



wwPDB EM Validation Summary Report ⓘ

May 18, 2025 – 04:14 AM EDT

PDB ID : 9BSS / pdb_00009bss
EMDB ID : EMD-44871
Title : 45SRbgA particle in complex with RbgA and YphC. Class B
Authors : Arpin, D.; Ortega, J.
Deposited on : 2024-05-13
Resolution : 3.10 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:

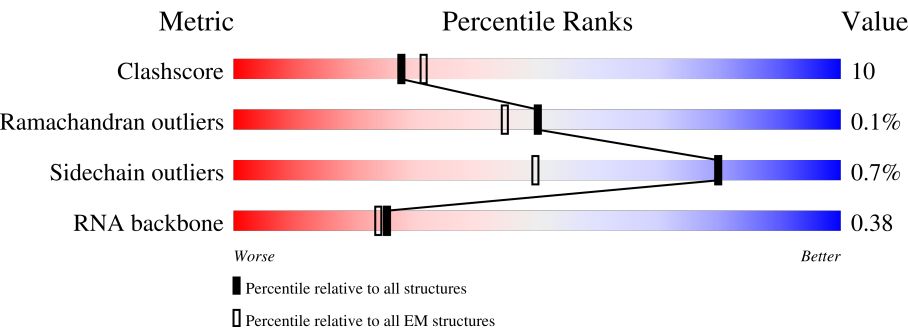
EMDB validation analysis : 0.0.1.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

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 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A	2927	<div><div>7%</div><div>45%</div><div>28%</div><div>15%</div><div>12%</div></div>
2	B	119	<div><div>58%</div><div>13%</div><div>48%</div><div>34%</div><div>6%</div></div>
3	C	277	<div><div>81%</div><div>8%</div><div>11%</div></div>
4	D	209	<div><div>90%</div><div>9%</div></div>
5	E	207	<div><div>7%</div><div>92%</div><div>7%</div></div>
6	F	179	<div><div>89%</div><div>66%</div><div>31%</div></div>
7	G	145	<div><div>97%</div></div>

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Mol	Chain	Length	Quality of chain
8	H	122	
9	I	146	
10	J	120	
11	K	115	
12	L	118	
13	M	102	
14	N	113	
15	O	95	
16	P	103	
17	Q	94	
18	R	66	
19	S	59	
20	T	59	
21	U	44	
22	V	282	
23	W	436	
24	Y	232	

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 81609 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2572	Total	C	N	O	P	0	0
			55237	24642	10204	17819	2572		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1558	C	G	conflict	GB 467326

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 3 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	246	Total	C	N	O	S	0	0
			1895	1177	373	340	5		

- Molecule 4 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	207	Total	C	N	O	S	0	0
			1575	988	290	292	5		

- Molecule 5 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	205	Total	C	N	O	S	0	0
			1551	974	288	287	2		

- Molecule 6 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	175	Total	C	N	O	S	0	0
			1285	793	237	254	1		

- Molecule 7 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 8 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 9 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	108	Total	C	N	O	S	0	0
			753	461	146	145	1		

- Molecule 10 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 11 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	113	Total	C	N	O		0	0
			925	589	180	156			

- Molecule 12 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	117	Total	C	N	O	S	0	0
			934	588	186	156	4		

- Molecule 13 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	M	101	Total	C	N	O	0	0
			786	501	139	146		

- Molecule 14 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 15 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	92	Total	C	N	O	S	0	0
			741	464	136	138	3		

- Molecule 16 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	98	Total	C	N	O	S	0	0
			737	463	137	133	4		

- Molecule 17 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	61	Total	C	N	O	0	0
			423	261	79	83		

- Molecule 18 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 19 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 20 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	54	Total	C	N	O	S	0	0
			394	241	80	68	5		

- Molecule 21 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 22 is a protein called Ribosome biogenesis GTPase A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	267	Total	C	N	O	S	0	0
			2119	1349	378	387	5		

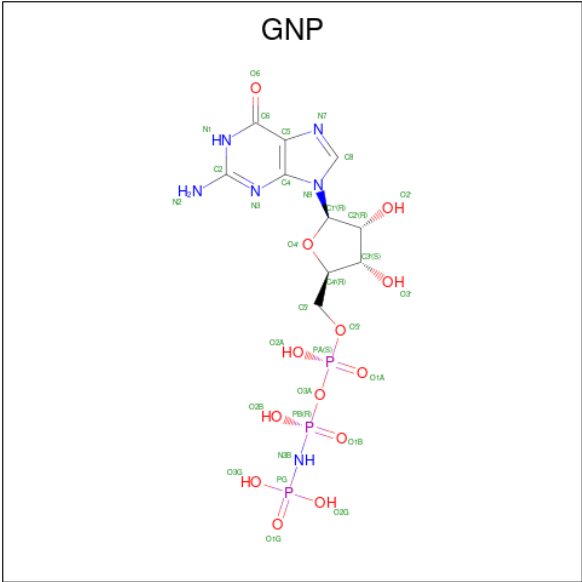
- Molecule 23 is a protein called GTPase Der.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	417	Total	C	N	O	S	0	0
			3239	2056	559	615	9		

- Molecule 24 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	178	Total	C	N	O	S	0	0
			1334	853	223	254	4		

- Molecule 25 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).



Mol	Chain	Residues	Atoms					AltConf
25	V	1	Total	C	N	O	P	0
			32	10	6	13	3	
25	W	1	Total	C	N	O	P	0
			32	10	6	13	3	
25	W	1	Total	C	N	O	P	0
			32	10	6	13	3	

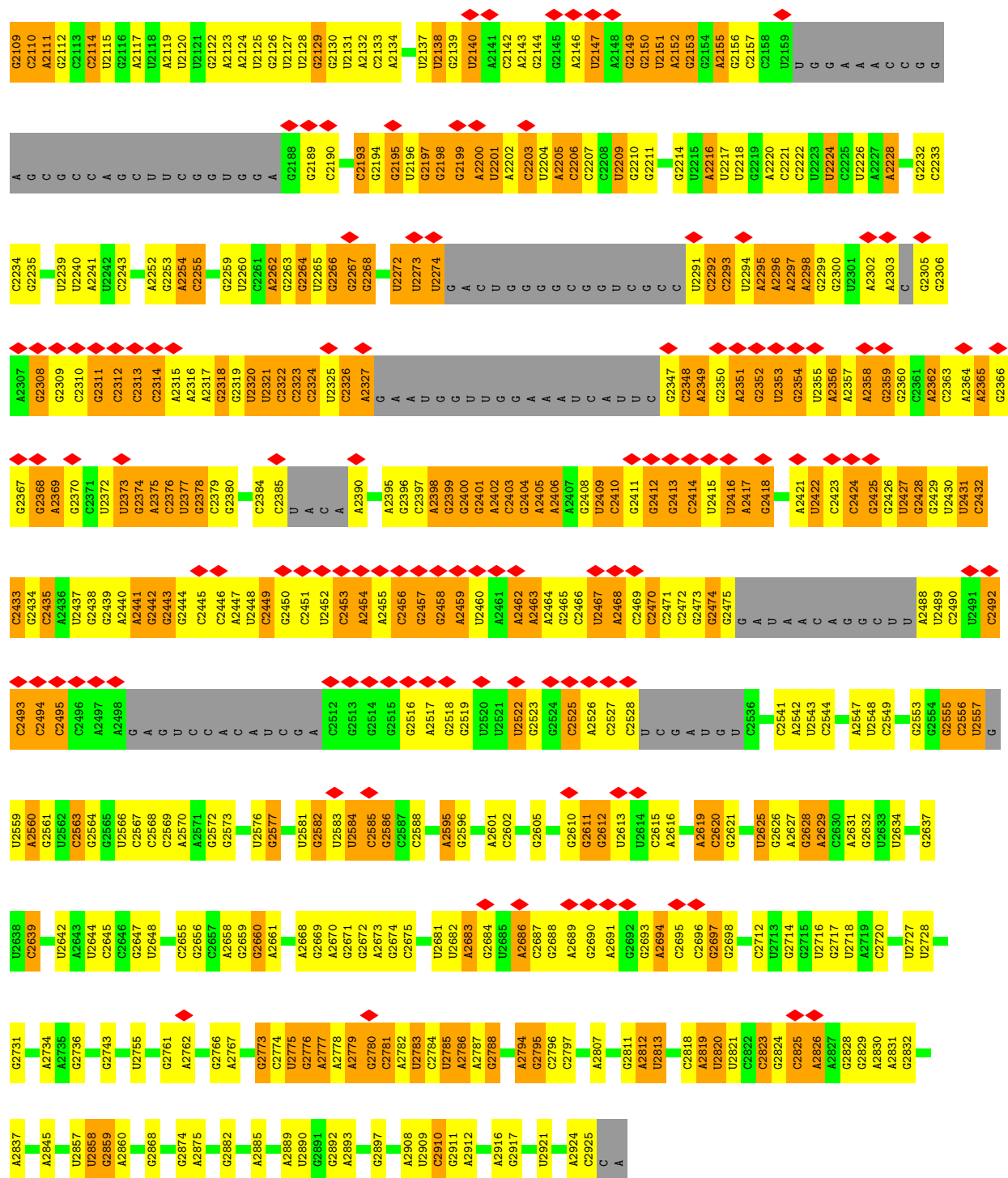
3 Residue-property plots

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.

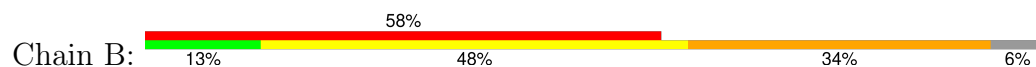
• Molecule 1: 23S rRNA





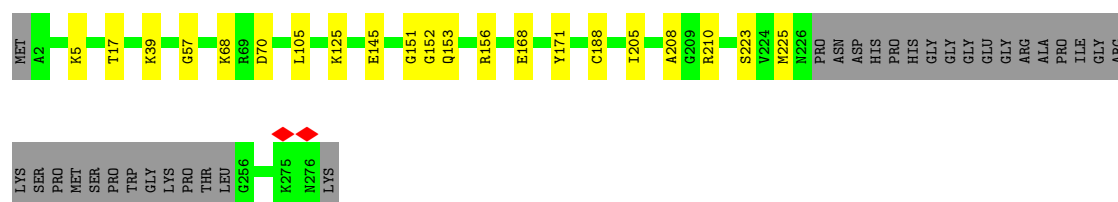
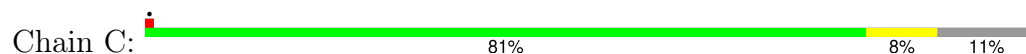


• Molecule 2: 5S rRNA

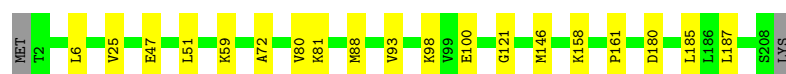
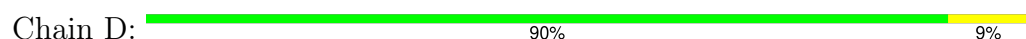




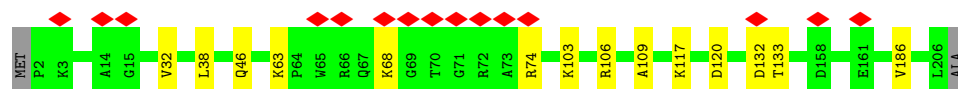
- Molecule 3: Large ribosomal subunit protein uL2



