



wwPDB EM Validation Summary Report ⓘ

Jul 2, 2026 – 08:58 PM JST

PDB ID : 9L94 / pdb_00009194
EMDB ID : EMD-62893
Title : State G of archaeal pre-50S ribosome
Authors : Li, Z.Q.; Yang, X.Y.
Deposited on : 2024-12-29
Resolution : 2.07 Å(reported)

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:

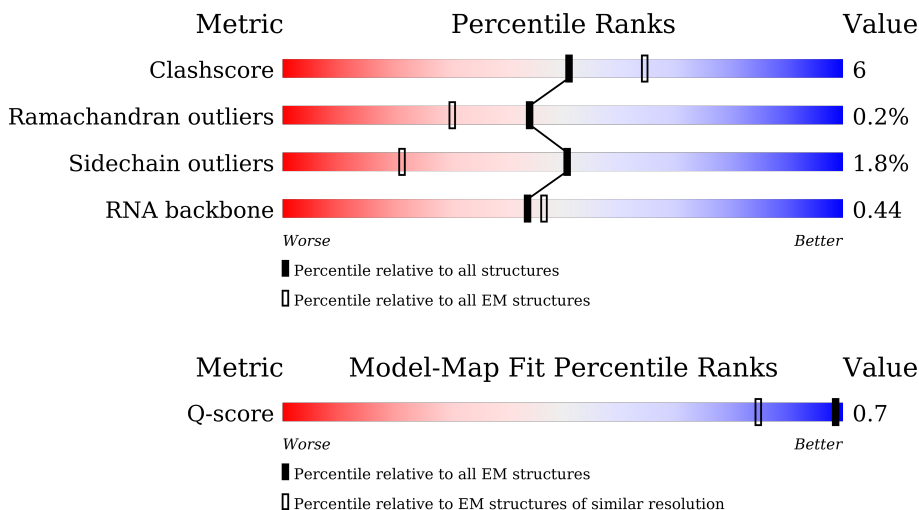
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using 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)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.07 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	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1932 (1.58 - 2.57)

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 $\leq 5\%$. 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	2916	
2	1	122	
3	i	168	

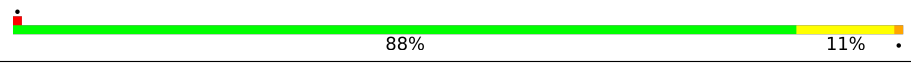
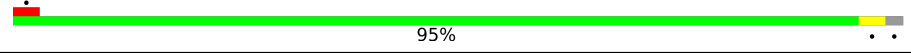

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Mol	Chain	Length	Quality of chain
4	E	120	76% 22% ..
5	F	176	7% 85% 13% ..
6	G	196	89% 10% ..
7	H	116	96% ..
8	I	184	80% 18% ..
9	J	151	87% 10% .
10	K	96	86% 12% .
11	L	153	89% 8% ..
12	M	67	79% 7% 13%
13	N	118	84% 12% ..
14	O	154	95% ..
15	P	92	9% 85% 11% ..
16	Q	234	56% 5% 39%
17	R	89	80% 9% 10%
18	S	58	95% ..
19	T	93	89% 11%
20	U	241	90% 5% ..
21	V	338	95% .
22	W	248	90% 10%
23	X	172	42% 74% 23% ..
24	Y	178	86% 12% .
25	b	145	90% 8% ...
26	j	48	83% 6% 10%
27	c	83	81% 17% ..
28	d	70	11% 77% 20% .

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Mol	Chain	Length	Quality of chain
29	f	132	 88% 11%
30	e	58	 95%
31	A	50	 80% 18%

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
32	BGC	0	3002	-	-	X	-
33	SPD	0	3003	-	-	X	-
33	SPD	0	3004	-	-	X	-

2 Entry composition [i](#)

There are 36 unique types of molecules in this entry. The entry contains 95953 atoms, of which 88 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 23S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	0	2624	56268	25116	10373	18155	2624	0	0

- Molecule 2 is a RNA chain called 5S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	1	120	2551	1138	453	840	120	0	0

- Molecule 3 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	i	155	1184	710	234	240	1	0

- Molecule 4 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	119	880	546	141	192	1	0	

- Molecule 5 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	174	1372	852	251	261	8	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	195	1599	975	344	278	2	1	0

- Molecule 7 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	H	115	887	544	167	176	0	0

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	I	183	1413	878	258	276	1	0	0

- Molecule 9 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	J	147	1179	712	243	223	1	0	0

- Molecule 10 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	K	95	744	456	151	134	3	1	0

- Molecule 11 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L	151	1174	730	214	226	4	0	0

- Molecule 12 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	58	466	287	83	94	2	0	0

- Molecule 13 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	N	114	909	549	172	188	1	0

- Molecule 14 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	154	Total	C	N	O	S	0	0
			1200	731	220	245	4		

- Molecule 15 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	89	Total	C	N	O	S	0	0
			719	445	138	135	1		

- Molecule 16 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	142	Total	C	N	O	S	1	0
			1140	696	231	212	1		

- Molecule 17 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	80	Total	C	N	O	S	1	0
			625	379	128	117	1		

- Molecule 18 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	57	Total	C	N	O	S	1	0
			447	270	93	80	4		

- Molecule 19 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	93	Total	C	N	O	S	0	0
			746	457	152	129	8		

- Molecule 20 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	232	Total	C	N	O	S	0	0
			1721	1066	339	311	5		

- Molecule 21 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	V	337	2615	1621	484	500	10	0	0

- Molecule 22 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	W	248	1898	1164	354	377	3	0	0

- Molecule 23 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	X	169	1186	729	216	239	2	0	0

- Molecule 24 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Y	174	1342	829	227	283	3	0	0

- Molecule 25 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	b	144	1127	701	201	220	5	0	0

- Molecule 26 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	j	43	350	211	79	55	5	0	0

- Molecule 27 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	c	82	645	397	112	133	3	0	0

- Molecule 28 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	d	68	515	317	88	109	1	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	f	132	1004	617	191	191	5	1	0

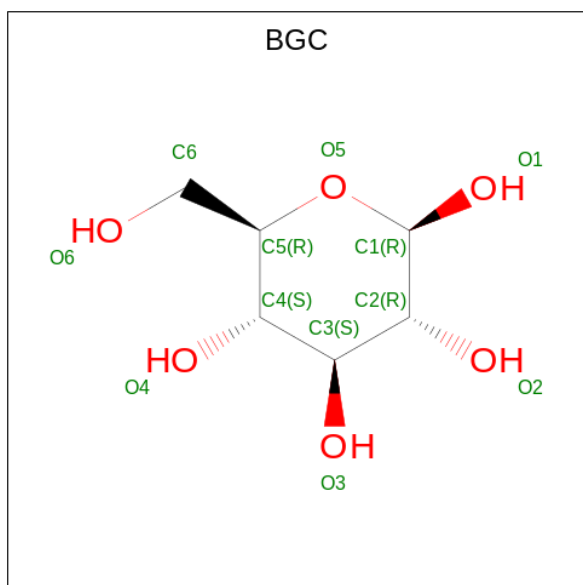
- Molecule 30 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
30	e	57	435	269	76	90	0	0

- Molecule 31 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	A	49	414	252	89	71	2	0	0

- Molecule 32 is beta-D-glucopyranose (CCD ID: BGC) (formula: C₆H₁₂O₆).



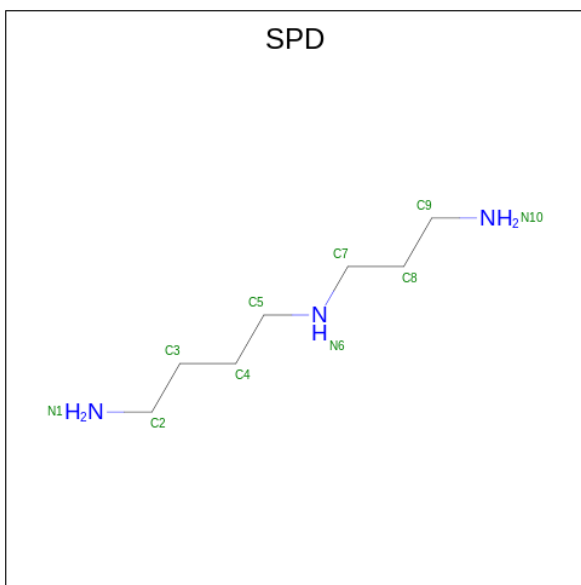
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
32	0	1	12	6	6	0

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Mol	Chain	Residues	Atoms				AltConf
			Total	C	H	O	
32	0	1	24	6	12	6	0

- Molecule 33 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	H	N	
33	0	1	29	7	19	3	0
33	0	1	29	7	19	3	0
33	0	1	29	7	19	3	0
33	0	1	29	7	19	3	0

- Molecule 34 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
34	0	292	292	292	0
34	1	5	5	5	0
34	F	1	1	1	0
34	G	4	4	4	0

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Mol	Chain	Residues	Atoms		AltConf
34	K	1	Total 1	Mg 1	0
34	N	1	Total 1	Mg 1	0
34	O	2	Total 2	Mg 2	0
34	P	1	Total 1	Mg 1	0
34	Q	1	Total 1	Mg 1	0
34	S	1	Total 1	Mg 1	0
34	T	1	Total 1	Mg 1	0
34	U	2	Total 2	Mg 2	0
34	V	3	Total 3	Mg 3	0
34	W	1	Total 1	Mg 1	0
34	f	1	Total 1	Mg 1	0

- Molecule 35 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
35	S	1	Total 1	Zn 1	0
35	T	1	Total 1	Zn 1	0

- Molecule 36 is water.

Mol	Chain	Residues	Atoms		AltConf
36	0	5625	Total 5625	O 5625	0
36	1	85	Total 85	O 85	0
36	i	45	Total 45	O 45	0
36	E	3	Total 3	O 3	0

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Mol	Chain	Residues	Atoms		AltConf
36	F	45	Total 45	O 45	0
36	G	101	Total 101	O 101	0
36	H	15	Total 15	O 15	0
36	I	8	Total 8	O 8	0
36	J	44	Total 44	O 44	0
36	K	41	Total 41	O 41	0
36	L	47	Total 47	O 47	0
36	M	9	Total 9	O 9	0
36	N	21	Total 21	O 21	0
36	O	57	Total 57	O 57	0
36	P	23	Total 23	O 23	0
36	Q	66	Total 66	O 66	0
36	R	18	Total 18	O 18	0
36	S	33	Total 33	O 33	0
36	T	35	Total 35	O 35	0
36	U	67	Total 67	O 67	0
36	V	118	Total 118	O 118	0
36	W	89	Total 89	O 89	0
36	Y	15	Total 15	O 15	0
36	b	44	Total 44	O 44	0
36	j	8	Total 8	O 8	0

