



## wwPDB EM Validation Summary Report ⓘ

Nov 1, 2025 – 07:39 am GMT

PDB ID : 9RTU / pdb\_00009rtu  
EMDB ID : EMD-54253  
Title : Structure of the 70S-EF-G(P610L)-GDP-Pi ribosome complex with tRNAs in hybrid state 1 (H1-EF-G(P610L)-GDP-Pi)  
Authors : Ghosh Dastidar, N.; Freyer, N.; Petrychenko, V.; Schwarzer, A.C.; Peng, B.Z.; Samatova, E.; Kothe, C.; Schmidt, M.; Peske, F.; Politi, A.; Urlaub, H.; Fischer, N.; Rodnina, M.V.; Wohlgemuth, I.  
Deposited on : 2025-07-03  
Resolution : 3.00 Å(reported)  
Based on initial model : 7PJV

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:

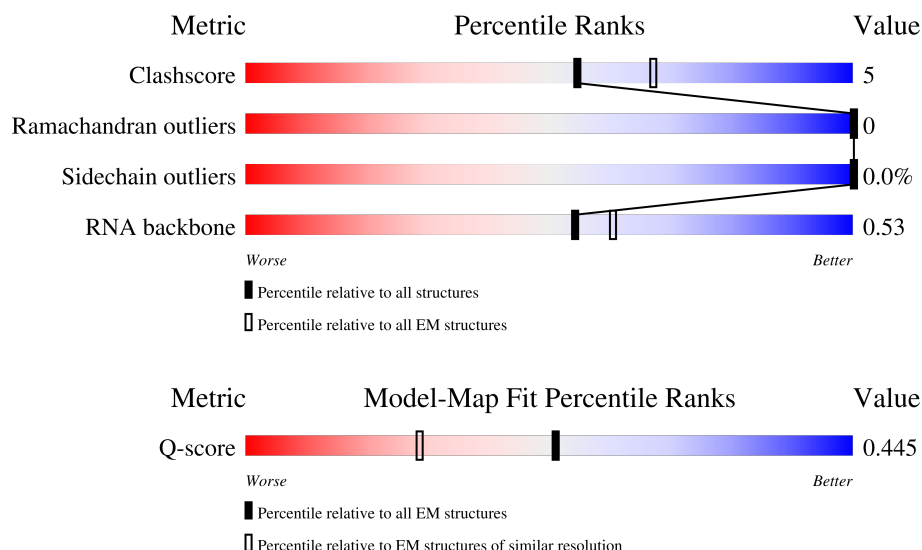
EMDB validation analysis : 0.0.1.dev129  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

# 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 3.00 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	14081 ( 2.50 - 3.50 )

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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	57	


























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Mol	Chain	Length	Quality of chain
2	1	55	
3	2	46	
4	3	65	
5	4	38	
6	5	165	
7	6	70	
8	A	2903	
9	B	120	
10	C	273	
11	D	209	
12	E	201	
13	F	179	
14	G	177	
15	H	149	
16	I	142	
17	J	142	
18	K	123	
19	L	144	
20	M	136	
21	N	127	
22	O	117	
23	P	115	
24	Q	118	
25	R	103	
26	S	110	








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Mol	Chain	Length	Quality of chain
27	T	100	
28	U	104	
29	V	94	
30	W	85	
31	X	78	
32	Y	63	
33	Z	59	
34	a	1542	
35	b	240	
36	c	233	
37	d	206	
38	e	167	
39	f	135	
40	g	179	
41	h	130	
42	i	130	
43	j	103	
44	k	129	
45	l	124	
46	m	118	
47	n	102	
48	o	89	
49	p	82	
50	q	84	
51	r	75	

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Mol	Chain	Length	Quality of chain
52	s	92	
53	t	87	
54	u	71	
55	v	77	
56	w	76	
57	x	704	
58	y	2	
59	z	33	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
64	PO4	x	802	-	-	X	-

## 2 Entry composition [i](#)

There are 65 unique types of molecules in this entry. The entry contains 256907 atoms, of which 103761 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 protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	0	56	Total	C	H	N	O	S	0	0
			904	269	460	94	80	1		

- Molecule 2 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	50	Total	C	H	N	O	0	0
			849	263	440	75	71		

- Molecule 3 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace	
3	2	46	Total	C	H	N	O	S	0	0
			796	228	419	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	3	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	4	38	Total	C	H	N	O	S	0	0
			642	185	340	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	131	Total	C	H	N	O	0	0
			983	385	336	131	131		

- Molecule 7 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	6	66	Total	C	H	N	O	S	0	0
			1042	323	520	99	94	6		

- Molecule 8 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	A	2903	Total	C	H	N	O	P	0	0
			93694	27816	31356	11471	20148	2903		

- Molecule 9 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	B	120	Total	C	H	N	O	P	0	0
			3871	1144	1301	468	838	120		

- Molecule 10 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	C	271	Total	C	H	N	O	S	0	0
			4237	1288	2155	423	364	7		

- Molecule 11 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	D	209	Total	C	H	N	O	S	0	0
			3183	979	1618	288	294	4		

- Molecule 12 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	E	201	Total	C	H	N	O	S	0	0
			3172	974	1620	283	290	5		

- Molecule 13 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	F	177	Total	C	H	N	O	S	0	0
			2855	899	1445	249	256	6		

- Molecule 14 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	G	176	Total	C	H	N	O	S	0	0
			2695	832	1372	243	246	2		

- Molecule 15 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	H	149	Total	C	H	N	O	S	0	0
			2259	699	1148	197	214	1		

- Molecule 16 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	I	141	Total	C	H	N	O		0	0
			1038	411	345	141	141			

- Molecule 17 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	J	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	K	122	Total	C	H	N	O	S	0	0
			1950	587	1012	180	165	6		

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	L	143	Total	C	H	N	O	S	0	0
			2162	649	1117	206	189	1		

- Molecule 20 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	M	136	Total	C	H	N	O	S	0	0
			2231	686	1157	205	177	6		

- Molecule 21 is a protein called 50S ribosomal protein L17.



Mol	Chain	Residues	Atoms						AltConf	Trace
21	N	120	Total	C	H	N	O	S	0	0
			1961	593	1001	196	166	5		

- Molecule 22 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	O	116	Total	C	H	N	O		0	0
			1815	552	923	178	162			

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	P	114	Total	C	H	N	O	S	0	0
			1880	574	963	179	163	1		

- Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	Q	117	Total	C	H	N	O		0	0
			1967	604	1020	192	151			

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	R	103	Total	C	H	N	O	S	0	0
			1655	516	839	153	145	2		

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	S	110	Total	C	H	N	O	S	0	0
			1779	532	922	166	156	3		

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	T	93	Total	C	H	N	O	S	0	0
			1546	466	808	139	131	2		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U	102	Total	C	H	N	O	0	0
			1611	492	832	146	141		

- Molecule 29 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	V	94	Total	C	H	N	O	S	0	0
			1534	479	781	137	134	3		

- Molecule 30 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	W	75	Total	C	H	N	O	S	0	0
			1169	356	594	116	102	1		

- Molecule 31 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	X	77	Total	C	H	N	O	S	0	0
			1279	388	654	129	106	2		

- Molecule 32 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace	
32	Y	63	Total	C	H	N	O	S	0	0
			1052	313	543	99	95	2		

- Molecule 33 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	Z	58	Total	C	H	N	O	S	0	0
			938	281	489	87	79	2		

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	a	1540	Total	C	H	N	O	P	0	0
			49687	14748	16637	6057	10705	1540		

- Molecule 35 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	b	218	Total	C	H	N	O	S	0	0
			3437	1081	1733	305	311	7		

- Molecule 36 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	c	206	Total	C	H	N	O	S	0	0
			3322	1028	1698	305	288	3		

- Molecule 37 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	d	205	Total	C	H	N	O	S	0	0
			3351	1026	1708	315	298	4		

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	e	157	Total	C	H	N	O	S	0	0
			2311	709	1170	218	208	6		

- Molecule 39 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	f	100	Total	C	H	N	O	S	0	0
			1626	515	809	148	148	6		

- Molecule 40 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	g	151	Total	C	H	N	O	S	0	0
			2419	735	1238	227	215	4		

- Molecule 41 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	h	129	Total	C	H	N	O	S	0	0
			2011	616	1032	173	184	6		

- Molecule 42 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	i	127	Total	C	H	N	O	S	0	0
			2092	634	1070	206	179	3		

- Molecule 43 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	j	98	Total	C	H	N	O	S	0	0
			1615	493	829	150	142	1		

- Molecule 44 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	k	116	Total	C	H	N	O	S	0	0
			1748	535	879	173	158	3		

- Molecule 45 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	l	123	Total	C	H	N	O	S	0	0
			1972	590	1017	196	165	4		

- Molecule 46 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	m	114	Total	C	H	N	O	S	0	0
			1825	546	942	178	156	3		

- Molecule 47 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	n	101	Total	C	H	N	O	S	0	0
			1638	498	839	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP P0AG59

- Molecule 48 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	o	88	Total	C	H	N	O	S	0	0
			1451	439	737	144	130	1		

- Molecule 49 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	p	82	Total	C	H	N	O	S	0	0
			1315	406	666	128	114	1		

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	q	80	Total	C	H	N	O	S	0	0
			1340	411	692	121	113	3		

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	r	65	Total	C	H	N	O	S	0	0
			1087	339	552	100	95	1		

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	s	82	Total	C	H	N	O	S	0	0
			1343	421	685	125	110	2		

- Molecule 53 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	t	85	Total	C	H	N	O	S	0	0
			1381	411	716	137	114	3		

- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	u	65	Total	C	H	N	O	S	0	0
			1008	313	502	105	87	1		

- Molecule 55 is a RNA chain called P/E-site tRNA(fMet).

Mol	Chain	Residues	Atoms							AltConf	Trace
55	v	76	Total	C	H	N	O	P	S	0	0
			2449	724	827	295	526	76	1		

- Molecule 56 is a RNA chain called A/P-site tRNA(Phe).

Mol	Chain	Residues	Atoms							AltConf	Trace
56	w	76	Total	C	H	N	O	P	S	0	0
			2462	731	831	291	531	76	2		

- Molecule 57 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms							AltConf	Trace
57	x	703	Total	C	H	N	O	S		0	0
			10865	3430	5420	942	1048	25			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	609	LEU	PRO	conflict	UNP C4ZUJ5

- Molecule 58 is a protein called Dipeptide (FME-PHE).

Mol	Chain	Residues	Atoms							AltConf	Trace
58	y	2	Total	C	H	N	O	S		0	0
			40	15	19	2	3	1			

- Molecule 59 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms							AltConf	Trace
59	z	11	Total	C	H	N	O	P		0	0
			345	103	115	35	81	11			

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	0	1	Total	Mg	0
			1	1	
60	A	262	Total	Mg	0
			262	262	
60	B	7	Total	Mg	0
			7	7	

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Mol	Chain	Residues	Atoms		AltConf
60	C	3	Total 3	Mg 3	0
60	N	1	Total 1	Mg 1	0
60	O	1	Total 1	Mg 1	0
60	P	1	Total 1	Mg 1	0
60	Z	1	Total 1	Mg 1	0
60	a	84	Total 84	Mg 84	0
60	m	2	Total 2	Mg 2	0
60	n	1	Total 1	Mg 1	0
60	v	1	Total 1	Mg 1	0
60	w	1	Total 1	Mg 1	0
60	x	2	Total 2	Mg 2	0
60	z	1	Total 1	Mg 1	0

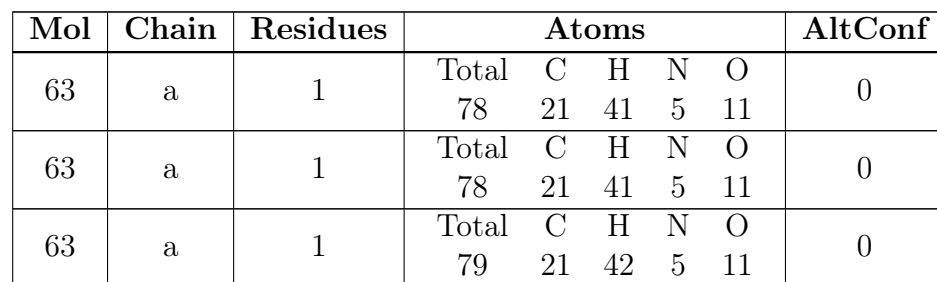
- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
61	4	1	Total 1	Zn 1	0
61	6	1	Total 1	Zn 1	0

- Molecule 62 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
62	A	1	Total 1	Na 1	0
62	B	1	Total 1	Na 1	0

- Molecule 63 is APRAMYCIN (CCD ID: AM2) (formula: C<sub>21</sub>H<sub>41</sub>N<sub>5</sub>O<sub>11</sub>).



- 
- The diagram shows a central phosphorus atom (P) bonded to four oxygen atoms. The bonds are colored: a double bond to the right (orange), and three single bonds to the top, left, and bottom (purple). The oxygen atoms are red circles with a minus sign (-) indicating a negative charge. Labels in green text identify the atoms: 'O1' for the right oxygen, 'O2' for the left oxygen, 'O3' for the top oxygen, and 'O4' for the bottom oxygen. The label 'P' is placed below the phosphorus atom. The text 'PO4' is at the top of the diagram.

Mol	Chain	Residues	Atoms			AltConf
64	x	1	Total	O	P	0
			5	4	1	




- # GDP
- 
- The image displays the chemical structure of Guanosine Diphosphate (GDP). It consists of a guanine base (a purine ring system with an amino group at the 2-position) linked to a ribose sugar, which is in turn linked to a diphosphate group. The structure is labeled with various atoms and bonds, including the phosphate groups (P, O, OH) and the sugar (C, O, H). The guanine base is shown in blue, the ribose sugar in black, and the diphosphate group in red. The structure is oriented with the guanine base at the top and the diphosphate group at the bottom.

