



wwPDB EM Validation Summary Report ⓘ

Jul 8, 2024 – 03:42 pm BST

PDB ID : 7QWP
EMDB ID : EMD-14190
Title : CryoEM structure of bacterial transcription close complex (RPc)
Authors : Ye, F.Z.; Zhang, X.D.
Deposited on : 2022-01-25
Resolution : 3.40 Å(reported)
Based on initial model : 5NSR

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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

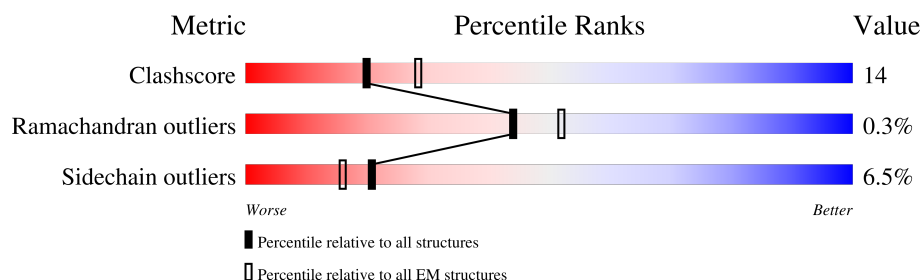
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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

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	329	
1	B	329	
2	C	1342	
3	D	1407	
4	E	91	
5	M	497	
6	N	63	
7	T	63	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 29006 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
1	A	309	Total	C	N	O	S	0	0
			2316	1450	404	455	7		
1	B	223	Total	C	N	O	S	0	0
			1673	1045	291	332	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1341	Total	C	N	O	S	0	0
			10135	6365	1764	1966	40		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1333	Total	C	N	O	S	0	0
			9638	6054	1731	1815	38		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	74	Total	C	N	O	S	0	0
			552	341	109	101	1		

- Molecule 5 is a protein called RNA polymerase sigma-54 factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	405	Total	C	N	O	S	0	0
			3216	2015	557	633	11		

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-19	MET	-	initiating methionine	UNP A0A0N9UTC1

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Chain	Residue	Modelled	Actual	Comment	Reference
M	-18	GLY	-	expression tag	UNP A0A0N9UTC1
M	-17	SER	-	expression tag	UNP A0A0N9UTC1
M	-16	SER	-	expression tag	UNP A0A0N9UTC1
M	-15	HIS	-	expression tag	UNP A0A0N9UTC1
M	-14	HIS	-	expression tag	UNP A0A0N9UTC1
M	-13	HIS	-	expression tag	UNP A0A0N9UTC1
M	-12	HIS	-	expression tag	UNP A0A0N9UTC1
M	-11	HIS	-	expression tag	UNP A0A0N9UTC1
M	-10	HIS	-	expression tag	UNP A0A0N9UTC1
M	-9	SER	-	expression tag	UNP A0A0N9UTC1
M	-8	SER	-	expression tag	UNP A0A0N9UTC1
M	-7	GLY	-	expression tag	UNP A0A0N9UTC1
M	-6	LEU	-	expression tag	UNP A0A0N9UTC1
M	-5	VAL	-	expression tag	UNP A0A0N9UTC1
M	-4	PRO	-	expression tag	UNP A0A0N9UTC1
M	-3	ARG	-	expression tag	UNP A0A0N9UTC1
M	-2	GLY	-	expression tag	UNP A0A0N9UTC1
M	-1	SER	-	expression tag	UNP A0A0N9UTC1
M	0	HIS	-	expression tag	UNP A0A0N9UTC1
M	49	GLU	GLN	conflict	UNP A0A0N9UTC1

- Molecule 6 is a DNA chain called Non-Template promoter DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	36	Total	C	N	O	P	0	0
			738	349	137	216	36		

