
69	AD	0	4
70	AE	0	6
71	AF	0	10
72	AG	0	3
73	AU	0	5
74	AH	0	2
75	AV	0	6
76	Ag	0	3
77	AX	0	1
78	AJ	0	2
All	All	5	692

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	AA	2915	U	C2-N3	70.80	1.87	1.37
34	AA	2915	U	C4-C5	67.04	2.03	1.43
34	AA	2915	U	N1-C2	60.98	1.93	1.38
34	AA	2915	U	N1-C6	57.12	1.89	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	AA	2915	U	N3-C4	56.47	1.89	1.38

The worst 5 of 3550 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AA	181	C	P-O3'-C3'	14.44	137.03	119.70
1	A	981	U	P-O3'-C3'	14.26	136.81	119.70
1	A	844	G	P-O3'-C3'	13.99	136.49	119.70
1	A	1912	C	P-O3'-C3'	13.97	136.47	119.70
34	AA	1202	C	P-O3'-C3'	13.95	136.44	119.70

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	7	31	G	C3'
25	B	225	ILE	CB
34	AA	3018	A	C3'
41	A2	55	THR	CA
41	A2	116	SER	CA

5 of 692 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3	C	Sidechain
1	A	38	C	Sidechain
1	A	39	A	Sidechain
1	A	47	A	Sidechain
1	A	62	A	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	34207	0	17266	45	0
2	7	1598	0	816	1	0
3	Q	1129	0	1196	3	0
4	S	1047	0	1101	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	T	405	0	419	0	0
6	M	1099	0	1183	1	0
7	U	1202	0	1299	1	0
8	V	1206	0	1239	1	0
9	E	1515	0	1605	0	0
10	X	777	0	832	2	0
11	G	1758	0	1811	1	0
12	W	786	0	858	0	0
13	R	747	0	754	0	0
14	I	1424	0	1471	1	0
15	O	687	0	695	0	0
16	Y	1267	0	1316	0	0
17	Z	557	0	558	0	0
18	1	986	0	1076	0	0
19	2	321	0	338	0	0
20	C	1539	0	1600	0	0
21	3	782	0	820	1	0
22	4	586	0	604	1	0
23	5	458	0	496	0	0
24	6	346	0	381	0	0
25	B	1714	0	1838	2	0
26	D	1229	0	1311	0	0
27	F	2062	0	2200	1	0
28	H	1648	0	1803	0	0
29	K	1037	0	1099	3	0
30	J	1529	0	1680	1	0
31	N	772	0	813	0	0
32	P	954	0	997	1	0
33	L	1383	0	1434	1	0
34	AA	67862	0	34233	156	0
35	AC	3215	0	1633	6	0
36	AB	2522	0	1275	2	0
37	AL	1757	0	1888	1	0
38	A0	522	0	539	0	0
39	AO	1172	0	1230	1	0
40	Ai	779	0	861	0	0
41	A2	831	0	887	1	0
42	A4	555	0	599	3	0
43	A6	741	0	763	1	0
44	A7	794	0	869	0	0
45	A1	1134	0	1245	1	0
46	AN	1202	0	1316	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	A8	1037	0	1139	1	0
48	A9	845	0	886	1	0
49	Aa	859	0	912	0	0
50	Ab	757	0	842	0	0
51	Ad	604	0	686	0	0
52	Ae	388	0	421	0	0
53	Af	414	0	452	0	0
54	AP	1697	0	1802	2	0
55	Ah	659	0	727	0	0
56	AI	1685	0	1849	0	0
57	Ac	710	0	761	0	0
58	AK	1660	0	1785	1	0
59	AM	996	0	1044	0	0
60	AS	1503	0	1636	0	0
61	AQ	1545	0	1582	0	0
62	AR	2050	0	2140	1	0
63	AW	1319	0	1303	0	0
64	AY	797	0	850	0	0
65	AT	1509	0	1682	0	0
66	AZ	1001	0	1099	1	0
67	A3	995	0	1121	1	0
68	A5	1879	0	2005	0	0
69	AD	1867	0	1964	1	0
70	AE	3062	0	3205	4	0
71	AF	3095	0	3333	3	0
72	AG	1011	0	1073	1	0
73	AU	1497	0	1556	2	0
74	AH	1476	0	1574	0	0
75	AV	1276	0	1355	1	0
76	Ag	343	0	388	0	0
77	AX	825	0	882	1	0
78	AJ	1813	0	1985	25	0
All	All	193017	0	144286	249	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

