



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 11:27 PM UTC

PDB ID : 8W8F / pdb_00008w8f
EMDB ID : EMD-37353
Title : human co-transcriptional RNA capping enzyme RNGTT-CMTR1
Authors : Li, Y.; Wang, Q.; Xu, Y.; Li, Z.
Deposited on : 2023-09-02
Resolution : 4.00 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

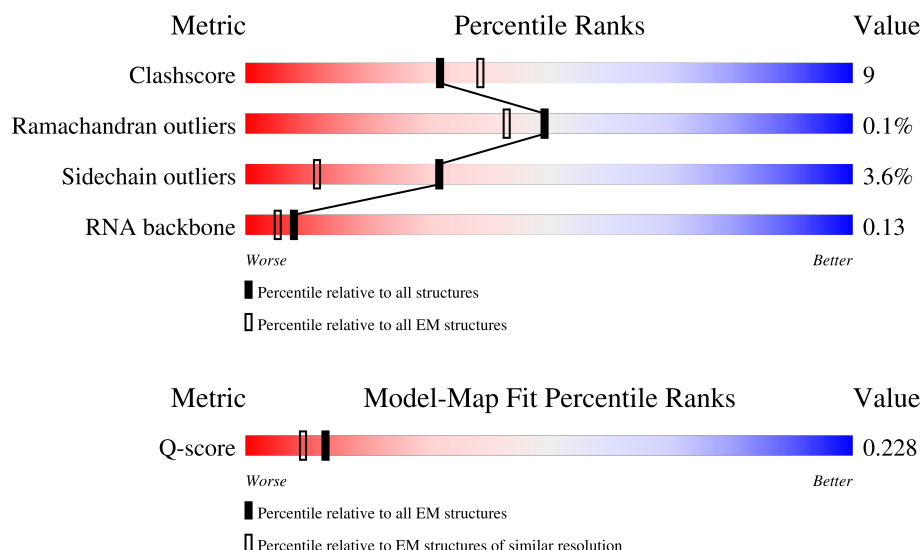
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

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



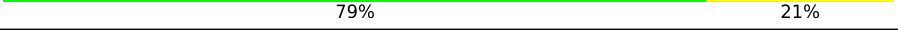
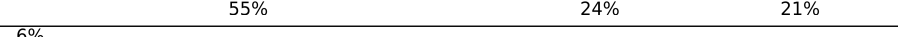
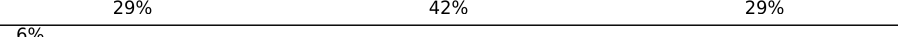
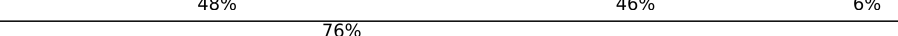
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7587 (3.50 - 4.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	597	
2	b	835	
3	A	1970	

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Mol	Chain	Length	Quality of chain
4	B	1174	
5	C	271	
6	D	142	
7	E	210	
8	F	127	
9	G	172	
10	H	150	
11	I	125	
12	J	67	
13	K	117	
14	L	58	
15	N	48	
16	P	17	
17	T	48	
18	Y	121	
19	Z	1087	

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 46667 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 mRNA-capping enzyme.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	517	Total	C	N	O	S	6	0
			4203	2684	726	759	34		

- Molecule 2 is a protein called Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	693	Total	C	N	O	S	0	0
			5584	3574	951	1024	35		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	1426	Total	C	N	O	S	0	0
			11299	7111	2020	2099	69		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	1133	Total	C	N	O	S	0	0
			9046	5723	1594	1665	64		

- Molecule 5 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	258	Total	C	N	O	S	0	0
			2072	1301	353	412	6		

- Molecule 6 is a protein called DNA-directed RNA polymerase II subunit RPB4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	129	Total	C	N	O	S	0	1
			998	629	170	195	4		

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	209	Total	C	N	O	S	0	0
			1721	1089	300	324	8		

- Molecule 8 is a protein called DNA-directed RNA polymerase II subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	82	Total	C	N	O	S	0	0
			658	418	113	122	5		

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	171	Total	C	N	O	S	0	0
			1305	852	205	240	8		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

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

- Molecule 11 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	117	Total	C	N	O	S	0	0
			950	587	169	183	11		

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	67	Total	C	N	O	S	0	0
			533	345	90	92	6		

- Molecule 13 is a protein called DNA-directed RNA polymerase II subunit RPB11-a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K	115	Total	C	N	O	S	0	0
			920	593	152	173	2		

- Molecule 14 is a protein called RPB12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	46	Total	C	N	O	S	0	0
			389	241	75	67	6		

- Molecule 15 is a DNA chain called DNA (36-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	34	Total	C	N	O	P	0	0
			714	333	147	200	34		

- Molecule 16 is a RNA chain called RNA (5'-R(P*GP*AP*GP*AP*GP*AP*GP*GP*GP*A P*AP*CP*CP*CP*AP*CP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	16	Total	C	N	O	P	0	0
			347	155	69	107	16		

- Molecule 17 is a DNA chain called DNA (45-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	45	Total	C	N	O	P	0	0
			910	432	156	277	45		

- Molecule 18 is a protein called Transcription elongation factor SPT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Y	116	Total	C	N	O	S	0	0
			911	570	159	173	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	-3	GLY	-	expression tag	UNP P63272
Y	-2	PRO	-	expression tag	UNP P63272
Y	-1	GLY	-	expression tag	UNP P63272
Y	0	SER	-	expression tag	UNP P63272

- Molecule 19 is a protein called Transcription elongation factor SPT5.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Z	360	Total	C	N	O	S	0	0
			2880	1835	495	537	13		

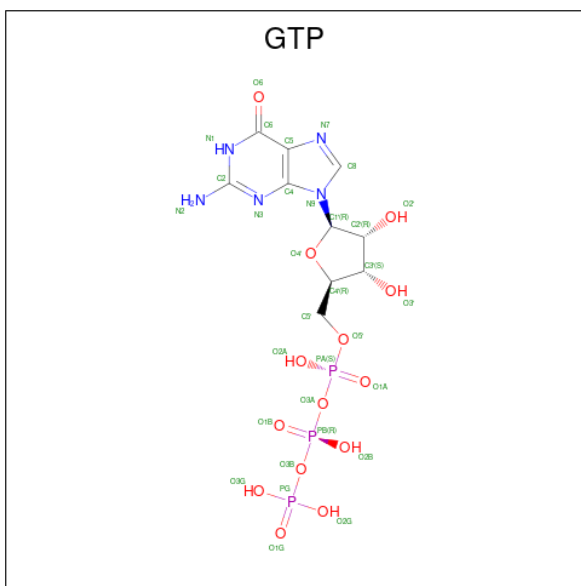
- Molecule 20 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

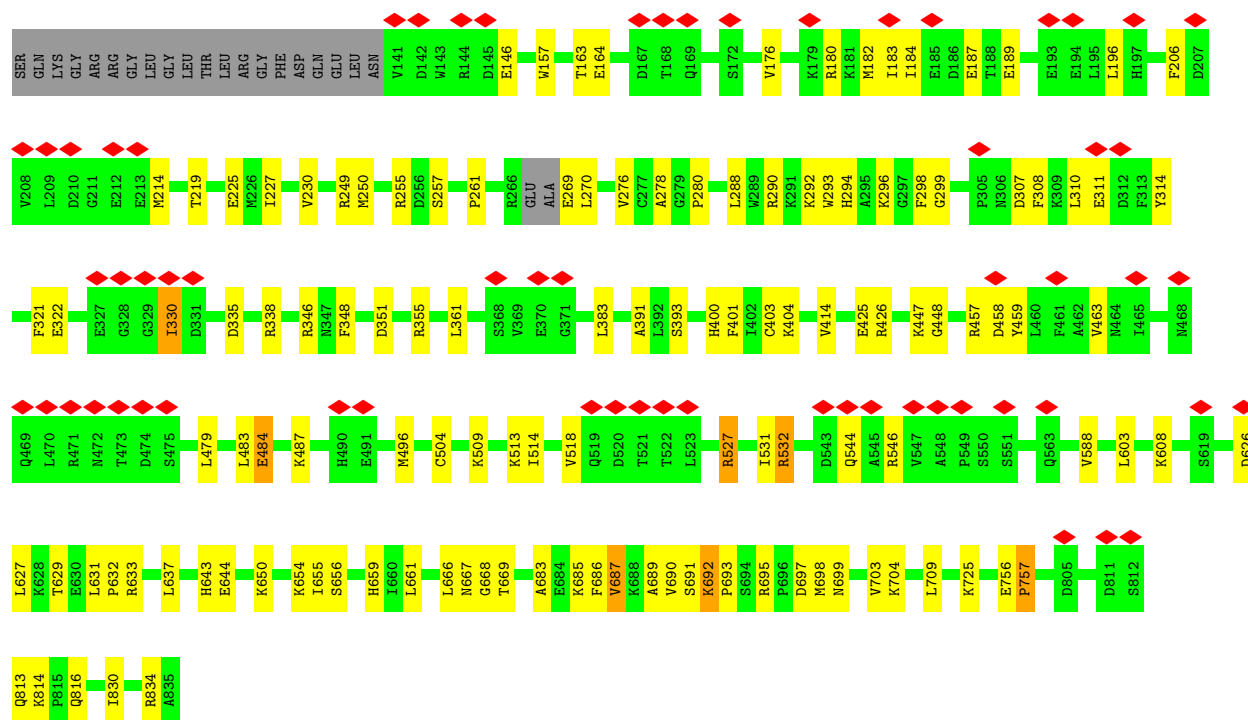
- Molecule 21 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
21	A	2	Total 2	Zn 2	0
21	B	1	Total 1	Zn 1	0
21	C	1	Total 1	Zn 1	0
21	I	2	Total 2	Zn 2	0
21	L	1	Total 1	Zn 1	0
21	Y	1	Total 1	Zn 1	0

- Molecule 22 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃) (labeled as "Ligand of Interest" by depositor).