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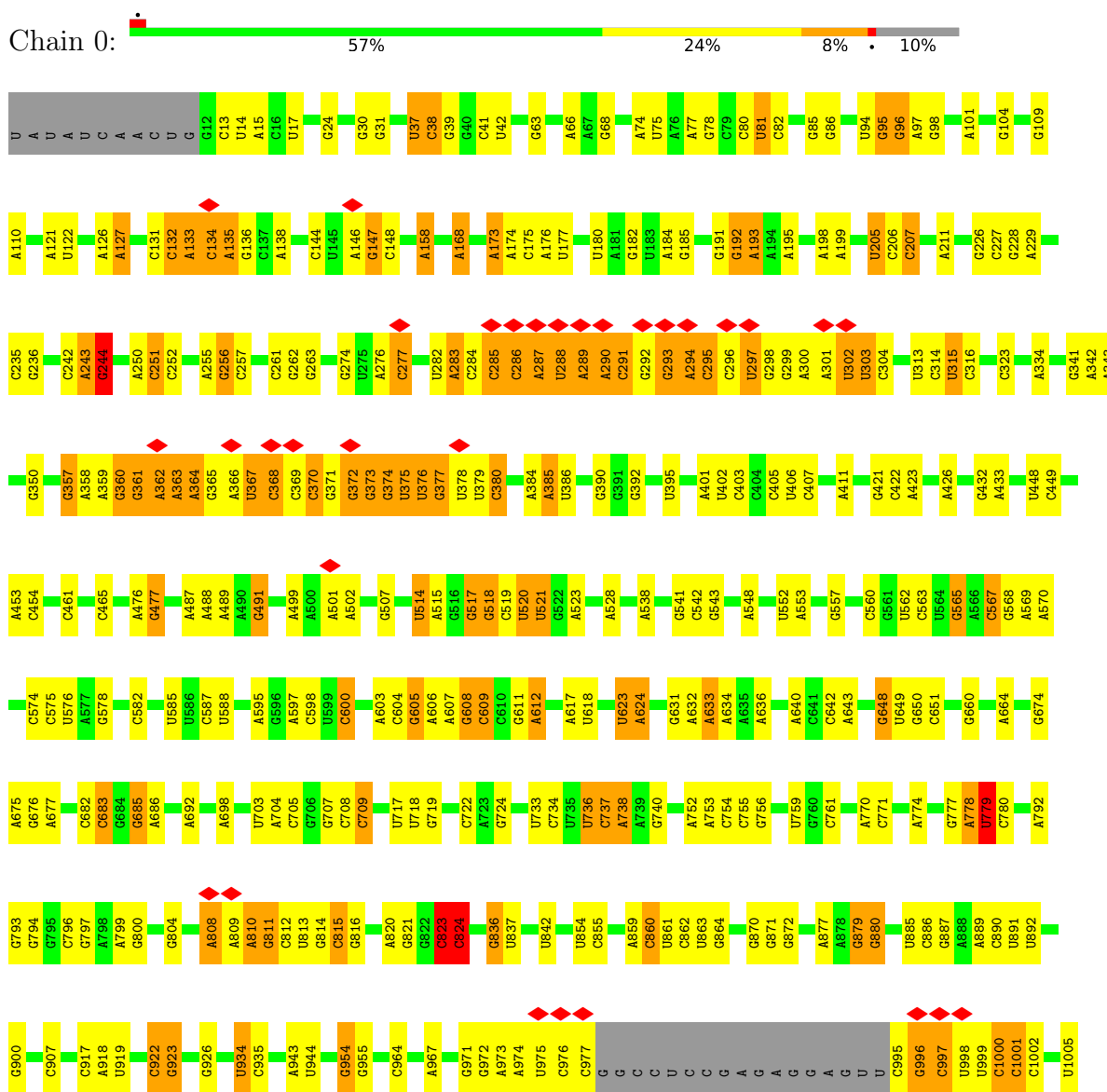
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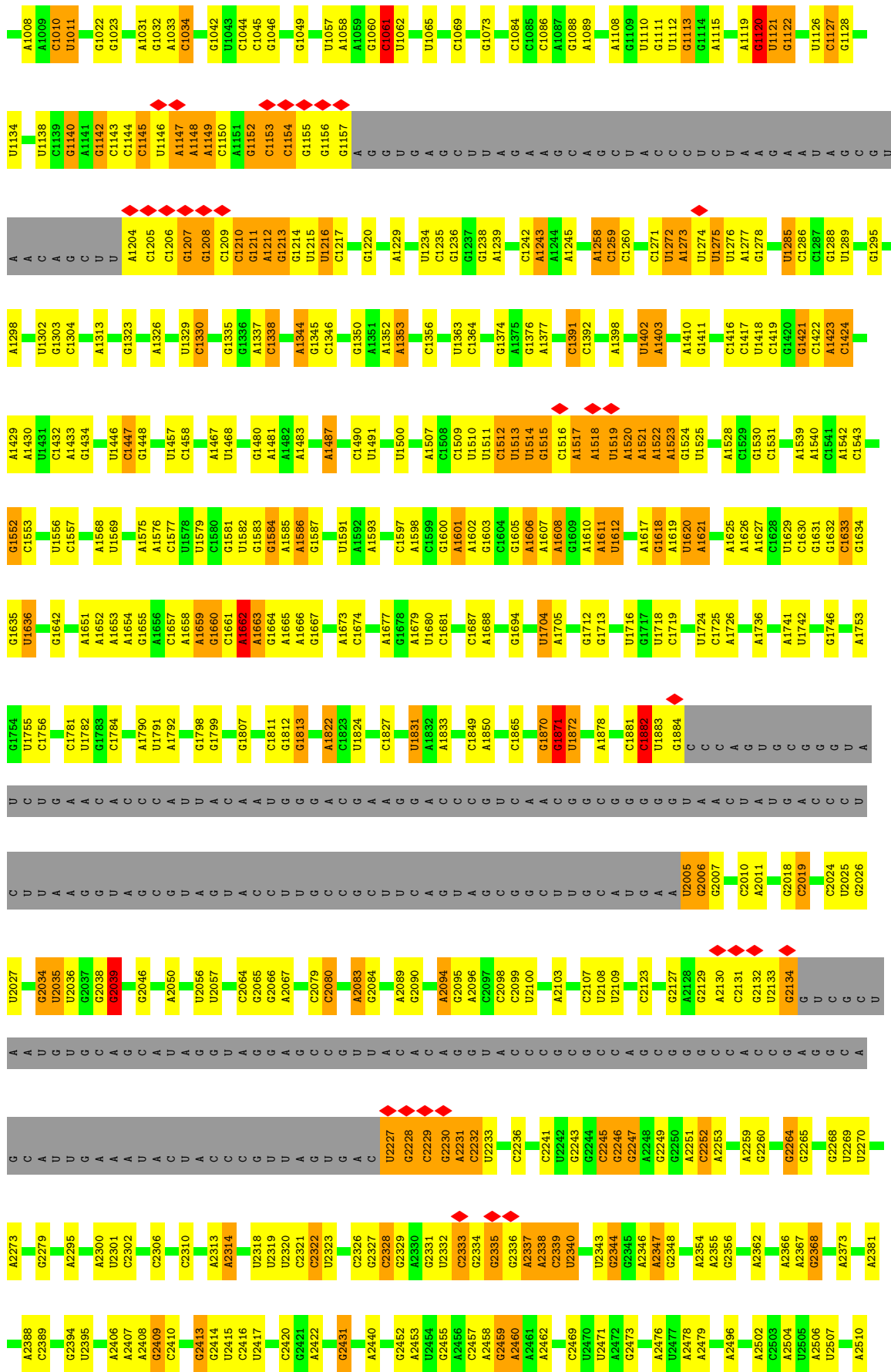
Mol	Chain	Residues	Atoms		AltConf
36	c	14	Total 14	O 14	0
36	f	33	Total 33	O 33	0
36	e	1	Total 1	O 1	0
36	A	17	Total 17	O 17	0

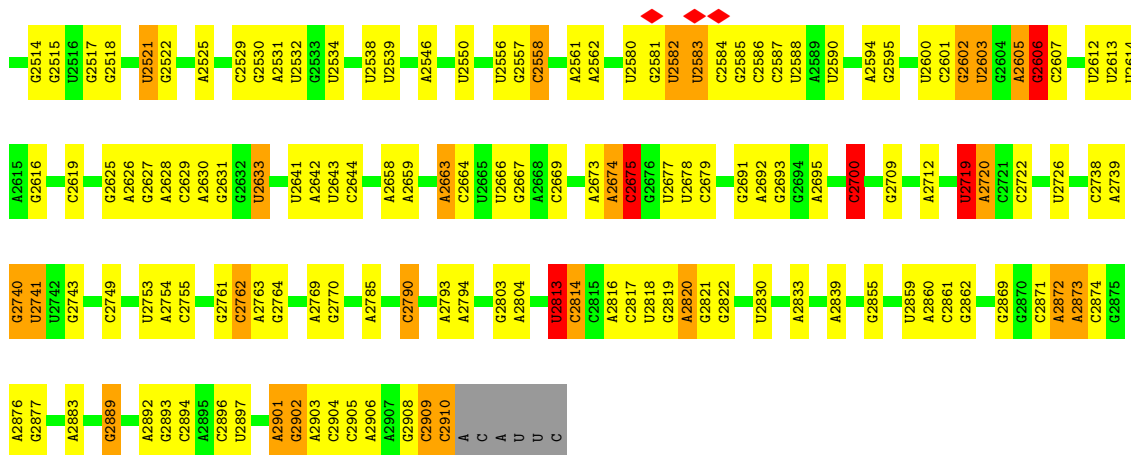
3 Residue-property plots

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 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.

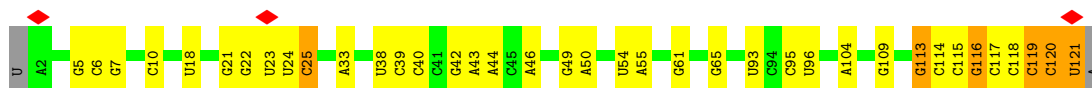
• Molecule 1: 23S RNA



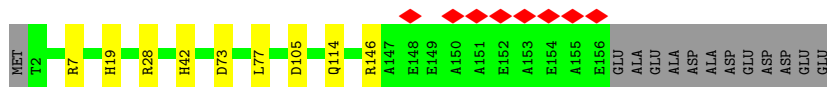
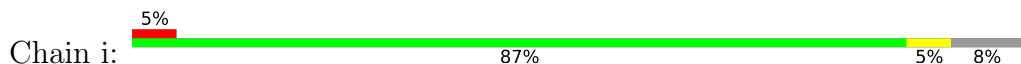




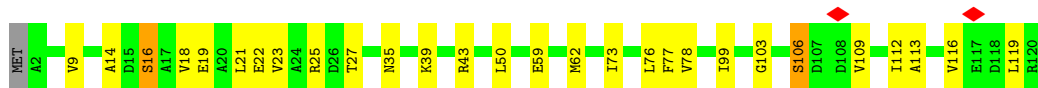
• Molecule 2: 5S RNA



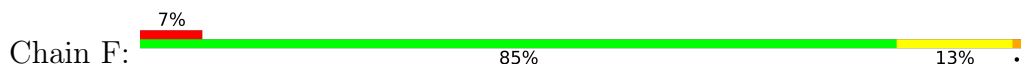
• Molecule 3: Large ribosomal subunit protein uL15



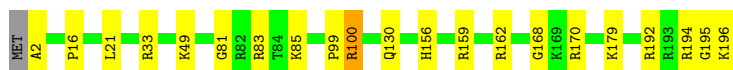
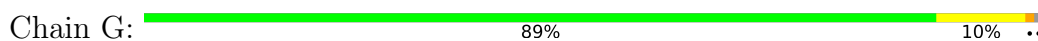
• Molecule 4: Large ribosomal subunit protein eL8



• Molecule 5: Large ribosomal subunit protein uL16



• Molecule 6: Large ribosomal subunit protein eL15




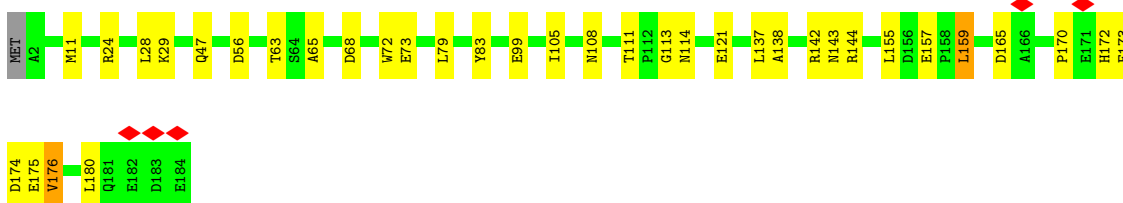
- Molecule 7: Large ribosomal subunit protein eL18

Chain H:  96%




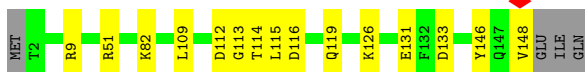
- Molecule 8: Large ribosomal subunit protein uL18

Chain I:  80% 18%




- Molecule 9: Large ribosomal subunit protein eL19

Chain J:  87% 10%




- Molecule 10: Large ribosomal subunit protein eL21

Chain K:  86% 12%




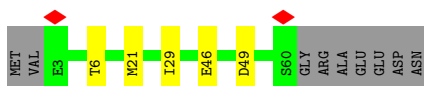
- Molecule 11: Large ribosomal subunit protein uL22

Chain L:  89% 8%




- Molecule 12: Large ribosomal subunit protein eL24

Chain M:  79% 7% 13%



- Molecule 13: Large ribosomal subunit protein uL24

Chain N:  84% 12% ..




