



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 01:02 AM UTC

PDB ID : 9LXN / pdb_00009lxn
EMDB ID : EMD-63482
Title : Human RNA Polymerase III de novo transcribing complex 5 (TC5)(without 3'dATP)
Authors : Wang, Q.; Ren, Y.; Jin, Q.; Chen, X.; Xu, Y.
Deposited on : 2025-02-18
Resolution : 3.30 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:

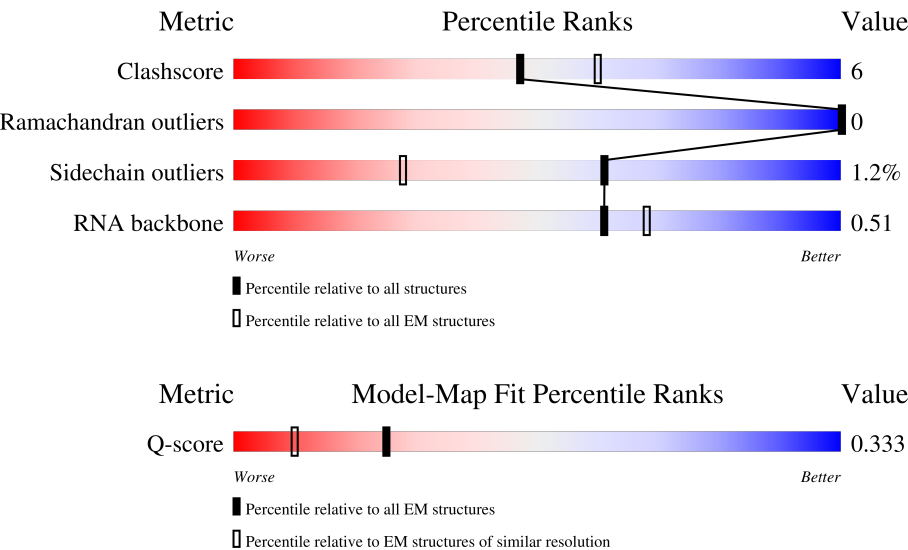
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.49

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 3.30 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.



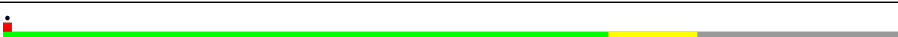
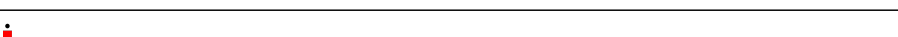
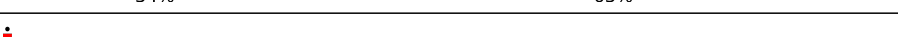
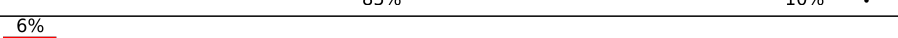
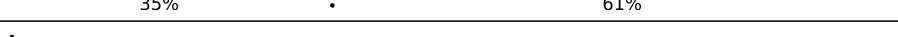
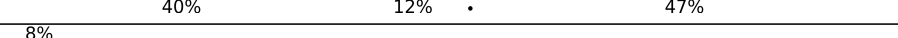
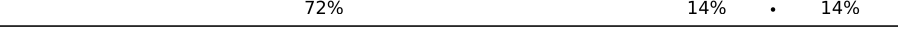
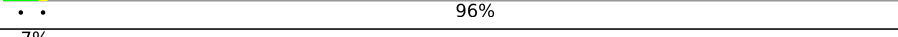
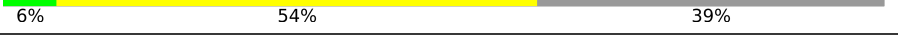
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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 <=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	1	368	30% 28%11%60%
2	3	411	73% 76%14%9%
3	4	1469	11% 15%83%

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Mol	Chain	Length	Quality of chain
4	A	1390	
5	B	1133	
6	C	346	
7	D	148	
8	E	210	
9	F	127	
10	G	204	
11	H	150	
12	I	108	
13	J	67	
14	K	133	
15	L	58	
16	M	708	
17	N	398	
18	O	534	
19	P	316	
20	Q	223	
21	U	339	
22	V	419	
23	W	2624	
24	X	127	
25	Y	127	
26	Z	4	

2 Entry composition

There are 30 unique types of molecules in this entry. The entry contains 56785 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 protein called snRNA-activating protein complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	146	Total	C	N	O	S	0	0
			1233	804	212	209	8		

- Molecule 2 is a protein called snRNA-activating protein complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	374	Total	C	N	O	S	0	0
			3038	1925	521	571	21		

- Molecule 3 is a protein called snRNA-activating protein complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	247	Total	C	N	O	S	0	0
			2066	1295	378	388	5		

- Molecule 4 is a protein called DNA-directed RNA polymerase III subunit RPC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	1378	Total	C	N	O	S	0	0
			10814	6850	1886	2005	73		

- Molecule 5 is a protein called DNA-directed RNA polymerase III subunit RPC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	1097	Total	C	N	O	S	0	0
			8680	5499	1516	1597	68		

- Molecule 6 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	343	Total	C	N	O	S	0	0
			2736	1723	488	514	11		

- Molecule 7 is a protein called DNA-directed RNA polymerase III subunit RPC9.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	122	Total	C	N	O	S	0	0
			985	614	172	196	3		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	209	Total	C	N	O	S	0	0
			1715	1083	300	324	8		

- Molecule 9 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	76	Total	C	N	O	S	0	0
			610	392	103	110	5		

- Molecule 10 is a protein called DNA-directed RNA polymerase III subunit RPC8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	166	Total	C	N	O	S	0	0
			1337	876	211	245	5		

- Molecule 11 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	148	Total	C	N	O	S	0	0
			1186	750	194	237	5		

- Molecule 12 is a protein called DNA-directed RNA polymerase III subunit RPC10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	54	Total	C	N	O	S	0	0
			426	267	79	74	6		

- Molecule 13 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	65	Total	C	N	O	S	0	0
			512	331	87	88	6		

- Molecule 14 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	103	Total	C	N	O	S	0	0
			822	513	145	157	7		

- Molecule 15 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	46	Total	C	N	O	S	0	0
			388	241	75	66	6		

- Molecule 16 is a protein called DNA-directed RNA polymerase III subunit RPC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	422	Total	C	N	O	S	0	0
			3382	2138	588	636	20		

- Molecule 17 is a protein called DNA-directed RNA polymerase III subunit RPC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	146	Total	C	N	O	S	0	0
			1128	710	191	221	6		

- Molecule 18 is a protein called DNA-directed RNA polymerase III subunit RPC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	512	Total	C	N	O	S	0	0
			4075	2565	712	774	24		

- Molecule 19 is a protein called DNA-directed RNA polymerase III subunit RPC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	303	Total	C	N	O	S	0	0
			2403	1516	411	460	16		

- Molecule 20 is a protein called DNA-directed RNA polymerase III subunit RPC7.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	87	Total	C	N	O	S	0	0
			754	488	126	134	6		

- Molecule 21 is a protein called TATA-box-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	178	Total	C	N	O	S	1	0
			1411	915	246	243	7		

- Molecule 22 is a protein called Transcription factor IIIB 50 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	361	Total	C	N	O	S	1	0
			2853	1792	507	531	23		

- Molecule 23 is a protein called Transcription factor TFIIB component B'' homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	111	Total	C	N	O	S	0	0
			943	606	163	170	4		

- Molecule 24 is a DNA chain called DNA (127-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	77	Total	C	N	O	P	0	0
			1577	757	275	468	77		

- Molecule 25 is a DNA chain called DNA (127-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	77	Total	C	N	O	P	0	0
			1580	756	291	456	77		

- Molecule 26 is a RNA chain called RNA (5'-R(P*UP*GP*CP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	4	Total	C	N	O	P	0	0
			83	37	12	30	4		

- Molecule 27 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
27	A	2	Total	Zn	0
			2	2	
27	B	1	Total	Zn	0
			1	1	
27	I	1	Total	Zn	0
			1	1	

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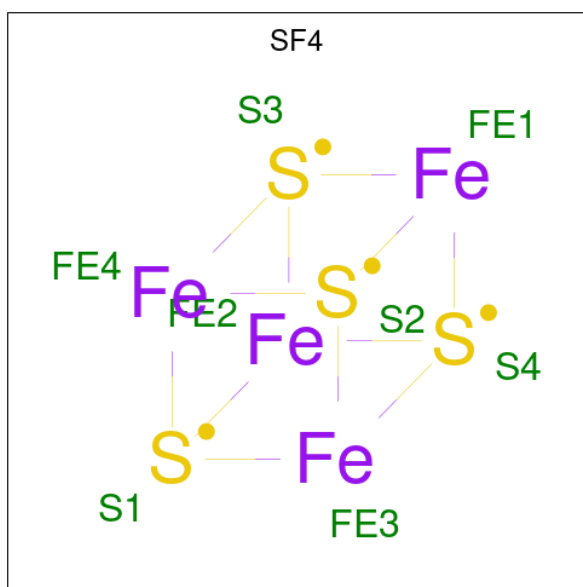
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Mol	Chain	Residues	Atoms		AltConf
27	J	1	Total	Zn	0
			1	1	
27	L	1	Total	Zn	0
			1	1	
27	V	1	Total	Zn	0
			1	1	