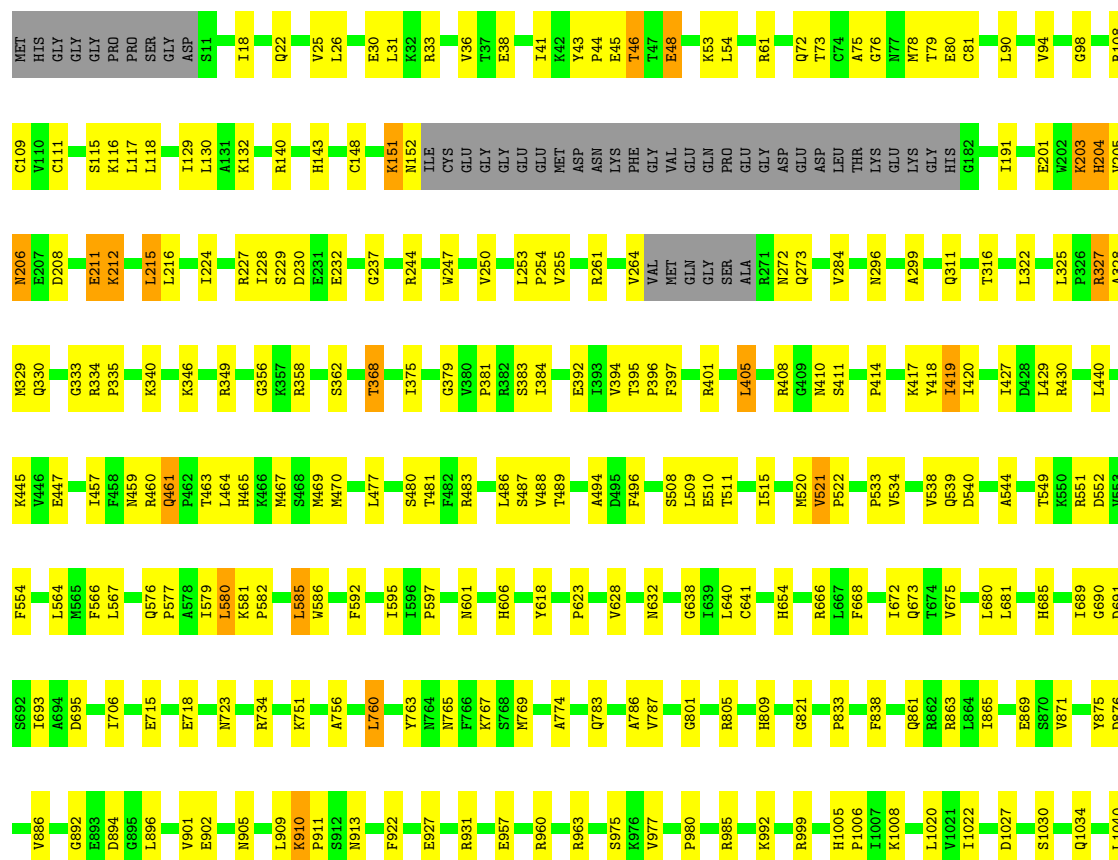


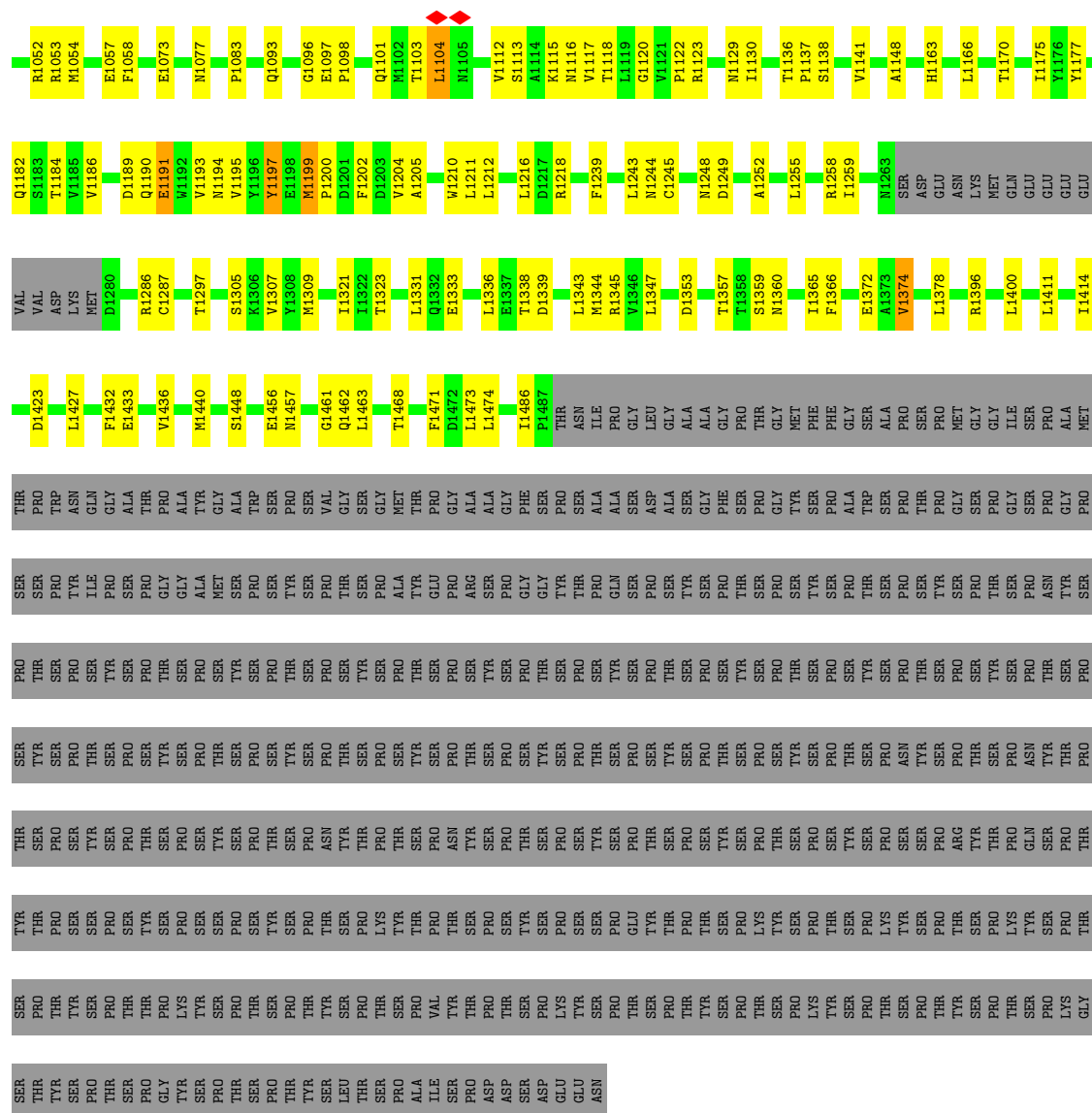
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
22	P	1	32	10	5	14	3	0



