



## wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 11:14 AM EST

PDB ID : 3JBN  
EMDB ID : EMD-6456  
Title : Cryo-electron microscopy reconstruction of the Plasmodium falciparum 80S ribosome bound to P-tRNA  
Authors : Sun, M.; Li, W.; Blomqvist, K.; Das, S.; Hashem, Y.; Dvorin, J.D.; Frank, J.  
Deposited on : 2015-09-16  
Resolution : 4.70 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev43  
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) : 2.31.3

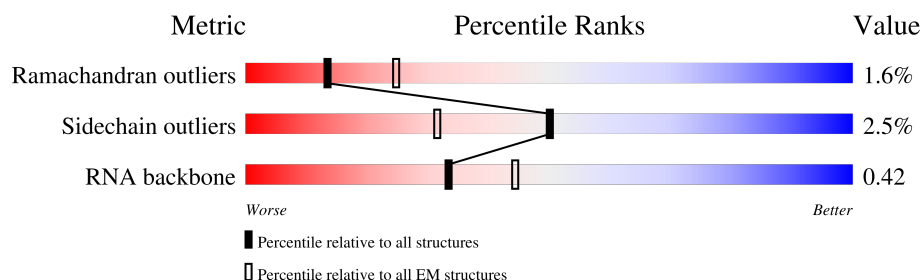
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.70 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.






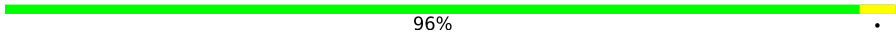
















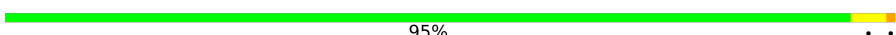




Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	
2	7	76	
3	D	209	
4	E	185	
5	G	224	
6	I	189	
7	K	129	
8	M	138	
9	W	108	






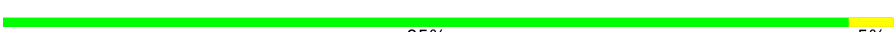






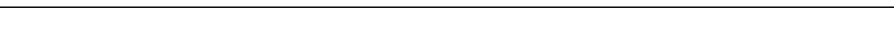

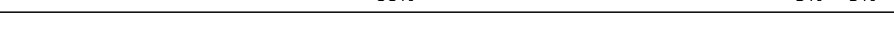

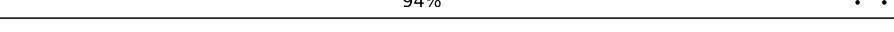

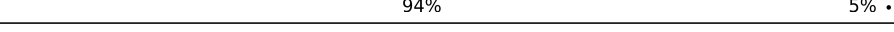





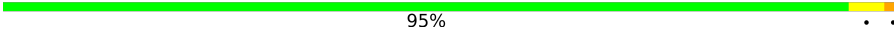
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Mol	Chain	Length	Quality of chain
10	R	114	
11	O	79	
12	Y	154	
13	Z	72	
14	1	120	
15	2	68	
16	3	95	
17	4	76	
18	5	65	
19	6	43	
20	B	210	
21	F	257	
22	H	214	
23	J	188	
24	L	214	
25	N	98	
26	P	127	
27	Q	144	
28	S	128	
29	T	48	
30	U	149	
31	V	156	
32	X	103	
33	C	195	
34	AA	3193	





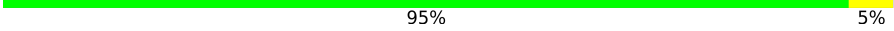




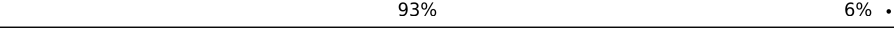

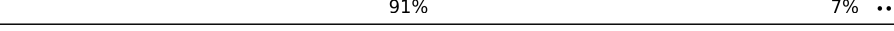


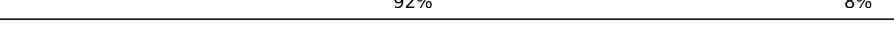


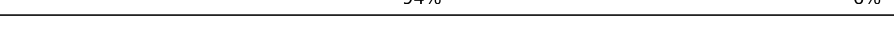

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Mol	Chain	Length	Quality of chain
35	AC	151	 28% 52% 19% .
36	AB	118	 32% 55% 13%
37	AL	211	 91% 7% .
38	A1	145	 90% 6% .
39	A2	118	 82% 6% 12%
40	A4	66	 95% 5%
41	A6	98	 96% .
42	A7	102	 85% 7% . 6%
43	AN	146	 91% 9%
44	A8	125	 86% 12% .
45	A9	103	 89% 10% .
46	Aa	106	 88% 8% .
47	Ab	105	 83% 8% 10%
48	Ad	76	 88% 5% . 5%
49	Ae	50	 72% 14% 14%
50	Af	51	 94% . .
51	AP	204	 84% 12% .
52	Ah	85	 94% 5% .
53	Ai	95	 91% 8% .
54	AI	213	 92% 6% .
55	AJ	244	 83% 8% 9%
56	Ac	89	 87% 10% .
57	AK	201	 92% . .
58	AM	132	 95% . .
59	AS	186	 88% 9% .

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Mol	Chain	Length	Quality of chain
60	AO	147	 87% 11% .
61	AQ	205	 80% 10% . 8%
62	AR	289	 77% 9% . 13%
63	AW	170	 92% 7% .
64	AY	101	 95% 5%
65	AT	181	 92% 8%
66	AZ	121	 88% 9% .
67	A3	119	 92% 8% .
68	A5	223	 88% 10% ..
69	AD	247	 93% 6% .
70	AE	380	 90% 9% .
71	AF	390	 91% 7% ..
72	AG	159	 70% 6% .. 22%
73	AU	180	 90% 7% .
74	AH	185	 92% 8% .
75	AV	155	 89% 10% .
76	Ag	37	 70% 24% 5%
77	AX	97	 94% 6%
78	A0	62	 90% 5% 5%

## 2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 193061 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
1	A	1608	Total	C	N	O	P	0	0
			34207	15346	6106	11169	1586		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	76	Total	C	N	O	P	0	0
			1620	723	295	527	75		

- Molecule 3 is a protein called 40S ribosomal protein uS3.

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

- Molecule 4 is a protein called 40S ribosomal protein uS4.

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

- Molecule 5 is a protein called 40S ribosomal protein uS5.

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

- Molecule 6 is a protein called 40S ribosomal protein uS7.

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

- Molecule 7 is a protein called 40S ribosomal protein uS8.

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

- Molecule 8 is a protein called 40S ribosomal protein uS9.

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

- Molecule 9 is a protein called 40S ribosomal protein eS17.

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

- Molecule 10 is a protein called 40S ribosomal protein eS12.

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

- Molecule 11 is a protein called 40S ribosomal protein eS10.

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

- Molecule 12 is a protein called 40S ribosomal protein eS19.

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

- Molecule 13 is a protein called 40S ribosomal protein eS21.

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

- Molecule 14 is a protein called 40S ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	1	120	Total	C	N	O	S	0	0
			986	632	189	163	2		

- Molecule 15 is a protein called 40S ribosomal protein eS25.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	2	41	Total	C	N	O	0	0
			321	208	56	57		

- Molecule 16 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	3	95	Total	C	N	O	S	0	0
			782	478	169	129	6		

- Molecule 17 is a protein called 40S ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	4	76	Total	C	N	O	S	0	0
			586	368	102	107	9		

- Molecule 18 is a protein called 40S ribosomal protein eS28.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	5	58	Total	C	N	O	0	0
			458	285	93	80		

- Molecule 19 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	6	43	Total	C	N	O	0	0
			346	213	75	58		

- Molecule 20 is a protein called 40S ribosomal protein eS1.

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

- Molecule 21 is a protein called 40S ribosomal protein eS4.



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

- Molecule 22 is a protein called 40S ribosomal protein eS6.

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

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 23 is a protein called 40S ribosomal protein eS7.

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

- Molecule 24 is a protein called 40S ribosomal protein eS8.

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

- Molecule 25 is a protein called 40S ribosomal protein uS10.

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

- Molecule 26 is a protein called 40S ribosomal protein uS11.

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

- Molecule 27 is a protein called 40S ribosomal protein uS12.

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

- Molecule 28 is a protein called 40S ribosomal protein uS13.

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

- Molecule 29 is a protein called 40S ribosomal protein uS14.

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

- Molecule 30 is a protein called 40S ribosomal protein uS15.

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

- Molecule 31 is a protein called 40S ribosomal protein uS17.

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

- Molecule 32 is a protein called 40S ribosomal protein uS19.

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

- Molecule 33 is a protein called 40S ribosomal protein uS2.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AA	3193	Total	C	N	O	P	0	0
			67884	30446	12054	22223	3161		

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

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

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

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

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

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

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 eL27.

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

- Molecule 39 is a protein called 60S ribosomal protein eL28.

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

- Molecule 40 is a protein called 60S ribosomal protein eL29.

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

- Molecule 41 is a protein called 60S ribosomal protein eL30.

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

- Molecule 42 is a protein called 60S ribosomal protein eL31.

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

- Molecule 43 is a protein called 60S ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	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 44 is a protein called 60S ribosomal protein eL32.

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

- Molecule 45 is a protein called 60S ribosomal protein eL33.

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

- Molecule 46 is a protein called 60S ribosomal protein eL34.

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

- Molecule 47 is a protein called 60S ribosomal protein eL36.

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

- Molecule 48 is a protein called 60S ribosomal protein eL38.

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

- Molecule 49 is a protein called 60S ribosomal protein eL39.

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

- Molecule 50 is a protein called 60S ribosomal protein eL40.

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

- Molecule 51 is a protein called 60S ribosomal protein eL15.

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

- Molecule 52 is a protein called 60S ribosomal protein eL43.

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

- Molecule 53 is a protein called 60S ribosomal protein eL44.

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

- Molecule 54 is a protein called 60S ribosomal protein eL6.

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

- Molecule 55 is a protein called 60S ribosomal protein eL8.