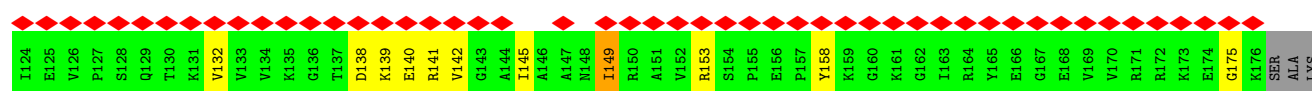
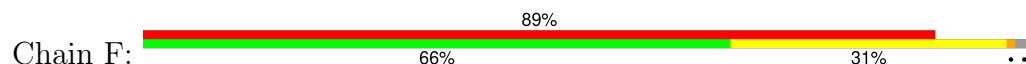
- Molecule 4: Large ribosomal subunit protein uL3



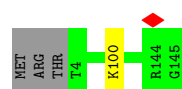
- Molecule 5: Large ribosomal subunit protein uL4



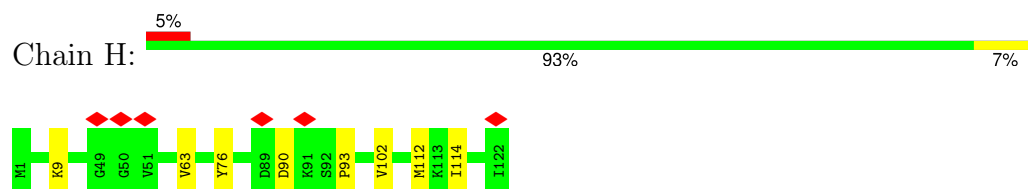
- Molecule 6: Large ribosomal subunit protein uL6



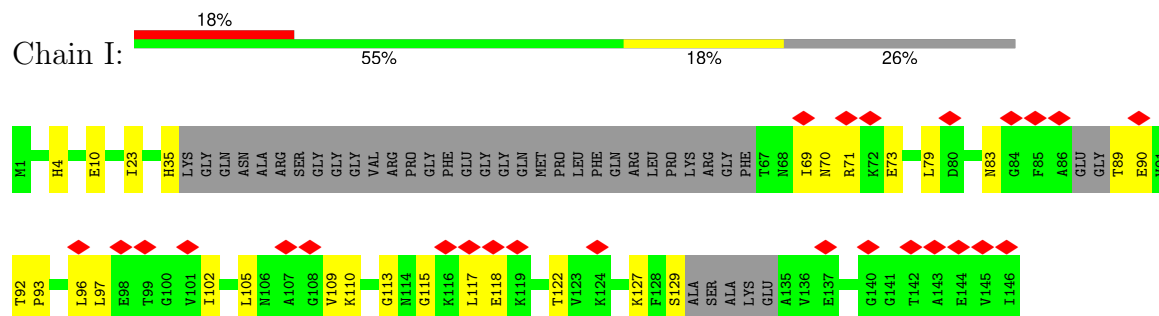
- Molecule 7: Large ribosomal subunit protein uL13



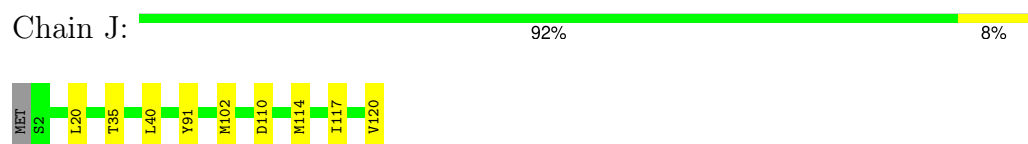
- Molecule 8: Large ribosomal subunit protein uL14



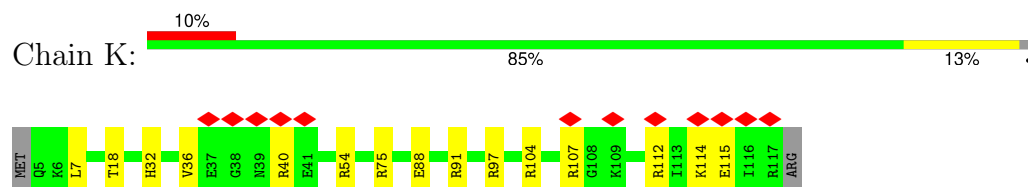
- Molecule 9: Large ribosomal subunit protein uL15



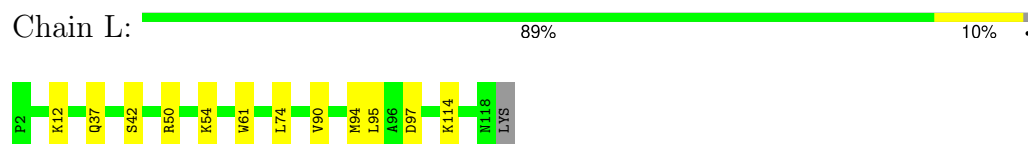
- Molecule 10: Large ribosomal subunit protein bL17



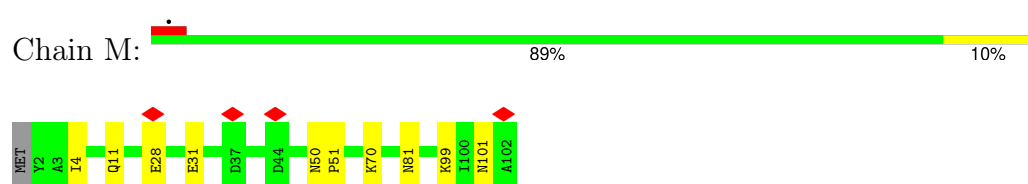
- Molecule 11: Large ribosomal subunit protein bL19




- Molecule 12: Large ribosomal subunit protein bL20



- Molecule 13: Large ribosomal subunit protein bL21




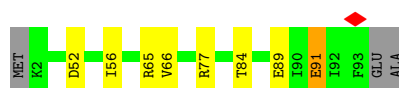
- Molecule 14: Large ribosomal subunit protein uL22

Chain N:  89% 7% •




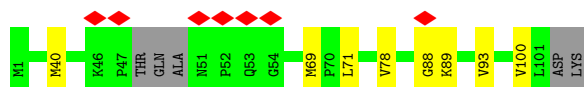
- Molecule 15: Large ribosomal subunit protein uL23

Chain O:  88% 7% ••



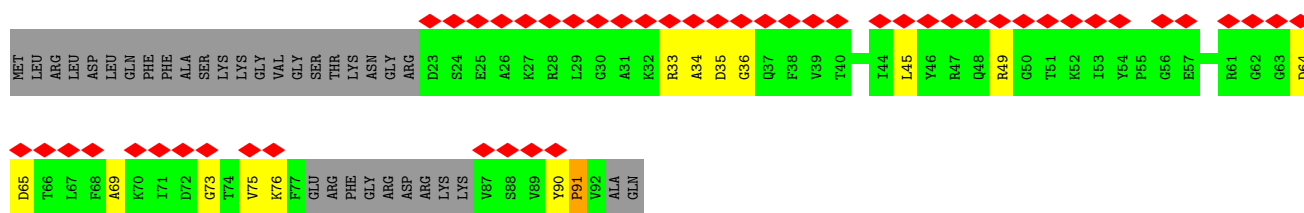
- Molecule 16: Large ribosomal subunit protein uL24

Chain P:  7% 87% 8% 5%



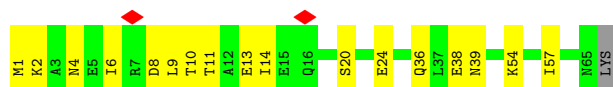
- Molecule 17: Large ribosomal subunit protein bL27

Chain Q:  52% 50% 14% 35%



- Molecule 18: Large ribosomal subunit protein uL29

Chain R:  73% 26% •



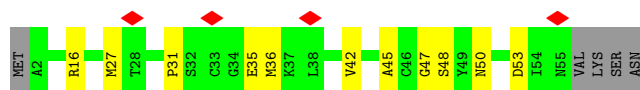
- Molecule 19: Large ribosomal subunit protein uL30

Chain S:  92% 7% •



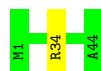
- Molecule 20: Large ribosomal subunit protein bL32

Chain T:  7% 73% 19% 8%



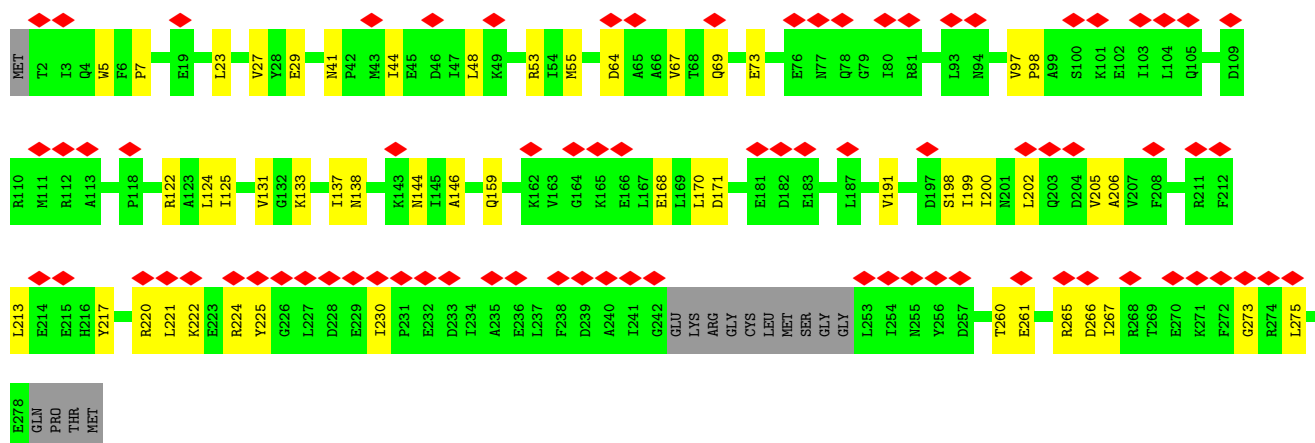
- Molecule 21: Large ribosomal subunit protein bL34

