



wwPDB EM Validation Summary Report

Apr 10, 2023 – 10:24 AM EDT

PDB ID : 8GZH
EMDB ID : EMD-34398
Title : Cryo-EM structure of Synechocystis sp. PCC 6803 CTP-bound RPitc
Authors : You, L.L.; Shen, L.Q.; Zhang, Y.
Deposited on : 2022-09-27
Resolution : 2.96 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:

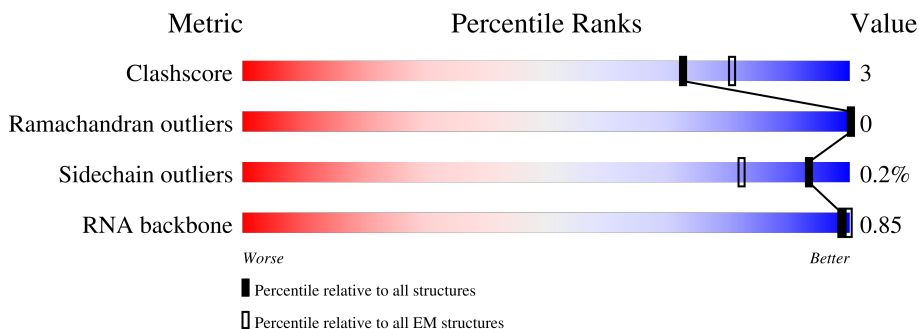
EMDB validation analysis : 0.0.1.dev50
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.32.2

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 2.96 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.





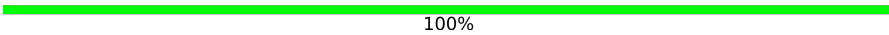
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	328	 62% 5% 33%
1	B	328	 61% 5% 34%
2	C	1104	 86% 10% 5%
3	D	626	 89% 9%
4	E	76	 72% 5% 22%
5	F	429	 66% 7% 27%
6	Z	1323	 83% 9% 8%

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Mol	Chain	Length	Quality of chain
7	1	67	 67% 7% 25%
8	2	67	 69% 6% 25%
9	3	4	 100%

2 Entry composition i

There are 12 unique types of molecules in this entry. The entry contains 30339 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 DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	219	Total	C	N	O	S	0	0
			1675	1060	287	322	6		
1	B	217	Total	C	N	O	S	0	0
			1673	1057	284	327	5		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP P73297
A	-12	GLY	-	expression tag	UNP P73297
A	-11	SER	-	expression tag	UNP P73297
A	-10	SER	-	expression tag	UNP P73297
A	-9	HIS	-	expression tag	UNP P73297
A	-8	HIS	-	expression tag	UNP P73297
A	-7	HIS	-	expression tag	UNP P73297
A	-6	HIS	-	expression tag	UNP P73297
A	-5	HIS	-	expression tag	UNP P73297
A	-4	HIS	-	expression tag	UNP P73297
A	-3	SER	-	expression tag	UNP P73297
A	-2	GLN	-	expression tag	UNP P73297
A	-1	ASP	-	expression tag	UNP P73297
A	0	PRO	-	expression tag	UNP P73297
B	-13	MET	-	initiating methionine	UNP P73297
B	-12	GLY	-	expression tag	UNP P73297
B	-11	SER	-	expression tag	UNP P73297
B	-10	SER	-	expression tag	UNP P73297
B	-9	HIS	-	expression tag	UNP P73297
B	-8	HIS	-	expression tag	UNP P73297
B	-7	HIS	-	expression tag	UNP P73297
B	-6	HIS	-	expression tag	UNP P73297
B	-5	HIS	-	expression tag	UNP P73297
B	-4	HIS	-	expression tag	UNP P73297
B	-3	SER	-	expression tag	UNP P73297
B	-2	GLN	-	expression tag	UNP P73297

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	ASP	-	expression tag	UNP P73297
B	0	PRO	-	expression tag	UNP P73297

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	1052	8171	5142	1450	1557	22	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	MET	-	initiating methionine	UNP P77965
C	0	ALA	-	expression tag	UNP P77965

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	615	4862	3088	875	877	22	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	59	450	278	84	86	2	0	0

- Molecule 5 is a protein called RNA polymerase sigma factor SigA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	314	2474	1560	447	462	5	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-3	GLY	-	expression tag	UNP P74565
F	-2	ALA	-	expression tag	UNP P74565
F	-1	MET	-	expression tag	UNP P74565
F	0	GLY	-	expression tag	UNP P74565

- Molecule 6 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	Z	1217	8860	5535	1556	1747	22	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	-5	GLY	-	expression tag	UNP P73334
Z	-4	SER	-	expression tag	UNP P73334
Z	-3	GLY	-	expression tag	UNP P73334
Z	-2	SER	-	expression tag	UNP P73334
Z	-1	GLY	-	expression tag	UNP P73334
Z	0	SER	-	expression tag	UNP P73334

- Molecule 7 is a DNA chain called Nontemplate strand DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	1	50	1029	489	192	299	49	0	0

- Molecule 8 is a DNA chain called Template strand DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	2	50	1031	488	196	297	50	0	0

- Molecule 9 is a RNA chain called RNA (5'-R(*CP*CP*GP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
9	3	4	81	38	16	24	3	0	0

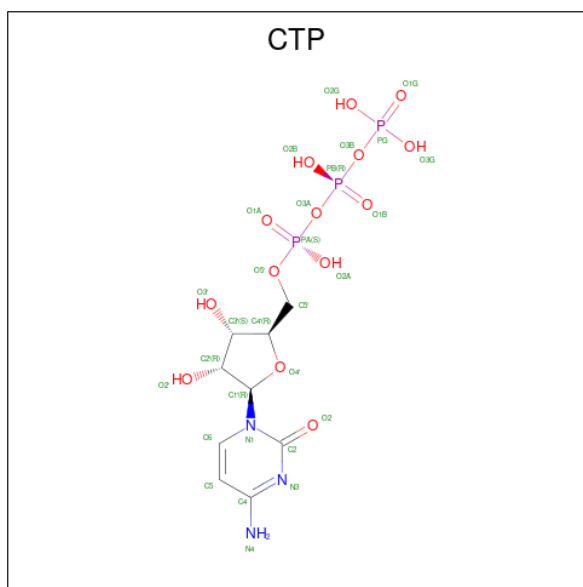
- Molecule 10 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
10	D	2	Total	Mg	0
			2	2	

- Molecule 11 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
11	D	1	Total	Zn	0
			1	1	
11	Z	1	Total	Zn	0
			1	1	

- Molecule 12 is CYTIDINE-5'-TRIPHOSPHATE (three-letter code: CTP) (formula: $C_9H_{16}N_3O_{14}P_3$).