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

- Molecule 56 is a protein called 60S ribosomal protein eL37.

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

- Molecule 57 is a protein called 60S ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	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 58 is a protein called 60S ribosomal protein uL14.

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

- Molecule 59 is a protein called 60S ribosomal protein eL18.

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

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

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

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

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

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

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

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
63	AW	170	Total	C	N	O	S	0	0
			1319	824	266	222	7		

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

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

- 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
72	AG	124	Total	C	N	O	S	0	0
			1011	636	197	172	6		

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

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

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

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

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

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

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

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

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

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

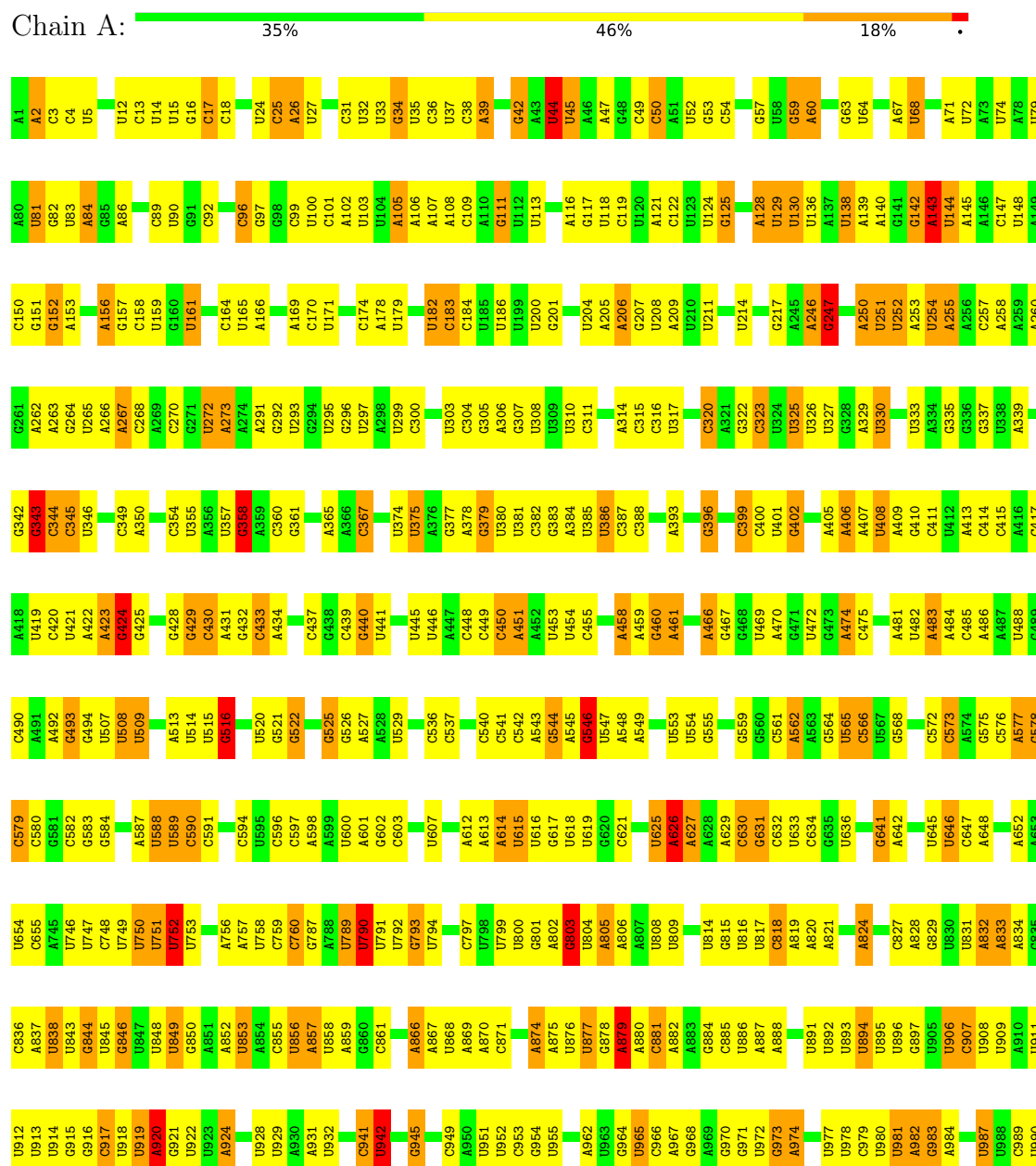
- Molecule 78 is a protein called 60S ribosomal protein eL24.

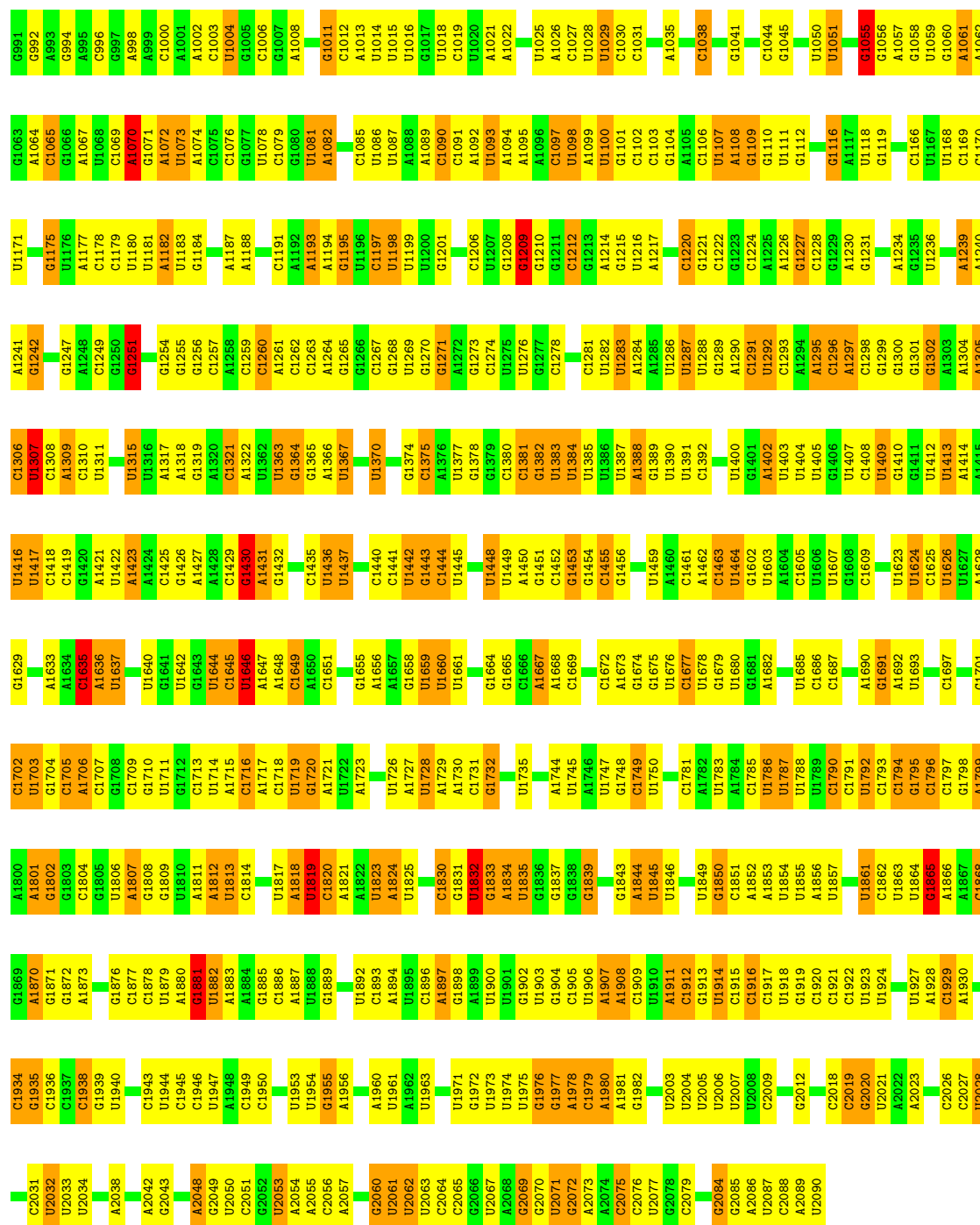
Mol	Chain	Residues	Atoms					AltConf	Trace
78	A0	62	Total	C	N	O	S	0	0
			522	336	97	88	1		

### 3 Residue-property plots

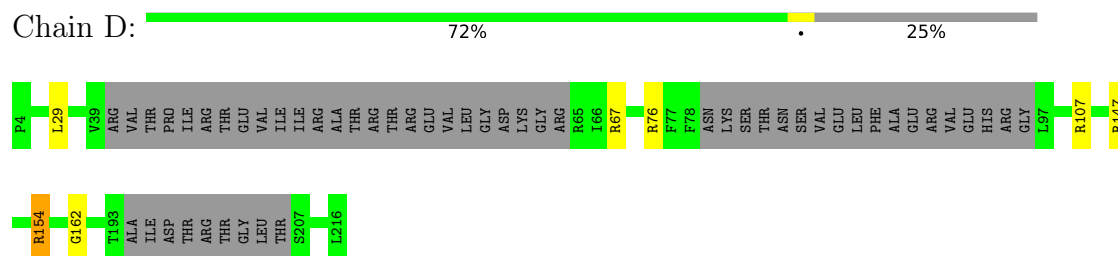
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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