Chain U: 98%



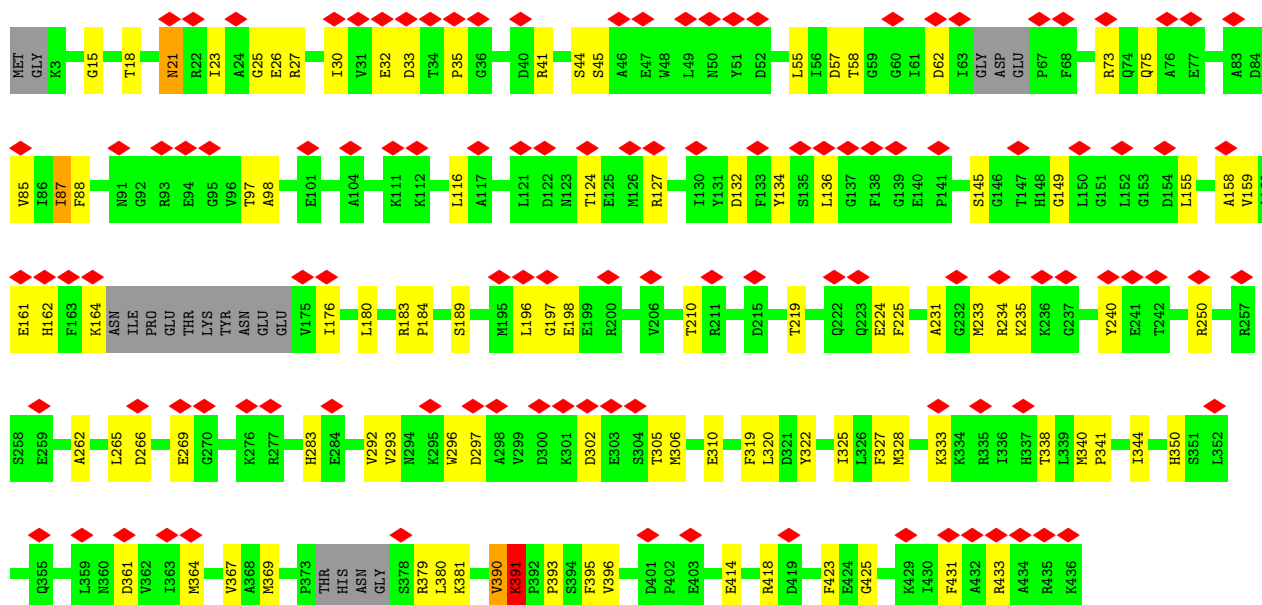
- Molecule 22: Ribosome biogenesis GTPase A

Chain V: 28% 77% 18% 5%

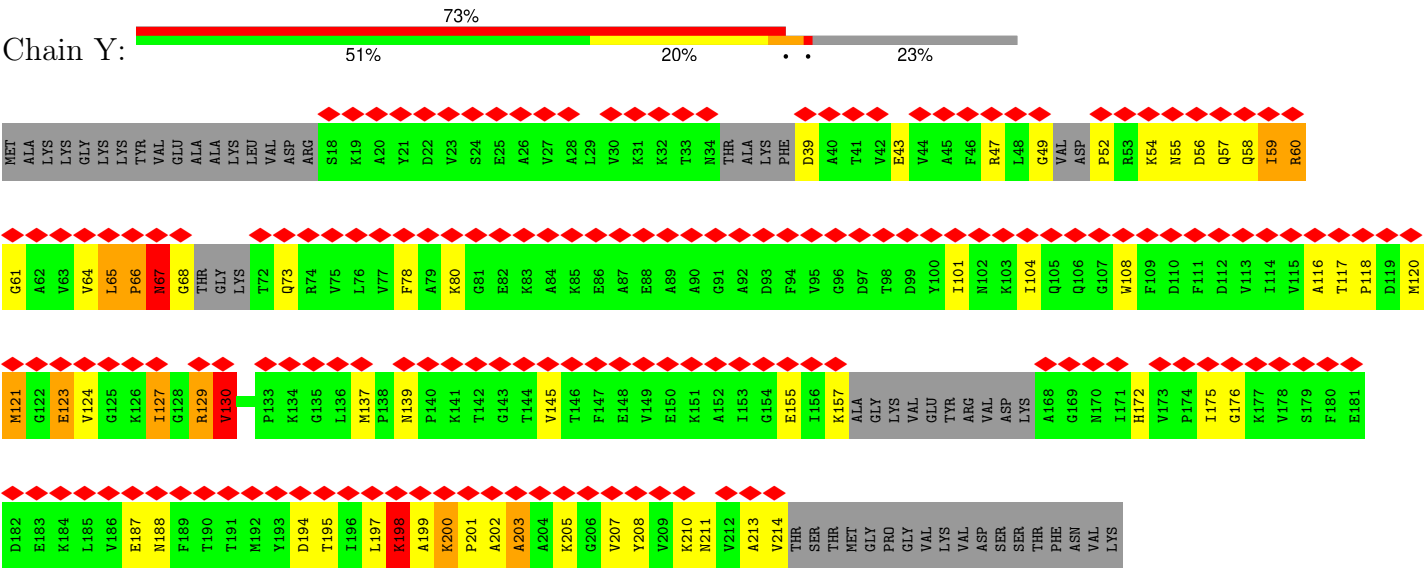


- Molecule 23: GTPase Der

Chain W: 26% 73% 22%



● Molecule 24: Large ribosomal subunit protein uL1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	47897	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2750	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.607	Depositor
Minimum map value	-0.197	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.146	Depositor
Map size (Å)	383.04, 383.04, 383.04	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.855, 0.855, 0.855	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: GNP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.17	0/61858	0.32	0/96468
2	B	0.13	0/2678	0.34	0/4174
3	C	0.17	0/1921	0.42	3/2570 (0.1%)
4	D	0.16	0/1597	0.35	0/2140
5	E	0.15	0/1570	0.31	0/2119
6	F	0.16	0/1303	0.46	1/1760 (0.1%)
7	G	0.16	0/1146	0.29	0/1542
8	H	0.16	0/927	0.32	0/1245
9	I	0.18	0/754	0.50	0/1007
10	J	0.17	0/960	0.31	0/1284
11	K	0.15	0/938	0.35	0/1255
12	L	0.20	0/946	0.35	0/1259
13	M	0.18	0/797	0.39	0/1070
14	N	0.18	0/851	0.36	0/1146
15	O	0.19	0/748	0.45	1/997 (0.1%)
16	P	0.16	0/746	0.38	0/996
17	Q	0.36	1/427 (0.2%)	0.68	1/575 (0.2%)
18	R	0.19	0/531	0.49	0/707
19	S	0.17	0/457	0.40	0/613
20	T	0.18	0/400	0.51	0/536
21	U	0.15	0/370	0.25	0/483
22	V	0.14	0/2152	0.39	0/2902
23	W	0.15	0/3295	0.49	7/4463 (0.2%)
24	Y	0.42	1/1352 (0.1%)	0.90	7/1822 (0.4%)
All	All	0.17	2/88724 (0.0%)	0.36	20/133133 (0.0%)

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
23	W	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	Q	91	PRO	N-CD	5.50	1.55	1.47
24	Y	129	ARG	CA-C	5.50	1.61	1.52

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	W	23	ILE	N-CA-C	-9.64	101.16	110.42
24	Y	54	LYS	N-CA-CB	-8.80	98.42	110.56
24	Y	198	LYS	N-CA-C	-8.61	100.91	111.33
24	Y	54	LYS	N-CA-C	8.46	122.41	112.93
24	Y	61	GLY	N-CA-C	8.07	123.78	110.55

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
23	W	391	LYS	Peptide

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	A	55237	0	27809	804	0
2	B	2395	0	1212	68	0
3	C	1895	0	1985	12	0
4	D	1575	0	1642	15	0
5	E	1551	0	1630	10	0
6	F	1285	0	1246	45	0
7	G	1123	0	1162	1	0
8	H	920	0	977	6	0
9	I	753	0	754	23	0
10	J	953	0	983	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	K	925	0	995	10	0
12	L	934	0	994	10	0
13	M	786	0	826	8	0
14	N	842	0	899	6	0
15	O	741	0	781	6	0
16	P	737	0	789	5	0
17	Q	423	0	392	13	0
18	R	530	0	568	12	0
19	S	455	0	491	2	0
20	T	394	0	373	7	0
21	U	367	0	410	1	0
22	V	2119	0	2190	31	0
23	W	3239	0	3203	112	0
24	Y	1334	0	1351	126	0
25	V	32	0	13	0	0
25	W	64	0	26	5	0
All	All	81609	0	53701	1241	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 10.

The worst 5 of 1241 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)
23:W:132:ASP:HA	24:Y:137:MET:CE	1.21	1.59
23:W:132:ASP:CA	24:Y:137:MET:HE1	1.56	1.35
23:W:98:ALA:N	24:Y:52:PRO:HD3	1.48	1.26
23:W:98:ALA:H	24:Y:52:PRO:CD	1.46	1.26
23:W:132:ASP:CA	24:Y:137:MET:CE	2.16	1.17

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	C	242/277 (87%)	234 (97%)	8 (3%)	0	100	100
4	D	205/209 (98%)	198 (97%)	7 (3%)	0	100	100
5	E	203/207 (98%)	194 (96%)	9 (4%)	0	100	100
6	F	173/179 (97%)	159 (92%)	14 (8%)	0	100	100
7	G	140/145 (97%)	134 (96%)	6 (4%)	0	100	100
8	H	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
9	I	100/146 (68%)	94 (94%)	6 (6%)	0	100	100
10	J	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
11	K	111/115 (96%)	109 (98%)	2 (2%)	0	100	100
12	L	115/118 (98%)	107 (93%)	8 (7%)	0	100	100
13	M	99/102 (97%)	93 (94%)	6 (6%)	0	100	100
14	N	107/113 (95%)	102 (95%)	5 (5%)	0	100	100
15	O	90/95 (95%)	87 (97%)	3 (3%)	0	100	100
16	P	94/103 (91%)	89 (95%)	5 (5%)	0	100	100
17	Q	57/94 (61%)	51 (90%)	6 (10%)	0	100	100
18	R	63/66 (96%)	57 (90%)	6 (10%)	0	100	100
19	S	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
20	T	52/59 (88%)	49 (94%)	3 (6%)	0	100	100
21	U	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
22	V	263/282 (93%)	252 (96%)	11 (4%)	0	100	100
23	W	409/436 (94%)	393 (96%)	16 (4%)	0	100	100
24	Y	168/232 (72%)	148 (88%)	17 (10%)	3 (2%)	7	29
All	All	3026/3323 (91%)	2876 (95%)	147 (5%)	3 (0%)	50	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
24	Y	66	PRO
24	Y	67	ASN
24	Y	130	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	200/225 (89%)	200 (100%)	0	100	100
4	D	168/170 (99%)	168 (100%)	0	100	100
5	E	166/170 (98%)	166 (100%)	0	100	100
6	F	131/151 (87%)	131 (100%)	0	100	100
7	G	120/123 (98%)	120 (100%)	0	100	100
8	H	101/101 (100%)	101 (100%)	0	100	100
9	I	71/110 (64%)	71 (100%)	0	100	100
10	J	99/100 (99%)	99 (100%)	0	100	100
11	K	98/100 (98%)	98 (100%)	0	100	100
12	L	95/97 (98%)	95 (100%)	0	100	100
13	M	83/84 (99%)	83 (100%)	0	100	100
14	N	90/93 (97%)	90 (100%)	0	100	100
15	O	82/85 (96%)	82 (100%)	0	100	100
16	P	82/87 (94%)	82 (100%)	0	100	100
17	Q	38/74 (51%)	38 (100%)	0	100	100
18	R	56/57 (98%)	56 (100%)	0	100	100
19	S	52/53 (98%)	52 (100%)	0	100	100
20	T	38/53 (72%)	37 (97%)	1 (3%)	41	68
21	U	39/39 (100%)	39 (100%)	0	100	100
22	V	227/244 (93%)	227 (100%)	0	100	100
23	W	343/371 (92%)	341 (99%)	2 (1%)	84	91
24	Y	138/185 (75%)	124 (90%)	14 (10%)	6	23
All	All	2517/2772 (91%)	2500 (99%)	17 (1%)	80	90

