



## wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 12:29 PM 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](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

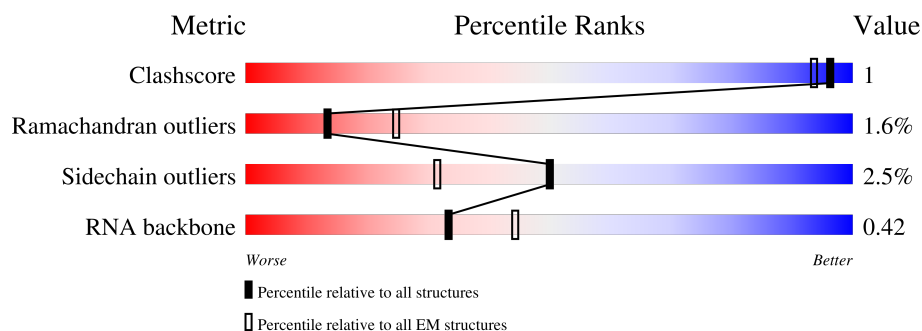
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 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.






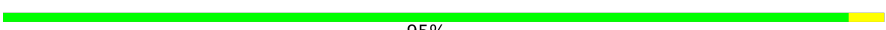






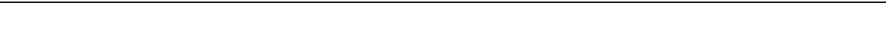

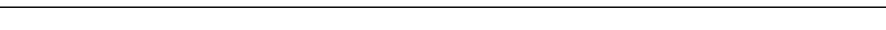
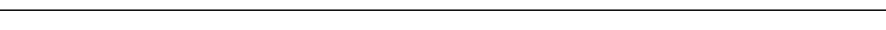

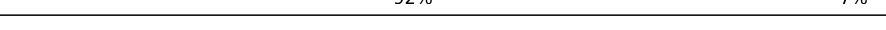


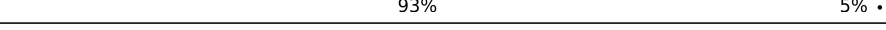

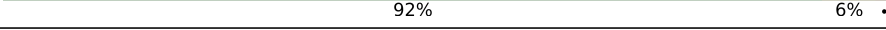



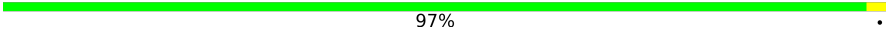
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	75	
3	Q	144	
4	S	128	
5	T	48	
6	M	138	
7	U	149	


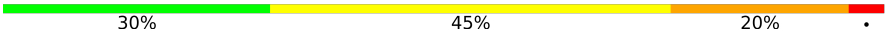
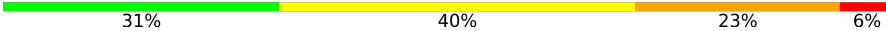


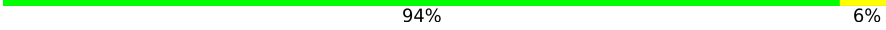



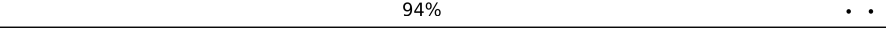
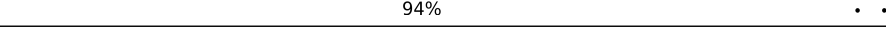
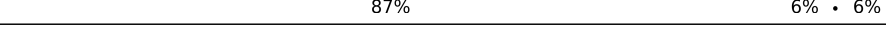
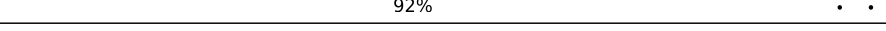
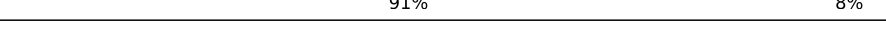


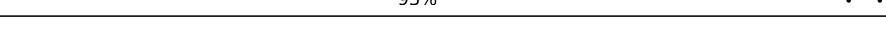


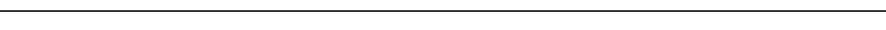

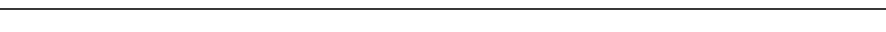
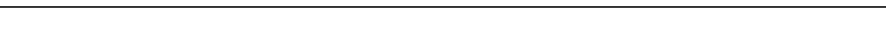


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Mol	Chain	Length	Quality of chain
8	V	156	 83% 9% • 6%
9	E	185	 91% 8% •
10	X	103	 83% 9% • 7%
11	G	224	 95% •
12	W	108	 81% 7% 12%
13	R	114	 82% • 14%
14	I	189	 87% 7% • 5%
15	O	79	 87% 13%
16	Y	154	 86% 14%
17	Z	72	 97% •
18	1	120	 88% 12% •
19	2	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% ••
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% •


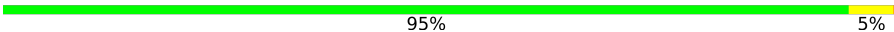




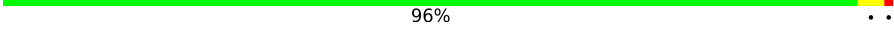


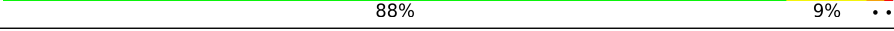


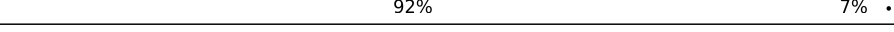
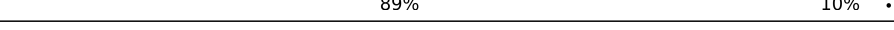