Mol	Chain	Residues	Atoms					AltConf	
65	x	1	Total	C	H	N	O	P	0
			38	10	10	5	11	2	

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. 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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: 50S ribosomal protein L32

Chain 0: 



- Molecule 2: Large ribosomal subunit protein bL33

Chain 1: 



- Molecule 3: Large ribosomal subunit protein bL34

Chain 2: 



- Molecule 4: 50S ribosomal protein L35

Chain 3: 

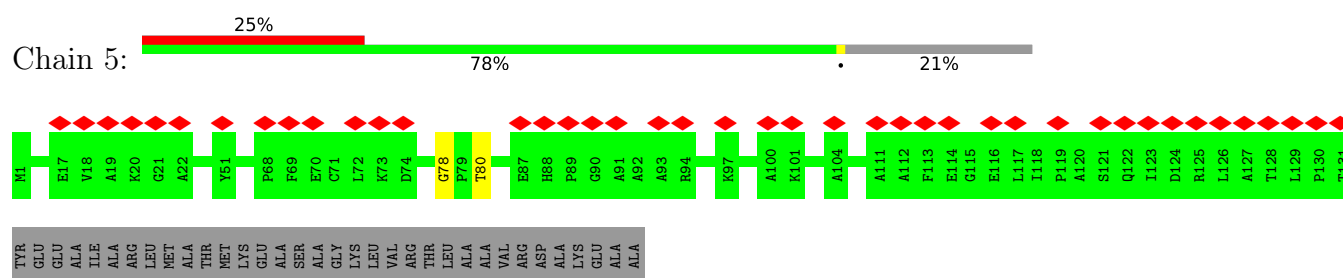


- Molecule 5: 50S ribosomal protein L36

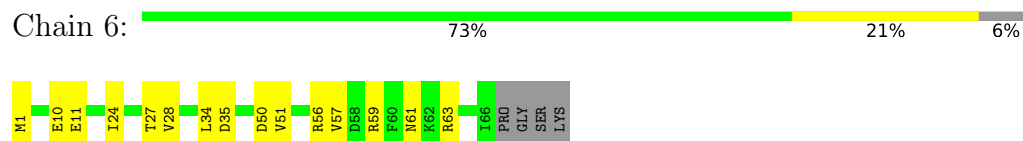
Chain 4: 



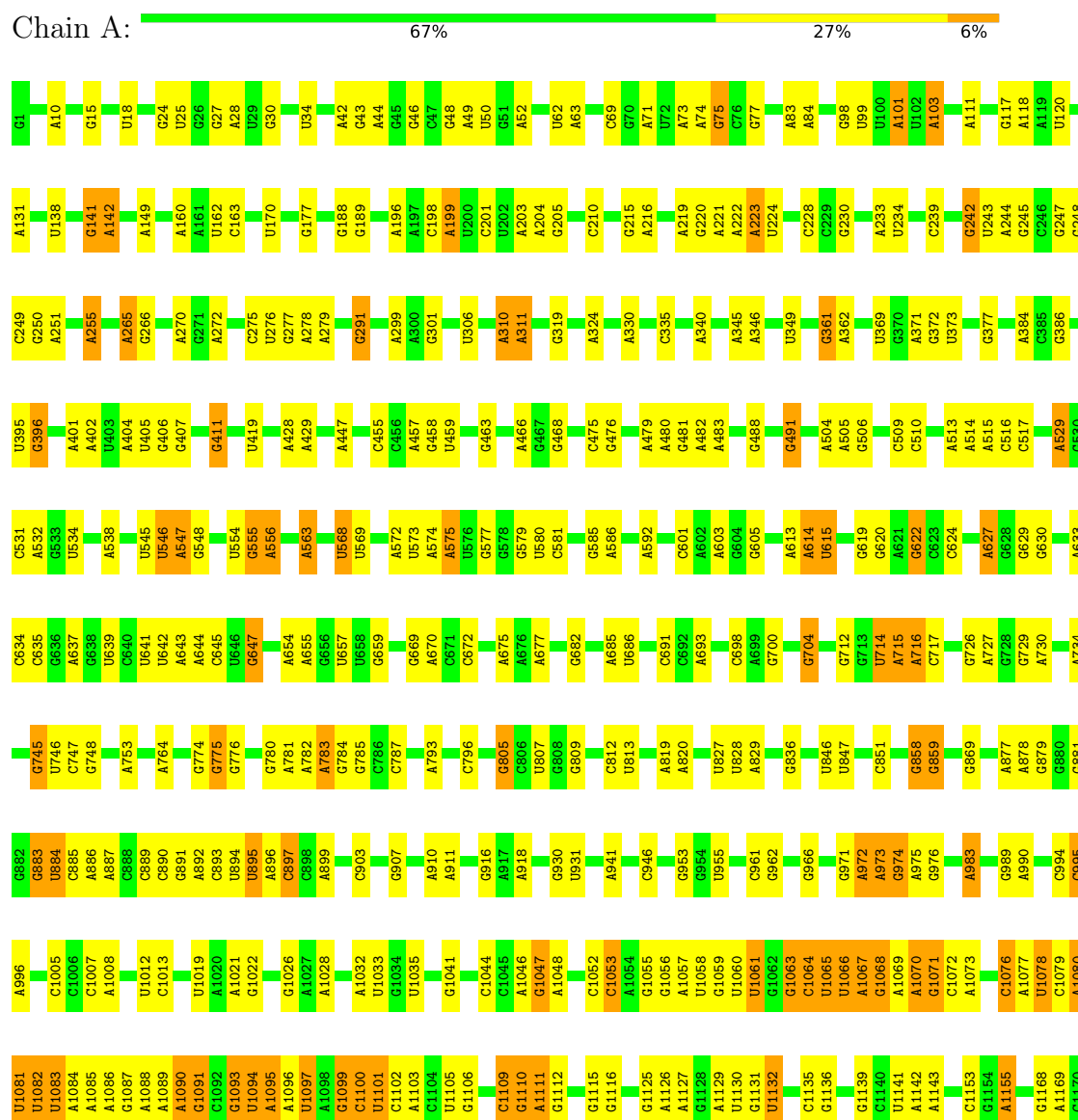
- Molecule 6: 50S ribosomal protein L10



- Molecule 7: 50S ribosomal protein L31



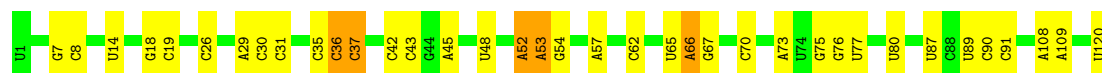
- Molecule 8: 23S ribosomal RNA




G2819	U2890	A2572	A2469	G2369	A2268	U2155	G2069	C1958	A1808	A1668	C1557	G1315	G1171
A2820	G2702	G2576	C2475	G2156	G2271	G2157	A2070	G1964	A1809	A1671	C1558	C1322	C1172
G2821	A2577	A2577	A2476	A2158	C2275	A2158	A2071	A1810	G1811	A1672	U1563	A1322	U1173
A2823	A2705	C2578	U2477	C2159	G2279	C2160	U2079	C1967	U1812	G1673	C1564	C1323	A1175
A2826	A2706	C2579	A2478	G2379	G2279	C2161	U2092	A1970	G1813	G1674	U1329	U1329	U1176
G2839	G2714	U2585	G2481	G2383	C2283	G2162	G2093	G1972	G1814	G1682	C1447	C1330	G1179
G2848	C2715	U2384	G2484	U2384	A2284	C2164	G2100	U1970	A1815	G1682	A1566	G1331	U1180
U2849	C2716	G2595	G2488	U2385	A2288	U2167	G2101	G1972	G1816	G1682	G1567	G1332	G1187
G2852	G2717	A2598	G2488	A2386	A2288	G2168	G2102	U1982	G1817	G1682	A1569	G1333	G1187
G2852	G2718	G2598	G2488	A2386	A2288	G2168	G2103	U1982	G1818	G1682	A1572	G1334	U1188
G2852	G2719	G2598	G2488	A2386	A2288	G2168	G2104	U1982	G1818	G1682	A1572	G1334	U1188
G2852	G2720	G2598	G2488	A2386	A2288	G2168	G2105	U1982	G1818	G1682	A1572	G1334	U1188
G2857	C2723	G2603	G2494	C2394	A2297	A2170	U2106	G1992	G1826	G1699	U1578	G1338	U1199
A2860	G2726	U2605	C2496	U2402	A2297	A2171	U2106	G1992	G1826	G1699	U1578	G1338	U1199
U2865	A2727	G2608	U2500	G2405	U2302	A2175	G2110	C1996	G1826	G1699	U1578	G1338	U1199
U2866	U2728	U2609	C2501	A2406	G2303	A2176	G2111	U1991	G1828	U1712	U1460	G1339	U1199
G2867	G2729	G2502	G2502	G2410	G2304	A2176	G2112	G1992	A1829	U1713	C1461	U1340	A1205
A2872	G2732	U2613	A2503	G2419	U2305	U2180	G2115	G2012	G1835	G1715	U1466	G1341	G1206
G2873	A2733	U2614	U2504	U2419	C2306	A2183	G2116	A2014	C1836	U1716	U1474	A1353	U1209
C2874	G2733	U2615	G2505	U2423	G2307	A2184	A2117	U2016	G1837	U1716	U1474	A1353	U1209
U2878	G2744	C2424	U2506	C2424	G2308	U2185	A2119	U2016	A1900	G1730	G1492	G1360	G1212
A2879	A2748	A2425	C2512	A2425	A2309	G2186	G2123	A2019	A1901	G1730	A1496	G1361	A1214
U2884	G2751	G2623	G2518	G2429	U2312	U2189	G2124	A2020	G1906	G1730	A1496	U1372	G1236
G2885	C2752	G2624	A2518	A2430	C2313	U2190	G2125	C2021	G1907	A1744	U1497	A1372	A1237
G2886	G2627	U2627	U2522	A2431	A2314	A2191	A2126	U2022	C1908	A1754	A1508	A1378	A1247
A2883	C2628	C2628	G2526	A2432	G2319	G2192	G2127	U2022	C1909	A1754	U1508	U1379	G1248
U2888	U2756	U2629	G2527	A2433	U2320	G2193	G2128	A2030	G1910	G1764	A1509	G1380	U1249
A2889	A2765	C2636	U2528	A2434	U2321	U2199	G2130	G2032	A1911	U1769	A1515	A1383	G1250
U2903	G2769	G2640	G2531	A2435	G2322	C2200	U2130	A2033	A1912	U1769	G1516	A1384	G1250
G2777	G2777	G2645	A2531	A2439	U2324	G2200	U2131	A2033	A1913	U1769	G1516	A1384	G1250
A2778	U2778	C2646	G2532	U2441	G2325	G2201	U2132	G2035	A1916	A1773	G1521	A1385	A1253
U2779	U2779	U2647	G2532	U2442	G2325	G2202	U2133	C2036	A1917	A1773	A1522	A1386	A1254
G2780	G2780	G2648	G2535	C2443	G2331	G2204	A2135	C2043	G1922	U1782	G1524	A1392	G1256
A2781	A2781	G2648	G2539	G2444	G2332	A2211	G2136	C2047	C1925	A1783	A1532	A1393	A1264
C2788	C2788	G2653	A2547	G2445	U2334	A2212	G2138	G2048	U1926	A1783	C1533	U1394	A1265
C2789	U2789	G2655	U2548	G2446	A2335	A2215	U2139	G2049	A1927	A1784	U1534	U1395	G1266
U2790	U2790	U2656	G2554	A2448	A2336	C2215	G2140	C2050	A1928	C1788	G1536	U1396	G1266
U2796	U2796	G2661	U2554	U2449	G2345	A2225	G2143	A2051	G1930	A1781	G1537	U1415	G1271
U2797	U2797	A2662	G2559	A2450	C2347	G2238	C2145	C2055	A1937	U1796	G1538	G1417	A1272
U2798	U2798	G2663	A2564	A2451	U2348	G2239	C2146	G2056	A1938	U1797	U1539	G1418	A1294
A2799	A2799	C2664	A2565	G2452	G2349	G2240	A2147	A2060	U1939	U1798	G1540	A1419	U1294
A2800	A2800	U2684	A2566	G2453	C2350	U2245	G2148	G2061	G1939	G1800	A1544	G1421	G1300
G2808	G2808	U2684	A2566	G2453	U2356	U2245	U2149	A2062	A1953	G1800	A1544	G1421	G1300
A2809	A2809	U2688	G2567	A2459	G2361	G2250	U2151	A2062	G1954	A1801	G1663	G1426	A1301
U2818	U2818	G2688	G2569	C2467	G2365	G2251	G2152	C2066	U1955	A1802	U1662	A1427	C1306
		G2688	G2569	A2468	G2365	A2267	A2154	U2068	C1957	G1807	G1666	G1429	G1429

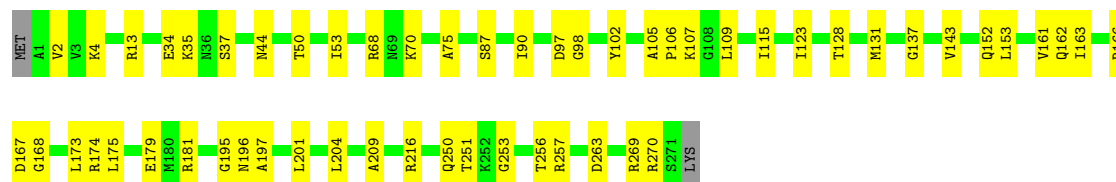
- Molecule 9: 5S ribosomal RNA

Chain B:  69% 27%




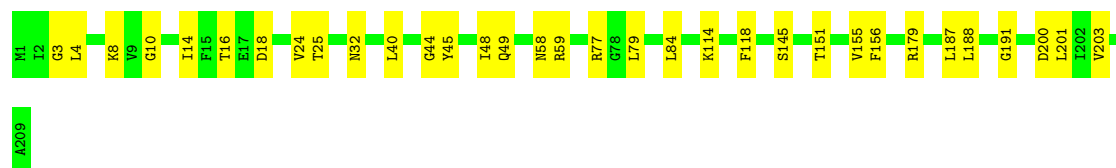
- Molecule 10: 50S ribosomal protein L2

Chain C:  79% 20%




- Molecule 11: 50S ribosomal protein L3

Chain D:  84% 16%




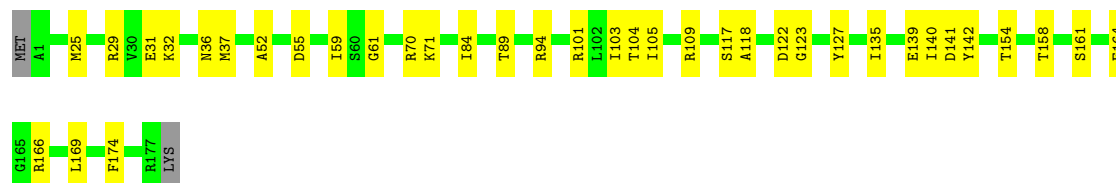
- Molecule 12: 50S ribosomal protein L4

Chain E:  84% 16%




- Molecule 13: 50S ribosomal protein L5

Chain F:  78% 21%

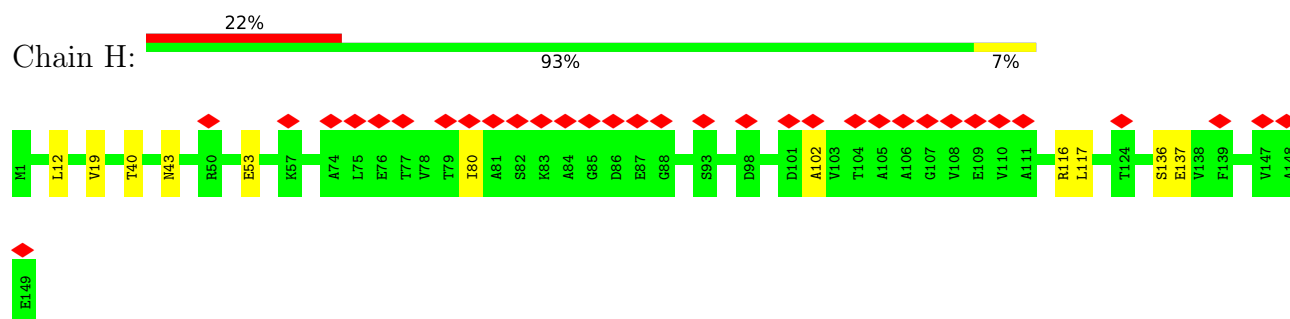


- Molecule 14: 50S ribosomal protein L6

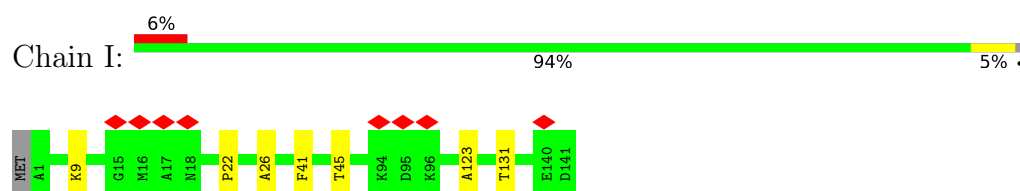
Chain G:  90% 10%



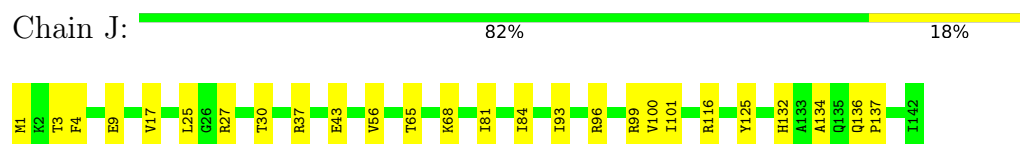
- Molecule 15: 50S ribosomal protein L9



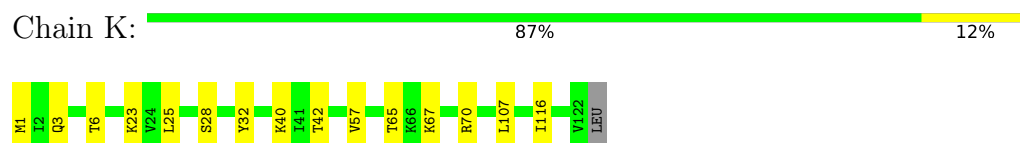
- Molecule 16: 50S ribosomal protein L11