- Molecule 28 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

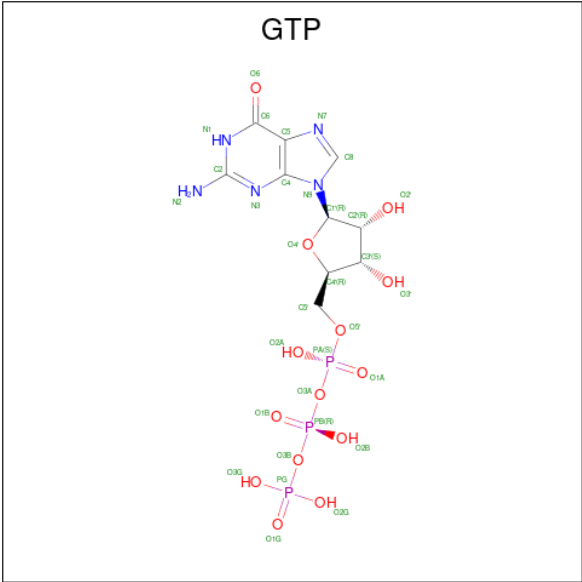
Mol	Chain	Residues	Atoms		AltConf
28	A	1	Total	Mg	0
			1	1	

- Molecule 29 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			AltConf
29	P	1	Total	Fe	S	0
			8	4	4	

- Molecule 30 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

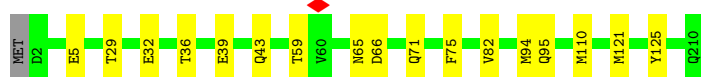


Mol	Chain	Residues	Atoms					AltConf
30	Z	1	Total	C	N	O	P	0
			32	10	5	14	3	



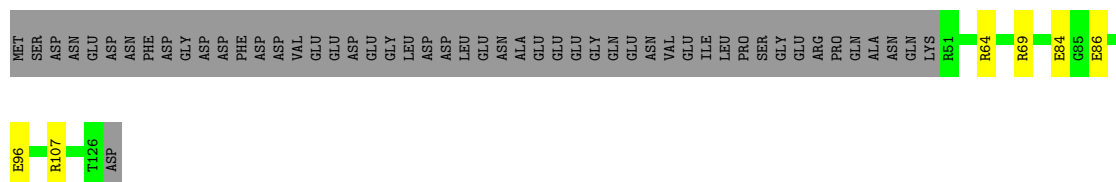
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E:  91% 8%



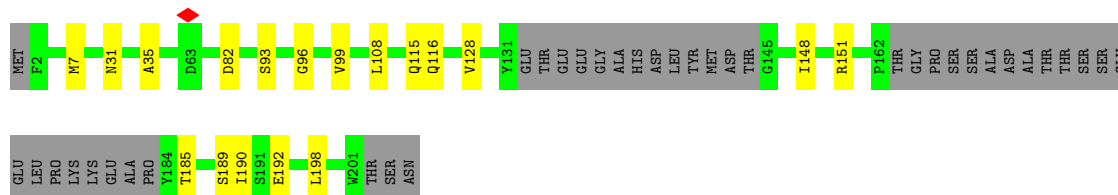
- Molecule 9: DNA-directed RNA polymerases I, II, and III subunit RPABC2

Chain F:  55% 5% 40%



- Molecule 10: DNA-directed RNA polymerase III subunit RPC8

Chain G:  73% 9% 19%



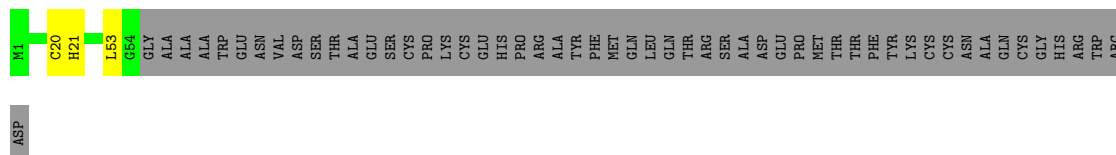
- Molecule 11: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H:  85% 13%



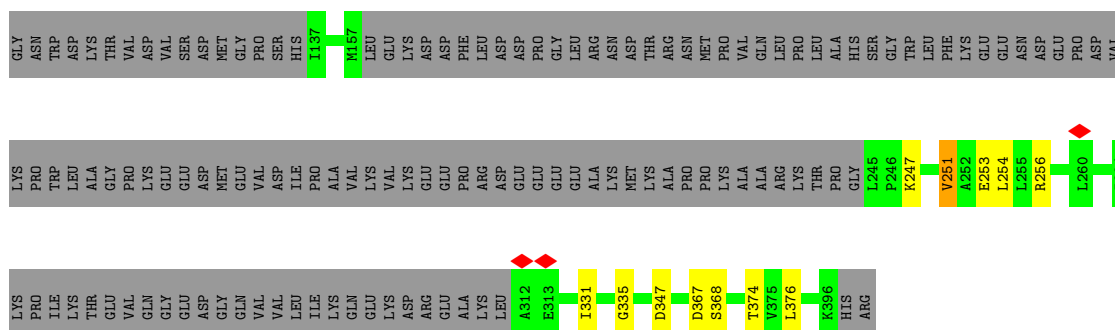
- Molecule 12: DNA-directed RNA polymerase III subunit RPC10

Chain I:  47% 50%



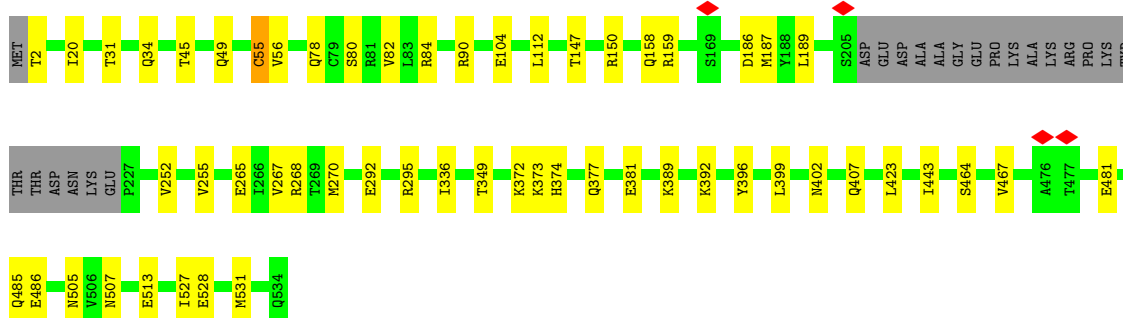
- Molecule 13: DNA-directed RNA polymerases I, II, and III subunit RPABC5

Chain J:  82% 13%



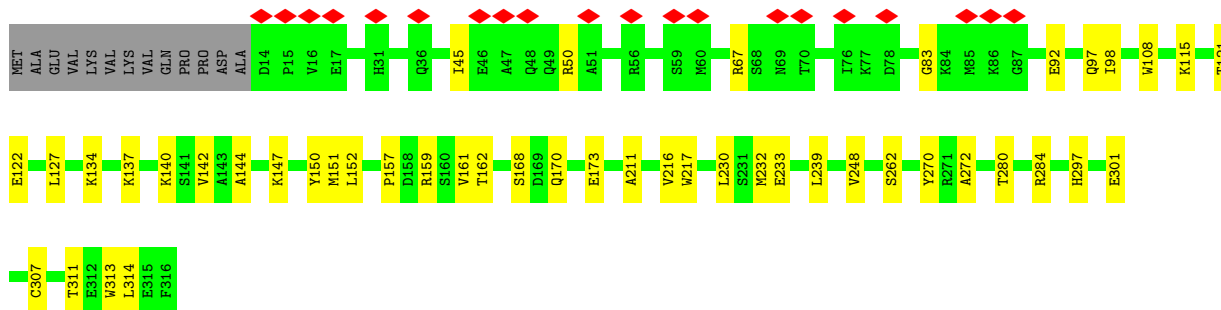
• Molecule 18: DNA-directed RNA polymerase III subunit RPC3

Chain O: 85% 10% .



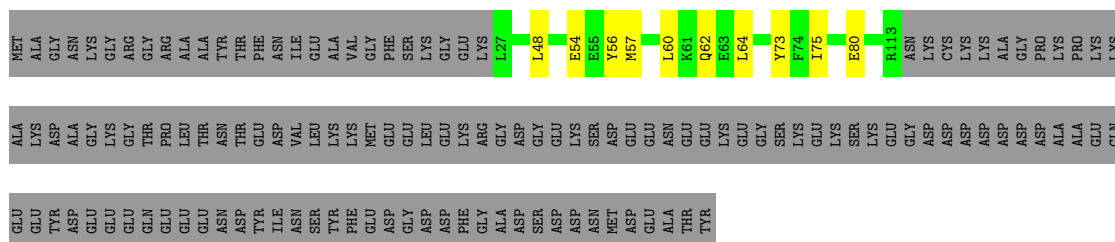
• Molecule 19: DNA-directed RNA polymerase III subunit RPC6

Chain P: 6% 81% 15% .