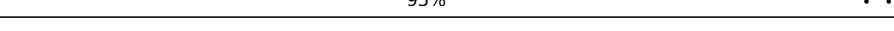




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Mol	Chain	Length	Quality of chain
33	L	214	
34	AA	3192	
35	AC	151	
36	AB	118	
37	AL	211	
38	A0	62	
39	AO	147	
40	Ai	95	
41	A2	118	
42	A4	66	
43	A6	98	
44	A7	102	
45	A1	145	
46	AN	146	
47	A8	125	
48	A9	103	
49	Aa	106	
50	Ab	105	
51	Ad	76	
52	Ae	50	
53	Af	51	
54	AP	204	
55	Ah	85	
56	AI	213	
57	Ac	89	

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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

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
1	A	1608	Total	C	N	O	P	0	0
			34207	15346	6106	11169	1586		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
28	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 29 is a protein called 40S ribosomal protein uS8.

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

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

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

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

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

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

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

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

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

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

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

- 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 eL24.

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

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

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

- 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
47	A8	125	Total	C	N	O	S	0	0
			1037	660	206	164	7		

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

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

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

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

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

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

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

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

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

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

- 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
59	AM	132	Total	C	N	O	S	0	0
			996	631	179	178	8		

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

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

- 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		

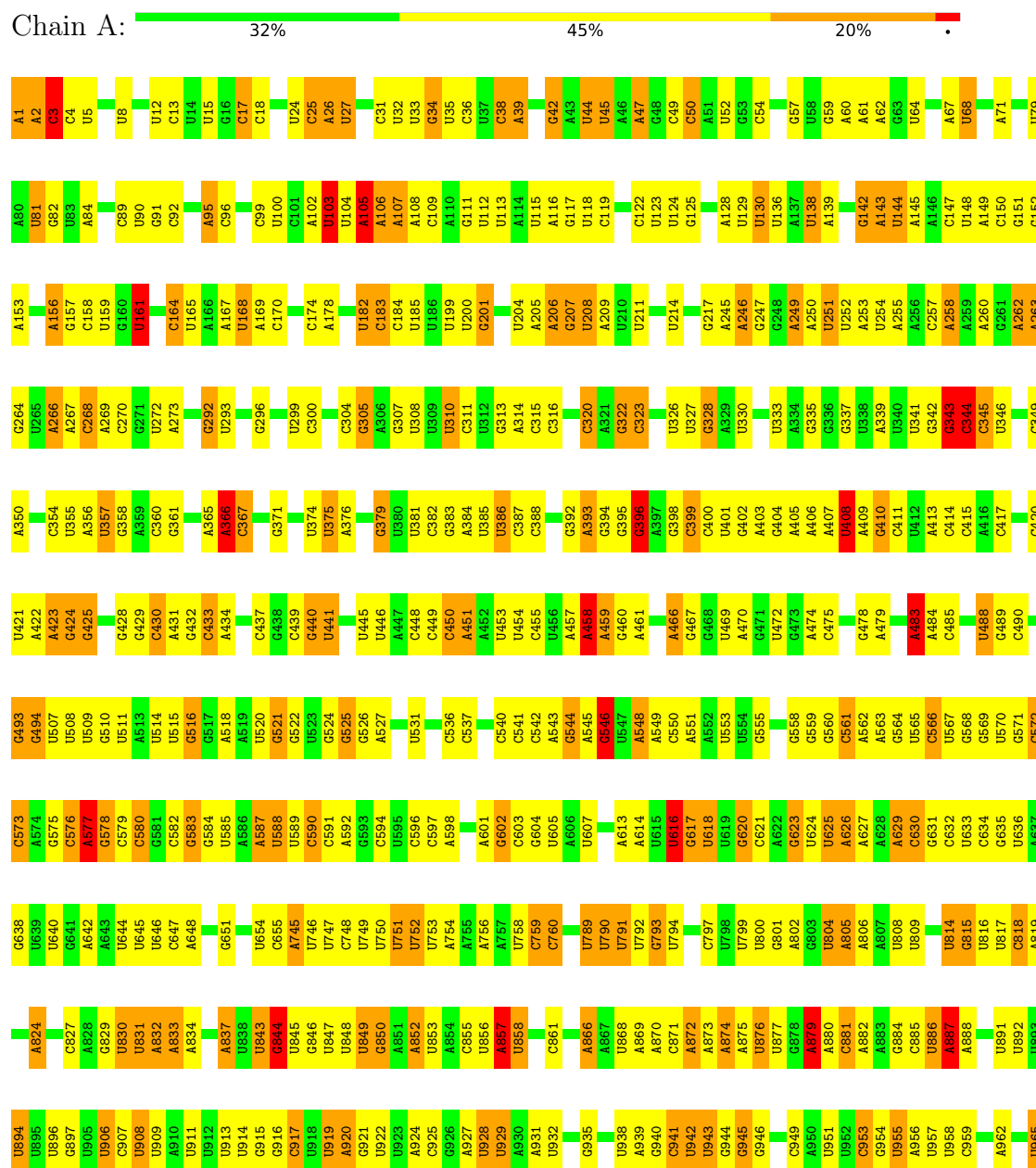
- Molecule 78 is a protein called 60S ribosomal protein eL8.

