



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 01:40 PM EST

PDB ID : 3JBP
EMDB ID : EMD-6454
Title : Cryo-electron microscopy reconstruction of the Plasmodium falciparum 80S ribosome bound to E-tRNA
Authors : Sun, M.; Li, W.; Blomqvist, K.; Das, S.; Hashem, Y.; Dvorin, J.D.; Frank, J.
Deposited on : 2015-09-16
Resolution : 6.70 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

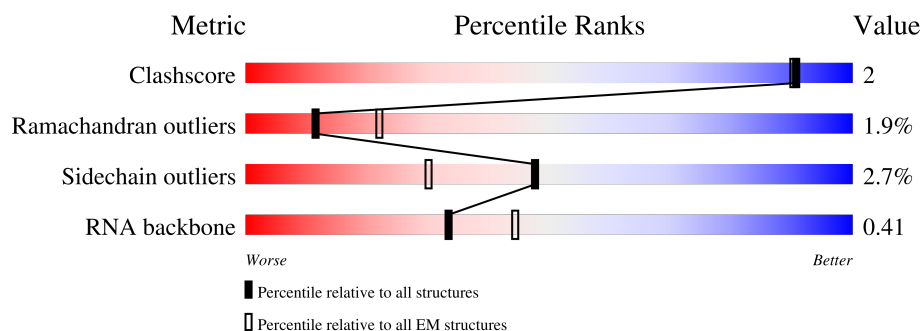
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 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 6.70 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	A	1608	29% 44% 22% 5%
2	7	74	9% 41% 38% 12%
3	D	209	70% . . 25%
4	E	185	88% 11% .
5	G	224	93% 7%
6	I	189	87% 5% . 5%
7	K	129	90% 5% . .


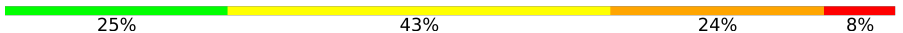
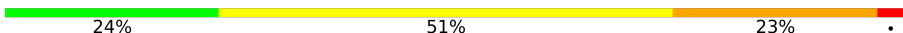















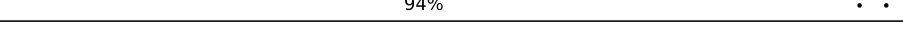

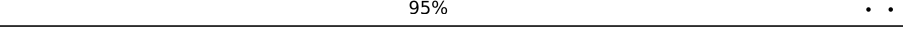




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Mol	Chain	Length	Quality of chain
8	M	138	
9	W	108	
10	R	114	
11	O	79	
12	Y	154	
13	Z	72	
14	1	120	
15	2	68	
16	3	95	
17	4	76	
18	5	65	
19	6	43	
20	B	210	
21	F	257	
22	H	214	
23	J	188	
24	L	214	
25	N	98	
26	P	127	
27	Q	144	
28	S	128	
29	T	48	
30	U	149	
31	V	156	
32	X	103	

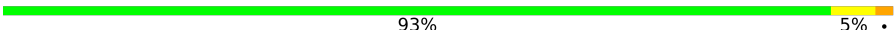





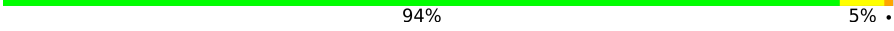

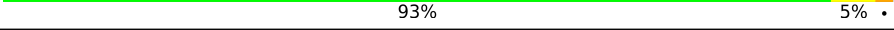




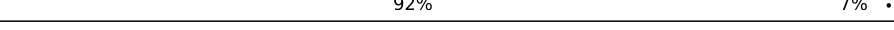







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Mol	Chain	Length	Quality of chain
33	C	195	 89% 10% .
34	AA	3193	 25% 43% 24% 8%
35	AC	151	 24% 51% 23% .
36	AB	118	 29% 52% 13% 7%
37	AL	211	 92% 7% .
38	A1	145	 89% 8% .
39	A2	118	 82% 6% 12%
40	A4	66	 86% 8% 5% .
41	A6	98	 90% 8% ..
42	A7	102	 86% 8% 6%
43	AN	146	 90% 8% .
44	A8	125	 88% 10% ..
45	A9	103	 88% 9% ..
46	Aa	106	 83% 16% .
47	Ab	105	 87% . . 10%
48	Ad	76	 91% . 5%
49	Ae	50	 68% 14% . 14%
50	Af	51	 94% . .
51	AP	204	 84% 15% .
52	Ah	85	 95% . .
53	Ai	95	 91% 8% .
54	AI	213	 91% 6% .
55	AJ	244	 87% . 9%
56	Ac	89	 82% 16% ..
57	AK	201	 90% 9% .

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Mol	Chain	Length	Quality of chain
58	AM	132	 93% 5% .
59	AS	186	 86% 12% .
60	AO	147	 89% 10% .
61	AQ	205	 80% 11% . 8%
62	AR	289	 77% 9% . 13%
63	AW	170	 88% 9% .
64	AY	101	 94% 5% .
65	AT	181	 91% 8% ..
66	AZ	121	 93% 5% .
67	A3	119	 92% 8% .
68	A5	223	 86% 11% .
69	AD	247	 89% 9% ..
70	AE	380	 89% 10% .
71	AF	390	 92% 7% .
72	AG	159	 70% 6% . 22%
73	AU	180	 88% 7% . .
74	AH	185	 91% 8% .
75	AV	155	 89% 10% .
76	Ag	37	 76% 16% 8%
77	AX	97	 94% 6%
78	A0	62	 92% 6% .

2 Entry composition

There are 78 unique types of molecules in this entry. The entry contains 193012 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 E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	74	Total	C	N	O	P	0	0
			1571	702	275	521	73		

- 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		

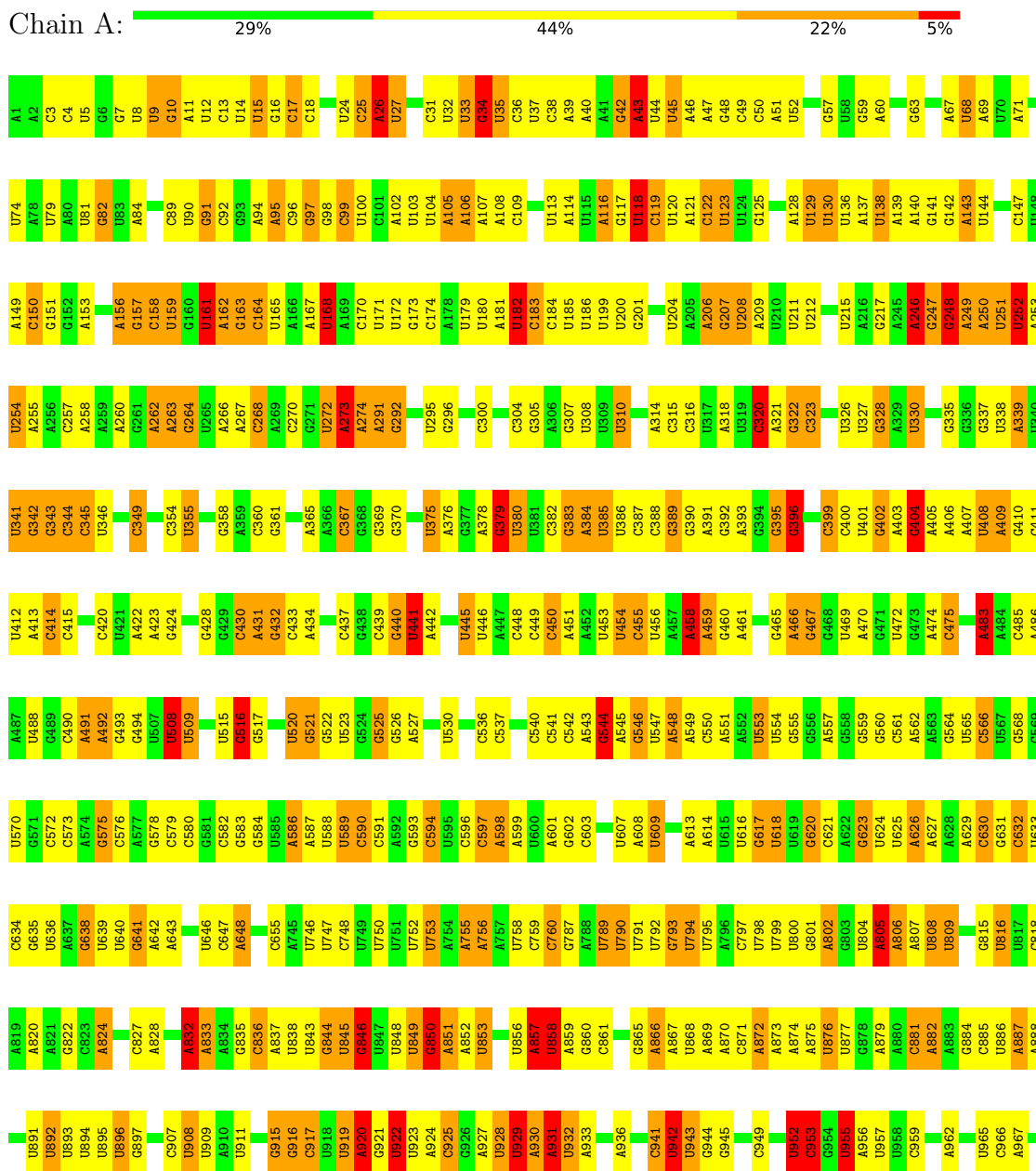
- Molecule 78 is a protein called 60S ribosomal protein eL24.