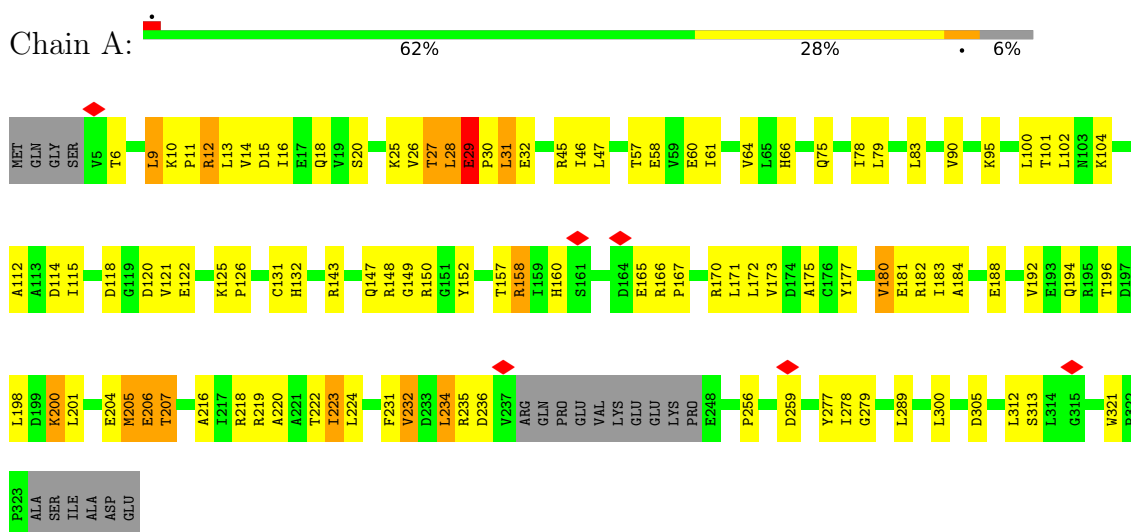
- Molecule 7 is a DNA chain called Template promoter DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	T	36	Total	C	N	O	P	0	0
			738	349	137	216	36		