The worst 5 of 249 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:2915:U:C5	34:AA:2915:U:C4	2.03	1.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:2915:U:N3	34:AA:2915:U:C2	1.87	1.42
34:AA:2915:U:N1	34:AA:2915:U:C6	1.89	1.39
34:AA:2915:U:C4	34:AA:2915:U:N3	1.89	1.37
34:AA:2915:U:C2	34:AA:2915:U:N1	1.93	1.35

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	Q	142/144 (99%)	134 (94%)	6 (4%)	2 (1%)	11	46
4	S	126/128 (98%)	107 (85%)	11 (9%)	8 (6%)	1	16
5	T	46/48 (96%)	44 (96%)	2 (4%)	0	100	100
6	M	136/138 (99%)	128 (94%)	6 (4%)	2 (2%)	10	45
7	U	147/149 (99%)	144 (98%)	2 (1%)	1 (1%)	22	62
8	V	142/156 (91%)	134 (94%)	4 (3%)	4 (3%)	5	30
9	E	183/185 (99%)	176 (96%)	7 (4%)	0	100	100
10	X	92/103 (89%)	82 (89%)	6 (6%)	4 (4%)	2	22
11	G	222/224 (99%)	209 (94%)	10 (4%)	3 (1%)	11	46
12	W	91/108 (84%)	87 (96%)	3 (3%)	1 (1%)	14	51
13	R	92/114 (81%)	78 (85%)	10 (11%)	4 (4%)	2	22
14	I	176/189 (93%)	166 (94%)	7 (4%)	3 (2%)	9	42
15	O	77/79 (98%)	70 (91%)	3 (4%)	4 (5%)	2	19
16	Y	152/154 (99%)	141 (93%)	7 (5%)	4 (3%)	5	31
17	Z	70/72 (97%)	65 (93%)	4 (6%)	1 (1%)	11	46
18	1	118/120 (98%)	109 (92%)	7 (6%)	2 (2%)	9	42

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	2	35/68 (52%)	32 (91%)	1 (3%)	2 (6%)	1	17
20	C	193/195 (99%)	180 (93%)	11 (6%)	2 (1%)	15	54
21	3	93/95 (98%)	81 (87%)	12 (13%)	0	100	100
22	4	74/76 (97%)	67 (90%)	4 (5%)	3 (4%)	3	22
23	5	54/65 (83%)	52 (96%)	1 (2%)	1 (2%)	8	38
24	6	41/43 (95%)	38 (93%)	3 (7%)	0	100	100
25	B	208/210 (99%)	188 (90%)	16 (8%)	4 (2%)	8	38
26	D	149/209 (71%)	143 (96%)	4 (3%)	2 (1%)	12	48
27	F	255/257 (99%)	244 (96%)	10 (4%)	1 (0%)	34	72
28	H	200/214 (94%)	186 (93%)	13 (6%)	1 (0%)	29	69
29	K	127/129 (98%)	119 (94%)	6 (5%)	2 (2%)	9	43
30	J	186/188 (99%)	175 (94%)	7 (4%)	4 (2%)	6	35
31	N	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
32	P	125/127 (98%)	110 (88%)	15 (12%)	0	100	100
33	L	165/214 (77%)	149 (90%)	15 (9%)	1 (1%)	25	66
37	AL	209/211 (99%)	190 (91%)	13 (6%)	6 (3%)	4	29
38	A0	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
39	AO	145/147 (99%)	134 (92%)	8 (6%)	3 (2%)	7	36
40	Ai	93/95 (98%)	84 (90%)	6 (6%)	3 (3%)	4	26
41	A2	96/118 (81%)	92 (96%)	3 (3%)	1 (1%)	15	54
42	A4	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
43	A6	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
44	A7	92/102 (90%)	90 (98%)	2 (2%)	0	100	100
45	A1	136/145 (94%)	131 (96%)	5 (4%)	0	100	100
46	AN	144/146 (99%)	138 (96%)	4 (3%)	2 (1%)	11	46
47	A8	123/125 (98%)	111 (90%)	10 (8%)	2 (2%)	9	43
48	A9	101/103 (98%)	93 (92%)	5 (5%)	3 (3%)	4	28
49	Aa	104/106 (98%)	97 (93%)	7 (7%)	0	100	100
50	Ab	91/105 (87%)	86 (94%)	3 (3%)	2 (2%)	6	35
51	Ad	68/76 (90%)	65 (96%)	2 (3%)	1 (2%)	10	45
52	Ae	39/50 (78%)	38 (97%)	1 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	Af	49/51 (96%)	44 (90%)	5 (10%)	0	100	100
54	AP	202/204 (99%)	182 (90%)	11 (5%)	9 (4%)	2	21
55	Ah	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
56	AI	203/213 (95%)	188 (93%)	10 (5%)	5 (2%)	5	32
57	Ac	87/89 (98%)	78 (90%)	6 (7%)	3 (3%)	3	26
58	AK	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	29	69
59	AM	130/132 (98%)	122 (94%)	7 (5%)	1 (1%)	19	60
60	AS	184/186 (99%)	166 (90%)	13 (7%)	5 (3%)	5	31
61	AQ	185/205 (90%)	169 (91%)	11 (6%)	5 (3%)	5	31
62	AR	244/289 (84%)	219 (90%)	19 (8%)	6 (2%)	5	32
63	AW	149/170 (88%)	137 (92%)	10 (7%)	2 (1%)	12	48
64	AY	99/101 (98%)	96 (97%)	2 (2%)	1 (1%)	15	54
65	AT	179/181 (99%)	174 (97%)	3 (2%)	2 (1%)	14	51
66	AZ	119/121 (98%)	113 (95%)	5 (4%)	1 (1%)	19	60
67	A3	117/119 (98%)	110 (94%)	5 (4%)	2 (2%)	9	42
68	A5	221/223 (99%)	197 (89%)	19 (9%)	5 (2%)	6	33
69	AD	245/247 (99%)	232 (95%)	9 (4%)	4 (2%)	9	43
70	AE	378/380 (100%)	350 (93%)	27 (7%)	1 (0%)	41	76
71	AF	388/390 (100%)	355 (92%)	24 (6%)	9 (2%)	6	33
72	AG	116/159 (73%)	106 (91%)	7 (6%)	3 (3%)	5	31
73	AU	178/180 (99%)	162 (91%)	12 (7%)	4 (2%)	6	35
74	AH	183/185 (99%)	163 (89%)	17 (9%)	3 (2%)	9	43
75	AV	153/155 (99%)	142 (93%)	10 (6%)	1 (1%)	22	62
76	Ag	35/37 (95%)	29 (83%)	5 (14%)	1 (3%)	4	29
77	AX	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
78	AJ	216/244 (88%)	201 (93%)	12 (6%)	3 (1%)	11	46
All	All	10111/10698 (94%)	9380 (93%)	565 (6%)	166 (2%)	13	43