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

### 3 Residue-property plots

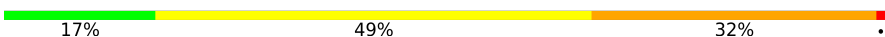
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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



C966	U1008	U1100	C1206	U1275	A1376	U1450	U1661	A1730	U1829	U1891	U1954	C2052
A967	U1029	G1101	U1207	C1278	U1377	G1451	C1664	C1731	C1830	U1892	G1955	U2053
G968	C1030	C1102	G1208	G1279	C1380	C1452	G1665	A1732	G1831	C1893	C2054	A2054
A969	C1031	C1103	G1209	G1280	G1381	G1453	G1666	G1733	U1832	A1894	G1959	A2055
G970	A1035	G1104	G1210	G1281	G1382	G1454	A1667	U1735	G1833	U1895	U1960	C2056
G971	A1036	G1105	G1211	U1282	G1383	G1455	A1668	A1741	A1834	C1896	U1961	A2057
U972	C1038	C1106	C1212	U1283	U1384	G1456	A1669	A1742	U1835	A1897	A1962	A2058
A973	G1041	U1107	G1215	U1284	U1385	A1457	C1672	C1743	G1836	G1898	U1963	G2059
A974	G1042	A1108	G1219	A1285	A1388	A1458	A1673	U1745	G1837	A1899	U1964	G2060
A976	G1044	G1109	U1219	U1286	A1389	A1459	G1674	A1746	G1838	U1900	A1965	U2061
U977	C1044	G1110	C1220	U1287	G1390	C1461	G1675	U1747	U1839	U1901	U1966	U2062
U978	U1051	U1111	G1221	U1288	U1391	A1462	G1676	G1748	U1841	G1902	G1972	C2063
C979	A1052	G1112	C1222	G1289	U1392	C1463	U1677	C1749	A1842	G1903	U1973	C2064
U980	A1053	G1116	G1223	A1290	C1392	U1464	C1678	C1781	G1843	C1904	C1905	C2065
A981	G1054	A1117	C1224	U1291	U1403	A1604	U1678	C1782	A1844	U1906	U1974	A2068
A982	G1055	U1118	A1225	C1292	U1404	C1605	U1679	U1783	U1845	A1907	U1975	G2069
G983	G1056	G1119	G1227	A1293	U1405	C1606	U1680	A1784	U1846	A1908	G1976	G2070
A984	G1058	G1123	C1228	A1294	U1406	U1607	A1681	C1785	A1847	C1909	A1978	U2071
U985	A1057	U1124	G1229	U1295	G1407	G1608	A1682	C1786	U1848	U1910	C1979	C2072
G986	U1059	U1125	G1230	C1296	U1408	C1609	U1683	U1787	U1849	A1911	A1980	A2073
U987	G1060	C1166	G1231	U1297	U1409	C1609	U1684	U1788	C1851	G1912	A1981	A2074
C989	A1061	C1169	A1232	U1298	U1410	C1622	C1685	U1789	A1852	U1913	U1982	C2075
U990	A1062	C1170	C1233	G1300	G1411	G1623	C1687	C1790	A1853	C1914	U2004	C2076
G991	G1063	C1171	U1236	G1301	U1412	U1624	C1688	C1791	U1854	C1915	U2005	C2079
A993	A1064	U1172	A1239	G1302	U1413	C1625	G1691	U1792	U1855	C1916	U2006	U2079
G994	G1066	C1173	A1240	A1303	A1414	U1626	A1692	C1793	A1856	U1917	U2007	G2084
A995	A1067	A1174	A1241	A1304	A1415	G1627	U1693	G1794	U1857	U1918	G2008	C2085
C996	C1068	G1175	G1242	A1305	U1416	U1628	C1697	U1795	U1858	G1919	C2009	A2086
C1000	C1069	U1176	G1254	U1307	U1417	G1629	U1698	C1796	G1803	C1920	U2010	U2087
A1001	A1070	A1177	G1255	C1308	C1418	A1630	U1699	C1797	C1804	C1921	G2011	U2090
A1002	G1071	C1178	G1256	A1309	U1419	G1631	G1701	U1798	U1809	U1922	G2012	
G1003	A1072	C1179	G1257	C1310	G1420	C1635	U1702	A1800	A1811	U1923	A2013	
U1004	U1073	U1180	G1258	U1311	A1421	A1636	U1703	A1801	A1812	U1924	A2014	
G1005	A1074	A1181	G1259	G1312	U1422	U1637	G1704	G1802	C1813	U1927	C2018	
C1006	C1075	A1182	G1261	G1313	A1423	U1638	C1705	G1803	C1814	A1928	C2019	
G1007	C1076	U1183	G1262	U1314	U1424	U1639	U1706	C1804	U1815	C1929	G2020	
G1008	C1077	G1184	G1263	U1315	C1425	G1640	C1707	C1804	U1816	U1930	U2021	
A1009	U1078	A1185	G1264	U1316	U1426	G1641	G1708	U1810	U1817	A1932	A2022	
G1010	G1080	G1186	G1265	A1317	A1427	U1642	C1709	U1811	A1818	C1933	A2023	
A1011	U1081	A1187	G1266	G1318	C1429	G1643	C1713	A1812	U1819	G1934	U2025	
C1012	A1082	A1188	G1267	U1319	U1432	U1644	U1714	U1813	A1820	G1935	C2026	
A1013	U1086	U1189	A1261	A1320	G1432	U1645	U1715	C1814	C1821	C1936	C2027	
U1014	U1087	C1191	C1262	C1321	A1433	A1646	G1716	U1815	A1822	U1937	U2028	
G1015	A1088	A1192	C1263	U1362	U1434	A1647	U1717	U1816	A1823	C1938	A2029	
U1016	A1089	A1193	G1264	U1363	C1435	U1648	A1718	U1817	U1824	G1939	U2030	
G1017	C1090	A1194	G1265	U1364	U1436	C1649	C1719	U1818	A1824	U1940	C2031	
U1018	C1091	G1195	G1266	G1365	U1437	A1650	U1719	A1819	G1881	C1941	U2032	
C1019	U1092	U1196	G1267	A1366	C1440	C1651	A1720	U1820	U1882	U1944	U2033	
U1020	A1092	C1197	G1268	U1367	U1441	A1652	A1721	C1821	A1883	C1945	U2034	
A1021	U1093	U1198	G1269	U1368	U1442	A1653	U1722	U1822	A1884	U1946	A2042	
A1022	A1094	U1199	G1270	G1369	G1443	G1655	U1723	U1823	G1885	U1947	A2043	
A1023	A1095	U1200	G1271	U1370	U1444	A1656	U1724	U1824	C1886	A1948	A2047	
A1024	A1096	G1201	G1272	U1371	U1445	A1657	U1725	U1825	A1887	C1949	A2048	
C1025	U1097	U1204	A1272	U1372	U1446	G1658	U1726	U1826	U1888	U1950	G2049	
A1026	U1098	G1374	G1273	U1373	U1447	G1659	U1727	U1827	G1889	C2051	U2050	
C1027	A1099	U1205	C1274	C1375	U1449	U1660	A1729	A1828	A1890	U1953	C2051	