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	Y	200	LYS
24	Y	207	VAL
24	Y	65	LEU
24	Y	67	ASN
24	Y	121	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
23	W	349	ASN
24	Y	57	GLN
24	Y	188	ASN
24	Y	67	ASN
24	Y	55	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2555/2927 (87%)	825 (32%)	64 (2%)
2	B	111/119 (93%)	66 (59%)	6 (5%)
All	All	2666/3046 (87%)	891 (33%)	70 (2%)

5 of 891 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	10	A
1	A	28	A
1	A	34	U
1	A	36	G
1	A	39	C

5 of 70 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2583	U
1	A	2683	A
2	B	37	A
1	A	837	U
1	A	682	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 ligands 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$
25	GNP	V	301	-	29,34,34	1.56	7 (24%)	33,54,54	2.20	5 (15%)
25	GNP	W	502	-	29,34,34	1.65	7 (24%)	33,54,54	2.22	6 (18%)
25	GNP	W	501	-	29,34,34	1.62	7 (24%)	33,54,54	2.20	5 (15%)

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
25	GNP	V	301	-	-	6/14/38/38	0/3/3/3
25	GNP	W	502	-	-	5/14/38/38	0/3/3/3
25	GNP	W	501	-	-	6/14/38/38	0/3/3/3

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	W	502	GNP	PB-O3A	4.72	1.64	1.59
25	W	501	GNP	PB-O3A	4.49	1.64	1.59
25	V	301	GNP	PB-O3A	4.05	1.64	1.59

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	W	502	GNP	PB-O1B	3.22	1.51	1.46
25	W	501	GNP	PB-O1B	3.11	1.50	1.46

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	W	501	GNP	C5-C6-N1	-8.60	111.92	123.42
25	W	502	GNP	C5-C6-N1	-8.60	111.93	123.42
25	V	301	GNP	C5-C6-N1	-8.55	111.98	123.42
25	W	501	GNP	C2-N1-C6	6.64	125.20	115.96
25	W	502	GNP	C2-N1-C6	6.64	125.19	115.96

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

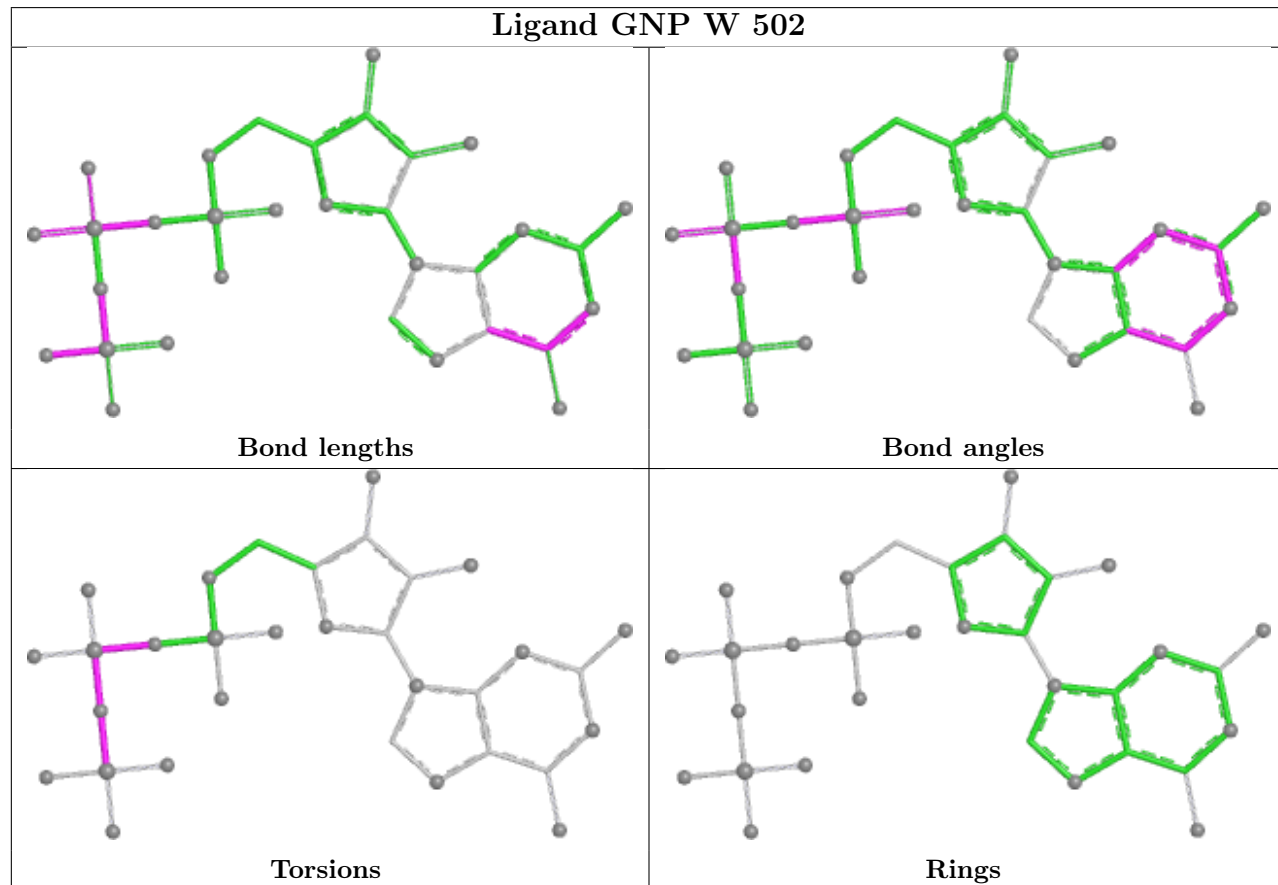
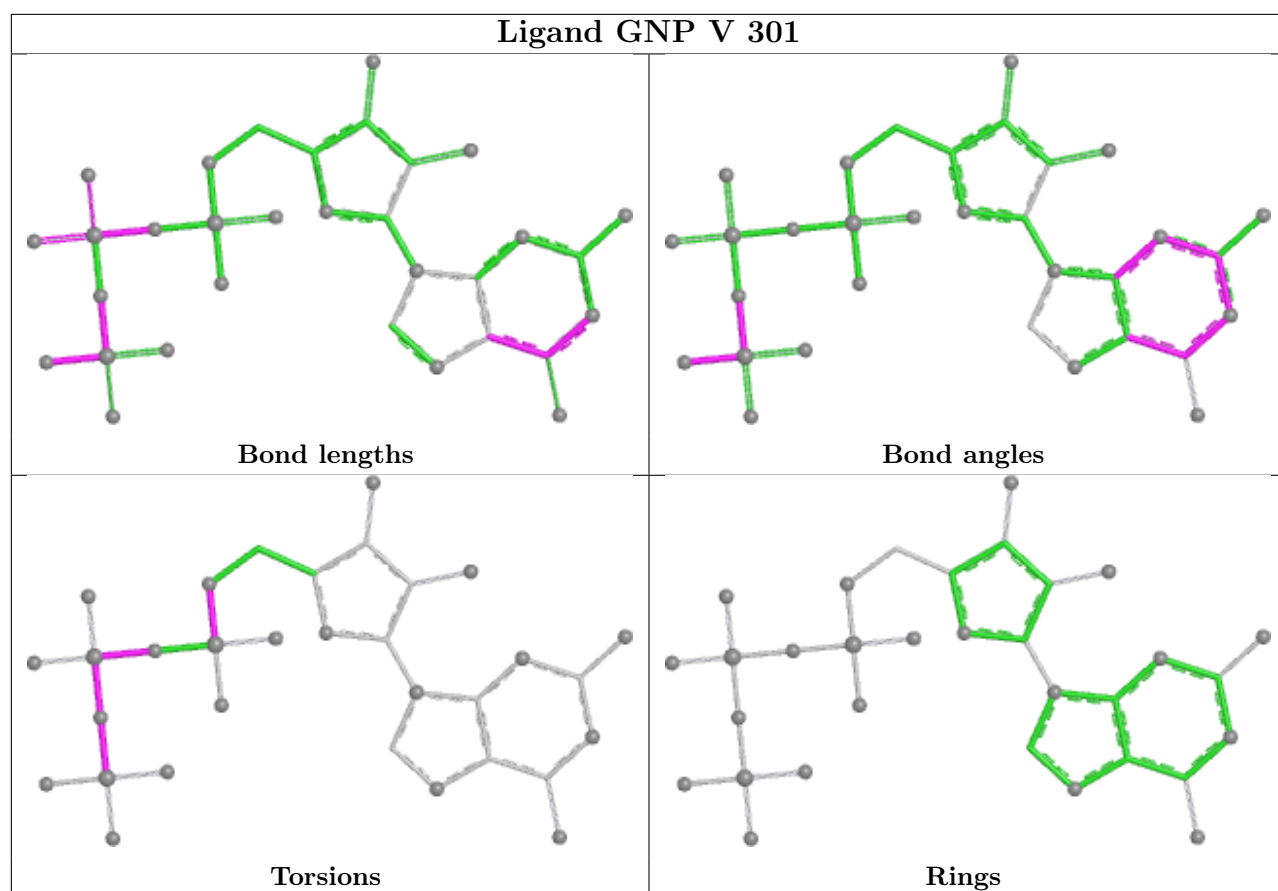
Mol	Chain	Res	Type	Atoms
25	V	301	GNP	PB-N3B-PG-O1G
25	V	301	GNP	PG-N3B-PB-O1B
25	V	301	GNP	PA-O3A-PB-O2B
25	V	301	GNP	C5'-O5'-PA-O3A
25	W	501	GNP	PG-N3B-PB-O1B

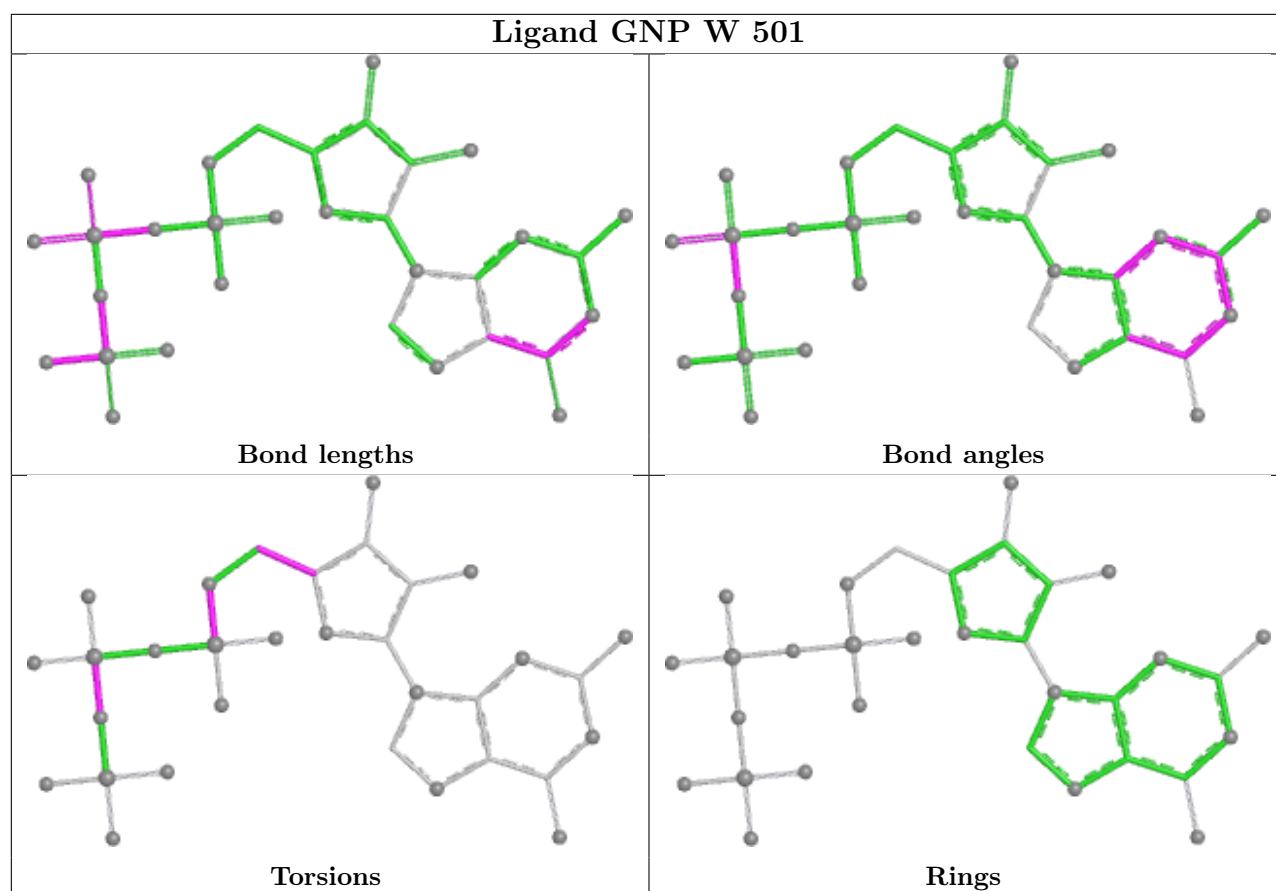
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	W	502	GNP	2	0
25	W	501	GNP	3	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.