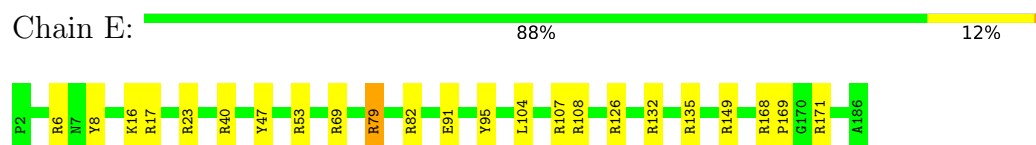




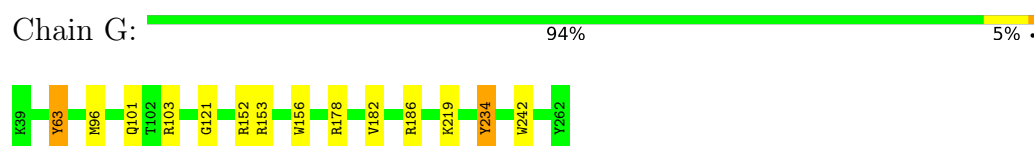
- Molecule 3: 40S ribosomal protein uS3



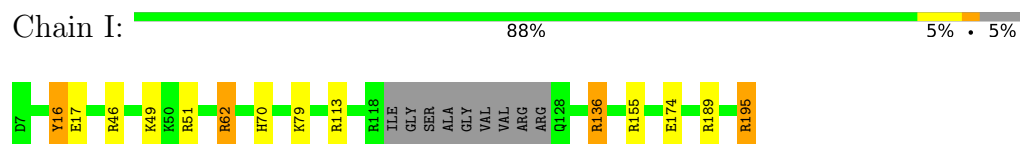
- Molecule 4: 40S ribosomal protein uS4



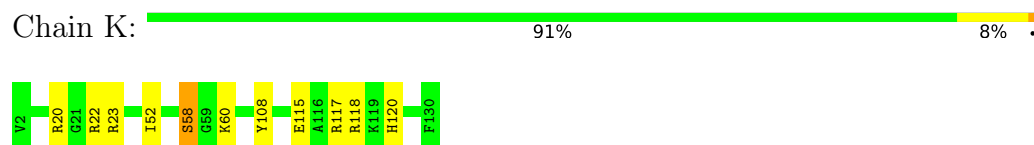
- Molecule 5: 40S ribosomal protein uS5



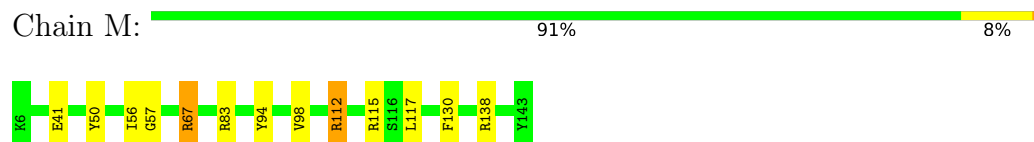
- Molecule 6: 40S ribosomal protein uS7



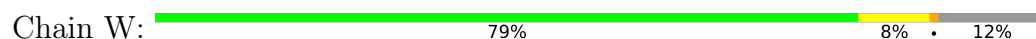
- Molecule 7: 40S ribosomal protein uS8

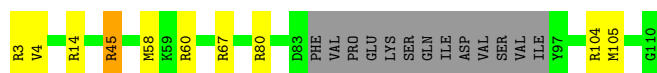


- Molecule 8: 40S ribosomal protein uS9



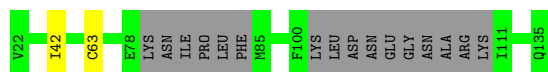
- Molecule 9: 40S ribosomal protein eS17





- Molecule 10: 40S ribosomal protein eS12

Chain R: 84% 14%



- Molecule 11: 40S ribosomal protein eS10

Chain O: 87% 13%



- Molecule 12: 40S ribosomal protein eS19

Chain Y: 88% 11%



- Molecule 13: 40S ribosomal protein eS21

Chain Z: 96%



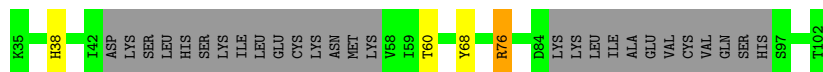
- Molecule 14: 40S ribosomal protein eS24

Chain 1: 88% 11%



- Molecule 15: 40S ribosomal protein eS25

Chain 2: 54% 40%

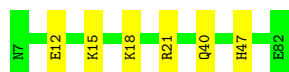


- Molecule 16: 40S ribosomal protein eS26

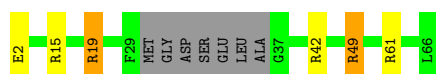
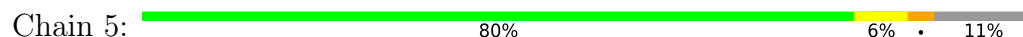
Chain 3: 85% 14%



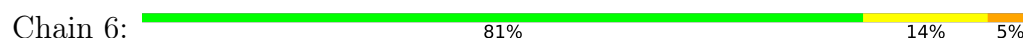
- Molecule 17: 40S ribosomal protein eS27



- Molecule 18: 40S ribosomal protein eS28



- Molecule 19: 40S ribosomal protein eS30



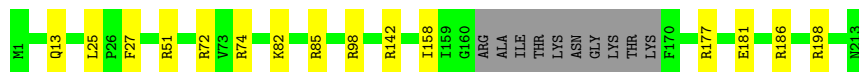
- Molecule 20: 40S ribosomal protein eS1



- Molecule 21: 40S ribosomal protein eS4



- Molecule 22: 40S ribosomal protein eS6

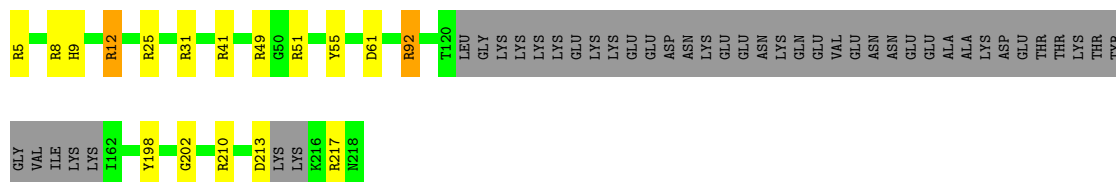


- Molecule 23: 40S ribosomal protein eS7





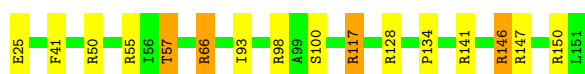
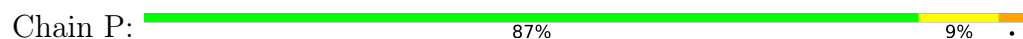
- Molecule 24: 40S ribosomal protein eS8



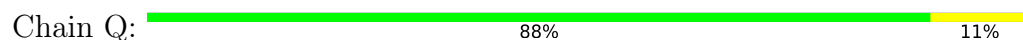
- Molecule 25: 40S ribosomal protein uS10



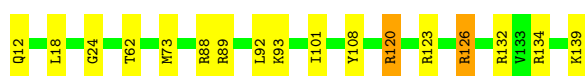
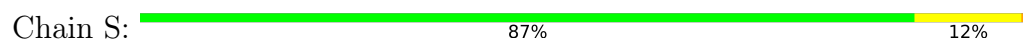
- Molecule 26: 40S ribosomal protein uS11



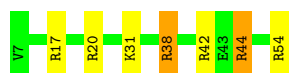
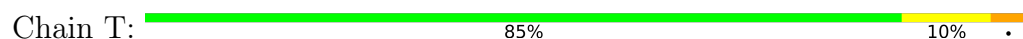
- Molecule 27: 40S ribosomal protein uS12



- Molecule 28: 40S ribosomal protein uS13



- Molecule 29: 40S ribosomal protein uS14




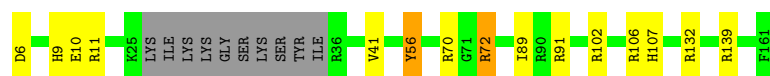
- Molecule 30: 40S ribosomal protein uS15

Chain U:  95% . .




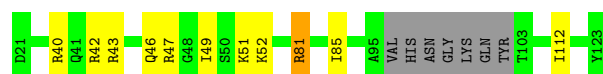
- Molecule 31: 40S ribosomal protein uS17

Chain V:  84% 8% 6%



- Molecule 32: 40S ribosomal protein uS19

Chain X:  83% 10% 7%



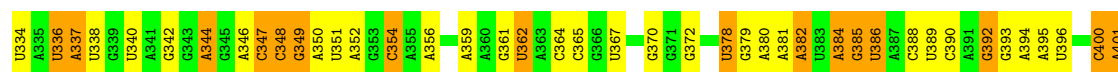
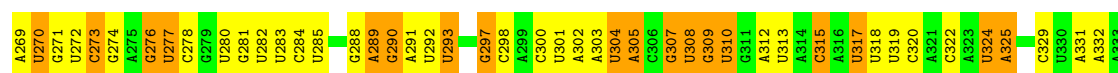
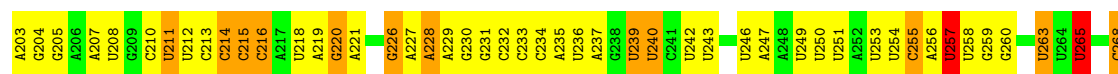
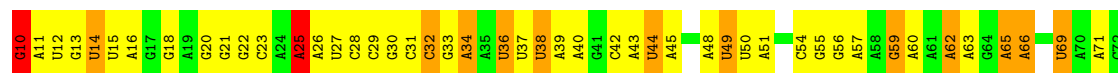
- Molecule 33: 40S ribosomal protein uS2