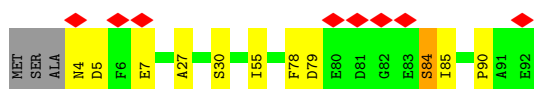
- Molecule 14: Large ribosomal subunit protein uL30

Chain O:  95% ..



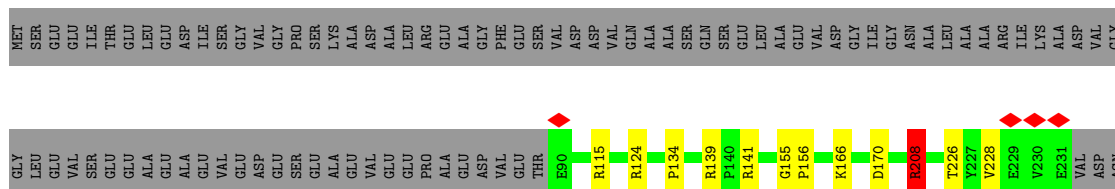
- Molecule 15: Large ribosomal subunit protein eL31

Chain P:  9% 85% 11% ..




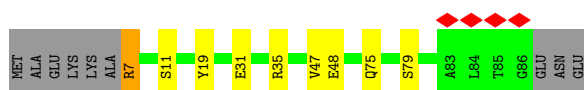
- Molecule 16: Large ribosomal subunit protein eL32

Chain Q:  56% 5% 39% ..



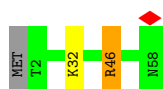
- Molecule 17: Large ribosomal subunit protein eL43

Chain R:  80% 9% 10% ..




- Molecule 18: Large ribosomal subunit protein eL37

Chain S:  95% ...

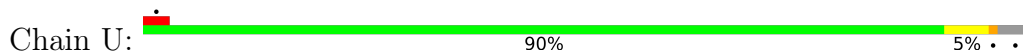


- Molecule 19: Large ribosomal subunit protein eL42

Chain T:  89% 11% ..



- Molecule 20: Large ribosomal subunit protein uL2



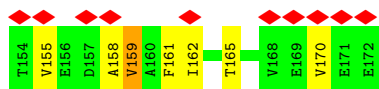
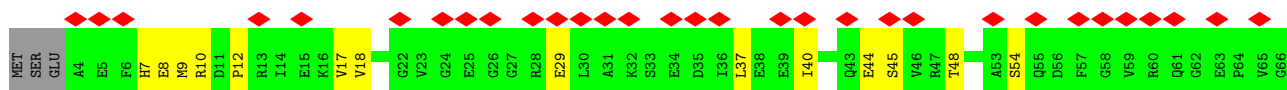
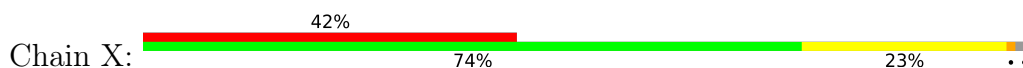
- Molecule 21: Large ribosomal subunit protein uL3



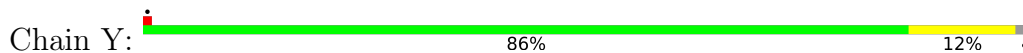
- Molecule 22: Large ribosomal subunit protein uL4




- Molecule 23: Large ribosomal subunit protein uL5



- Molecule 24: Large ribosomal subunit protein uL6




- Molecule 25: Large ribosomal subunit protein uL13

Chain b:  90% 8% ...




- Molecule 26: Large ribosomal subunit protein eL40

Chain j:  83% 6% 10%




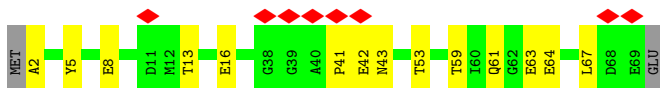
- Molecule 27: Large ribosomal subunit protein uL23

Chain c:  81% 17% ..




- Molecule 28: Large ribosomal subunit protein uL29

Chain d:  11% 77% 20% .



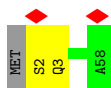
- Molecule 29: Large ribosomal subunit protein uL14

Chain f:  88% 11% .




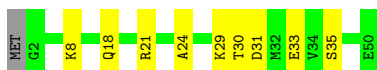
- Molecule 30: Large ribosomal subunit protein eL20

Chain e:  95% . .



- Molecule 31: Large ribosomal subunit protein eL39

Chain A:  80% 18% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	918876	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	5.535	Depositor
Minimum map value	-2.481	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.135	Depositor
Recommended contour level	0.33	Depositor
Map size (Å)	427.52, 427.52, 427.52	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.668, 0.668, 0.668	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: UR3, BGC, PSU, 1MA, ZN, SPD, 6MZ, MG

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	0.61	1/62820 (0.0%)	1.03	119/97974 (0.1%)
2	1	0.22	0/2848	0.44	2/4436 (0.0%)
3	i	0.23	0/1199	0.43	0/1607
4	E	0.20	0/889	0.41	0/1209
5	F	0.18	0/1395	0.42	0/1875
6	G	0.21	0/1626	0.38	0/2170
7	H	0.15	0/895	0.37	0/1210
8	I	0.15	0/1443	0.34	0/1964
9	J	0.17	0/1191	0.38	0/1587
10	K	0.16	0/758	0.41	0/1011
11	L	0.17	0/1199	0.39	0/1619
12	M	0.12	0/474	0.32	0/634
13	N	0.35	2/920 (0.2%)	0.53	4/1244 (0.3%)
14	O	0.18	0/1218	0.39	0/1651
15	P	0.19	0/734	0.43	0/989
16	Q	0.36	2/1162 (0.2%)	0.52	2/1558 (0.1%)
17	R	0.17	0/635	0.36	0/849
18	S	0.59	2/457 (0.4%)	0.58	0/600
19	T	0.13	0/764	0.29	0/1015
20	U	0.16	0/1755	0.40	0/2365
21	V	0.14	0/2673	0.35	0/3612
22	W	0.16	0/1925	0.37	0/2598
23	X	0.15	0/1203	0.42	0/1637
24	Y	0.14	0/1364	0.35	0/1855
25	b	0.26	0/1144	0.51	4/1541 (0.3%)
26	j	0.13	0/353	0.34	0/463
27	c	0.17	0/650	0.35	0/872
28	d	0.15	0/518	0.43	0/699
29	f	0.37	2/1015 (0.2%)	0.56	4/1361 (0.3%)
30	e	0.12	0/441	0.31	0/594
31	A	0.20	0/419	0.38	0/553
All	All	0.51	9/96087 (0.0%)	0.88	135/143352 (0.1%)

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
5	F	0	1
6	G	0	1
7	H	0	1
9	J	0	1
11	L	0	1
13	N	0	1
16	Q	0	2
17	R	0	1
18	S	0	2
20	U	0	1
29	f	0	2
All	All	0	14

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	S	46[A]	ARG	C-O	6.24	1.31	1.23
18	S	46[B]	ARG	C-O	6.24	1.31	1.23
29	f	77[A]	ARG	C-O	6.15	1.31	1.24
29	f	77[B]	ARG	C-O	6.15	1.31	1.24
13	N	23[A]	GLN	C-O	5.58	1.32	1.24

The worst 5 of 135 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	1326	A	O3'-P-O5'	9.97	118.95	104.00
1	0	1824	U	O3'-P-O5'	9.49	118.23	104.00
1	0	520	U	O3'-P-O5'	9.43	118.14	104.00
1	0	1831	U	O3'-P-O5'	9.29	117.93	104.00
1	0	476	A	O3'-P-O5'	9.00	117.50	104.00

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	F	20	ARG	Sidechain
6	G	100[A]	ARG	Sidechain
7	H	116	ARG	Sidechain

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Mol	Chain	Res	Type	Group
9	J	51	ARG	Sidechain
11	L	133	ARG	Sidechain

5.2 Too-close contacts [i](#)

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	56268	0	28385	574	0
2	1	2551	0	1298	20	0
3	i	1184	0	1131	5	0
4	E	880	0	852	16	0
5	F	1372	0	1371	16	0
6	G	1599	0	1631	22	0
7	H	887	0	907	4	0
8	I	1413	0	1361	25	0
9	J	1179	0	1183	8	0
10	K	744	0	753	7	0
11	L	1174	0	1146	12	0
12	M	466	0	443	2	0
13	N	909	0	894	6	0
14	O	1200	0	1159	4	0
15	P	719	0	697	6	0
16	Q	1140	0	1140	9	0
17	R	625	0	631	4	0
18	S	447	0	458	0	0
19	T	746	0	736	7	0
20	U	1721	0	1741	7	0
21	V	2615	0	2568	11	0
22	W	1898	0	1895	18	0
23	X	1186	0	1070	27	0
24	Y	1342	0	1281	11	0
25	b	1127	0	1118	5	0
26	j	350	0	381	1	0
27	c	645	0	645	8	0
28	d	515	0	515	6	0
29	f	1004	0	1059	9	0
30	e	435	0	426	1	0
31	A	414	0	442	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	0	24	12	24	9	0
33	0	40	76	76	29	0
34	0	292	0	0	1	0
34	1	5	0	0	0	0
34	F	1	0	0	0	0
34	G	4	0	0	0	0
34	K	1	0	0	0	0
34	N	1	0	0	0	0
34	O	2	0	0	0	0
34	P	1	0	0	0	0
34	Q	1	0	0	0	0
34	S	1	0	0	0	0
34	T	1	0	0	0	0
34	U	2	0	0	0	0
34	V	3	0	0	0	0
34	W	1	0	0	0	0
34	f	1	0	0	0	0
35	S	1	0	0	0	0
35	T	1	0	0	0	0
36	0	5625	0	0	26	0
36	1	85	0	0	1	0
36	A	17	0	0	1	0
36	E	3	0	0	0	0
36	F	45	0	0	2	0
36	G	101	0	0	3	0
36	H	15	0	0	0	0
36	I	8	0	0	0	0
36	J	44	0	0	1	0
36	K	41	0	0	0	0
36	L	47	0	0	1	0
36	M	9	0	0	0	0
36	N	21	0	0	0	0
36	O	57	0	0	0	0
36	P	23	0	0	0	0
36	Q	66	0	0	2	0
36	R	18	0	0	1	0
36	S	33	0	0	0	0
36	T	35	0	0	2	0
36	U	67	0	0	0	0
36	V	118	0	0	0	0
36	W	89	0	0	0	0
36	Y	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	b	44	0	0	0	0
36	c	14	0	0	1	0
36	e	1	0	0	0	0
36	f	33	0	0	1	0
36	i	45	0	0	2	0
36	j	8	0	0	0	0
All	All	95865	88	59417	821	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 6.

