



wwPDB EM Validation Summary Report ⓘ

Aug 6, 2025 – 11:27 AM EDT

PDB ID : 9MSF / pdb_00009msf
EMDB ID : EMD-48587
Title : de novo SigN RNA polymerase transcription initiation intermediate with post-catalytic bEBP state (RPi1 closed ring)
Authors : Mueller, A.U.; Darst, S.A.
Deposited on : 2025-01-09
Resolution : 2.60 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.dev126
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) : 2.45.1

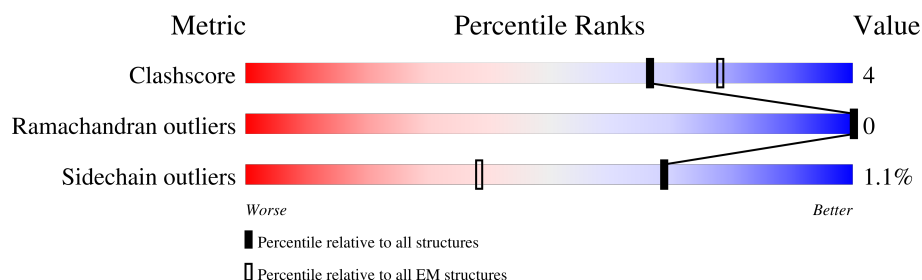
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 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.





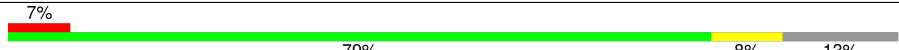
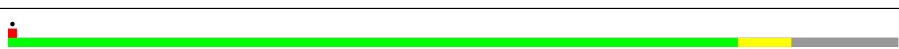

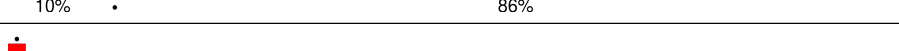
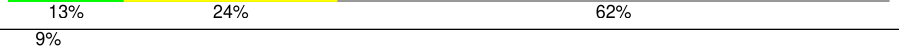

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	268	
1	B	268	
1	C	268	
1	D	268	
1	E	268	
1	F	268	
2	G	329	
2	H	329	

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Mol	Chain	Length	Quality of chain
3	I	1342	
4	J	1415	
5	K	91	
6	M	477	
7	S	90	
7	U	90	
8	T	90	
8	V	90	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 44073 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 Transcriptional regulator (NtrC family).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	247	Total	C	N	O	S	0	0
			1979	1278	333	364	4		
1	B	247	Total	C	N	O	S	0	0
			1979	1278	333	364	4		
1	C	247	Total	C	N	O	S	0	0
			1979	1278	333	364	4		
1	D	247	Total	C	N	O	S	0	0
			1979	1278	333	364	4		
1	E	247	Total	C	N	O	S	0	0
			1979	1278	333	364	4		
1	F	246	Total	C	N	O	S	0	0
			1964	1270	329	361	4		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	120	MET	-	initiating methionine	UNP O67198
B	120	MET	-	initiating methionine	UNP O67198
C	120	MET	-	initiating methionine	UNP O67198
D	120	MET	-	initiating methionine	UNP O67198
E	120	MET	-	initiating methionine	UNP O67198
F	120	MET	-	initiating methionine	UNP O67198

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	305	Total	C	N	O	S	0	0
			2357	1477	414	458	8		
2	H	223	Total	C	N	O	S	0	0
			1718	1074	302	336	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	1340	Total	C	N	O	S	0	0
			10567	6631	1841	2052	43		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	1352	Total	C	N	O	S	0	0
			10524	6614	1876	1983	51		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	1408	LEU	-	expression tag	UNP P0A8T7
J	1409	GLU	-	expression tag	UNP P0A8T7
J	1410	LEU	-	expression tag	UNP P0A8T7
J	1411	GLU	-	expression tag	UNP P0A8T7
J	1412	VAL	-	expression tag	UNP P0A8T7
J	1413	LEU	-	expression tag	UNP P0A8T7
J	1414	PHE	-	expression tag	UNP P0A8T7
J	1415	GLN	-	expression tag	UNP P0A8T7

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	79	Total	C	N	O	S	0	0
			627	382	118	126	1		

- Molecule 6 is a protein called RNA polymerase sigma-54 factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	M	421	Total	C	N	O	S	0	0
			3353	2098	582	662	11		

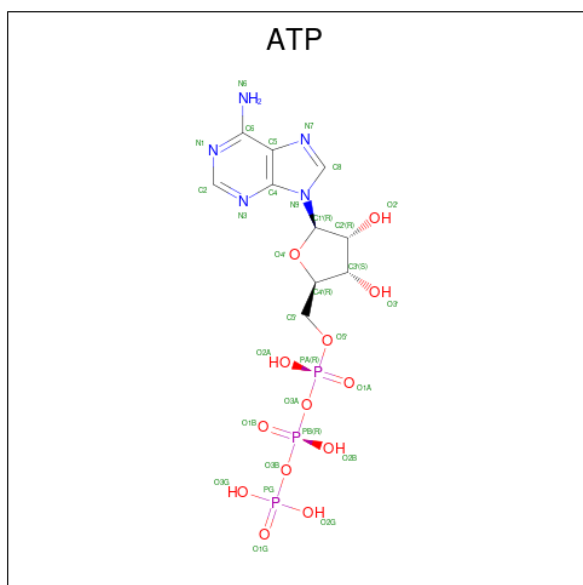
- Molecule 7 is a DNA chain called dhsU (-60 to +30) non-template strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	S	13	Total	C	N	O	P	0	0
			276	130	56	77	13		
7	U	34	Total	C	N	O	P	0	0
			701	334	140	193	34		

- Molecule 8 is a DNA chain called dhsU (-60 to +30) template strand.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	T	11	Total	C	N	O	P	0	0
			217	105	33	68	11		
8	V	34	Total	C	N	O	P	0	0
			693	335	109	215	34		

- Molecule 9 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



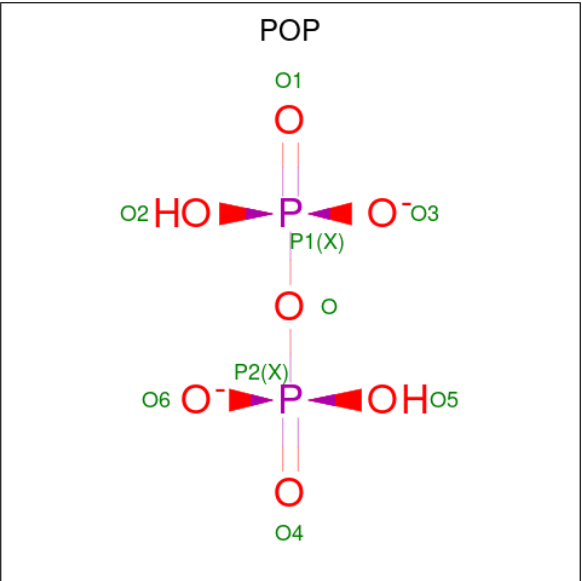
Mol	Chain	Residues	Atoms					AltConf
9	A	1	Total	C	N	O	P	0
			31	10	5	13	3	
9	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
9	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
9	D	1	Total	C	N	O	P	0
			31	10	5	13	3	
9	F	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
10	A	1	Total	Mg	0
			1	1	
10	J	1	Total	Mg	0
			1	1	

- # ADP

- Molecule 12 is PYROPHOSPHATE 2- (CCD ID: POP) (formula: $\text{H}_2\text{O}_7\text{P}_2$).



Mol	Chain	Residues	Atoms			AltConf
12	J	1	Total	O	P	0
			9	7	2	

- Molecule 13 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
13	J	2	Total	Zn	0
			2	2	

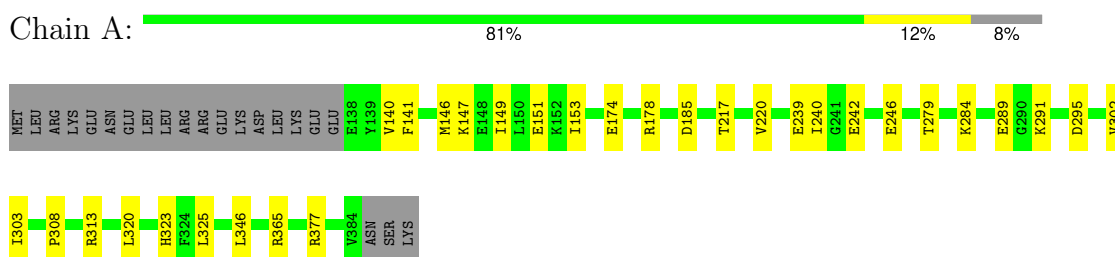
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		AltConf
14	A	3	Total	O	0
			3	3	
14	B	5	Total	O	0
			5	5	
14	C	5	Total	O	0
			5	5	
14	D	8	Total	O	0
			8	8	
14	E	15	Total	O	0
			15	15	
14	F	2	Total	O	0
			2	2	
14	G	89	Total	O	0
			89	89	
14	H	45	Total	O	0
			45	45	
14	I	367	Total	O	0
			367	367	
14	J	333	Total	O	0
			333	333	
14	K	26	Total	O	0
			26	26	
14	M	64	Total	O	0
			64	64	
14	S	1	Total	O	0
			1	1	
14	U	13	Total	O	0
			13	13	
14	V	10	Total	O	0
			10	10	

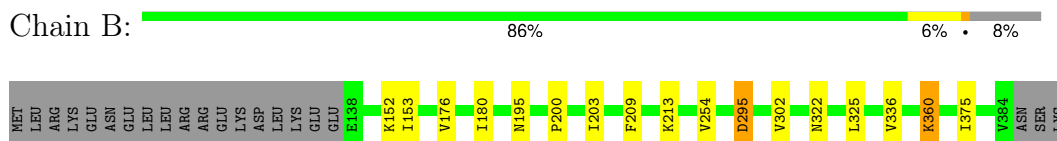
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

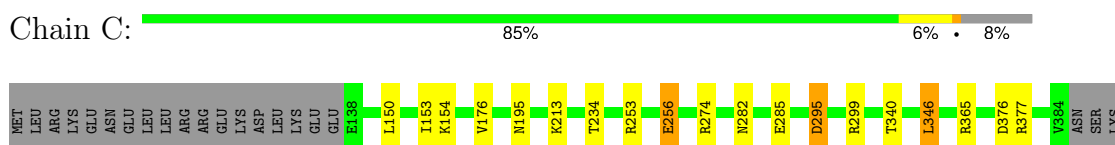
- Molecule 1: Transcriptional regulator (NtrC family)



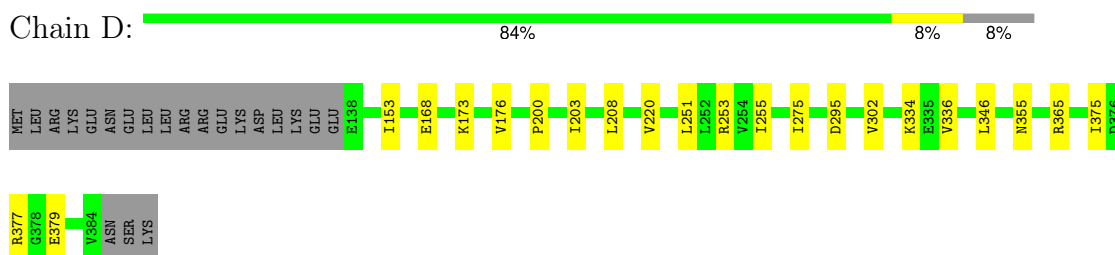
- Molecule 1: Transcriptional regulator (NtrC family)