• Molecule 2: P/E-tRNA

Chain 7:  17% 49% 32%

C1	G2	C3	G4	G5	G6	G7	U8	G9	G12	C13	G14	G15	C16	C17	G18	G19	C20	A21	G22	C23	U24	C25	G26	U27	C28	G29	G30	G31	C32	C33	C34	A35	U36	A37	A38	C39	C40	C41	G42	A43	A44	G45	G46	U47	C48	G49	U50	C51	G52	G53	U54	U55	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% .



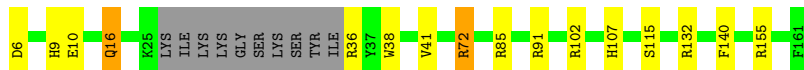
- Molecule 7: 40S ribosomal protein uS15

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% .



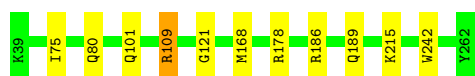
- Molecule 10: 40S ribosomal protein uS19

Chain X: 83% 9% 7%



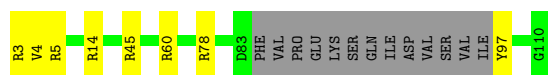
- Molecule 11: 40S ribosomal protein uS5

Chain G: 95%



- Molecule 12: 40S ribosomal protein eS17

Chain W: 81% 7% 12%



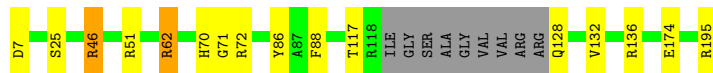
- Molecule 13: 40S ribosomal protein eS12

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% .



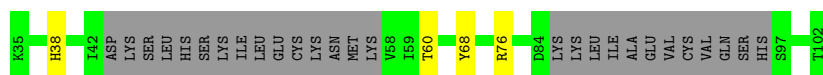
- Molecule 18: 40S ribosomal protein eS24

Chain 1: 88% 12% .



- Molecule 19: 40S ribosomal protein eS25

Chain 2: 54% 6% 40% .



- Molecule 20: 40S ribosomal protein uS2

Chain C: 95% 5% .



- Molecule 21: 40S ribosomal protein eS26

Chain 3: 87% 12% .



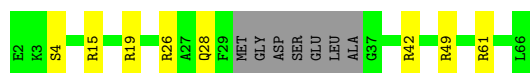
- Molecule 22: 40S ribosomal protein eS27

Chain 4: 92% 7% .



- Molecule 23: 40S ribosomal protein eS28

Chain 5: 77% 12% 11% .



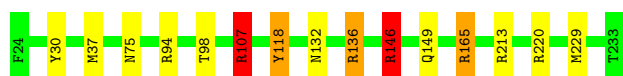
- Molecule 24: 40S ribosomal protein eS30

Chain 6: 86% 9% 5%



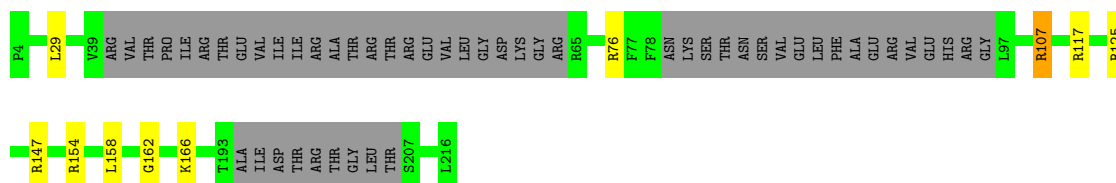
- Molecule 25: 40S ribosomal protein eS1

Chain B: 93% 5% ..



- Molecule 26: 40S ribosomal protein uS3

Chain D: 70% 25% .