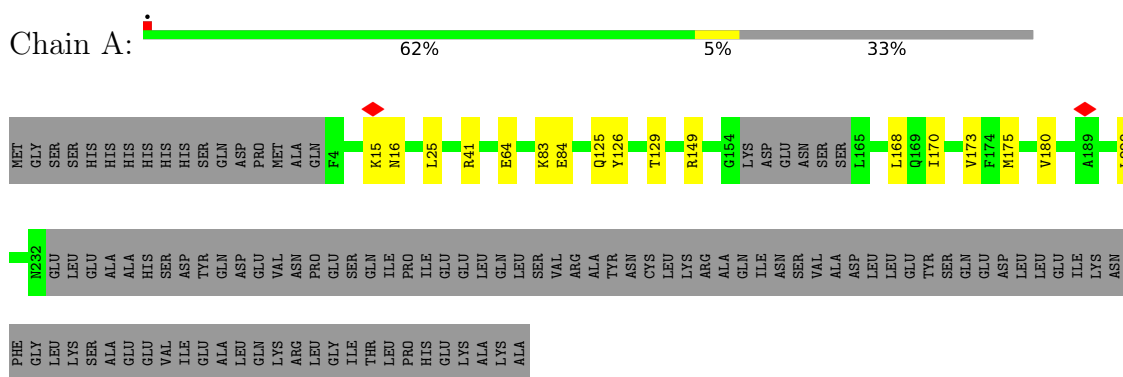


Mol	Chain	Residues	Atoms					AltConf
12	2	1	Total	C	N	O	P	0
			29	9	3	14	3	

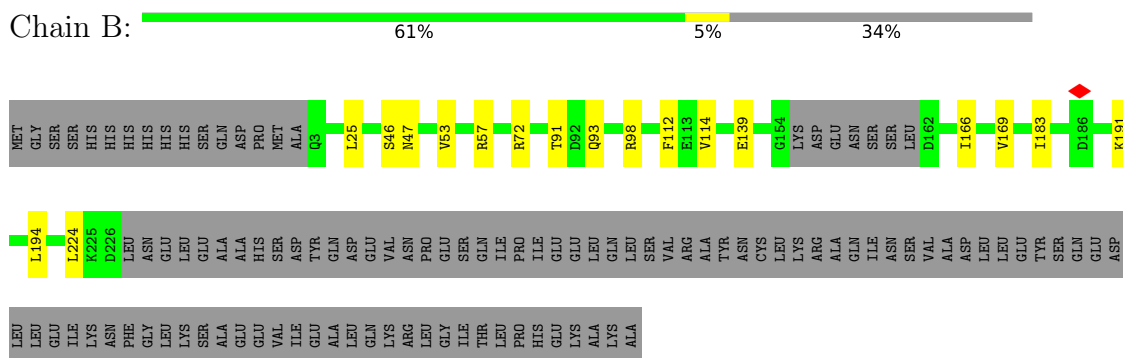
3 Residue-property plots

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

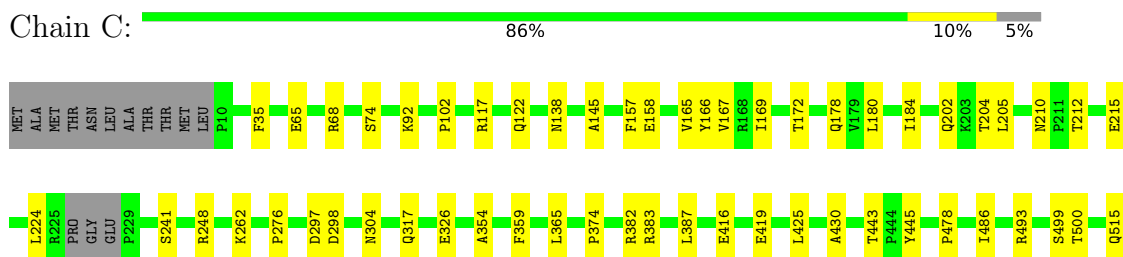
- Molecule 1: DNA-directed RNA polymerase subunit alpha

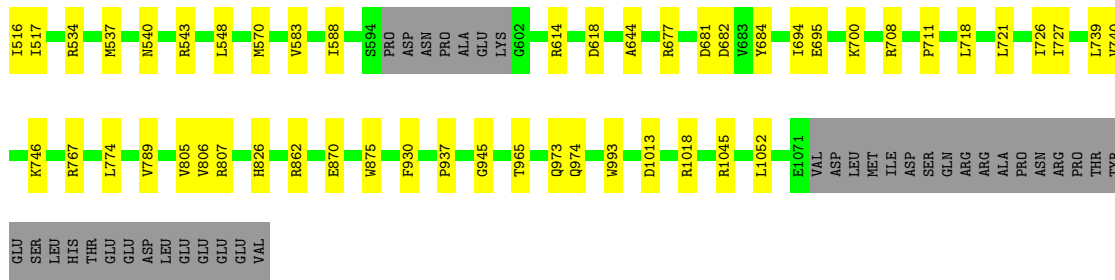


- Molecule 1: DNA-directed RNA polymerase subunit alpha



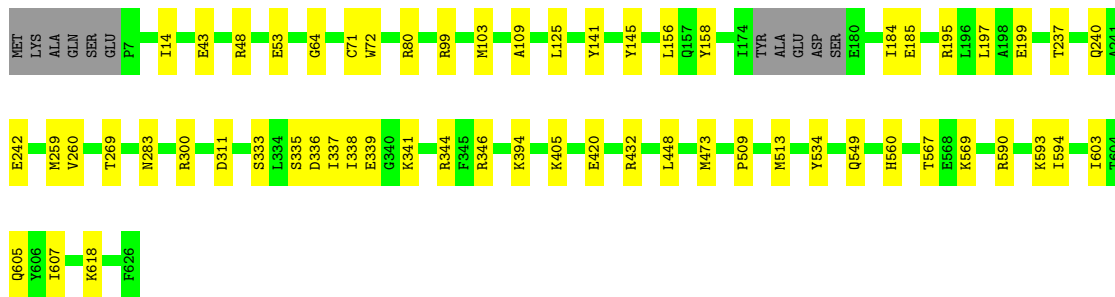
- Molecule 2: DNA-directed RNA polymerase subunit beta





- Molecule 3: DNA-directed RNA polymerase subunit gamma

Chain D: 89% 9%



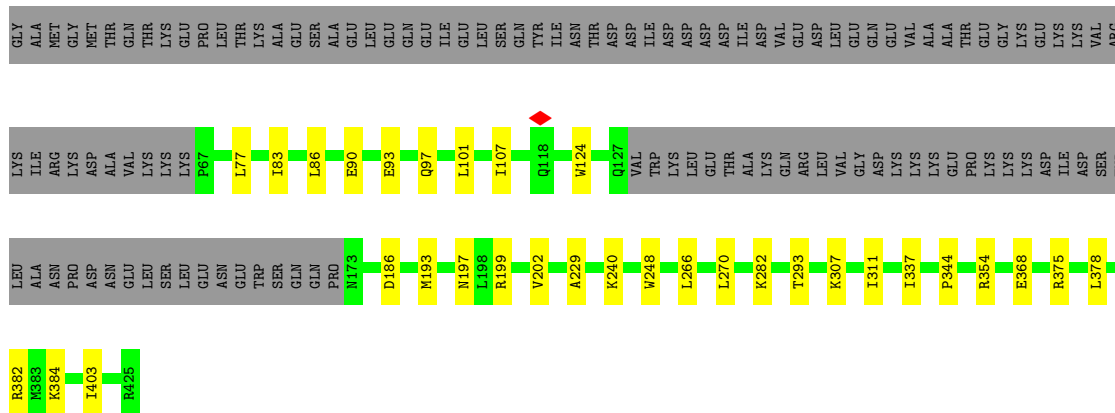
- Molecule 4: DNA-directed RNA polymerase subunit omega

Chain E: 72% 5% 22%



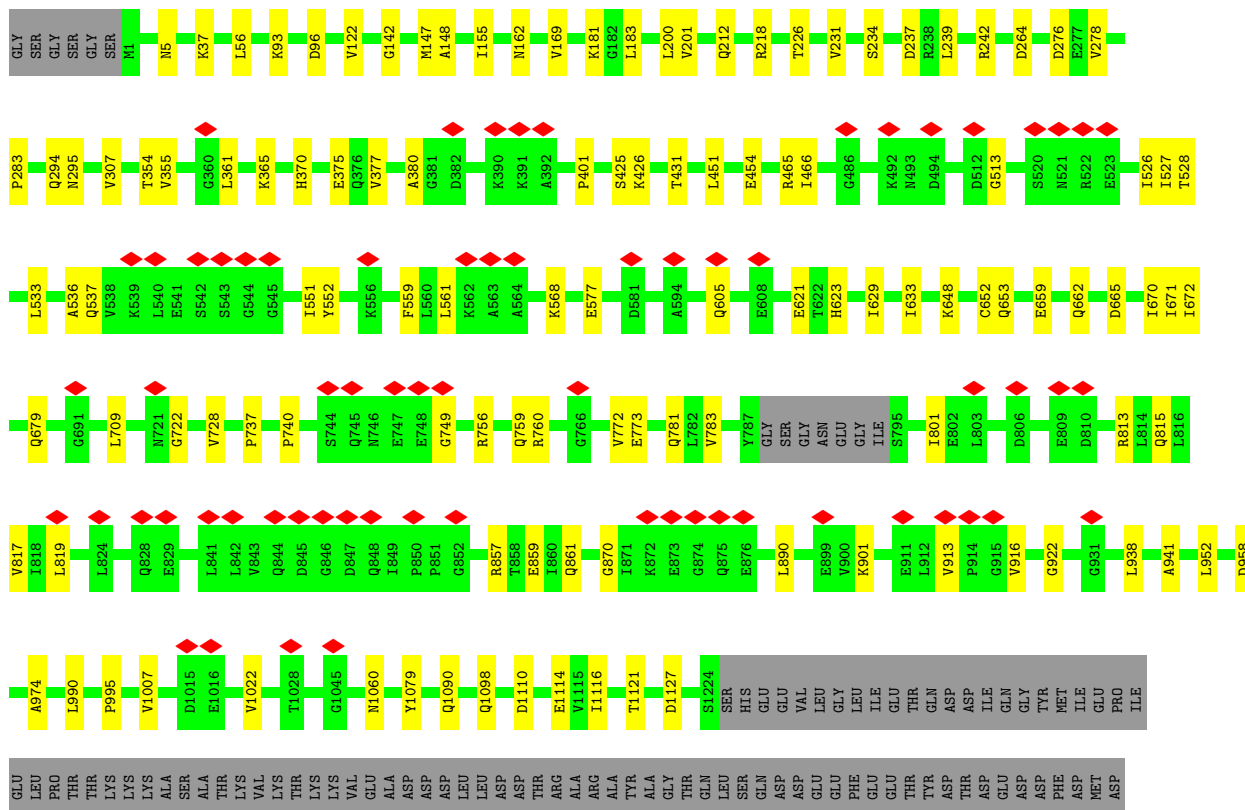
- Molecule 5: RNA polymerase sigma factor SigA