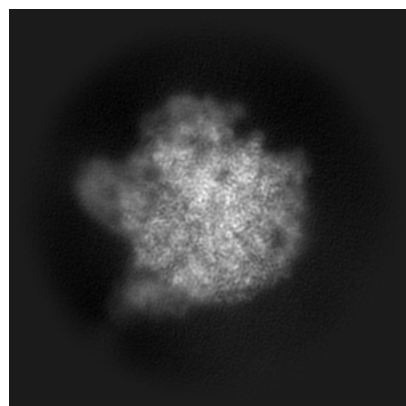
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44871. These allow visual inspection of the internal detail of the map and identification of artifacts.

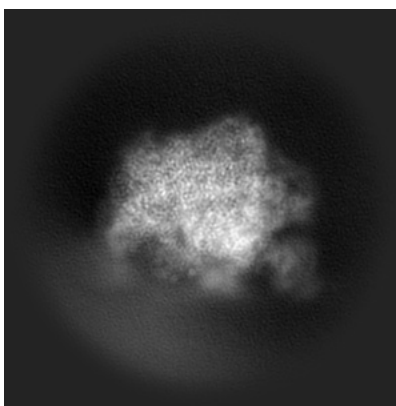
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

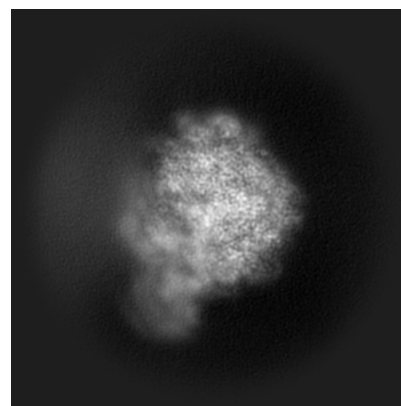
6.1.1 Primary map



X

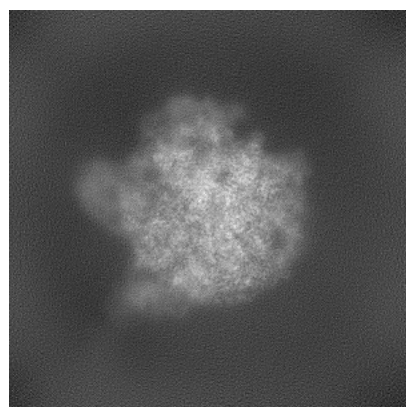


Y

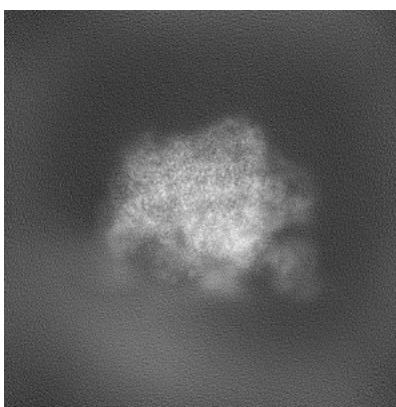


Z

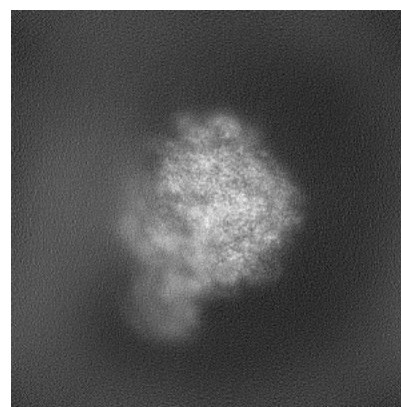
6.1.2 Raw map



X



Y

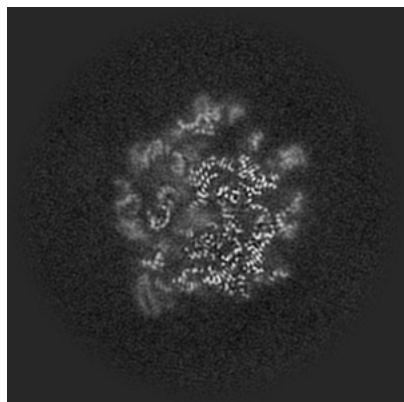


Z

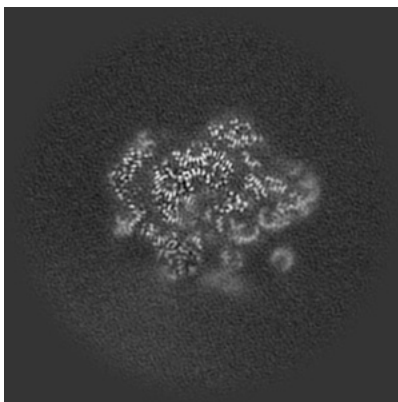
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

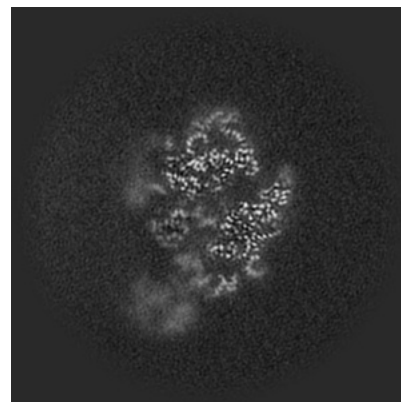
6.2.1 Primary map



X Index: 224

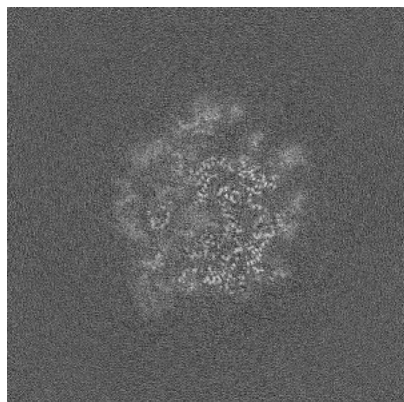


Y Index: 224

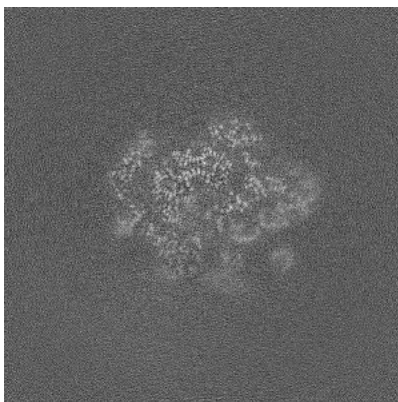


Z Index: 224

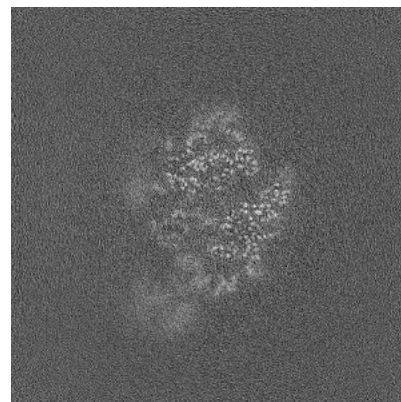
6.2.2 Raw map



X Index: 224



Y Index: 224

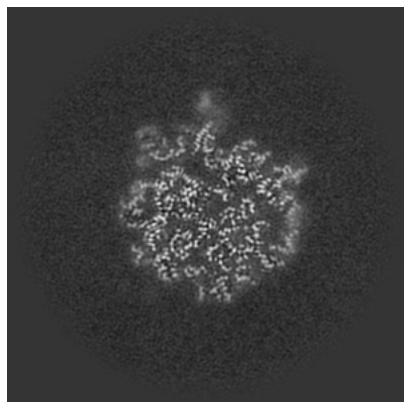


Z Index: 224

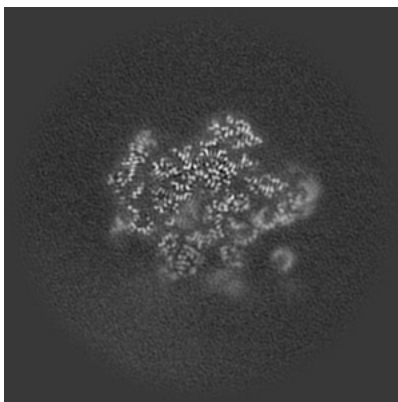
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