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

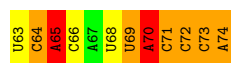


U2038	C1945	U1728	U1661	G1378	U1275	U1207	C1097	G1031	G970
A2029	C1946	A1729	U1662	G1379	U1276	G1208	U1098	A1032	G971
U2030	U1947	A1730	G1664	C1380	G1277	G1209	A1099	A1035	U972
C2031	C1886	A1731	G1665	C1381	G1278	G1210	U1100		G973
U2032	A1948	G1732	G1666	G1382	G1279	G1211	G1101	G1038	A974
A2033	C1949	G1733	G1667	U1383	G1280	G1212	C1102	A1039	A975
U2034	C1889	G1734	A1668	U1384	C1281	G1213	C1103	A1040	A976
U2035	G1951	G1735	G1454	U1385	U1282	G1214	G1104	A1041	U977
A1891	A1952	A1736	G1455	U1386	U1283	G1215	A1105	G1042	U978
A1892	U1953	A1741	G1456	U1387	A1284	U1216	C1106	A1043	G979
C1893	C1954	A1742	C1672	A1388	A1285		U1107	A1044	U981
A1894	G1955	A1743	G1673	U1389	U1286	C1220	A1108	G1045	A982
U1896	A1956	A1744	A1673	U1390	U1287	G1221	G1109	A1046	G983
A1897	U1896	A1745	G1674	U1391	U1288	G1222		A1047	A984
G1898	G1898	G1746	G1675	C1392	G1289	G1223	G1112		U986
A1900	A1899	U1747	C1677	U1400	A1290	G1224	U1116	U1050	U987
U1901	U1900	C1749	U1678	G1401	U1291	A1225	G1117	U1051	U988
U1902	G1901	U1750	G1679	A1402	C1293	A1226	U1118		U989
U1903	U1902	C1781		U1403	A1294	G1227	G1119	G1054	C989
G1904	A1903	A1782	A1682	U1404	A1295	C1228		G1055	U990
C1905	U1904	U1783	U1683	U1407	C1296		C1166	G1056	A993
U1906	A1905	A1784	G1684	U1408	A1297	G1229	U1167	A1057	G994
A1907	U1906	G1785	U1685	U1409	C1298	G1230	U1168	G1058	A995
U1908	A1907	C1786	C1686	G1409	G1299	G1231	C1169	U1059	C996
C1909	U1908	U1787	C1687	G1410	G1300	U1236	C1170	G1060	G997
U1910	U1909	U1788	U1688	G1411	G1301		U1171	A1061	
A1911	G1910	U1789	G1691	U1412	G1302	A1239	U1172	A1062	A998
C1912	U1911	U1790	A1692	U1413	A1303	G1240	C1173	G1063	A999
G1913	A1912	C1791	U1693	U1414	A1304	A1241	A1174	A1064	C1000
U1914	U1913	U1792	C1694	A1415	A1305	G1242	G1175	A1065	A1001
C1915	A1914	G1793	A1695	U1416	C1306	A1243	U1176		A1002
U1916	U1915	C1794	U1696	U1417	U1307	A1244	U1177	U1068	C1003
A1917	A1916	G1795	C1697	C1418	A1308		C1178	C1069	U1004
U1918	U1917	U1796	G1699	C1419	A1309	G1247	U1180	G1070	G1005
G1919	A1918	C1797	G1700	U1420	C1310		A1071	C1006	C1006
C1920	U1919	U1798	G1632	G1421		G1248	U1181	G1007	G1007
A1921	A1920	A1799	G1635	U1422	G1313	A1249	A1182	A1008	A1008
C1922	U1921	A1800	A1636	A1423	U1314	G1250	A1183	A1009	A1009
U1923	A1922	U1801	U1637	U1424	U1315	G1251	G1184	A1010	A1010
U1924	U1923	G1802	C1705	C1425		A1252	A1185	C1075	C1075
	U1924	G1803	U1706	U1426			G1186	C1076	
U1927	U1925	U1804	C1707	G1427	A1318	G1255	A1187	G1079	A1013
A1928	A1926	G1805	U1708	U1428	G1319	G1256	A1188	U1014	U1014
C1929	U1927	U1806	C1709	A1429	A1320	C1257	A1189	U1015	U1015
A1930	U1928	A1807	U1710	C1429	C1321	A1258	U1190	A1082	U1016
C1931	A1929	G1808	G1712	U1430	U1322	C1259	C1191	A1083	G1017
U1932	U1930	U1809	U1713	A1431	U1362	C1260	A1192	U1018	U1018
A1933	A1931	C1810	C1714	G1432	G1363	A1261	A1193	C1085	C1019
C1934	U1932	U1811	U1715	U1433	G1364	C1262	A1194	U1086	U1020
G1935	U1933	A1812	A1716	U1434	G1365	C1263	G1195	U1087	A1021
A1936	G1935	U1813	C1717	C1435	A1366	A1264	U1196	A1088	A1022
C1937	U1936	U1814	U1718	U1436	U1367	G1265	C1197	A1089	A1023
U1938	A1937	G1815	U1719	U1437	G1368	C1266	U1198	C1090	A1024
G1939	U1938	U1816	G1720	C1440	U1370	G1268	U1199	C1091	U1025
A1940	U1939	U1817	A1721	U1441			U1200	A1092	A1026
C1941	U1940	A1818	U1722	U1442	G1374	G1271	G1201	U1093	C1027
U1942	A1941	U1819	A1723	U1443	C1375	A1272	G1202	A1094	U1029
G1943	U1942	U1820	U1724	G1444	A1376	G1273		A1095	U1029
A1944	A1943	A1821	A1727	U1445	U1377	C1274	C1206	A1096	C1030

• Molecule 2: E-tRNA

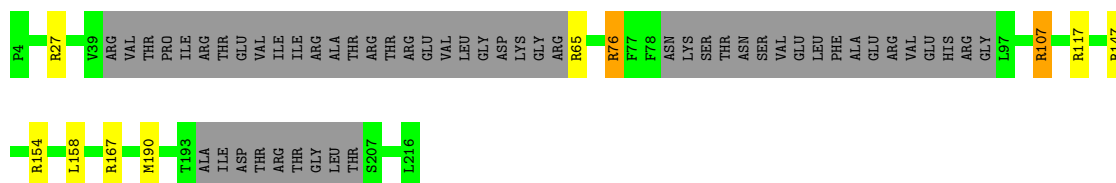
Chain 7:  9% 41% 38% 12%

G1	G1
G2	G2
G3	G3
U4	U4
A5	A5
A6	A6
U7	U7
U8	U8
G9	G9
C11	C11
G12	G12
C13	C13
A14	A14
G15	G15
U16	U16
U17	U17
G18	G18
G19	G19
U20	U20
U21	U21
A22	A22
G23	G23
C24	C24
G25	G25
C26	C26
G27	G27
C28	C28
G29	G29
C30	C30
G31	G31
U32	U32
C33	C33
C34	C34
C35	C35
A36	A36
U37	U37
A38	A38
A39	A39
U40	U40
C41	C41
C42	C42
C43	C43
C44	C44
A45	A45
G46	G46
U48	U48
C49	C49
G50	G50
U51	U51
C52	C52
A53	A53
G54	G54
U55	U55
C56	C56
G57	G57
C61	C61
C62	C62



- Molecule 3: 40S ribosomal protein uS3

Chain D: 70% 25%



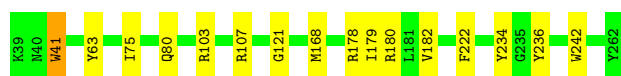
- Molecule 4: 40S ribosomal protein uS4

Chain E: 88% 11%



- Molecule 5: 40S ribosomal protein uS5

Chain G: 93% 7%



- Molecule 6: 40S ribosomal protein uS7

Chain I: 87% 5% 5%



- Molecule 7: 40S ribosomal protein uS8

Chain K: 90% 5% 5%




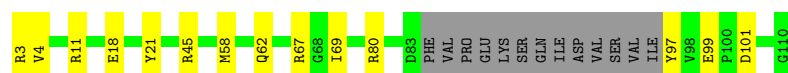
- Molecule 8: 40S ribosomal protein uS9

Chain M: 94% 6%




- Molecule 9: 40S ribosomal protein eS17

Chain W:  75% 13% 12%




- Molecule 10: 40S ribosomal protein eS12

Chain R:  80% 6% 14%




- Molecule 11: 40S ribosomal protein eS10

Chain O:  86% 14%



- Molecule 12: 40S ribosomal protein eS19

Chain Y:  86% 13% .