Chain F: 66% 7% 27%



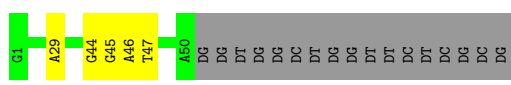
- Molecule 6: DNA-directed RNA polymerase subunit beta'

Chain Z: 5% 83% 9% 8%

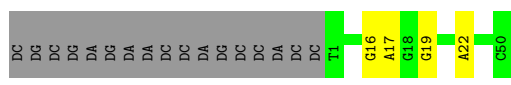


ASP
ASP
ASP
PRO
THR
THR
THR
THR
THR
LYS
LYS
LYS
ALA
SER
SER
ALA
ALA
THR
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THR
LYS
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ALA
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ASP
THR
THR
ARG
ALA
ARG
ALA
TYR
ALA
ALA
GLY
THR
GLN
LEU
SER
GLN
ASP
ASP
GLU
GLU
GLU
PHE
GLU
GLU
THR
TYR
ASP
THR
ASP
ASP
GLN
GLY
ASP
ASP
PHE
MET
ASP
MET
ASP

• Molecule 7: Nontemplate strand DNA



• Molecule 8: Template strand DNA



• Molecule 9: RNA (5'-R(*CP*CP*GP*A)-3')



There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	145731	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.249	Depositor
Minimum map value	-0.113	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0112	Depositor
Map size (\AA)	308.0, 308.0, 308.0	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, CTP

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	0.27	0/1699	0.52	0/2305
1	B	0.26	0/1697	0.49	0/2302
2	C	0.28	0/8328	0.50	1/11289 (0.0%)
3	D	0.28	0/4952	0.49	0/6708
4	E	0.25	0/454	0.43	0/611
5	F	0.26	0/2505	0.47	0/3376
6	Z	0.27	0/8978	0.52	1/12209 (0.0%)
7	1	0.57	0/1155	0.94	0/1783
8	2	0.59	0/1158	0.91	0/1786
9	3	0.39	0/90	1.10	0/138
All	All	0.31	0/31016	0.55	2/42507 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
6	Z	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	Z	819	LEU	CA-CB-CG	5.21	127.28	115.30
2	C	138	ASN	C-N-CA	5.10	133.01	122.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	Z	870	GLY	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1675	0	1674	10	0
1	B	1673	0	1674	12	0
2	C	8171	0	8067	65	0
3	D	4862	0	4939	36	0
4	E	450	0	440	3	0
5	F	2474	0	2452	18	0
6	Z	8860	0	8530	69	0
7	1	1029	0	564	3	0
8	2	1031	0	561	3	0
9	3	81	0	44	0	0
10	D	2	0	0	0	0
11	D	1	0	0	0	0
11	Z	1	0	0	0	0
12	2	29	0	12	1	0
All	All	30339	0	28957	199	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 3.

The worst 5 of 199 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)
6:Z:629:ILE:HD12	6:Z:665:ASP:HA	1.52	0.91
3:D:109:ALA:H	3:D:283:ASN:HD21	1.39	0.70
6:Z:629:ILE:HD11	6:Z:662:GLN:HB2	1.73	0.69
6:Z:737:PRO:HG3	6:Z:759:GLN:HE21	1.65	0.61
2:C:387:LEU:HD21	2:C:425:LEU:HD13	1.83	0.60

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	215/328 (66%)	201 (94%)	14 (6%)	0	100	100
1	B	213/328 (65%)	207 (97%)	6 (3%)	0	100	100
2	C	1046/1104 (95%)	1005 (96%)	41 (4%)	0	100	100
3	D	611/626 (98%)	587 (96%)	24 (4%)	0	100	100
4	E	57/76 (75%)	55 (96%)	2 (4%)	0	100	100
5	F	310/429 (72%)	302 (97%)	8 (3%)	0	100	100
6	Z	1213/1323 (92%)	1141 (94%)	72 (6%)	0	100	100
All	All	3665/4214 (87%)	3498 (95%)	167 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	180/284 (63%)	180 (100%)	0	100	100
1	B	182/284 (64%)	182 (100%)	0	100	100
2	C	867/946 (92%)	867 (100%)	0	100	100
3	D	516/537 (96%)	515 (100%)	1 (0%)	93	98
4	E	45/69 (65%)	45 (100%)	0	100	100
5	F	250/386 (65%)	249 (100%)	1 (0%)	91	96
6	Z	882/1107 (80%)	878 (100%)	4 (0%)	88	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2922/3613 (81%)	2916 (100%)	6 (0%)	93 98

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	Z	756	ARG
6	Z	857	ARG
6	Z	901	LYS
5	F	293	THR
3	D	237	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
6	Z	108	GLN
6	Z	1210	ASN
6	Z	1102	GLN
3	D	283	ASN
5	F	402	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
9	3	2/4 (50%)	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 monosaccharides in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 4 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
12	CTP	2	3001	10	26,30,30	0.76	0	39,47,47	1.12	3 (7%)

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
12	CTP	2	3001	10	-	5/22/38/38	0/2/2/2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	2	3001	CTP	PB-O3B-PG	-2.80	123.21	132.83
12	2	3001	CTP	C3'-C2'-C1'	2.68	106.52	101.43
12	2	3001	CTP	PB-O3A-PA	-2.61	123.87	132.83

There are no chirality outliers.

All (5) torsion outliers are listed below:

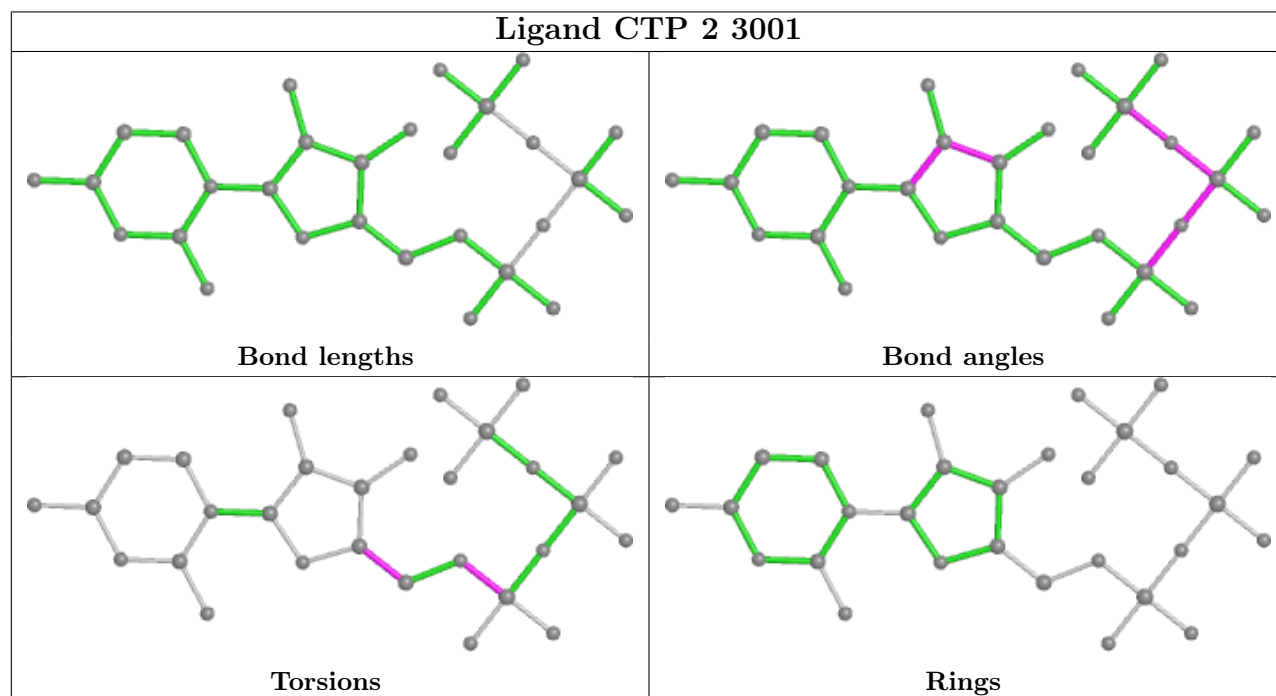
Mol	Chain	Res	Type	Atoms
12	2	3001	CTP	C5'-O5'-PA-O1A
12	2	3001	CTP	C3'-C4'-C5'-O5'
12	2	3001	CTP	O4'-C4'-C5'-O5'
12	2	3001	CTP	C5'-O5'-PA-O3A
12	2	3001	CTP	C5'-O5'-PA-O2A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	2	3001	CTP	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.