The worst 5 of 821 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)
1:0:736:U:H1'	1:0:737:C:H5'	1.27	1.11
1:0:1353:A:H5'	36:0:6031:HOH:O	1.47	1.10
1:0:390:G:H21	33:0:3006:SPD:H32	1.13	1.09
1:0:290:A:H3'	1:0:291:C:H5''	1.37	1.03
19:T:42:ARG:NH1	36:T:201:HOH:O	1.92	1.02

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	i	154/168 (92%)	149 (97%)	5 (3%)	0	100	100
4	E	117/120 (98%)	116 (99%)	1 (1%)	0	100	100
5	F	172/176 (98%)	163 (95%)	8 (5%)	1 (1%)	21	13
6	G	194/196 (99%)	190 (98%)	4 (2%)	0	100	100
7	H	113/116 (97%)	112 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	I	181/184 (98%)	177 (98%)	4 (2%)	0	100	100
9	J	145/151 (96%)	142 (98%)	3 (2%)	0	100	100
10	K	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
11	L	149/153 (97%)	146 (98%)	3 (2%)	0	100	100
12	M	56/67 (84%)	54 (96%)	2 (4%)	0	100	100
13	N	113/118 (96%)	104 (92%)	9 (8%)	0	100	100
14	O	152/154 (99%)	150 (99%)	2 (1%)	0	100	100
15	P	87/92 (95%)	85 (98%)	2 (2%)	0	100	100
16	Q	141/234 (60%)	141 (100%)	0	0	100	100
17	R	79/89 (89%)	75 (95%)	4 (5%)	0	100	100
18	S	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
19	T	91/93 (98%)	91 (100%)	0	0	100	100
20	U	230/241 (95%)	220 (96%)	8 (4%)	2 (1%)	14	7
21	V	335/338 (99%)	331 (99%)	4 (1%)	0	100	100
22	W	246/248 (99%)	240 (98%)	6 (2%)	0	100	100
23	X	167/172 (97%)	156 (93%)	10 (6%)	1 (1%)	21	13
24	Y	172/178 (97%)	167 (97%)	5 (3%)	0	100	100
25	b	142/145 (98%)	141 (99%)	0	1 (1%)	18	10
26	j	41/48 (85%)	40 (98%)	1 (2%)	0	100	100
27	c	80/83 (96%)	78 (98%)	2 (2%)	0	100	100
28	d	66/70 (94%)	61 (92%)	4 (6%)	1 (2%)	8	2
29	f	131/132 (99%)	127 (97%)	4 (3%)	0	100	100
30	e	55/58 (95%)	55 (100%)	0	0	100	100
31	A	47/50 (94%)	44 (94%)	2 (4%)	1 (2%)	5	1
All	All	3806/4028 (94%)	3702 (97%)	97 (2%)	7 (0%)	44	38

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	F	103	ALA
25	b	4	ALA
28	d	42	GLU
20	U	208	HIS
31	A	31	ASP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	i	114/123 (93%)	112 (98%)	2 (2%)	51	51
4	E	93/94 (99%)	90 (97%)	3 (3%)	34	29
5	F	145/147 (99%)	144 (99%)	1 (1%)	76	79
6	G	163/163 (100%)	162 (99%)	1 (1%)	78	82
7	H	98/99 (99%)	96 (98%)	2 (2%)	48	47
8	I	143/145 (99%)	137 (96%)	6 (4%)	26	20
9	J	117/121 (97%)	116 (99%)	1 (1%)	70	74
10	K	78/78 (100%)	77 (99%)	1 (1%)	61	62
11	L	122/124 (98%)	120 (98%)	2 (2%)	55	55
12	M	48/55 (87%)	47 (98%)	1 (2%)	47	45
13	N	99/102 (97%)	95 (96%)	4 (4%)	28	22
14	O	132/132 (100%)	131 (99%)	1 (1%)	73	77
15	P	76/80 (95%)	75 (99%)	1 (1%)	61	62
16	Q	118/191 (62%)	116 (98%)	2 (2%)	53	53
17	R	62/68 (91%)	59 (95%)	3 (5%)	23	16
18	S	49/49 (100%)	48 (98%)	1 (2%)	48	47
19	T	77/77 (100%)	77 (100%)	0	100	100
20	U	175/186 (94%)	172 (98%)	3 (2%)	53	53
21	V	276/278 (99%)	275 (100%)	1 (0%)	84	87
22	W	198/198 (100%)	192 (97%)	6 (3%)	36	32
23	X	112/147 (76%)	109 (97%)	3 (3%)	39	35
24	Y	148/151 (98%)	147 (99%)	1 (1%)	76	79
25	b	122/123 (99%)	119 (98%)	3 (2%)	42	38
26	j	37/40 (92%)	36 (97%)	1 (3%)	39	35
27	c	74/76 (97%)	70 (95%)	4 (5%)	20	12
28	d	53/56 (95%)	51 (96%)	2 (4%)	29	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	f	107/106 (101%)	107 (100%)	0	100	100
30	e	48/49 (98%)	48 (100%)	0	100	100
31	A	45/46 (98%)	44 (98%)	1 (2%)	45	43
All	All	3129/3304 (95%)	3072 (98%)	57 (2%)	51	51

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	R	7	ARG
28	d	64	GLU
21	V	294	SER
28	d	53	THR
26	j	46	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
19	T	13	ASN
21	V	337	GLN
21	V	231	GLN
22	W	9	ASN
11	L	95	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2621/2916 (89%)	524 (19%)	92 (3%)
2	1	119/122 (97%)	19 (15%)	1 (0%)
All	All	2740/3038 (90%)	543 (19%)	93 (3%)

5 of 543 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	13	C
1	0	14	U
1	0	15	A
1	0	17	U
1	0	24	G

5 of 93 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	0	1523	A
1	0	2089	A
1	0	1584	G
1	0	1807	G
1	0	2246	G

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

8 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
1	1MA	0	632	1	21,25,26	0.43	0	31,37,40	0.66	0
1	UR3	0	2612	1	19,22,23	0.32	0	26,32,35	0.67	0
1	PSU	0	37	1	18,21,22	1.49	3 (16%)	22,30,33	2.16	6 (27%)
1	PSU	0	2600	1	18,21,22	1.71	6 (33%)	22,30,33	2.56	9 (40%)
1	UR3	0	75	1	19,22,23	0.30	0	26,32,35	0.73	0
1	PSU	0	934	1	18,21,22	1.51	3 (16%)	22,30,33	2.06	5 (22%)
1	PSU	0	2726	1	18,21,22	1.75	3 (16%)	22,30,33	2.16	5 (22%)
1	6MZ	0	698	1	22,25,26	1.42	4 (18%)	30,36,39	2.40	13 (43%)

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
1	1MA	0	632	1	-	0/7/25/26	0/3/3/3
1	UR3	0	2612	1	-	0/7/25/26	0/2/2/2
1	PSU	0	37	1	-	1/7/25/26	0/2/2/2
1	PSU	0	2600	1	-	1/7/25/26	0/2/2/2
1	UR3	0	75	1	-	0/7/25/26	0/2/2/2
1	PSU	0	934	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	0	2726	1	-	0/7/25/26	0/2/2/2
1	6MZ	0	698	1	-	0/9/27/28	0/3/3/3

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	0	2726	PSU	C4-N3	-4.44	1.30	1.38
1	0	698	6MZ	C5-C4	3.96	1.46	1.39
1	0	2600	PSU	C4-N3	-3.82	1.31	1.38
1	0	934	PSU	C4-N3	-3.70	1.32	1.38
1	0	37	PSU	C4-N3	-3.39	1.32	1.38

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	2600	PSU	N1-C2-N3	6.82	122.86	115.13
1	0	934	PSU	N1-C2-N3	6.77	122.80	115.13
1	0	2726	PSU	N1-C2-N3	6.55	122.56	115.13
1	0	37	PSU	N1-C2-N3	6.49	122.48	115.13
1	0	698	6MZ	C5-C4-N3	-5.85	119.12	126.75

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	0	2600	PSU	O4'-C1'-C5-C4
1	0	37	PSU	O4'-C1'-C5-C6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	0	2612	UR3	1	0
1	0	934	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 325 ligands modelled in this entry, 319 are monoatomic - leaving 6 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
33	SPD	0	3004	-	9,9,9	0.15	0	8,8,8	0.21	0
33	SPD	0	3005	-	9,9,9	0.15	0	8,8,8	0.74	0
33	SPD	0	3006	-	9,9,9	0.16	0	8,8,8	0.16	0
33	SPD	0	3003	34	9,9,9	0.50	0	8,8,8	0.67	0
32	BGC	0	3002	-	12,12,12	0.34	0	17,17,17	0.98	1 (5%)
32	BGC	0	3001	-	12,12,12	0.23	0	17,17,17	0.66	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	SPD	0	3004	-	-	4/7/7/7	-
33	SPD	0	3005	-	-	3/7/7/7	-
33	SPD	0	3006	-	-	4/7/7/7	-
33	SPD	0	3003	34	-	1/7/7/7	-
32	BGC	0	3002	-	-	2/2/22/22	0/1/1/1
32	BGC	0	3001	-	-	2/2/22/22	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	0	3002	BGC	C3-C4-C5	-2.02	106.63	110.24

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

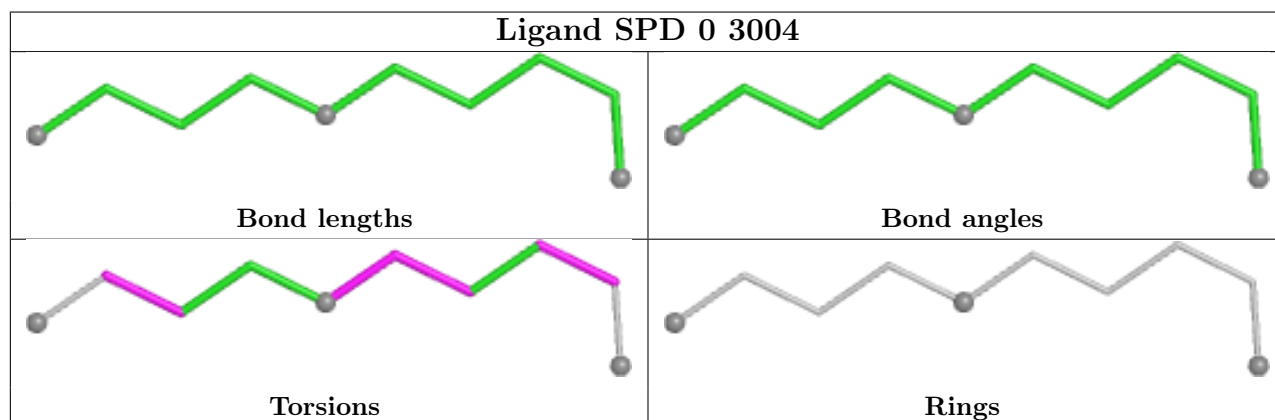
Mol	Chain	Res	Type	Atoms
32	0	3001	BGC	O5-C5-C6-O6
33	0	3004	SPD	C3-C4-C5-N6
32	0	3001	BGC	C4-C5-C6-O6
33	0	3006	SPD	C3-C4-C5-N6
32	0	3002	BGC	O5-C5-C6-O6