5 of 166 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	M	41	GLU
8	V	41	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
10	X	52	LYS
13	R	42	ILE
14	I	70	HIS

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	Q	120/120 (100%)	116 (97%)	4 (3%)	38	61
4	S	114/114 (100%)	111 (97%)	3 (3%)	46	66
5	T	43/43 (100%)	41 (95%)	2 (5%)	26	51
6	M	116/116 (100%)	112 (97%)	4 (3%)	37	60
7	U	132/132 (100%)	129 (98%)	3 (2%)	50	70
8	V	131/140 (94%)	128 (98%)	3 (2%)	50	70
9	E	161/164 (98%)	159 (99%)	2 (1%)	71	83
10	X	88/94 (94%)	87 (99%)	1 (1%)	73	84
11	G	191/191 (100%)	186 (97%)	5 (3%)	46	66
12	W	86/99 (87%)	86 (100%)	0	100	100
13	R	83/97 (86%)	83 (100%)	0	100	100
14	I	154/160 (96%)	150 (97%)	4 (3%)	46	66
15	O	76/76 (100%)	74 (97%)	2 (3%)	46	66
16	Y	137/137 (100%)	132 (96%)	5 (4%)	35	59
17	Z	60/60 (100%)	60 (100%)	0	100	100
18	1	104/104 (100%)	102 (98%)	2 (2%)	57	75
19	2	35/61 (57%)	34 (97%)	1 (3%)	42	64
20	C	167/167 (100%)	164 (98%)	3 (2%)	59	77
21	3	87/87 (100%)	87 (100%)	0	100	100
22	4	70/70 (100%)	68 (97%)	2 (3%)	42	64
23	5	47/52 (90%)	46 (98%)	1 (2%)	53	72