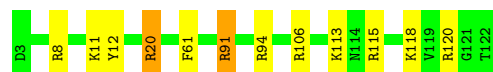
- Molecule 13: 40S ribosomal protein eS21

Chain Z:  94% 6%



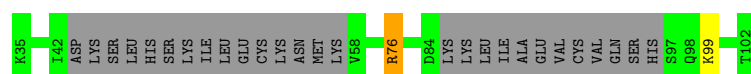
- Molecule 14: 40S ribosomal protein eS24

Chain 1:  90% 8% .




- Molecule 15: 40S ribosomal protein eS25

Chain 2:  57% .. 40%




- Molecule 16: 40S ribosomal protein eS26

Chain 3:  85% 13%




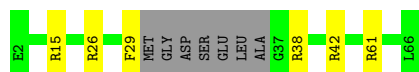
- Molecule 17: 40S ribosomal protein eS27

Chain 4:  88% 11%




- Molecule 18: 40S ribosomal protein eS28

Chain 5:  80% 9% 11%



- Molecule 19: 40S ribosomal protein eS30

Chain 6:  86% 14%




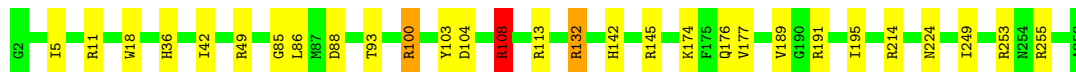
- Molecule 20: 40S ribosomal protein eS1

Chain B:  92% 5%




- Molecule 21: 40S ribosomal protein eS4

Chain F:  89% 10%




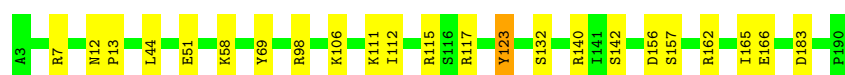
- Molecule 22: 40S ribosomal protein eS6

Chain H:  86% 8% 5%



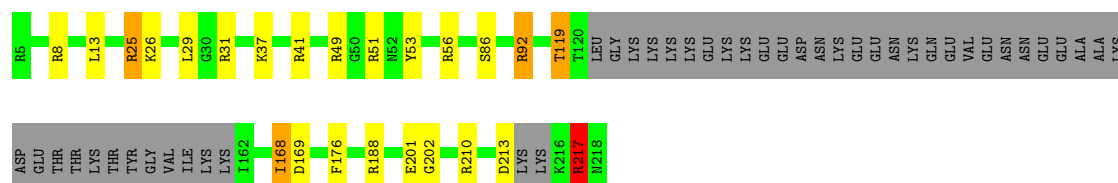
- Molecule 23: 40S ribosomal protein eS7

Chain J:  88% 12% .




- Molecule 24: 40S ribosomal protein eS8

Chain L:  69% 9% 20% .




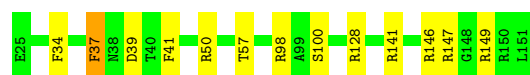
- Molecule 25: 40S ribosomal protein uS10

Chain N:  90% 8% .



- Molecule 26: 40S ribosomal protein uS11

Chain P:  90% 9% .




- Molecule 27: 40S ribosomal protein uS12

Chain Q:  92% 7% .




- Molecule 28: 40S ribosomal protein uS13

Chain S:  84% 14% .



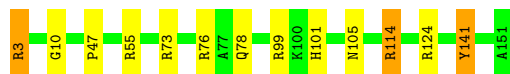
- Molecule 29: 40S ribosomal protein uS14

Chain T:  85% 12% .




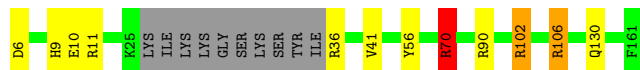
- Molecule 30: 40S ribosomal protein uS15

Chain U:  91% 7%




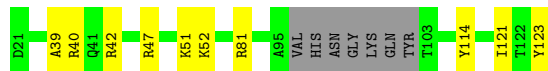
- Molecule 31: 40S ribosomal protein uS17

Chain V:  86% 6% 6%



- Molecule 32: 40S ribosomal protein uS19

Chain X:  83% 10% 7%



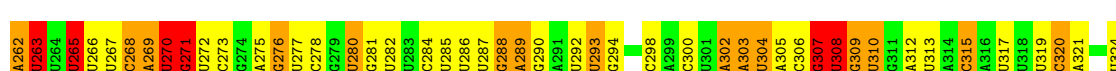
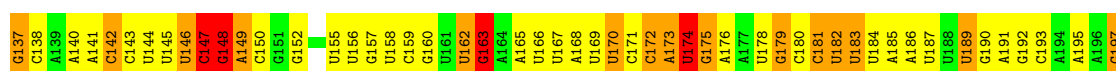
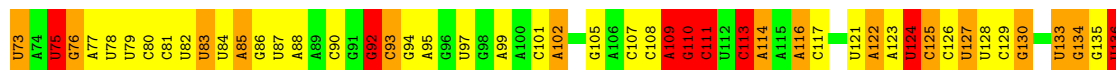
- Molecule 33: 40S ribosomal protein uS2