- Molecule 27: 40S ribosomal protein eS4

Chain F: 92% 6% .



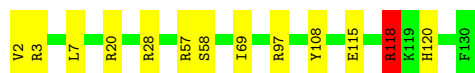
- Molecule 28: 40S ribosomal protein eS6

Chain H: 88% 7% 5%



- Molecule 29: 40S ribosomal protein uS8

Chain K: 90% 9% .



- Molecule 30: 40S ribosomal protein eS7

Topic	Number of Publications
A3	3
V4	4
Q5	5
P13	13
S31	31
K58	58
K67	67
P68	68
Y69	69
Y72	72
R78	78
A96	96
K97	97
R98	98
I112	112
Y123	123
L127	127
S132	132
R140	140
R149	149
R181	181
P190	190

- Chain N:  97%

- Chain P:  89% 9%

Topic	Number of Publications
E25	1
F41	4
B50	4
B55	4
B66	3
D67	6
E68	4
M75	1
R98	4
R121	3
R128	4
D131	7
R141	7
R146	10
R147	9
G148	10
R149	9
R150	10
L151	10

- Chain L:  71% 8% 20%

THR	R5
THR	
LYS	R8
THR	
TYR	R12
GLY	
VAL	R25
ILE	R26
LYS	Y27
LYS	E28
	L29
I162	G30
	R31
F176	
R210	R47
	G48
D213	R49
LYS	
K216	R56
R217	S64
N218	
	F70
	R77
	R92
	T120
	LEU
	GLY
	LYS
	LYS
	LYS
	LYS
	GLU
	LYS
	LYS
	GLU
	GLU
	ASP
	ASN
	GLU
	GLU
	GLU
	LYS
	GLN
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	VAL
	GLU
	ASN
	ASN
	GLU
	ALA
	ALA
	LYS
	ASP
	GLU

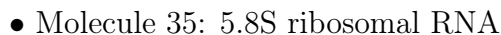
- Chain AA:  30% 45% 20% .

U286	A200	G137	A74	G10
U287	A201	C138	U75	A11
C288	C202	A139	G76	U12
A269		A140	A77	G13
U270	G205	A141	U78	U14
G271	A206	C142	U79	U15
U272	A207	C143	C80	A16
C273	U208	U144	C31	G17
	G209	U145	U82	A18
G276	C210	U146	U83	A19
U277	U211	C147	U84	G20
C278	U212	G148	A85	G21
G281	C213	A149	G86	G22
U282	C214	C150	U87	C23
U283	C215	G151	A88	A24
C284	C216	G152	A89	A25
	U217	A153	A26	A26
	U218	A154	C91	U27
A289	A219	U155	G92	C28
G290	G220	U156	C93	C29
U291	A221	G94	G30	G31
U292		U158		C31
U293	U225	C159	U97	G32
C294	G226		G98	G33
	A227	U162	A99	A34
G297	A228	G163	A100	A35
C298	A229	A164	C101	U36
A299	G230	U165	U37	U37
C300	G231	U166	G104	U38
U301	C232	U167	G105	A39
A302	C233	A168	A106	A40
A303	C234	U169	C107	G41
U304	A235	C170	C108	C42
A305	U236	C171	A109	A43
C306	A237	C172	G110	U44
G307	G238	A173	C111	A45
U308	U239	U174	U112	U46
G309	G240	G175	C113	A47
U310	C241		C13	A48
G311	U242	U178	A116	U49
A312	U243	G179	C117	
U313		C180	G118	C54
A314	U246	C181	G119	G55
C315	A247	U182	U120	G56
A316		U183	A121	A57
U317	U250	U184	U122	A58
U318	U251	A185	A123	G59
		A186	U124	A60
	U254		C125	A61
C320	C255	U189	A62	
A321	A256	G190	C126	A63
C322		A191	U127	A64
A323	U257	G192	U128	A65
U324	U258	C193	C129	A66
A325	C259	A194	G130	
	G260	C195	U131	
	A261	U196	U132	U69
U330	A262	G197	U133	A70
A331	U263	A198	G134	A71
A332	U264	U199	C135	C72
C323	U265		U136	U73