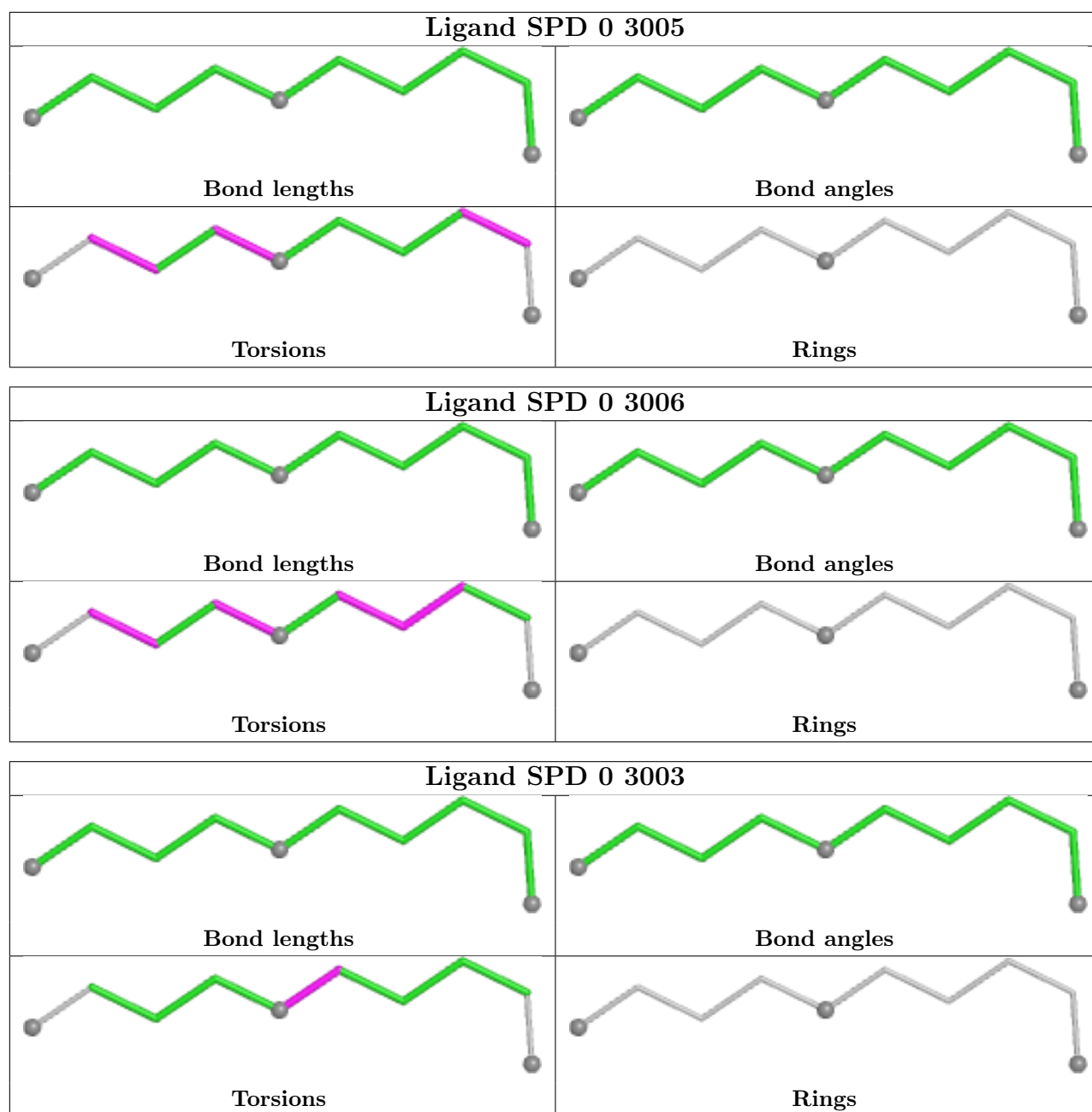
There are no ring outliers.

6 monomers are involved in 38 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	0	3004	SPD	11	0
33	0	3005	SPD	1	0
33	0	3006	SPD	5	0
33	0	3003	SPD	12	0
32	0	3002	BGC	7	0
32	0	3001	BGC	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.

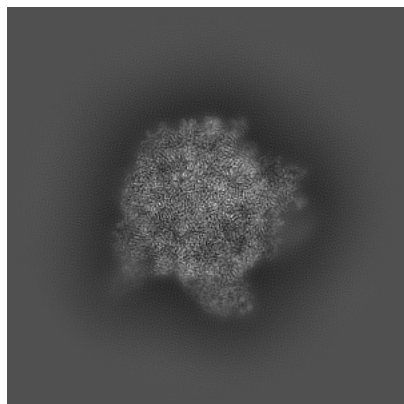
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62893. These allow visual inspection of the internal detail of the map and identification of artifacts.

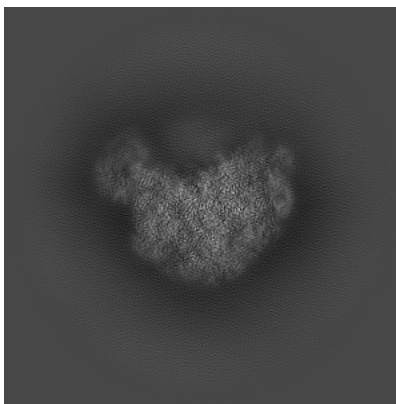
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

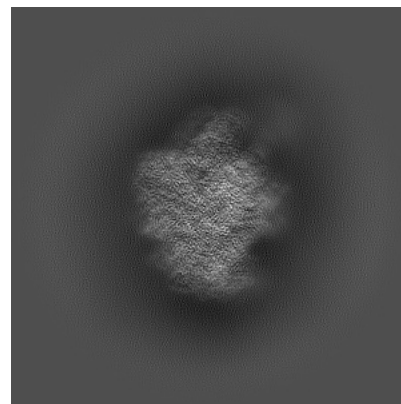
6.1.1 Primary map



X

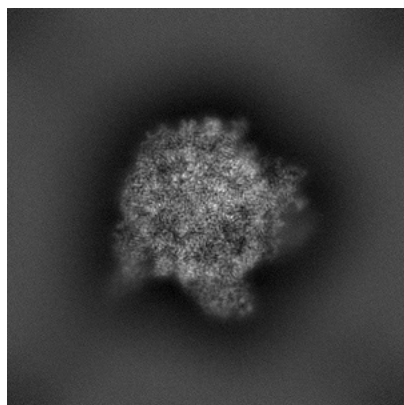


Y

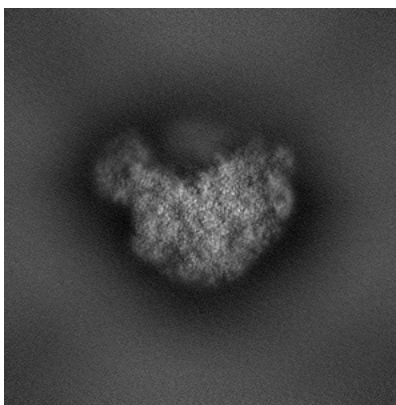


Z

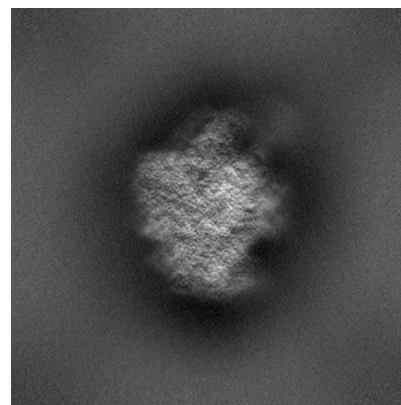
6.1.2 Raw map



X



Y

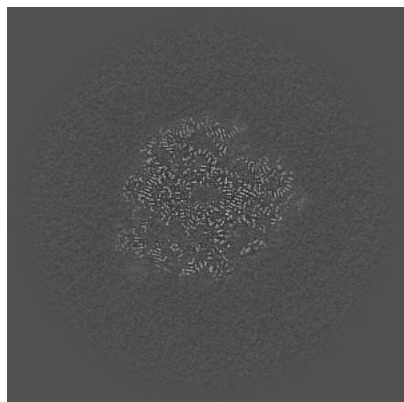


Z

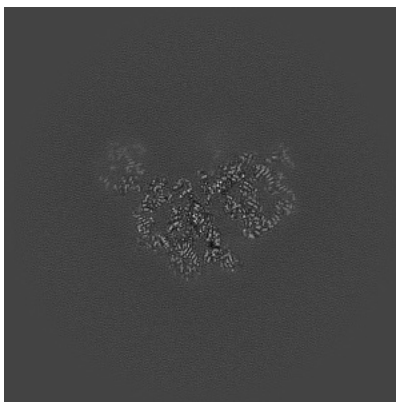
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

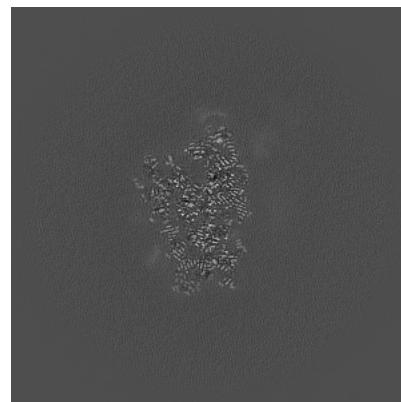
6.2.1 Primary map



X Index: 320

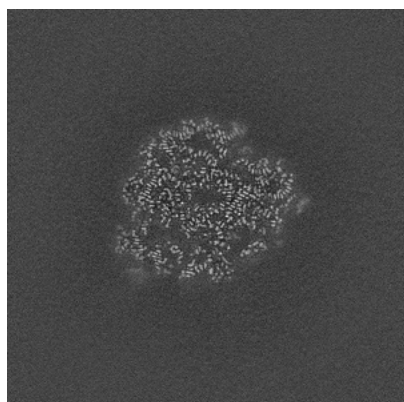


Y Index: 320

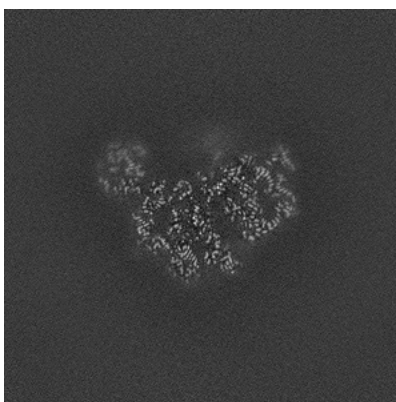


Z Index: 320

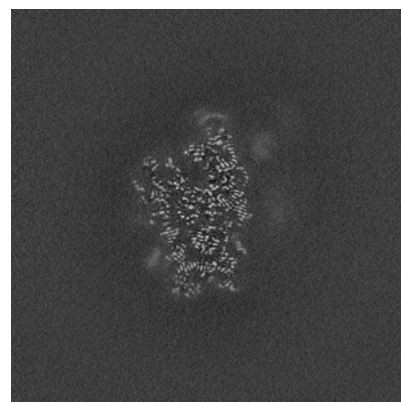
6.2.2 Raw map



X Index: 320



Y Index: 320

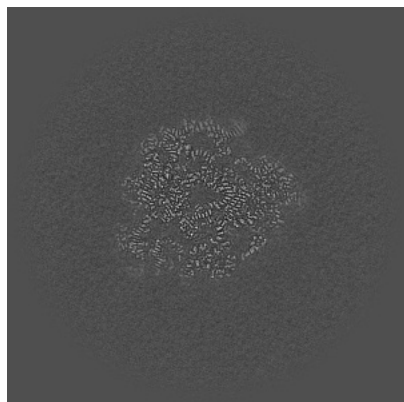


Z Index: 320

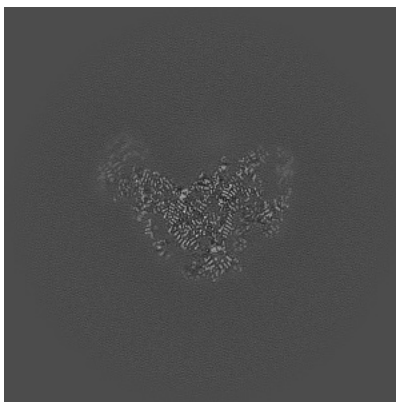
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