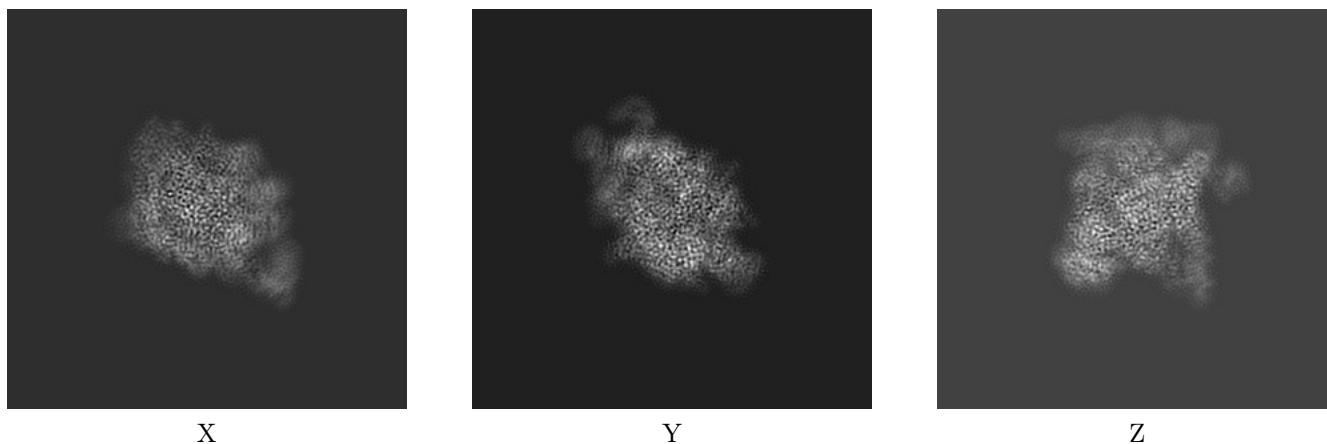
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34398. These allow visual inspection of the internal detail of the map and identification of artifacts.

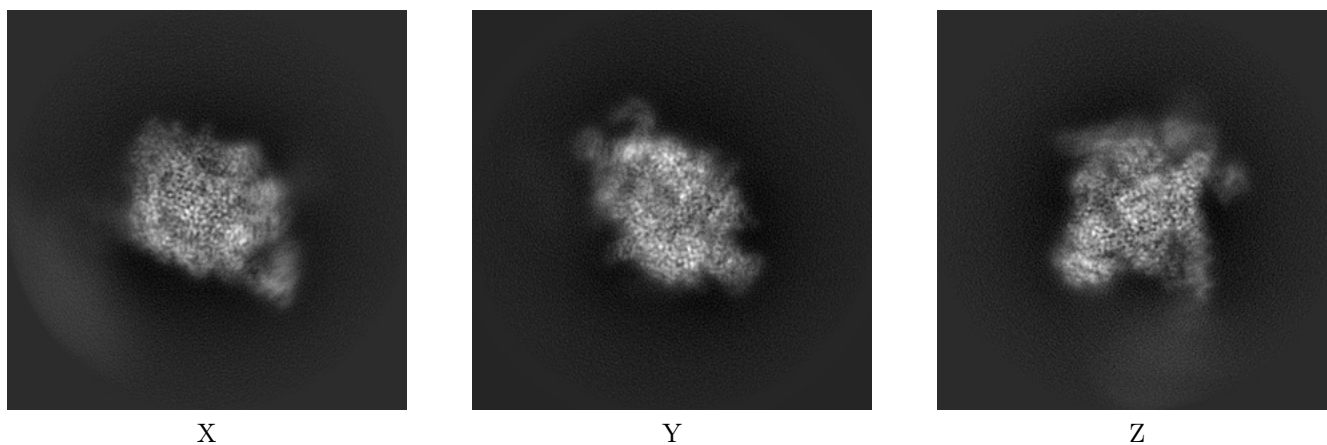
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



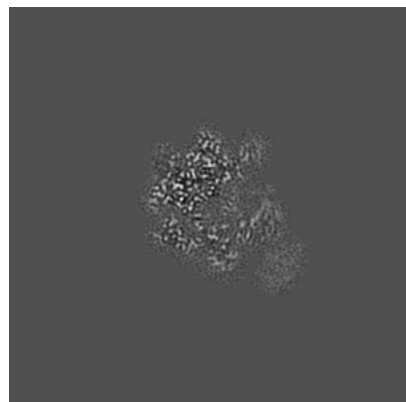
6.1.2 Raw map



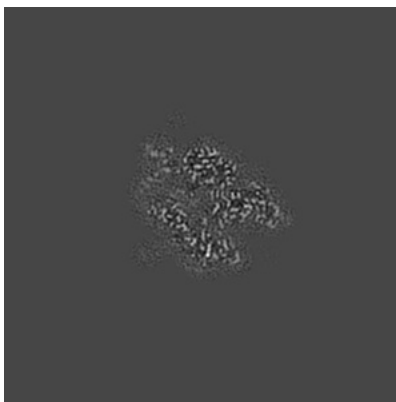
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

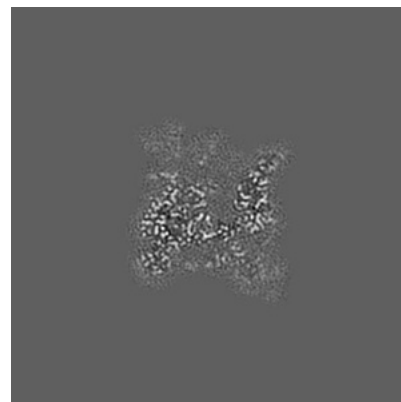
6.2.1 Primary map



X Index: 140

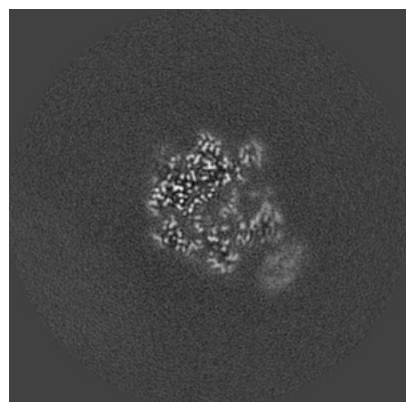


Y Index: 140

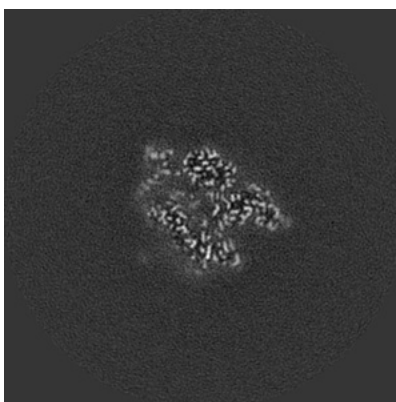


Z Index: 140

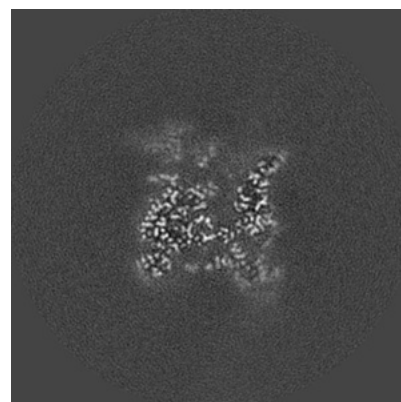
6.2.2 Raw map



X Index: 140



Y Index: 140

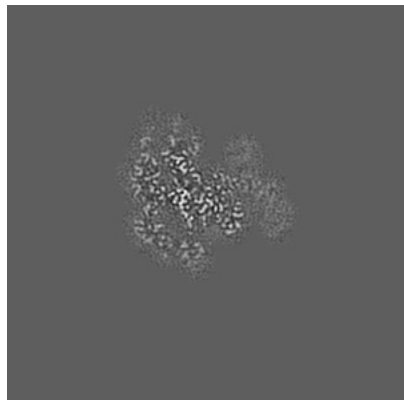


Z Index: 140

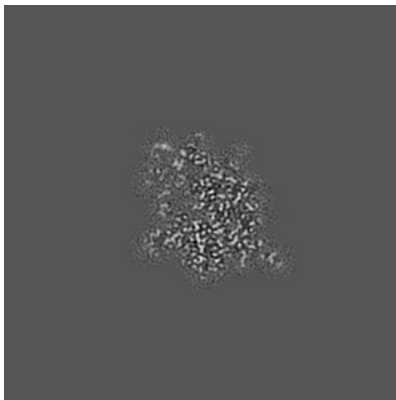
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