Chain C:  89% 10%



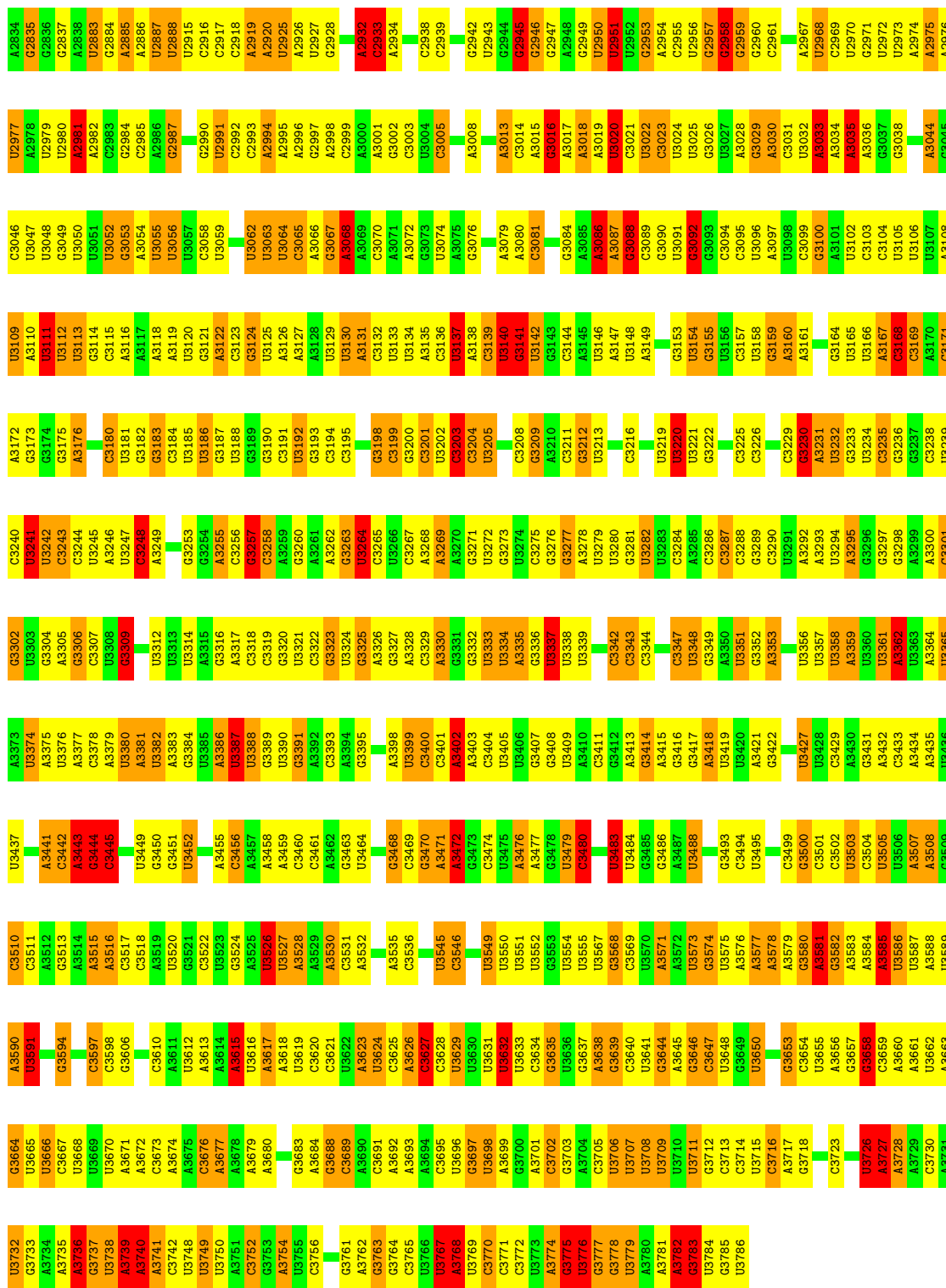
- Molecule 34: 28S ribosomal RNA

Chain AA:  25% 43% 24% 8%





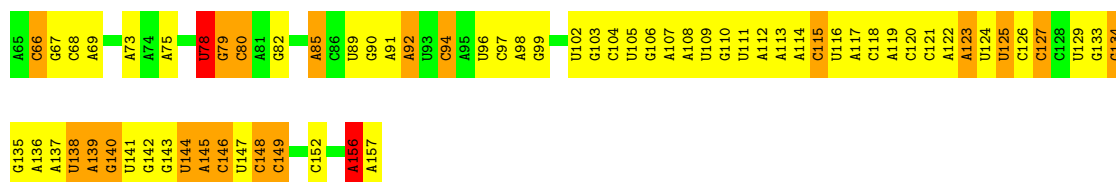
G2639	A2572	A2506	A2442	G2214	U2148	C2080	G1973	C1866	U1800	A1732	U1661	G1593	A1522
U2640	A2573	A2507	G2443	G2215	A2149	U2081	U1974	U1867	G1801	G1733	G1662	A1594	A1523
C2643	A2574	C2508	C2444	G2216	A2152	C2082	A1976	U1868	C1804	G1735	A1663	A1595	U1524
U2644	G2576	U2510	U2446	C2217	A2153	U2083	U1977	A1871	C1805	U1736	G1665	U1597	G1526
C2647	C2577	G2514	U2449	G2218	A2154	C2089	U1978	A1872	C1806	A1737	A1666	A1598	
G2648	U2579	A2515	G2450	U2220	A2156	U2090	C1980	U1873	U1807	U1738	A1667	G1599	G1529
A2649	A2451	A2516	A2451	U2221	G2157	U2091	U1981	C1874	U1808	C1739	G1668	C1600	G1530
C2652	A2452	A2517	A2452	A2386	U2158	C2092	A1989	A1875	U1809	A1740	A1669	A1601	G1531
C2653	G2581	U2518	A2453	A2387	U2159	U2093	A1990	U1876	C1812	G1741	U1671	C1602	
A2654	A2584	C2520	A2454	U2388	G2160	A2094	U1991	U1877	U1813	G1742		C1603	U1534
C2655		A2521	C2455	G2389	G2161	U2096		U1878	A1813	U1743		U1604	G1535
A2656	U2587	A2522	C2456	U2390	U2162	G2096	U1994	A1880	U1814	U1744		U1605	U1536
G2657	U2588	G2523	A2457		G2165	A2097	C1995	U1881	A1815	U1745	C1675	U1606	G1537
C2658	A2589	C2524	A2458	A2393	G2166	C2098	C1996	U1882	G1816	U1746	C1676	U1607	U1538
C2659	U2590	A2525	A2459	C2394	G2167	C2099	G1997	U1883	A1817	U1747	G1677	U1539	U1540
A2660	U2591	A2526	A2461	U2395	A2168		A1998	A1886	U1818	U1748	C1678	A1612	
A2661	A2592	C2527	C2462	C2396	A2169	A2102	G2000	A1887	U1820	U1749	A1679	G1613	A1541
G2662	A2593	C2528	A2463	A2400	G2170	C2103	G2001	A1888	U1821	C1751	C1681	A1614	G1543
G2663	U2594	G2529	G2464	C2401	U2171	A2105	G2002	A1889	U1822	C1752	A1682	G1615	C1544
G2664	G2595	G2534	G2465	U2402	C2172	A2106	G2003		A1823	U1753	A1683	A1616	
A2665	A2596	U2534	U2466	G2403	G2173	C2107	U2004	U1894	A1824	G1754	A1684	A1617	A1548
A2666	C2597	A2535		A2404	G2174	A2108	A2005	C1896	U1826	U1755	G1685	C1618	U1549
C2667	C2598	A2536	U2469	A2405	C2175	A2109		C1897	C1827	C1757		U1619	U1550
G2668	G2599	A2537			A2176	C2110	G2008	U1898	G1828		A1688	C1551	C1552
C2669	C2600	C2538	C2472	G2408	A2177	C2111	A2009	U1899	G1829	C1758	U1689	G1625	U1553
G2670	C2601	G2539	A2473	G2409	A2178	G2112	C2010	C1900	G1830	A1762	A1690	A1626	G1554
C2671	A2602	G2540	C2474	A2410	A2179	C2113	U2011	A1901	G1831	G1763	C1692	C1627	G1554
C2672	U2603	C2541		C2411	U2180	A2114	A2012	U1902	U1832		A1693	G1628	A1585
U2673	G2604	G2542	U2477	A2412	A2181	U2115	U2013	C1903	G1833	U1766	G1694	G1629	G1556
G2674	A2605	G2543	G2478	A2413	G2182	C2116	C2014	U1904	C1834	U1767	A1695	A1630	U1560
G2675	G2606	G2544	U2479	G2414	A2183	A2117	C2015	C1905	G1835	A1768	A1696	A1631	C1561
A2676	U2607	A2545	G2480	G2415	U2184	G2118	U2016	A1906	U1836	G1770	A1697	G1632	
A2677	G2608		A2481	G2416	C2185		U2017	A1907	U1837	A1771	A1698	G1633	G1564
U2679		A2548	U2482		C2186	C2121	G2018	U1908	U1838	G1772	G1699	G1635	U1564
A2680	U2611	A2549	U2483	A2419	G2187	U2122	A2019	U1909	U1839	A1773	U1700	A1636	A1566
U2681	U2612	C2550	U2484	U2420	U2188	C2123	A2020	C1910	C1840	U1774	G1701	G1637	A1567
C2682	A2613	U2551	C2485	C2421	A2189	C2124	A2021		U1841	U1775	U1702	C1568	C1569
A2683	A2614	A2552	U2486	G2422	A2190	A2126	A2022	A1913	U1842	A1779	U1703	G1640	U1572
G2684	G2615	U2553	G2487	G2423	C2191	A2126		A1914	U1843	G1780	U1704	G1641	G1642
C2685		G2554	A2488	A2424	U2192	G2127	G2030	A1915	G1844	A1781	A1705	U1643	C1573
U2686	G2618	A2555	C2489	C2425	U2193	G2128		U1956	C1845	U1782	U1706	U1644	C1574
		C2556	C2490	U2426	U2194		C2033	U1957	A1846	G1783	A1707	G1645	U1575
C2689	U2621	U2557	A2491	G2427	G2197	A2131	G2034	U1958	C1847		G1712	U1646	U1576
U2690	C2622	C2558	G2492	U2428	U2198	A2132	G2035	G1959	U1848	U1785	G1724	C1646	A1577
C2693	C2623	U2559	U2493	U2429	A2199	C2133	C2036	U1960	U1849	A1786	U1725	U1647	G1578
U2694	G2624	C2560	G2494	U2430	A2199	A2134	U2037	U1961	U1850	U1787	C1720	U1648	
A2695		U2561	C2495	A2431	A2200	G2135		U1962	A1851	C1788	C1721	G1649	
U2496	C2626	U2562	A2496	A2432	A2201	C2136	U2041	U1963	C1852	A1789	C1722	U1650	G1643
C2627	U2627	A2563	U2497	U2433	G2202	C2137	G2068	G1964	C1853	U1790	G1723	C1651	G1644
G2628	C2628	A2564	U2498	A2434	G2203	U2138	C2069	U1965	U1854		G1724	C1654	U1585
C2629	U2629	G2565	A2499	A2435	A2204	C2139	U2070	A1966	U1855	A1793	G1726	U1655	U1587
A2630	G2630	U2566	A2500	A2436	U2205	U2140	U2071	U1967	U1856	U1794	C1726	G1656	U1587
U2631	C2631	G2567	A2501	A2437	U2206	G2141	U2072	C1968	A1857	U1795	U1727	U1657	U1588
U2701		A2568	U2502	A2438	G2207		G2073	A1969		U1796	C1728	U1657	G1589
G2702	C2635	C2569	G2503	A2439	C2208	A2145	C2074	A1970	C1861	A1797	A1729	G1658	U1590
U2703	U2636	C2570	A2440	C2439	C2209	A2146	U2075	U1971		A1798	A1730	U1591	U1591
U2704		C2571	C2505	U2441	U2210	A2147	A2079	A1972	C1865	A1799	A1731	G1592	



- Molecule 35: 5.8S ribosomal RNA

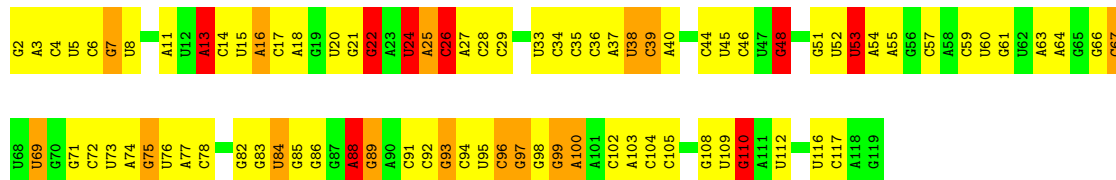
Chain AC: 24% 51% 23% .