- Molecule 1: Transcriptional regulator (NtrC family)



- Molecule 1: Transcriptional regulator (NtrC family)



- Molecule 1: Transcriptional regulator (NtrC family)

G354
E358
E371
R377
V384
ASN
SER
LYS

MET
LEU
ARG
LYS
GLU
ASN
GLU
LEU
LEU
ARG
ARG
GLU
LYS
ASP
LEU
LYS
GLU
GLU

E138
V139
V140

M146

E168

K173

L194

I199

K213

I240

T279

V302

I307

R313

P319

K326

R330

T340

S342

K343

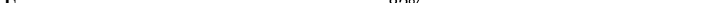
Q344

E345


L346

L347

L348

- Chain F:  82% 10% 8%

[illegible]

- Chain G:  84% 9% 7%

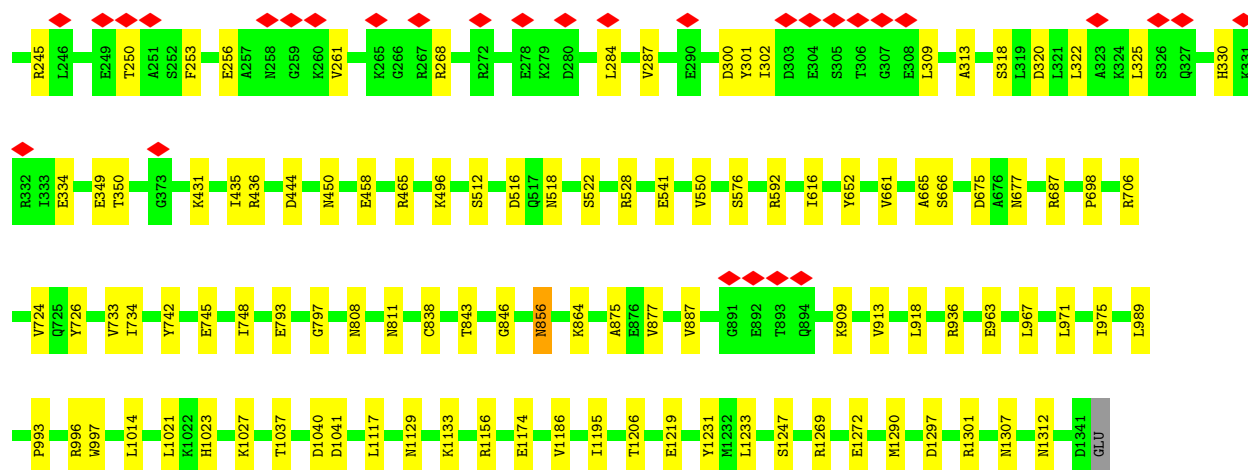
ARG	GLN	PRO	GLU	VAL	LYS	GLU	GLU	LYS	PRO	E248	E261	D280	E288	L289	T292	W321	S325	ILE	ALA	ASP	GLU																			
MET	GLN	GLY	S4	V5	T6	L31	E32	F35	G36	D62	G63	V64	K71	D96	L102	W103	K104	V110	T111	V129	S141	M142	R148	R158	ILE	HIS	SER	GLU	GLU	ASP	E165	G169	R182	E206	D212	E215	L228	F231	D236	W1

- Chain H:  56% 12% 32%

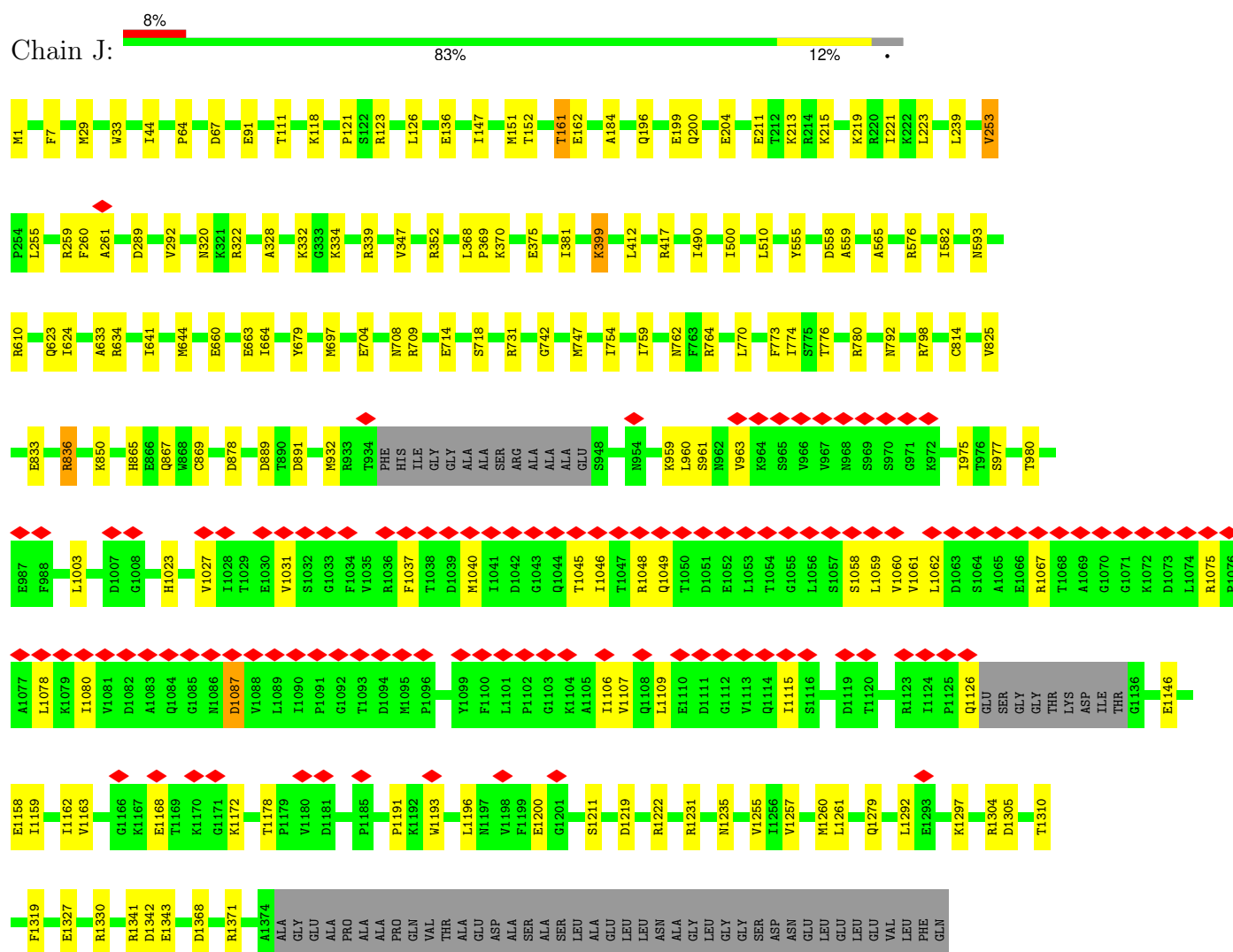
ALA	GLU	ALA	ILE	HIS	ILE	GLY	ASP	LEU	VAL	GLN	ARG	THR	GLU	VAL	GLU	LEU	LEU	LYS	THR	PRO	ASN	LEU	GLY	LYS	SER	LEU	THR	GLU	ILE	LYS	ASP	VAL	LEU	ALA	SER	ARG	GLY	MET	LEU	GLU	ASN	TRP	PRO	PRO	ALA	SER	ILE	ASP	GLU							
S178	P179	R191	V192	E193	T196	M205	T210	I211	E215	R218	L224	D233	LEU	ARG	ASP	VAL	ARG	GLN	PRO	GLU	VAL	LYS	GLU	LYS	GLU	LYS	PRO	GLU	LYS	GLU	LYS	PRO	LEU	GLU	ARG	PHE	ASP	PRO	ILE	LEU	SER	LEU	GLY	MET	ARG	LEU	GLU	ASN	THR	PRO	PRO	ALA	SER	ILE	ASP	GLU
GLN	GLY	S4	L13	L39	I46	V59	E60	T61	G63	V64	L65	H66	E67	V68	D77	L78	L79	V90	R91	V92	R95	L102	D120	I123	D135	E136	M142	L148	G149	R150	I159	HIS	SER	GLU	GLU	ASP	GLU	ARG	P167	I168	G169	R170	L171													

- Chain I:  90% 10%

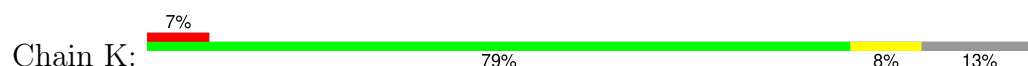
[illegible]

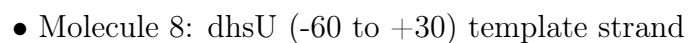


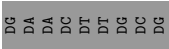
• Molecule 4: DNA-directed RNA polymerase subunit beta'



• Molecule 5: DNA-directed RNA polymerase subunit omega







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	260106	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 ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.942	Depositor
Minimum map value	-0.289	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	385.28, 385.28, 385.28	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, ADP, ATP, POP, 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	A	0.08	0/2013	0.22	0/2700
1	B	0.09	0/2013	0.24	0/2700
1	C	0.09	0/2013	0.24	0/2700
1	D	0.10	0/2013	0.27	1/2700 (0.0%)
1	E	0.09	0/2013	0.23	0/2700
1	F	0.07	0/1998	0.22	0/2681
2	G	0.09	0/2386	0.27	0/3234
2	H	0.09	0/1738	0.24	0/2355
3	I	0.10	0/10736	0.25	0/14487
4	J	0.09	0/10682	0.24	0/14418
5	K	0.09	0/629	0.23	0/847
6	M	0.10	0/3404	0.25	0/4613
7	S	0.15	0/311	0.33	0/480
7	U	0.17	0/790	0.35	0/1216
8	T	0.14	0/240	0.33	0/366
8	V	0.18	0/772	0.40	0/1190
All	All	0.10	0/43751	0.25	1/59387 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	355	ASN	CB-CA-C	-5.35	110.42	116.63

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	1979	0	2040	18	0
1	B	1979	0	2040	13	0
1	C	1979	0	2040	12	0
1	D	1979	0	2040	12	0
1	E	1979	0	2040	14	0
1	F	1964	0	2023	15	0
2	G	2357	0	2410	18	0
2	H	1718	0	1756	20	0
3	I	10567	0	10585	70	0
4	J	10524	0	10765	101	0
5	K	627	0	634	4	0
6	M	3353	0	3347	19	0
7	S	276	0	147	3	0
7	U	701	0	381	13	0
8	T	217	0	126	0	0
8	V	693	0	392	5	0
9	A	31	0	12	1	0
9	B	31	0	12	0	0
9	C	31	0	12	0	0
9	D	31	0	12	0	0
9	F	31	0	12	2	0
10	A	1	0	0	0	0
10	J	1	0	0	0	0
11	E	27	0	12	0	0
12	J	9	0	0	0	0
13	J	2	0	0	0	0
14	A	3	0	0	0	0
14	B	5	0	0	0	0
14	C	5	0	0	0	0
14	D	8	0	0	0	0
14	E	15	0	0	0	0
14	F	2	0	0	0	0
14	G	89	0	0	2	0
14	H	45	0	0	0	0
14	I	367	0	0	1	0
14	J	333	0	0	4	0
14	K	26	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	M	64	0	0	0	0
14	S	1	0	0	0	0
14	U	13	0	0	0	0
14	V	10	0	0	0	0
All	All	44073	0	42838	314	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 4.