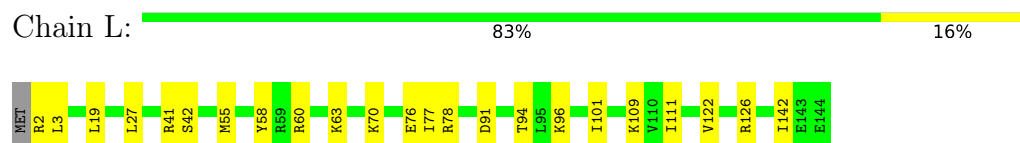
- Molecule 17: 50S ribosomal protein L13



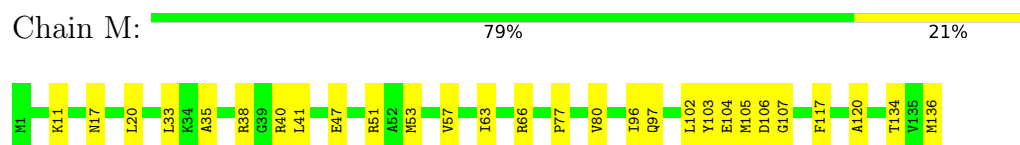
- Molecule 18: 50S ribosomal protein L14



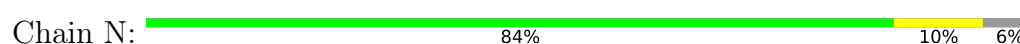
- Molecule 19: 50S ribosomal protein L15

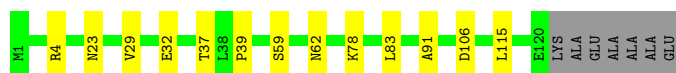


- Molecule 20: 50S ribosomal protein L16

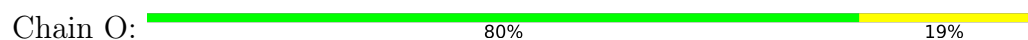


- Molecule 21: 50S ribosomal protein L17





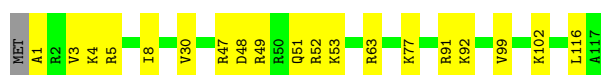
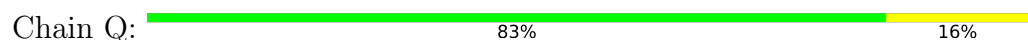
- Molecule 22: 50S ribosomal protein L18



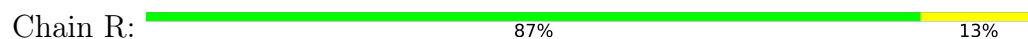
- Molecule 23: 50S ribosomal protein L19



- Molecule 24: 50S ribosomal protein L20



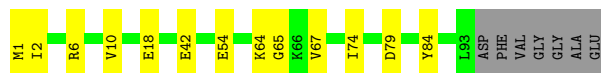
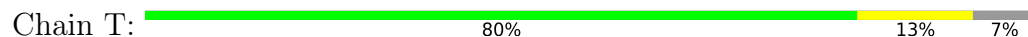
- Molecule 25: 50S ribosomal protein L21



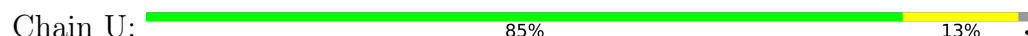
- Molecule 26: 50S ribosomal protein L22



- Molecule 27: 50S ribosomal protein L23



- Molecule 28: 50S ribosomal protein L24





- Molecule 29: 50S ribosomal protein L25

Chain V: 83% 17%



- Molecule 30: Large ribosomal subunit protein bL27

Chain W: 78% 11% 12%



- Molecule 31: 50S ribosomal protein L28

Chain X: 86% 13% .



- Molecule 32: 50S ribosomal protein L29

Chain Y: 90% 10%



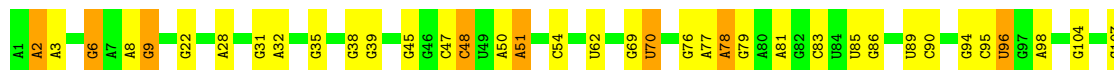
- Molecule 33: 50S ribosomal protein L30

Chain Z: 76% 22% .

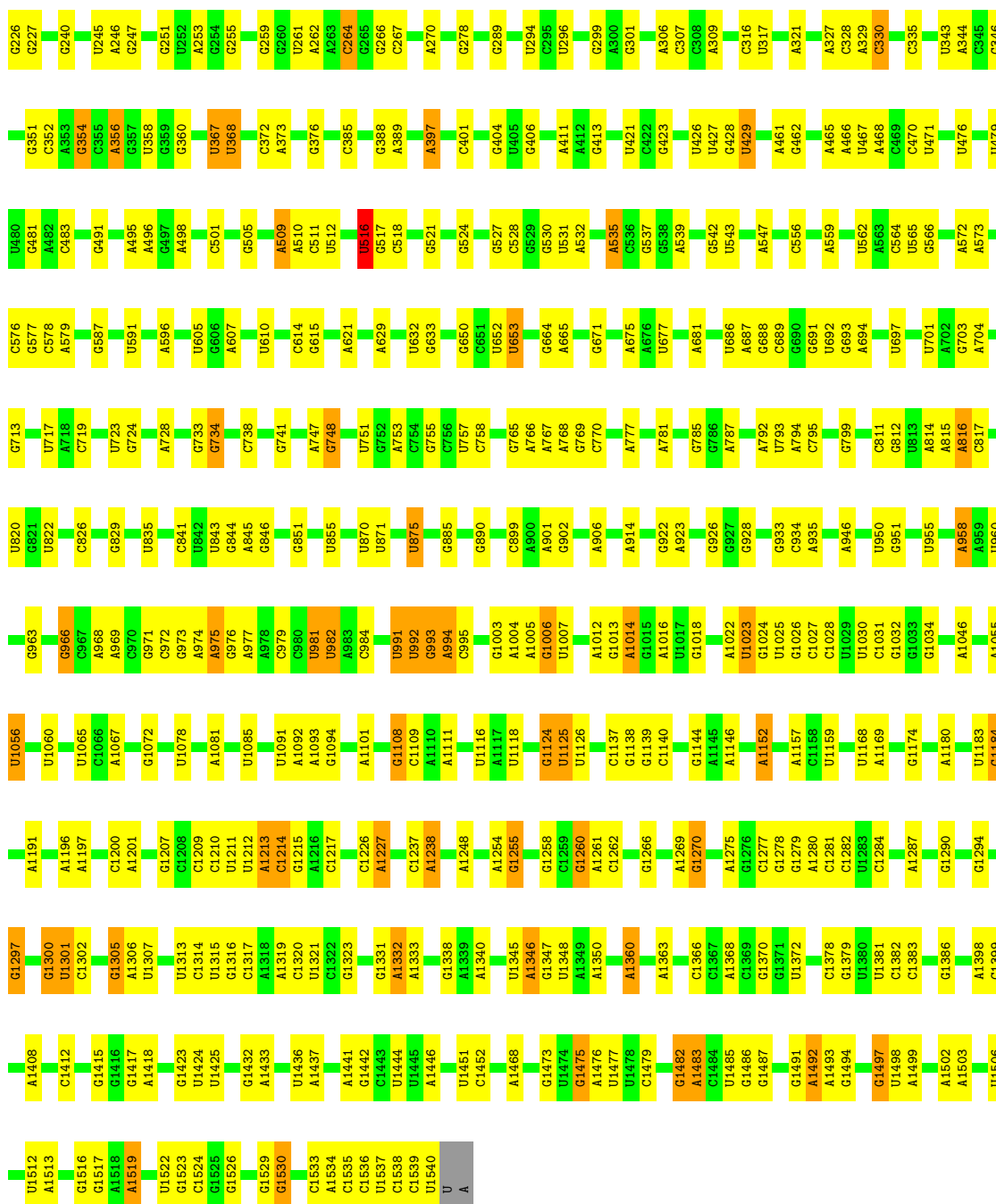


- Molecule 34: 16S ribosomal RNA

Chain a: 67% 29% .

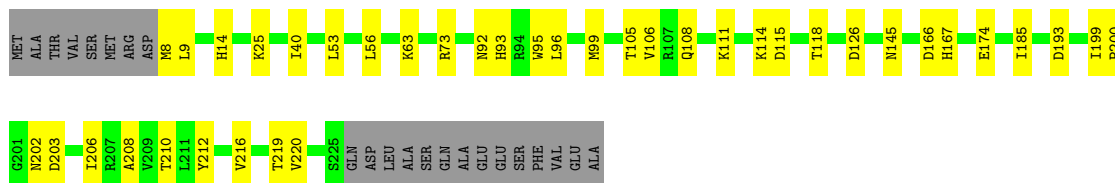






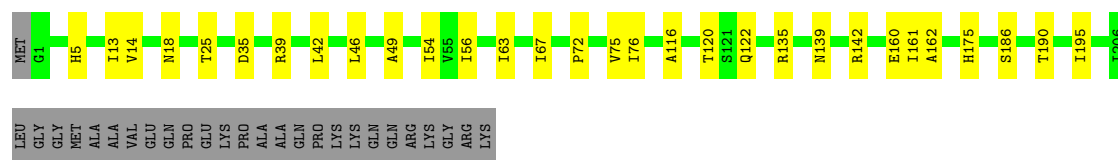
• Molecule 35: 30S ribosomal protein S2

Chain b: 75% 16% 9%




• Molecule 36: Small ribosomal subunit protein uS3

Chain c:  76% 13% 12%




- Molecule 37: Small ribosomal subunit protein uS4

Chain d:  81% 18%



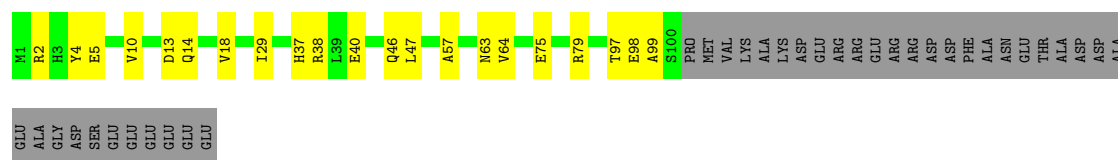
- Molecule 38: 30S ribosomal protein S5

Chain e:  80% 14% 6%



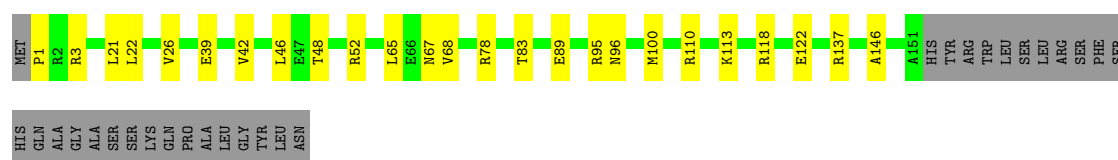
- Molecule 39: 30S ribosomal protein S6

Chain f:  59% 16% 26%




- Molecule 40: 30S ribosomal protein S7

Chain g:  70% 14% 16%




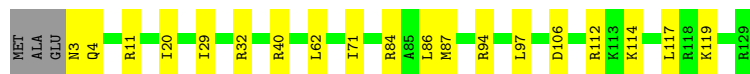
- Molecule 41: 30S ribosomal protein S8

Chain h:  82% 18%



- Molecule 42: 30S ribosomal protein S9

Chain i:  83% 15% .



- Molecule 43: 30S ribosomal protein S10

Chain j:  71% 24% 5%




- Molecule 44: 30S ribosomal protein S11

Chain k:  74% 16% 10%




- Molecule 45: 30S ribosomal protein S12

Chain l:  85% 14% .




- Molecule 46: 30S ribosomal protein S13

Chain m:  81% 15% .



- Molecule 47: 30S ribosomal protein S14

Chain n:  79% 20% .




- Molecule 48: Small ribosomal subunit protein uS15

Chain o:  90% 9% .




- Molecule 49: 30S ribosomal protein S16

Chain p:  91% 9%




- Molecule 50: 30S ribosomal protein S17

Chain q:  80% 15% 5%



- Molecule 51: 30S ribosomal protein S18

Chain r:  79% 8% 13%




- Molecule 52: 30S ribosomal protein S19

Chain s:  66% 23% 11%




- Molecule 53: 30S ribosomal protein S20

Chain t:  84% 14% 2%



- Molecule 54: 30S ribosomal protein S21

Chain u:  77% 14% 8%



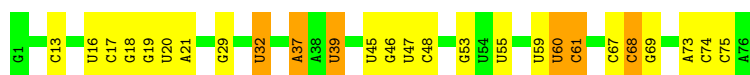
- Molecule 55: P/E-site tRNA(fMet)

Chain v:  73% 18% 8% 1%




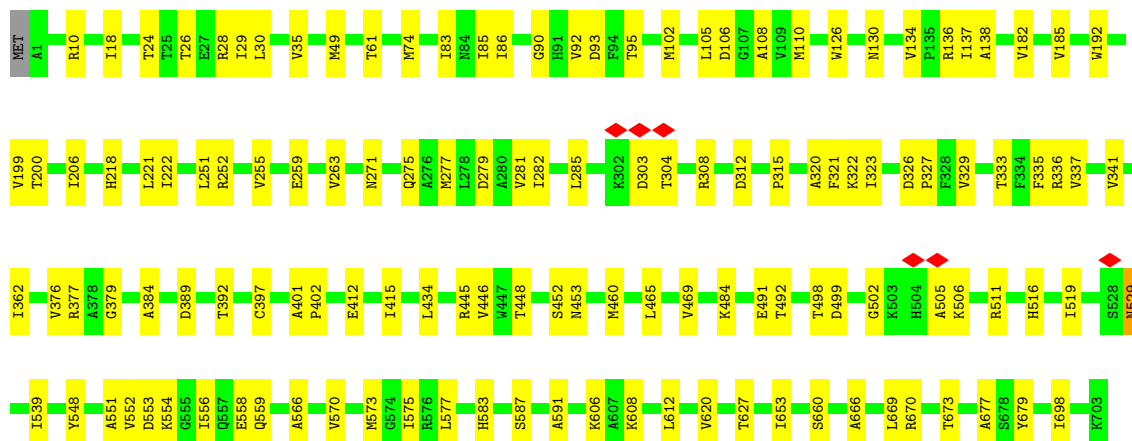
- Molecule 56: A/P-site tRNA(Phe)

Chain w:  66% 26% 8%



• Molecule 57: Elongation factor G

Chain x:  81% 18%



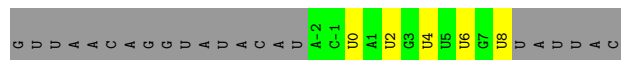
• Molecule 58: Dipeptide (FME-PHE)

Chain y:  50% 50%



• Molecule 59: mRNA

Chain z:  18% 15% 67%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	106477	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.130	Depositor
Minimum map value	-0.029	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	334.08, 334.08, 334.08	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, ZN, MIA, 5MC, AM2, 2MG, MA6, NA, MG, PSU, 2MA, OMG, PO4, 1MG, OMC, OMU, 4OC, 6MZ, 3TD, FME, UR3, 4SU, H2U, G7M, GDP

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	0	0.17	0/450	0.35	0/599
2	1	0.18	0/416	0.37	0/554
3	2	0.16	0/380	0.31	0/498
4	3	0.17	0/513	0.42	0/676
5	4	0.16	0/303	0.40	0/397
6	5	0.13	0/646	0.36	0/898
7	6	0.19	0/531	0.43	0/709
8	A	0.17	0/69266	0.30	0/108055
9	B	0.13	0/2873	0.27	0/4478
10	C	0.18	0/2121	0.40	0/2852
11	D	0.18	0/1586	0.37	0/2134
12	E	0.16	0/1571	0.33	0/2113
13	F	0.19	0/1434	0.43	0/1926
14	G	0.15	0/1343	0.34	0/1816
15	H	0.15	0/1122	0.38	0/1515
16	I	0.14	0/692	0.37	0/960
17	J	0.19	0/1152	0.35	0/1551
18	K	0.16	0/947	0.35	0/1268
19	L	0.17	0/1054	0.40	0/1403
20	M	0.18	0/1093	0.41	0/1460
21	N	0.16	0/973	0.36	0/1301
22	O	0.15	0/902	0.36	0/1209
23	P	0.17	0/929	0.37	0/1242
24	Q	0.19	0/960	0.34	0/1278
25	R	0.19	0/829	0.42	0/1107
26	S	0.18	0/864	0.40	0/1156
27	T	0.17	0/744	0.36	0/994
28	U	0.16	0/787	0.37	0/1051
29	V	0.17	0/766	0.42	0/1025
30	W	0.16	0/582	0.38	0/769
31	X	0.19	0/635	0.37	0/848