• Molecule 36: 5S ribosomal RNA

Chain AB: 29% 52% 13% 7%



• Molecule 37: 60S ribosomal protein eL13

Chain AL: 92% 7%



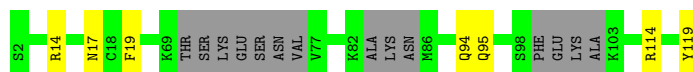
• Molecule 38: 60S ribosomal protein eL27

Chain A1: 89% 8%



• Molecule 39: 60S ribosomal protein eL28

Chain A2: 82% 6% 12%



• Molecule 40: 60S ribosomal protein eL29

Chain A4: 86% 8% 5%



• Molecule 41: 60S ribosomal protein eL30

Chain A6: 90% 8%



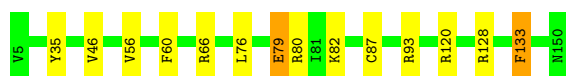
- Molecule 42: 60S ribosomal protein eL31

Chain A7: 86% 8% 6%



- Molecule 43: 60S ribosomal protein eL14

Chain AN: 90% 8% .



- Molecule 44: 60S ribosomal protein eL32

Chain A8: 88% 10% ..



- Molecule 45: 60S ribosomal protein eL33

Chain A9: 88% 9% ..



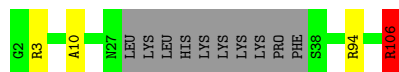
- Molecule 46: 60S ribosomal protein eL34

Chain Aa: 83% 16% .



- Molecule 47: 60S ribosomal protein eL36

Chain Ab: 87% . . 10%



- Molecule 48: 60S ribosomal protein eL38

Chain Ad: 91% . 5%



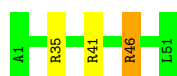
- Molecule 49: 60S ribosomal protein eL39

Chain Ae: 68% 14% 14%



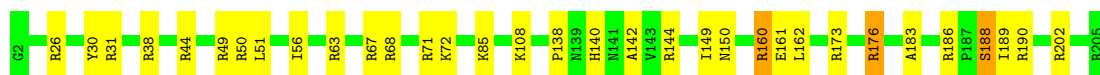
- Molecule 50: 60S ribosomal protein eL40

Chain Af: 94% . .



- Molecule 51: 60S ribosomal protein eL15

Chain AP: 84% 15% .



- Molecule 52: 60S ribosomal protein eL43

Chain Ah: 95% . .



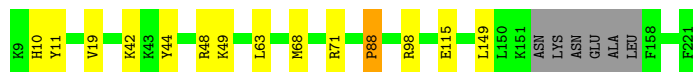
- Molecule 53: 60S ribosomal protein eL44

Chain Ai: 91% 8% .



- Molecule 54: 60S ribosomal protein eL6

Chain AI: 91% 6% .



- Molecule 55: 60S ribosomal protein eL8

Chain AJ: 87% . 9%



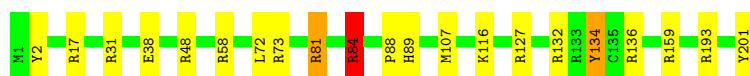
- Molecule 56: 60S ribosomal protein eL37

Chain Ac: 82% 16% ..



- Molecule 57: 60S ribosomal protein uL13

Chain AK: 90% 9% .



- Molecule 58: 60S ribosomal protein uL14

Chain AM: 93% 5% .



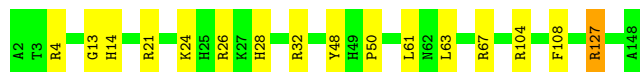
- Molecule 59: 60S ribosomal protein eL18

Chain AS: 86% 12% .



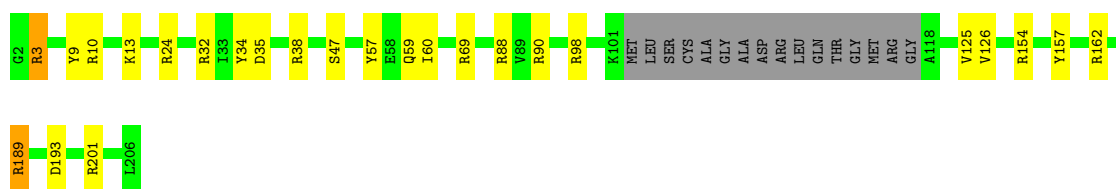
- Molecule 60: 60S ribosomal protein uL15

Chain AO: 89% 10% .




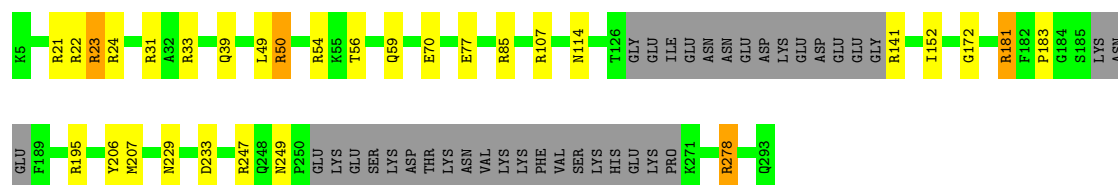
- Molecule 61: 60S ribosomal protein uL16

Chain AQ: 80% 11% 8%



- Molecule 62: 60S ribosomal protein uL18

Chain AR:  77% 9% 13%



- Molecule 63: 60S ribosomal protein uL22

Chain AW:  88% 9%



- Molecule 64: 60S ribosomal protein uL23

Chain AY:  94% 5%



- Molecule 65: 60S ribosomal protein eL19

Chain AT:  91% 8%



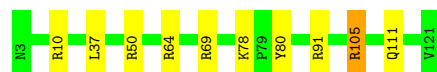
- Molecule 66: 60S ribosomal protein uL24

Chain AZ:  93% 5%




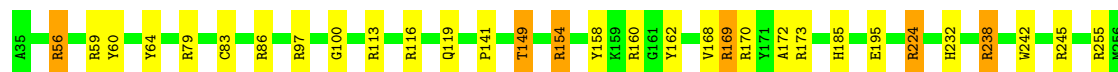
- Molecule 67: 60S ribosomal protein uL29

Chain A3:  92% 8%



- Molecule 68: 60S ribosomal protein uL30

Chain A5:  86% 11%

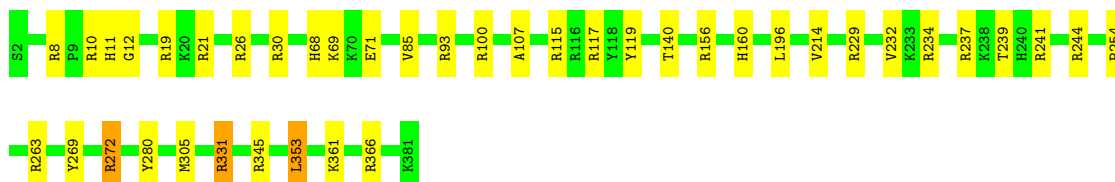


1257

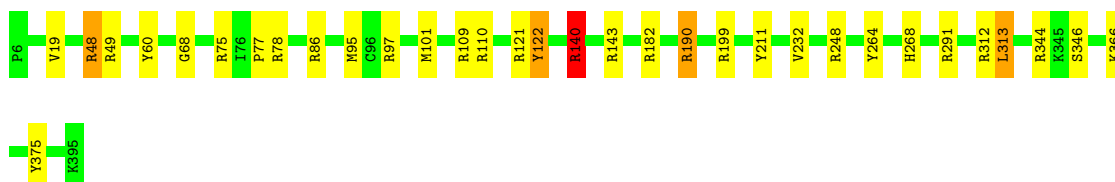
- Molecule 69: 60S ribosomal protein uL2

Chain AD:  89% 9% ..

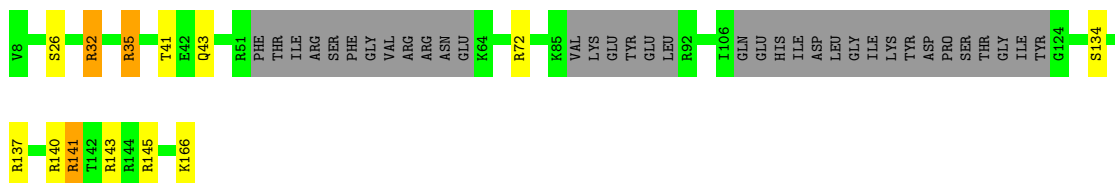

- Molecule 70: 60S ribosomal protein uL3

Chain AE:  89% 10% .