• Molecule 3: DNA-directed RNA polymerase subunit

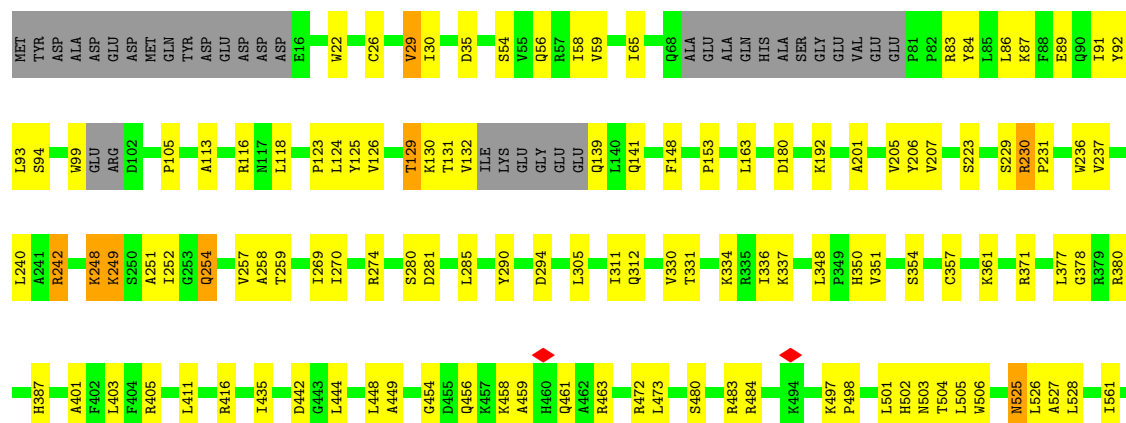
Chain A: 54% 17% 28%

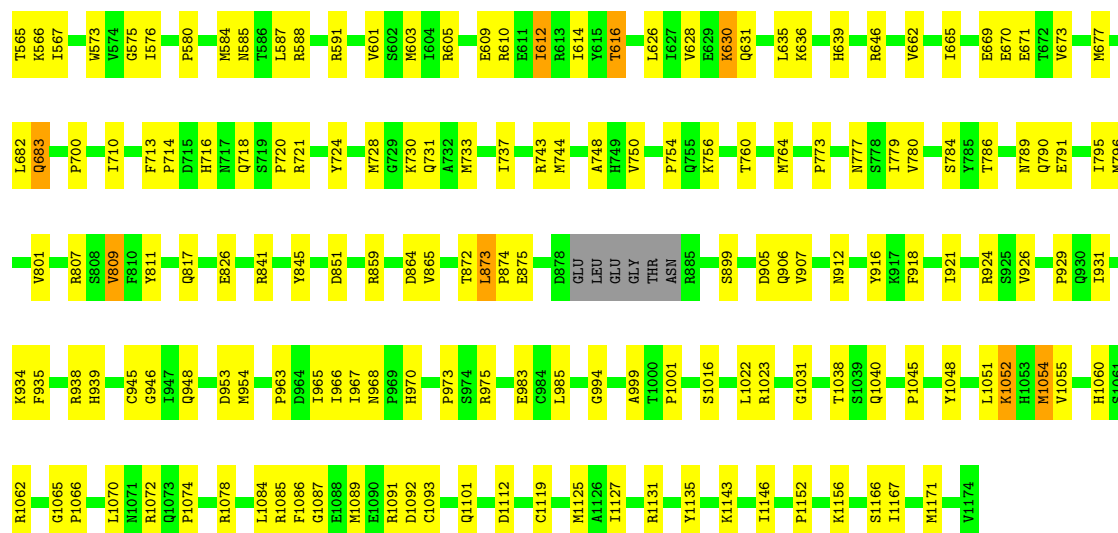




• Molecule 4: DNA-directed RNA polymerase subunit beta

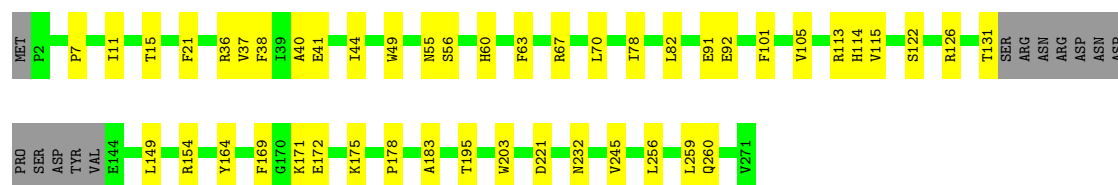
Chain B: 72% 23%





• Molecule 5: DNA-directed RNA polymerase II subunit RPB3

Chain C: 78% 17% 5%



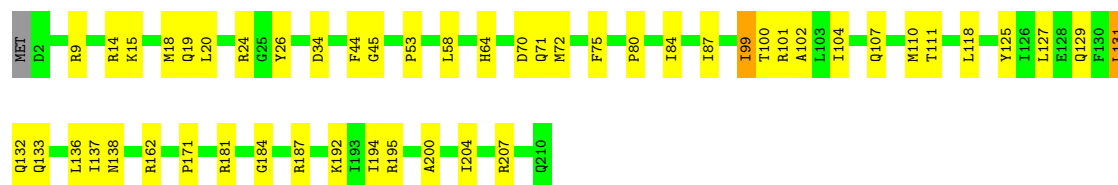
• Molecule 6: DNA-directed RNA polymerase II subunit RPB4

Chain D: 80% 11% 9%



• Molecule 7: DNA-directed RNA polymerase II subunit E

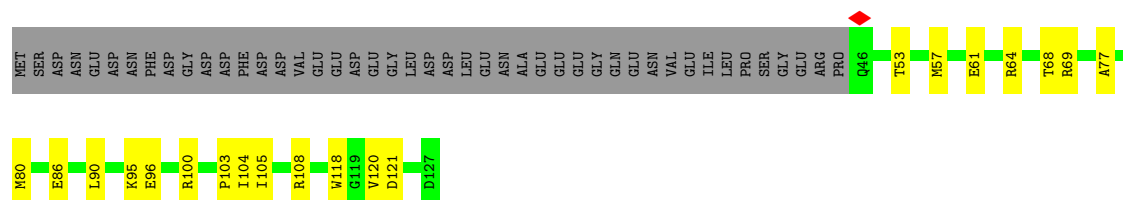
Chain E: 76% 23%



• Molecule 8: DNA-directed RNA polymerase II subunit F

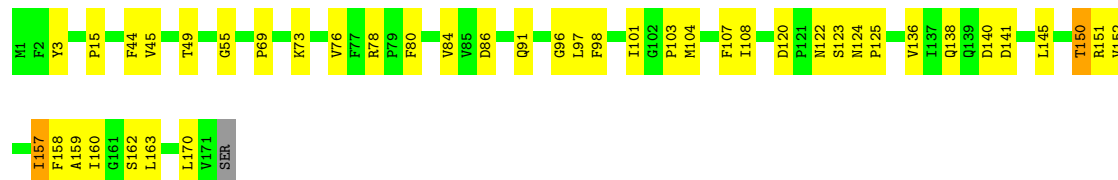
Chain F: 49% 16% 35%





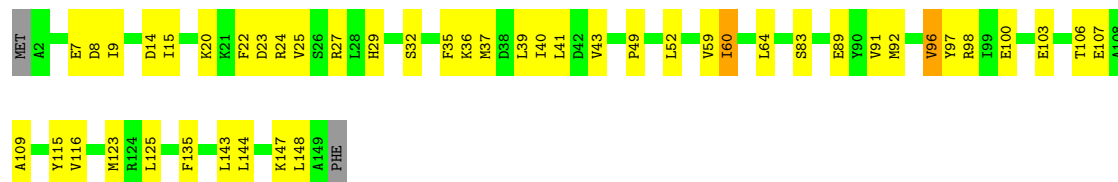
- Molecule 9: DNA-directed RNA polymerase II subunit RPB7

Chain G: 75% 23% ..



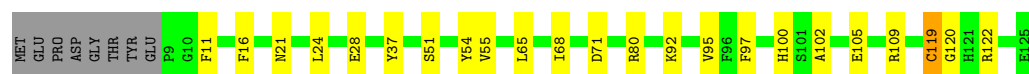
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC3

Chain H: 68% 29% ..



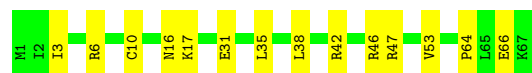
- Molecule 11: DNA-directed RNA polymerase II subunit RPB9

Chain I: 75% 18% 6%



- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC5

Chain J: 79% 21%



- Molecule 13: DNA-directed RNA polymerase II subunit RPB11-a

Chain K: 79% 18% ..



- Molecule 14: RPB12



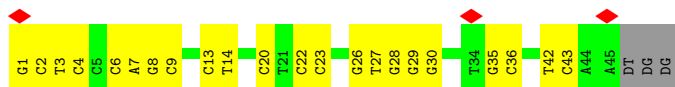
Chain N: 6% 29% 42% 29%



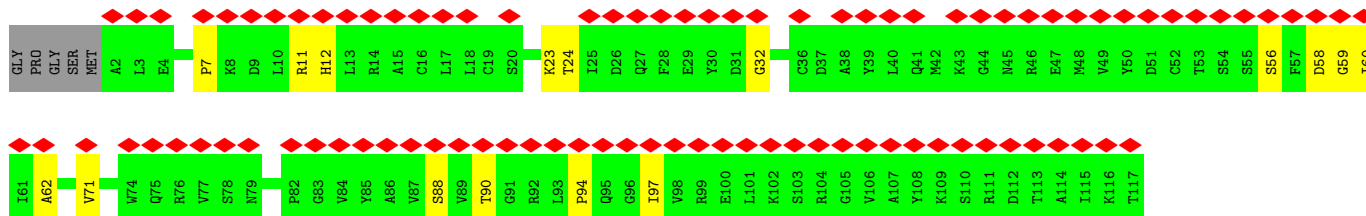
Chain P:



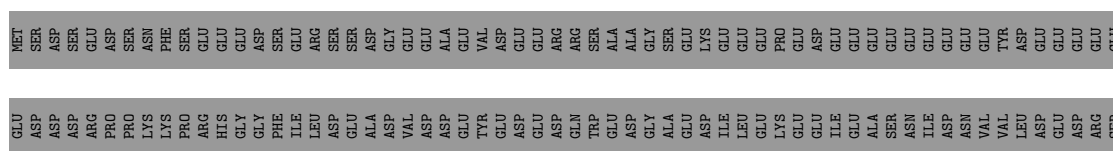
Chain T:



Chain Y: 76% 83% 13%



Chain Z:





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	92000	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.604	Depositor
Minimum map value	-1.299	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.070	Depositor
Recommended contour level	0.26	Depositor
Map size ($\text{\AA}$)	426.88, 426.88, 426.88	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.334, 1.334, 1.334	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: MG, GTP, ZN

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	0.14	0/4322	0.38	0/5831
2	b	0.17	0/5715	0.39	0/7708
3	A	0.09	0/11509	0.29	2/15542 (0.0%)
4	B	0.08	0/9226	0.28	0/12451
5	C	0.08	0/2115	0.27	0/2873
6	D	0.07	0/1012	0.21	0/1366
7	E	0.09	0/1752	0.27	0/2366
8	F	0.07	0/668	0.23	0/901
9	G	0.10	0/1336	0.29	0/1820
10	H	0.08	0/1207	0.25	0/1628
11	I	0.07	0/973	0.25	0/1316
12	J	0.08	0/542	0.27	0/730
13	K	0.09	0/939	0.25	0/1271
14	L	0.09	0/395	0.27	0/524
15	N	0.16	0/804	0.38	0/1240
16	P	0.10	0/389	0.30	0/605
17	T	0.20	0/1015	0.46	0/1562
18	Y	0.05	0/927	0.20	0/1250
19	Z	0.06	0/2928	0.23	0/3940
All	All	0.11	0/47774	0.31	2/64924 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1120	GLY	CA-C-N	5.02	123.40	120.24
3	A	1120	GLY	C-N-CA	5.02	123.40	120.24

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	a	4203	0	4182	62	0
2	b	5584	0	5509	98	0
3	A	11299	0	11416	244	0
4	B	9046	0	9078	196	0
5	C	2072	0	2016	37	0
6	D	998	0	953	12	0
7	E	1721	0	1737	34	0
8	F	658	0	684	14	0
9	G	1305	0	1267	33	0
10	H	1186	0	1147	34	0
11	I	950	0	880	17	0
12	J	533	0	557	10	0
13	K	920	0	942	16	0
14	L	389	0	395	11	0
15	N	714	0	379	23	0
16	P	347	0	175	11	0
17	T	910	0	507	20	0
18	Y	911	0	905	12	0
19	Z	2880	0	2925	40	0
20	A	1	0	0	0	0
21	A	2	0	0	0	0
21	B	1	0	0	0	0
21	C	1	0	0	0	0
21	I	2	0	0	0	0
21	L	1	0	0	0	0
21	Y	1	0	0	0	0
22	P	32	0	11	0	0
All	All	46667	0	45665	791	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 9.