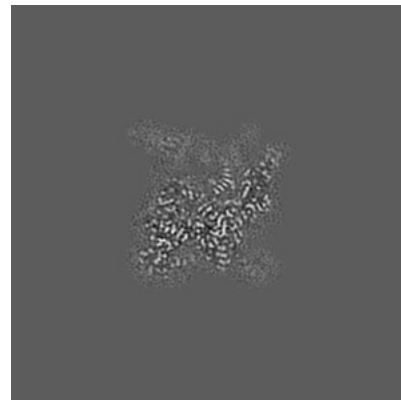
6.3.1 Primary map



X Index: 109

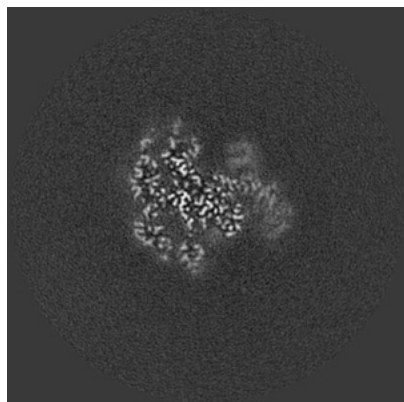


Y Index: 126

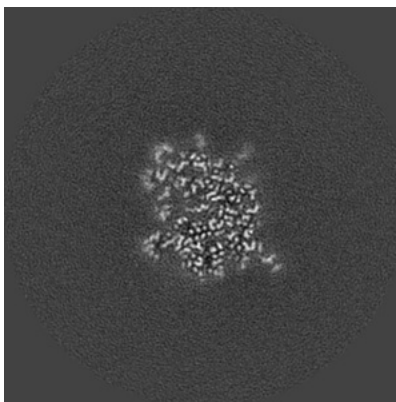


Z Index: 146

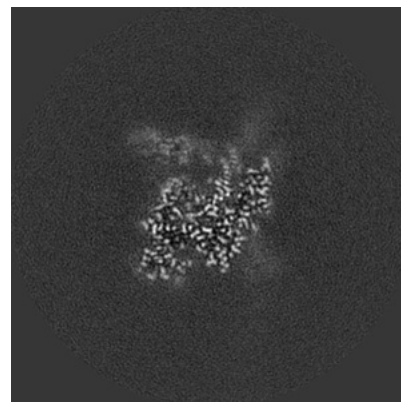
6.3.2 Raw map



X Index: 109



Y Index: 127

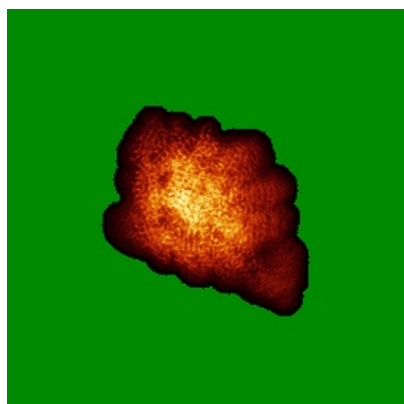


Z Index: 148

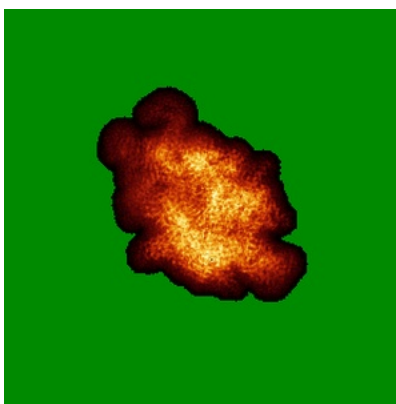
The images above show the largest variance slices of the map in three orthogonal directions.

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

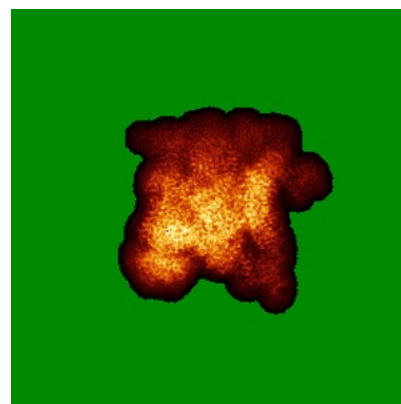
6.4.1 Primary map



X

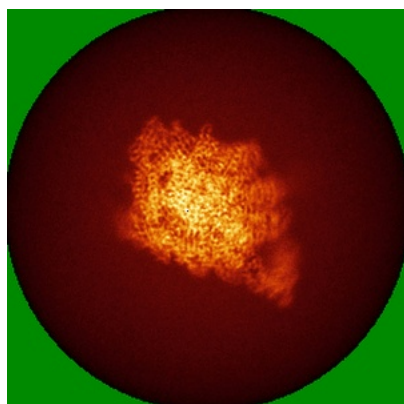


Y

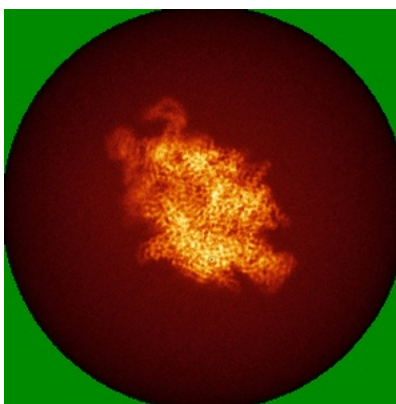


Z

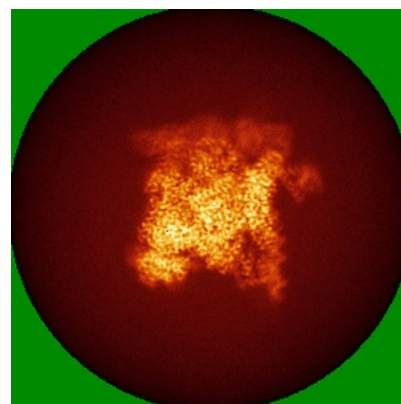
6.4.2 Raw map



X



Y

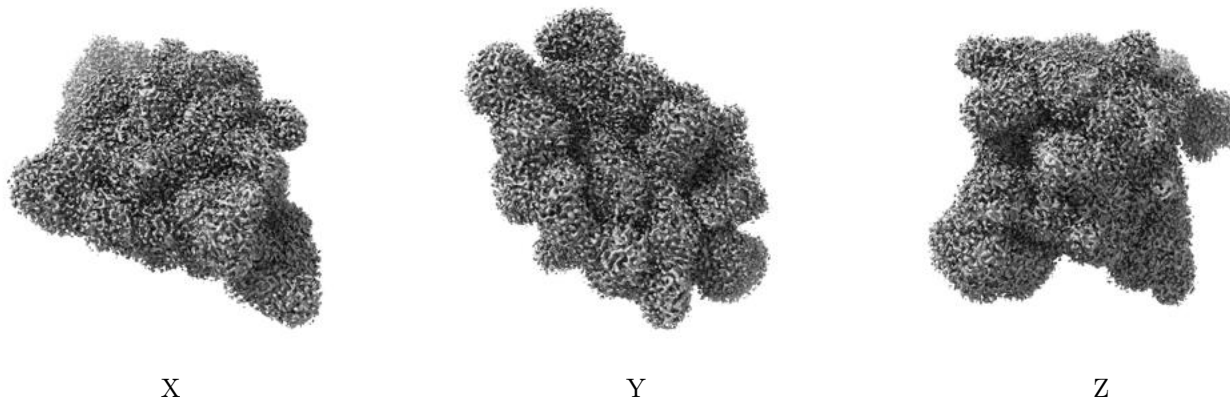


Z

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.

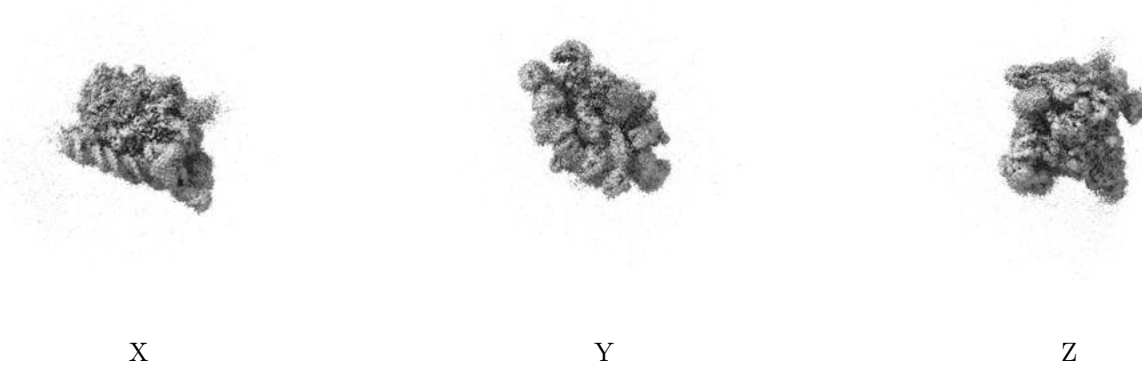
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0112. 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.