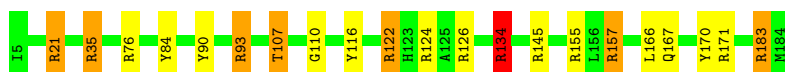
- Molecule 71: 60S ribosomal protein uL4

Chain AF:  92% 7% .


- Molecule 72: 60S ribosomal protein uL5

Chain AG:  70% 6% • 22%


- Molecule 73: 60S ribosomal protein eL20


Chain AU:  88% 7% • •


- Molecule 74: 60S ribosomal protein uL6

Chain AH:  91% 8% .




- Molecule 75: 60S ribosomal protein eL21

Chain AV:  89% 10% .



- Molecule 76: 60S ribosomal protein eL41

Chain Ag:  76% 16% 8%



- Molecule 77: 60S ribosomal protein eL22

Chain AX:  94% 6%



- Molecule 78: 60S ribosomal protein eL24

Chain A0:  92% 6% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	96732	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	1.23	26/38275 (0.1%)	1.58	870/59596 (1.5%)
2	7	1.23	4/1754 (0.2%)	1.79	69/2732 (2.5%)
3	D	0.75	0/1241	1.13	10/1652 (0.6%)
4	E	0.70	0/1539	1.16	13/2055 (0.6%)
5	G	0.70	0/1800	1.01	5/2429 (0.2%)
6	I	0.69	0/1443	1.22	15/1936 (0.8%)
7	K	0.70	0/1054	1.15	10/1411 (0.7%)
8	M	0.71	0/1114	1.12	4/1487 (0.3%)
9	W	0.71	0/793	1.18	4/1053 (0.4%)
10	R	0.74	0/755	1.06	0/1013
11	O	0.72	0/706	1.03	3/950 (0.3%)
12	Y	0.70	0/1295	1.18	9/1742 (0.5%)
13	Z	0.70	0/565	1.08	2/758 (0.3%)
14	1	0.70	0/999	1.17	11/1321 (0.8%)
15	2	0.75	0/324	0.98	1/435 (0.2%)
16	3	0.71	0/794	1.24	10/1055 (0.9%)
17	4	0.68	0/597	1.09	0/801
18	5	0.75	0/459	1.33	9/606 (1.5%)
19	6	0.73	0/349	1.24	3/458 (0.7%)
20	B	0.65	0/1738	1.11	9/2321 (0.4%)
21	F	0.67	0/2098	1.14	11/2819 (0.4%)
22	H	0.67	0/1665	1.10	5/2210 (0.2%)
23	J	0.68	0/1545	1.07	7/2064 (0.3%)
24	L	0.71	0/1407	1.23	16/1879 (0.9%)
25	N	0.70	0/780	1.24	7/1053 (0.7%)
26	P	0.70	0/966	1.23	8/1295 (0.6%)
27	Q	0.69	0/1149	1.25	11/1532 (0.7%)
28	S	0.65	0/1063	1.27	11/1425 (0.8%)
29	T	0.73	0/412	1.25	6/544 (1.1%)
30	U	0.67	0/1223	1.14	9/1634 (0.6%)
31	V	0.71	0/1233	1.10	4/1645 (0.2%)
32	X	0.71	0/788	1.18	7/1050 (0.7%)
33	C	0.67	0/1570	1.08	4/2129 (0.2%)
34	AA	1.30	70/75947 (0.1%)	1.59	1892/118255 (1.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AC	1.30	7/3599 (0.2%)	1.55	88/5603 (1.6%)
36	AB	1.27	2/2823 (0.1%)	1.52	57/4400 (1.3%)
37	AL	0.67	0/1789	1.14	9/2381 (0.4%)
38	A1	0.68	0/1151	1.02	1/1531 (0.1%)
39	A2	0.72	0/840	1.01	3/1114 (0.3%)
40	A4	0.66	0/564	1.01	3/737 (0.4%)
41	A6	0.69	0/749	0.99	2/1001 (0.2%)
42	A7	0.70	0/806	1.14	3/1073 (0.3%)
43	AN	0.69	0/1218	1.12	6/1621 (0.4%)
44	A8	0.70	0/1054	1.24	10/1399 (0.7%)
45	A9	0.72	0/865	1.20	7/1160 (0.6%)
46	Aa	0.68	0/872	1.26	11/1161 (0.9%)
47	Ab	0.71	0/763	1.13	5/1008 (0.5%)
48	Ad	0.72	0/612	1.09	2/812 (0.2%)
49	Ae	0.75	0/396	1.41	6/521 (1.2%)
50	Af	0.67	0/419	1.16	3/556 (0.5%)
51	AP	0.69	0/1735	1.31	21/2320 (0.9%)
52	Ah	0.68	0/668	1.13	2/887 (0.2%)
53	Ai	0.67	0/789	1.16	6/1032 (0.6%)
54	AI	0.66	0/1708	1.04	6/2274 (0.3%)
55	AJ	0.67	0/1840	1.03	3/2456 (0.1%)
56	Ac	0.72	0/723	1.29	8/951 (0.8%)
57	AK	0.67	0/1690	1.15	13/2260 (0.6%)
58	AM	0.68	0/1012	1.15	5/1363 (0.4%)
59	AS	0.69	0/1531	1.24	17/2040 (0.8%)
60	AO	0.66	0/1199	1.18	10/1597 (0.6%)
61	AQ	0.73	0/1580	1.21	16/2113 (0.8%)
62	AR	0.68	0/2079	1.16	20/2777 (0.7%)
63	AW	0.68	0/1244	1.22	12/1663 (0.7%)
64	AY	0.67	0/806	1.15	5/1074 (0.5%)
65	AT	0.66	0/1525	1.17	15/2016 (0.7%)
66	AZ	0.68	0/1013	1.17	9/1339 (0.7%)
67	A3	0.65	0/1005	1.09	8/1329 (0.6%)
68	A5	0.70	0/1917	1.25	22/2562 (0.9%)
69	AD	0.68	0/1902	1.19	17/2544 (0.7%)
70	AE	0.68	0/3130	1.16	25/4195 (0.6%)
71	AF	0.68	0/3145	1.16	23/4205 (0.5%)
72	AG	0.73	0/1021	1.19	9/1349 (0.7%)
73	AU	0.70	0/1527	1.18	15/2043 (0.7%)
74	AH	0.69	0/1501	1.17	10/2025 (0.5%)
75	AV	0.68	0/1301	1.20	11/1732 (0.6%)
76	Ag	0.74	0/348	1.57	8/448 (1.8%)
77	AX	0.72	0/842	1.06	3/1125 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
78	A0	0.73	0/534	1.12	4/711 (0.6%)
All	All	1.07	109/207275 (0.1%)	1.44	3594/303853 (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	231
2	7	0	18
3	D	0	1
4	E	0	6
5	G	0	4
6	I	0	4
7	K	0	2
8	M	0	1
9	W	0	3
11	O	0	1
12	Y	0	6
14	1	0	2
15	2	0	1
16	3	0	2
17	4	0	3
19	6	0	2
20	B	0	4
21	F	0	5
22	H	0	3
23	J	0	5
24	L	0	3
25	N	0	1
26	P	0	3
27	Q	0	2
29	T	0	1
30	U	0	2
31	V	0	6
32	X	0	1
33	C	0	6
34	AA	1	546
35	AC	0	19
36	AB	0	14
37	AL	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
38	A1	0	1
39	A2	0	1
40	A4	0	2
41	A6	0	4
42	A7	0	1
43	AN	0	3
44	A8	0	2
45	A9	0	2
46	Aa	0	4
47	Ab	0	1
49	Ae	0	5
50	Af	0	2
51	AP	0	6
52	Ah	0	2
53	Ai	0	3
54	AI	0	2
55	AJ	0	2
56	Ac	0	3
57	AK	0	5
58	AM	0	5
59	AS	0	8
60	AO	0	3
61	AQ	0	4
62	AR	0	4
63	AW	0	6
64	AY	0	1
65	AT	0	6
66	AZ	0	4
67	A3	0	1
68	A5	0	7
69	AD	0	6
70	AE	0	4
71	AF	0	6
72	AG	0	3
73	AU	0	7
74	AH	0	3
75	AV	0	5
76	Ag	0	2
77	AX	0	1
78	A0	0	2
All	All	1	1052

The worst 5 of 109 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	AA	2552	A	N9-C4	-8.94	1.32	1.37
2	7	74	A	C4'-C3'	8.62	1.62	1.53
34	AA	275	A	O3'-P	-7.93	1.51	1.61
34	AA	3122	A	N9-C4	-7.49	1.33	1.37
1	A	2055	A	N9-C4	-7.09	1.33	1.37