The worst 5 of 791 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)
3:A:1115:LYS:HE3	3:A:1339:ASP:HA	1.48	0.92
15:N:43:DG:N2	17:T:6:DC:N3	2.18	0.92
2:b:270:LEU:HA	2:b:685:LYS:HE3	1.51	0.91
1:a:157:ALA:HA	1:a:163:GLY:H	1.37	0.88
2:b:687:VAL:HA	2:b:690:VAL:HG22	1.58	0.83

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	a	515/597 (86%)	497 (96%)	17 (3%)	1 (0%)	43	75
2	b	689/835 (82%)	664 (96%)	22 (3%)	3 (0%)	30	65
3	A	1418/1970 (72%)	1320 (93%)	97 (7%)	1 (0%)	48	81
4	B	1123/1174 (96%)	1057 (94%)	66 (6%)	0	100	100
5	C	254/271 (94%)	248 (98%)	6 (2%)	0	100	100
6	D	127/142 (89%)	122 (96%)	5 (4%)	0	100	100
7	E	207/210 (99%)	200 (97%)	7 (3%)	0	100	100
8	F	80/127 (63%)	79 (99%)	1 (1%)	0	100	100
9	G	169/172 (98%)	162 (96%)	7 (4%)	0	100	100
10	H	146/150 (97%)	139 (95%)	7 (5%)	0	100	100
11	I	115/125 (92%)	108 (94%)	7 (6%)	0	100	100
12	J	65/67 (97%)	64 (98%)	1 (2%)	0	100	100
13	K	113/117 (97%)	109 (96%)	4 (4%)	0	100	100
14	L	44/58 (76%)	42 (96%)	2 (4%)	0	100	100
18	Y	114/121 (94%)	112 (98%)	2 (2%)	0	100	100
19	Z	348/1087 (32%)	334 (96%)	14 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	5527/7223 (76%)	5257 (95%)	265 (5%)	5 (0%)	49 81

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	a	162	PRO
2	b	280	PRO
2	b	757	PRO
3	A	1205	ALA
2	b	230	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
1	a	468/534 (88%)	426 (91%)	42 (9%)	9 31
2	b	610/741 (82%)	587 (96%)	23 (4%)	29 51
3	A	1255/1749 (72%)	1196 (95%)	59 (5%)	23 46
4	B	989/1027 (96%)	960 (97%)	29 (3%)	37 58
5	C	235/248 (95%)	234 (100%)	1 (0%)	84 84
6	D	104/126 (82%)	104 (100%)	0	100 100
7	E	191/192 (100%)	187 (98%)	4 (2%)	47 65
8	F	71/111 (64%)	70 (99%)	1 (1%)	59 71
9	G	138/153 (90%)	131 (95%)	7 (5%)	21 45
10	H	129/131 (98%)	125 (97%)	4 (3%)	35 56
11	I	105/112 (94%)	104 (99%)	1 (1%)	68 76
12	J	56/56 (100%)	55 (98%)	1 (2%)	51 68
13	K	104/106 (98%)	100 (96%)	4 (4%)	29 51
14	L	43/55 (78%)	43 (100%)	0	100 100
18	Y	102/105 (97%)	102 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	Z	319/940 (34%)	318 (100%)	1 (0%)	86	85
All	All	4919/6386 (77%)	4742 (96%)	177 (4%)	32	53

5 of 177 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	1191	GLU
4	B	616	THR
3	A	1204	VAL
4	B	240	LEU
4	B	1054	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 93 such sidechains are listed below:

Mol	Chain	Res	Type
4	B	518	HIS
4	B	1145	GLN
4	B	639	HIS
4	B	749	HIS
6	D	129	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	P	15/17 (88%)	11 (73%)	0

5 of 11 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
16	P	32	G
16	P	33	A
16	P	34	G
16	P	35	A
16	P	36	G

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, 9 are monoatomic - leaving 1 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
22	GTP	P	101	16	33,34,34	0.96	1 (3%)	50,54,54	1.56	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
22	GTP	P	101	16	-	5/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	P	101	GTP	C2-N3	2.17	1.38	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	P	101	GTP	C5-C4-N3	-4.88	120.62	128.39
22	P	101	GTP	C2-N3-C4	4.59	120.21	112.30
22	P	101	GTP	N9-C4-N3	3.12	132.19	125.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	P	101	GTP	C2-N1-C6	-2.87	119.91	125.11
22	P	101	GTP	N9-C8-N7	-2.69	108.42	113.40

There are no chirality outliers.

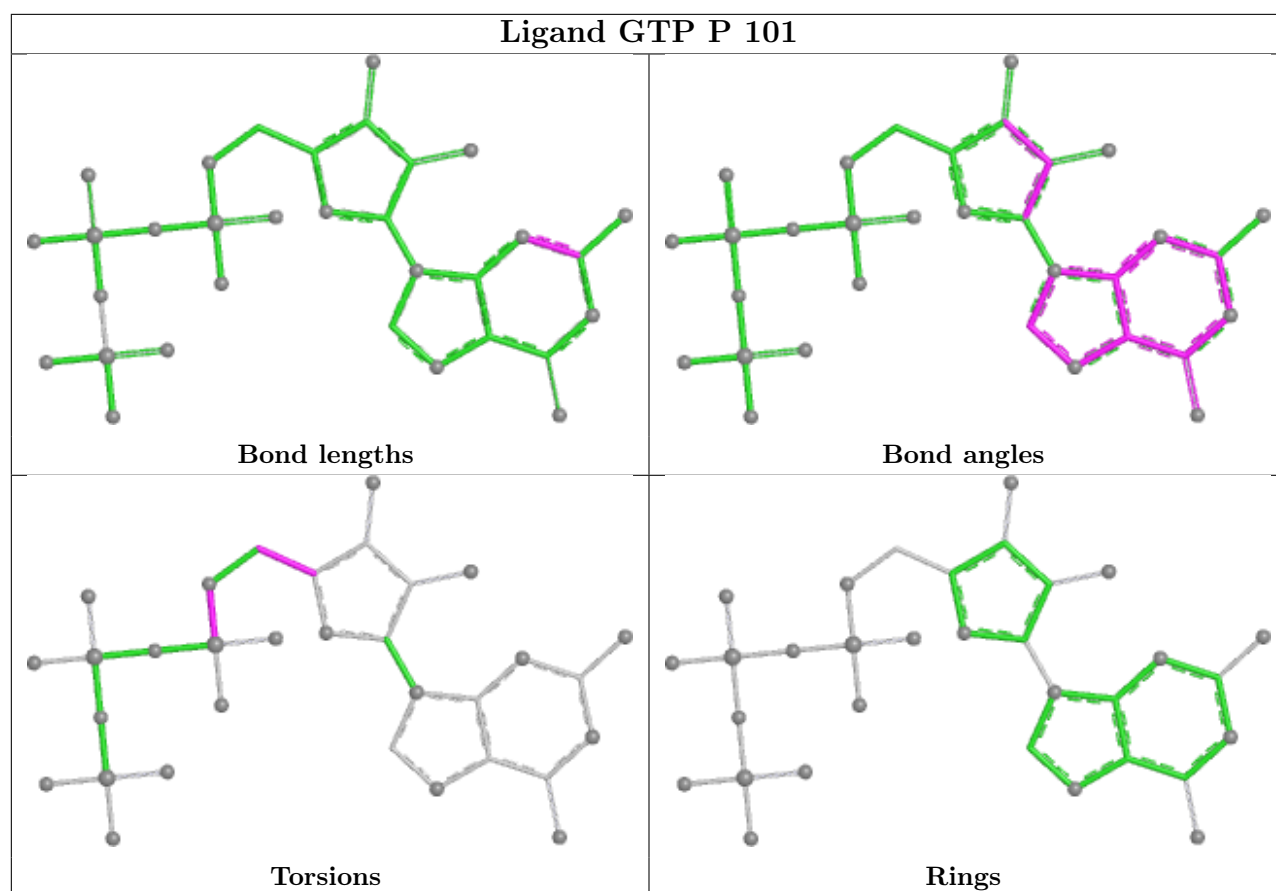
All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	P	101	GTP	C5'-O5'-PA-O3A
22	P	101	GTP	C5'-O5'-PA-O1A
22	P	101	GTP	C5'-O5'-PA-O2A
22	P	101	GTP	O4'-C4'-C5'-O5'
22	P	101	GTP	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

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.

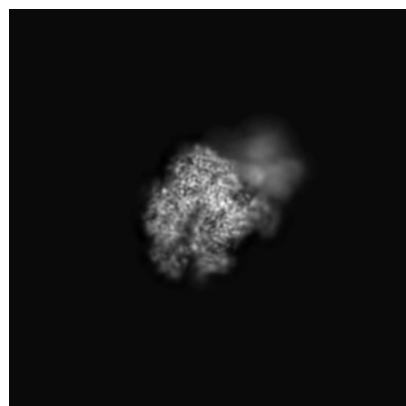
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37353. These allow visual inspection of the internal detail of the map and identification of artifacts.

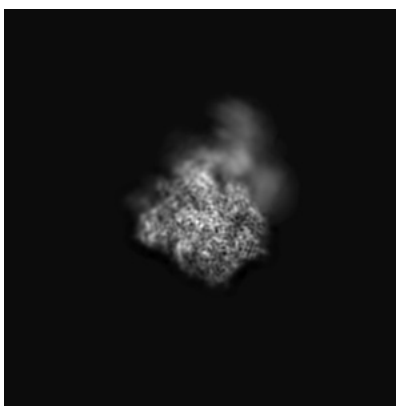
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