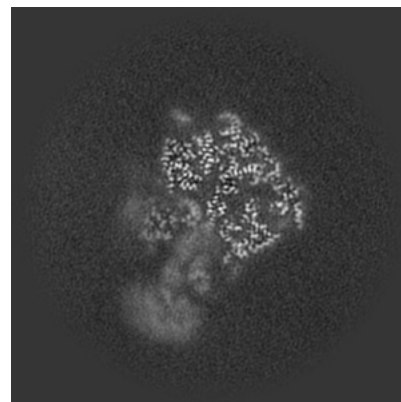
6.3.1 Primary map



X Index: 246

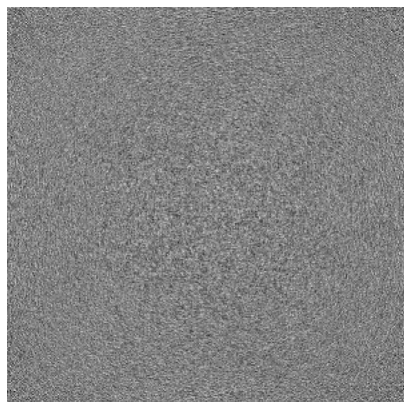


Y Index: 221

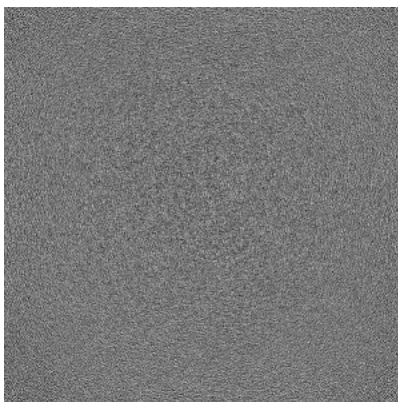


Z Index: 255

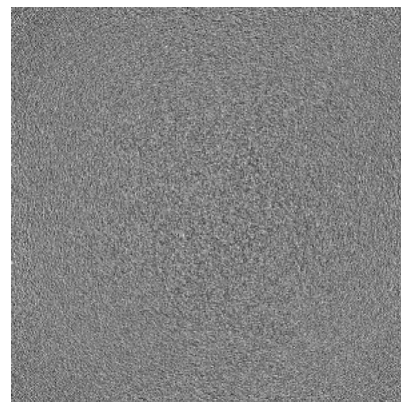
6.3.2 Raw map



X Index: 0



Y Index: 0

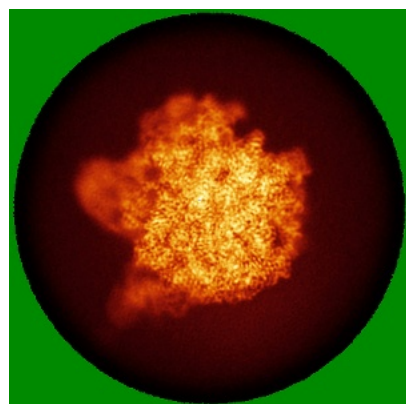


Z Index: 0

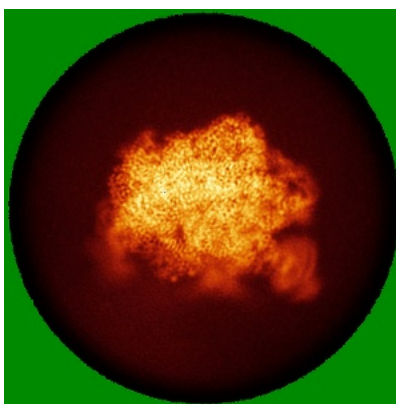
The images above show the largest variance slices of the map in three orthogonal directions.

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

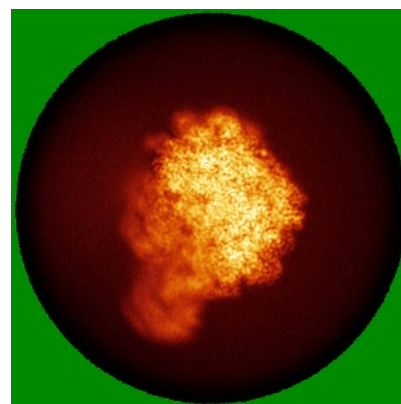
6.4.1 Primary map



X

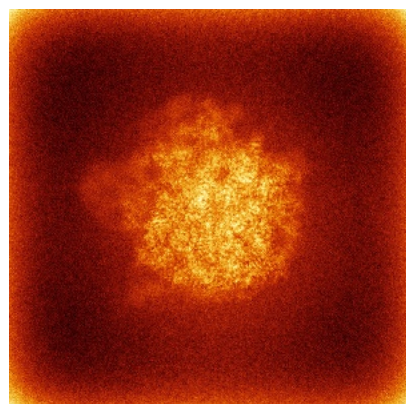


Y

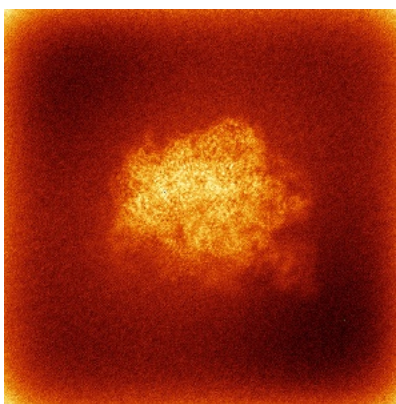


Z

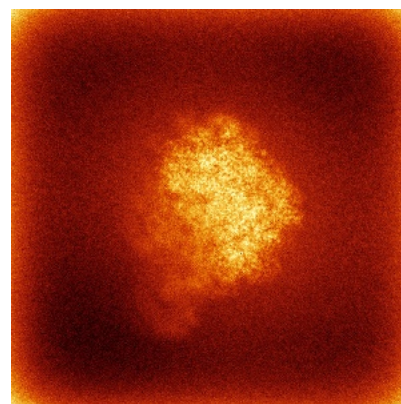
6.4.2 Raw map



X



Y

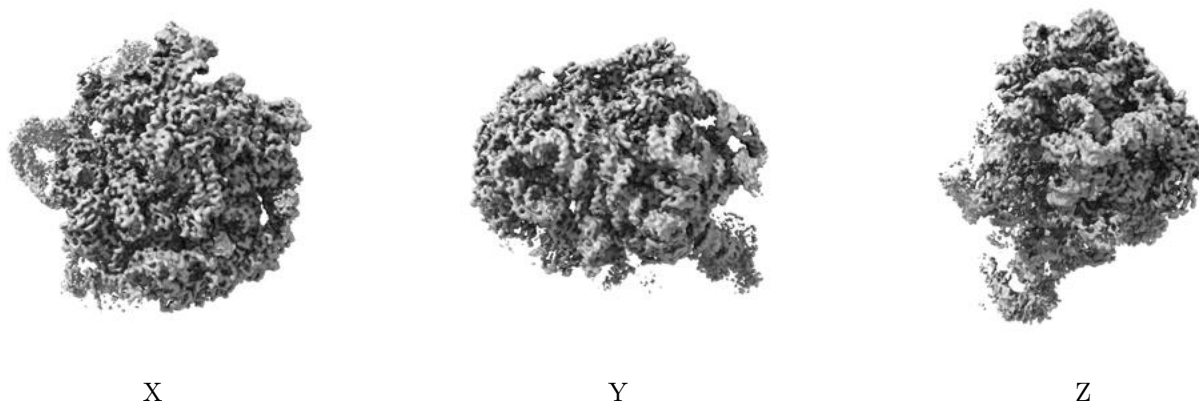


Z

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.

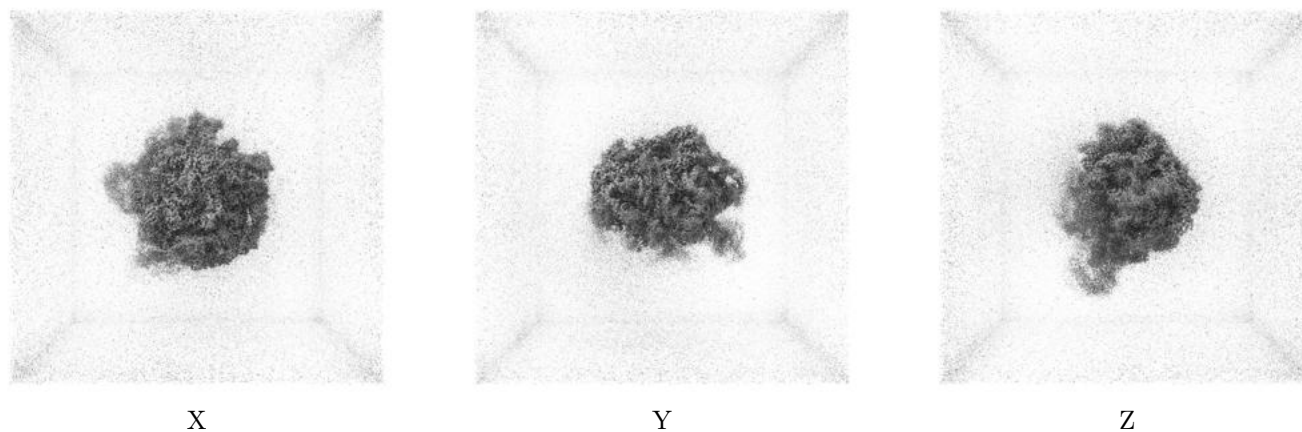
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.146. 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.

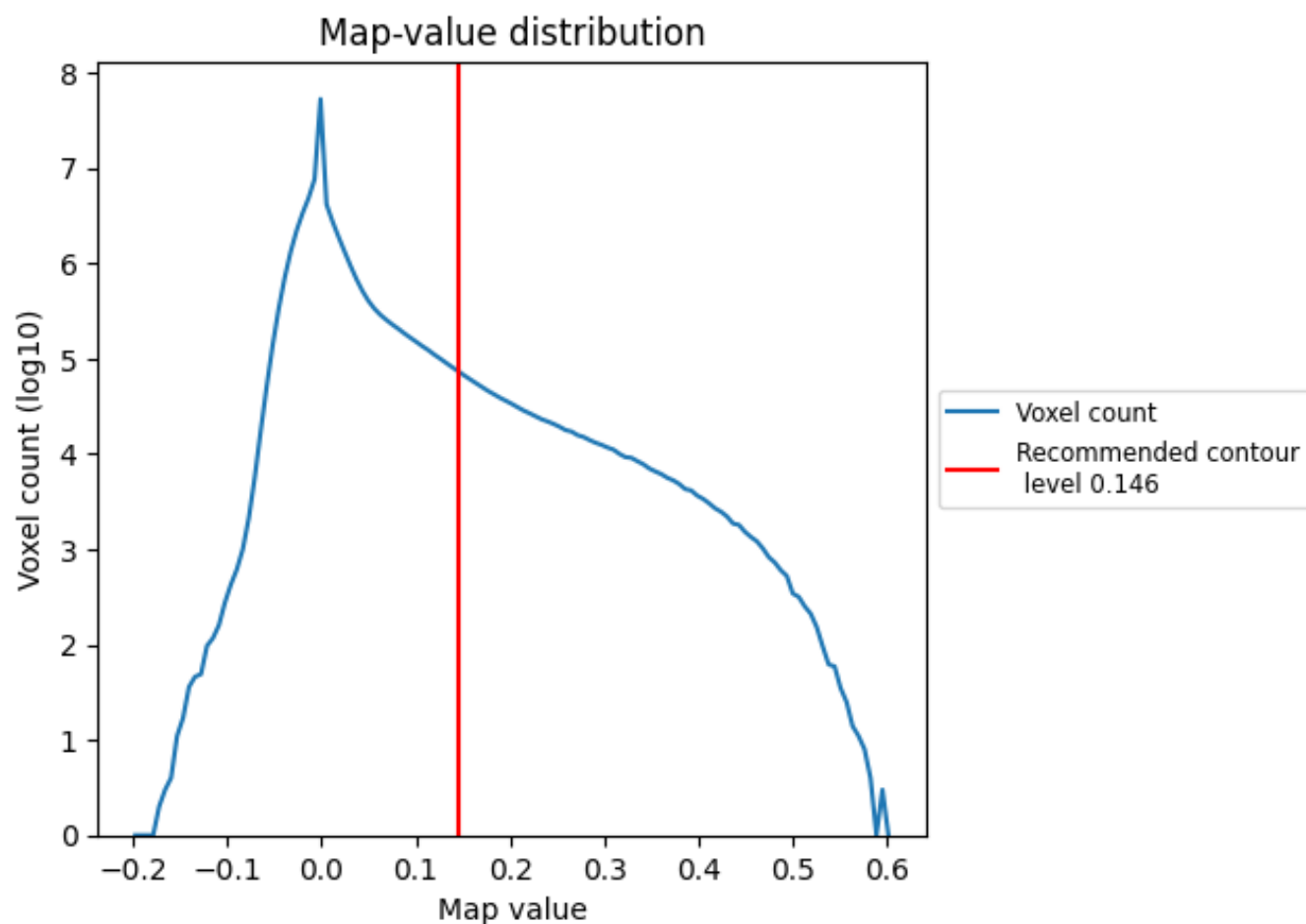
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