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	Y	0.18	0/510	0.45	0/677
33	Z	0.17	0/453	0.33	0/605
34	a	0.15	0/36725	0.29	0/57285
35	b	0.17	0/1735	0.40	0/2338
36	c	0.16	0/1651	0.34	0/2225
37	d	0.16	0/1665	0.35	0/2227
38	e	0.16	0/1154	0.42	0/1554
39	f	0.17	0/835	0.43	0/1128
40	g	0.92	5/1195 (0.4%)	0.99	5/1602 (0.3%)
41	h	0.18	0/989	0.42	0/1326
42	i	0.16	0/1034	0.41	0/1375
43	j	0.17	0/796	0.46	0/1077
44	k	0.19	0/885	0.39	0/1195
45	l	0.18	0/969	0.42	0/1300
46	m	0.19	0/892	0.47	0/1193
47	n	0.19	0/811	0.45	0/1081
48	o	0.16	0/722	0.37	0/964
49	p	0.16	0/659	0.37	0/884
50	q	0.16	0/657	0.40	0/881
51	r	0.15	0/544	0.36	0/731
52	s	0.16	0/675	0.39	0/908
53	t	0.16	0/671	0.33	0/888
54	u	0.18	0/512	0.41	0/683
55	v	0.17	0/1722	0.27	0/2678
56	w	0.22	0/1650	0.32	0/2569
57	x	0.18	0/5546	0.44	0/7503
58	y	0.14	0/11	0.33	0/13
59	z	0.14	0/255	0.23	0/394
All	All	0.18	5/164387 (0.0%)	0.34	5/245126 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	g	1	PRO	CB-CG	24.33	2.71	1.49
40	g	1	PRO	CG-CD	-16.38	0.95	1.50
40	g	1	PRO	CA-CB	-7.65	1.38	1.53
40	g	1	PRO	N-CA	-5.20	1.39	1.47
40	g	1	PRO	N-CD	5.00	1.54	1.47

All (5) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	g	1	PRO	CB-CG-CD	-29.23	12.56	106.10
40	g	1	PRO	N-CA-CB	-12.90	88.81	103.00
40	g	1	PRO	CA-CB-CG	-10.79	84.00	104.50
40	g	1	PRO	N-CD-CG	-8.00	91.20	103.20
40	g	1	PRO	CA-N-CD	-7.39	101.66	112.00

There are no chirality outliers.

There are no planarity outliers.

## 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	0	444	460	461	7	0
2	1	409	440	440	8	0
3	2	377	419	418	7	0
4	3	504	572	574	18	0
5	4	302	340	340	9	0
6	5	647	336	336	1	0
7	6	522	520	520	11	0
8	A	62338	31356	31371	387	0
9	B	2570	1301	1301	20	0
10	C	2082	2155	2157	39	0
11	D	1565	1618	1616	24	0
12	E	1552	1620	1619	23	0
13	F	1410	1445	1447	28	0
14	G	1323	1372	1374	11	0
15	H	1111	1148	1148	7	0
16	I	693	345	347	6	0
17	J	1129	1162	1162	26	0
18	K	938	1012	1012	13	0
19	L	1045	1117	1117	20	0
20	M	1074	1157	1157	19	0
21	N	960	1001	1000	10	0
22	O	892	923	923	16	0
23	P	917	963	965	9	0
24	Q	947	1020	1022	16	0
25	R	816	839	839	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	S	857	922	922	21	0
27	T	738	808	807	11	0
28	U	779	832	834	11	0
29	V	753	781	780	13	0
30	W	575	594	592	7	0
31	X	625	654	655	10	0
32	Y	509	543	543	5	0
33	Z	449	489	491	10	0
34	a	33050	16637	16653	210	0
35	b	1704	1733	1732	27	0
36	c	1624	1698	1699	23	0
37	d	1643	1708	1710	28	0
38	e	1141	1170	1170	17	0
39	f	817	809	808	17	0
40	g	1181	1238	1240	18	0
41	h	979	1032	1034	18	0
42	i	1022	1070	1070	14	0
43	j	786	829	828	22	0
44	k	869	879	878	18	0
45	l	955	1017	1019	14	0
46	m	883	942	944	15	0
47	n	799	839	841	21	0
48	o	714	737	737	7	0
49	p	649	666	666	6	0
50	q	648	692	691	8	0
51	r	535	552	552	7	0
52	s	658	685	685	19	0
53	t	665	716	714	10	0
54	u	506	502	502	7	0
55	v	1622	827	831	9	0
56	w	1631	831	837	4	0
57	x	5445	5420	5422	95	0
58	y	21	19	19	1	0
59	z	230	115	116	5	0
60	0	1	0	0	0	0
60	A	262	0	0	0	0
60	B	7	0	0	0	0
60	C	3	0	0	0	0
60	N	1	0	0	0	0
60	O	1	0	0	0	0
60	P	1	0	0	0	0
60	Z	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	a	84	0	0	0	0
60	m	2	0	0	0	0
60	n	1	0	0	0	0
60	v	1	0	0	0	0
60	w	1	0	0	0	0
60	x	2	0	0	0	0
60	z	1	0	0	0	0
61	4	1	0	0	0	0
61	6	1	0	0	0	0
62	A	1	0	0	0	0
62	B	1	0	0	0	0
63	a	111	124	123	6	0
64	x	5	0	0	2	0
65	x	28	10	12	1	0
All	All	153146	103761	103823	1189	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 5.

The worst 5 of 1189 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)
8:A:1071:G:H21	8:A:1089:A:N6	1.68	0.90
8:A:2386:A:O2'	30:W:37:ARG:NH2	2.06	0.87
40:g:21:LEU:HD21	40:g:65:LEU:HD11	1.57	0.85
8:A:1361:G:HO2'	8:A:2215:C:HO2'	1.07	0.84
8:A:1508:A:O2'	8:A:1509:A:O4'	1.95	0.82

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	
1	0	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
2	1	48/55 (87%)	47 (98%)	1 (2%)	0	100	100
3	2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
4	3	62/65 (95%)	58 (94%)	4 (6%)	0	100	100
5	4	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
6	5	129/165 (78%)	106 (82%)	23 (18%)	0	100	100
7	6	64/70 (91%)	55 (86%)	9 (14%)	0	100	100
10	C	269/273 (98%)	260 (97%)	9 (3%)	0	100	100
11	D	207/209 (99%)	195 (94%)	12 (6%)	0	100	100
12	E	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
13	F	175/179 (98%)	161 (92%)	14 (8%)	0	100	100
14	G	174/177 (98%)	169 (97%)	5 (3%)	0	100	100
15	H	147/149 (99%)	137 (93%)	10 (7%)	0	100	100
16	I	139/142 (98%)	125 (90%)	14 (10%)	0	100	100
17	J	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
18	K	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
19	L	141/144 (98%)	131 (93%)	10 (7%)	0	100	100
20	M	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
21	N	118/127 (93%)	113 (96%)	5 (4%)	0	100	100
22	O	114/117 (97%)	113 (99%)	1 (1%)	0	100	100
23	P	112/115 (97%)	108 (96%)	4 (4%)	0	100	100
24	Q	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
25	R	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
26	S	108/110 (98%)	102 (94%)	6 (6%)	0	100	100
27	T	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
28	U	100/104 (96%)	95 (95%)	5 (5%)	0	100	100
29	V	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
30	W	73/85 (86%)	73 (100%)	0	0	100	100
31	X	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
32	Y	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
33	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
35	b	216/240 (90%)	199 (92%)	17 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	c	204/233 (88%)	199 (98%)	5 (2%)	0	100	100
37	d	203/206 (98%)	193 (95%)	10 (5%)	0	100	100
38	e	155/167 (93%)	151 (97%)	4 (3%)	0	100	100
39	f	98/135 (73%)	87 (89%)	11 (11%)	0	100	100
40	g	149/179 (83%)	138 (93%)	11 (7%)	0	100	100
41	h	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
42	i	125/130 (96%)	111 (89%)	14 (11%)	0	100	100
43	j	96/103 (93%)	88 (92%)	8 (8%)	0	100	100
44	k	114/129 (88%)	108 (95%)	6 (5%)	0	100	100
45	l	121/124 (98%)	111 (92%)	10 (8%)	0	100	100
46	m	112/118 (95%)	102 (91%)	10 (9%)	0	100	100
47	n	99/102 (97%)	93 (94%)	6 (6%)	0	100	100
48	o	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
49	p	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
50	q	78/84 (93%)	75 (96%)	3 (4%)	0	100	100
51	r	63/75 (84%)	61 (97%)	2 (3%)	0	100	100
52	s	80/92 (87%)	71 (89%)	9 (11%)	0	100	100
53	t	83/87 (95%)	79 (95%)	4 (5%)	0	100	100
54	u	63/71 (89%)	61 (97%)	2 (3%)	0	100	100
57	x	701/704 (100%)	652 (93%)	49 (7%)	0	100	100
All	All	6551/6924 (95%)	6175 (94%)	376 (6%)	0	100	100

There are no Ramachandran outliers to report.

### 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	
1	0	47/48 (98%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/52 (98%)	51 (100%)	0	100	100
5	4	34/34 (100%)	34 (100%)	0	100	100
7	6	59/62 (95%)	59 (100%)	0	100	100
10	C	216/218 (99%)	216 (100%)	0	100	100
11	D	164/164 (100%)	164 (100%)	0	100	100
12	E	165/165 (100%)	165 (100%)	0	100	100
13	F	148/150 (99%)	148 (100%)	0	100	100
14	G	137/138 (99%)	137 (100%)	0	100	100
15	H	114/114 (100%)	114 (100%)	0	100	100
17	J	116/116 (100%)	116 (100%)	0	100	100
18	K	103/104 (99%)	103 (100%)	0	100	100
19	L	102/103 (99%)	102 (100%)	0	100	100
20	M	109/109 (100%)	109 (100%)	0	100	100
21	N	100/103 (97%)	100 (100%)	0	100	100
22	O	86/87 (99%)	86 (100%)	0	100	100
23	P	99/100 (99%)	99 (100%)	0	100	100
24	Q	89/90 (99%)	89 (100%)	0	100	100
25	R	84/84 (100%)	84 (100%)	0	100	100
26	S	93/93 (100%)	93 (100%)	0	100	100
27	T	80/84 (95%)	80 (100%)	0	100	100
28	U	83/85 (98%)	83 (100%)	0	100	100
29	V	78/78 (100%)	78 (100%)	0	100	100
30	W	57/63 (90%)	57 (100%)	0	100	100
31	X	67/68 (98%)	67 (100%)	0	100	100
32	Y	55/55 (100%)	55 (100%)	0	100	100
33	Z	48/49 (98%)	48 (100%)	0	100	100
35	b	180/198 (91%)	180 (100%)	0	100	100
36	c	170/190 (90%)	170 (100%)	0	100	100
37	d	172/173 (99%)	171 (99%)	1 (1%)	84	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	e	114/126 (90%)	114 (100%)	0	100	100
39	f	87/116 (75%)	87 (100%)	0	100	100
40	g	124/147 (84%)	124 (100%)	0	100	100
41	h	104/105 (99%)	104 (100%)	0	100	100
42	i	105/107 (98%)	105 (100%)	0	100	100
43	j	86/90 (96%)	86 (100%)	0	100	100
44	k	89/99 (90%)	89 (100%)	0	100	100
45	l	103/104 (99%)	103 (100%)	0	100	100
46	m	92/96 (96%)	92 (100%)	0	100	100
47	n	79/84 (94%)	79 (100%)	0	100	100
48	o	76/77 (99%)	76 (100%)	0	100	100
49	p	65/65 (100%)	65 (100%)	0	100	100
50	q	74/78 (95%)	74 (100%)	0	100	100
51	r	56/65 (86%)	56 (100%)	0	100	100
52	s	72/79 (91%)	72 (100%)	0	100	100
53	t	65/66 (98%)	65 (100%)	0	100	100
54	u	46/61 (75%)	46 (100%)	0	100	100
57	x	577/578 (100%)	576 (100%)	1 (0%)	92	97
58	y	1/1 (100%)	1 (100%)	0	100	100
All	All	5204/5408 (96%)	5202 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	d	139	ASN
57	x	529	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
45	l	95	HIS
57	x	454	GLN
57	x	350	ASN
36	c	99	GLN

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Mol	Chain	Res	Type
40	g	96	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1539/1542 (99%)	295 (19%)	0
55	v	74/77 (96%)	12 (16%)	0
56	w	75/76 (98%)	22 (29%)	0
59	z	10/33 (30%)	1 (10%)	0
8	A	2902/2903 (99%)	560 (19%)	38 (1%)
9	B	119/120 (99%)	19 (15%)	3 (2%)
All	All	4719/4751 (99%)	909 (19%)	41 (0%)

5 of 909 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	A	10	A
8	A	15	G
8	A	34	U
8	A	42	A
8	A	43	G

5 of 41 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	2287	A
8	A	2728	U
8	A	2319	G
8	A	2468	A
8	A	2808	G

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

46 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection.



RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
34	2MG	a	1207	34	18,26,27	0.94	1 (5%)	16,38,41	0.67	0
8	5MC	A	1962	8	18,22,23	0.28	0	26,32,35	0.42	0
8	5MU	A	1939	8	19,22,23	0.29	0	28,32,35	0.40	0
8	6MZ	A	1618	8	18,25,26	0.73	0	16,36,39	0.77	1 (6%)
55	4SU	v	8	55	18,21,22	0.30	0	26,30,33	0.37	0
56	G7M	w	46	56	20,26,27	0.51	0	17,39,42	0.41	0
55	H2U	v	20	55	18,21,22	0.37	0	21,30,33	0.34	0
34	UR3	a	1498	34	19,22,23	0.31	0	26,32,35	0.45	0
56	4SU	w	8	56	18,21,22	0.31	0	26,30,33	0.37	0
34	4OC	a	1402	34	20,23,24	0.31	0	26,32,35	0.46	0
8	PSU	A	2604	8	18,21,22	1.05	1 (5%)	22,30,33	1.86	5 (22%)
8	1MG	A	745	8	18,26,27	0.94	2 (11%)	19,39,42	0.55	0
34	MA6	a	1519	34	18,26,27	0.76	0	19,38,41	0.69	0
8	OMU	A	2552	8	19,22,23	0.33	0	26,31,34	0.45	0
34	2MG	a	966	34	18,26,27	0.97	2 (11%)	16,38,41	0.67	0
8	OMG	A	2251	56,8	18,26,27	0.96	2 (11%)	19,38,41	0.55	0
8	PSU	A	955	8	18,21,22	1.09	1 (5%)	22,30,33	1.84	5 (22%)
56	MIA	w	37	56	24,31,32	0.61	0	26,44,47	0.89	2 (7%)
34	PSU	a	516	34	18,21,22	1.01	1 (5%)	22,30,33	1.84	5 (22%)
8	PSU	A	1911	8	18,21,22	1.05	1 (5%)	22,30,33	1.80	5 (22%)
8	PSU	A	1917	8	18,21,22	1.01	1 (5%)	22,30,33	1.78	4 (18%)
34	5MC	a	1407	34	18,22,23	0.33	0	26,32,35	0.48	0
8	2MA	A	2503	8,60	19,25,26	1.03	2 (10%)	21,37,40	3.12	5 (23%)
8	PSU	A	2580	8	18,21,22	1.10	2 (11%)	22,30,33	1.95	6 (27%)
58	FME	y	101	58	8,9,10	0.97	0	7,9,11	0.79	0
34	MA6	a	1518	34	18,26,27	0.76	0	19,38,41	0.62	0
8	PSU	A	2457	8	18,21,22	0.99	1 (5%)	22,30,33	2.01	6 (27%)
34	G7M	a	527	34	20,26,27	0.59	0	17,39,42	0.42	0
56	PSU	w	55	56	18,21,22	1.08	1 (5%)	22,30,33	1.79	5 (22%)
8	3TD	A	1915	8	18,22,23	0.48	0	22,32,35	0.62	0
8	6MZ	A	2030	8,60	18,25,26	0.76	0	16,36,39	0.77	1 (6%)
8	OMC	A	2498	8,60	19,22,23	0.30	0	26,31,34	0.44	0
56	PSU	w	39	56	18,21,22	1.09	1 (5%)	22,30,33	1.68	4 (18%)
56	PSU	w	32	56	18,21,22	1.07	1 (5%)	22,30,33	1.65	4 (18%)
8	PSU	A	2504	8	18,21,22	1.06	1 (5%)	22,30,33	1.79	4 (18%)
8	PSU	A	746	8,60	18,21,22	1.09	1 (5%)	22,30,33	1.65	4 (18%)
8	G7M	A	2069	8	20,26,27	0.60	0	17,39,42	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	PSU	A	2605	8	18,21,22	1.04	1 (5%)	22,30,33	1.78	4 (18%)
34	2MG	a	1516	34	18,26,27	0.97	2 (11%)	16,38,41	0.69	0
8	2MG	A	1835	8	18,26,27	0.95	2 (11%)	16,38,41	0.67	0
56	5MU	w	54	56	19,22,23	0.31	0	28,32,35	0.30	0
8	2MG	A	2445	8	18,26,27	1.02	3 (16%)	16,38,41	0.60	0
55	5MU	v	54	55	19,22,23	0.29	0	28,32,35	0.29	0
8	5MC	A	747	8	18,22,23	0.30	0	26,32,35	0.41	0
55	PSU	v	55	55	18,21,22	1.08	1 (5%)	22,30,33	1.72	4 (18%)
34	5MC	a	967	34	18,22,23	0.28	0	26,32,35	0.42	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	2MG	a	1207	34	-	2/5/27/28	0/3/3/3
8	5MC	A	1962	8	-	0/7/25/26	0/2/2/2
8	5MU	A	1939	8	-	1/7/25/26	0/2/2/2
8	6MZ	A	1618	8	-	0/5/27/28	0/3/3/3
55	4SU	v	8	55	-	0/7/25/26	0/2/2/2
56	G7M	w	46	56	-	1/3/25/26	0/3/3/3
55	H2U	v	20	55	-	2/7/38/39	0/2/2/2
34	UR3	a	1498	34	-	2/7/25/26	0/2/2/2
56	4SU	w	8	56	-	0/7/25/26	0/2/2/2
34	4OC	a	1402	34	-	0/9/29/30	0/2/2/2
8	PSU	A	2604	8	-	0/7/25/26	0/2/2/2
8	1MG	A	745	8	-	0/3/25/26	0/3/3/3
34	MA6	a	1519	34	-	2/7/29/30	0/3/3/3
8	OMU	A	2552	8	-	2/9/27/28	0/2/2/2
34	2MG	a	966	34	-	0/5/27/28	0/3/3/3
8	OMG	A	2251	56,8	-	0/5/27/28	0/3/3/3
8	PSU	A	955	8	-	0/7/25/26	0/2/2/2
56	MIA	w	37	56	-	0/11/33/34	0/3/3/3
34	PSU	a	516	34	-	0/7/25/26	0/2/2/2
8	PSU	A	1911	8	-	0/7/25/26	0/2/2/2
8	PSU	A	1917	8	-	0/7/25/26	0/2/2/2
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2
8	2MA	A	2503	8,60	-	1/3/25/26	0/3/3/3
8	PSU	A	2580	8	-	0/7/25/26	0/2/2/2

Continued on next page...

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	FME	y	101	58	-	3/7/9/11	-
34	MA6	a	1518	34	-	0/7/29/30	0/3/3/3
8	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
34	G7M	a	527	34	-	3/3/25/26	0/3/3/3
56	PSU	w	55	56	-	0/7/25/26	0/2/2/2
8	3TD	A	1915	8	-	3/7/25/26	0/2/2/2
8	6MZ	A	2030	8,60	-	2/5/27/28	0/3/3/3
8	OMC	A	2498	8,60	-	0/9/27/28	0/2/2/2
56	PSU	w	39	56	-	5/7/25/26	0/2/2/2
56	PSU	w	32	56	-	3/7/25/26	0/2/2/2
8	PSU	A	2504	8	-	2/7/25/26	0/2/2/2
8	PSU	A	746	8,60	-	1/7/25/26	0/2/2/2
8	G7M	A	2069	8	-	1/3/25/26	0/3/3/3
8	PSU	A	2605	8	-	0/7/25/26	0/2/2/2
34	2MG	a	1516	34	-	0/5/27/28	0/3/3/3
8	2MG	A	1835	8	-	0/5/27/28	0/3/3/3
56	5MU	w	54	56	-	0/7/25/26	0/2/2/2
8	2MG	A	2445	8	-	0/5/27/28	0/3/3/3
55	5MU	v	54	55	-	0/7/25/26	0/2/2/2
8	5MC	A	747	8	-	0/7/25/26	0/2/2/2
55	PSU	v	55	55	-	3/7/25/26	0/2/2/2
34	5MC	a	967	34	-	0/7/25/26	0/2/2/2

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	w	32	PSU	C6-C5	3.65	1.39	1.35
56	w	39	PSU	C6-C5	3.64	1.39	1.35
55	v	55	PSU	C6-C5	3.61	1.39	1.35
8	A	746	PSU	C6-C5	3.52	1.39	1.35
56	w	55	PSU	C6-C5	3.48	1.39	1.35

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2503	2MA	C5-C6-N1	-12.57	112.76	121.01
8	A	2457	PSU	C4-N3-C2	-5.22	118.82	126.34
8	A	2457	PSU	N1-C2-N3	5.03	120.83	115.13
34	a	516	PSU	C4-N3-C2	-4.84	119.36	126.34
8	A	2605	PSU	C4-N3-C2	-4.82	119.39	126.34

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	a	1207	2MG	N1-C2-N2-CM2
34	a	1207	2MG	N3-C2-N2-CM2
34	a	1498	UR3	O4'-C1'-N1-C2
55	v	55	PSU	O4'-C1'-C5-C4
55	v	55	PSU	O4'-C1'-C5-C6

There are no ring outliers.

11 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	a	1498	UR3	1	0
8	A	745	1MG	1	0
34	a	1519	MA6	1	0
56	w	37	MIA	2	0
34	a	516	PSU	1	0
8	A	1917	PSU	2	0
58	y	101	FME	1	0
34	a	527	G7M	1	0
8	A	2030	6MZ	1	0
56	w	32	PSU	1	0
8	A	2504	PSU	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 378 ligands modelled in this entry, 373 are monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
63	AM2	a	1630	-	40,40,40	0.51	0	53,60,60	0.73	1 (1%)
63	AM2	a	1633	-	40,40,40	0.54	0	53,60,60	0.69	2 (3%)
65	GDP	x	804	60	24,30,30	0.85	1 (4%)	30,47,47	0.80	1 (3%)
63	AM2	a	1618	-	40,40,40	0.51	0	53,60,60	0.71	2 (3%)
64	PO4	x	802	-	4,4,4	0.99	0	6,6,6	0.41	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
63	AM2	a	1630	-	-	3/12/84/84	0/4/4/4
65	GDP	x	804	60	-	1/12/32/32	0/3/3/3
63	AM2	a	1618	-	-	4/12/84/84	0/4/4/4
63	AM2	a	1633	-	-	0/12/84/84	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
65	x	804	GDP	C5-C6	-2.08	1.43	1.47

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	x	804	GDP	PA-O3A-PB	3.05	143.28	132.83
63	a	1618	AM2	OA1-CA1-CA2	2.45	112.33	108.23
63	a	1618	AM2	OA4-CA1-CA2	2.43	115.66	110.25
63	a	1633	AM2	OA4-CA1-CA2	2.38	115.55	110.25
63	a	1633	AM2	OA1-CA1-CA2	2.33	112.14	108.23

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

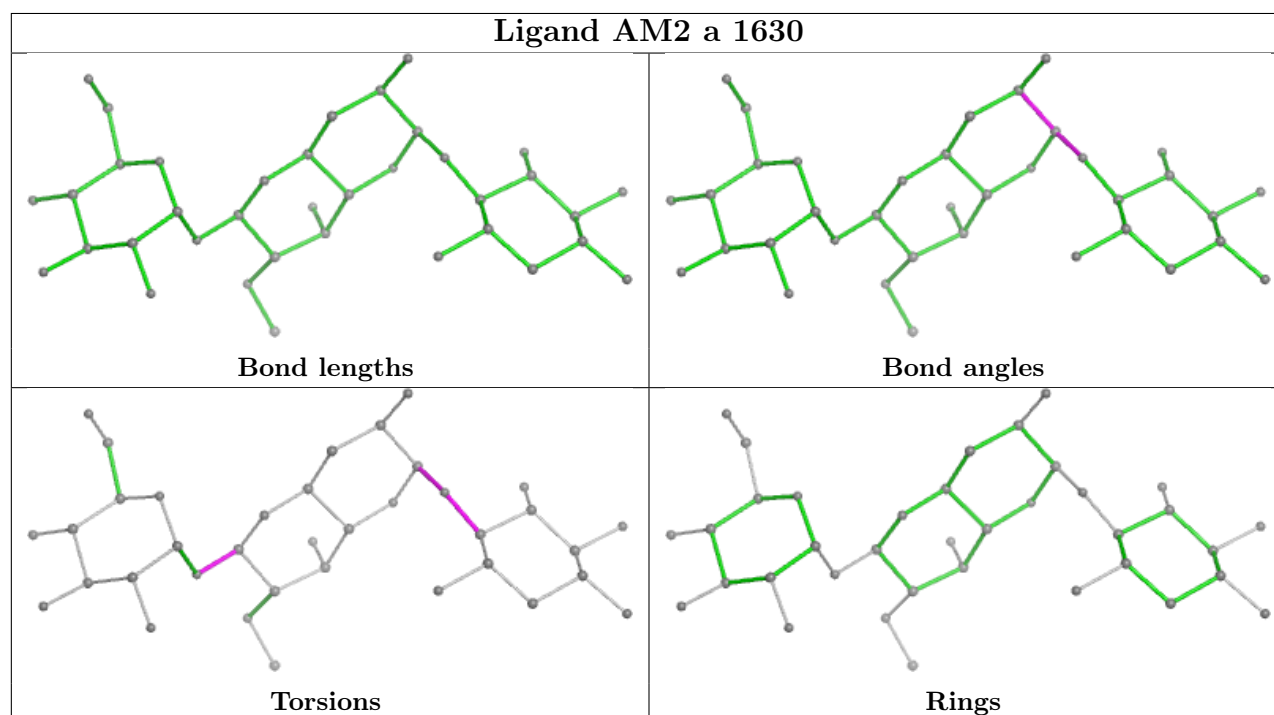
Mol	Chain	Res	Type	Atoms
63	a	1630	AM2	OA5-CA8-OA8-CB1
63	a	1630	AM2	OA4-CA1-OA1-CC1
63	a	1618	AM2	OB1-CB5-CB6-OB6
63	a	1618	AM2	OB1-CB1-OA8-CA8
63	a	1618	AM2	CB2-CB1-OA8-CA8

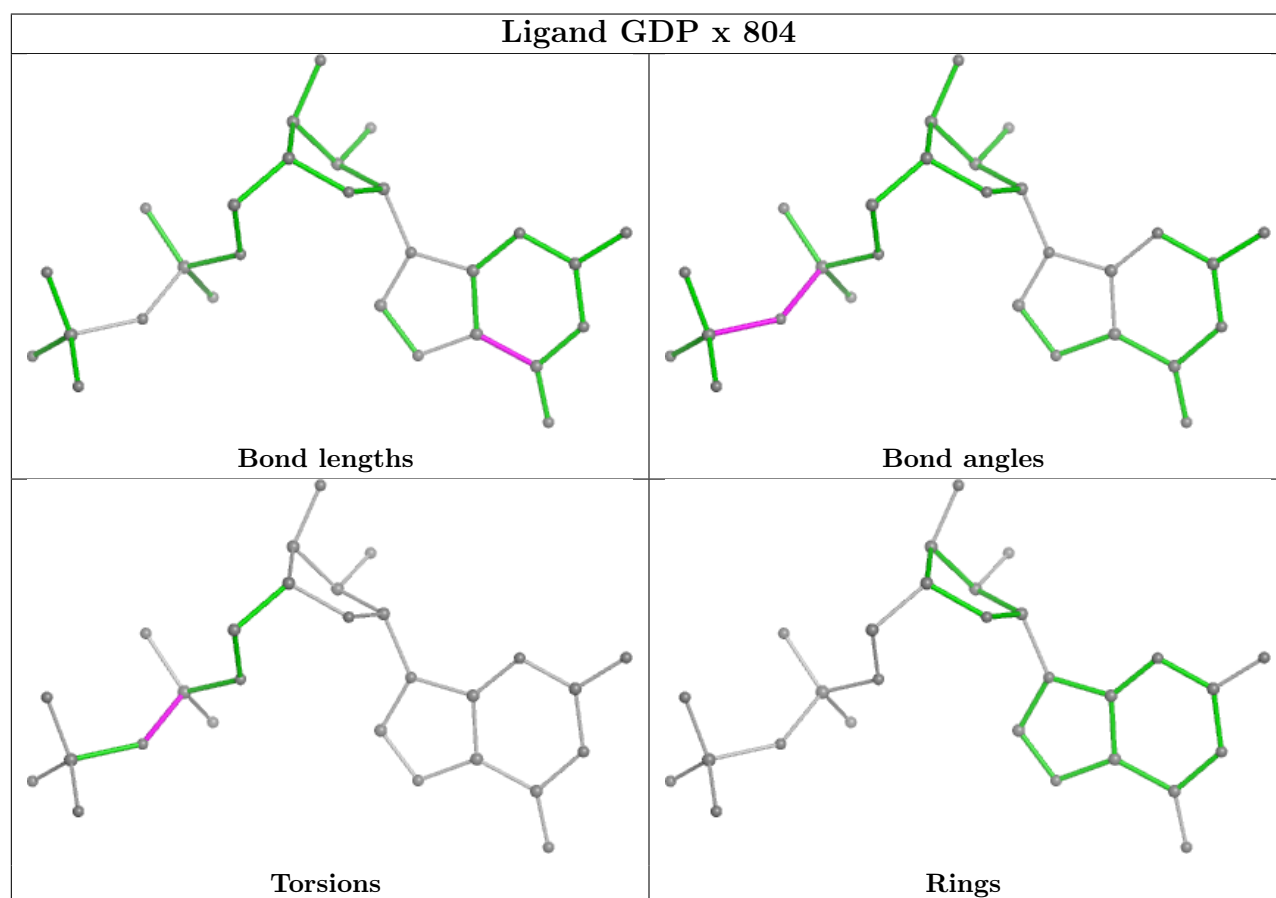
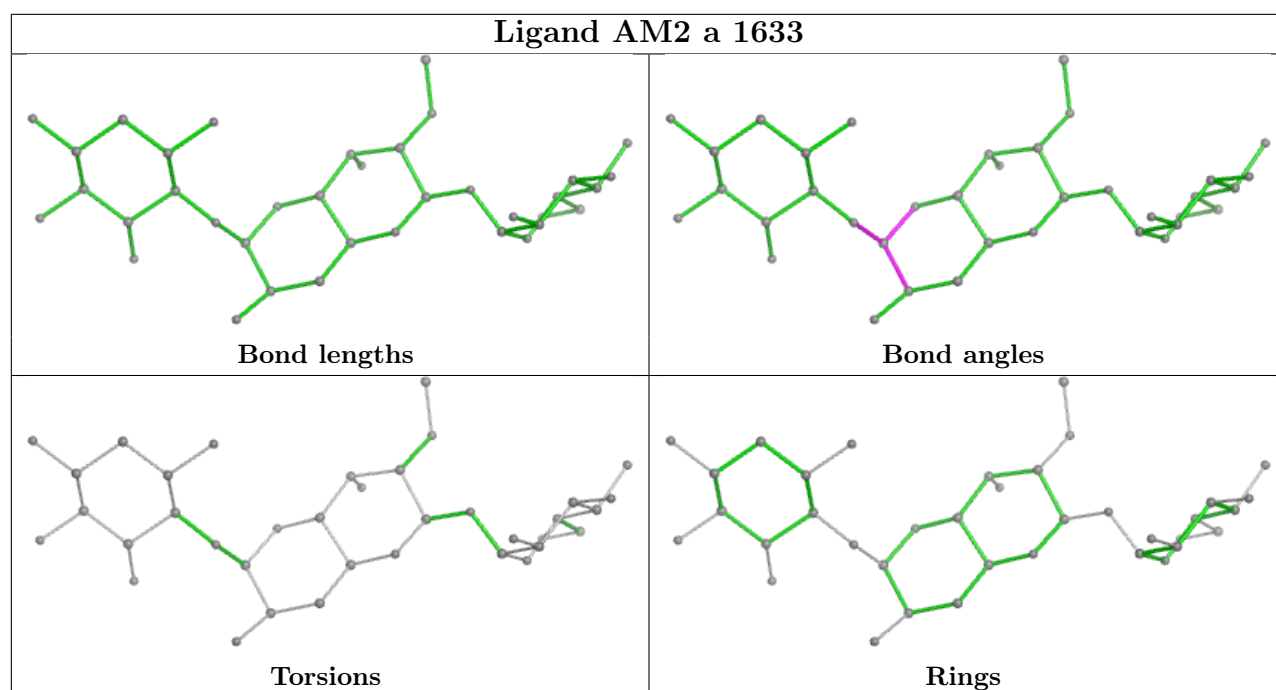
There are no ring outliers.