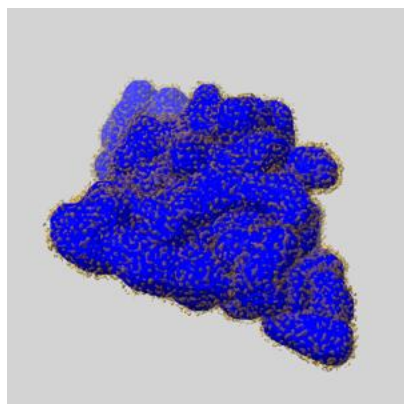
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

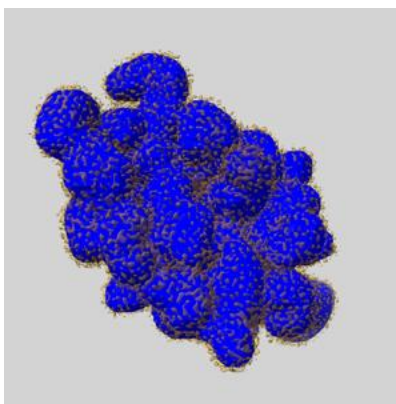
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

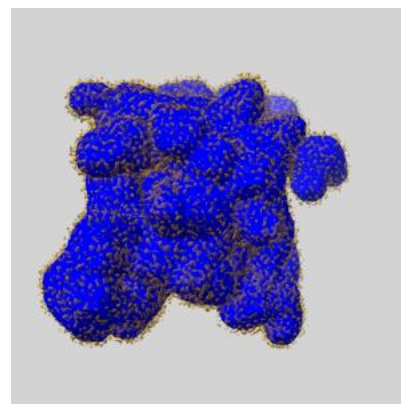
6.6.1 emd_34398_msk_1.map [i](#)



X



Y

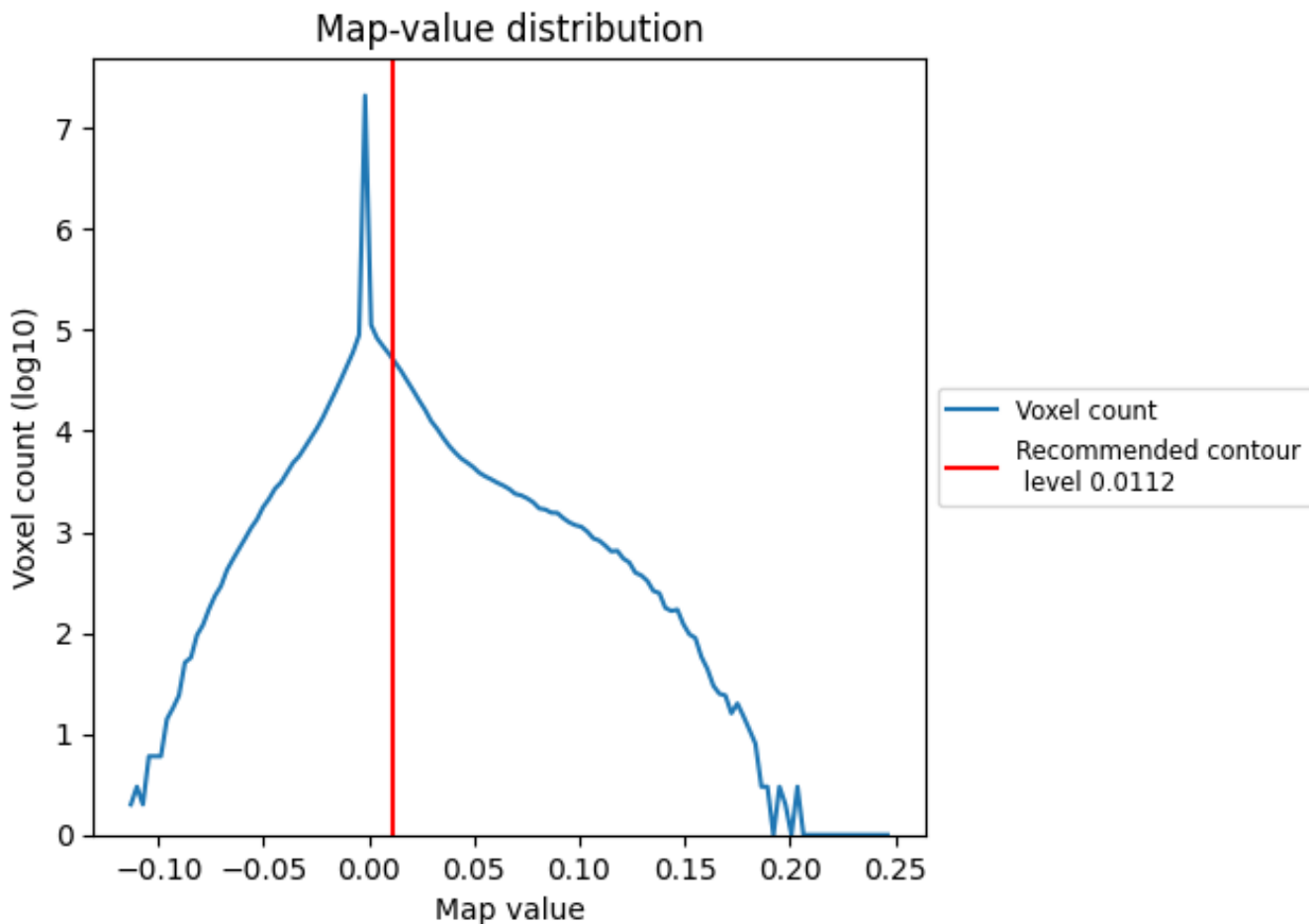


Z

7 Map analysis [i](#)

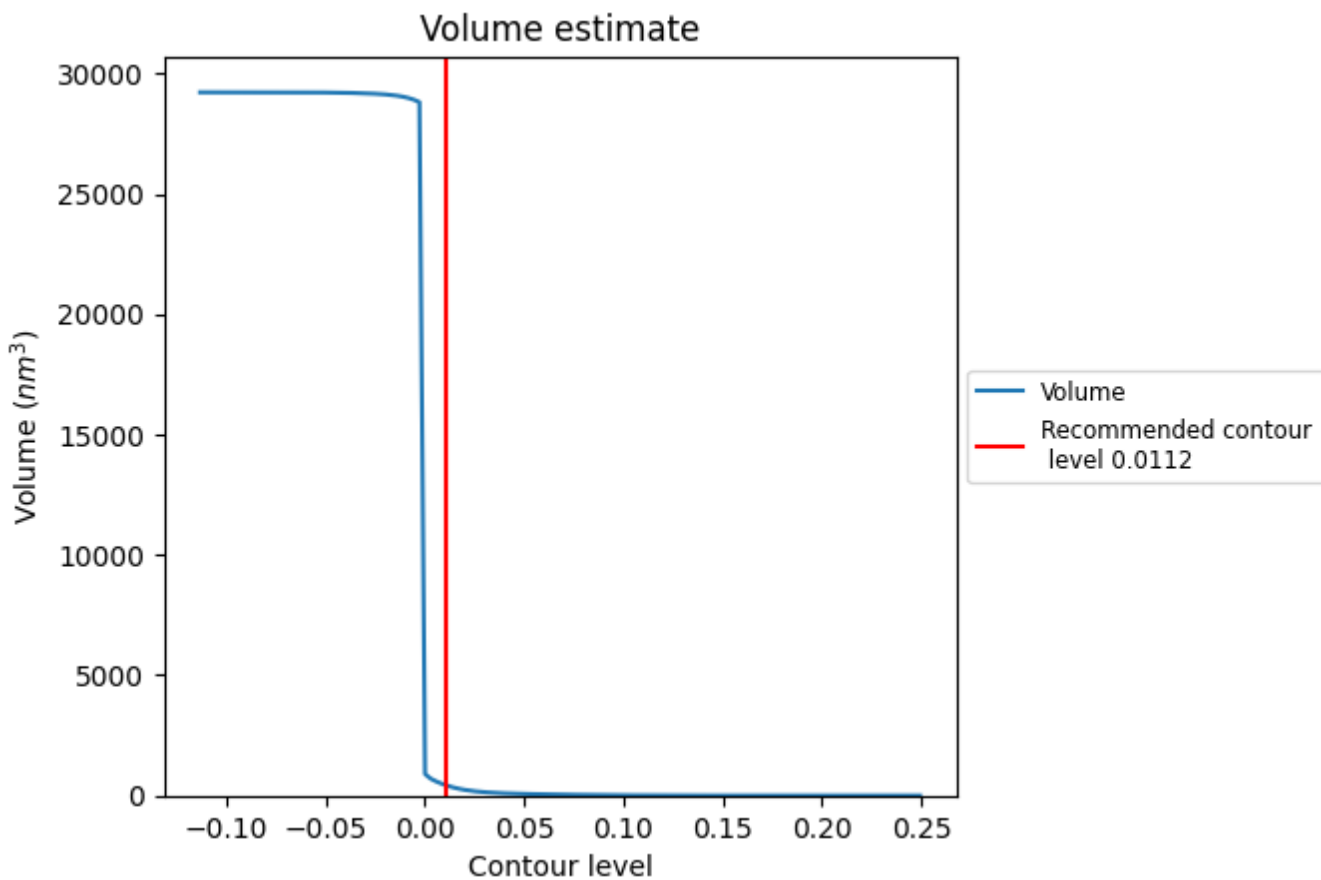
This section contains the results of statistical analysis of the map.

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.