Chain C:  94% 6%



- Molecule 34: 28S ribosomal RNA

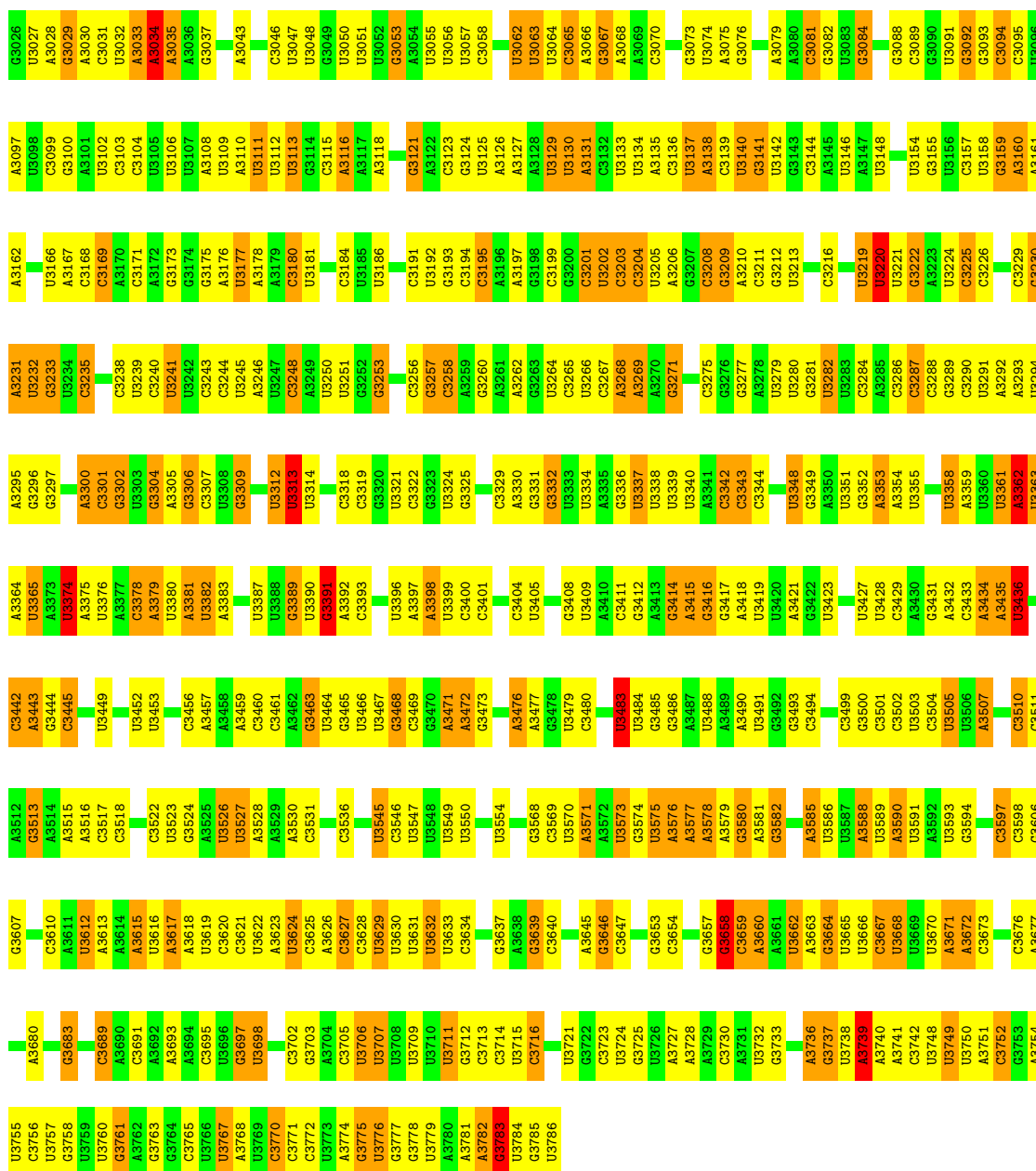
Chain AA:  33% 46% 19%





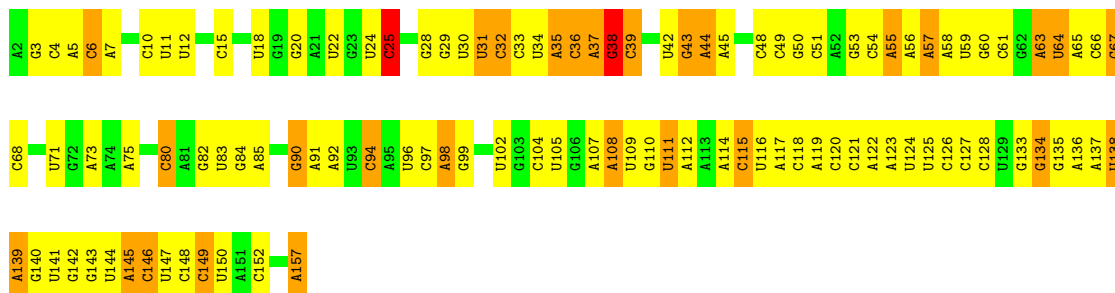
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U1421	A1422	G1423	C1424	G1425	G1426	U1427	G1428	A1429	U1430	A1431	G1432	U1433	U1434	G1435	A1436	U1437	G1440	G1441	G1442	U1443	A1444	G1445	G1446	G1447	G1448	G1449	G1450	A1451	U1452	G1453	G1454	G1455	G1456	G1457	A1458	U1459	A1460	C1461	G1462	G1463	G1464	G1465	G1466	A1467	U1468	G1469	G1470	A1471	A1472	A1473	A1474	G1475	A1476	A1477	G1478	G1479	G1480	A1481	G1482	U1483	A1484	U1485	U1486	U1487	U1488	U1489	U1490	U1491	U1492	U1493	U1494	U1495																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
G1289	C1290	U1291	U1292	U1293	G1294	A1295	U1296	U1297	U1298	G1299	G1300	U1301	G1302	C1303	G1304	U1305	A1306	U1307	A1308	U1309	A1310	U1311	U1312	G1313	G1314	G1315	U1316	U1317	G1320	A1321	G1322	U1323	U1324	G1325	G1326	U1327	U1328	U1329	A1330	A1331	G1332	G1333	G1334	U1335	U1336	G1337	U1338	U1339	G1340	G1341	U1342	U1343	U1344	U1345	U1346	U1347	U1348	U1349	U1350	U1351	U1352	U1353	U1354	U1355	U1356	U1357	U1358	U1359	U1360	U1361	U1362	U1363	U1364	U1365	U1366	U1367	U1368	U1369	U1370	U1371	U1372	U1373	U1374	U1375	U1376	U1377	U1378	U1379	U1380	U1381	U1382	U1383	U1384	U1385	U1386	U1387	U1388	U1389	U1390	U1391	U1392	U1393	U1394	U1395	U1396	U1397	U1398	U1399	U1400	U1401	U1402	U1403	U1404	U1405	U1406	U1407	U1408	U1409	U1410	U1411	U1412	U1413	U1414	U1415	U1416	U1417	U1418	U1419	U1420	U1421	U1422	U1423	U1424	U1425	U1426	U1427	U1428	U1429	U1430	U1431	U1432	U1433	U1434	U1435	U1436	U1437	U1438	U1439	U1440	U1441	U1442	U1443	U1444	U1445	U1446	U1447	U1448	U1449	U1450	U1451	U1452	U1453	U1454	U1455	U1456	U1457	U1458	U1459	U1460	U1461	U1462	U1463	U1464	U1465	U1466	U1467	U1468	U1469	U1470	U1471	U1472	U1473	U1474	U1475	U1476	U1477	U1478	U1479	U1480	U1481	U1482	U1483	U1484	U1485	U1486	U1487	U1488	U1489	U1490	U1491	U1492	U1493	U1494	U1495																																																																																																																																																																																																																																																																																																																																																																																																																	
A1221	U1222	U1223	U1224	U1225	A1226	U1227	U1228	U1229	U1230	A1231	U1232	U1233	A1234	C1235	U1236	U1237	U1238	U1239	A1240	U1241	U1242	U1243	G1244	U1245	C1246	C1247	U1251	U1252	U1253	U1254	U1255	U1256	U1257	U1258	U1259	C1260	U1261	U1262	U1263	U1264	U1265	U1266	U1267	U1268	U1269	U1270	U1271	U1272	U1273	U1274	U1275	U1276	U1277	U1278	U1279	U1280	U1281	U1282	U1283	U1284	U1285	U1286	U1287	U1288	U1289	U1290	U1291	U1292	U1293	U1294	U1295	U1296	U1297	U1298	U1299	U1300	U1301	U1302	U1303	U1304	U1305	U1306	U1307	U1308	U1309	U1310	U1311	U1312	U1313	U1314	U1315	U1316	U1317	U1318	U1319	U1320	U1321	U1322	U1323	U1324	U1325	U1326	U1327	U1328	U1329	U1330	U1331	U1332	U1333	U1334	U1335	U1336	U1337	U1338	U1339	U1340	U1341	U1342	U1343	U1344	U1345	U1346	U1347	U1348	U1349	U1350	U1351	U1352	U1353	U1354	U1355	U1356	U1357	U1358	U1359	U1360	U1361	U1362	U1363	U1364	U1365	U1366	U1367	U1368	U1369	U1370	U1371	U1372	U1373	U1374	U1375	U1376	U1377	U1378	U1379	U1380	U1381	U1382	U1383	U1384	U1385	U1386	U1387	U1388	U1389	U1390	U1391	U1392	U1393	U1394	U1395	U1396	U1397	U1398	U1399	U1400	U1401	U1402	U1403	U1404	U1405	U1406	U1407	U1408	U1409	U1410	U1411	U1412	U1413	U1414	U1415	U1416	U1417	U1418	U1419	U1420	U1421	U1422	U1423	U1424	U1425	U1426	U1427	U1428	U1429	U1430	U1431	U1432	U1433	U1434	U1435	U1436	U1437	U1438	U1439	U1440	U1441	U1442	U1443	U1444	U1445	U1446	U1447	U1448	U1449	U1450	U1451	U1452	U1453	U1454	U1455	U1456	U1457	U1458	U1459	U1460	U1461	U1462	U1463	U1464	U1465	U1466	U1467	U1468	U1469	U1470	U1471	U1472	U1473	U1474	U1475	U1476	U1477	U1478	U1479	U1480	U1481	U1482	U1483	U1484	U1485	U1486	U1487	U1488	U1489	U1490	U1491	U1492	U1493	U1494	U1495																																																																																																																																																																																																																																																																																																																																														
U1776	U1777	U1778	U1779	U1780	U1781	U1782	U1783	U1784	U1785	U1786	U1787	U1788	U1789	U1790	U1791	U1792	U1793	U1794	U1795	U1796	U1797	U1798	U1799	U1800	U1801	U1802	U1803	U1804	U1805	U1806	U1807	U1808	U1809	U1810	U1811	U1812	U1813	U1814	U1815	U1816	U1817	U1818	U1819	U1820	U1821	U1822	U1823	U1824	U1825	U1826	U1827	U1828	U1829	U1830	U1831	U1832	U1833	U1834	U1835	U1836	U1837	U1838	U1839	U1840	U1841	U1842	U1843	U1844	U1845	U1846	U1847	U1848	U1849	U1850	U1851	U1852	U1853	U1854	U1855	U1856	U1857	U1858	U1859	U1860	U1861	U1862	U1863	U1864	U1865	U1866	U1867	U1868	U1869	U1870	U1871	U1872	U1873	U1874	U1875	U1876	U1877	U1878	U1879	U1880	U1881	U1882	U1883	U1884	U1885	U1886	U1887	U1888	U1889	U1890	U1891	U1892	U1893	U1894	U1895	U1896	U1897	U1898	U1899	U1900	U1901	U1902	U1903	U1904	U1905	U1906	U1907	U1908	U1909	U1910	U1911	U1912	U1913	U1914	U1915	U1916	U1917	U1918	U1919	U1920	U1921	U1922	U1923	U1924	U1925	U1926	U1927	U1928	U1929	U1930	U1931	U1932	U1933	U1934	U1935	U1936	U1937	U1938	U1939	U1940	U1941	U1942	U1943	U1944	U1945	U1946	U1947	U1948	U1949	U1950	U1951	U1952	U1953	U1954	U1955	U1956	U1957	U1958	U1959	U1960	U1961	U1962	U1963	U1964	U1965	U1966	U1967	U1968	U1969	U1970	U1971	U1972	U1973	U1974	U1975	U1976	U1977	U1978	U1979	U1980	U1981	U1982	U1983	U1984	U1985	U1986	U1987	U1988	U1989	U1990	U1991	U1992	U1993	U1994	U1995	U1996	U1997	U1998	U1999	U2000	U2001	U2002	U2003	U2004	U2005	U2006	U2007	U2008	U2009	U2010	U2011	U2012	U2013	U2014	U2015	U2016	U2017	U2018	U2019	U2020	U2021	U2022	U2023	U2024	U2025	U2026	U2027	U2028	U2029	U2030	U2031	U2032	U2033	U2034	U2035	U2036	U2037	U2038	U2039	U2040	U2041	U2042	U2043	U2044	U2045	U2046	U2047	U2048	U2049	U2050	U2051	U2052	U2053	U2054	U2055	U2056	U2057	U2058	U2059	U2060	U2061	U2062	U2063	U2064	U2065	U2066	U2067	U2068	U2069	U2070	U2071	U2072	U2073	U2074	U2075	U2076	U2077	U2078	U2079	U2080	U2081	U2082	U2083	U2084	U2085	U2086	U2087	U2088	U2089	U2090	U2091	U2092	U2093	U2094	U2095	U2096	U2097	U2098	U2099	U2100	U2101	U2102	U2103	U2104	U2105	U2106	U2107	U2108	U2109	U2110	U2111	U2112	U2113	U2114	U2115	U2116	U2117	U2118	U2119	U2120	U2121	U2122	U2123	U2124	U2125	U2126	U2127	U2128	U2129	U2130	U2131	U2132	U2133	U2134	U2135	U2136	U2137	U2138	U2139	U2140	U2141	U2142	U2143	U2144	U2145	U2146	U2147	U2148	U2149	U2150	U2151	U2152	U2153	U2154	U2155	U2156	U2157	U2158	U2159	U2160	U2161	U2162	U2163	U2164	U2165	U2166	U2167	U2168	U2169	U2170	U2171	U2172	U2173	U2174	U2175	U2176	U2177	U2178	U2179	U2180	U2181	U2182	U2183	U2184	U2185	U2186	U2187	U2188	U2189	U2190	U2191	U2192	U2193	U2194	U2195	U2196	U2197	U2198	U2199	U2200	U2201	U2202	U2203	U2204	U2205	U2206	U2207	U2208	U2209	U2210	U2211	U2212	U2213	U2214	U2215	U2216	U2217	U2218	U2219	U2220	U2221	U2222	U2223	U2224	U2225	U2226	U2227	U2228	U2229	U2230	U2231	U2232	U2233	U2234	U2235	U2236	U2237	U2238	U2239	U2240	U2241	U2242	U2243	U2244	U2245	U2246	U2247	U2248	U2249	U2250	U2251	U2252	U2253	U2254	U2255	U2256	U2257	U2258	U2259	U2260	U2261	U2262	U2263	U2264	U2265	U2266	U2267	U2268	U2269	U2270	U2271	U2272	U2273	U2274	U2275	U2276	U2277	U2278	U2279	U2280	U2281	U2282	U2283	U2284	U2285	U2286	U2287	U2288	U2289	U2290	U2291	U2292	U2293	U2294	U2295	U2296	U2297	U2298	U2299	U2300	U2301	U2302	U2303	U2304	U2305	U2306	U2307	U2308	U2309	U2310	U2311	U2312	U2313	U2314	U2315	U2316	U2317	U2318	U2319	U2320	U2321	U2322	U2323	U2324	U2325	U2326	U2327	U2328	U2329	U2330	U2331	U2332	U2333	U2334	U2335	U2336	U2337	U2338	U2339	U2340	U2341	U2342	U2343	U2344	U2345	U2346	U2347	U2348	U2349	U2350	U2351	U2352	U2353	U2354	U2355	U2356	U2357	U2358	U2359	U2360	U2361	U2362	U2363	U2364	U2365	U2366	U2367	U2368	U2369	U2370	U2371	U2372	U2373	U2374	U2375	U2376	U2377	U2378	U2379	U2380	U2381