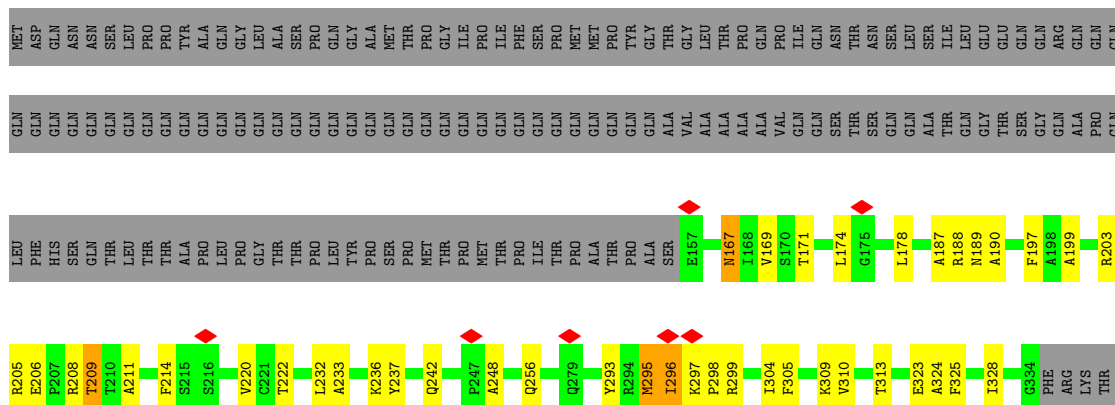
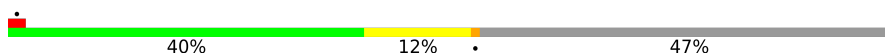


• Molecule 20: DNA-directed RNA polymerase III subunit RPC7

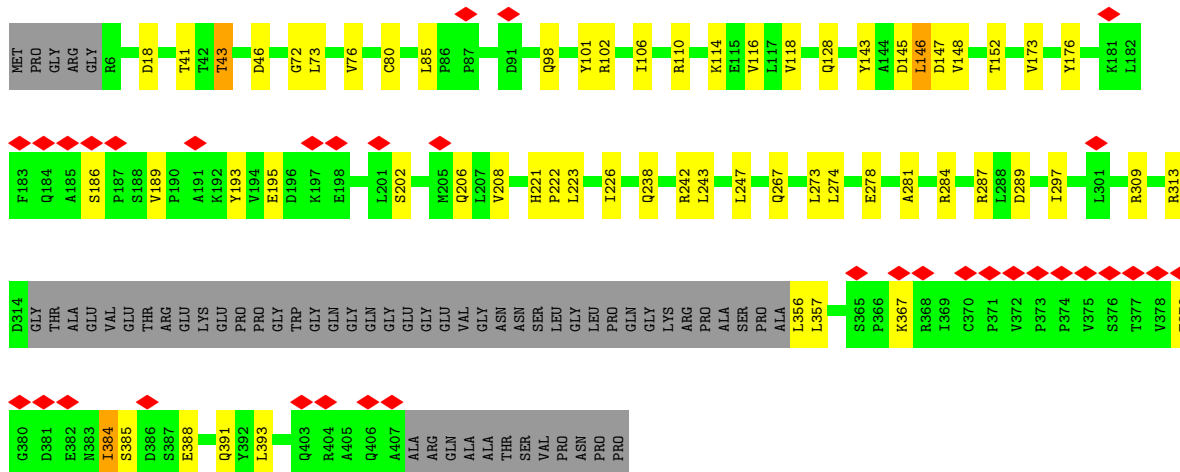
Chain Q: 35% 61% .



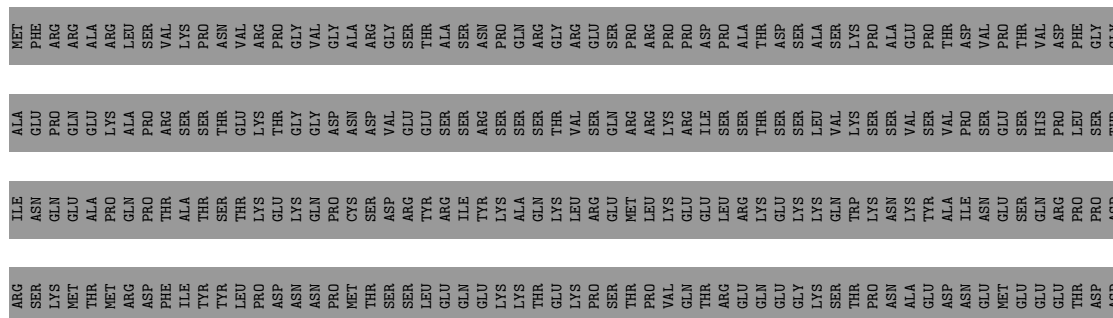
Chain U:



Chain V:



Chain W:









4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	341000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	6.436	Depositor
Minimum map value	-4.297	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.108	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	429.07724, 429.07724, 429.07724	wwPDB
Map dimensions	322, 322, 322	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.332538, 1.332538, 1.332538	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: ZN, SF4, GTP, 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	1	0.15	0/1266	0.32	0/1708
2	3	0.11	0/3113	0.31	0/4206
3	4	0.10	0/2107	0.25	0/2828
4	A	0.10	0/11008	0.24	0/14842
5	B	0.09	0/8845	0.23	0/11930
6	C	0.09	0/2790	0.22	0/3782
7	D	0.12	0/997	0.31	0/1343
8	E	0.09	0/1745	0.21	0/2358
9	F	0.08	0/620	0.21	0/839
10	G	0.10	0/1374	0.28	0/1868
11	H	0.08	0/1207	0.21	0/1628
12	I	0.12	0/434	0.25	0/584
13	J	0.10	0/521	0.27	0/703
14	K	0.10	0/837	0.24	0/1129
15	L	0.10	0/394	0.24	0/524
16	M	0.09	0/3455	0.22	0/4673
17	N	0.16	0/1137	0.25	0/1530
18	O	0.10	0/4141	0.22	0/5592
19	P	0.09	0/2446	0.22	0/3301
20	Q	0.09	0/777	0.23	0/1050
21	U	0.11	0/1439	0.27	0/1938
22	V	0.11	0/2904	0.25	0/3941
23	W	0.11	0/967	0.28	0/1293
24	X	0.26	0/1765	0.47	0/2720
25	Y	0.22	0/1773	0.40	0/2731
26	Z	0.39	0/91	0.62	0/139
All	All	0.12	0/58153	0.26	0/79180

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	1233	0	1231	26	0
2	3	3038	0	2911	54	0
3	4	2066	0	2049	19	0
4	A	10814	0	11057	119	0
5	B	8680	0	8805	104	0
6	C	2736	0	2712	32	0
7	D	985	0	1006	15	0
8	E	1715	0	1733	11	0
9	F	610	0	642	5	0
10	G	1337	0	1306	14	0
11	H	1186	0	1147	14	0
12	I	426	0	428	2	0
13	J	512	0	525	7	0
14	K	822	0	810	12	0
15	L	388	0	393	3	0
16	M	3382	0	3376	32	0
17	N	1128	0	1181	9	0
18	O	4075	0	4149	44	0
19	P	2403	0	2406	36	0
20	Q	754	0	759	11	0
21	U	1411	0	1501	32	0
22	V	2853	0	2890	36	0
23	W	943	0	924	13	0
24	X	1577	0	877	83	0
25	Y	1580	0	871	94	0
26	Z	83	0	41	5	0
27	A	2	0	0	0	0
27	B	1	0	0	0	0
27	I	1	0	0	0	0
27	J	1	0	0	0	0
27	L	1	0	0	0	0
27	V	1	0	0	0	0
28	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	P	8	0	0	0	0
30	Z	32	0	11	1	0
All	All	56785	0	55741	674	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 674 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)
24:X:-49:DG:H22	25:Y:49:DC:H42	1.15	0.93
24:X:-48:DT:H4'	24:X:-47:DA:H5'	1.58	0.85
24:X:-43:DC:O2	25:Y:43:DG:N2	2.10	0.84
1:1:46:MET:HG3	2:3:140:ARG:HH22	1.43	0.83
25:Y:36:DA:H2''	25:Y:37:DG:H5''	1.61	0.82

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	144/368 (39%)	137 (95%)	7 (5%)	0	100	100
2	3	368/411 (90%)	346 (94%)	22 (6%)	0	100	100
3	4	245/1469 (17%)	232 (95%)	13 (5%)	0	100	100
4	A	1376/1390 (99%)	1345 (98%)	31 (2%)	0	100	100
5	B	1091/1133 (96%)	1061 (97%)	30 (3%)	0	100	100
6	C	341/346 (99%)	338 (99%)	3 (1%)	0	100	100
7	D	120/148 (81%)	116 (97%)	4 (3%)	0	100	100
8	E	207/210 (99%)	203 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	F	74/127 (58%)	71 (96%)	3 (4%)	0	100	100
10	G	160/204 (78%)	149 (93%)	11 (7%)	0	100	100
11	H	146/150 (97%)	145 (99%)	1 (1%)	0	100	100
12	I	52/108 (48%)	51 (98%)	1 (2%)	0	100	100
13	J	63/67 (94%)	60 (95%)	3 (5%)	0	100	100
14	K	101/133 (76%)	100 (99%)	1 (1%)	0	100	100
15	L	44/58 (76%)	42 (96%)	2 (4%)	0	100	100
16	M	418/708 (59%)	404 (97%)	14 (3%)	0	100	100
17	N	140/398 (35%)	140 (100%)	0	0	100	100
18	O	508/534 (95%)	496 (98%)	12 (2%)	0	100	100
19	P	301/316 (95%)	292 (97%)	9 (3%)	0	100	100
20	Q	85/223 (38%)	83 (98%)	2 (2%)	0	100	100
21	U	177/339 (52%)	174 (98%)	3 (2%)	0	100	100
22	V	358/419 (85%)	342 (96%)	16 (4%)	0	100	100
23	W	109/2624 (4%)	102 (94%)	7 (6%)	0	100	100
All	All	6628/11883 (56%)	6429 (97%)	199 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	130/334 (39%)	123 (95%)	7 (5%)	20	49
2	3	330/356 (93%)	318 (96%)	12 (4%)	31	58
3	4	221/1213 (18%)	215 (97%)	6 (3%)	39	63
4	A	1200/1212 (99%)	1189 (99%)	11 (1%)	70	78
5	B	959/988 (97%)	956 (100%)	3 (0%)	86	86
6	C	299/302 (99%)	296 (99%)	3 (1%)	68	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	D	114/136 (84%)	114 (100%)	0	100	100
8	E	191/192 (100%)	191 (100%)	0	100	100
9	F	66/111 (60%)	66 (100%)	0	100	100
10	G	149/181 (82%)	148 (99%)	1 (1%)	76	80
11	H	129/131 (98%)	129 (100%)	0	100	100
12	I	48/93 (52%)	48 (100%)	0	100	100
13	J	53/56 (95%)	52 (98%)	1 (2%)	50	68
14	K	92/119 (77%)	92 (100%)	0	100	100
15	L	43/55 (78%)	43 (100%)	0	100	100
16	M	377/622 (61%)	377 (100%)	0	100	100
17	N	131/347 (38%)	130 (99%)	1 (1%)	73	79
18	O	458/476 (96%)	457 (100%)	1 (0%)	87	88
19	P	269/280 (96%)	268 (100%)	1 (0%)	84	84
20	Q	84/195 (43%)	83 (99%)	1 (1%)	63	75
21	U	154/293 (53%)	147 (96%)	7 (4%)	24	53
22	V	325/365 (89%)	314 (97%)	11 (3%)	32	59
23	W	102/2381 (4%)	96 (94%)	6 (6%)	18	46
All	All	5924/10438 (57%)	5852 (99%)	72 (1%)	61	75