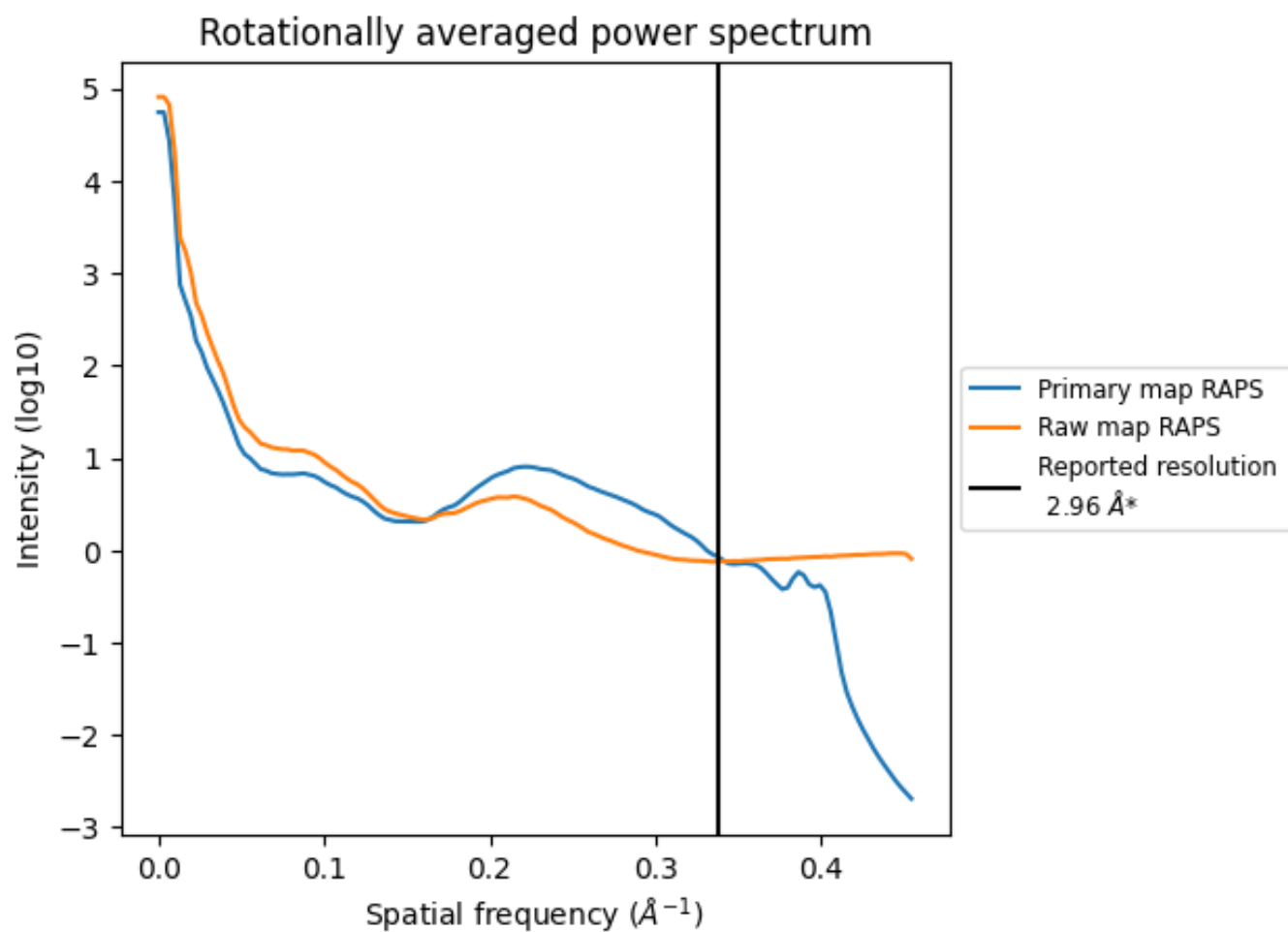
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 417 nm³; this corresponds to an approximate mass of 376 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum i

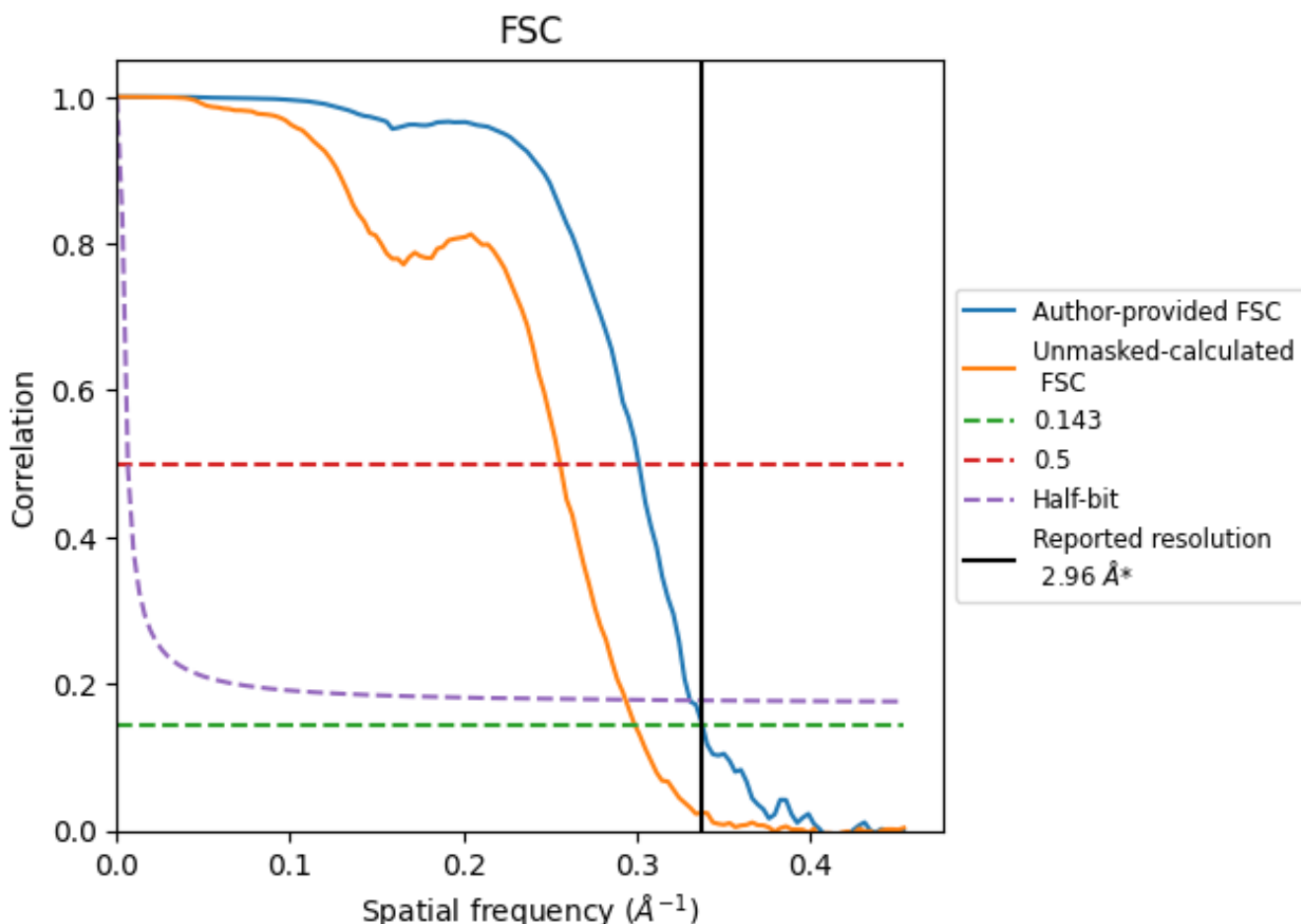


*Reported resolution corresponds to spatial frequency of 0.338 Å⁻¹

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 0.338 Å⁻¹

8.2 Resolution estimates [i](#)

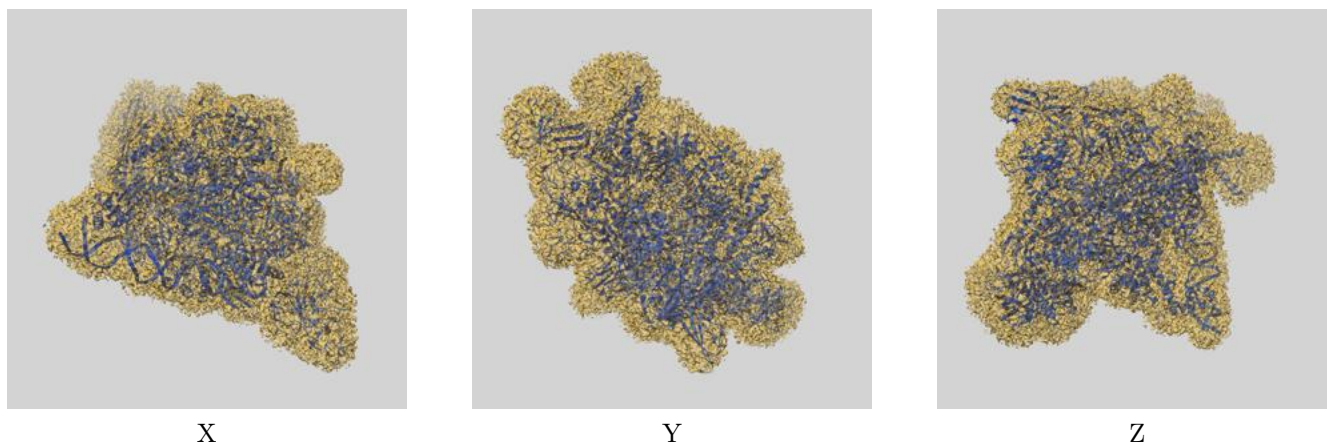
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.96	-	-
Author-provided FSC curve	2.96	3.32	3.02
Unmasked-calculated*	3.34	3.91	3.40