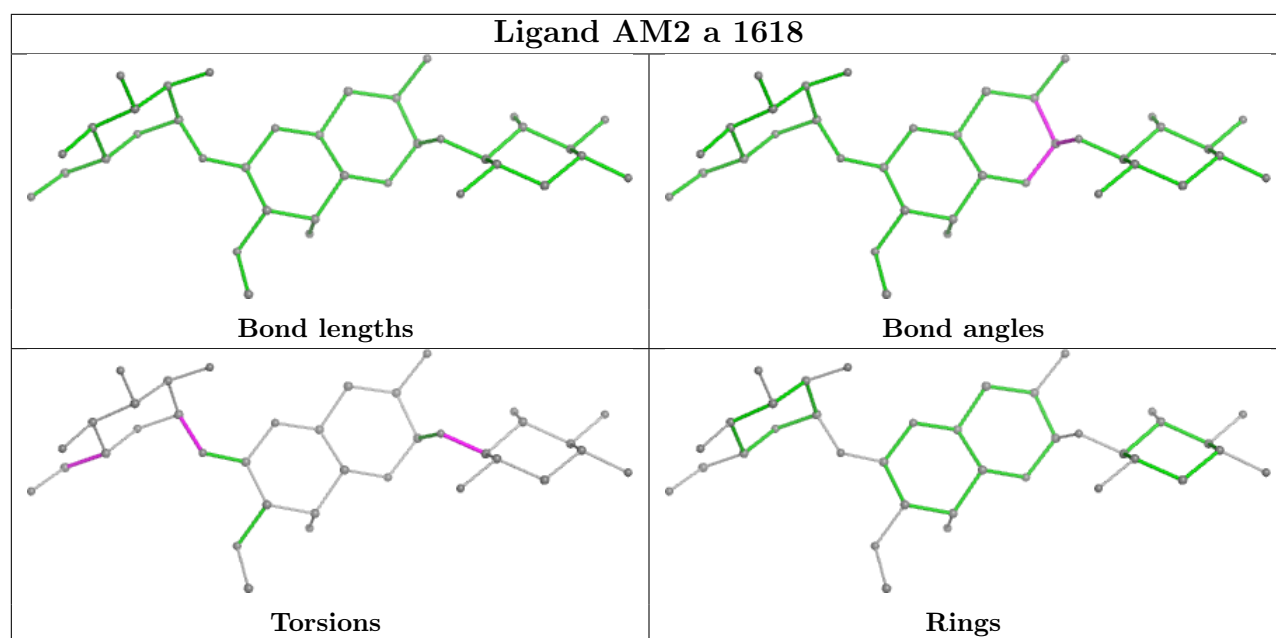
4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
63	a	1633	AM2	4	0
65	x	804	GDP	1	0
63	a	1618	AM2	2	0
64	x	802	PO4	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



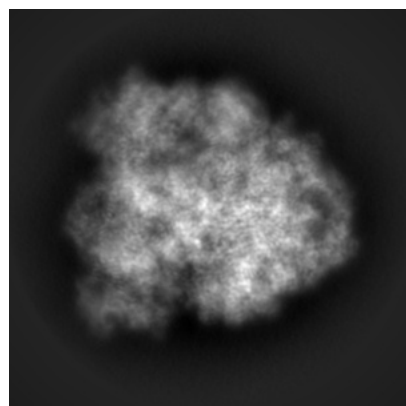
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-54253. These allow visual inspection of the internal detail of the map and identification of artifacts.

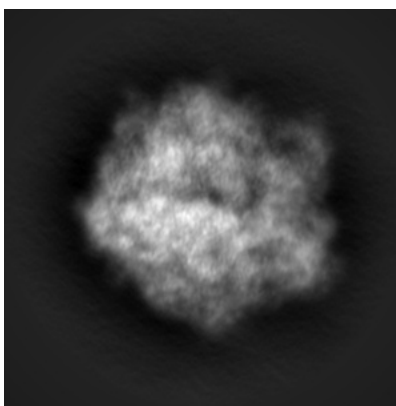
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

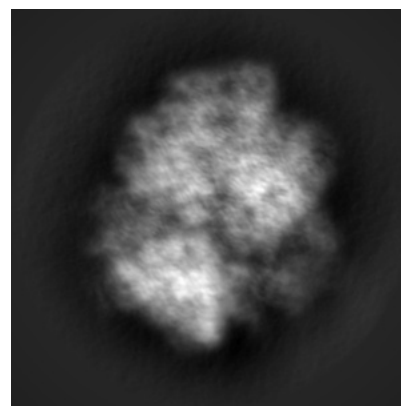
#### 6.1.1 Primary map



X

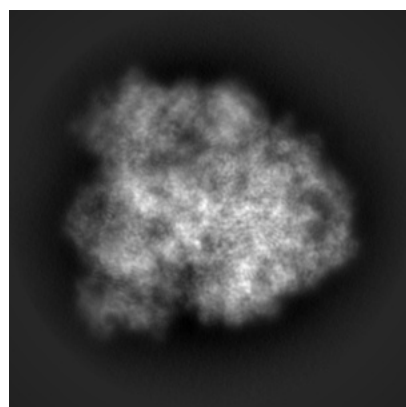


Y

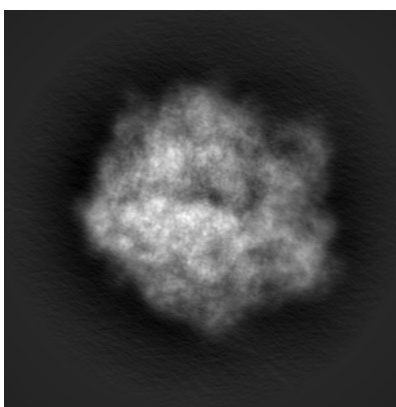


Z

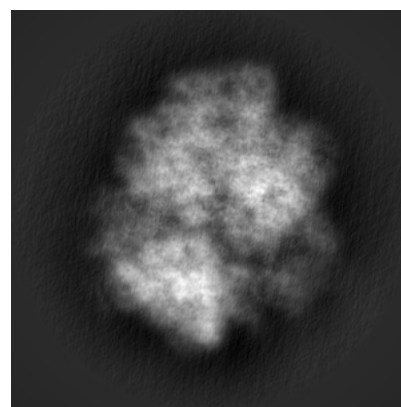
#### 6.1.2 Raw map



X



Y

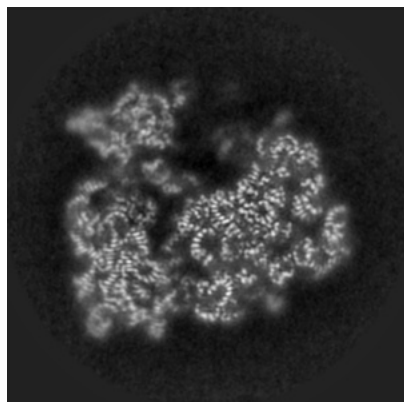


Z

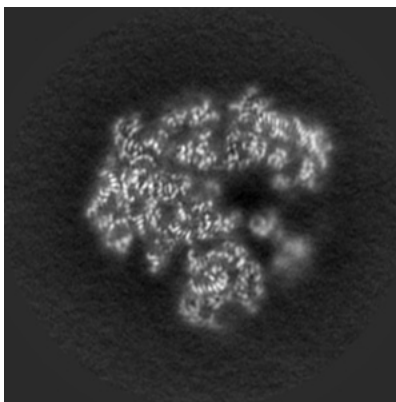
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

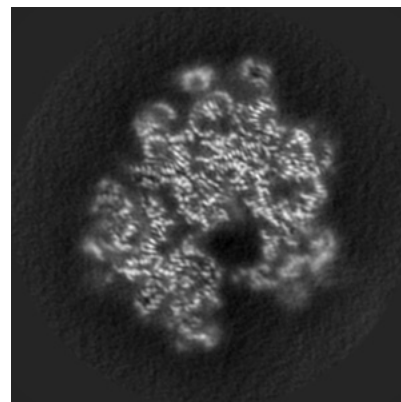
### 6.2.1 Primary map



X Index: 144

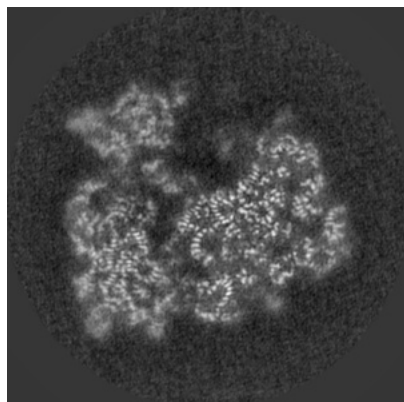


Y Index: 144

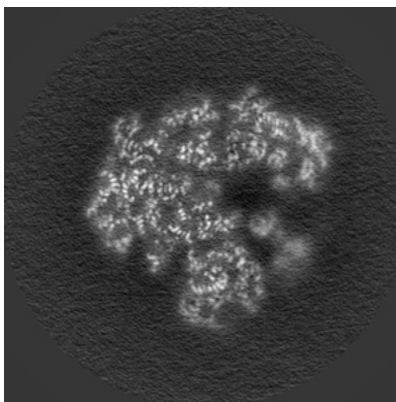


Z Index: 144

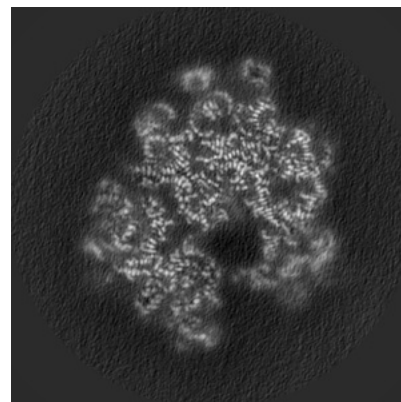
### 6.2.2 Raw map



X Index: 144



Y Index: 144

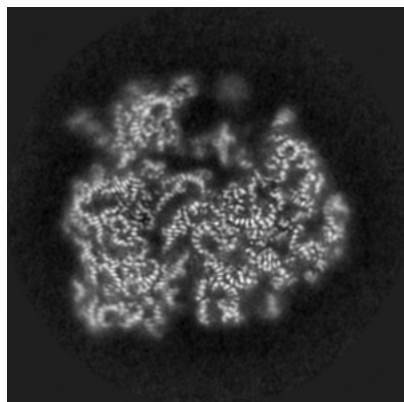


Z Index: 144

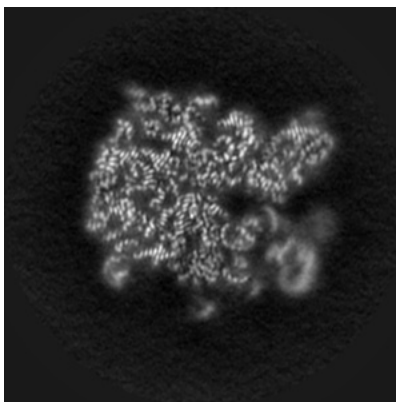
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

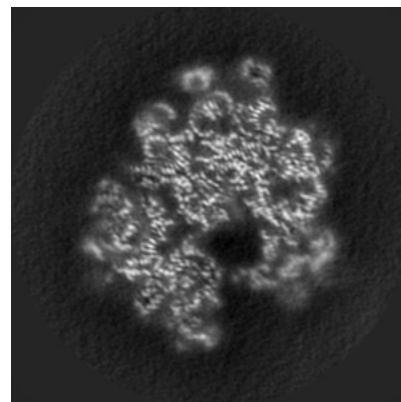
### 6.3.1 Primary map



X Index: 138

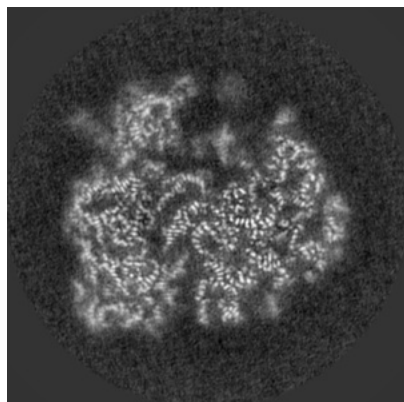


Y Index: 161

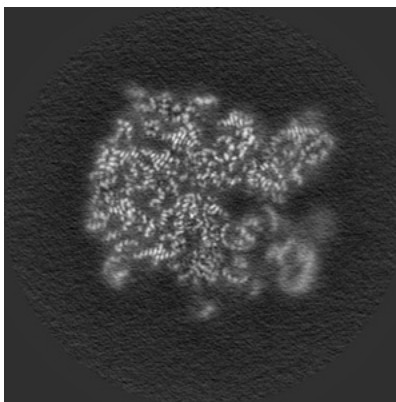


Z Index: 144

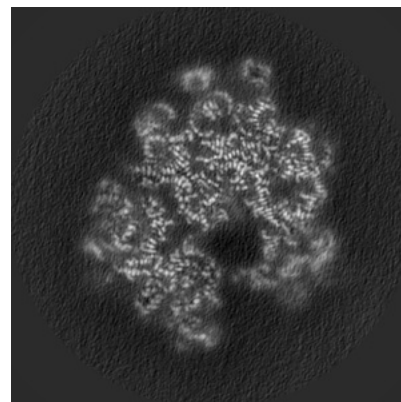
### 6.3.2 Raw map



X Index: 138



Y Index: 161

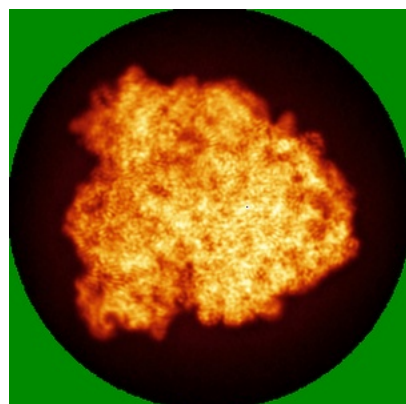


Z Index: 144

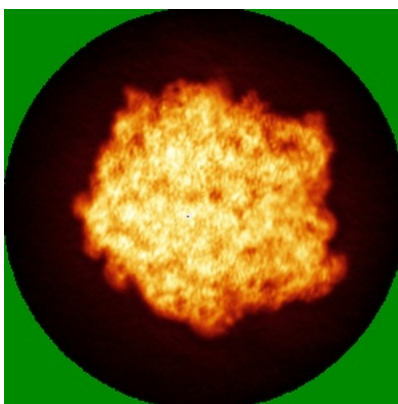
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