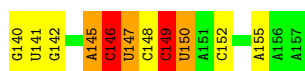
WORLDWIDE  
PDB  
PROTEIN DATA BANK

G3747	G2801	G2676	A2602	G2540	C2462	G2389	U2144	G2068	U1963	C1852	A1787	C1720	A1636	G1562	G1476
G2801	G2802	A2679	U2603	C2541	U2463	U2390	A2145	C2069	G1964	C1853	C1788	C1721	G1637	U1563	A1476
A2803	A2804	A2680	G2604	G2542	G2464	U2391	A2146	U2070	U1965	U1854	U1789	C1722	G1641	G1564	A1479
G2804	G2805	A2681	A2606	G2543	G2465	A2392	A2147	U2071	A1966	U1855	U1790	C1723	G1642	G1565	A1481
U2806	U2807	U2682	G2608	G2544	C2472	C2394	A2148	U2072	G1967	U1856	U1791	G1724	U1643	A1567	
U2808	U2809	A2683	G2608	G2545	A2473	U2395	A2149	G2074	G1968	A1857	U1792	C1725	U1644	C1568	A1486
A2809	A2810	U2684	U2611	A2548	C2474	C2396	A2153	C2080	A1969	C1861	U1793	U1726	U1645	U1569	A1487
G2811	G2812	G2685	U2611	A2549	U2477	C2401	A2154	U2081	U1971	U1971	U1794	C1727	U1646	U1570	U1493
U2813	U2814	G2686	U2611	A2550	U2478	U2402	G2157	U2082	U1974	C1865	A1797	A1729	U1647	C1571	
G2815	U2816	G2687	A2614	C2551	G2478	G2403	U2158	C2082	U1975	C1866	A1798	A1730	U1648	U1572	U1496
G2816	U2817	G2688	C2615	U2551	U2479	A2404	A2159	U2083	A1976	U1867	U1799	A1731	G1649	C1573	U1497
G2817	U2818	G2688	G2618	A2552	G2480	G2405	G2160	U2084	U1977	U1868	U1800	A1732	U1650	C1574	U1498
U2819	U2820	G2689	G2618	U2553	A2481	G2406	G2161	C2089	U1978	G1869	G1801		C1651	C1575	U1499
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G2827	U2828	G2693	U2621	U2557	G2487	C2411	G2165	G2093	U1982	U1873	C1806	A1738	U1656	U1505	U1505
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G2837	U2838	G2698	U2621	U2562	U2492	A2416	C2172	A2097	U1993	A1881	A1811	U1743	U1661	G1592	U1510
U2839	U2840	G2699	U2621	U2563	U2493	G2417	G2173	G2098	G1994	U1882	C1812	U1744	U1662	G1593	U1511
G2841	U2842	G2700	U2621	U2564	U2494	C2418	G2174	G2099	G1995	U1883	A1813	G1745	U1663	A1594	U1512
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U2845	U2846	G2702	U2621	U2566	U2496	A2420	A2176	A2102	A1998	U1885	A1815	A1748	U1665	G1596	G1514
G2847	U2848	U2703	U2621	U2567	U2497	C2421	A2177	C2103	A1999	U1886	A1816	U1749	U1666	A1596	A1515
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U2855	U2856	G2707	U2621	U2571	U2501	G2425	G2181	C2107	G2003	U1890	U1820	U1753	U1670	C1600	G1519
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U2863	U2864	U2711	U2621	U2575	U2505	U2429	G2185	A2111	G2007	U1895	A1824	C1758	U1674	G1603	G1526
G2865	U2866	U2712	U2621	U2576	U2506	U2430	A2189	C2112	A2009	C1896	A1825	A1759	U1675	A1604	U1527
U2867	U2868	U2713	U2621	U2577	U2507	A2431	A2190	G2113	G2010	G1897	C1826	U1760	U1676	A1605	
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U2871	U2872	U2715	U2621	U2579	U2509	A2433	U2192	C2114	U2012	U1899	U1827	U1762	U1678	U1607	U1533
G2873	U2874	U2716	U2621	U2580	U2510	A2434	U2193	A2115	G2013	G1900	U1828	U1763	U1679	U1608	U1534
U2875	U2876	U2717	U2621	U2581	U2511	A2435	G2202	U2116	C2014	A1901	U1829	U1764	U1680	G1535	G1535
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U2879	U2880	U2719	U2621	U2583	U2513	A2437	U2204	G2118	U2016	C1903	C1834	U1766	U1682	G1537	U1537
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U2891	U2892	U2725	U2621	U2589	U2519	A2443	U2210	A2125	A2022	U1909	C1840	G1772	U1688	U1541	U1541
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U2895	U2896	U2727	U2621	U2591	U2521	A2445	G2212	A2132	C2031	A1913	U1842	U1774	U1690	C1550	C1550
G2897	U2898	U2728	U2621	U2592	U2522	A2446	G2213	C2133	G2032	A1914	U1843	U1775	U1691	C1551	C1551
U2899	U2900	U2729	U2621	U2593	U2523	A2447	G2214	C2134	G2033	A1915	U1844	G1776	U1692	U1552	U1552
G2901	U2902	U2730	U2621	U2594	U2524	U2448	G2215	C2135	G2034	A1916	U1845	U1777	U1693	U1553	U1553
U2903	U2904	U2731	U2621	U2595	U2525	A2449	G2216	C2136	G2035	A1917	U1846	G1778	U1694	G1554	G1554
G2905	U2906	U2732	U2621	U2596	U2526	U2450	G2217	C2137	G2036	U1957	U1847	A1781	U1703	A1630	A1630
U2907	U2908	U2733	U2621	U2597	U2527	A2451	G2218	C2138	G2037	U1958	U1848	U1782	U1704	A1631	A1631
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U2911	U2912	U2735	U2621	U2599	U2529	A2453	G2220	U2140	U2039	U1960	U1850	U1784	A1706	G1556	G1556
G2913	U2914	U2736	U2621	U2600	U2530	A2454	G2221	U2141	G2040	U1961	U1851	U1785	G1712	U1630	U1630
U2915	U2916	U2737	U2621	U2601	U2531	A2455	G2222	U2142	U2041	U1962	A1851	A1786		G1633	G1633
G2917	U2918	U2738	U2621	U2602	U2532	A2456	G2223	U2143						G1634	G1634
U2919	U2920	U2739	U2621	U2603	U2533	A2457	G2224	U2144						G1635	G1635
G2921	U2922	U2740	U2621	U2604	U2534	A2458	G2225	U2145							
U2923	U2924	U2741	U2621	U2605	U2535	A2459	G2226	U2146							
G2925	U2926	U2742	U2621	U2606	U2536	A2460	G2227	U2147							
U2927	U2928	U2743	U2621	U2607	U2537	A2461	G2228	U2148							
G2929	U2930	U2744	U2621	U2608	U2538	A2462	G2229	U2149							
U2931	U2932	U2745	U2621	U2609	U2539	A2463	G2230	U2150							
G2933	U2934	U2746	U2621	U2610	U2540	A2464	G2231	U2151							
U2935	U2936	U2747	U2621	U2611	U2541	A2465	G2232	U2152							
G2937	U2938	U2748	U2621	U2612	U2542	A2466	G2233	U2153							
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G2941	U2942	U2750	U2621	U2614	U2544	A2468	G2235	U2155							
U2943	U2944	U2751	U2621	U2615	U2545	A2469	G2236	U2156							
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U2947	U2948	U2753	U2621	U2617	U2547	A2471	G2238	U2158							
G2949	U2950	U2754	U2621	U2618	U2548	A2472	G2239	U2159							
U2951	U2952	U2755	U2621	U2619	U2549	A2473	G2240	U2160							
G2953	U2954	U2756	U2621	U2620	U2550	A2474	G2241	U2161							
U2955	U2956	U2757	U2621	U2621	U2551	A2475	G2242	U2162							
G2957	U2958	U2758	U2621	U2622	U2552	A2476	G2243	U2163							
U2959	U2960	U2759	U2621	U2623	U2553	A2477	G2244	U2164							
G2961	U2962	U2760	U2621	U2624	U2554	A2478	G2245	U2165							
U2963	U														