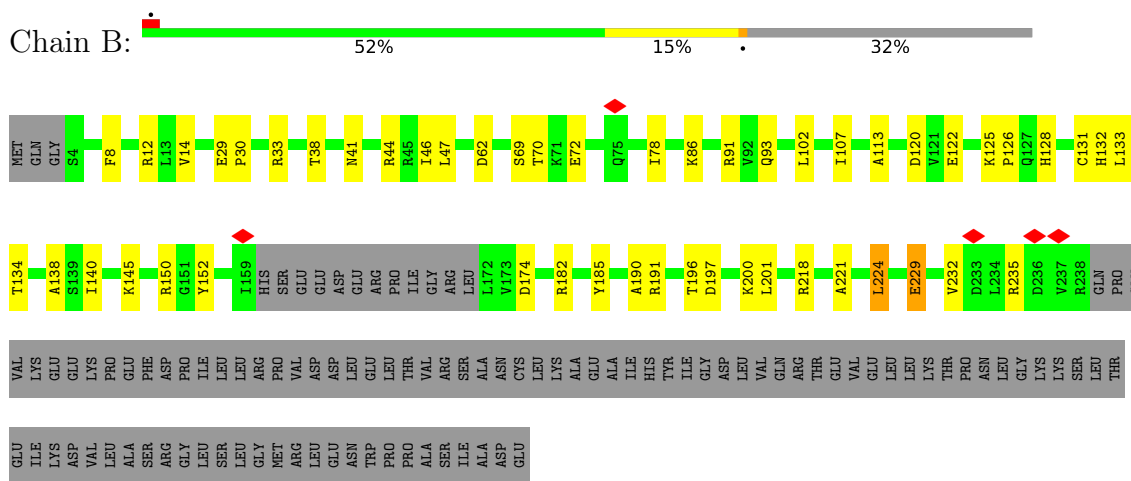
3 Residue-property plots

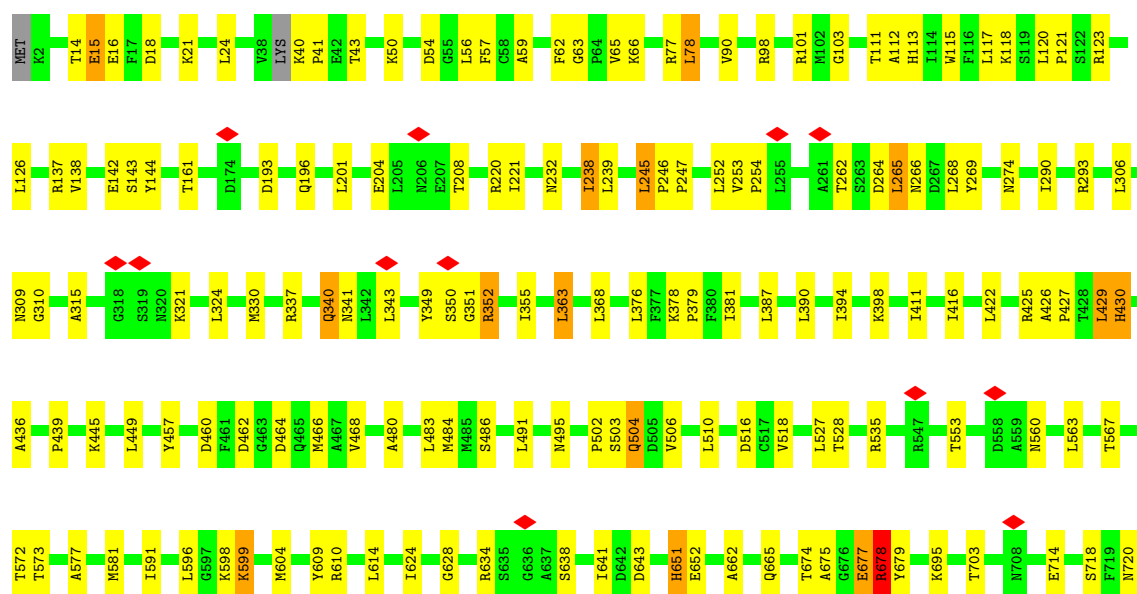
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

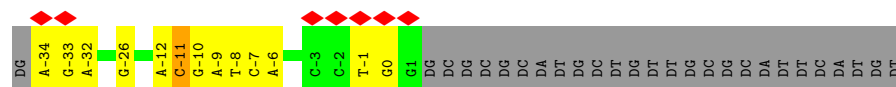
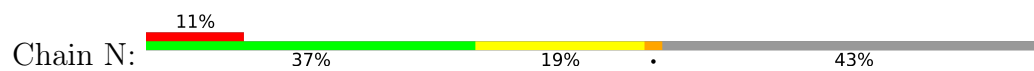


- Molecule 1: DNA-directed RNA polymerase subunit alpha





- Molecule 6: Non-Template promoter DNA



- Molecule 7: Template promoter DNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	31394	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)	1400	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.293	Depositor
Minimum map value	-0.159	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.021	Depositor
Map size (\AA)	281.6, 281.6, 281.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.24	0/2345	0.46	0/3195
1	B	0.23	0/1690	0.44	0/2297
2	C	0.23	0/10293	0.40	0/13952
3	D	0.24	0/9772	0.42	1/13273 (0.0%)
4	E	0.23	0/554	0.37	0/749
5	M	0.87	2/3263 (0.1%)	1.05	10/4420 (0.2%)
6	N	0.66	2/827 (0.2%)	0.85	3/1274 (0.2%)
7	T	1.15	12/827 (1.5%)	1.11	8/1274 (0.6%)
All	All	0.42	16/29571 (0.1%)	0.57	22/40434 (0.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	N	-11	DC	C4'-O4'	-13.40	1.31	1.45
7	T	23	DT	C4'-O4'	13.16	1.58	1.45
7	T	17	DA	C4'-O4'	11.91	1.56	1.45
7	T	13	DG	O3'-P	-11.08	1.47	1.61
7	T	9	DT	O3'-P	-9.80	1.49	1.61