The worst 5 of 314 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)
7:U:48:DC:H2''	7:U:49:DA:H5'	1.68	0.76
3:I:21:VAL:HG21	3:I:592:ARG:HD3	1.69	0.74
8:V:51:DC:H2'	8:V:52:DG:C8	2.24	0.72
4:J:644:MET:O	4:J:764:ARG:NH1	2.22	0.70
1:F:234:THR:HG22	1:F:274:ARG:HB3	1.73	0.69

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	245/268 (91%)	238 (97%)	7 (3%)	0	100	100
1	B	245/268 (91%)	241 (98%)	4 (2%)	0	100	100
1	C	245/268 (91%)	241 (98%)	4 (2%)	0	100	100
1	D	245/268 (91%)	238 (97%)	7 (3%)	0	100	100
1	E	245/268 (91%)	242 (99%)	3 (1%)	0	100	100
1	F	244/268 (91%)	238 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	G	299/329 (91%)	296 (99%)	3 (1%)	0	100	100
2	H	219/329 (67%)	217 (99%)	2 (1%)	0	100	100
3	I	1338/1342 (100%)	1307 (98%)	31 (2%)	0	100	100
4	J	1346/1415 (95%)	1327 (99%)	19 (1%)	0	100	100
5	K	77/91 (85%)	76 (99%)	1 (1%)	0	100	100
6	M	417/477 (87%)	410 (98%)	7 (2%)	0	100	100
All	All	5165/5591 (92%)	5071 (98%)	94 (2%)	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	A	212/233 (91%)	209 (99%)	3 (1%)	62	82
1	B	212/233 (91%)	210 (99%)	2 (1%)	75	90
1	C	212/233 (91%)	208 (98%)	4 (2%)	52	75
1	D	212/233 (91%)	209 (99%)	3 (1%)	62	82
1	E	212/233 (91%)	211 (100%)	1 (0%)	86	95
1	F	210/233 (90%)	208 (99%)	2 (1%)	73	88
2	G	262/286 (92%)	260 (99%)	2 (1%)	79	91
2	H	191/286 (67%)	188 (98%)	3 (2%)	58	79
3	I	1155/1157 (100%)	1146 (99%)	9 (1%)	79	91
4	J	1135/1176 (96%)	1120 (99%)	15 (1%)	65	84
5	K	67/75 (89%)	67 (100%)	0	100	100
6	M	377/428 (88%)	371 (98%)	6 (2%)	58	79
All	All	4457/4806 (93%)	4407 (99%)	50 (1%)	69	86

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	I	1206	THR
4	J	260	PHE
6	M	475	GLN
4	J	44	ILE
4	J	161	THR

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

Mol	Chain	Res	Type
4	J	80	HIS
4	J	739	GLN
4	J	665	GLN
4	J	1259	GLN
2	H	127	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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 11 ligands modelled in this entry, 4 are monoatomic - leaving 7 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
11	ADP	E	401	-	24,29,29	0.95	1 (4%)	29,45,45	1.19	2 (6%)
12	POP	J	1501	-	6,8,8	0.77	0	12,13,13	0.93	0
9	ATP	B	401	-	28,33,33	0.62	0	34,52,52	0.86	2 (5%)
9	ATP	A	401	10	28,33,33	0.67	0	34,52,52	0.70	1 (2%)
9	ATP	D	401	-	28,33,33	0.64	0	34,52,52	0.65	1 (2%)
9	ATP	C	401	-	28,33,33	0.63	0	34,52,52	0.67	1 (2%)
9	ATP	F	401	-	28,33,33	0.61	0	34,52,52	0.66	1 (2%)

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
11	ADP	E	401	-	-	2/12/32/32	0/3/3/3
12	POP	J	1501	-	-	0/6/6/6	-
9	ATP	B	401	-	-	10/18/38/38	0/3/3/3
9	ATP	A	401	10	-	1/18/38/38	0/3/3/3
9	ATP	D	401	-	-	5/18/38/38	0/3/3/3
9	ATP	C	401	-	-	7/18/38/38	0/3/3/3
9	ATP	F	401	-	-	1/18/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	E	401	ADP	PA-O3A	2.15	1.61	1.59

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	401	ATP	C4'-O4'-C1'	-3.59	106.64	109.92
11	E	401	ADP	N3-C2-N1	-3.56	123.84	128.67
11	E	401	ADP	C4-C5-N7	-2.58	106.61	109.34
9	D	401	ATP	C5-C6-N6	2.34	123.87	120.31
9	F	401	ATP	C5-C6-N6	2.31	123.83	120.31

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

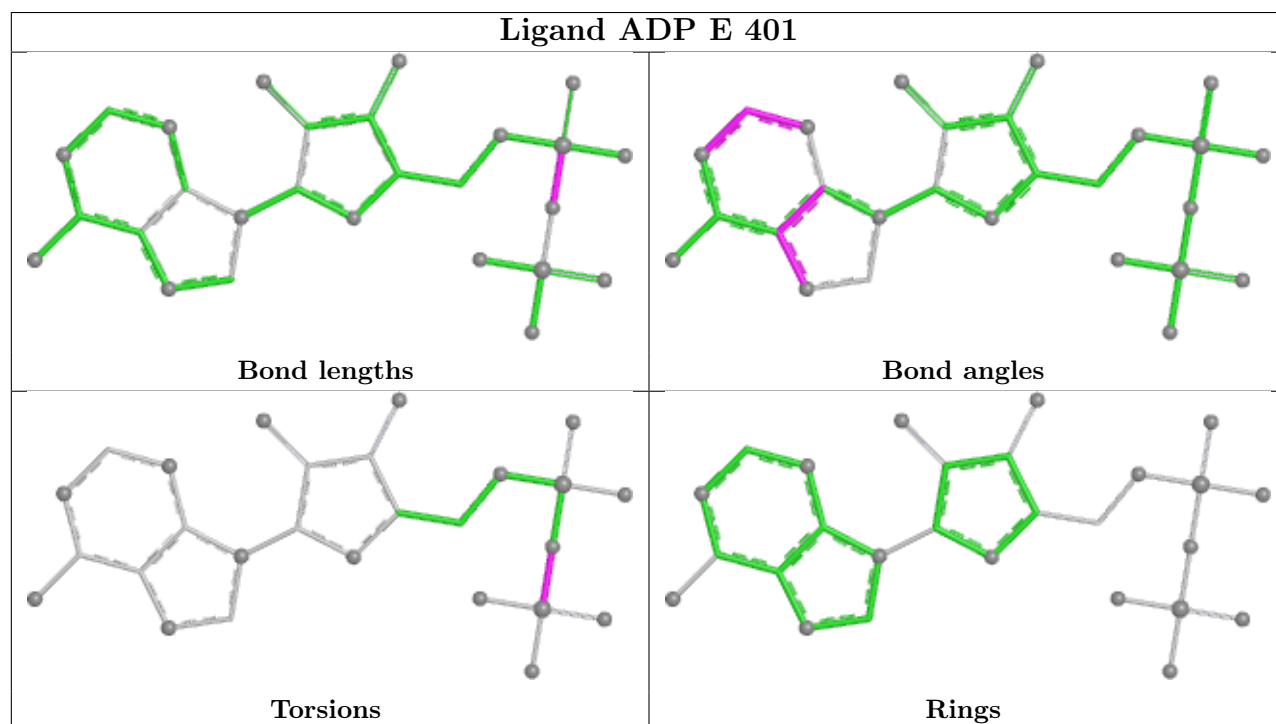
Mol	Chain	Res	Type	Atoms
9	B	401	ATP	PB-O3B-PG-O3G
9	B	401	ATP	C5'-O5'-PA-O1A
9	B	401	ATP	C5'-O5'-PA-O2A
9	B	401	ATP	C5'-O5'-PA-O3A
9	C	401	ATP	PB-O3B-PG-O2G

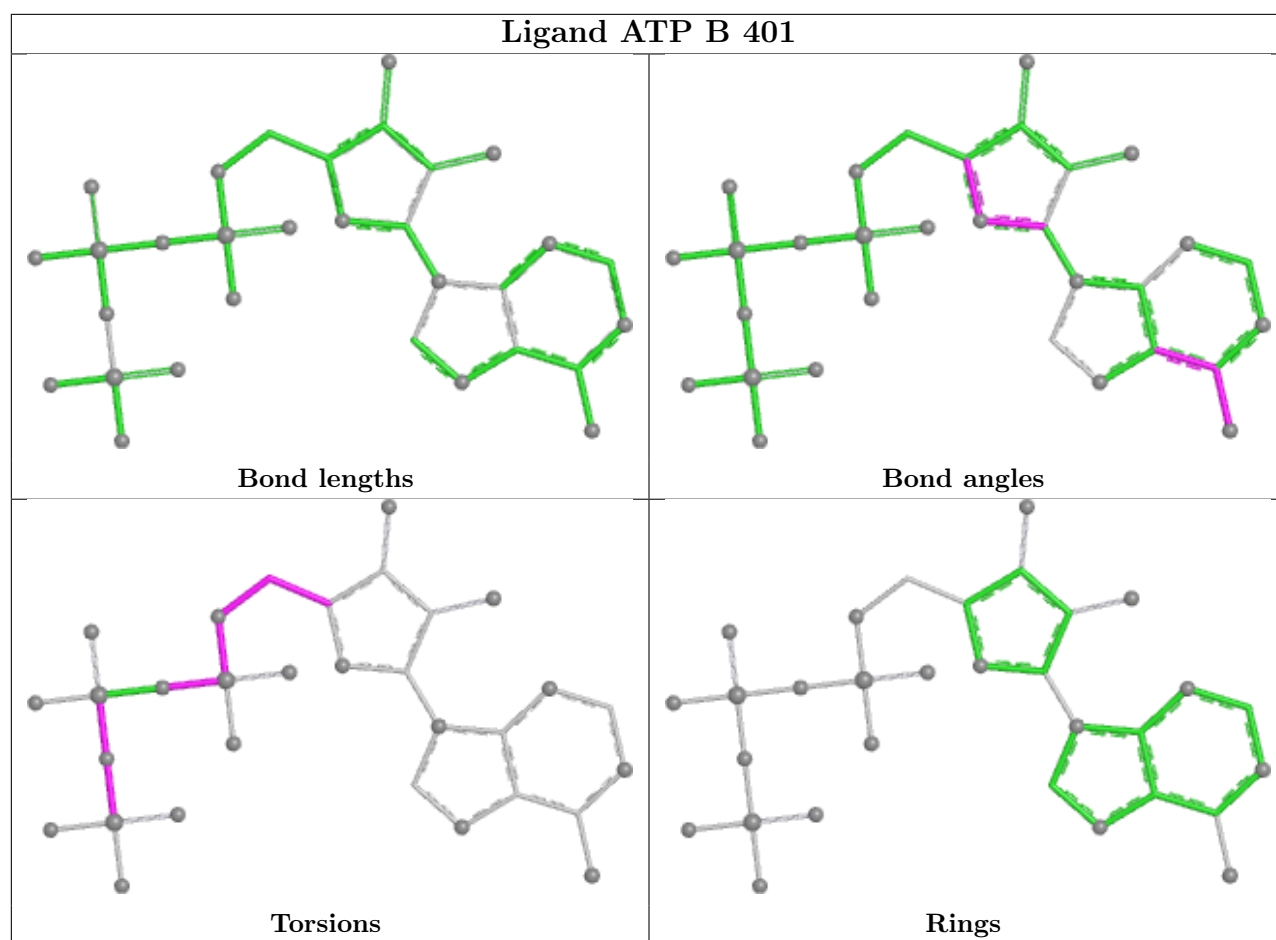
There are no ring outliers.