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	V	106	ILE
23	W	357	GLN
22	V	146	LEU
22	V	384	ILE
3	4	387	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
18	O	407	GLN
18	O	497	GLN
22	V	112	GLN
4	A	119	GLN

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Mol	Chain	Res	Type
4	A	44	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	Z	3/4 (75%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 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	$\# Z > 2$
29	SF4	P	401	19	0,12,12	-	-	-		
30	GTP	Z	101	26	33,34,34	0.91	1 (3%)	50,54,54	1.78	9 (18%)

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
29	SF4	P	401	19	-	-	0/6/5/5
30	GTP	Z	101	26	-	6/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	Z	101	GTP	C2-N3	2.44	1.39	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	Z	101	GTP	C5-C4-N3	-6.09	118.70	128.39
30	Z	101	GTP	C2-N3-C4	4.86	120.67	112.30
30	Z	101	GTP	N9-C4-N3	4.58	135.11	125.95
30	Z	101	GTP	C2-N1-C6	-2.95	119.77	125.11
30	Z	101	GTP	C3'-C2'-C1'	2.26	105.73	101.46

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
30	Z	101	GTP	C5'-O5'-PA-O3A
30	Z	101	GTP	C5'-O5'-PA-O1A
30	Z	101	GTP	O4'-C4'-C5'-O5'
30	Z	101	GTP	C3'-C4'-C5'-O5'
30	Z	101	GTP	PG-O3B-PB-O2B

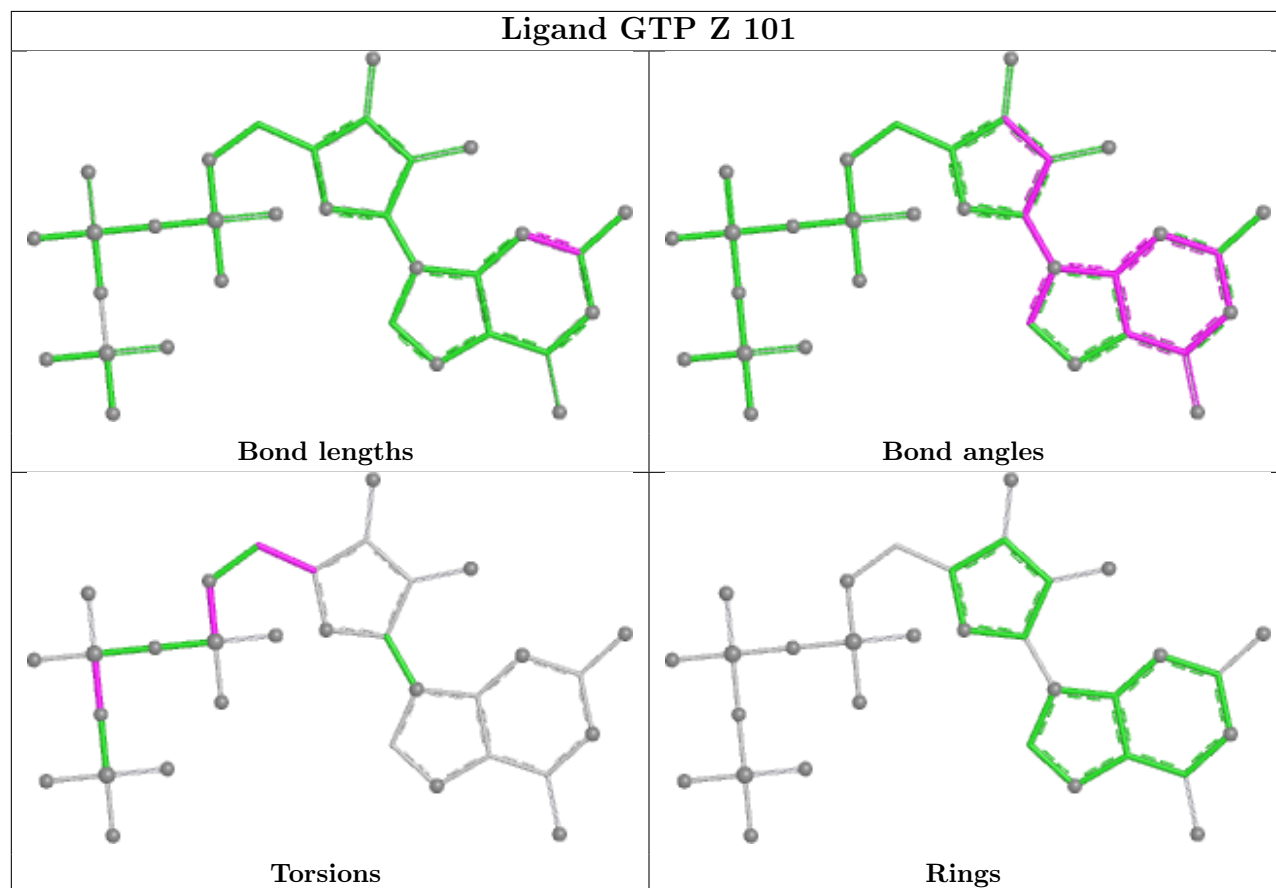
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	Z	101	GTP	1	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.

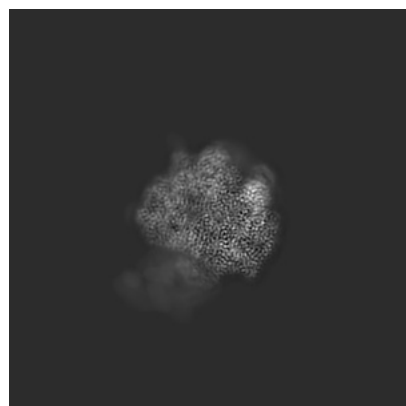
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63482. These allow visual inspection of the internal detail of the map and identification of artifacts.

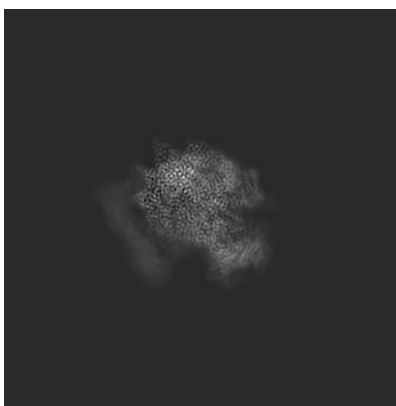
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

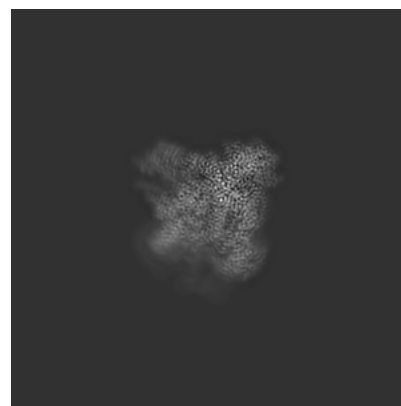
6.1.1 Primary map



X

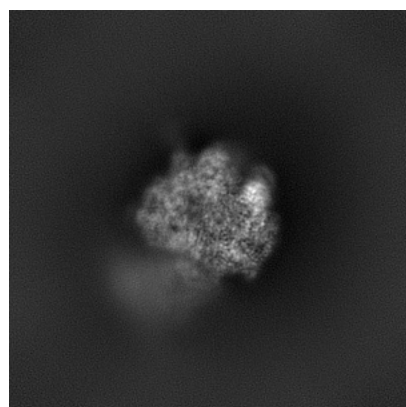


Y

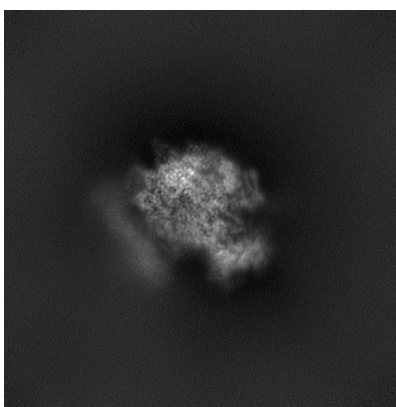


Z

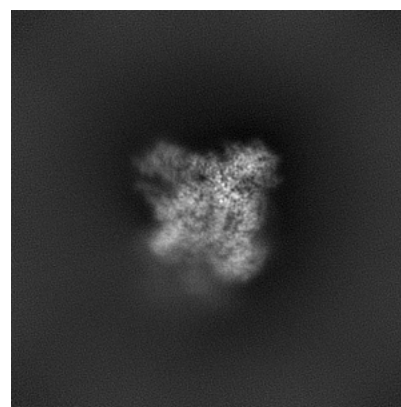
6.1.2 Raw map



X



Y

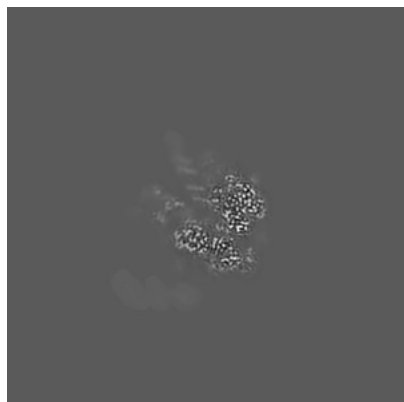


Z

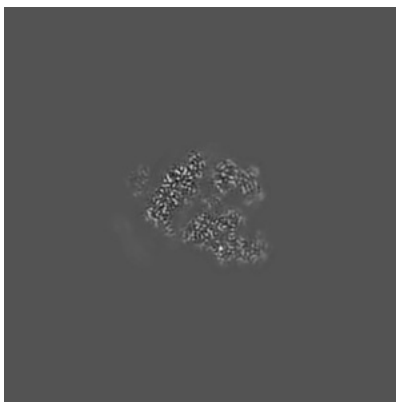
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 161