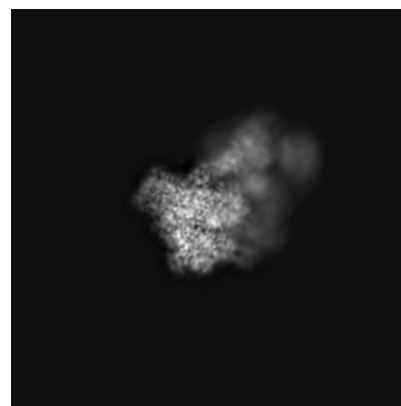
6.1.1 Primary map



X

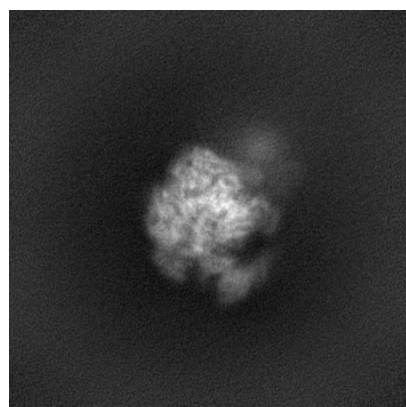


Y

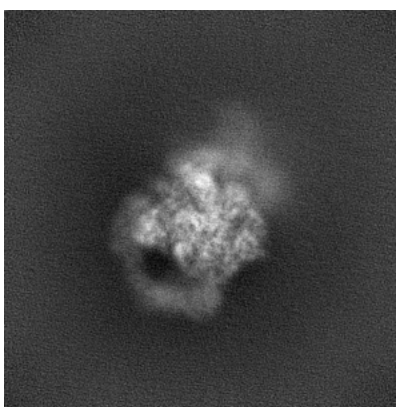


Z

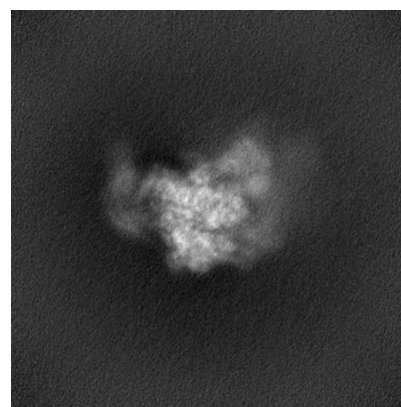
6.1.2 Raw map



X



Y

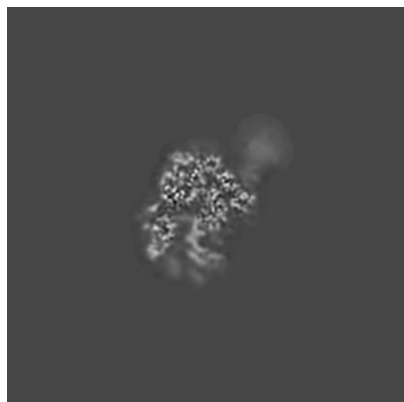


Z

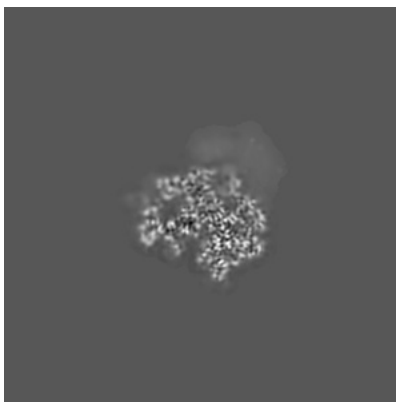
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

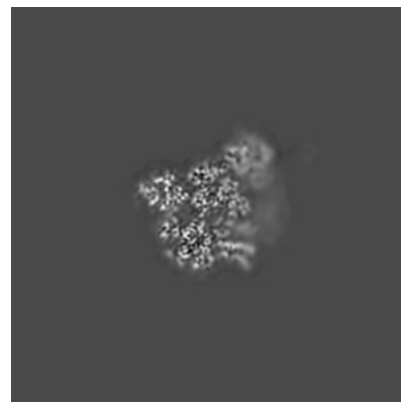
6.2.1 Primary map



X Index: 160

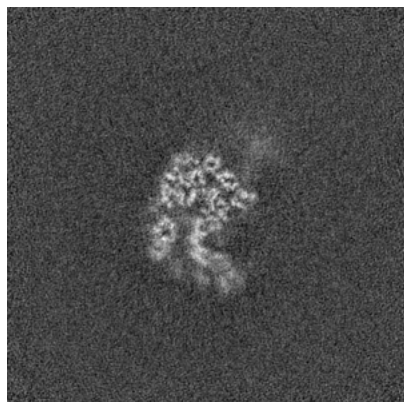


Y Index: 160

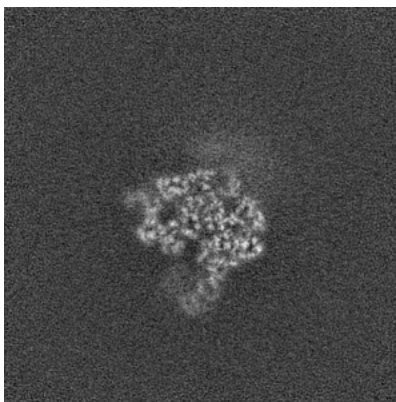


Z Index: 160

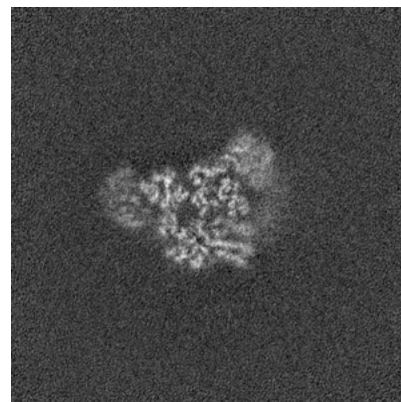
6.2.2 Raw map



X Index: 160



Y Index: 160

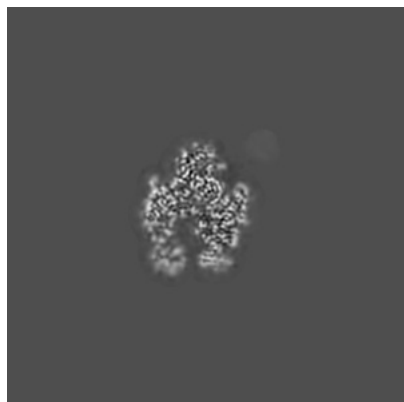


Z Index: 160

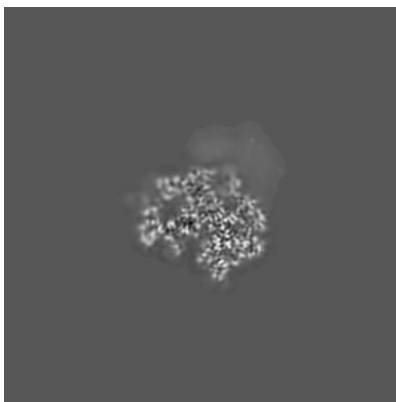
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

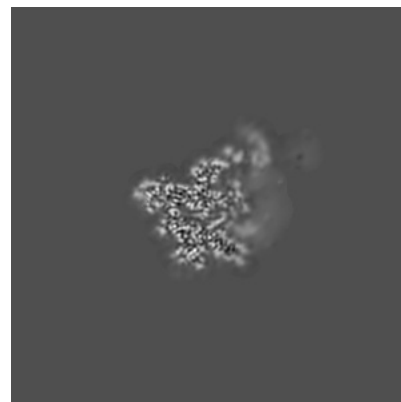
6.3.1 Primary map



X Index: 148

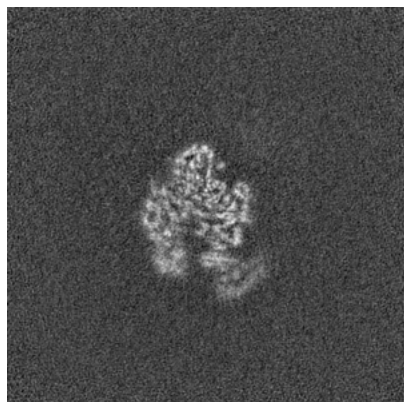


Y Index: 160

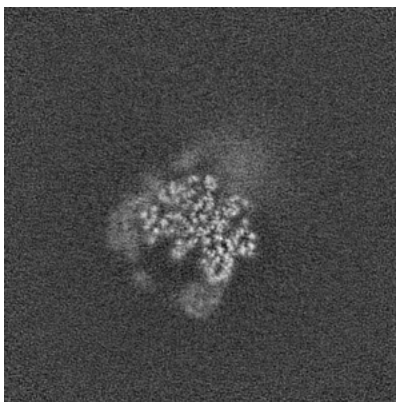


Z Index: 165

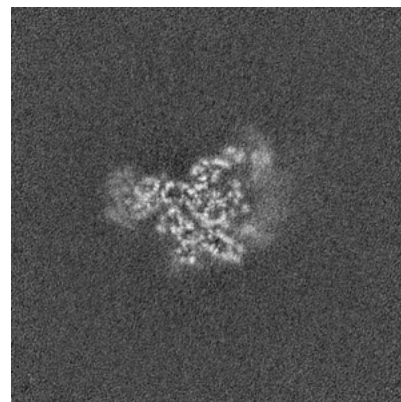
6.3.2 Raw map



X Index: 149



Y Index: 170

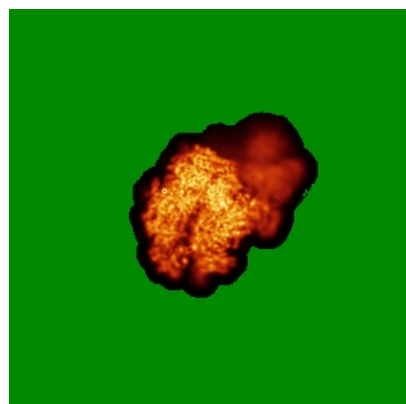


Z Index: 166

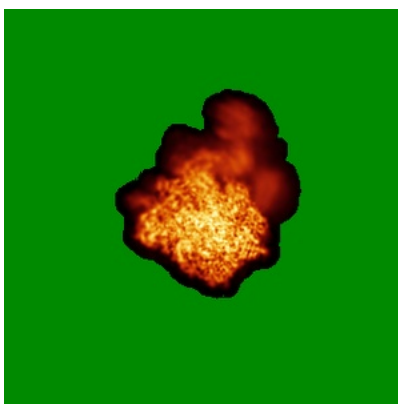
The images above show the largest variance slices of the map in three orthogonal directions.