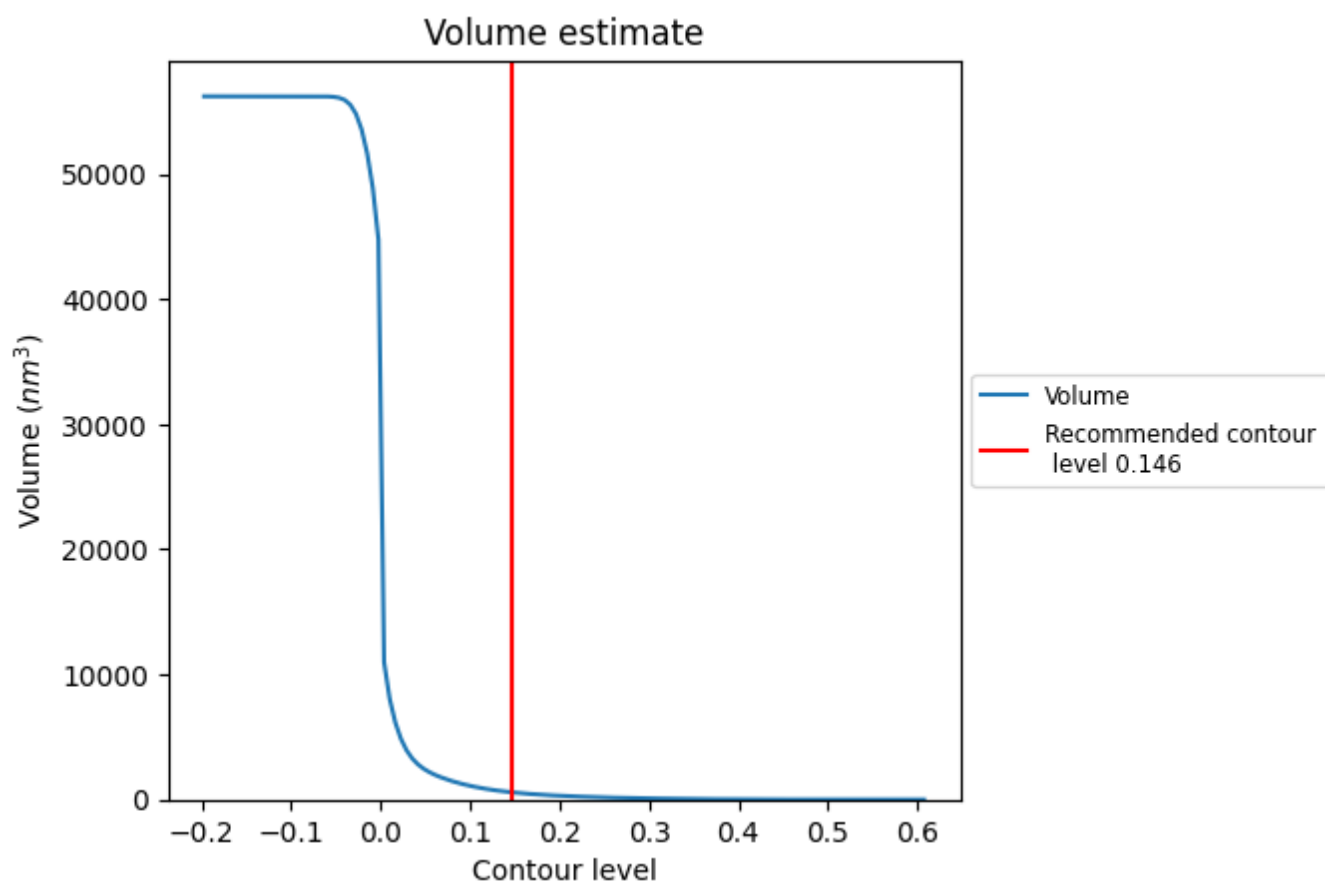
This section contains the results of statistical analysis of the map.

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.

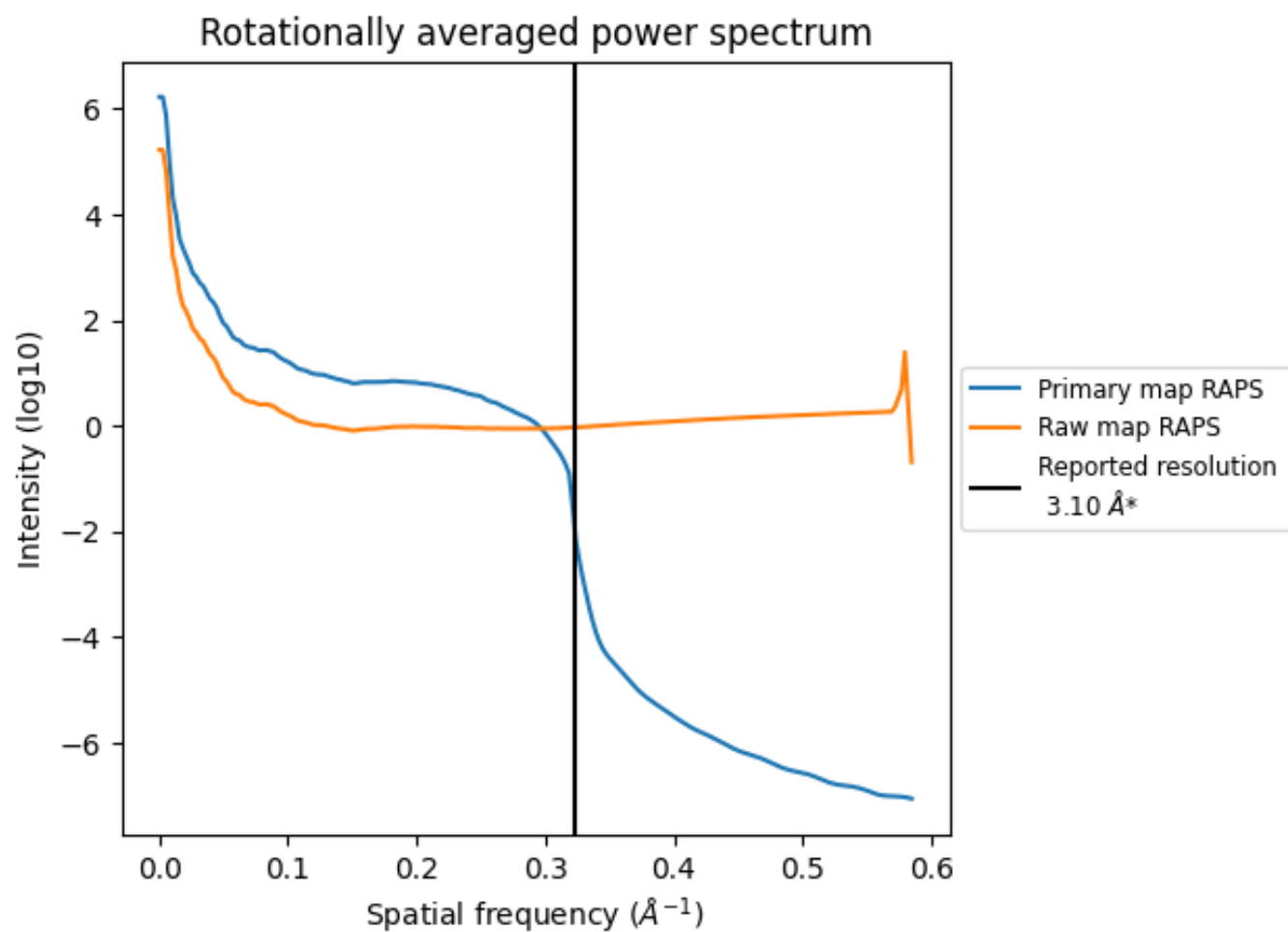
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 585 nm³; this corresponds to an approximate mass of 529 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 ⓘ