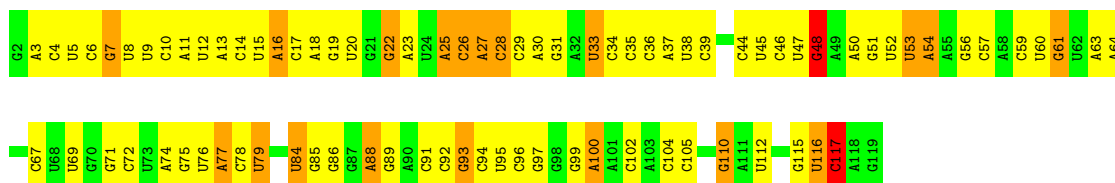
Frequency	Percentage
Daily	31%
Often	40%
Sometimes	23%
Never	6%





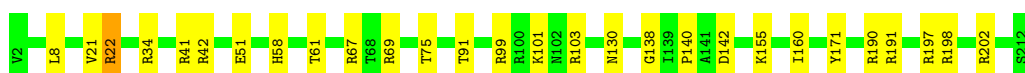
- Molecule 36: 5S ribosomal RNA

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%



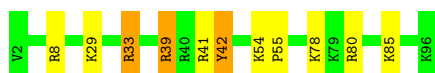
- Molecule 39: 60S ribosomal protein uL15

Chain AO: 90% 10%



- Molecule 40: 60S ribosomal protein eL44

Chain Ai: 88% 8%




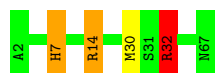
- Molecule 41: 60S ribosomal protein eL28

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% . . .



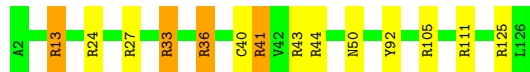
- Molecule 46: 60S ribosomal protein eL14

Chain AN:  91% 8% . . .




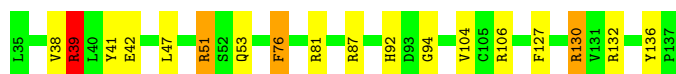
- Molecule 47: 60S ribosomal protein eL32

Chain A8:  89% 8% . . .



- Molecule 48: 60S ribosomal protein eL33

Chain A9:  83% 14% . . .

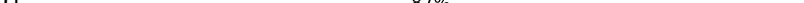


- Molecule 49: 60S ribosomal protein eL34

Category	Count
A2	10
Q3	10
R4	10
R8	10
R66	10
R67	10
R74	10
R86	10
R91	10
E107	10

- Chain Ab:  83% 7% • 10%

G2
F17
N18
S19
R26
N27
LEU
LYS
LEU
HIS
LYS
LYS
LYS
LYS
PRO
PHE
S38
K39
R40
R49
T86
R89
R94
R106


- Chain Ad:  87% 5% • 5%

- Chain Ae:  70% 12% 1% 14%

G2
R6
F7
R8
R18
R21
K30
LYS
ASP
THR
LYS
ILE
ARG
TYR
N38
R41
R42
R45
R46
L51

- Chain Af:  96% ..

A diagram showing a 4-bit bus system. It consists of four colored rectangular blocks connected by horizontal lines. From left to right, the blocks are: a blue block labeled 'A1', a yellow block labeled 'R41', a red block labeled 'R46', and a green block labeled 'L51'. The connections are as follows: a line from the right side of 'A1' to the left side of 'R41'; a line from the right side of 'R41' to the left side of 'R46'; and a line from the right side of 'R46' to the left side of 'L51'.

- Chain AP:  82% 16% .

G2	K13	S16	R24	V25	R26	R31	R38	R49	R50	I56	I61	V62	R63	K72	I79	K85	S94	T95	R96	C111	G112	N113	W121	Q124	I1149	N150	R160	E161	L162	R163	R173	R176	L181	R186	P187	S188	I189	R190
----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	-------	------	------	------	------	------	------	------	------	------	------	------	------	------

A191  
N192

R195  
R196

R205


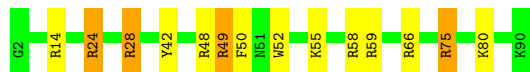
- Chain Ah:  94% 5%

A diagram showing a sequence of nodes: S2, R3, R4, R17, R23, R49, R85, and L86. Nodes S2, R3, R4, R23, R49, and L86 are yellow. Nodes R17 and R85 are orange. Green bars connect S2 to R3, R3 to R4, R4 to R17, R17 to R23, R23 to R49, and R49 to R85. R85 is connected to L86 by a thin line.