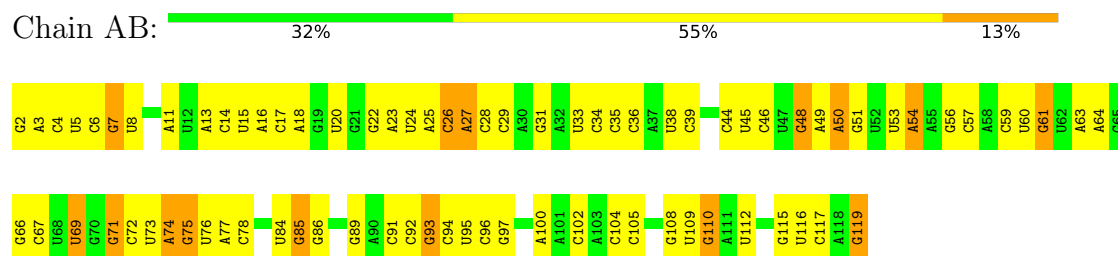


### ● Molecule 35: 5.8S ribosomal RNA

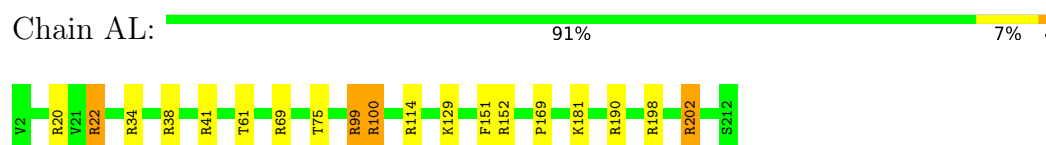
Chain AC: 28% 52% 19%



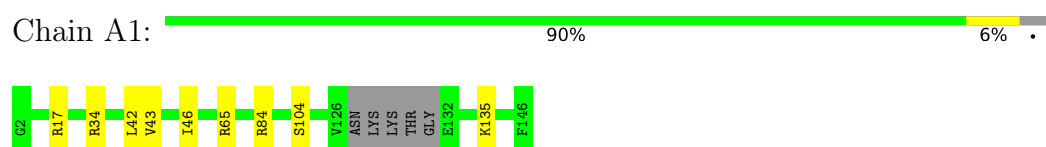
- Molecule 36: 5S ribosomal RNA



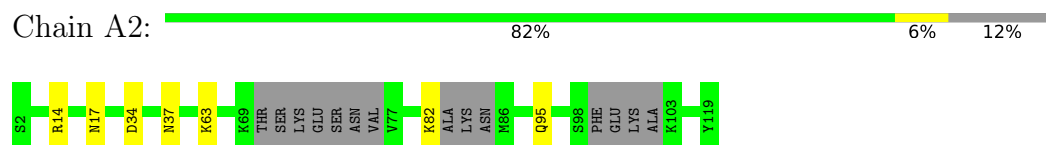
- Molecule 37: 60S ribosomal protein eL13



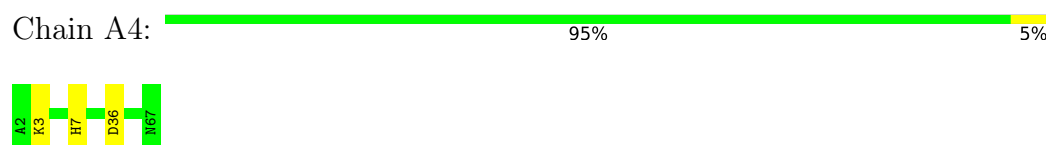
- Molecule 38: 60S ribosomal protein eL27



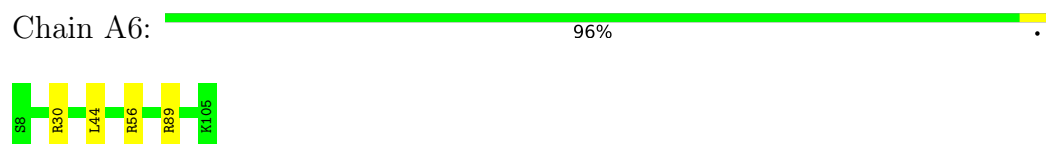
- Molecule 39: 60S ribosomal protein eL28