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

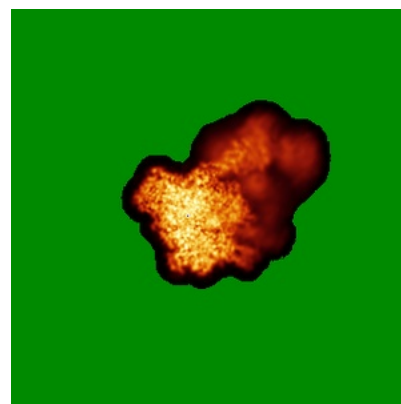
6.4.1 Primary map



X

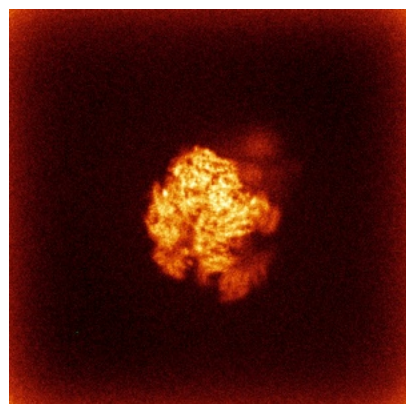


Y

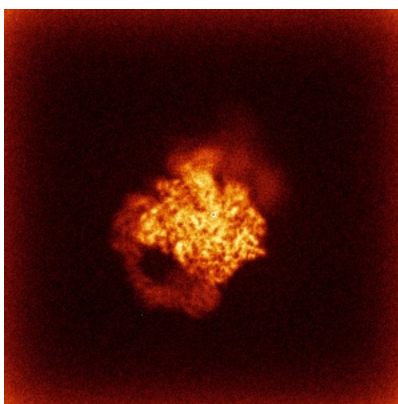


Z

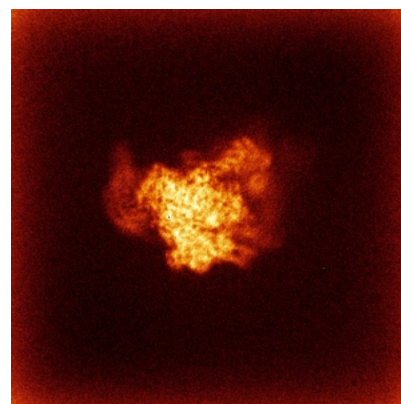
6.4.2 Raw map



X



Y

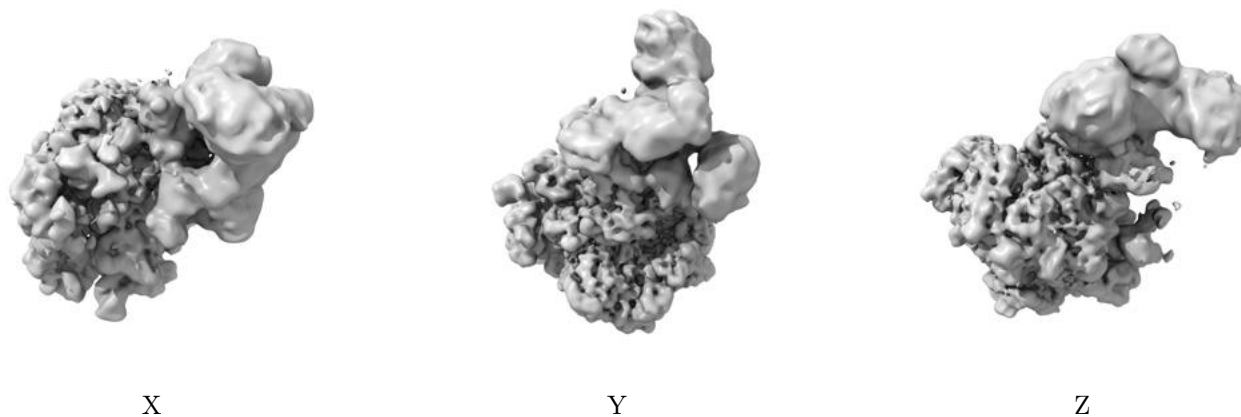


Z

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.

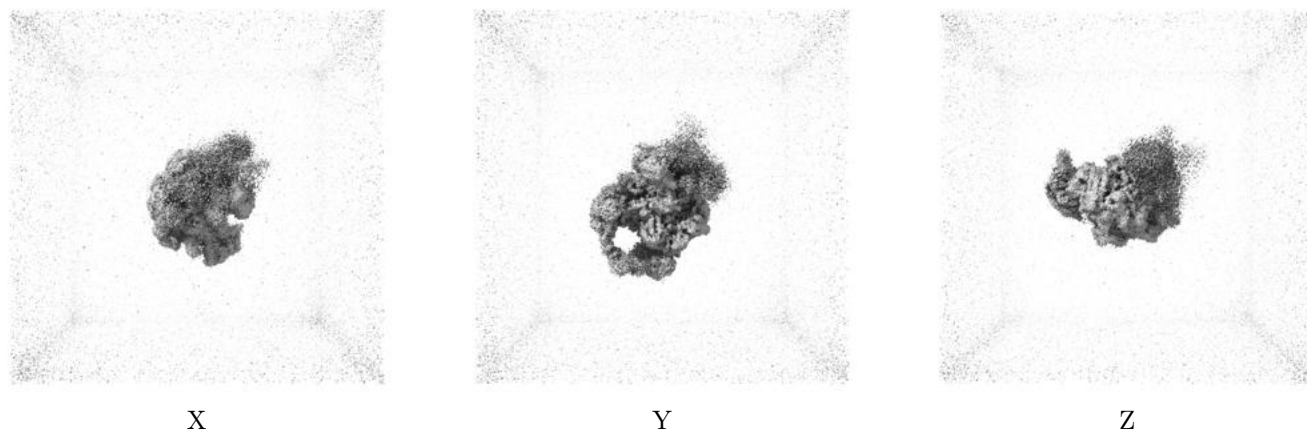
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.26. 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.

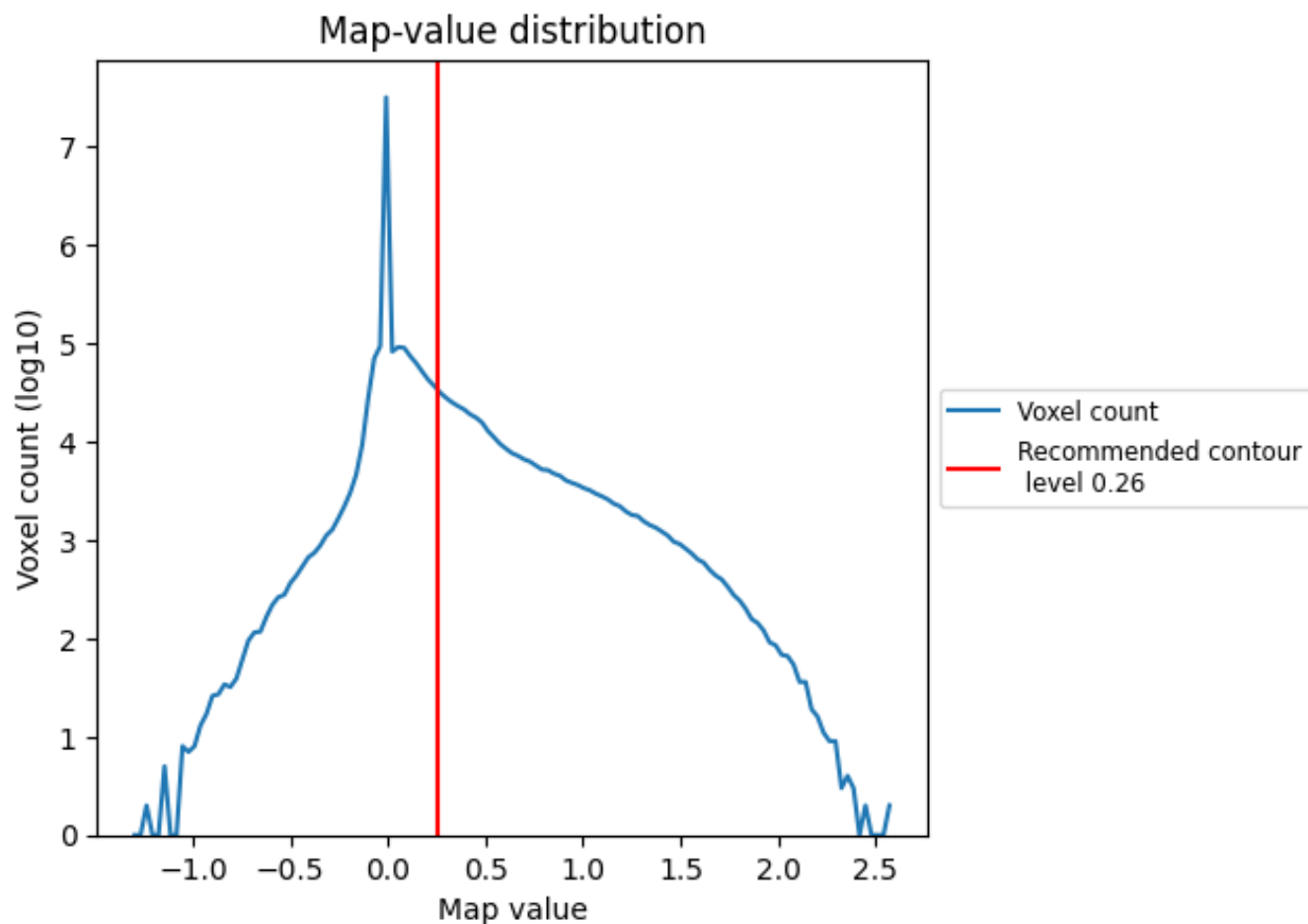
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