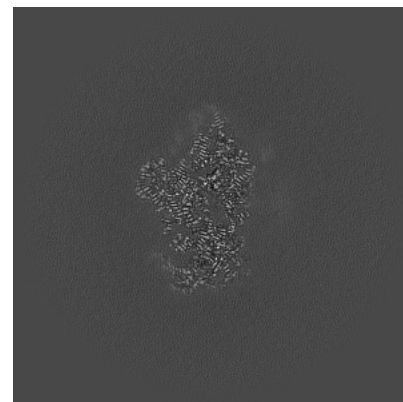
6.3.1 Primary map



X Index: 323

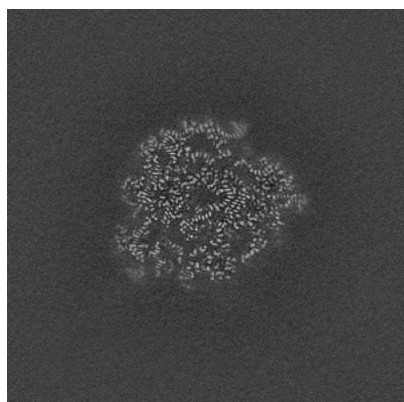


Y Index: 337

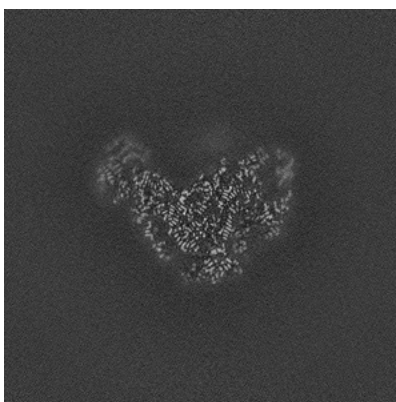


Z Index: 333

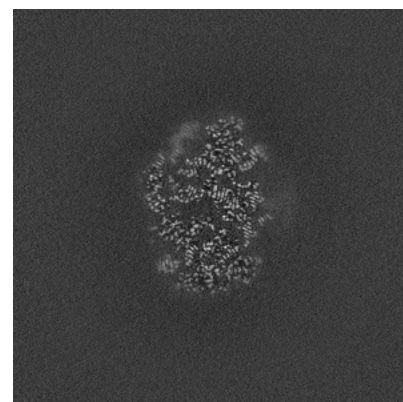
6.3.2 Raw map



X Index: 323



Y Index: 337

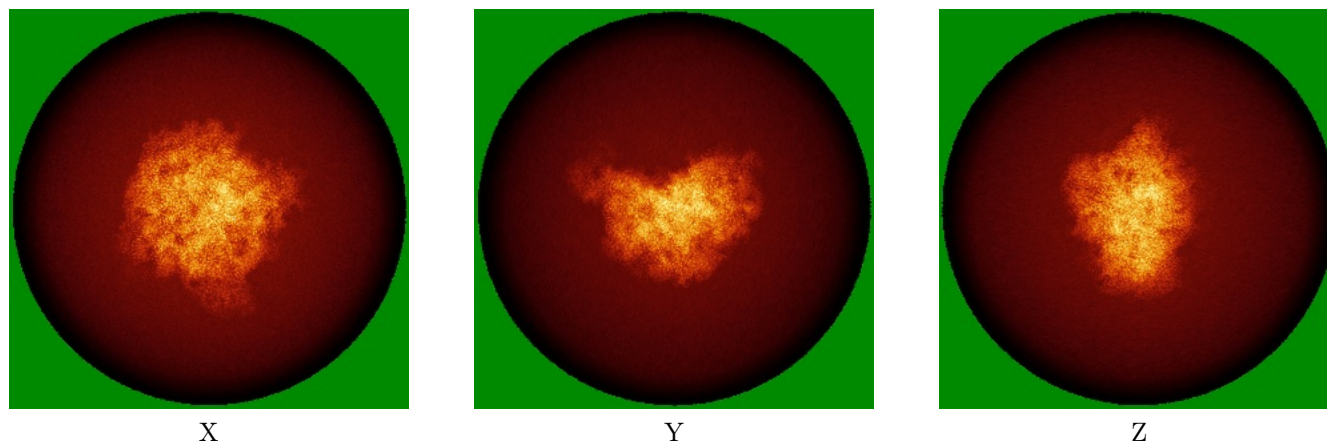


Z Index: 350

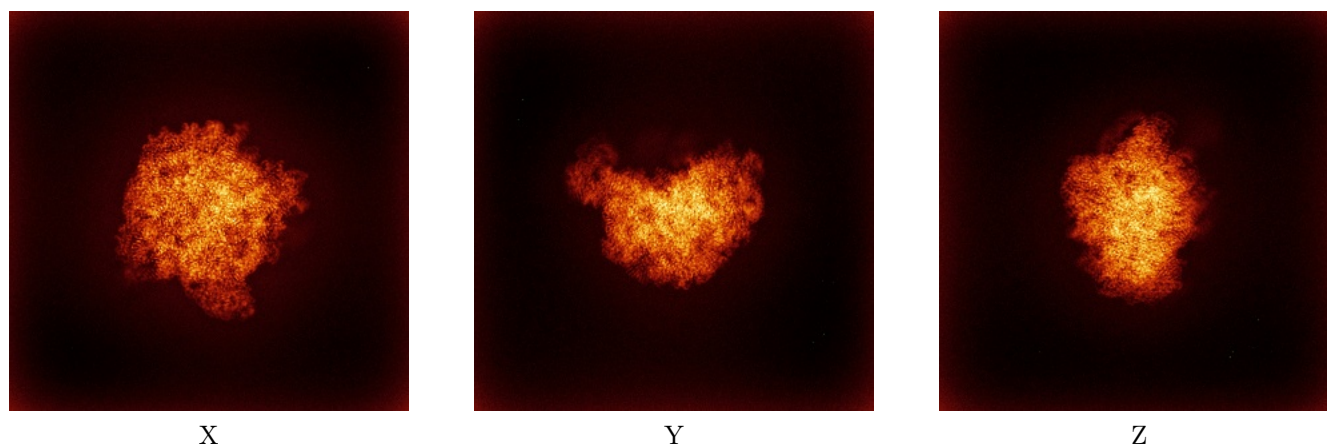
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



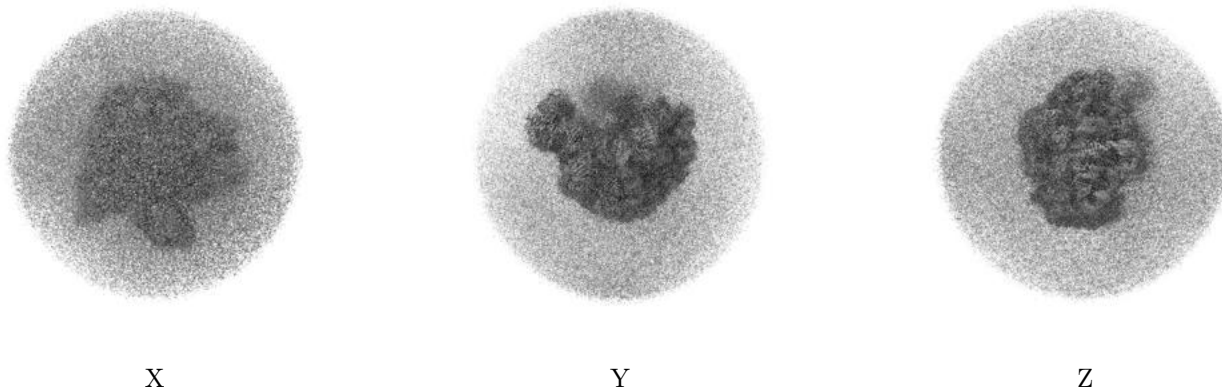
6.4.2 Raw map



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.

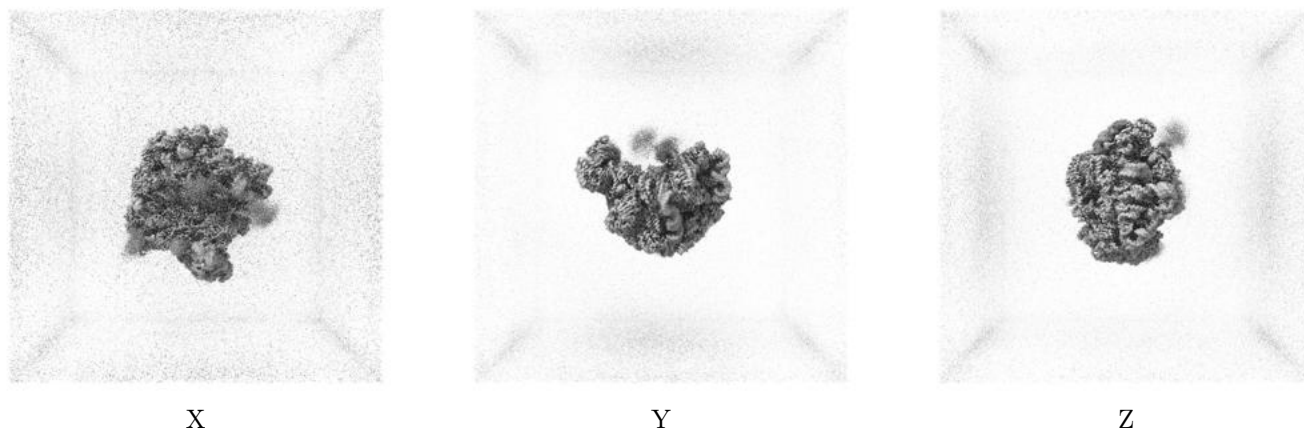
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.33. 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



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.

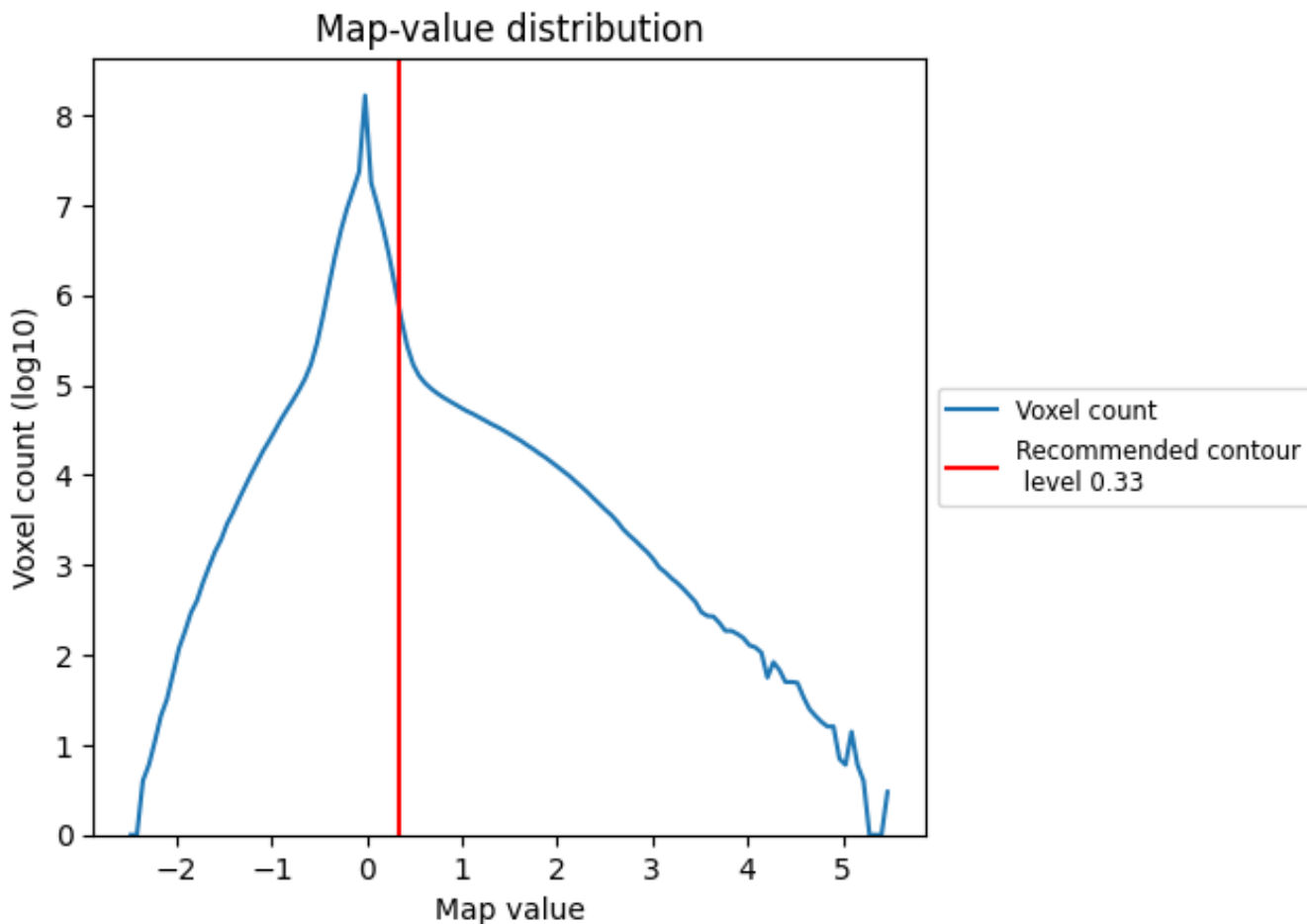
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