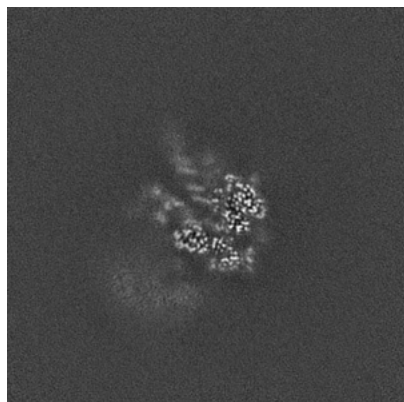


Y Index: 161

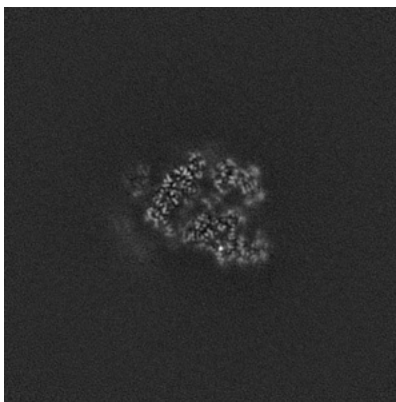


Z Index: 161

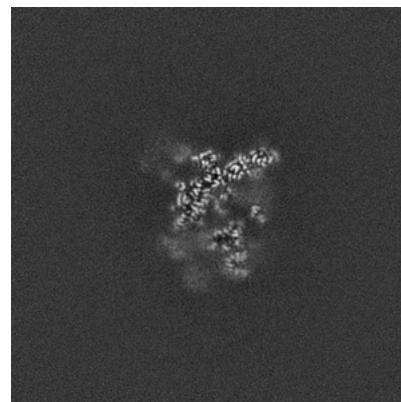
6.2.2 Raw map



X Index: 161



Y Index: 161

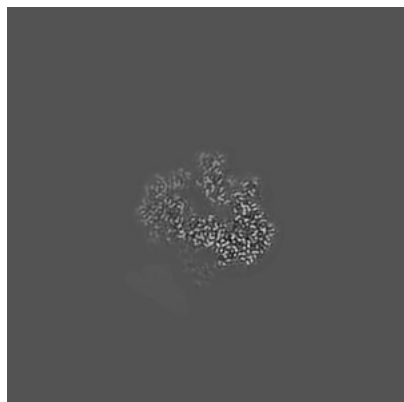


Z Index: 161

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

6.3 Largest variance slices [i](#)

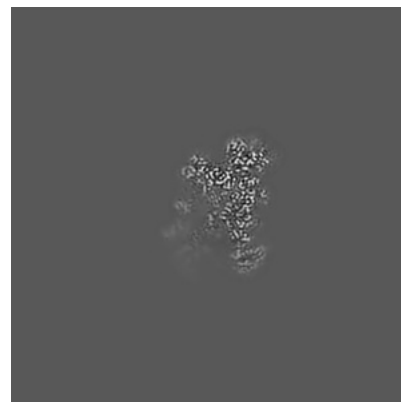
6.3.1 Primary map



X Index: 181

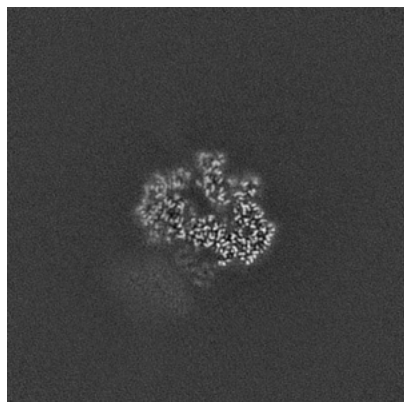


Y Index: 191

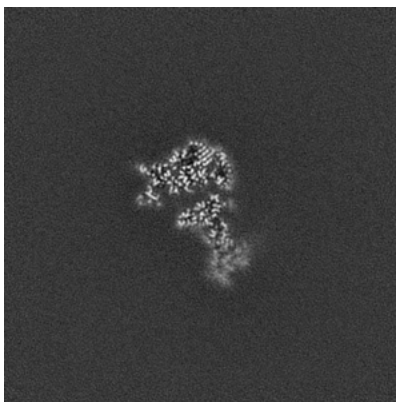


Z Index: 145

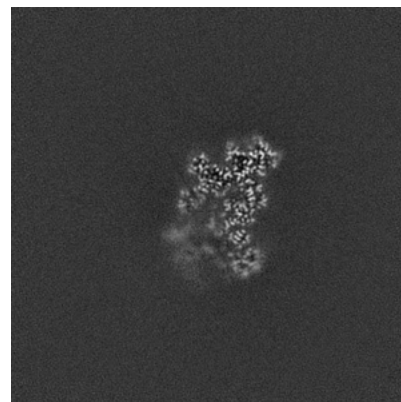
6.3.2 Raw map



X Index: 181



Y Index: 198

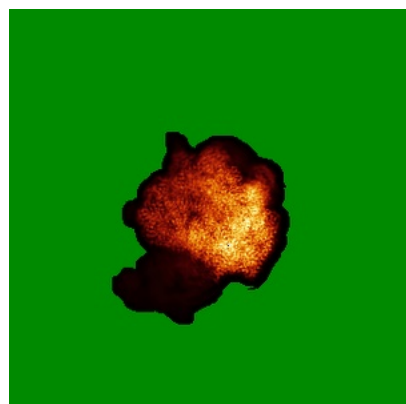


Z Index: 149

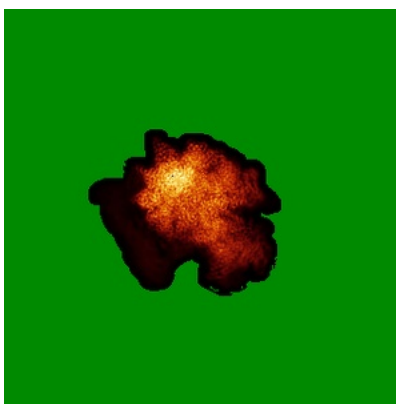
The images above show the largest variance slices of the map in three orthogonal directions.

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

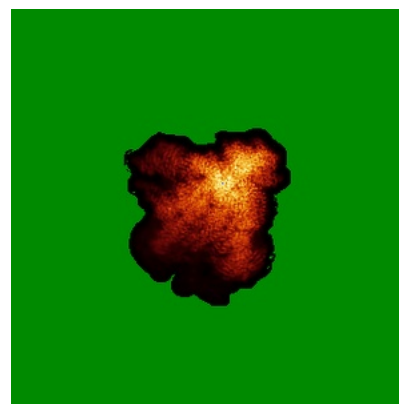
6.4.1 Primary map



X

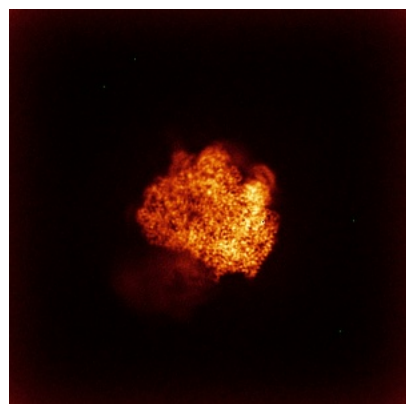


Y

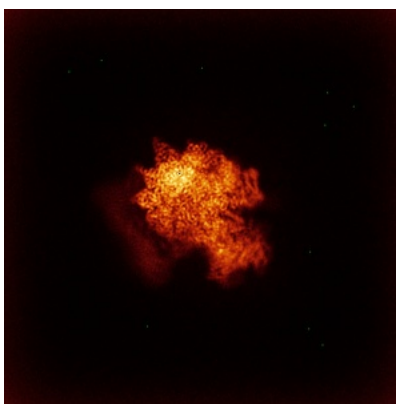


Z

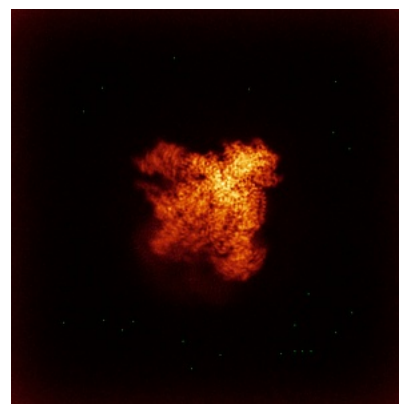
6.4.2 Raw map



X



Y

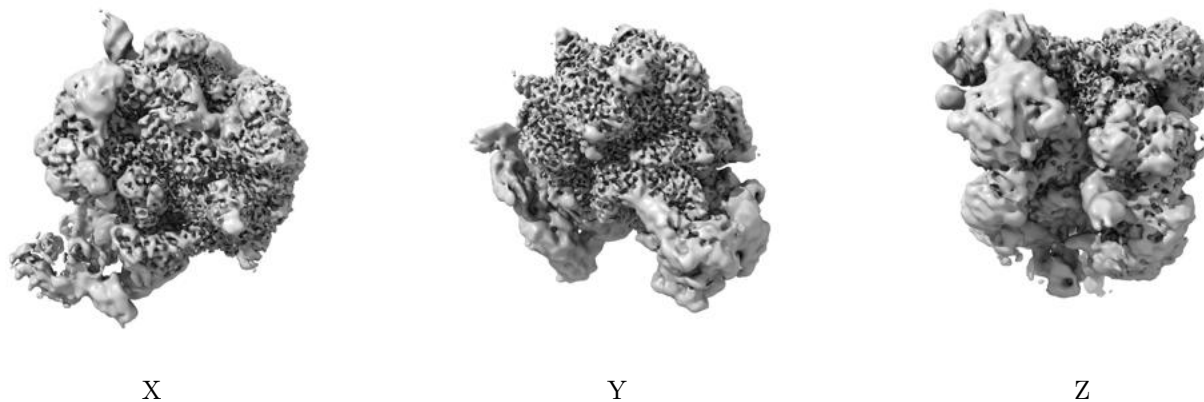


Z

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.