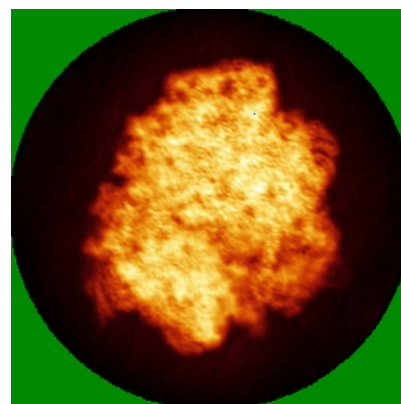
### 6.4.1 Primary map



X

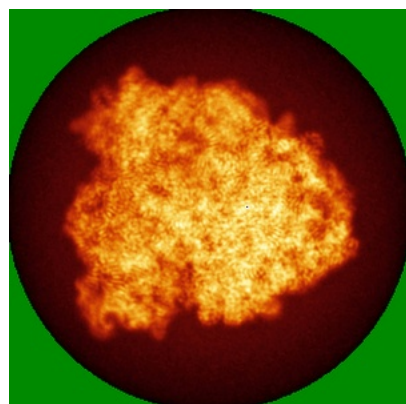


Y

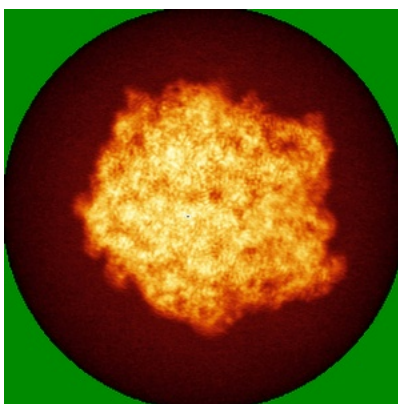


Z

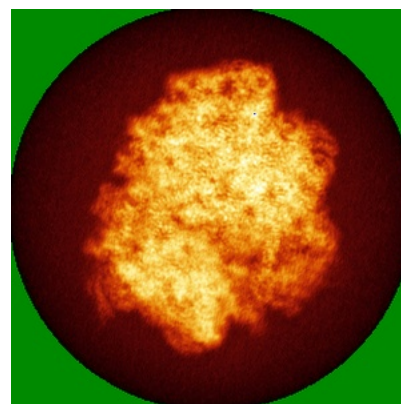
### 6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



X



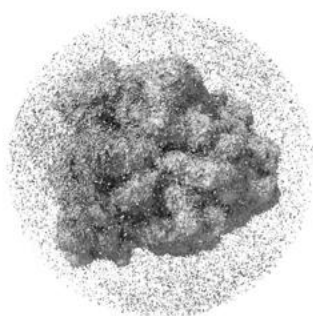
Y



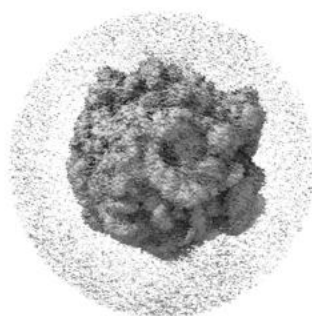
Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

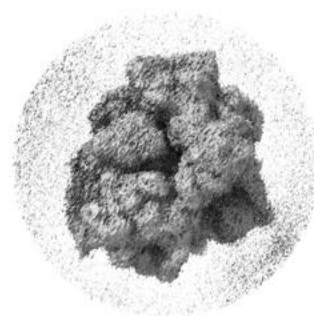
### 6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

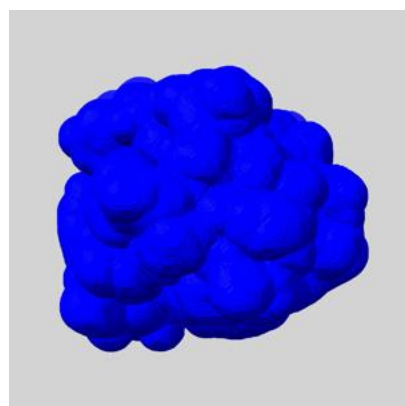
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

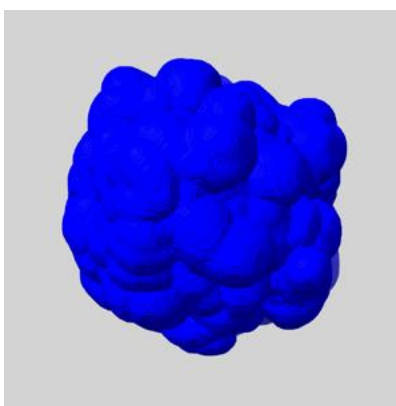
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

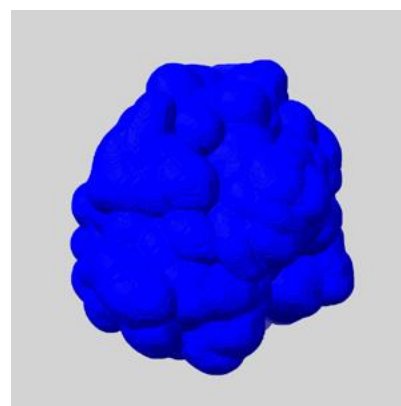
### 6.6.1 emd\_54253\_msk\_1.map [i](#)



X



Y

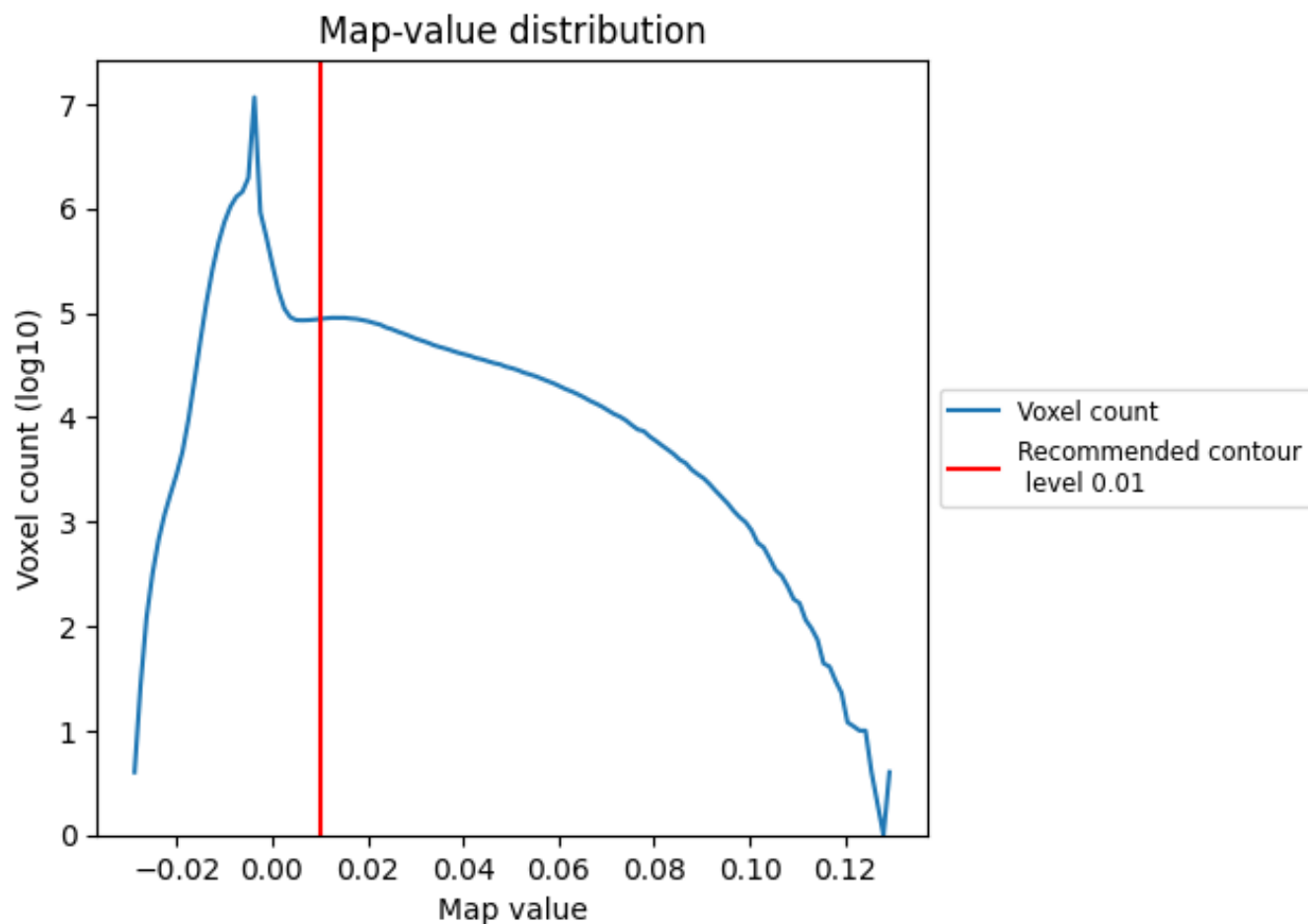


Z

## 7 Map analysis [i](#)

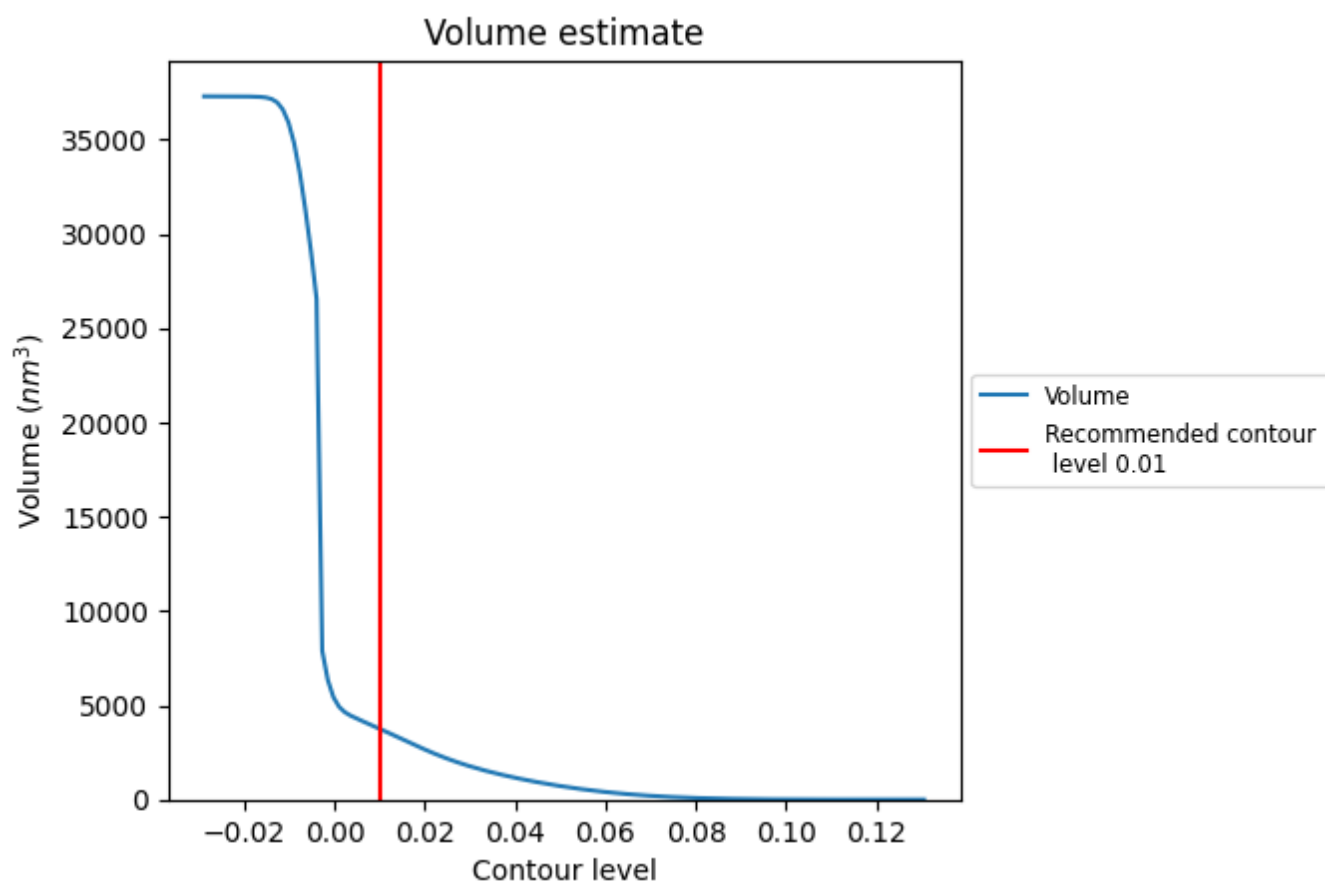
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

## 7.2 Volume estimate [i](#)

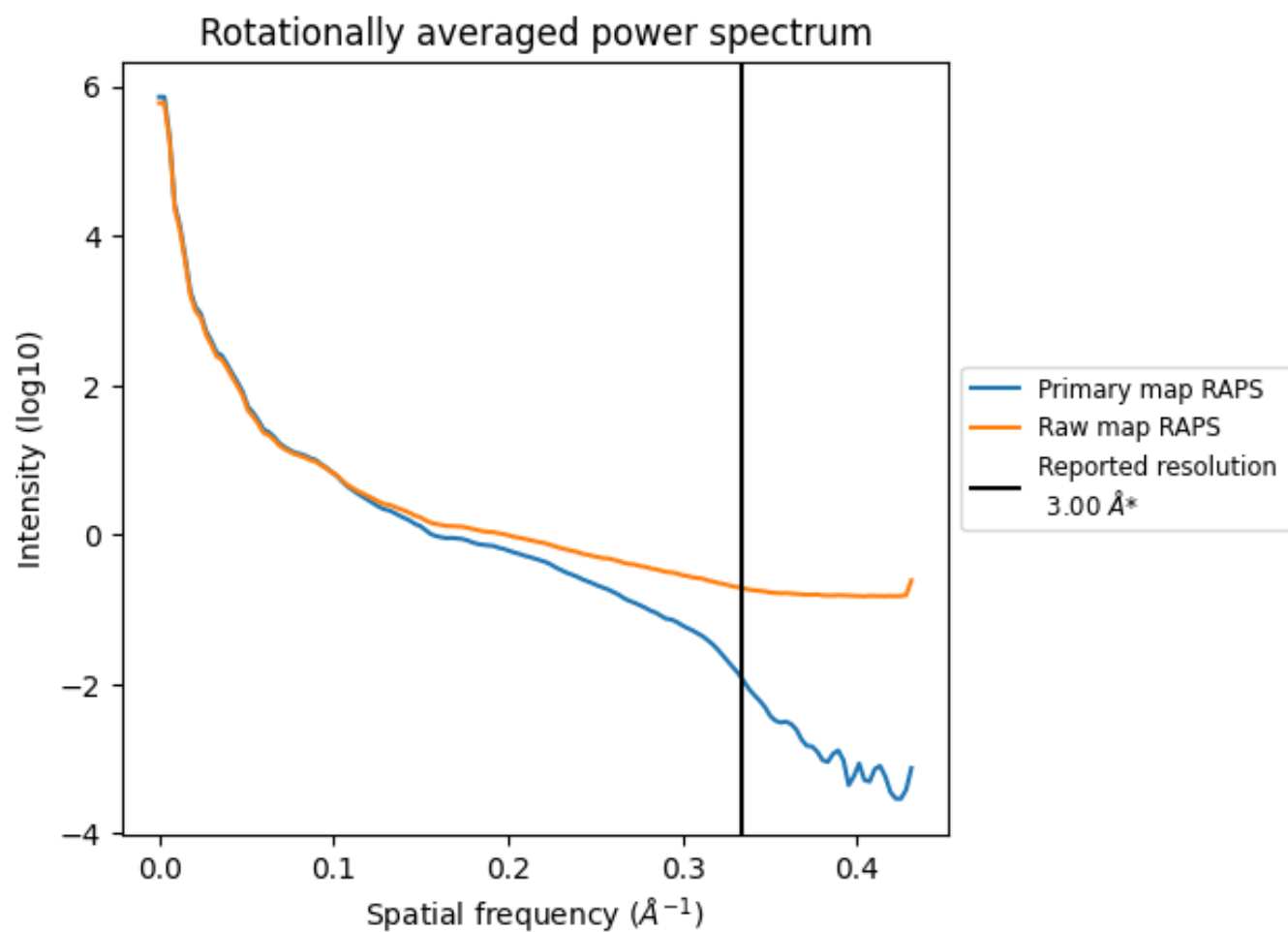


The volume at the recommended contour level is 3762 nm<sup>3</sup>; this corresponds to an approximate mass of 3398 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.