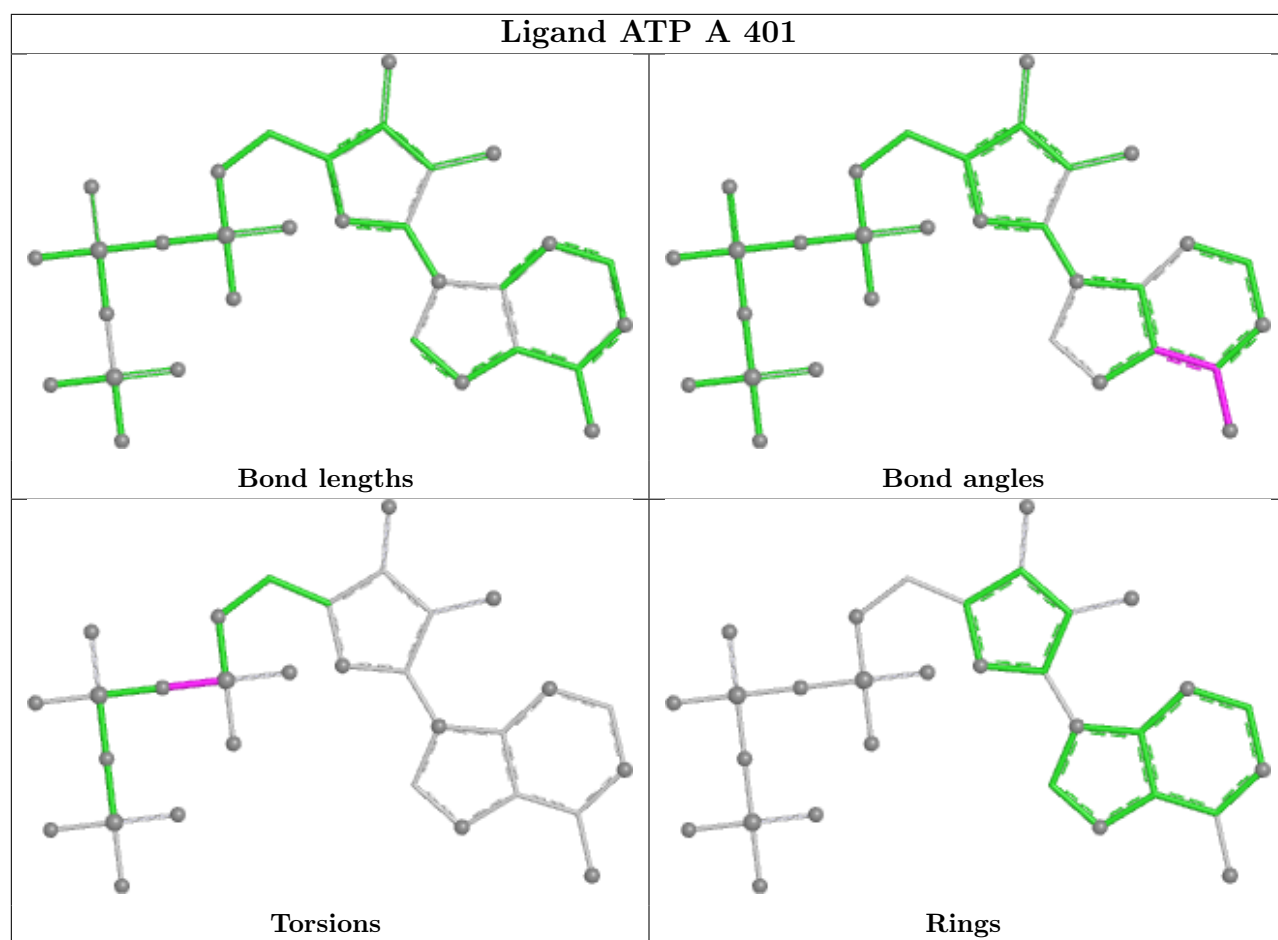
2 monomers are involved in 3 short contacts:

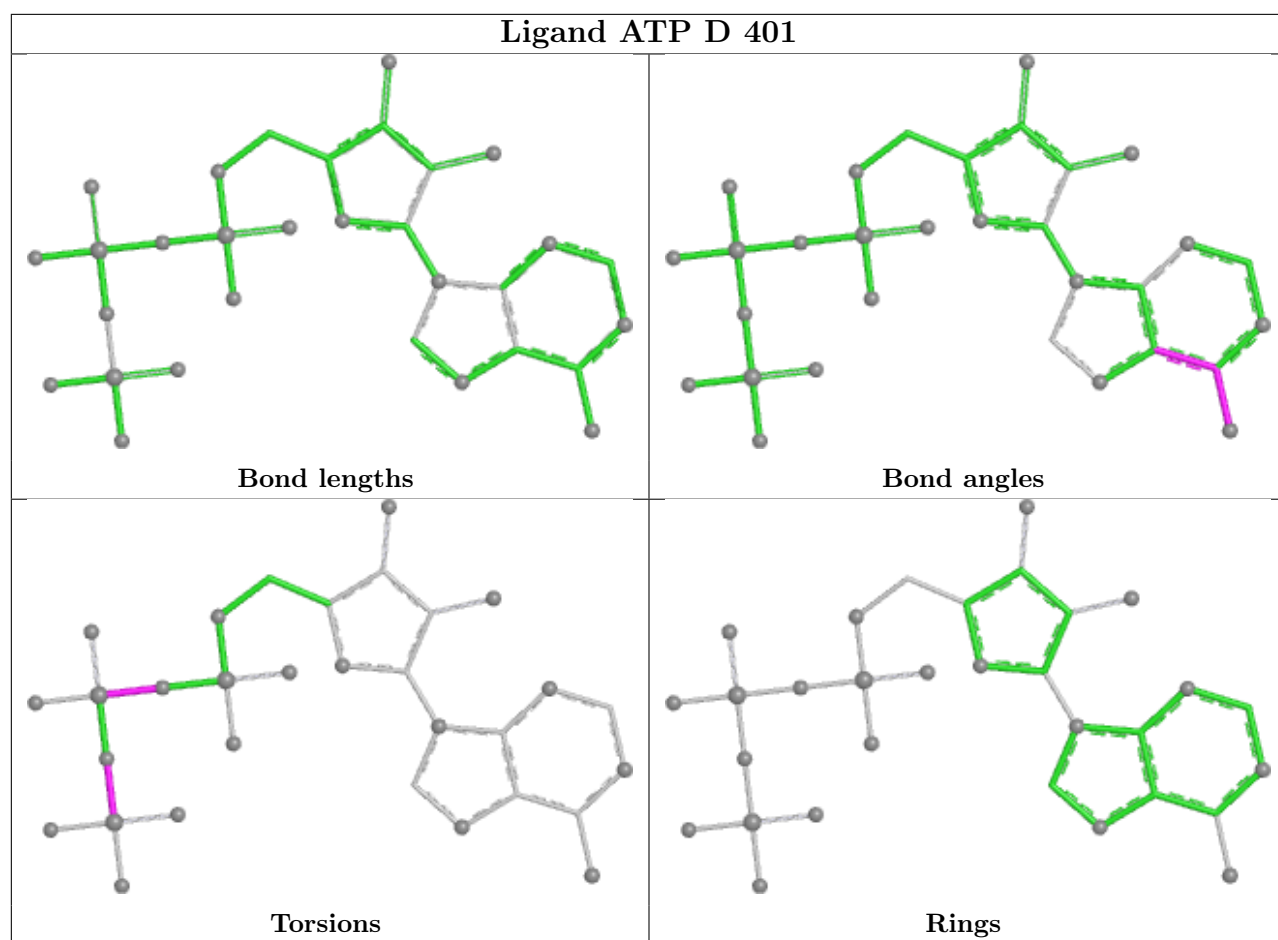
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	401	ATP	1	0
9	F	401	ATP	2	0

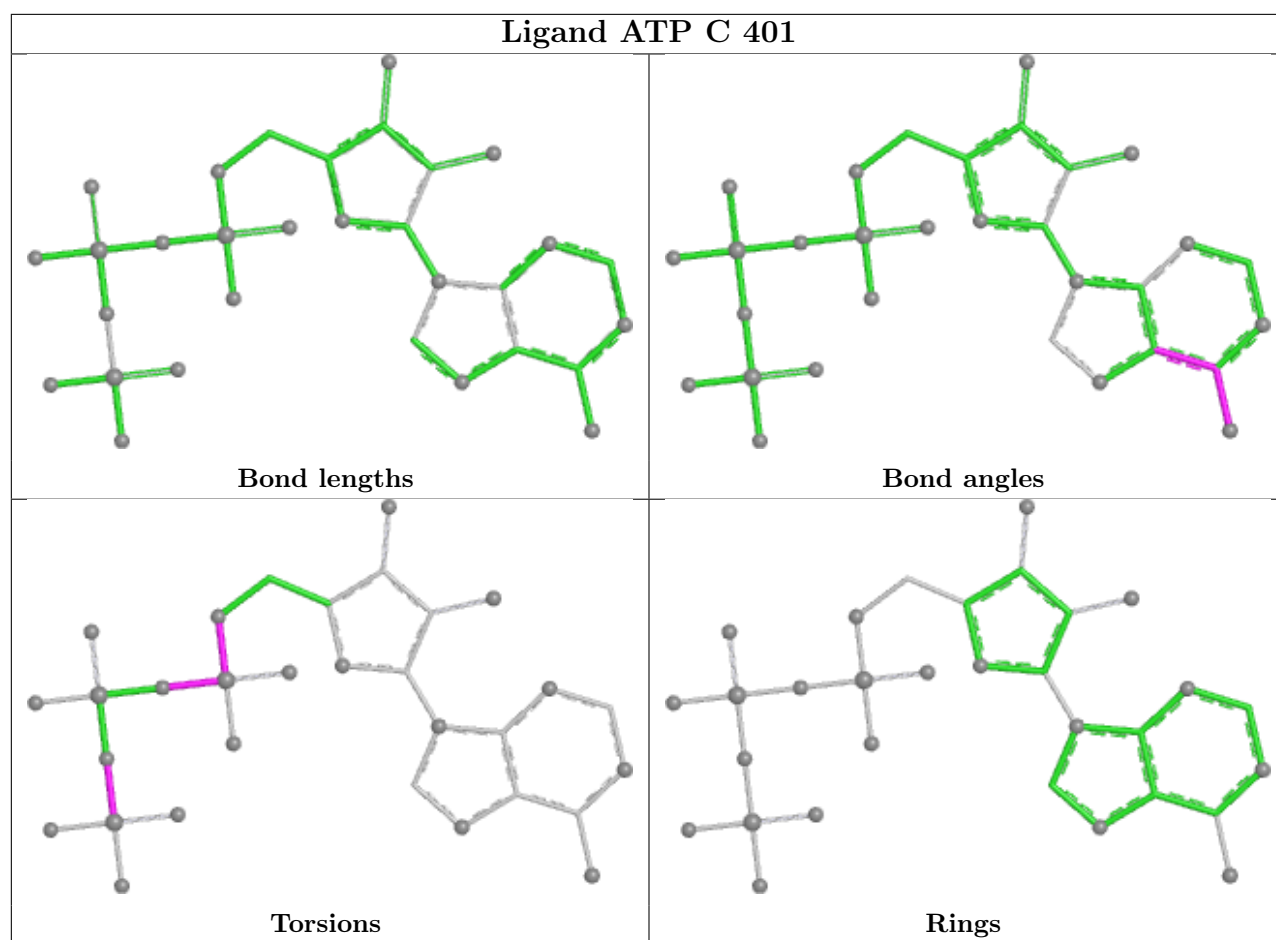
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