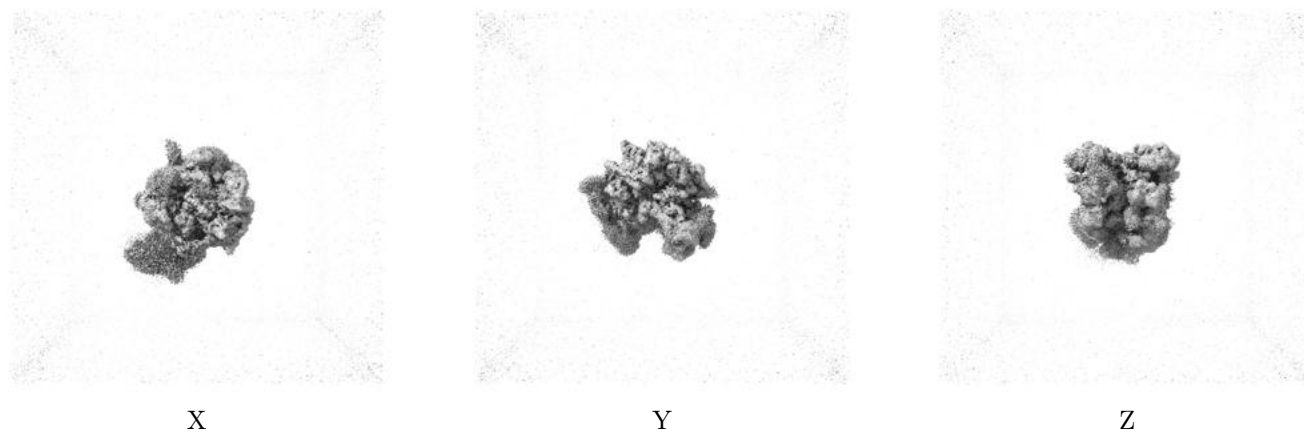
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

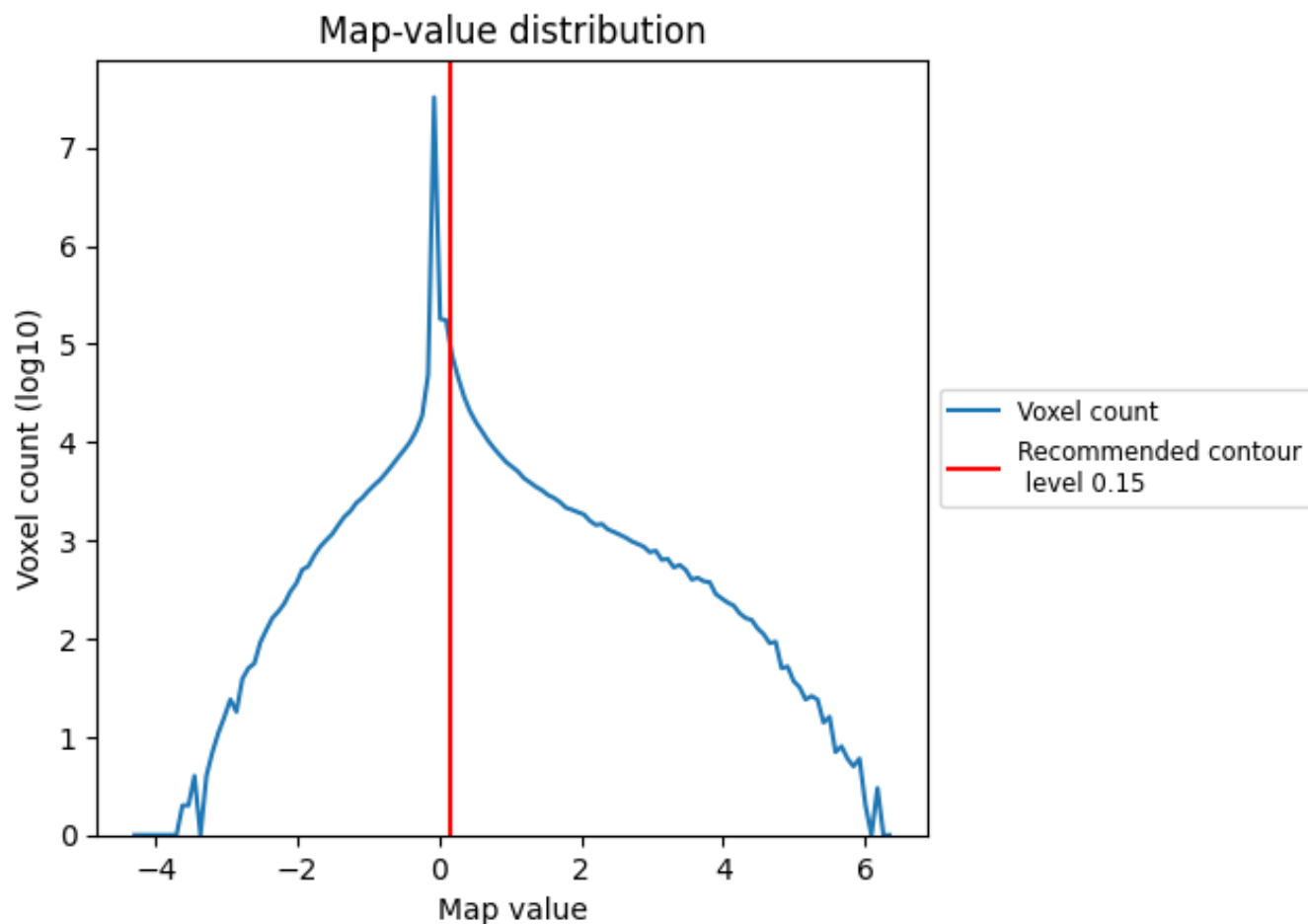
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

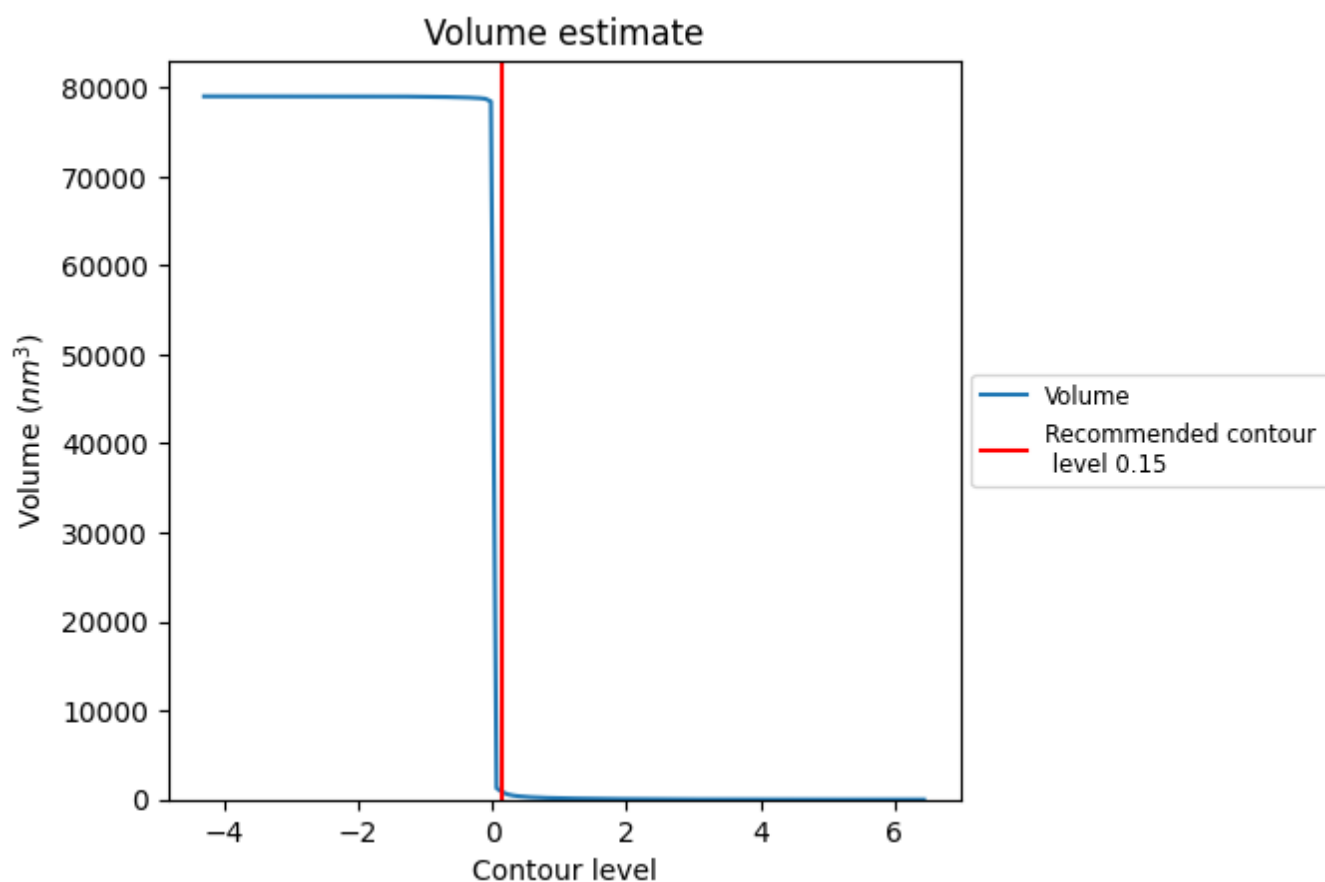
This section contains the results of statistical analysis of the map.