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	T	8	DA	O5'-P-OP2	-11.83	95.05	105.70
7	T	13	DG	C5'-C4'-O4'	11.06	130.32	109.30
7	T	7	DG	P-O3'-C3'	10.89	132.77	119.70
7	T	23	DT	C1'-O4'-C4'	-8.96	101.14	110.10
7	T	13	DG	O3'-P-O5'	8.45	120.05	104.00

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	2316	0	2297	133	0
1	B	1673	0	1674	35	0
2	C	10135	0	9844	182	0
3	D	9638	0	9243	204	0
4	E	552	0	555	13	0
5	M	3216	0	3227	265	0
6	N	738	0	404	33	0
7	T	738	0	404	33	0
All	All	29006	0	27648	774	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 14.

The worst 5 of 774 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)
1:A:29:GLU:CG	1:A:30:PRO:HD3	1.57	1.34
5:M:23:ILE:CD1	7:T:12:DT:H71	1.65	1.26
4:E:3:ARG:HH12	4:E:55:GLU:CB	1.57	1.17
5:M:15:MET:HB2	6:N:-12:DA:N6	1.60	1.17
5:M:109:LEU:HB3	5:M:110:PRO:CD	1.75	1.17

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	305/329 (93%)	274 (90%)	29 (10%)	2 (1%)	22	55
1	B	219/329 (67%)	206 (94%)	13 (6%)	0	100	100
2	C	1339/1342 (100%)	1266 (94%)	72 (5%)	1 (0%)	51	82
3	D	1319/1407 (94%)	1229 (93%)	89 (7%)	1 (0%)	51	82
4	E	72/91 (79%)	69 (96%)	2 (3%)	1 (1%)	11	37
5	M	401/497 (81%)	361 (90%)	33 (8%)	7 (2%)	9	34
All	All	3655/3995 (92%)	3405 (93%)	238 (6%)	12 (0%)	44	72

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	29	GLU
5	M	195	LEU
5	M	185	PHE
2	C	399	ALA
5	M	45	PRO

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	248/286 (87%)	225 (91%)	23 (9%)	9	31
1	B	180/286 (63%)	170 (94%)	10 (6%)	21	51
2	C	1049/1157 (91%)	1005 (96%)	44 (4%)	30	59
3	D	914/1168 (78%)	868 (95%)	46 (5%)	24	54
4	E	54/75 (72%)	49 (91%)	5 (9%)	9	31
5	M	358/440 (81%)	303 (85%)	55 (15%)	2	11
All	All	2803/3412 (82%)	2620 (94%)	183 (6%)	21	46

5 of 183 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	820	ILE

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Mol	Chain	Res	Type
5	M	131	THR
3	D	960	LEU
5	M	21	GLN
5	M	180	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	651	HIS
5	M	223	HIS
3	D	680	ASN
5	M	251	ASN
5	M	21	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

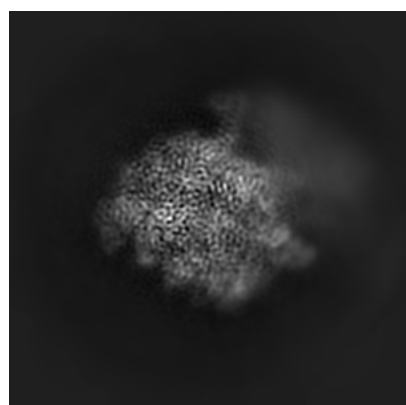
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14190. These allow visual inspection of the internal detail of the map and identification of artifacts.