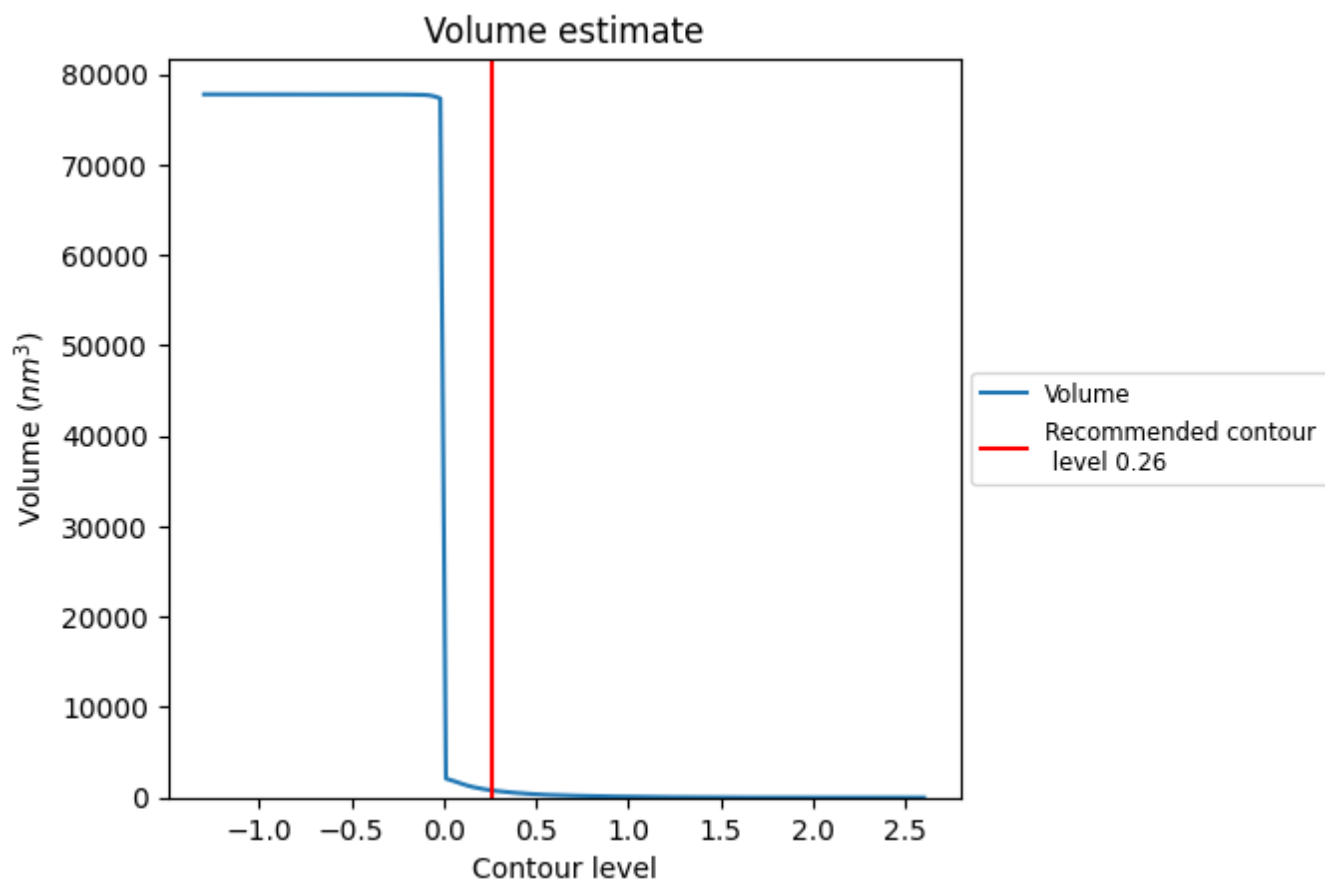
This section contains the results of statistical analysis of the map.

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.

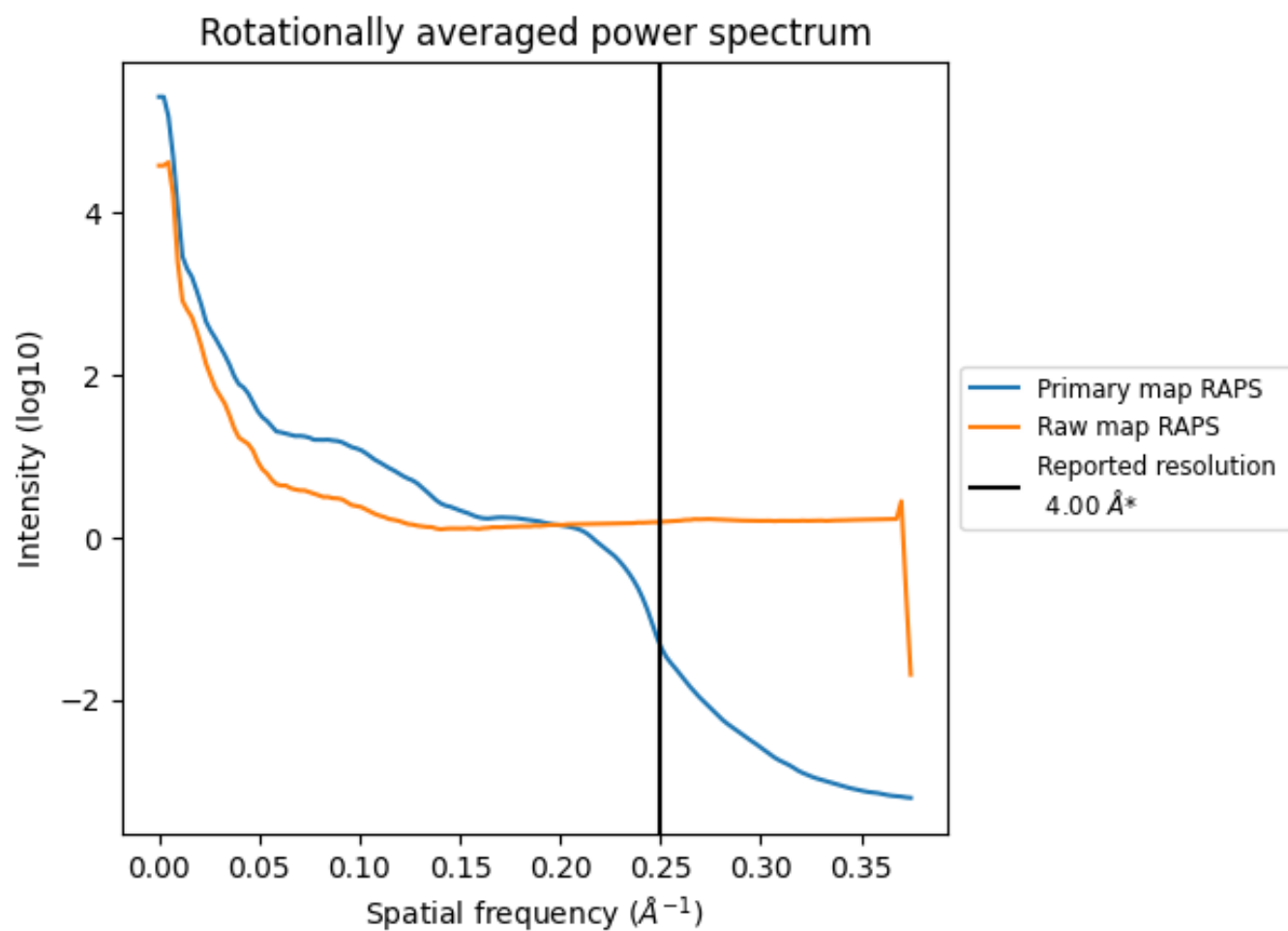
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 798 nm^3 ; this corresponds to an approximate mass of 720 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 ⓘ

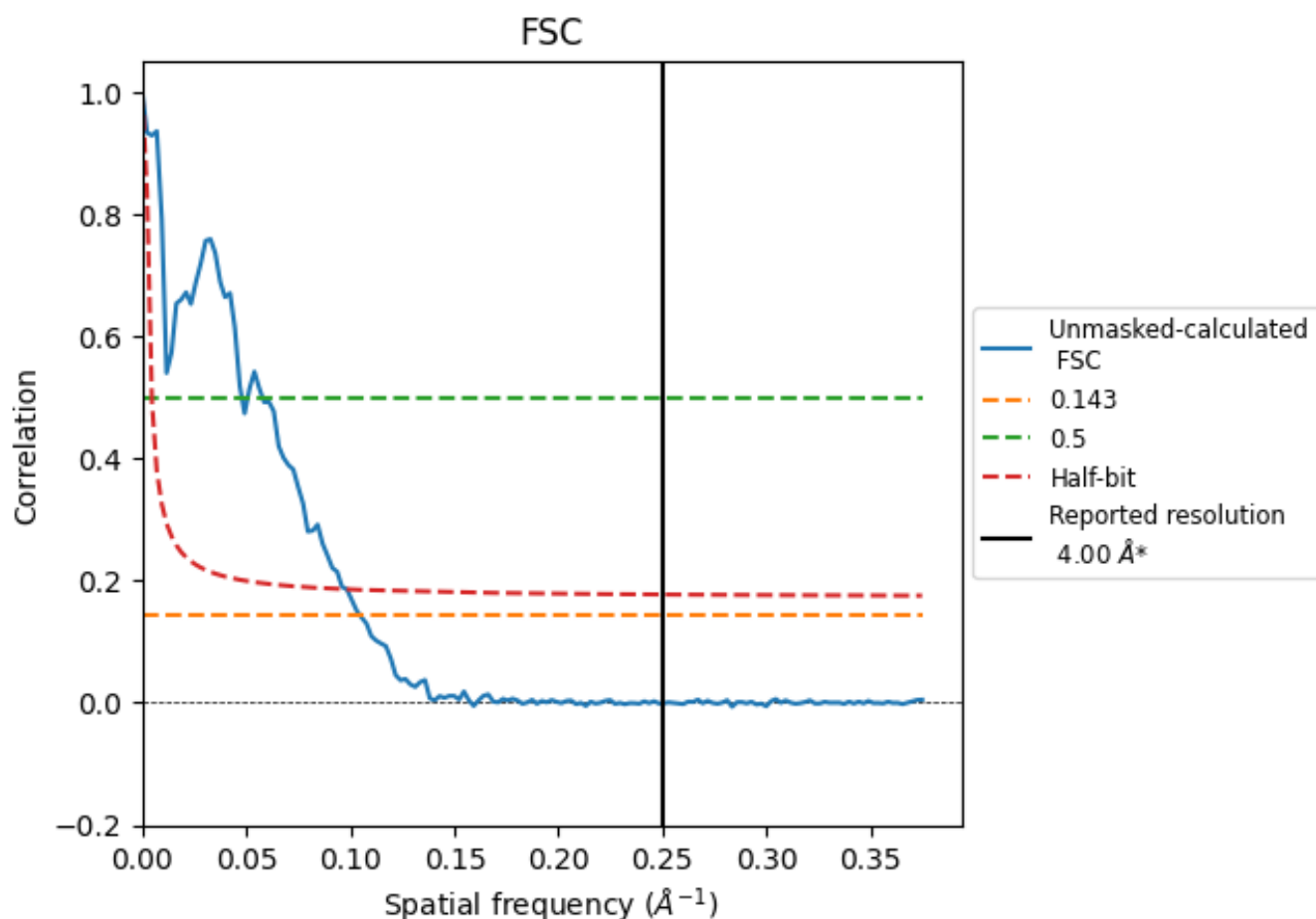


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

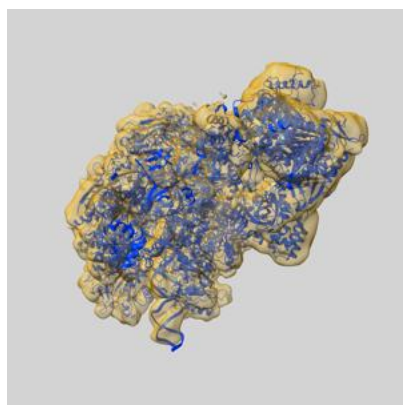
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	9.55	20.92	10.17