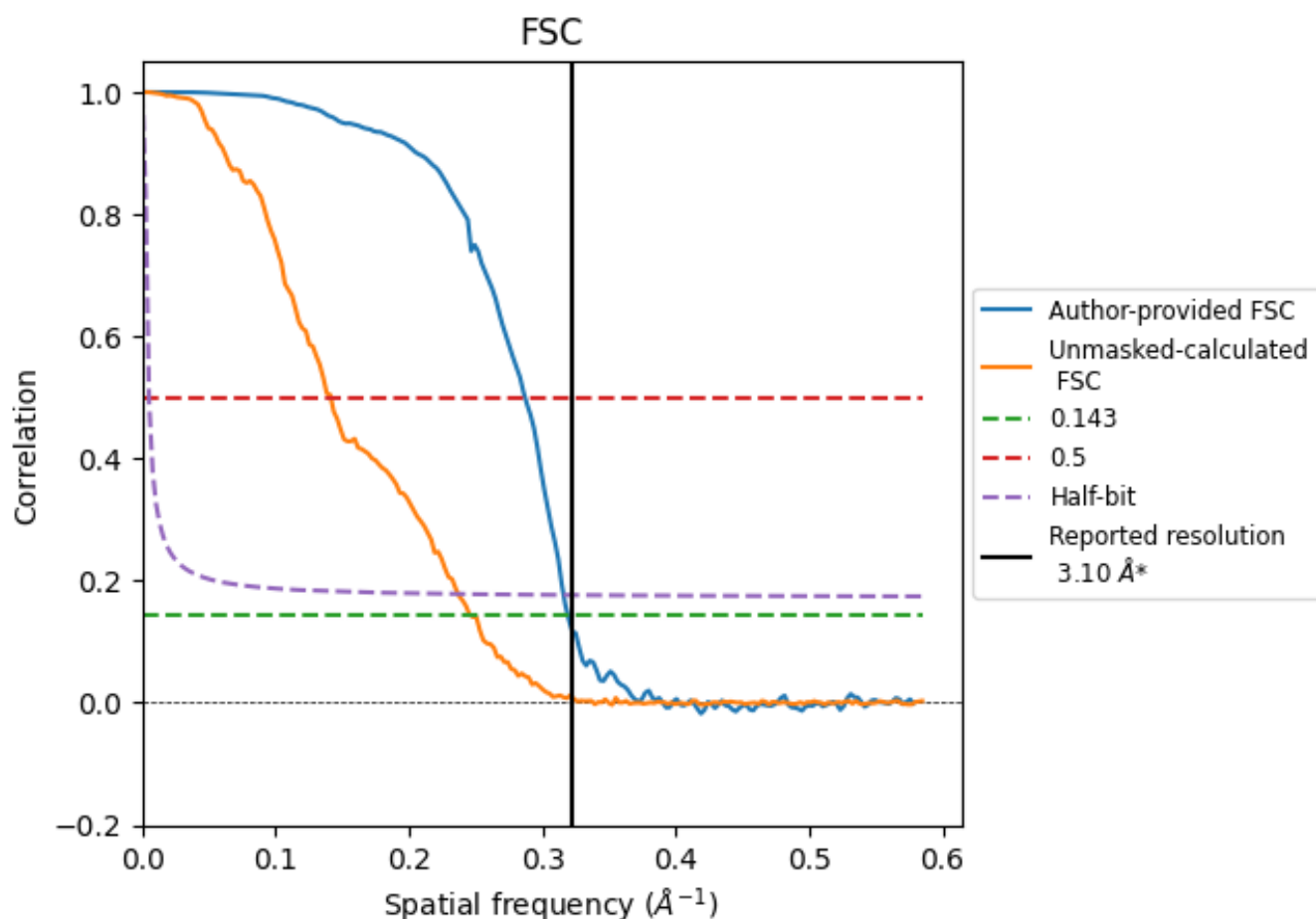


*Reported resolution corresponds to spatial frequency of 0.323 \AA^{-1}

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 0.323 \AA^{-1}

8.2 Resolution estimates [i](#)

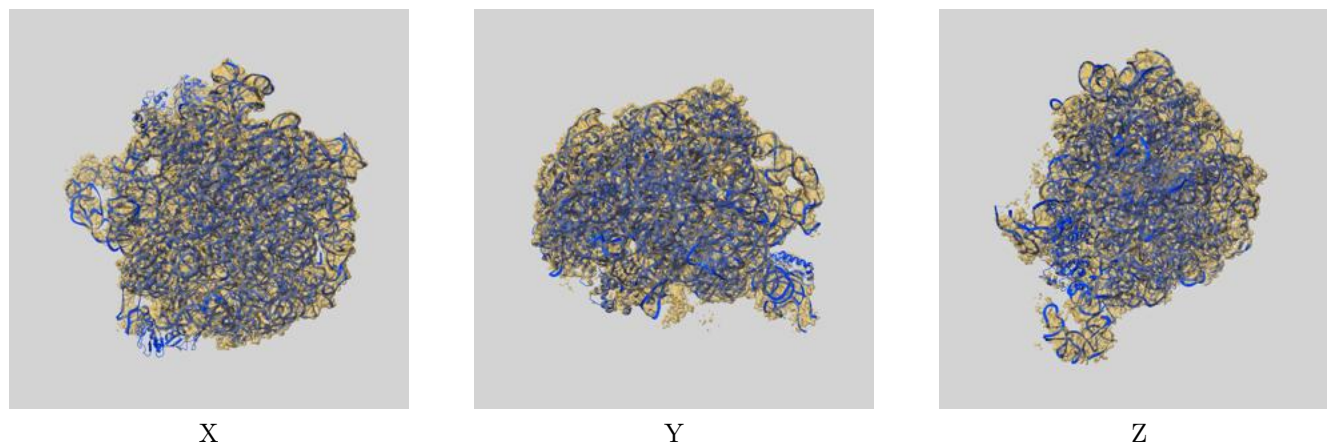
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.13	3.48	3.16
Unmasked-calculated*	4.06	7.07	4.22

*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 4.06 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

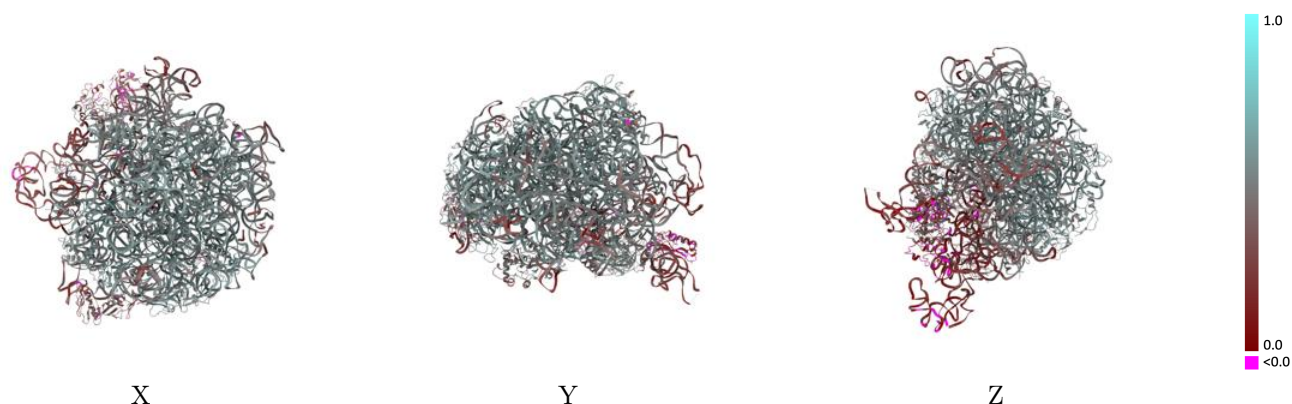
This section contains information regarding the fit between EMDB map EMD-44871 and PDB model 9BSS. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



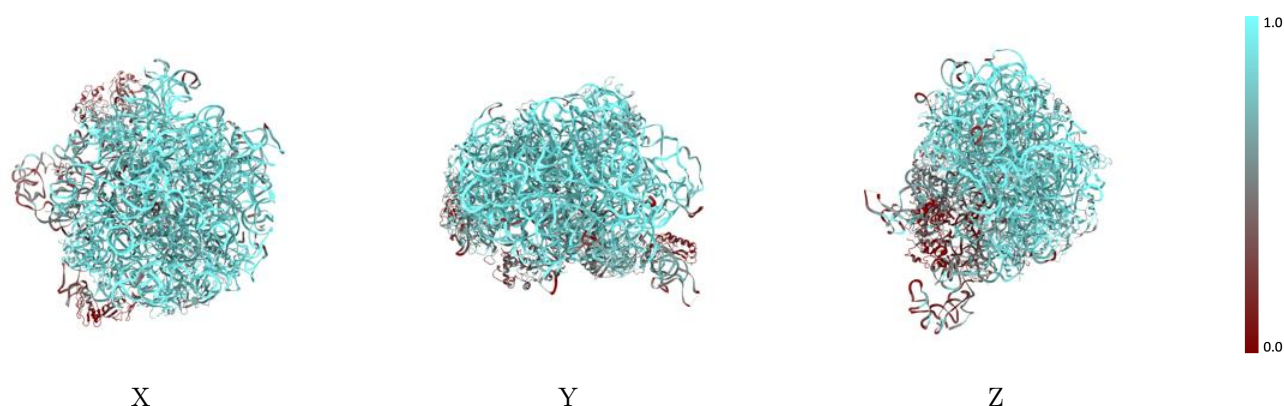
The images above show the 3D surface view of the map at the recommended contour level 0.146 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



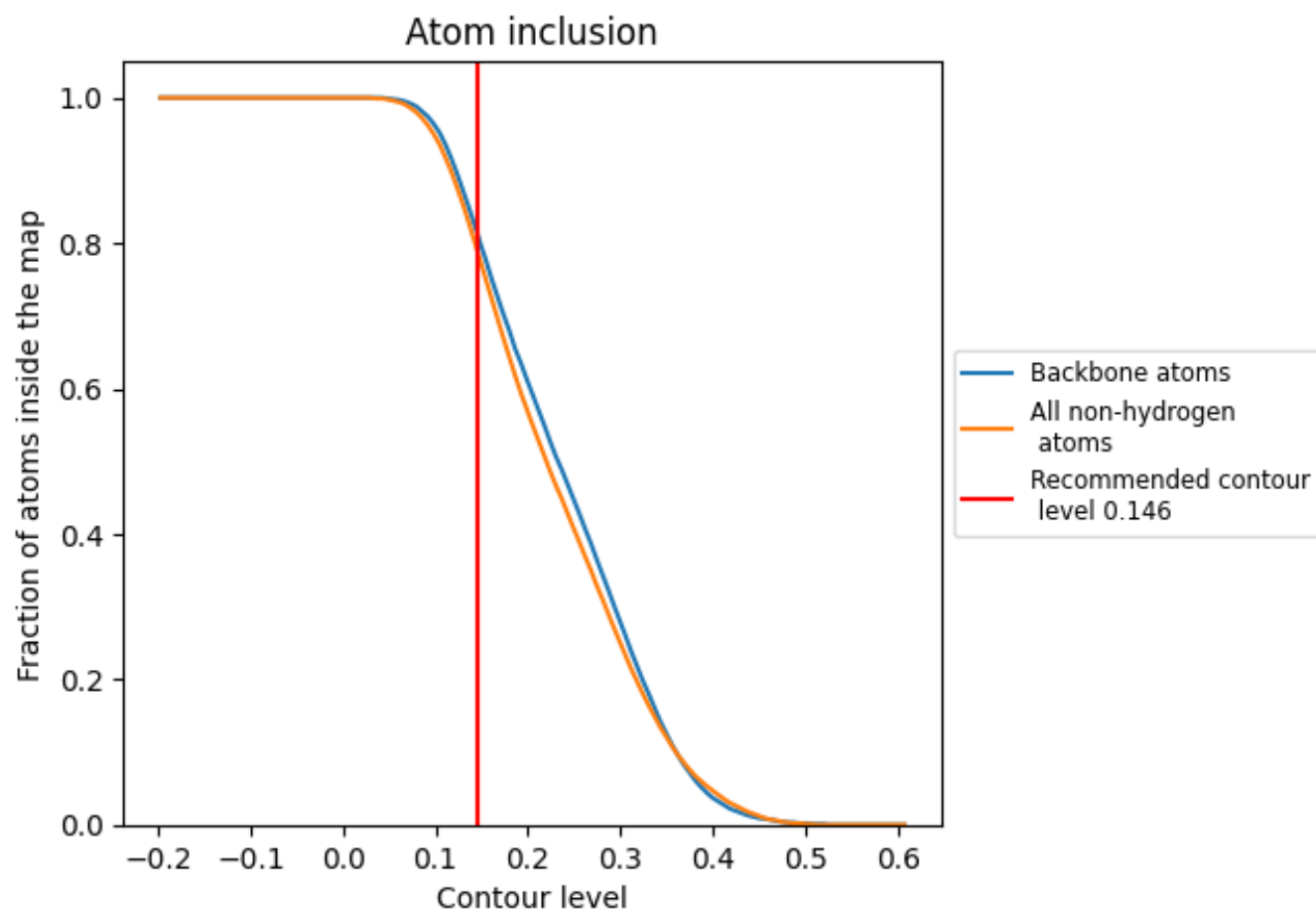
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.146).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 79% 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 (0.146) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7870	 0.4560
A	 0.8610	 0.4600
B	 0.3520	 0.1720
C	 0.8320	 0.5530
D	 0.8510	 0.5590
E	 0.7770	 0.5270
F	 0.1070	 0.2950
G	 0.8670	 0.5510
H	 0.7170	 0.5390
I	 0.6390	 0.4490
J	 0.8770	 0.5590
K	 0.7310	 0.5440
L	 0.8890	 0.5490
M	 0.8130	 0.5460
N	 0.8720	 0.5610
O	 0.8490	 0.5360
P	 0.7880	 0.5230
Q	 0.2130	 0.3510
R	 0.7920	 0.4850
S	 0.7620	 0.5140
T	 0.8150	 0.4430
U	 0.9250	 0.5730
V	 0.5150	 0.4630
W	 0.5250	 0.4300
Y	 0.0630	 0.0950