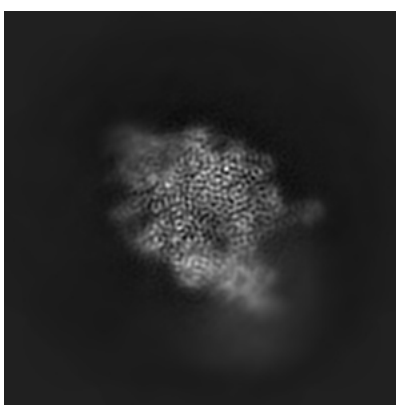
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

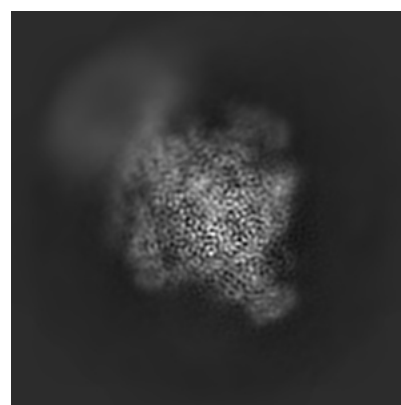
6.1.1 Primary map



X



Y

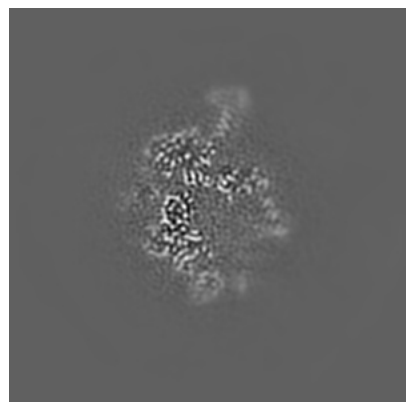


Z

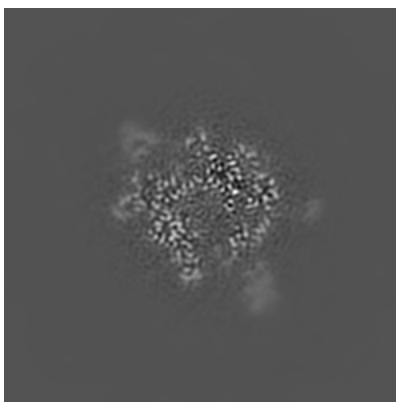
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

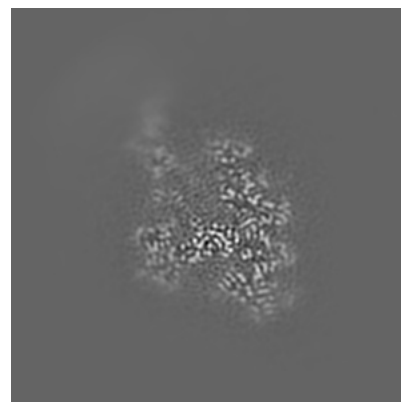
6.2.1 Primary map



X Index: 128



Y Index: 128

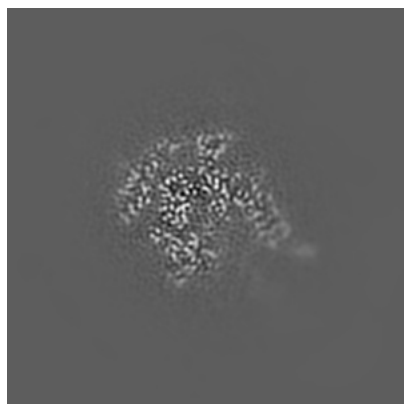


Z Index: 128

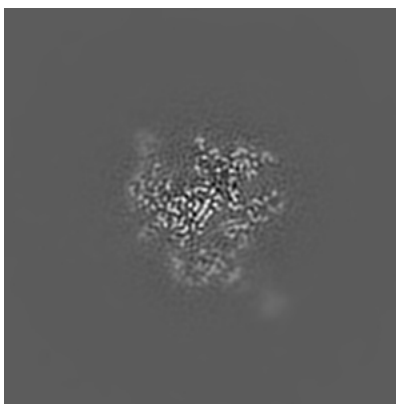
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