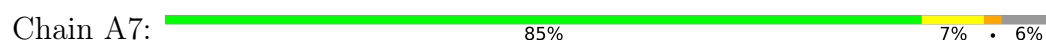
- Molecule 40: 60S ribosomal protein eL29

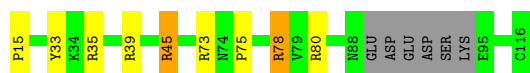


- Molecule 41: 60S ribosomal protein eL30



- Molecule 42: 60S ribosomal protein eL31





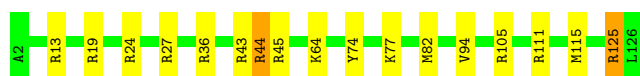
- Molecule 43: 60S ribosomal protein eL14

Chain AN: 91% 9%



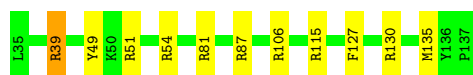
- Molecule 44: 60S ribosomal protein eL32

Chain A8: 86% 12%



- Molecule 45: 60S ribosomal protein eL33

Chain A9: 89% 10%



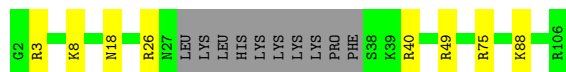
- Molecule 46: 60S ribosomal protein eL34

Chain Aa: 88% 8%



- Molecule 47: 60S ribosomal protein eL36

Chain Ab: 83% 8% 10%



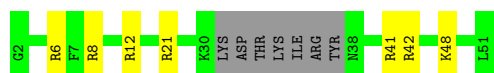
- Molecule 48: 60S ribosomal protein eL38

Chain Ad: 88% 5% 5%



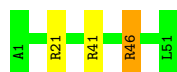
- Molecule 49: 60S ribosomal protein eL39

Chain Ae: 72% 14% 14%



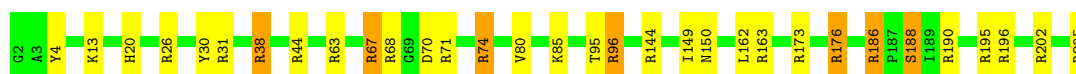
- Molecule 50: 60S ribosomal protein eL40

Chain Af: 94% . .



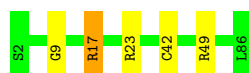
- Molecule 51: 60S ribosomal protein eL15

Chain AP: 84% 12% .



- Molecule 52: 60S ribosomal protein eL43

Chain Ah: 94% 5% .



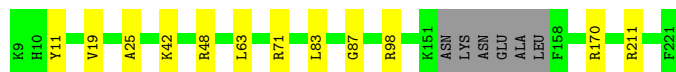
- Molecule 53: 60S ribosomal protein eL44

Chain Ai: 91% 8% .



- Molecule 54: 60S ribosomal protein eL6

Chain AI: 92% 6% .




- Molecule 55: 60S ribosomal protein eL8

Chain AJ: 83% 8% 9%



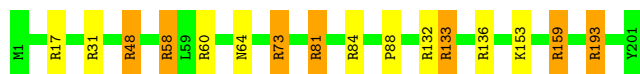
- Molecule 56: 60S ribosomal protein eL37

Chain Ac:  87% 10%



- Molecule 57: 60S ribosomal protein uL13

Chain AK:  92%




- Molecule 58: 60S ribosomal protein uL14

Chain AM:  95%



- Molecule 59: 60S ribosomal protein eL18

Chain AS:  88% 9%




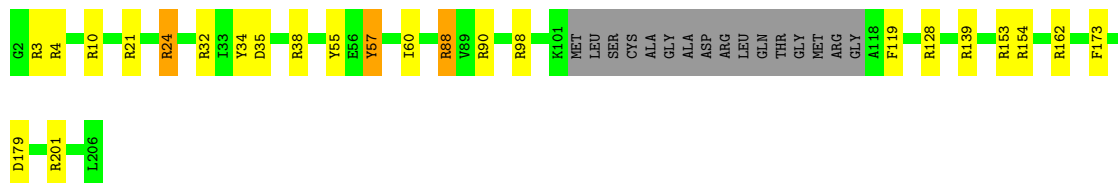
- Molecule 60: 60S ribosomal protein uL15

Chain AO:  87% 11%




- Molecule 61: 60S ribosomal protein uL16

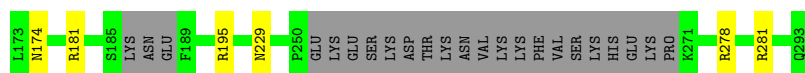
Chain AQ:  80% 10% 8%



- Molecule 62: 60S ribosomal protein uL18

Chain AR:  77% 9% 13%





- Molecule 63: 60S ribosomal protein uL22

Chain AW: 92% 7% .



- Molecule 64: 60S ribosomal protein uL23

Chain AY: 95% 5%



- Molecule 65: 60S ribosomal protein eL19

Chain AT: 92% 8%



- Molecule 66: 60S ribosomal protein uL24

Chain AZ: 88% 9% .



- Molecule 67: 60S ribosomal protein uL29

Chain A3: 92% 8% .



- Molecule 68: 60S ribosomal protein uL30

Chain A5: 88% 10% ..



- Molecule 69: 60S ribosomal protein uL2

Chain AD: 93% 6% .





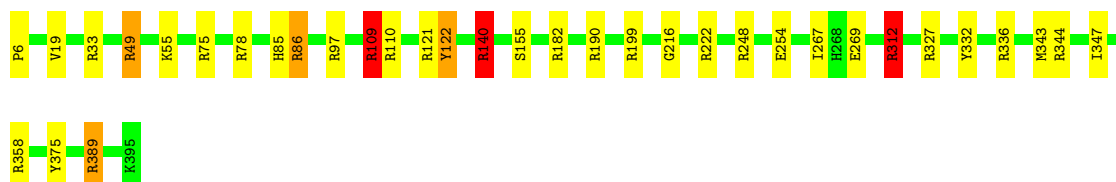
- Molecule 70: 60S ribosomal protein uL3

Chain AE: 90% 9% .



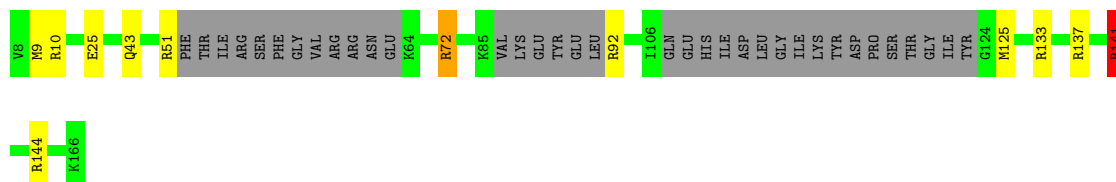
- Molecule 71: 60S ribosomal protein uL4

Chain AF: 91% 7% ..



- Molecule 72: 60S ribosomal protein uL5

Chain AG: 70% 6% .. 22%



- Molecule 73: 60S ribosomal protein eL20

Chain AU: 90% 7% .




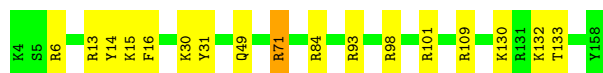
- Molecule 74: 60S ribosomal protein uL6

Chain AH: 92% 8% .



- Molecule 75: 60S ribosomal protein eL21

Chain AV:  89% 10%



- Molecule 76: 60S ribosomal protein eL41

Chain Ag:  70% 24% 5%



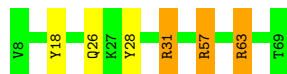
- Molecule 77: 60S ribosomal protein eL22

Chain AX:  94% 6%



- Molecule 78: 60S ribosomal protein eL24

Chain A0:  90% 5% 5%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	14696	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 ⓘ