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.

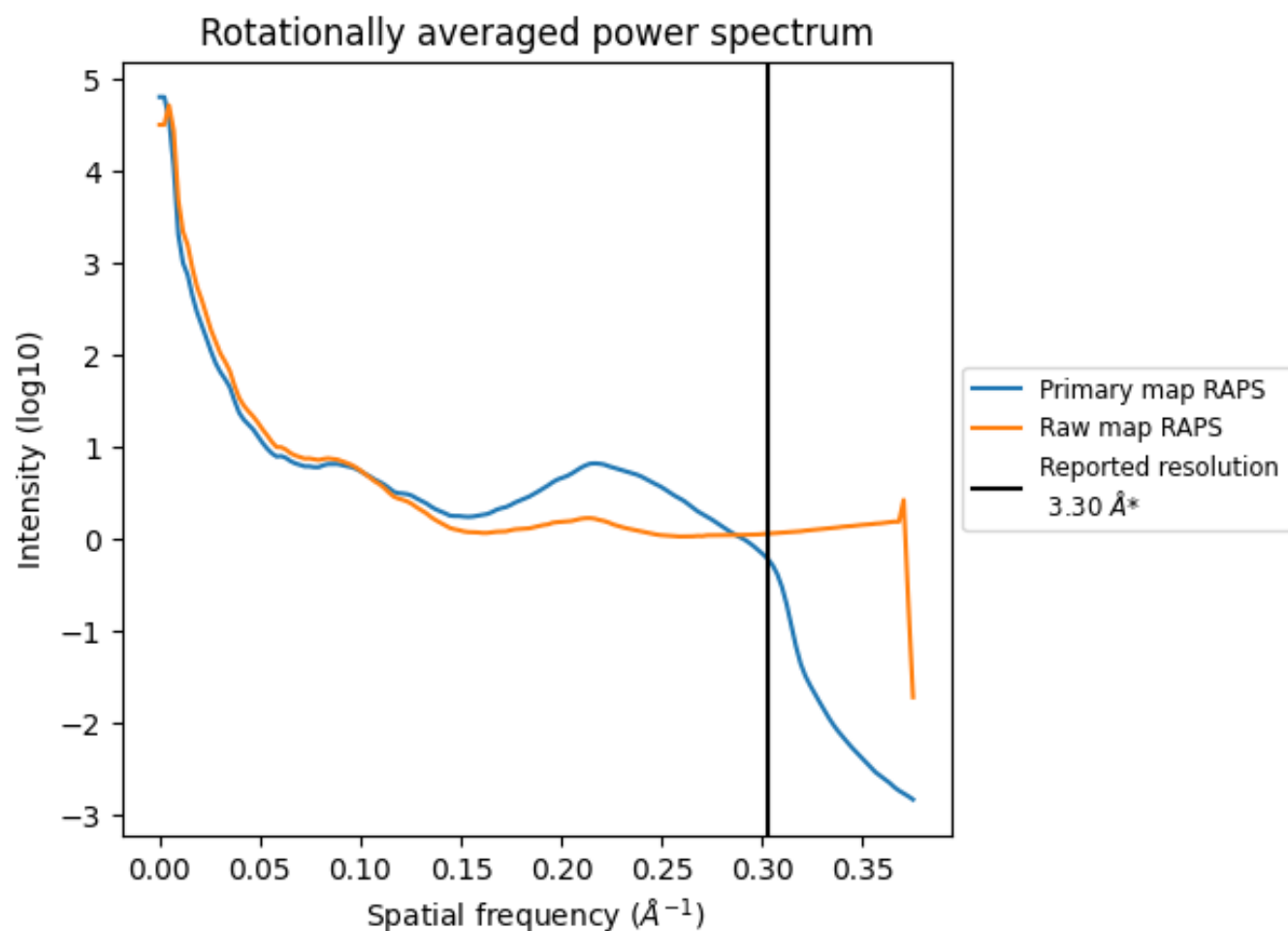
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 832 nm^3 ; this corresponds to an approximate mass of 752 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 ⓘ

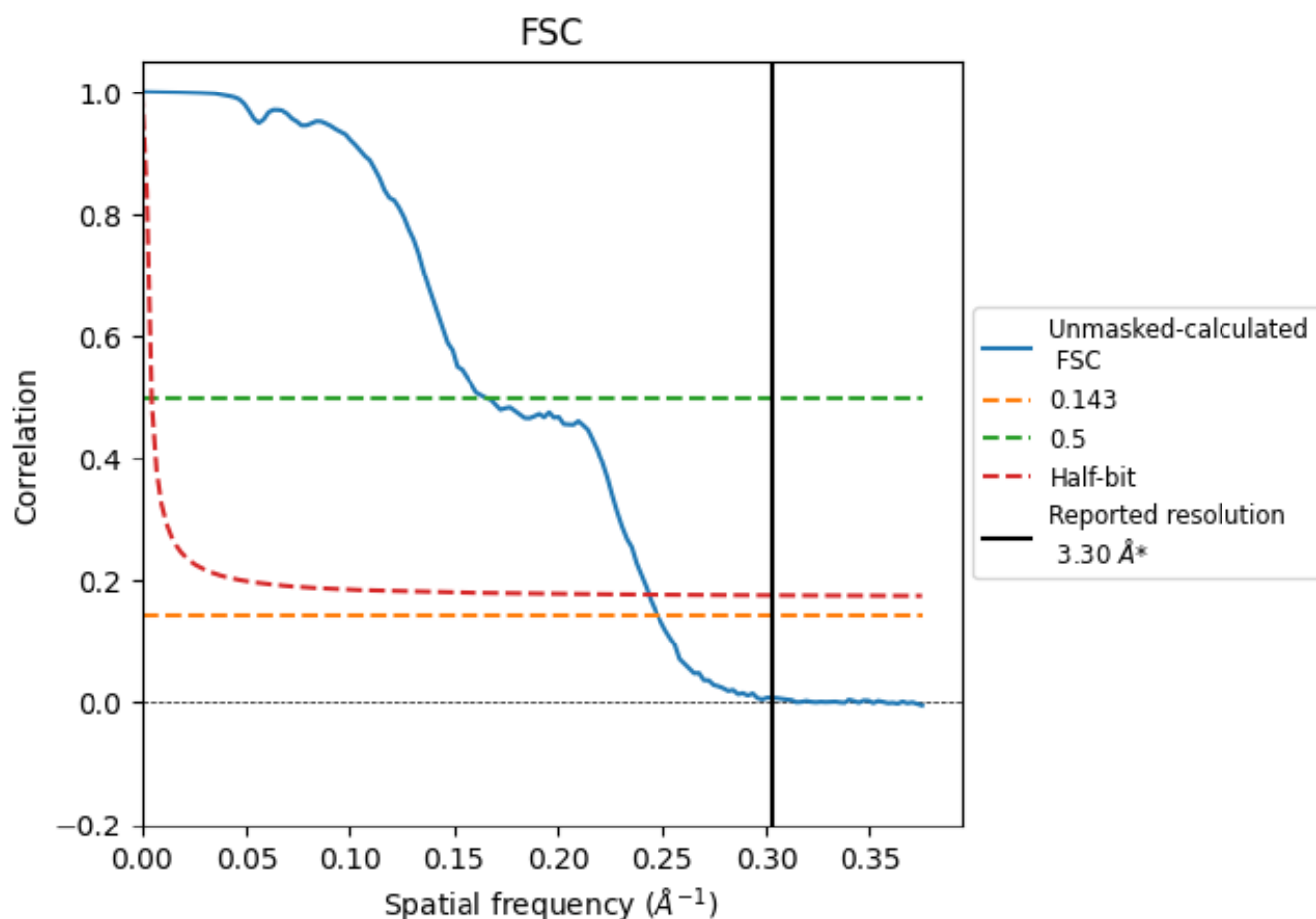


*Reported resolution corresponds to spatial frequency of $0.303 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