*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 9.55 differs from the reported value 4.0 by more than 10 %

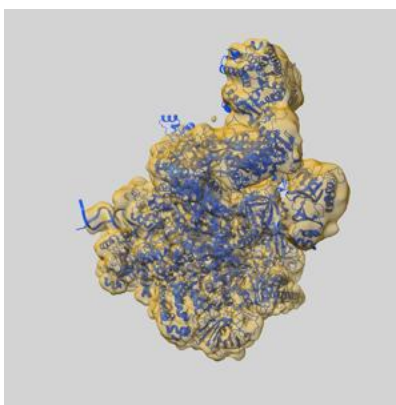
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37353 and PDB model 8W8F. Per-residue inclusion information can be found in section [3](#) on page [9](#).

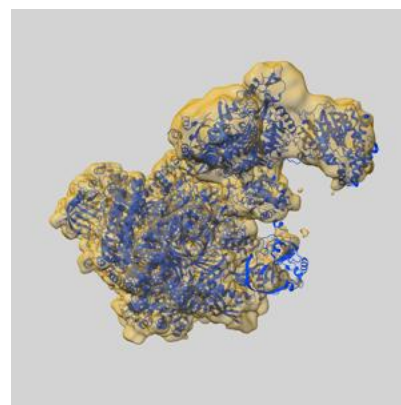
9.1 Map-model overlay [i](#)



X



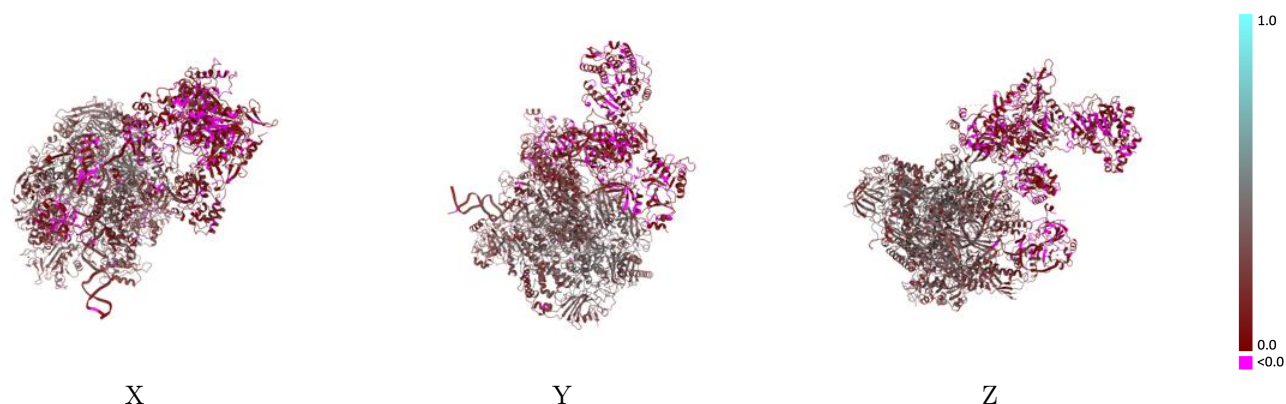
Y



Z

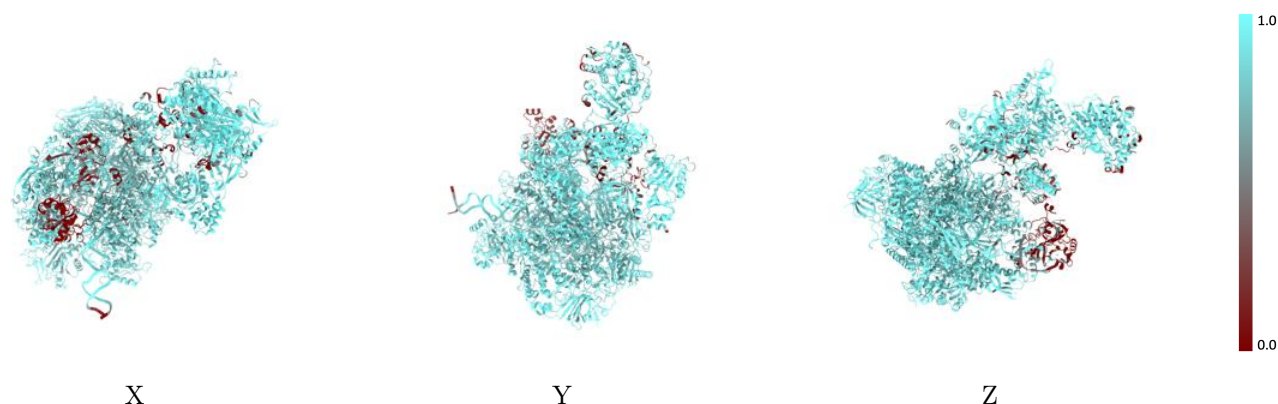
The images above show the 3D surface view of the map at the recommended contour level 0.26 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



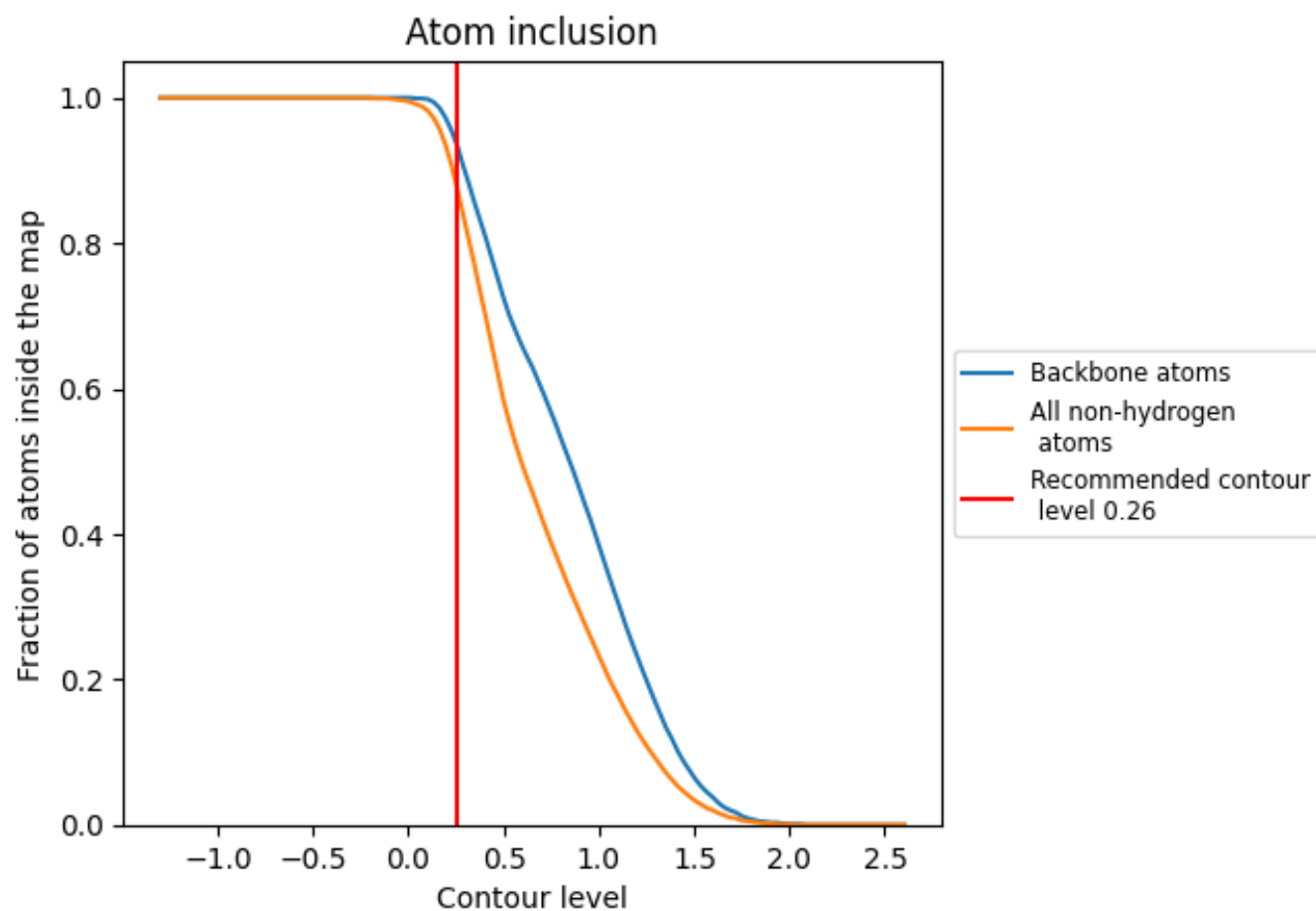
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.26).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 87% 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 (0.26) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8720	 0.2280
A	 0.9200	 0.3030
B	 0.9220	 0.3120
C	 0.9420	 0.3220
D	 0.9420	 0.1550
E	 0.9390	 0.2660
F	 0.8970	 0.3140
G	 0.9390	 0.1880
H	 0.9500	 0.3190
I	 0.9530	 0.2680
J	 0.9230	 0.3270
K	 0.9280	 0.3420
L	 0.9440	 0.2890
N	 0.8040	 0.1780
P	 0.8260	 0.2170
T	 0.8900	 0.2210
Y	 0.2110	 0.0700
Z	 0.5460	 0.0970
a	 0.8270	 0.0530
b	 0.8850	 0.0820