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	6	36/36 (100%)	36 (100%)	0	100	100
25	B	195/195 (100%)	191 (98%)	4 (2%)	53	72
26	D	132/177 (75%)	127 (96%)	5 (4%)	33	57
27	F	233/233 (100%)	223 (96%)	10 (4%)	29	53
28	H	182/190 (96%)	175 (96%)	7 (4%)	33	57
29	K	115/115 (100%)	114 (99%)	1 (1%)	78	87
30	J	177/177 (100%)	170 (96%)	7 (4%)	31	55
31	N	91/91 (100%)	90 (99%)	1 (1%)	73	84
32	P	99/99 (100%)	97 (98%)	2 (2%)	55	74
33	L	151/190 (80%)	147 (97%)	4 (3%)	46	66
37	AL	190/190 (100%)	185 (97%)	5 (3%)	46	66
38	A0	53/53 (100%)	52 (98%)	1 (2%)	57	75
39	AO	121/121 (100%)	117 (97%)	4 (3%)	38	61
40	Ai	87/87 (100%)	85 (98%)	2 (2%)	50	70
41	A2	97/109 (89%)	94 (97%)	3 (3%)	40	62
42	A4	60/60 (100%)	59 (98%)	1 (2%)	60	78
43	A6	83/83 (100%)	80 (96%)	3 (4%)	35	59
44	A7	90/96 (94%)	89 (99%)	1 (1%)	73	84
45	A1	127/131 (97%)	126 (99%)	1 (1%)	81	89
46	AN	135/135 (100%)	132 (98%)	3 (2%)	52	71
47	A8	114/114 (100%)	113 (99%)	1 (1%)	78	87
48	A9	90/90 (100%)	84 (93%)	6 (7%)	16	40
49	Aa	89/89 (100%)	86 (97%)	3 (3%)	37	60
50	Ab	82/92 (89%)	80 (98%)	2 (2%)	49	69
51	Ad	69/73 (94%)	67 (97%)	2 (3%)	42	64
52	Ae	40/47 (85%)	38 (95%)	2 (5%)	24	49
53	Af	45/45 (100%)	44 (98%)	1 (2%)	52	71
54	AP	179/179 (100%)	170 (95%)	9 (5%)	24	49
55	Ah	70/70 (100%)	70 (100%)	0	100	100
56	AI	189/195 (97%)	186 (98%)	3 (2%)	62	79
57	Ac	74/74 (100%)	71 (96%)	3 (4%)	30	55

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	AK	181/181 (100%)	175 (97%)	6 (3%)	38	61
59	AM	106/106 (100%)	105 (99%)	1 (1%)	78	87
60	AS	158/158 (100%)	154 (98%)	4 (2%)	47	68
61	AQ	165/176 (94%)	159 (96%)	6 (4%)	35	59
62	AR	215/250 (86%)	210 (98%)	5 (2%)	50	70
63	AW	128/128 (100%)	121 (94%)	7 (6%)	21	47
64	AY	90/90 (100%)	88 (98%)	2 (2%)	52	71
65	AT	162/162 (100%)	160 (99%)	2 (1%)	71	83
66	AZ	111/111 (100%)	109 (98%)	2 (2%)	59	77
67	A3	110/110 (100%)	106 (96%)	4 (4%)	35	59
68	A5	201/201 (100%)	197 (98%)	4 (2%)	55	74
69	AD	191/191 (100%)	181 (95%)	10 (5%)	23	48
70	AE	335/335 (100%)	332 (99%)	3 (1%)	78	87
71	AF	336/336 (100%)	327 (97%)	9 (3%)	44	65
72	AG	110/142 (78%)	107 (97%)	3 (3%)	44	65
73	AU	162/162 (100%)	160 (99%)	2 (1%)	71	83
74	AH	168/168 (100%)	166 (99%)	2 (1%)	71	83
75	AV	140/140 (100%)	137 (98%)	3 (2%)	53	72
76	Ag	34/34 (100%)	33 (97%)	1 (3%)	42	64
77	AX	92/92 (100%)	91 (99%)	1 (1%)	73	84
78	AJ	204/224 (91%)	200 (98%)	4 (2%)	55	74
All	All	9096/9417 (97%)	8871 (98%)	225 (2%)	50	68

5 of 225 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	A9	76	PHE
78	AJ	45	ILE
57	Ac	55	LYS
76	Ag	8	TYR
70	AE	237	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
54	AP	159	HIS
61	AQ	92	HIS
70	AE	253	HIS
61	AQ	59	GLN
62	AR	221	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1588/1608 (98%)	480 (30%)	100 (6%)
2	7	74/75 (98%)	33 (44%)	5 (6%)
34	AA	3165/3192 (99%)	971 (30%)	189 (5%)
35	AC	148/151 (98%)	49 (33%)	10 (6%)
36	AB	117/118 (99%)	27 (23%)	2 (1%)
All	All	5092/5144 (98%)	1560 (30%)	306 (6%)

5 of 1560 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	2	A
1	A	3	C
1	A	5	U
1	A	17	C
1	A	26	A

5 of 306 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	AA	2665	A
34	AA	3667	C
34	AA	2886	A
34	AA	3309	G
35	AC	114	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
63	AW	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AW	154:ASN	C	197:UNK	N	36.79

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-6452. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution

This section was not generated.

7.2 Volume estimate versus contour level

This section was not generated.

7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.