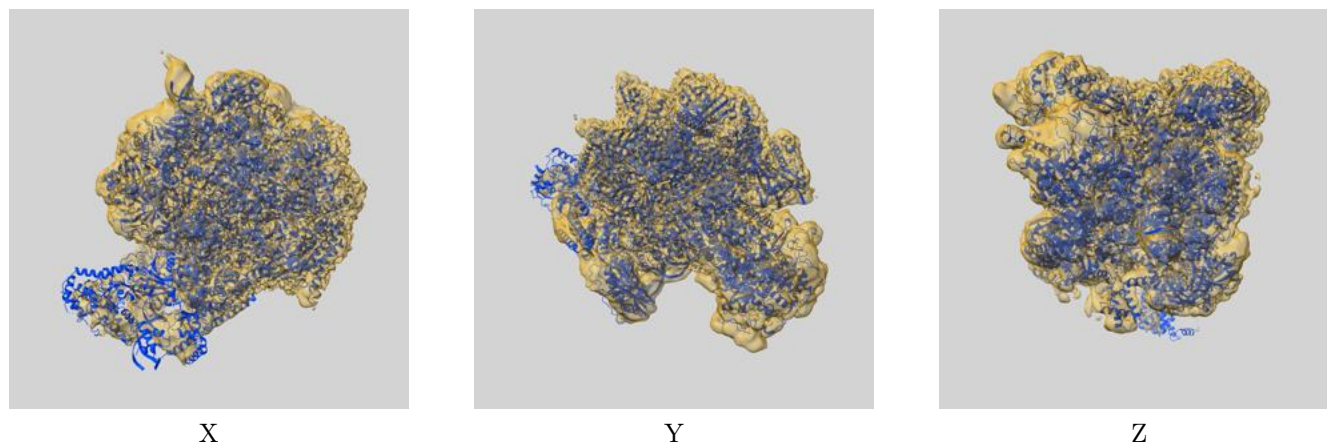
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.03	6.06	4.10

*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 4.03 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

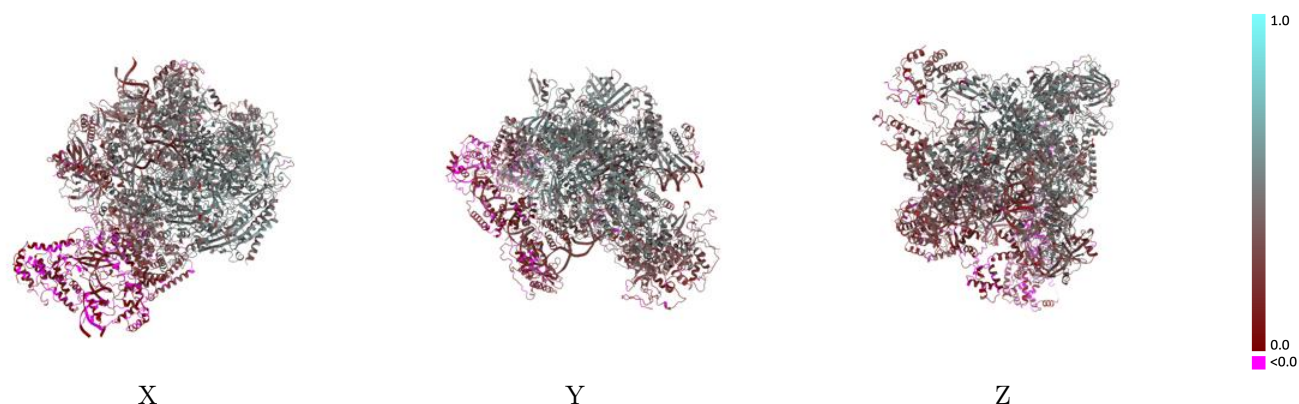
This section contains information regarding the fit between EMDB map EMD-63482 and PDB model 9LXN. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



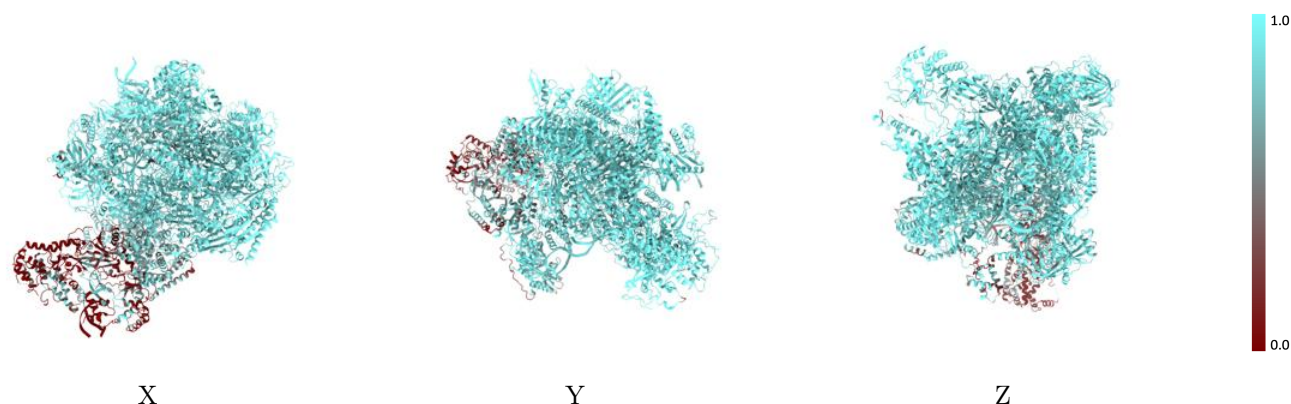
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



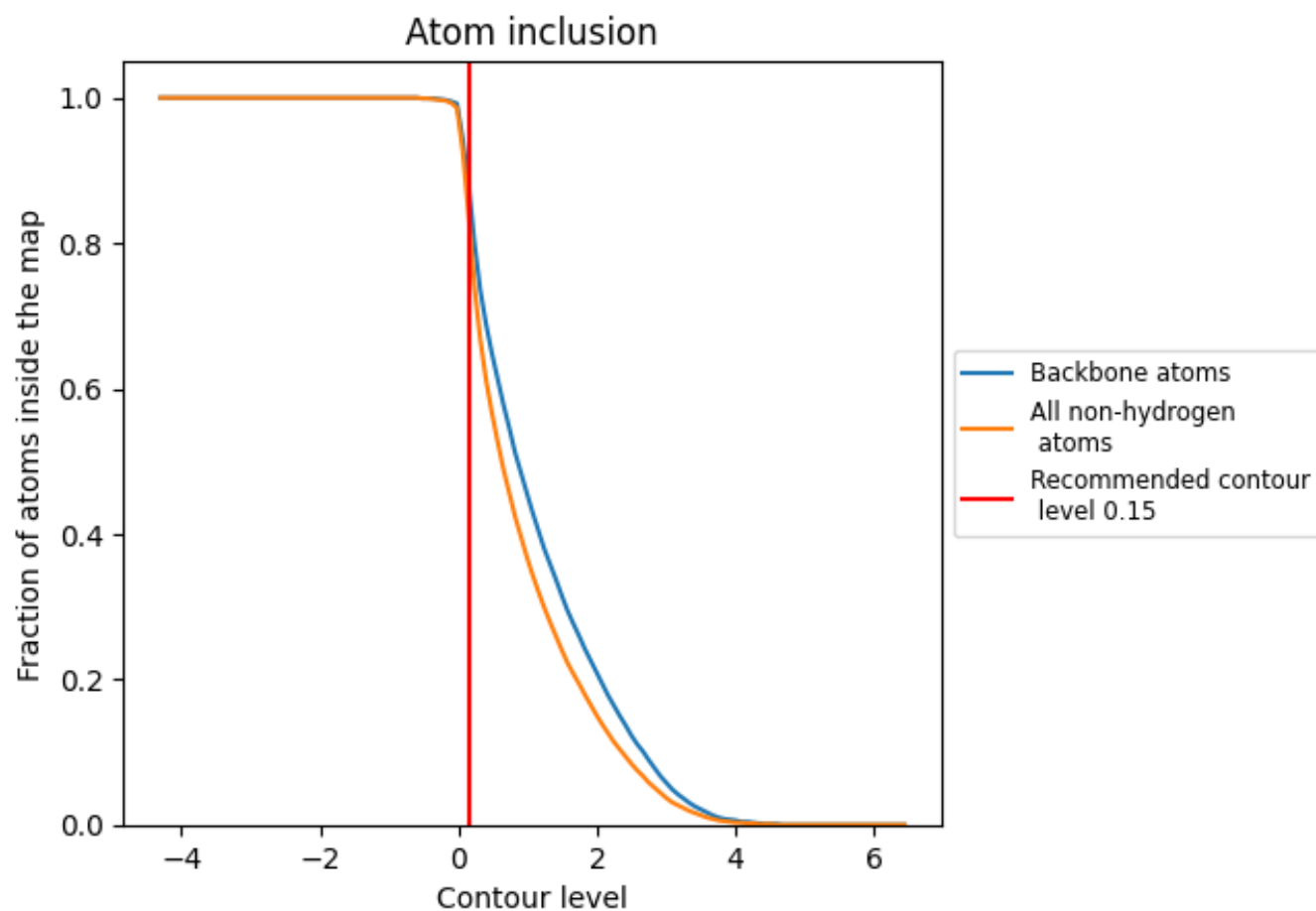
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 84% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8350	 0.3330
1	 0.2130	 0.0320
3	 0.1840	 0.0240
4	 0.3230	 0.0500
A	 0.9410	 0.4520
B	 0.9460	 0.4670
C	 0.9530	 0.4790
D	 0.9740	 0.2800
E	 0.9480	 0.3880
F	 0.9510	 0.4870
G	 0.9510	 0.3430
H	 0.9490	 0.4580
I	 0.9450	 0.4040
J	 0.9500	 0.4740
K	 0.9480	 0.4620
L	 0.9440	 0.4050
M	 0.7890	 0.3070
N	 0.9180	 0.2890
O	 0.9450	 0.3570
P	 0.8700	 0.2310
Q	 0.9260	 0.3030
U	 0.8920	 0.1360
V	 0.7890	 0.2290
W	 0.7780	 0.1250
X	 0.8300	 0.1670
Y	 0.8190	 0.2160
Z	 0.9650	 0.4920