### 5.1 Standard geometry ⓘ

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	4/38275 (0.0%)	1.54	870/59596 (1.5%)
2	7	1.12	0/1810	1.64	62/2821 (2.2%)
3	D	0.76	0/1241	1.05	5/1652 (0.3%)
4	E	0.72	0/1539	1.14	14/2055 (0.7%)
5	G	0.70	0/1800	1.03	10/2429 (0.4%)
6	I	0.71	0/1443	1.10	12/1936 (0.6%)
7	K	0.72	0/1054	1.09	4/1411 (0.3%)
8	M	0.72	0/1114	1.12	8/1487 (0.5%)
9	W	0.72	0/793	1.14	5/1053 (0.5%)
10	R	0.75	0/755	0.94	0/1013
11	O	0.74	0/706	1.02	4/950 (0.4%)
12	Y	0.71	0/1295	1.15	10/1742 (0.6%)
13	Z	0.70	0/565	0.99	2/758 (0.3%)
14	1	0.72	0/999	1.17	9/1321 (0.7%)
15	2	0.76	0/324	1.01	3/435 (0.7%)
16	3	0.75	0/794	1.32	14/1055 (1.3%)
17	4	0.66	0/597	1.01	2/801 (0.2%)
18	5	0.78	0/459	1.24	5/606 (0.8%)
19	6	0.75	0/349	1.21	5/458 (1.1%)
20	B	0.67	0/1738	1.11	8/2321 (0.3%)
21	F	0.68	0/2098	1.11	18/2819 (0.6%)
22	H	0.69	0/1665	1.09	11/2210 (0.5%)
23	J	0.69	0/1545	1.07	8/2064 (0.4%)
24	L	0.73	0/1407	1.18	12/1879 (0.6%)
25	N	0.68	0/780	1.17	5/1053 (0.5%)
26	P	0.70	0/966	1.26	14/1295 (1.1%)
27	Q	0.72	0/1149	1.19	13/1532 (0.8%)
28	S	0.65	0/1063	1.17	10/1425 (0.7%)
29	T	0.76	0/412	1.13	3/544 (0.6%)
30	U	0.70	0/1223	1.03	6/1634 (0.4%)
31	V	0.74	0/1233	1.06	8/1645 (0.5%)
32	X	0.71	0/788	1.17	7/1050 (0.7%)
33	C	0.68	0/1570	1.04	4/2129 (0.2%)
34	AA	1.11	8/75947 (0.0%)	1.54	1829/118255 (1.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	AC	1.13	0/3599	1.55	91/5603 (1.6%)
36	AB	1.11	2/2823 (0.1%)	1.50	67/4400 (1.5%)
37	AL	0.70	0/1789	1.16	13/2381 (0.5%)
38	A1	0.71	0/1151	1.02	5/1531 (0.3%)
39	A2	0.73	0/840	0.97	1/1114 (0.1%)
40	A4	0.67	0/564	0.99	0/737
41	A6	0.71	0/749	0.98	1/1001 (0.1%)
42	A7	0.72	0/806	1.20	9/1073 (0.8%)
43	AN	0.70	0/1218	1.04	3/1621 (0.2%)
44	A8	0.71	0/1054	1.25	11/1399 (0.8%)
45	A9	0.72	0/865	1.24	12/1160 (1.0%)
46	Aa	0.70	0/872	1.24	12/1161 (1.0%)
47	Ab	0.72	0/763	1.11	4/1008 (0.4%)
48	Ad	0.72	0/612	1.14	5/812 (0.6%)
49	Ae	0.81	0/396	1.27	4/521 (0.8%)
50	Af	0.71	0/419	1.06	2/556 (0.4%)
51	AP	0.72	0/1735	1.24	26/2320 (1.1%)
52	Ah	0.69	0/668	1.10	2/887 (0.2%)
53	Ai	0.69	0/789	1.14	8/1032 (0.8%)
54	AI	0.68	0/1708	1.01	5/2274 (0.2%)
55	AJ	0.68	0/1840	1.02	6/2456 (0.2%)
56	Ac	0.74	0/723	1.24	9/951 (0.9%)
57	AK	0.70	0/1690	1.11	12/2260 (0.5%)
58	AM	0.69	0/1012	1.12	9/1363 (0.7%)
59	AS	0.71	0/1531	1.24	25/2040 (1.2%)
60	AO	0.70	0/1199	1.13	11/1597 (0.7%)
61	AQ	0.75	0/1580	1.21	20/2113 (0.9%)
62	AR	0.72	0/2079	1.15	19/2777 (0.7%)
63	AW	0.71	0/1244	1.18	14/1663 (0.8%)
64	AY	0.66	0/806	1.03	4/1074 (0.4%)
65	AT	0.70	0/1525	1.09	12/2016 (0.6%)
66	AZ	0.71	0/1013	1.20	12/1339 (0.9%)
67	A3	0.70	0/1005	1.09	9/1329 (0.7%)
68	A5	0.72	0/1917	1.15	21/2562 (0.8%)
69	AD	0.68	0/1902	1.17	18/2544 (0.7%)
70	AE	0.70	0/3130	1.14	23/4195 (0.5%)
71	AF	0.70	0/3145	1.10	23/4205 (0.5%)
72	AG	0.76	0/1021	1.14	9/1349 (0.7%)
73	AU	0.73	0/1527	1.18	13/2043 (0.6%)
74	AH	0.67	0/1501	1.14	11/2025 (0.5%)
75	AV	0.69	0/1301	1.18	12/1732 (0.7%)
76	Ag	0.80	0/348	1.54	10/448 (2.2%)
77	AX	0.72	0/842	1.10	8/1125 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
78	A0	0.79	0/534	1.19	5/711 (0.7%)
All	All	0.96	14/207331 (0.0%)	1.40	3596/303942 (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	127
2	7	0	8
4	E	0	7
5	G	0	1
6	I	0	2
7	K	0	3
8	M	0	3
9	W	0	2
12	Y	0	3
14	1	0	3
15	2	0	1
16	3	0	3
18	5	0	2
19	6	0	3
20	B	1	5
21	F	0	3
22	H	0	2
23	J	0	4
24	L	0	4
25	N	0	1
26	P	0	3
27	Q	0	3
28	S	0	1
29	T	0	5
30	U	0	1
31	V	0	4
32	X	0	3
33	C	0	2
34	AA	1	304
35	AC	0	10
36	AB	0	9
37	AL	0	6
38	A1	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
40	A4	0	1
41	A6	0	1
42	A7	0	3
43	AN	0	5
44	A8	0	4
45	A9	0	2
46	Aa	0	3
47	Ab	0	1
48	Ad	0	1
49	Ae	0	2
50	Af	0	2
51	AP	0	7
52	Ah	0	1
53	Ai	0	1
54	AI	0	4
55	AJ	0	2
56	Ac	0	4
57	AK	0	7
58	AM	0	3
59	AS	0	7
60	AO	0	3
61	AQ	0	6
62	AR	0	4
63	AW	0	4
64	AY	0	1
65	AT	0	4
66	AZ	0	5
67	A3	0	1
68	A5	0	5
69	AD	0	1
70	AE	0	7
71	AF	0	10
72	AG	0	3
73	AU	0	5
75	AV	0	3
76	Ag	0	2
78	A0	0	4
All	All	2	668

The worst 5 of 14 bond length outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	AB	28	C	P-O5'	-6.19	1.53	1.59
1	A	1819	U	C5'-C4'	5.69	1.58	1.51
36	AB	5	U	O3'-P	-5.30	1.54	1.61
1	A	1853	A	P-O5'	-5.29	1.54	1.59
34	AA	211	U	N1-C2	-5.23	1.33	1.38

The worst 5 of 3596 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1659	U	P-O3'-C3'	16.14	139.06	119.70
1	A	981	U	P-O3'-C3'	15.61	138.43	119.70
34	AA	811	A	P-O3'-C3'	15.26	138.02	119.70
1	A	1865	G	P-O3'-C3'	13.78	136.24	119.70
1	A	1912	C	P-O3'-C3'	13.59	136.01	119.70

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
20	B	225	ILE	CB
34	AA	3018	A	C3'

5 of 668 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	129	U	Sidechain
1	A	143	A	Sidechain
1	A	39	A	Sidechain
1	A	44	U	Sidechain
1	A	84	A	Sidechain

## 5.2 Too-close contacts

Due to software issues we are unable to calculate clashes - this section is therefore empty.



## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	D	149/209 (71%)	144 (97%)	3 (2%)	2 (1%)	12	48
4	E	183/185 (99%)	175 (96%)	6 (3%)	2 (1%)	14	52
5	G	222/224 (99%)	206 (93%)	14 (6%)	2 (1%)	17	56
6	I	176/189 (93%)	161 (92%)	12 (7%)	3 (2%)	9	43
7	K	127/129 (98%)	118 (93%)	7 (6%)	2 (2%)	9	45
8	M	136/138 (99%)	127 (93%)	5 (4%)	4 (3%)	4	32
9	W	91/108 (84%)	84 (92%)	6 (7%)	1 (1%)	14	52
10	R	92/114 (81%)	80 (87%)	10 (11%)	2 (2%)	6	37
11	O	77/79 (98%)	67 (87%)	4 (5%)	6 (8%)	1	15
12	Y	152/154 (99%)	137 (90%)	11 (7%)	4 (3%)	5	34
13	Z	70/72 (97%)	65 (93%)	4 (6%)	1 (1%)	11	47
14	1	118/120 (98%)	111 (94%)	4 (3%)	3 (2%)	5	35
15	2	35/68 (52%)	31 (89%)	3 (9%)	1 (3%)	4	32
16	3	93/95 (98%)	81 (87%)	11 (12%)	1 (1%)	14	52
17	4	74/76 (97%)	65 (88%)	7 (10%)	2 (3%)	5	34
18	5	54/65 (83%)	53 (98%)	1 (2%)	0	100	100
19	6	41/43 (95%)	35 (85%)	5 (12%)	1 (2%)	6	35
20	B	208/210 (99%)	186 (89%)	19 (9%)	3 (1%)	11	47
21	F	255/257 (99%)	238 (93%)	13 (5%)	4 (2%)	9	45
22	H	200/214 (94%)	191 (96%)	8 (4%)	1 (0%)	29	68
23	J	186/188 (99%)	176 (95%)	5 (3%)	5 (3%)	5	34
24	L	165/214 (77%)	147 (89%)	14 (8%)	4 (2%)	6	35
25	N	96/98 (98%)	91 (95%)	3 (3%)	2 (2%)	7	38
26	P	125/127 (98%)	114 (91%)	8 (6%)	3 (2%)	6	35
27	Q	142/144 (99%)	130 (92%)	7 (5%)	5 (4%)	3	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	S	126/128 (98%)	108 (86%)	14 (11%)	4 (3%)	4	30
29	T	46/48 (96%)	44 (96%)	2 (4%)	0	100	100
30	U	147/149 (99%)	142 (97%)	4 (3%)	1 (1%)	22	62
31	V	142/156 (91%)	129 (91%)	10 (7%)	3 (2%)	7	38
32	X	92/103 (89%)	78 (85%)	10 (11%)	4 (4%)	2	25
33	C	193/195 (99%)	181 (94%)	9 (5%)	3 (2%)	9	45
37	AL	209/211 (99%)	190 (91%)	16 (8%)	3 (1%)	11	47
38	A1	136/145 (94%)	127 (93%)	7 (5%)	2 (2%)	10	46
39	A2	96/118 (81%)	89 (93%)	5 (5%)	2 (2%)	7	38
40	A4	64/66 (97%)	58 (91%)	4 (6%)	2 (3%)	4	30
41	A6	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
42	A7	92/102 (90%)	89 (97%)	3 (3%)	0	100	100
43	AN	144/146 (99%)	140 (97%)	2 (1%)	2 (1%)	11	47
44	A8	123/125 (98%)	114 (93%)	8 (6%)	1 (1%)	19	60
45	A9	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
46	Aa	104/106 (98%)	99 (95%)	5 (5%)	0	100	100
47	Ab	91/105 (87%)	85 (93%)	5 (6%)	1 (1%)	14	52
48	Ad	68/76 (90%)	68 (100%)	0	0	100	100
49	Ae	39/50 (78%)	39 (100%)	0	0	100	100
50	Af	49/51 (96%)	46 (94%)	3 (6%)	0	100	100
51	AP	202/204 (99%)	183 (91%)	14 (7%)	5 (2%)	5	35
52	Ah	83/85 (98%)	76 (92%)	5 (6%)	2 (2%)	6	35
53	Ai	93/95 (98%)	87 (94%)	5 (5%)	1 (1%)	14	52
54	AI	203/213 (95%)	187 (92%)	14 (7%)	2 (1%)	15	54
55	AJ	216/244 (88%)	196 (91%)	13 (6%)	7 (3%)	4	30
56	Ac	87/89 (98%)	74 (85%)	12 (14%)	1 (1%)	14	52
57	AK	199/201 (99%)	191 (96%)	6 (3%)	2 (1%)	15	54
58	AM	130/132 (98%)	121 (93%)	9 (7%)	0	100	100
59	AS	184/186 (99%)	171 (93%)	12 (6%)	1 (0%)	29	68
60	AO	145/147 (99%)	132 (91%)	10 (7%)	3 (2%)	7	38
61	AQ	185/205 (90%)	170 (92%)	12 (6%)	3 (2%)	9	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	AR	244/289 (84%)	224 (92%)	13 (5%)	7 (3%)	4	32
63	AW	149/170 (88%)	135 (91%)	12 (8%)	2 (1%)	12	48
64	AY	99/101 (98%)	97 (98%)	2 (2%)	0	100	100
65	AT	179/181 (99%)	173 (97%)	5 (3%)	1 (1%)	25	65
66	AZ	119/121 (98%)	113 (95%)	5 (4%)	1 (1%)	19	60
67	A3	117/119 (98%)	108 (92%)	9 (8%)	0	100	100
68	A5	221/223 (99%)	201 (91%)	15 (7%)	5 (2%)	6	36
69	AD	245/247 (99%)	230 (94%)	14 (6%)	1 (0%)	34	72
70	AE	378/380 (100%)	346 (92%)	26 (7%)	6 (2%)	9	45
71	AF	388/390 (100%)	363 (94%)	21 (5%)	4 (1%)	15	54
72	AG	116/159 (73%)	107 (92%)	6 (5%)	3 (3%)	5	34
73	AU	178/180 (99%)	167 (94%)	9 (5%)	2 (1%)	14	52
74	AH	183/185 (99%)	168 (92%)	12 (7%)	3 (2%)	9	45
75	AV	153/155 (99%)	141 (92%)	9 (6%)	3 (2%)	7	40
76	Ag	35/37 (95%)	29 (83%)	5 (14%)	1 (3%)	4	32
77	AX	95/97 (98%)	90 (95%)	4 (4%)	1 (1%)	14	52
78	A0	60/62 (97%)	57 (95%)	2 (3%)	1 (2%)	9	43
All	All	10111/10698 (94%)	9361 (93%)	590 (6%)	160 (2%)	13	45