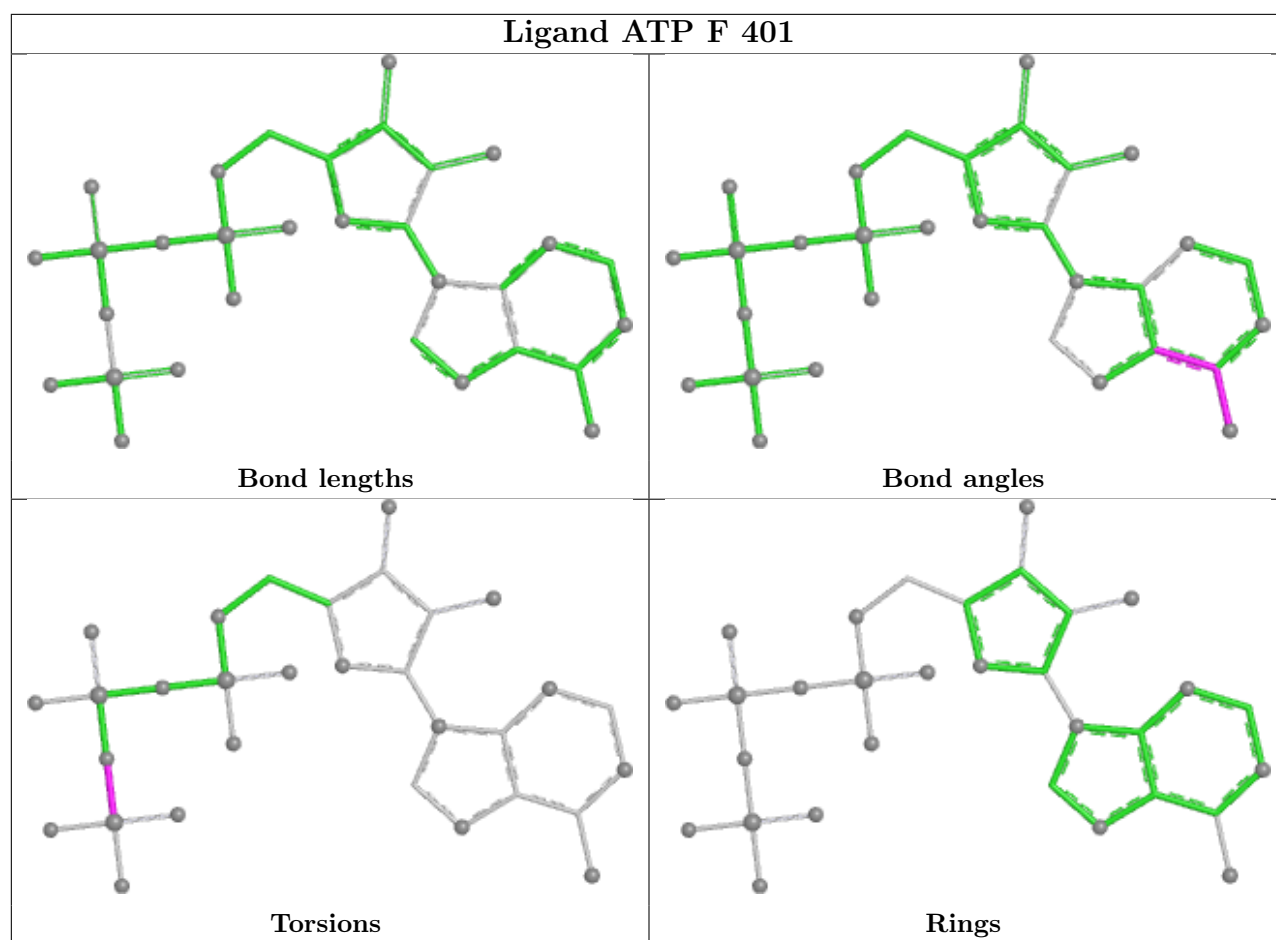












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

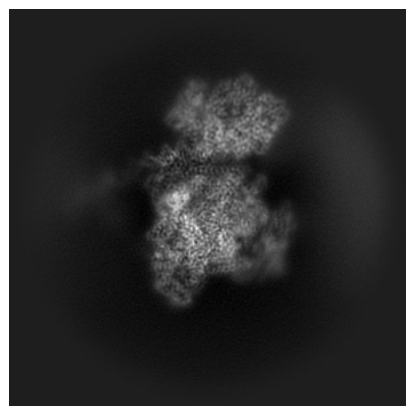
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-48587. These allow visual inspection of the internal detail of the map and identification of artifacts.

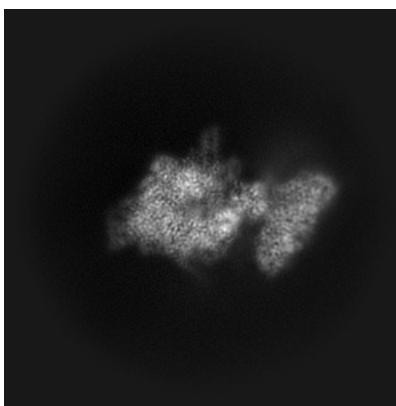
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

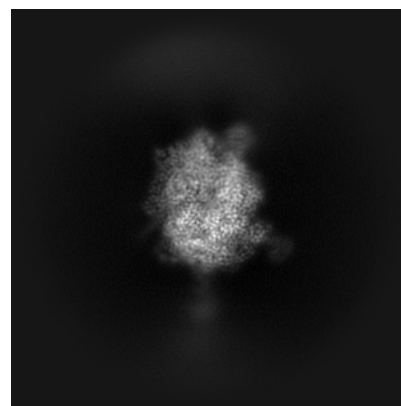
6.1.1 Primary map



X

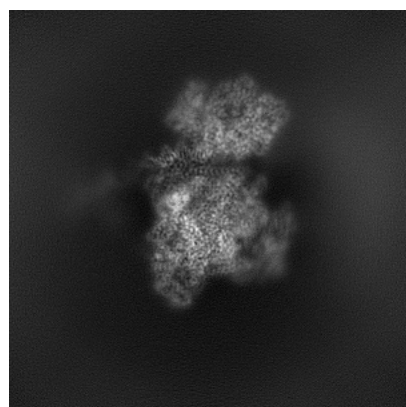


Y

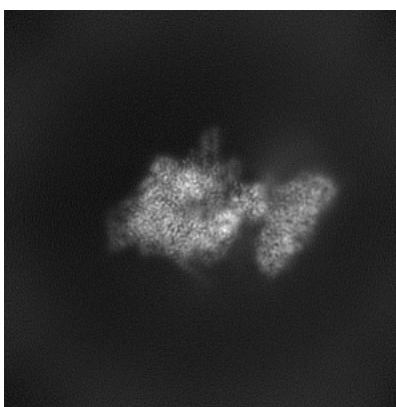


Z

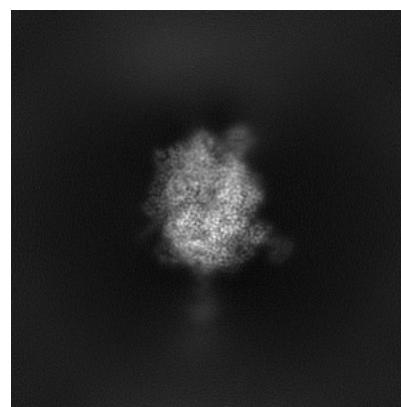
6.1.2 Raw map



X



Y

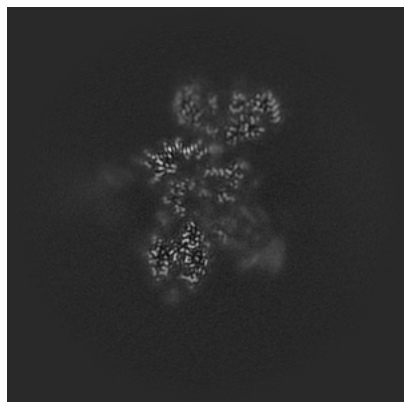


Z

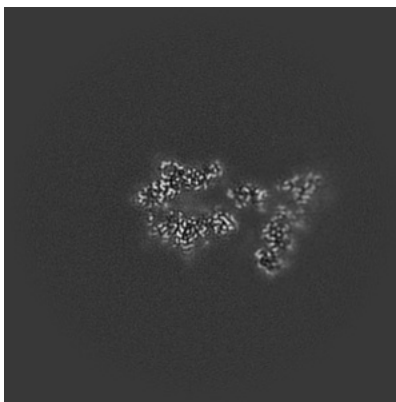
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

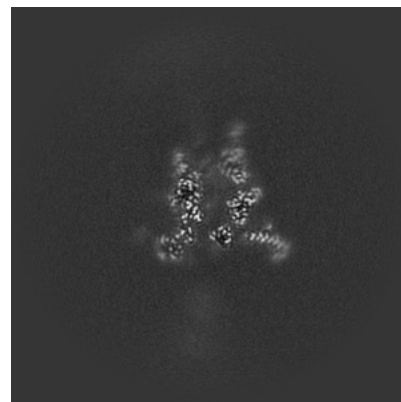
6.2.1 Primary map



X Index: 224

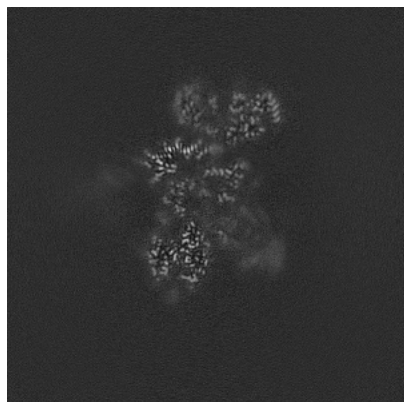


Y Index: 224

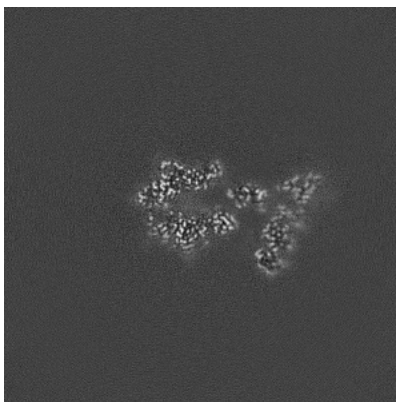


Z Index: 224

6.2.2 Raw map



X Index: 224



Y Index: 224

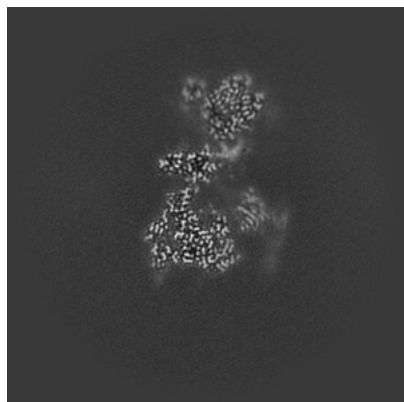


Z Index: 224

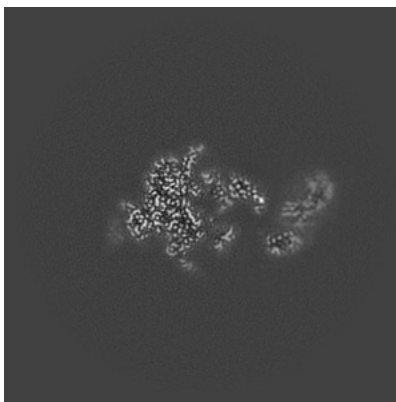
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