### 7.3 Rotationally averaged power spectrum ⓘ

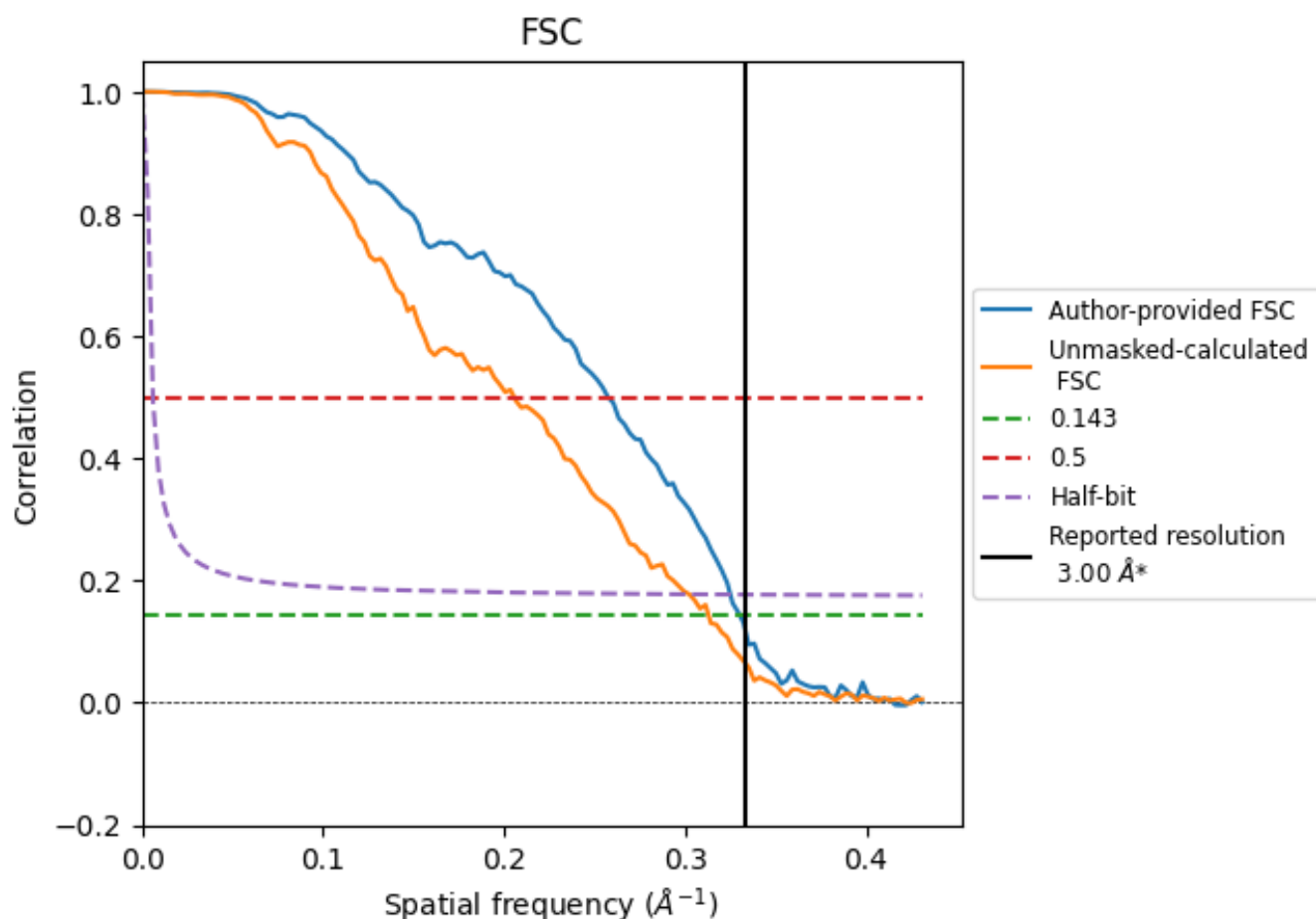


\*Reported resolution corresponds to spatial frequency of 0.333  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.333  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

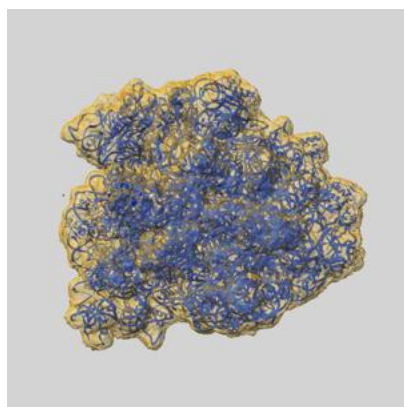
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.03	3.89	3.08
Unmasked-calculated*	3.19	4.86	3.31

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

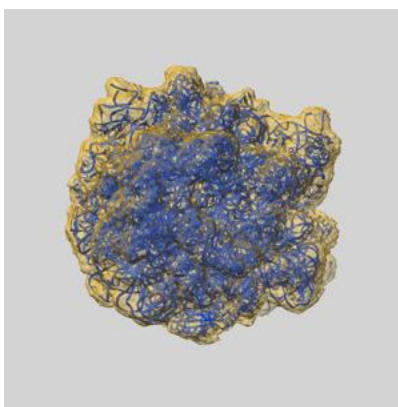
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-54253 and PDB model 9RTU. Per-residue inclusion information can be found in section 3 on page 18.

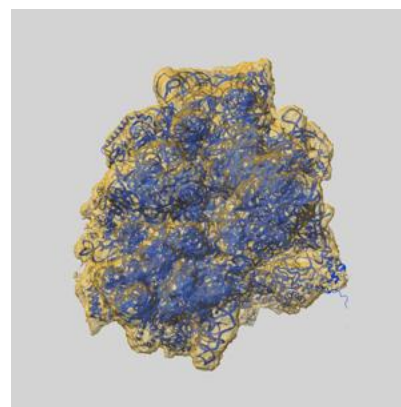
### 9.1 Map-model overlay [i](#)



X



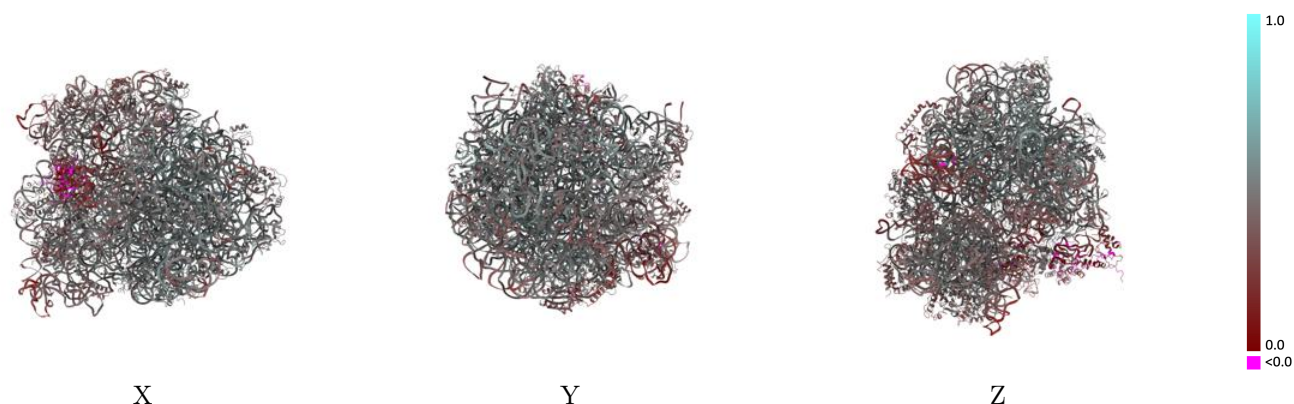
Y



Z

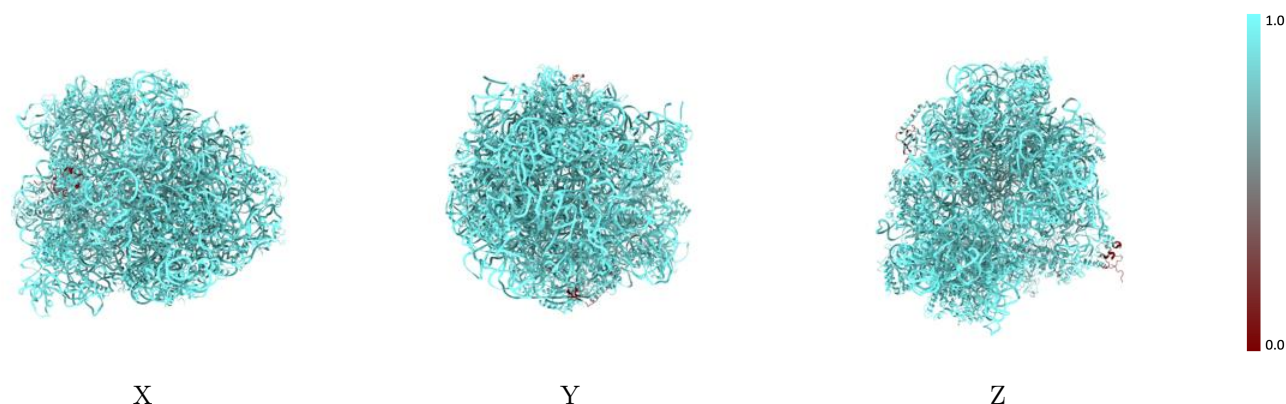
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



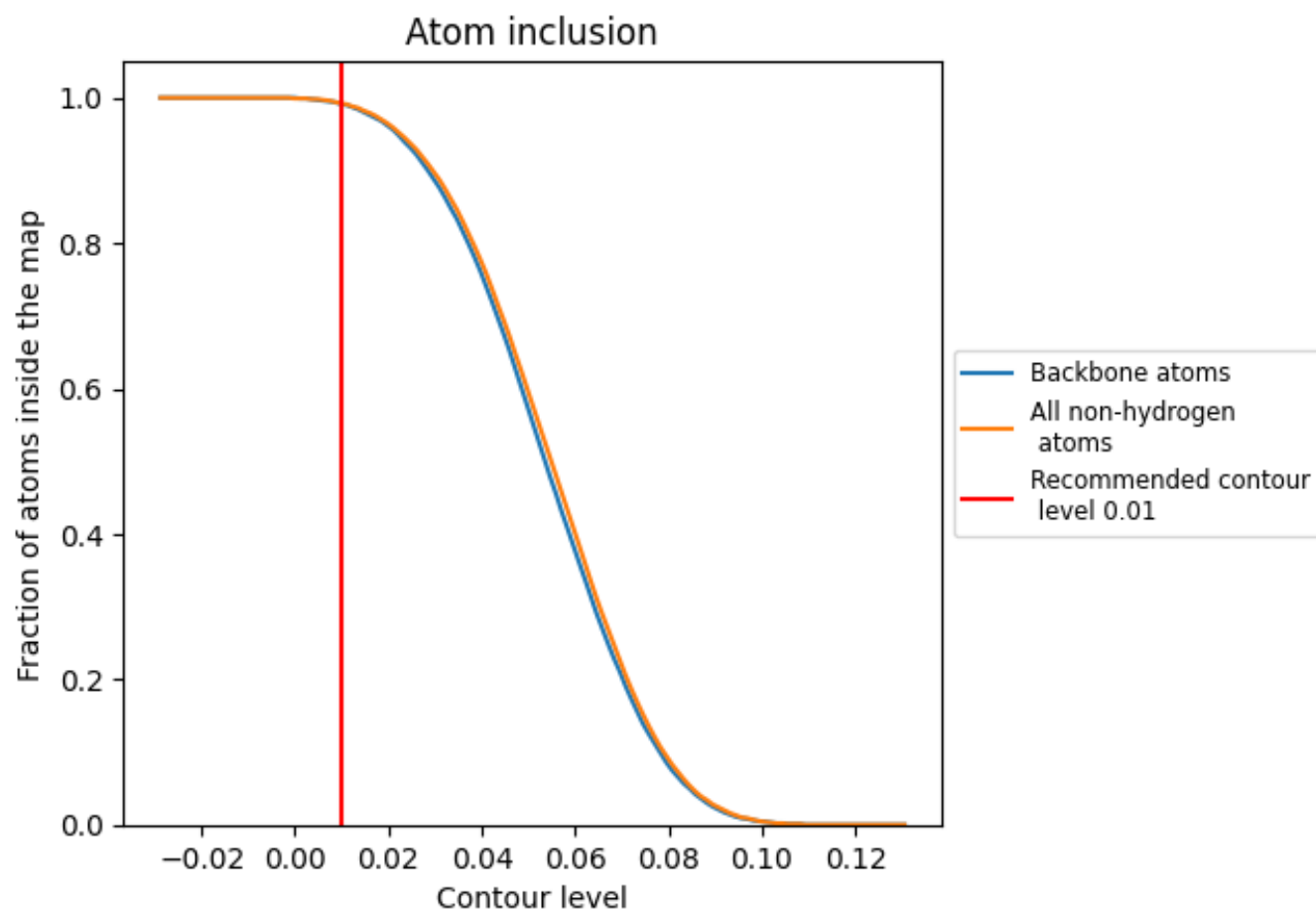
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ



















































The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9920	 0.4450
0	 0.9950	 0.4820
1	 1.0000	 0.4590
2	 1.0000	 0.5030
3	 0.9960	 0.5070
4	 1.0000	 0.4540
5	 0.6600	 0.1080
6	 0.9900	 0.3190
A	 0.9990	 0.4690
B	 1.0000	 0.4470
C	 0.9960	 0.4960
D	 0.9940	 0.4860
E	 0.9940	 0.4650
F	 0.9880	 0.3600
G	 0.9850	 0.4090
H	 0.6930	 0.3110
I	 0.9260	 0.1700
J	 0.9970	 0.4780
K	 0.9830	 0.4830
L	 0.9960	 0.4850
M	 0.9940	 0.4780
N	 0.9990	 0.4820
O	 0.9990	 0.4240
P	 0.9920	 0.4700
Q	 0.9990	 0.4830
R	 0.9940	 0.4760
S	 0.9960	 0.4730
T	 1.0000	 0.4550
U	 0.9910	 0.4320
V	 0.9910	 0.4520
W	 0.9950	 0.4870
X	 0.9930	 0.4680
Y	 0.9960	 0.3870
Z	 0.9890	 0.4740
a	 0.9990	 0.4480



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Chain	Atom inclusion	Q-score
b	 0.9740	 0.3870
c	 0.9910	 0.4190
d	 0.9970	 0.4110
e	 0.9980	 0.4590
f	 0.9750	 0.3830
g	 0.9870	 0.3470
h	 0.9970	 0.4670
i	 0.9940	 0.3970
j	 0.9960	 0.3860
k	 0.9950	 0.4410
l	 0.9860	 0.4810
m	 0.9910	 0.3700
n	 1.0000	 0.4080
o	 0.9960	 0.4240
p	 0.9950	 0.4520
q	 0.9970	 0.4520
r	 0.9960	 0.4240
s	 0.9890	 0.3690
t	 0.9950	 0.3860
u	 0.9940	 0.4010
v	 0.9960	 0.4080
w	 0.9960	 0.3600
x	 0.9640	 0.3450
y	 1.0000	 0.3420
z	 1.0000	 0.4660