## • Molecule 56: 60S ribosomal protein eL6

Chain AI:  91% 6% ..

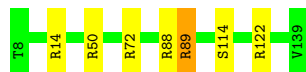
## • Molecule 57: 60S ribosomal protein eL37

Chain Ac:  84% 11% .


## • Molecule 58: 60S ribosomal protein uL13

Chain AK:  90% 8% .


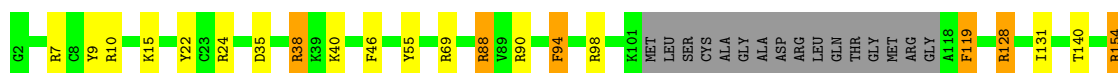
## • Molecule 59: 60S ribosomal protein uL14

Chain AM:  95% 5% .


## • Molecule 60: 60S ribosomal protein eL18

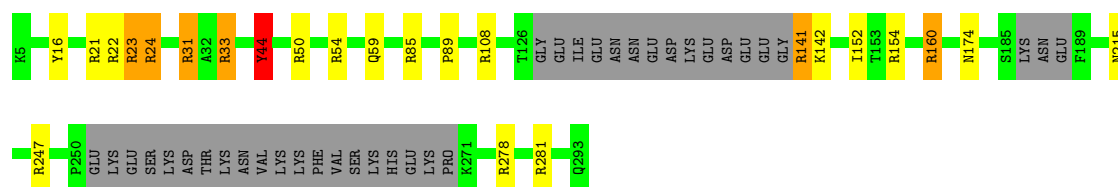
Chain AS:  87% 8% 5%

## • Molecule 61: 60S ribosomal protein uL16

Chain AQ:  79% 10% . 8%

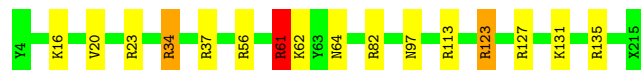
## • Molecule 62: 60S ribosomal protein uL18

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% .



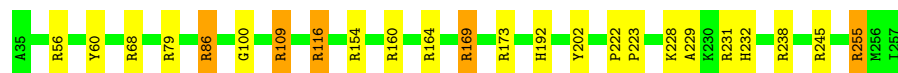
- Molecule 67: 60S ribosomal protein uL29

Chain A3: 88% 9% ..




- Molecule 68: 60S ribosomal protein uL30

Chain A5: 89% 9% .



- Molecule 69: 60S ribosomal protein uL2



Chain AD:  89% 9% .




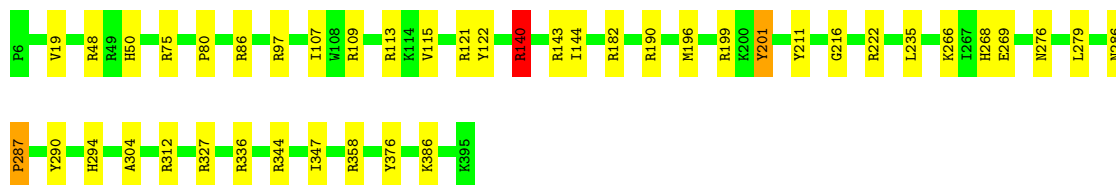
- Molecule 70: 60S ribosomal protein uL3

Chain AE:  92% 7% .



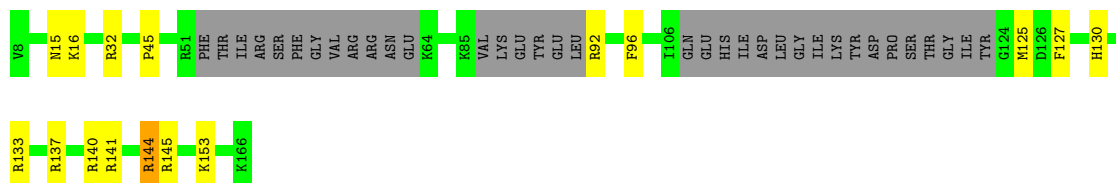
- Molecule 71: 60S ribosomal protein uL4

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% . .

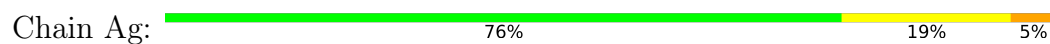


- Molecule 75: 60S ribosomal protein eL21

Chain AV:  90% 9% .



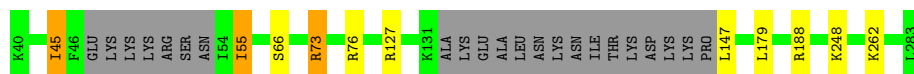
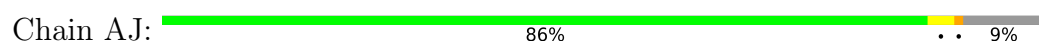
- Molecule 76: 60S ribosomal protein eL41



- 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 ⓘ

### 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	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

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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

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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

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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

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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

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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

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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

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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

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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

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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

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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 ⓘ

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 ⓘ

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

## 5.5 Carbohydrates ⓘ

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 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.