The worst 5 of 3594 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AA	3632	U	P-O5'-C5'	19.68	152.39	120.90
34	AA	257	U	P-O3'-C3'	18.75	142.20	119.70
34	AA	181	C	P-O3'-C3'	15.57	138.38	119.70
34	AA	3018	A	P-O3'-C3'	15.30	138.06	119.70
2	7	74	A	C5'-C4'-O4'	-14.85	91.28	109.10

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
34	AA	3018	A	C3'

5 of 1052 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	14	U	Sidechain
1	A	15	U	Sidechain
1	A	5	U	Sidechain
1	A	8	U	Sidechain
1	A	9	U	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	123	0
2	7	1571	0	797	12	0
3	D	1229	0	1311	0	0
4	E	1515	0	1605	2	0
5	G	1758	0	1811	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	I	1424	0	1471	0	0
7	K	1037	0	1099	2	0
8	M	1099	0	1183	1	0
9	W	786	0	858	1	0
10	R	747	0	754	0	0
11	O	687	0	695	0	0
12	Y	1267	0	1316	1	0
13	Z	557	0	558	0	0
14	1	986	0	1076	0	0
15	2	321	0	338	0	0
16	3	782	0	820	0	0
17	4	586	0	604	1	0
18	5	458	0	496	0	0
19	6	346	0	381	0	0
20	B	1714	0	1838	0	0
21	F	2062	0	2200	3	0
22	H	1648	0	1803	0	0
23	J	1529	0	1680	0	0
24	L	1383	0	1434	3	0
25	N	772	0	813	1	0
26	P	954	0	997	0	0
27	Q	1129	0	1196	0	0
28	S	1047	0	1101	2	0
29	T	405	0	419	0	0
30	U	1202	0	1299	1	0
31	V	1206	0	1239	1	0
32	X	777	0	832	1	0
33	C	1539	0	1600	1	0
34	AA	67884	0	34244	322	0
35	AC	3215	0	1633	8	0
36	AB	2522	0	1275	9	0
37	AL	1757	0	1888	0	0
38	A1	1134	0	1245	2	0
39	A2	831	0	887	1	0
40	A4	555	0	599	4	0
41	A6	741	0	763	1	0
42	A7	794	0	869	2	0
43	AN	1202	0	1316	2	0
44	A8	1037	0	1139	2	0
45	A9	845	0	886	3	0
46	Aa	859	0	912	0	0
47	Ab	757	0	842	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	Ad	604	0	686	0	0
49	Ae	388	0	421	0	0
50	Af	414	0	452	0	0
51	AP	1697	0	1802	2	0
52	Ah	659	0	727	0	0
53	Ai	779	0	861	0	0
54	AI	1685	0	1849	0	0
55	AJ	1813	0	1985	1	0
56	Ac	710	0	761	0	0
57	AK	1660	0	1785	2	0
58	AM	996	0	1044	0	0
59	AS	1503	0	1636	1	0
60	AO	1172	0	1230	3	0
61	AQ	1545	0	1582	0	0
62	AR	2050	0	2140	1	0
63	AW	1319	0	1304	1	0
64	AY	797	0	850	0	0
65	AT	1509	0	1682	0	0
66	AZ	1001	0	1099	0	0
67	A3	995	0	1121	0	0
68	A5	1879	0	2005	3	0
69	AD	1867	0	1964	4	0
70	AE	3062	0	3205	5	0
71	AF	3095	0	3333	1	0
72	AG	1011	0	1073	1	0
73	AU	1497	0	1556	2	0
74	AH	1476	0	1574	2	0
75	AV	1276	0	1355	0	0
76	Ag	343	0	388	0	0
77	AX	825	0	882	0	0
78	A0	522	0	539	0	0
All	All	193012	0	144279	522	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 2.

The worst 5 of 522 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)
70:AE:353:LEU:H	70:AE:353:LEU:HD23	1.55	0.71
34:AA:3632:U:H3	34:AA:3653:G:H1	1.42	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:AA:123:A:H3'	34:AA:124:U:H5''	1.81	0.62
34:AA:744:G:H1	34:AA:915:G:H1	1.47	0.62
34:AA:642:A:C6	34:AA:684:G:C8	2.89	0.61

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	D	149/209 (71%)	142 (95%)	7 (5%)	0	100	100
4	E	183/185 (99%)	171 (93%)	11 (6%)	1 (0%)	29	69
5	G	222/224 (99%)	204 (92%)	16 (7%)	2 (1%)	17	57
6	I	176/189 (93%)	165 (94%)	9 (5%)	2 (1%)	14	52
7	K	127/129 (98%)	113 (89%)	9 (7%)	5 (4%)	3	23
8	M	136/138 (99%)	125 (92%)	9 (7%)	2 (2%)	10	46
9	W	91/108 (84%)	82 (90%)	6 (7%)	3 (3%)	4	26
10	R	92/114 (81%)	80 (87%)	7 (8%)	5 (5%)	2	19
11	O	77/79 (98%)	69 (90%)	5 (6%)	3 (4%)	3	23
12	Y	152/154 (99%)	145 (95%)	4 (3%)	3 (2%)	7	38
13	Z	70/72 (97%)	64 (91%)	5 (7%)	1 (1%)	11	46
14	1	118/120 (98%)	112 (95%)	5 (4%)	1 (1%)	19	60
15	2	35/68 (52%)	33 (94%)	2 (6%)	0	100	100
16	3	93/95 (98%)	82 (88%)	10 (11%)	1 (1%)	14	52
17	4	74/76 (97%)	62 (84%)	8 (11%)	4 (5%)	2	19
18	5	54/65 (83%)	53 (98%)	1 (2%)	0	100	100
19	6	41/43 (95%)	33 (80%)	7 (17%)	1 (2%)	6	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	B	208/210 (99%)	189 (91%)	11 (5%)	8 (4%)	3	24
21	F	255/257 (99%)	232 (91%)	18 (7%)	5 (2%)	7	38
22	H	200/214 (94%)	187 (94%)	10 (5%)	3 (2%)	10	46
23	J	186/188 (99%)	169 (91%)	9 (5%)	8 (4%)	2	22
24	L	165/214 (77%)	146 (88%)	14 (8%)	5 (3%)	4	28
25	N	96/98 (98%)	90 (94%)	4 (4%)	2 (2%)	7	36
26	P	125/127 (98%)	109 (87%)	13 (10%)	3 (2%)	6	33
27	Q	142/144 (99%)	127 (89%)	13 (9%)	2 (1%)	11	46
28	S	126/128 (98%)	107 (85%)	12 (10%)	7 (6%)	2	18
29	T	46/48 (96%)	45 (98%)	1 (2%)	0	100	100
30	U	147/149 (99%)	141 (96%)	4 (3%)	2 (1%)	11	46
31	V	142/156 (91%)	128 (90%)	11 (8%)	3 (2%)	7	36
32	X	92/103 (89%)	78 (85%)	11 (12%)	3 (3%)	4	26
33	C	193/195 (99%)	171 (89%)	17 (9%)	5 (3%)	5	31
37	AL	209/211 (99%)	191 (91%)	14 (7%)	4 (2%)	8	38
38	A1	136/145 (94%)	125 (92%)	8 (6%)	3 (2%)	6	35
39	A2	96/118 (81%)	90 (94%)	4 (4%)	2 (2%)	7	36
40	A4	64/66 (97%)	60 (94%)	1 (2%)	3 (5%)	2	21
41	A6	96/98 (98%)	93 (97%)	3 (3%)	0	100	100
42	A7	92/102 (90%)	87 (95%)	5 (5%)	0	100	100
43	AN	144/146 (99%)	137 (95%)	5 (4%)	2 (1%)	11	46
44	A8	123/125 (98%)	102 (83%)	21 (17%)	0	100	100
45	A9	101/103 (98%)	92 (91%)	7 (7%)	2 (2%)	7	38
46	Aa	104/106 (98%)	96 (92%)	6 (6%)	2 (2%)	8	38
47	Ab	91/105 (87%)	85 (93%)	5 (6%)	1 (1%)	14	52
48	Ad	68/76 (90%)	65 (96%)	3 (4%)	0	100	100
49	Ae	39/50 (78%)	36 (92%)	3 (8%)	0	100	100
50	Af	49/51 (96%)	43 (88%)	6 (12%)	0	100	100
51	AP	202/204 (99%)	187 (93%)	7 (4%)	8 (4%)	3	23
52	Ah	83/85 (98%)	78 (94%)	4 (5%)	1 (1%)	13	50
53	Ai	93/95 (98%)	87 (94%)	4 (4%)	2 (2%)	6	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	AI	203/213 (95%)	183 (90%)	17 (8%)	3 (2%)	10	46
55	AJ	216/244 (88%)	202 (94%)	12 (6%)	2 (1%)	17	57
56	Ac	87/89 (98%)	76 (87%)	7 (8%)	4 (5%)	2	21
57	AK	199/201 (99%)	192 (96%)	5 (2%)	2 (1%)	15	54
58	AM	130/132 (98%)	123 (95%)	7 (5%)	0	100	100
59	AS	184/186 (99%)	168 (91%)	14 (8%)	2 (1%)	14	52
60	AO	145/147 (99%)	132 (91%)	12 (8%)	1 (1%)	22	63
61	AQ	185/205 (90%)	161 (87%)	19 (10%)	5 (3%)	5	31
62	AR	244/289 (84%)	224 (92%)	13 (5%)	7 (3%)	4	29
63	AW	149/170 (88%)	133 (89%)	10 (7%)	6 (4%)	3	23
64	AY	99/101 (98%)	95 (96%)	3 (3%)	1 (1%)	15	54
65	AT	179/181 (99%)	171 (96%)	5 (3%)	3 (2%)	9	42
66	AZ	119/121 (98%)	110 (92%)	7 (6%)	2 (2%)	9	42
67	A3	117/119 (98%)	107 (92%)	9 (8%)	1 (1%)	17	57
68	A5	221/223 (99%)	195 (88%)	21 (10%)	5 (2%)	6	34
69	AD	245/247 (99%)	223 (91%)	20 (8%)	2 (1%)	19	60
70	AE	378/380 (100%)	353 (93%)	21 (6%)	4 (1%)	14	52
71	AF	388/390 (100%)	356 (92%)	26 (7%)	6 (2%)	10	46
72	AG	116/159 (73%)	104 (90%)	11 (10%)	1 (1%)	17	57
73	AU	178/180 (99%)	169 (95%)	6 (3%)	3 (2%)	9	42
74	AH	183/185 (99%)	166 (91%)	14 (8%)	3 (2%)	9	44
75	AV	153/155 (99%)	141 (92%)	9 (6%)	3 (2%)	7	38
76	Ag	35/37 (95%)	30 (86%)	3 (9%)	2 (6%)	1	18
77	AX	95/97 (98%)	88 (93%)	5 (5%)	2 (2%)	7	36
78	A0	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
All	All	10111/10698 (94%)	9269 (92%)	652 (6%)	190 (2%)	11	38