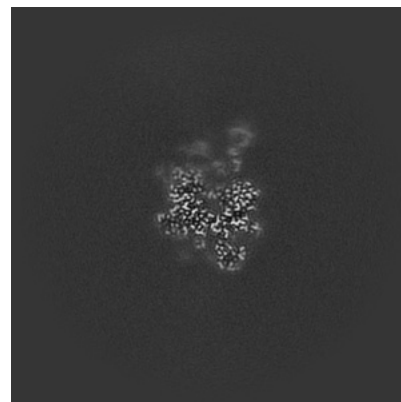
6.3.1 Primary map



X Index: 241

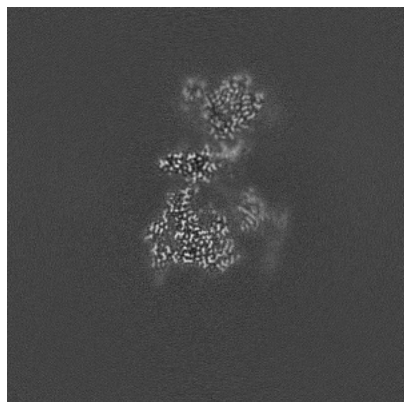


Y Index: 205

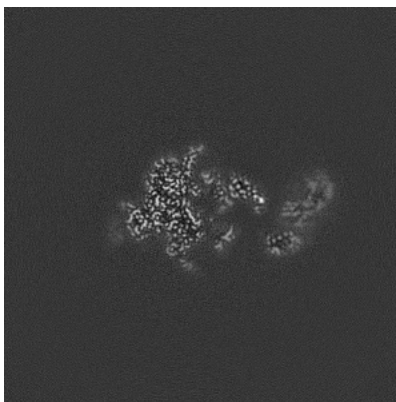


Z Index: 194

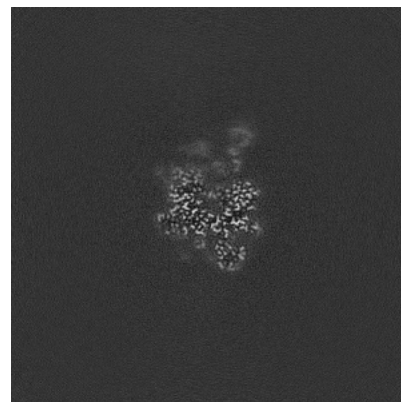
6.3.2 Raw map



X Index: 241



Y Index: 205

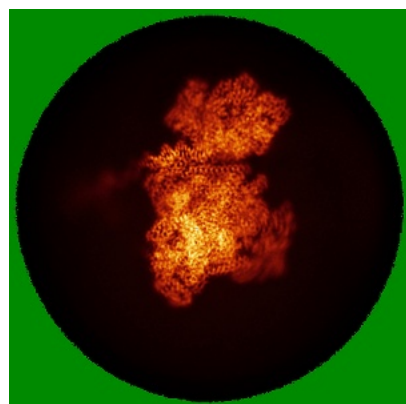


Z Index: 194

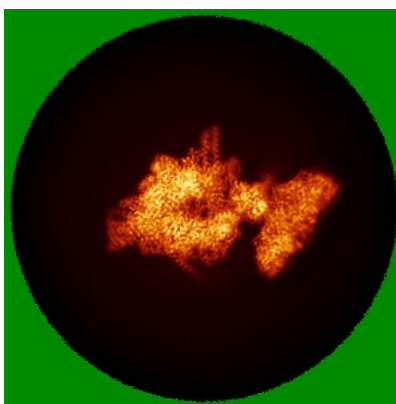
The images above show the largest variance slices of the map in three orthogonal directions.

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

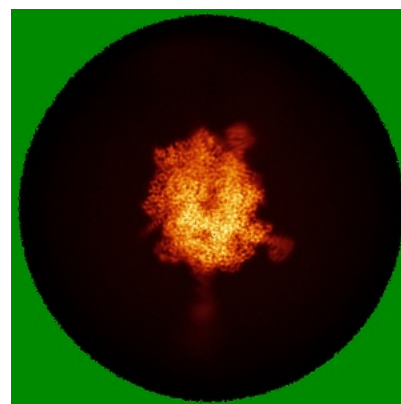
6.4.1 Primary map



X

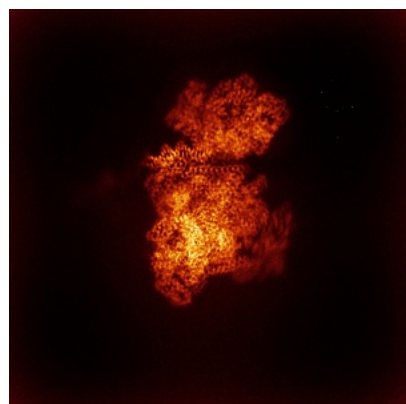


Y

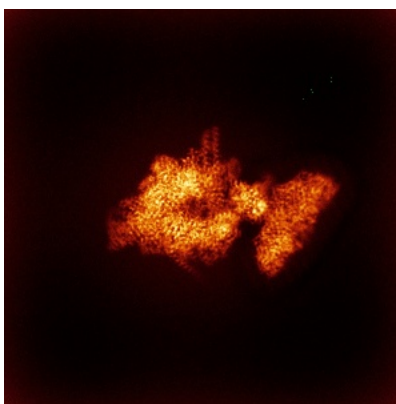


Z

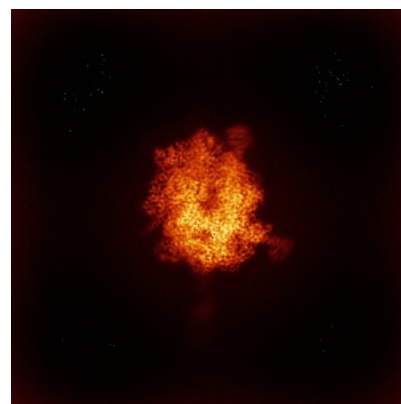
6.4.2 Raw map



X



Y

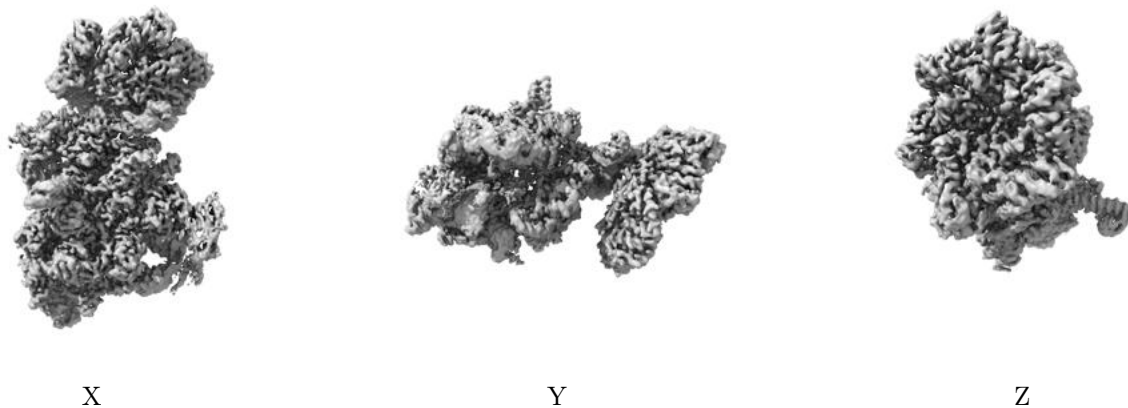


Z

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.

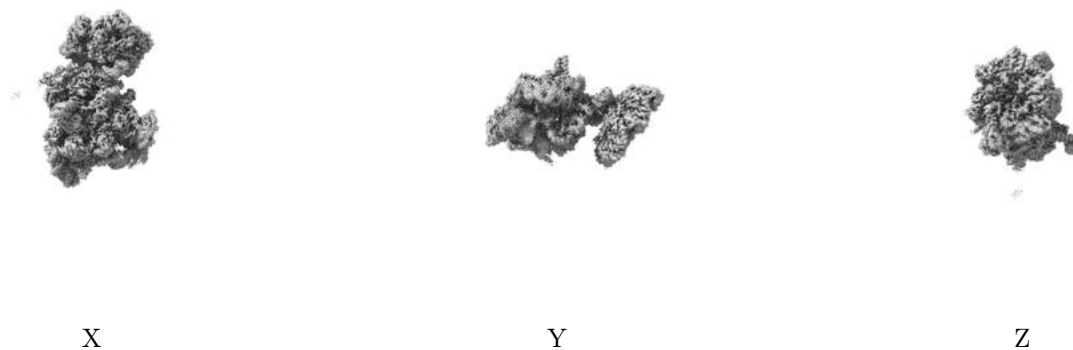
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.12. 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.

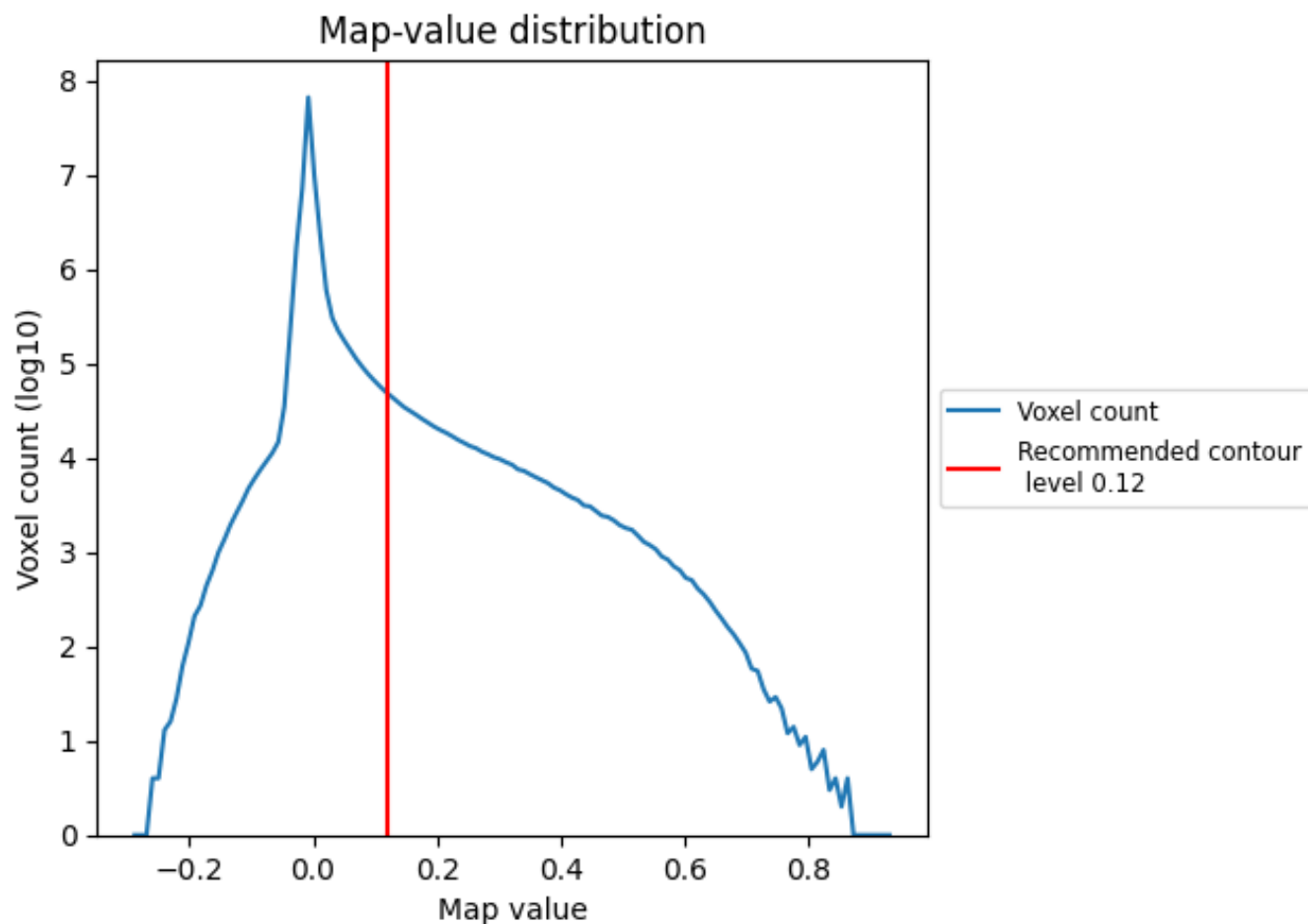
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