*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 3.34 differs from the reported value 2.96 by more than 10 %

9 Map-model fit [i](#)

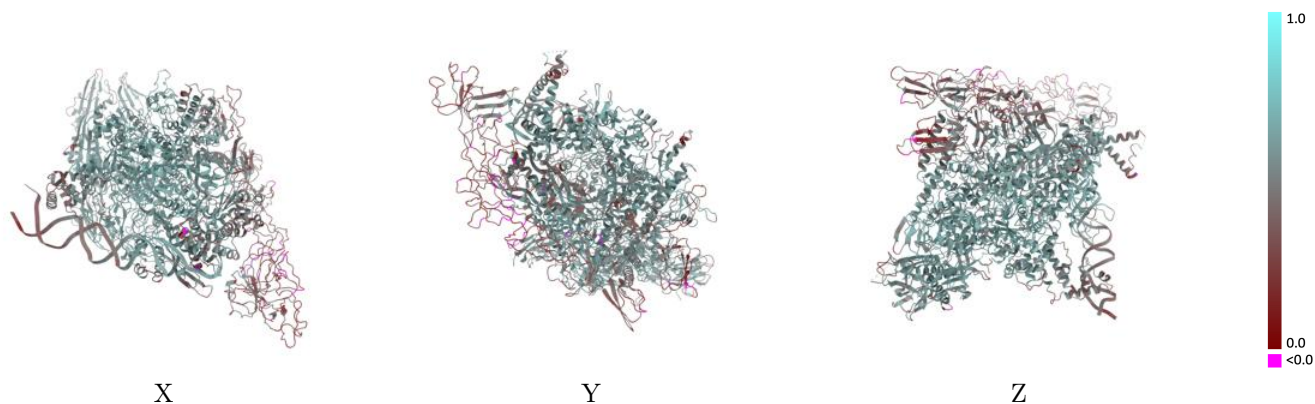
This section contains information regarding the fit between EMDB map EMD-34398 and PDB model 8GZH. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



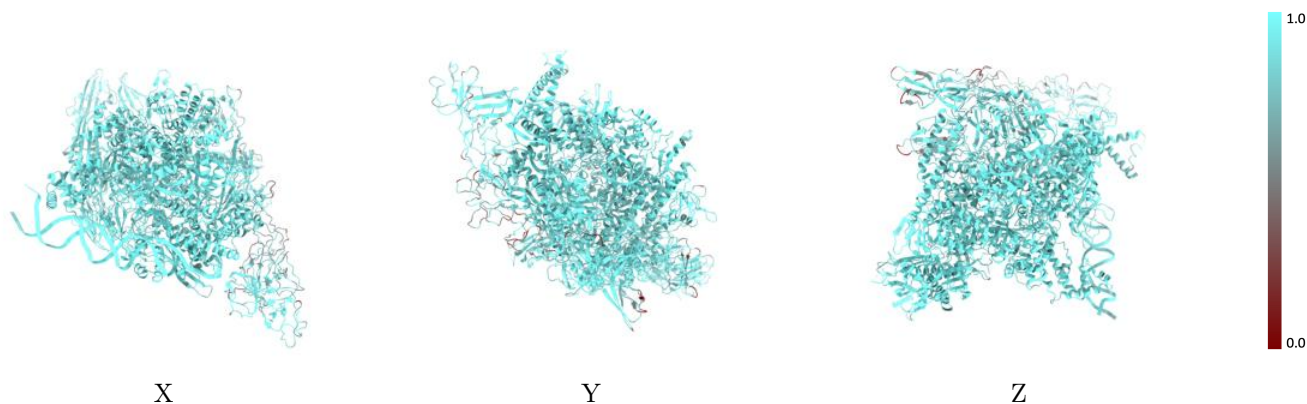
The images above show the 3D surface view of the map at the recommended contour level 0.0112 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



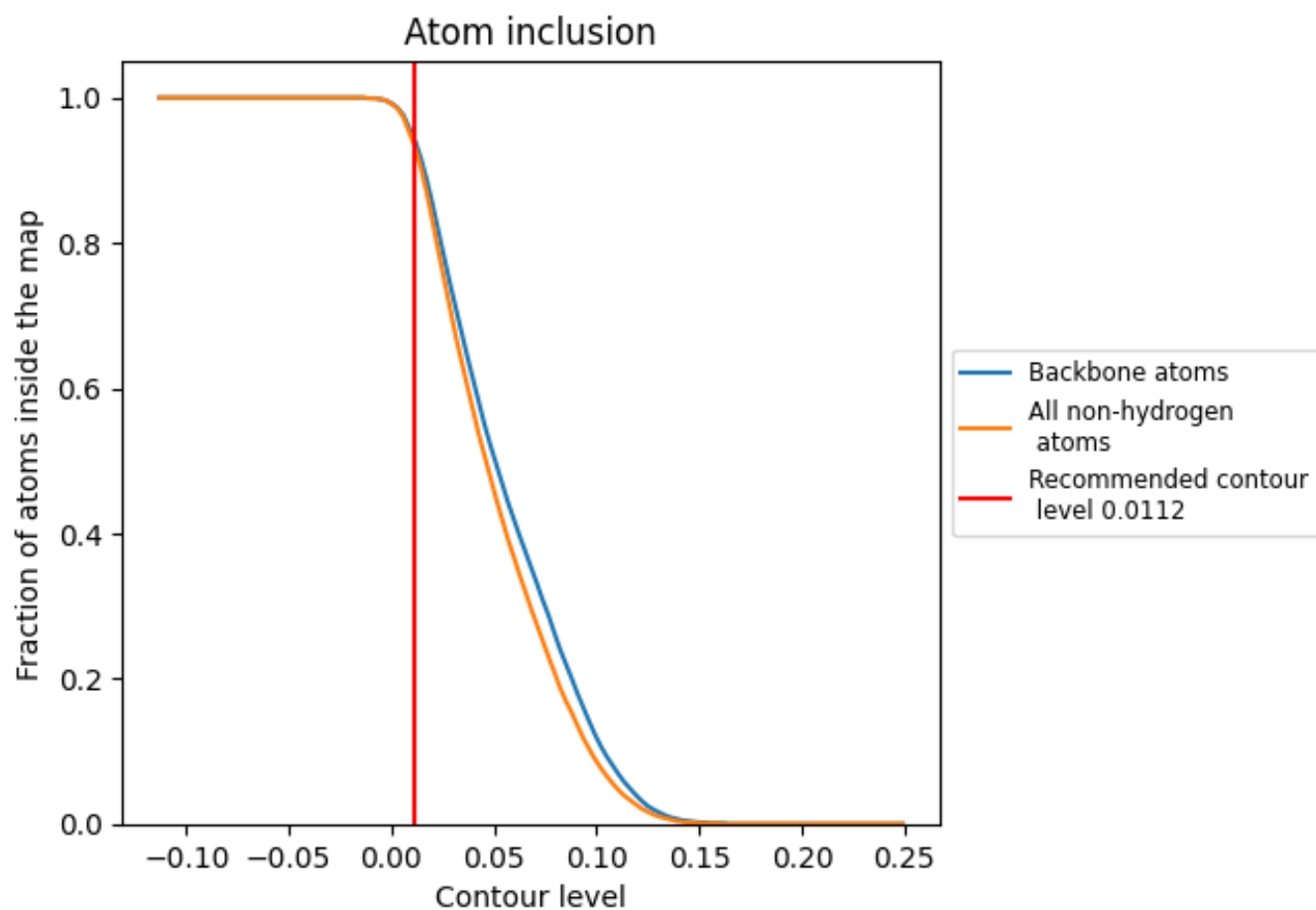
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0112).























9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0112) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9350	 0.5340
1	 0.9540	 0.4960
2	 0.9680	 0.5280
3	 1.0000	 0.6300
A	 0.9500	 0.5710
B	 0.9500	 0.5490
C	 0.9630	 0.5820
D	 0.9750	 0.6100
E	 0.9700	 0.5740
F	 0.9490	 0.5220
Z	 0.8700	 0.4450