5 of 190 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	I	42	HIS
6	I	70	HIS
8	M	41	GLU

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Mol	Chain	Res	Type
9	W	4	VAL
10	R	42	ILE

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%)	128 (97%)	4 (3%)	41	63
4	E	161/164 (98%)	156 (97%)	5 (3%)	40	62
5	G	191/191 (100%)	185 (97%)	6 (3%)	40	62
6	I	154/160 (96%)	151 (98%)	3 (2%)	57	75
7	K	115/115 (100%)	113 (98%)	2 (2%)	60	78
8	M	116/116 (100%)	115 (99%)	1 (1%)	78	87
9	W	86/99 (87%)	83 (96%)	3 (4%)	36	59
10	R	83/97 (86%)	81 (98%)	2 (2%)	49	69
11	O	76/76 (100%)	71 (93%)	5 (7%)	16	41
12	Y	137/137 (100%)	132 (96%)	5 (4%)	35	59
13	Z	60/60 (100%)	59 (98%)	1 (2%)	60	78
14	1	104/104 (100%)	100 (96%)	4 (4%)	33	57
15	2	35/61 (57%)	34 (97%)	1 (3%)	42	64
16	3	87/87 (100%)	83 (95%)	4 (5%)	27	52
17	4	70/70 (100%)	69 (99%)	1 (1%)	67	80
18	5	47/52 (90%)	46 (98%)	1 (2%)	53	72
19	6	36/36 (100%)	35 (97%)	1 (3%)	43	65
20	B	195/195 (100%)	191 (98%)	4 (2%)	53	72
21	F	233/233 (100%)	223 (96%)	10 (4%)	29	54
22	H	182/190 (96%)	173 (95%)	9 (5%)	25	50
23	J	177/177 (100%)	171 (97%)	6 (3%)	37	60
24	L	151/190 (80%)	144 (95%)	7 (5%)	27	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	N	91/91 (100%)	89 (98%)	2 (2%)	52	71
26	P	99/99 (100%)	97 (98%)	2 (2%)	55	74
27	Q	120/120 (100%)	119 (99%)	1 (1%)	81	89
28	S	114/114 (100%)	109 (96%)	5 (4%)	28	53
29	T	43/43 (100%)	40 (93%)	3 (7%)	15	40
30	U	132/132 (100%)	129 (98%)	3 (2%)	50	70
31	V	131/140 (94%)	128 (98%)	3 (2%)	50	70
32	X	88/94 (94%)	88 (100%)	0	100	100
33	C	167/167 (100%)	161 (96%)	6 (4%)	35	59
37	AL	190/190 (100%)	188 (99%)	2 (1%)	73	84
38	A1	127/131 (97%)	124 (98%)	3 (2%)	49	69
39	A2	97/109 (89%)	96 (99%)	1 (1%)	76	86
40	A4	60/60 (100%)	57 (95%)	3 (5%)	24	49
41	A6	83/83 (100%)	76 (92%)	7 (8%)	11	33
42	A7	90/96 (94%)	87 (97%)	3 (3%)	38	61
43	AN	135/135 (100%)	130 (96%)	5 (4%)	34	58
44	A8	114/114 (100%)	108 (95%)	6 (5%)	22	47
45	A9	90/90 (100%)	86 (96%)	4 (4%)	28	53
46	Aa	89/89 (100%)	85 (96%)	4 (4%)	27	52
47	Ab	82/92 (89%)	81 (99%)	1 (1%)	71	83
48	Ad	69/73 (94%)	68 (99%)	1 (1%)	67	80
49	Ae	40/47 (85%)	38 (95%)	2 (5%)	24	49
50	Af	45/45 (100%)	45 (100%)	0	100	100
51	AP	179/179 (100%)	175 (98%)	4 (2%)	52	71
52	Ah	70/70 (100%)	70 (100%)	0	100	100
53	Ai	87/87 (100%)	87 (100%)	0	100	100
54	AI	189/195 (97%)	183 (97%)	6 (3%)	39	61
55	AJ	204/224 (91%)	200 (98%)	4 (2%)	55	74
56	Ac	74/74 (100%)	68 (92%)	6 (8%)	11	35
57	AK	181/181 (100%)	178 (98%)	3 (2%)	60	78
58	AM	106/106 (100%)	104 (98%)	2 (2%)	57	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	AS	158/158 (100%)	151 (96%)	7 (4%)	28	53
60	AO	121/121 (100%)	119 (98%)	2 (2%)	60	78
61	AQ	165/176 (94%)	160 (97%)	5 (3%)	41	63
62	AR	215/250 (86%)	208 (97%)	7 (3%)	38	61
63	AW	128/128 (100%)	126 (98%)	2 (2%)	62	79
64	AY	90/90 (100%)	88 (98%)	2 (2%)	52	71
65	AT	162/162 (100%)	161 (99%)	1 (1%)	86	92
66	AZ	111/111 (100%)	111 (100%)	0	100	100
67	A3	110/110 (100%)	108 (98%)	2 (2%)	59	77
68	A5	201/201 (100%)	196 (98%)	5 (2%)	47	68
69	AD	191/191 (100%)	185 (97%)	6 (3%)	40	62
70	AE	335/335 (100%)	329 (98%)	6 (2%)	59	77
71	AF	336/336 (100%)	327 (97%)	9 (3%)	44	65
72	AG	110/142 (78%)	106 (96%)	4 (4%)	35	59
73	AU	162/162 (100%)	158 (98%)	4 (2%)	47	68
74	AH	168/168 (100%)	164 (98%)	4 (2%)	49	69
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	A0	53/53 (100%)	52 (98%)	1 (2%)	57	75
All	All	9096/9417 (97%)	8847 (97%)	249 (3%)	48	65

5 of 249 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	A2	94	GLN
70	AE	361	LYS
45	A9	136	TYR
70	AE	269	TYR
73	AU	107	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
60	AO	119	ASN
71	AF	286	ASN
63	AW	25	HIS
68	A5	232	HIS
73	AU	162	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1588/1608 (98%)	476 (29%)	86 (5%)
2	7	73/74 (98%)	23 (31%)	3 (4%)
34	AA	3167/3193 (99%)	966 (30%)	190 (5%)
35	AC	148/151 (98%)	51 (34%)	6 (4%)
36	AB	117/118 (99%)	28 (23%)	4 (3%)
All	All	5093/5144 (99%)	1544 (30%)	289 (5%)

5 of 1544 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	17	C
1	A	25	C
1	A	26	A
1	A	27	U
1	A	34	G

5 of 289 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	AA	2886	A
36	AB	39	C
34	AA	3034	A
34	AA	3505	U
34	AA	62	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	30.56

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-6454. 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.