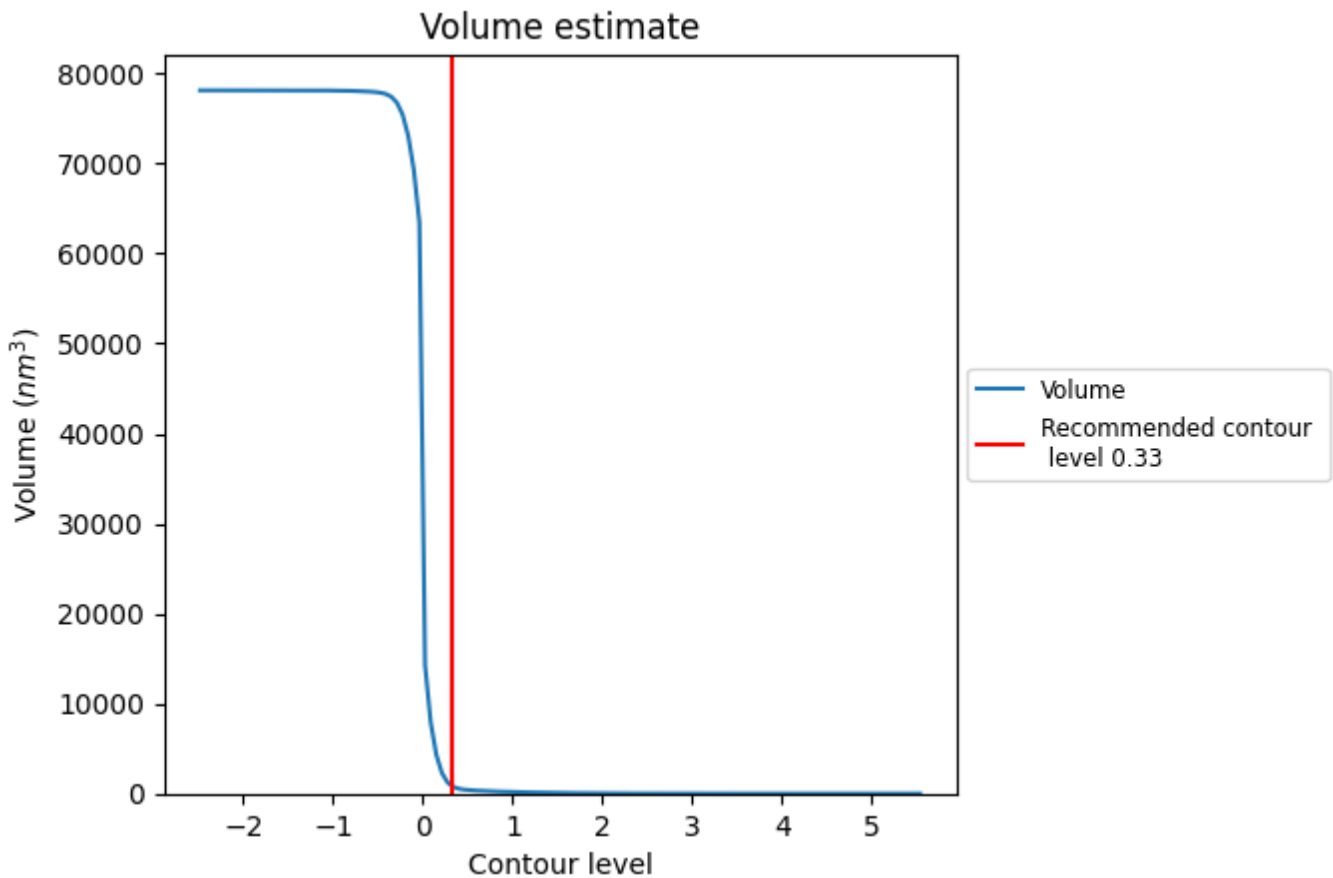
This section contains the results of statistical analysis of the map.

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.

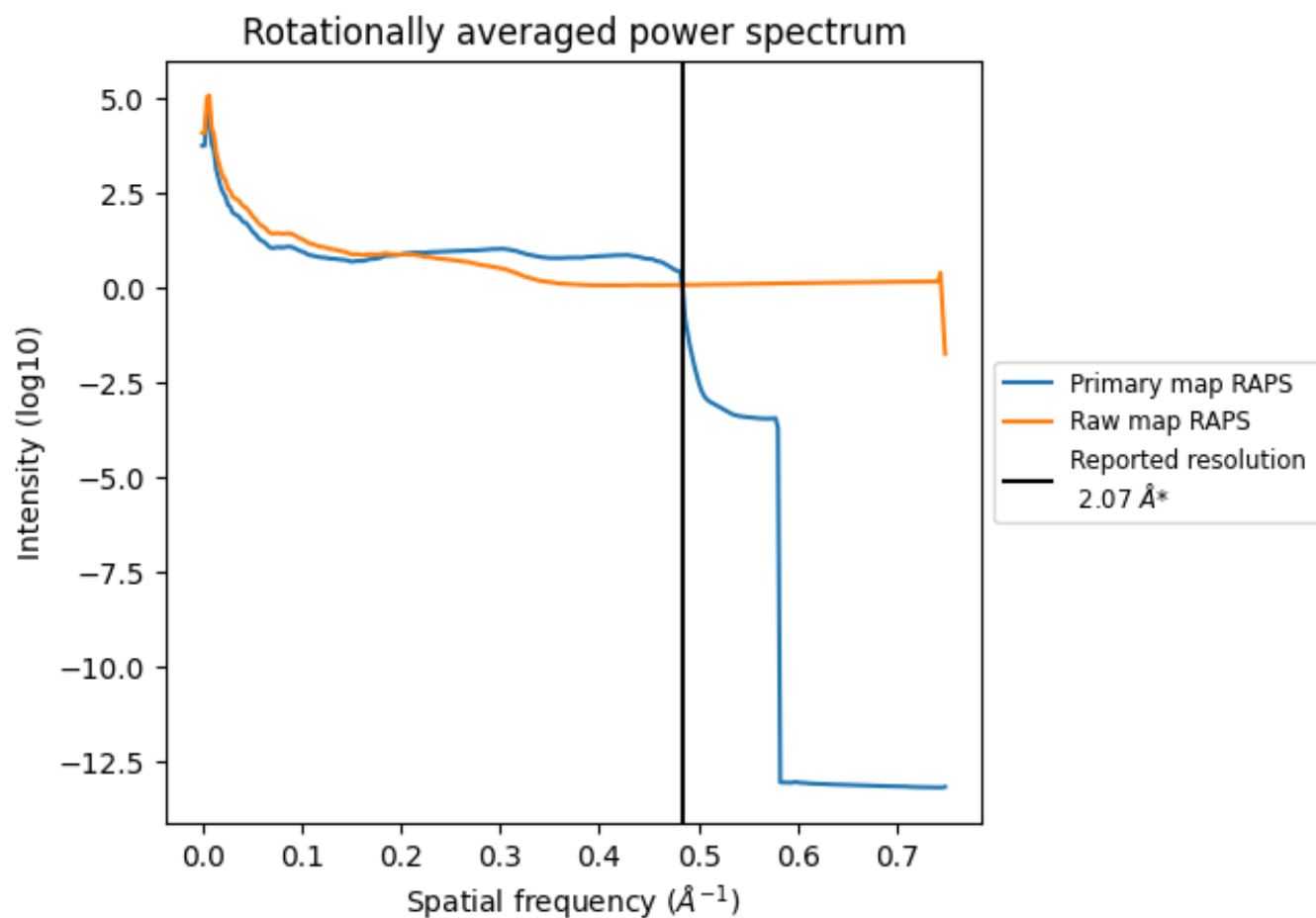
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 804 nm³; this corresponds to an approximate mass of 727 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 [i](#)