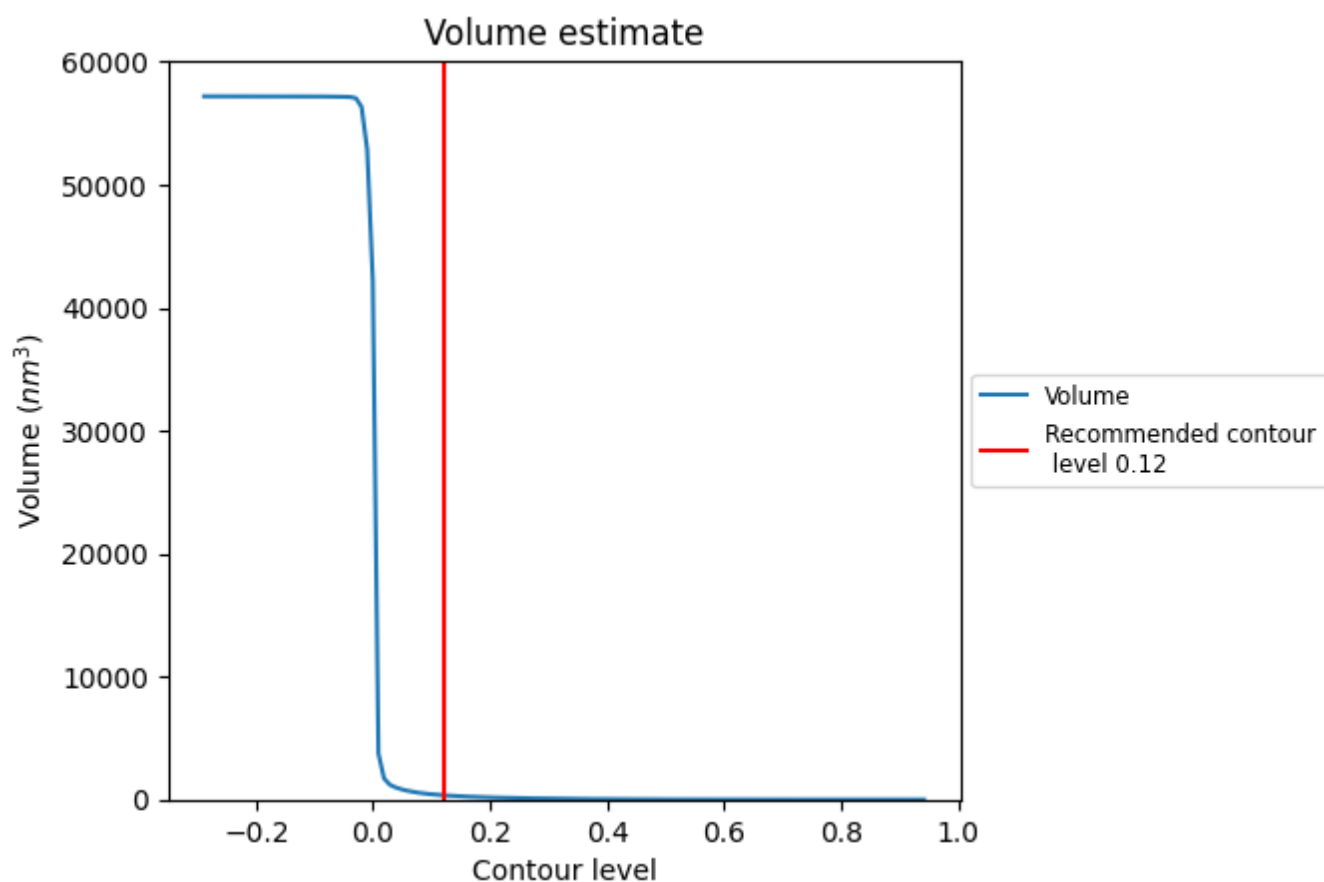
This section contains the results of statistical analysis of the map.

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.

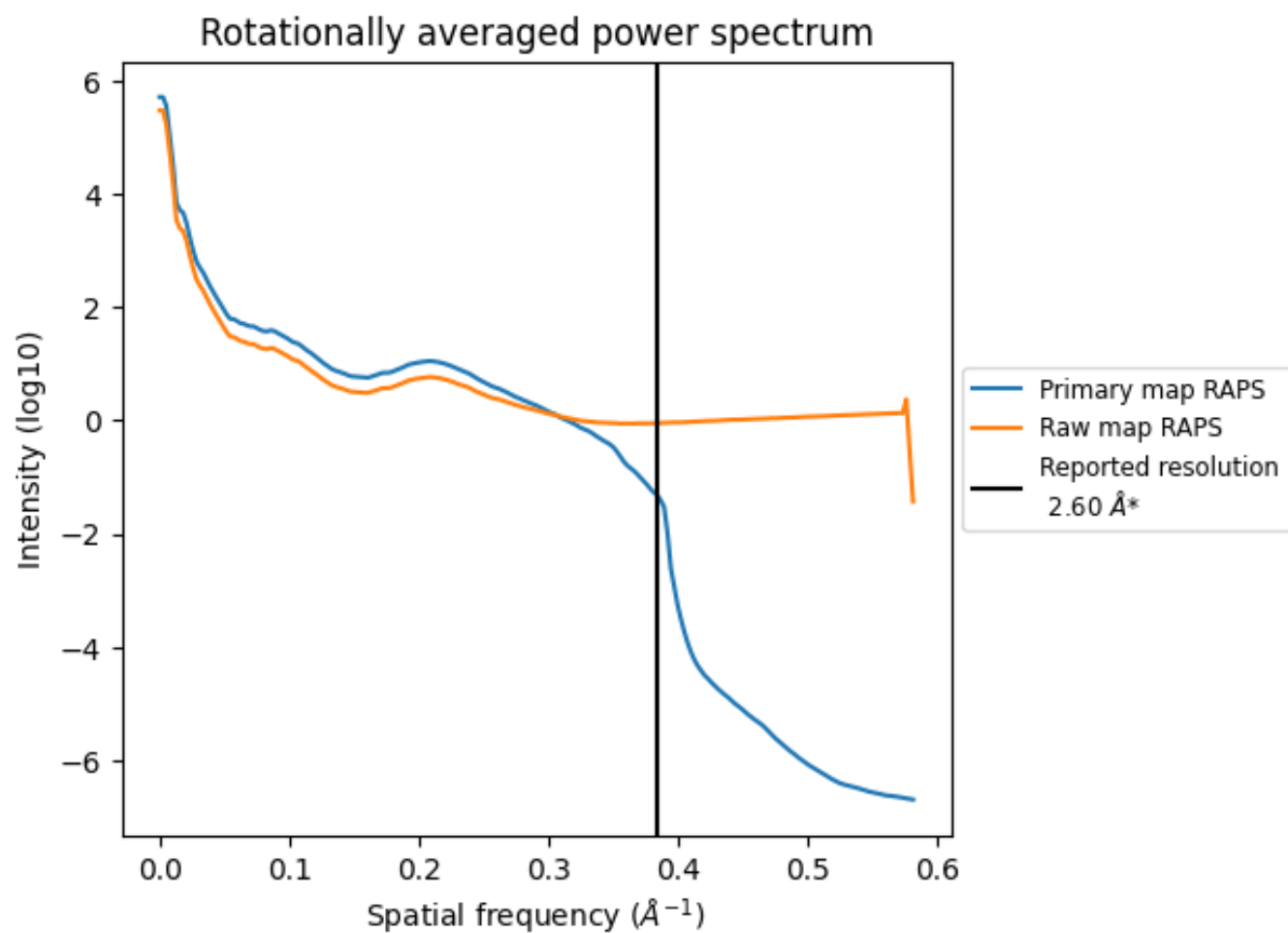
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 350 nm^3 ; this corresponds to an approximate mass of 316 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 ⓘ