5 of 160 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	K	120	HIS
8	M	41	GLU
9	W	4	VAL
10	R	42	ILE
12	Y	55	LYS

### 5.3.2 Protein sidechains ⓘ

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	D	132/177 (75%)	129 (98%)	3 (2%)	50	70
4	E	161/164 (98%)	159 (99%)	2 (1%)	71	84
5	G	191/191 (100%)	185 (97%)	6 (3%)	40	62
6	I	154/160 (96%)	150 (97%)	4 (3%)	46	67
7	K	115/115 (100%)	112 (97%)	3 (3%)	46	67
8	M	116/116 (100%)	114 (98%)	2 (2%)	60	78
9	W	86/99 (87%)	83 (96%)	3 (4%)	36	60
10	R	83/97 (86%)	83 (100%)	0	100	100
11	O	76/76 (100%)	74 (97%)	2 (3%)	46	67
12	Y	137/137 (100%)	131 (96%)	6 (4%)	28	54
13	Z	60/60 (100%)	60 (100%)	0	100	100
14	1	104/104 (100%)	102 (98%)	2 (2%)	57	75
15	2	35/61 (57%)	34 (97%)	1 (3%)	42	64
16	3	87/87 (100%)	87 (100%)	0	100	100
17	4	70/70 (100%)	67 (96%)	3 (4%)	29	54
18	5	47/52 (90%)	45 (96%)	2 (4%)	29	54
19	6	36/36 (100%)	35 (97%)	1 (3%)	43	65
20	B	195/195 (100%)	192 (98%)	3 (2%)	65	80
21	F	233/233 (100%)	230 (99%)	3 (1%)	69	82
22	H	182/190 (96%)	178 (98%)	4 (2%)	52	71
23	J	177/177 (100%)	176 (99%)	1 (1%)	86	92
24	L	151/190 (80%)	148 (98%)	3 (2%)	55	73
25	N	91/91 (100%)	88 (97%)	3 (3%)	38	61
26	P	99/99 (100%)	95 (96%)	4 (4%)	31	56
27	Q	120/120 (100%)	117 (98%)	3 (2%)	47	68
28	S	114/114 (100%)	108 (95%)	6 (5%)	22	49
29	T	43/43 (100%)	41 (95%)	2 (5%)	26	52
30	U	132/132 (100%)	129 (98%)	3 (2%)	50	70
31	V	131/140 (94%)	127 (97%)	4 (3%)	40	62
32	X	88/94 (94%)	87 (99%)	1 (1%)	73	85
33	C	167/167 (100%)	164 (98%)	3 (2%)	59	77
37	AL	190/190 (100%)	187 (98%)	3 (2%)	62	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	A1	127/131 (97%)	124 (98%)	3 (2%)	49	69
39	A2	97/109 (89%)	93 (96%)	4 (4%)	30	56
40	A4	60/60 (100%)	60 (100%)	0	100	100
41	A6	83/83 (100%)	81 (98%)	2 (2%)	49	69
42	A7	90/96 (94%)	89 (99%)	1 (1%)	73	85
43	AN	135/135 (100%)	131 (97%)	4 (3%)	41	63
44	A8	114/114 (100%)	109 (96%)	5 (4%)	28	54
45	A9	90/90 (100%)	89 (99%)	1 (1%)	73	85
46	Aa	89/89 (100%)	84 (94%)	5 (6%)	21	48
47	Ab	82/92 (89%)	80 (98%)	2 (2%)	49	69
48	Ad	69/73 (94%)	68 (99%)	1 (1%)	67	81
49	Ae	40/47 (85%)	38 (95%)	2 (5%)	24	51
50	Af	45/45 (100%)	44 (98%)	1 (2%)	52	71
51	AP	179/179 (100%)	173 (97%)	6 (3%)	37	61
52	Ah	70/70 (100%)	69 (99%)	1 (1%)	67	81
53	Ai	87/87 (100%)	83 (95%)	4 (5%)	27	53
54	AI	189/195 (97%)	186 (98%)	3 (2%)	62	79
55	AJ	204/224 (91%)	199 (98%)	5 (2%)	47	68
56	Ac	74/74 (100%)	71 (96%)	3 (4%)	30	56
57	AK	181/181 (100%)	178 (98%)	3 (2%)	60	78
58	AM	106/106 (100%)	105 (99%)	1 (1%)	78	88
59	AS	158/158 (100%)	156 (99%)	2 (1%)	69	82
60	AO	121/121 (100%)	113 (93%)	8 (7%)	16	43
61	AQ	165/176 (94%)	161 (98%)	4 (2%)	49	69
62	AR	215/250 (86%)	208 (97%)	7 (3%)	38	61
63	AW	128/128 (100%)	127 (99%)	1 (1%)	81	89
64	AY	90/90 (100%)	88 (98%)	2 (2%)	52	71
65	AT	162/162 (100%)	162 (100%)	0	100	100
66	AZ	111/111 (100%)	110 (99%)	1 (1%)	78	88
67	A3	110/110 (100%)	107 (97%)	3 (3%)	44	66
68	A5	201/201 (100%)	195 (97%)	6 (3%)	41	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	AD	191/191 (100%)	184 (96%)	7 (4%)	34	59
70	AE	335/335 (100%)	325 (97%)	10 (3%)	41	63
71	AF	336/336 (100%)	323 (96%)	13 (4%)	32	57
72	AG	110/142 (78%)	108 (98%)	2 (2%)	59	77
73	AU	162/162 (100%)	156 (96%)	6 (4%)	34	59
74	AH	168/168 (100%)	163 (97%)	5 (3%)	41	63
75	AV	140/140 (100%)	136 (97%)	4 (3%)	42	64
76	Ag	34/34 (100%)	33 (97%)	1 (3%)	42	64
77	AX	92/92 (100%)	92 (100%)	0	100	100
78	A0	53/53 (100%)	52 (98%)	1 (2%)	57	75
All	All	9096/9417 (97%)	8870 (98%)	226 (2%)	50	68

5 of 226 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	Ae	48	LYS
75	AV	15	LYS
59	AS	18	HIS
74	AH	131	VAL
71	AF	140	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
70	AE	310	HIS
72	AG	20	ASN
44	A8	107	GLN
40	A4	17	HIS
73	AU	114	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1586/1608 (98%)	481 (30%)	89 (5%)
2	7	75/76 (98%)	13 (17%)	2 (2%)
34	AA	3168/3193 (99%)	979 (30%)	187 (5%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	AC	148/151 (98%)	50 (33%)	9 (6%)
36	AB	117/118 (99%)	27 (23%)	1 (0%)
All	All	5094/5146 (98%)	1550 (30%)	288 (5%)

5 of 1550 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	C
1	A	5	U
1	A	17	C
1	A	25	C
1	A	26	A

5 of 288 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	AA	2966	C
35	AC	145	A
34	AA	3137	U
34	AA	3576	A
34	AA	138	C

## 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

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	33.92



## 6 Map visualisation

This section contains visualisations of the EMDB entry EMD-6456. 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 surface views

This section was not generated.

### 6.5 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.