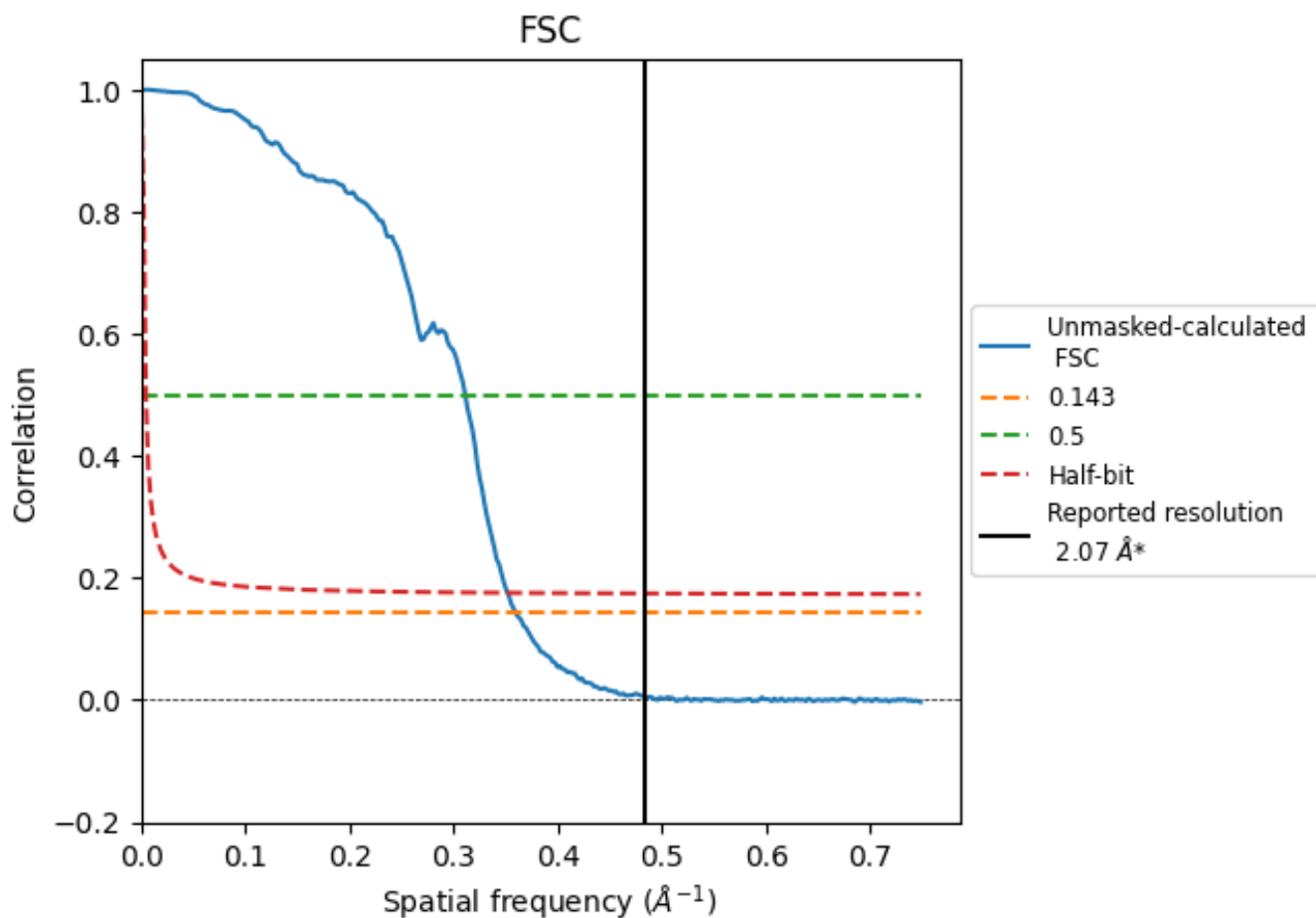


*Reported resolution corresponds to spatial frequency of 0.483 Å⁻¹

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 0.483 \AA^{-1}

8.2 Resolution estimates [i](#)

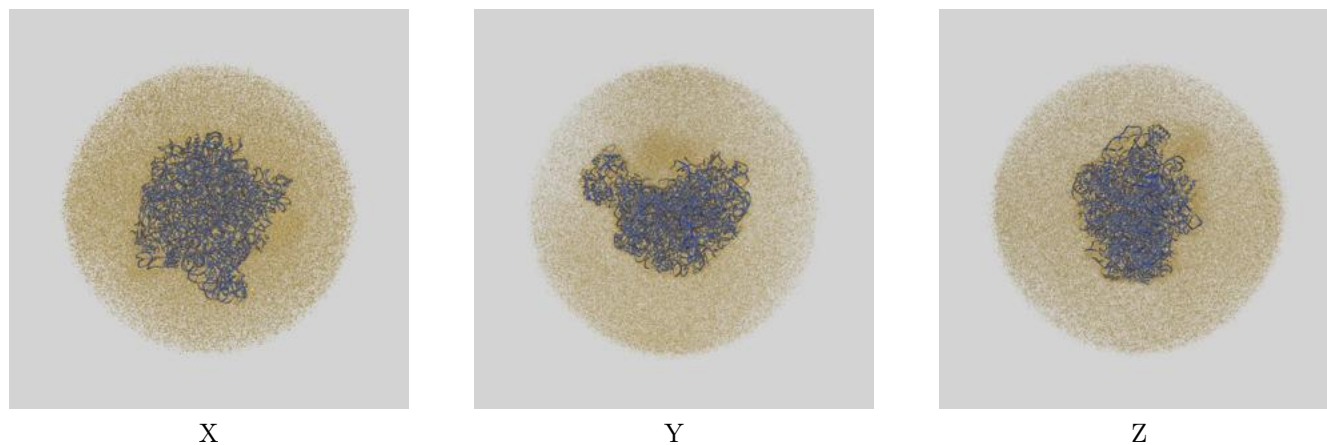
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.07	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.78	3.21	2.84

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.78 differs from the reported value 2.07 by more than 10 %

9 Map-model fit [i](#)

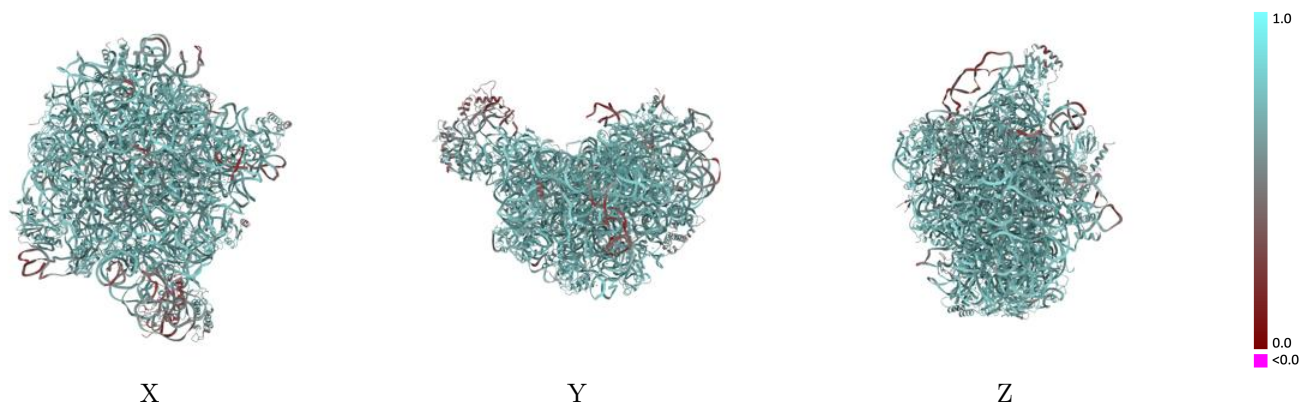
This section contains information regarding the fit between EMDB map EMD-62893 and PDB model 9L94. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



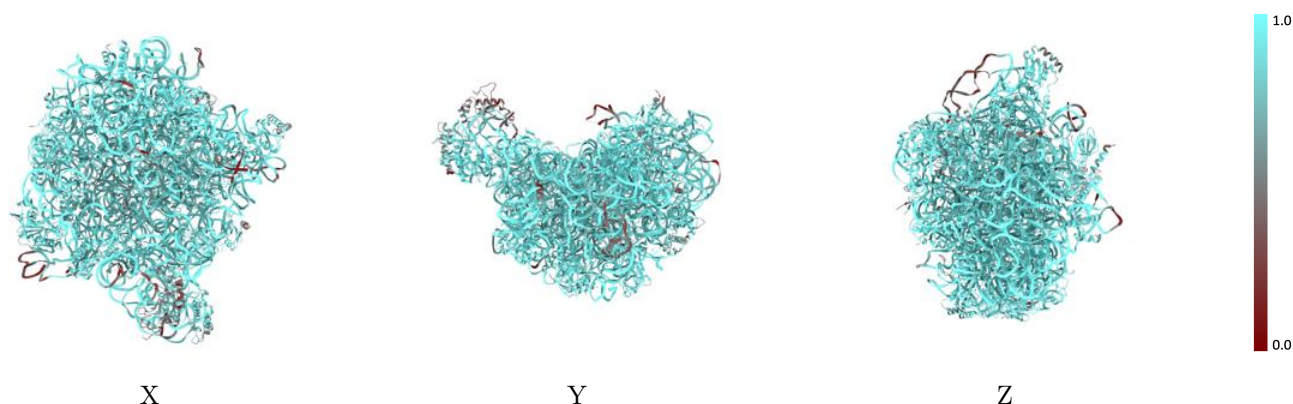
The images above show the 3D surface view of the map at the recommended contour level 0.33 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



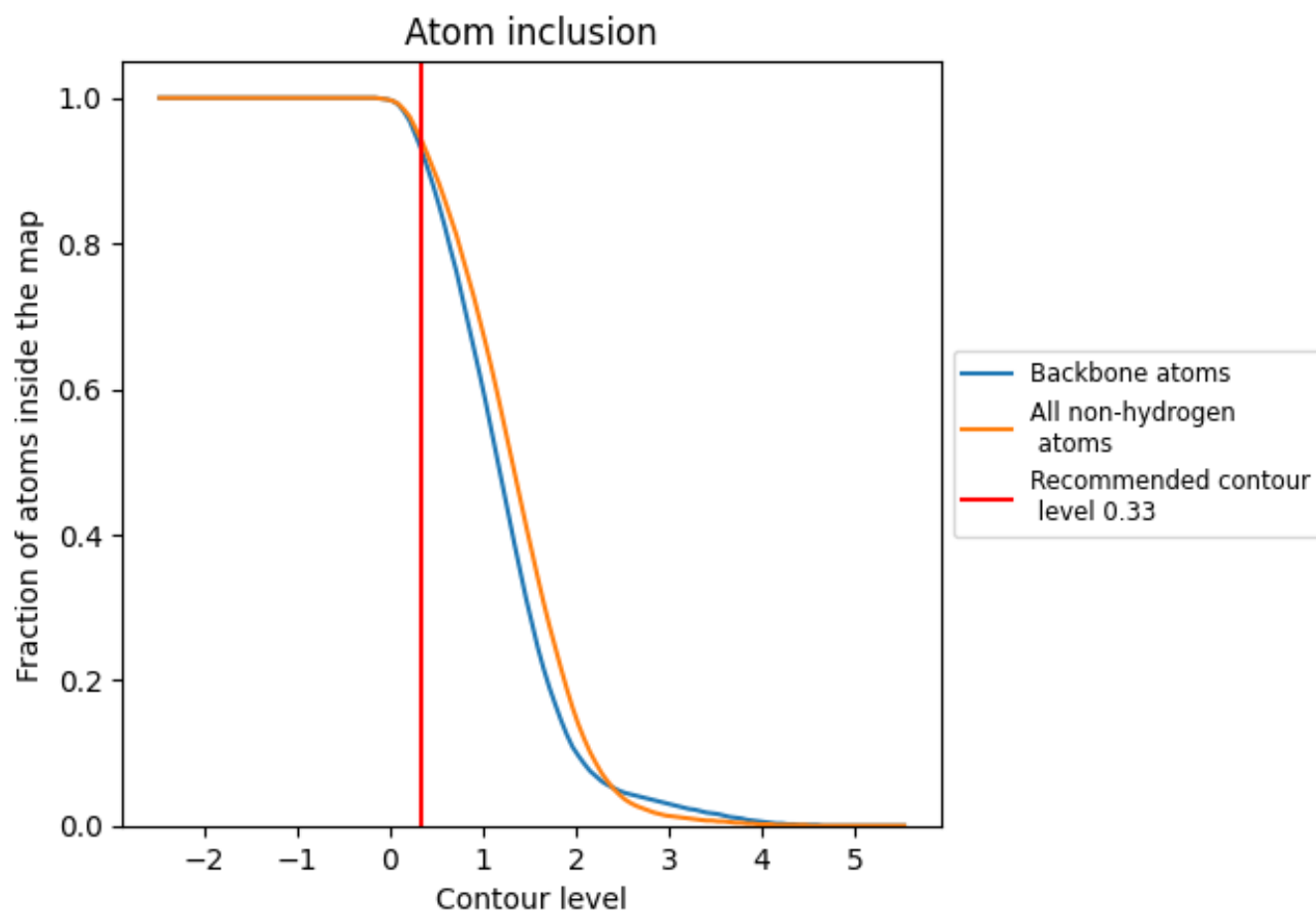
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.33).

































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 94% 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 (0.33) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.7000
0	 0.9620	 0.7080
1	 0.9190	 0.6220
A	 0.9220	 0.7060
E	 0.8610	 0.6330
F	 0.9010	 0.6990
G	 0.9880	 0.7620
H	 0.9570	 0.7150
I	 0.8610	 0.6290
J	 0.9420	 0.7050
K	 0.9710	 0.7440
L	 0.9740	 0.7420
M	 0.9090	 0.6940
N	 0.9550	 0.7110
O	 0.9730	 0.7430
P	 0.8830	 0.6750
Q	 0.9400	 0.7150
R	 0.9120	 0.6950
S	 0.9790	 0.7630
T	 0.9540	 0.7220
U	 0.9380	 0.7110
V	 0.9600	 0.7350
W	 0.9490	 0.7270
X	 0.5190	 0.4080
Y	 0.9060	 0.6700
b	 0.9570	 0.7380
c	 0.8820	 0.6510
d	 0.7350	 0.5440
e	 0.8510	 0.6490
f	 0.9440	 0.7130
i	 0.8830	 0.6740
j	 0.8810	 0.6660