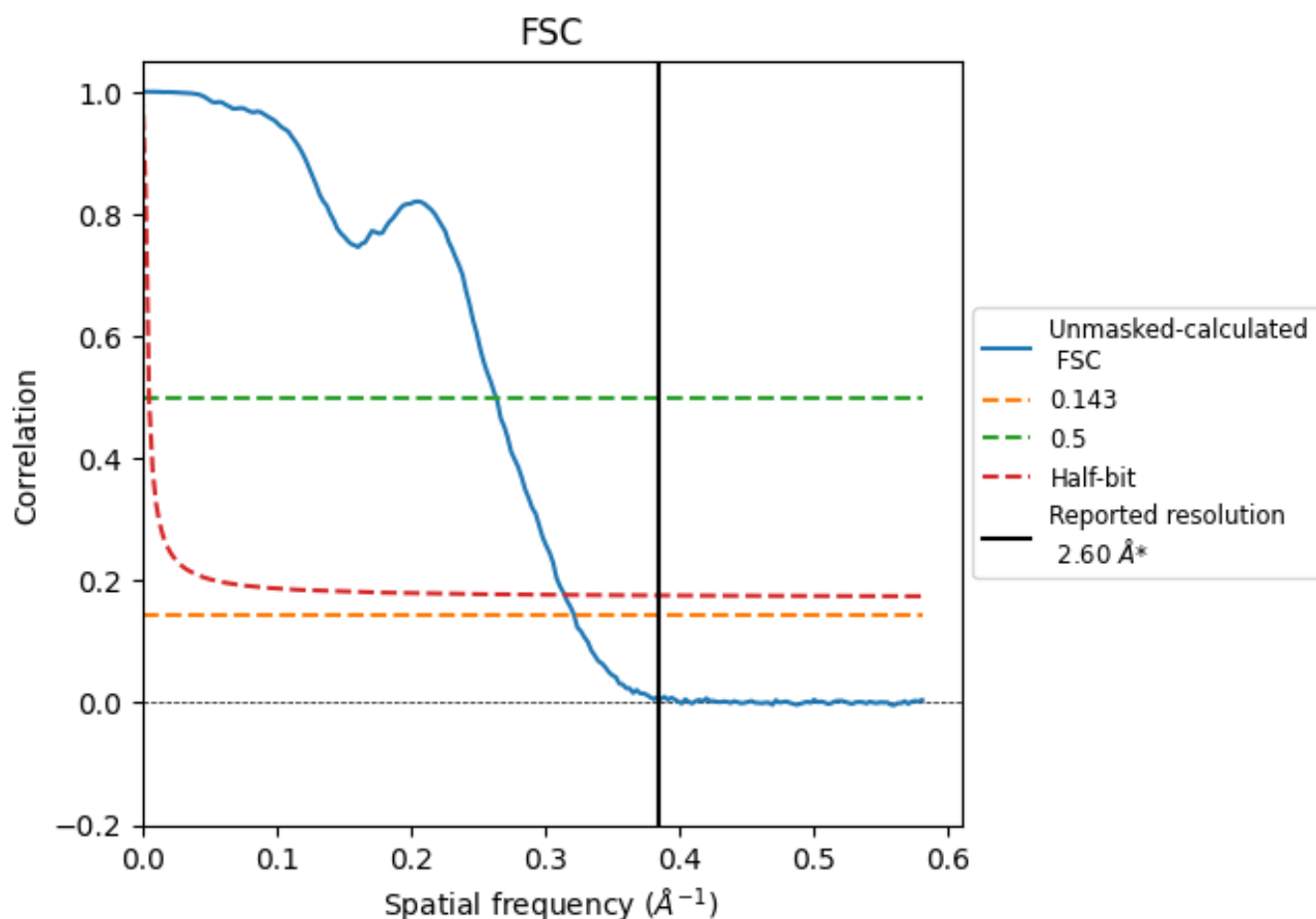


*Reported resolution corresponds to spatial frequency of 0.385 \AA^{-1}

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 0.385 Å⁻¹

8.2 Resolution estimates [i](#)

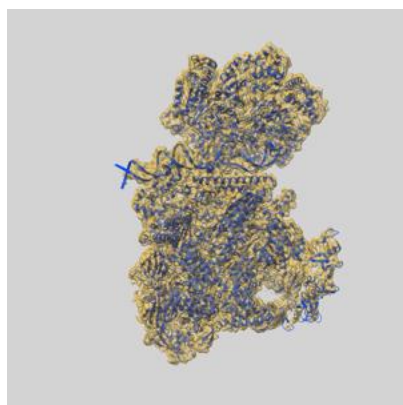
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.11	3.79	3.18

*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 3.11 differs from the reported value 2.6 by more than 10 %

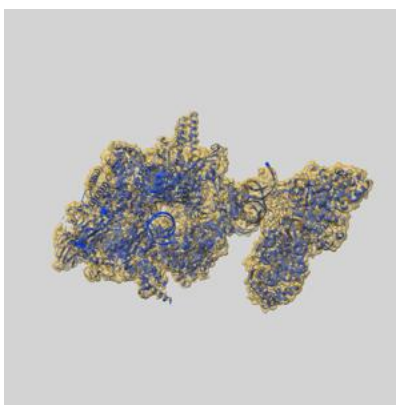
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-48587 and PDB model 9MSF. Per-residue inclusion information can be found in section [3](#) on page [9](#).

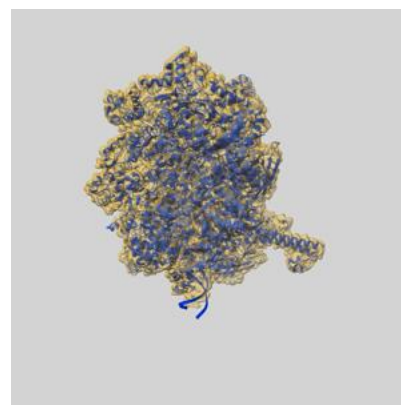
9.1 Map-model overlay [i](#)



X



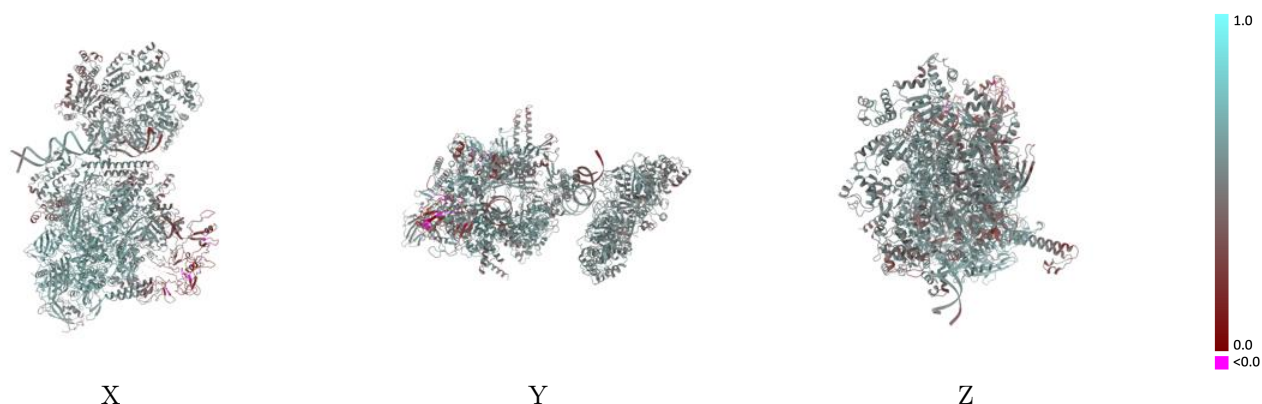
Y



Z

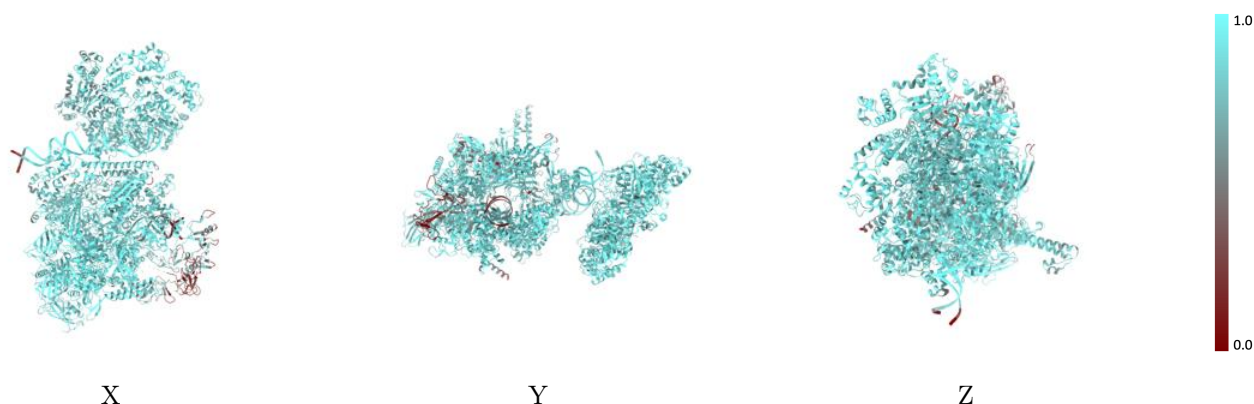
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



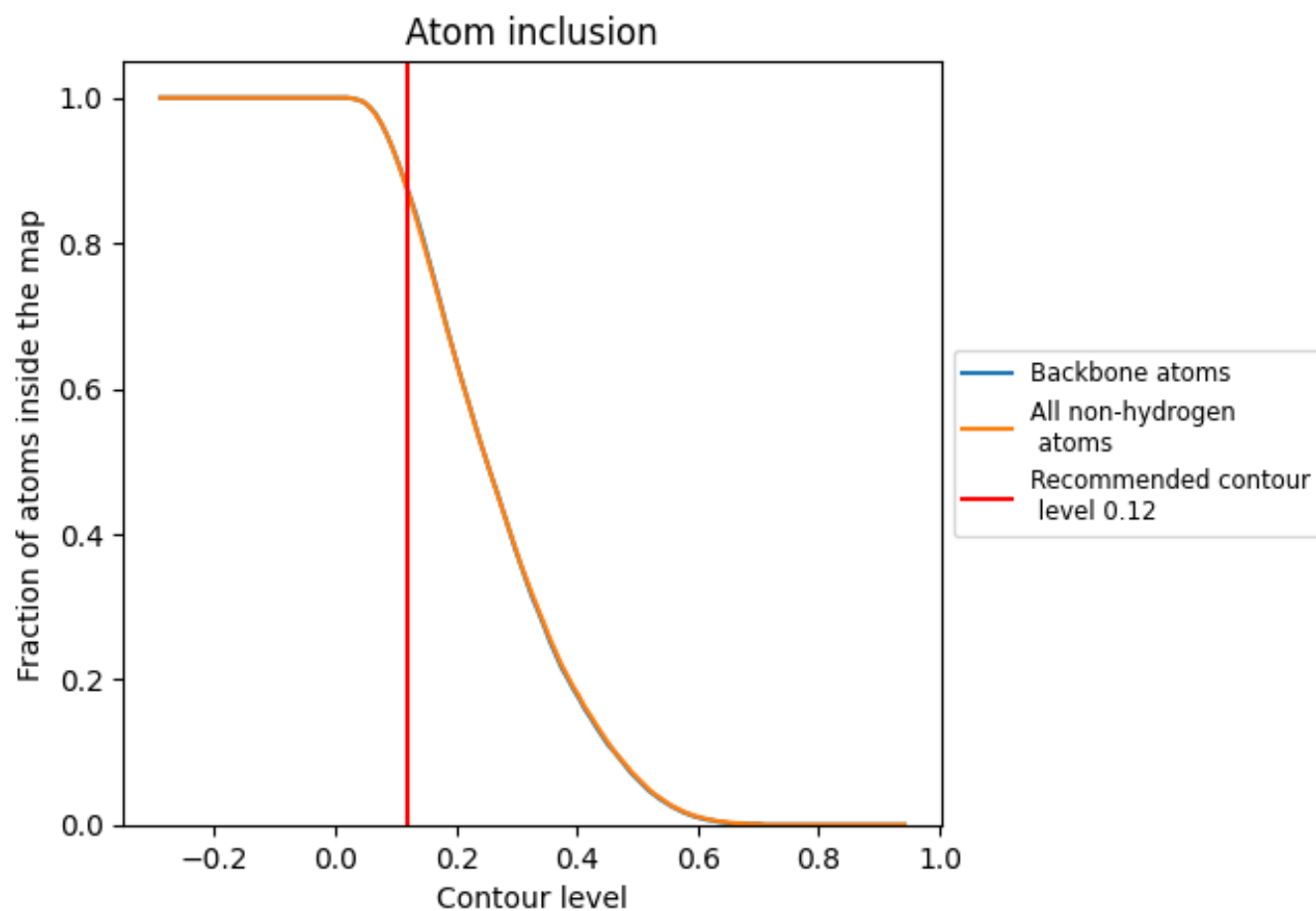
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).



































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8720	 0.5310
A	 0.8870	 0.5050
B	 0.9080	 0.5310
C	 0.9120	 0.5460
D	 0.9060	 0.5450
E	 0.8570	 0.4990
F	 0.8080	 0.4530
G	 0.9270	 0.5880
H	 0.9200	 0.5610
I	 0.8960	 0.5530
J	 0.8460	 0.5170
K	 0.8480	 0.5680
M	 0.9020	 0.5470
S	 0.3800	 0.3730
T	 0.2770	 0.2970
U	 0.8970	 0.4950
V	 0.9060	 0.4860