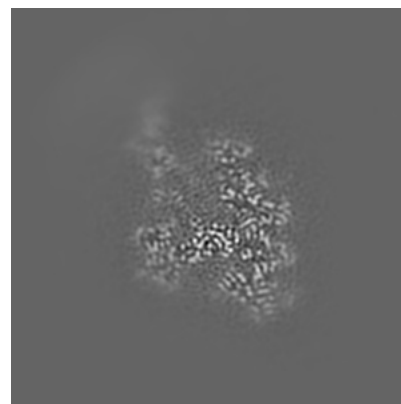
6.3.1 Primary map



X Index: 139



Y Index: 112

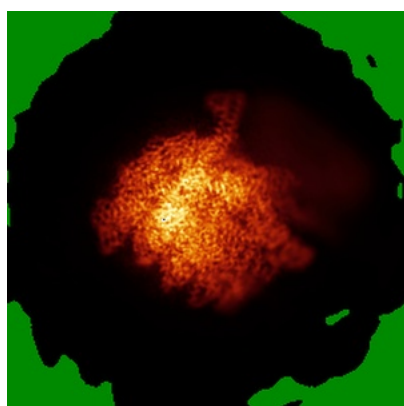


Z Index: 128

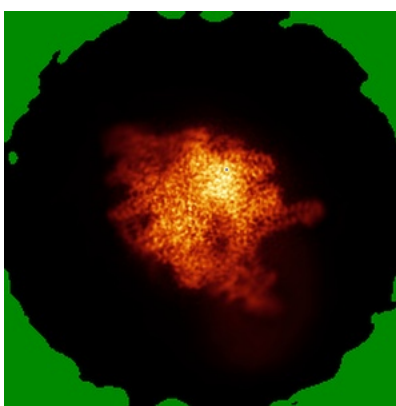
The images above show the largest variance slices of the map in three orthogonal directions.

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

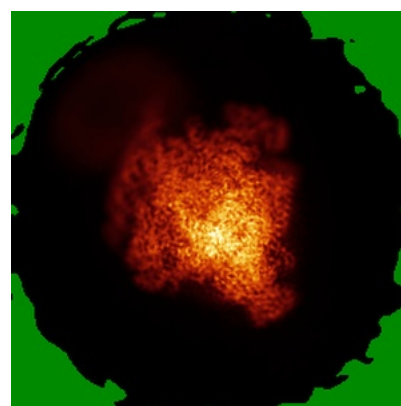
6.4.1 Primary map



X



Y

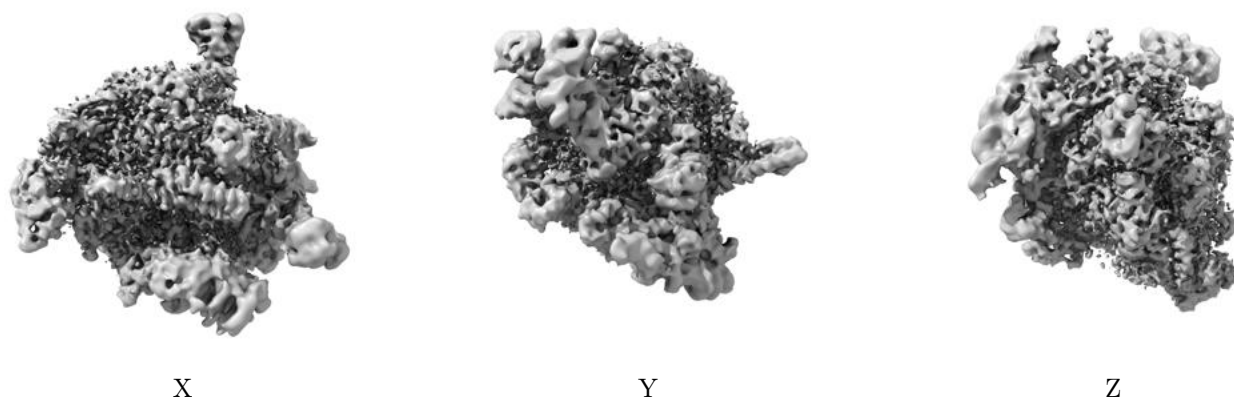


Z

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 0.021. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

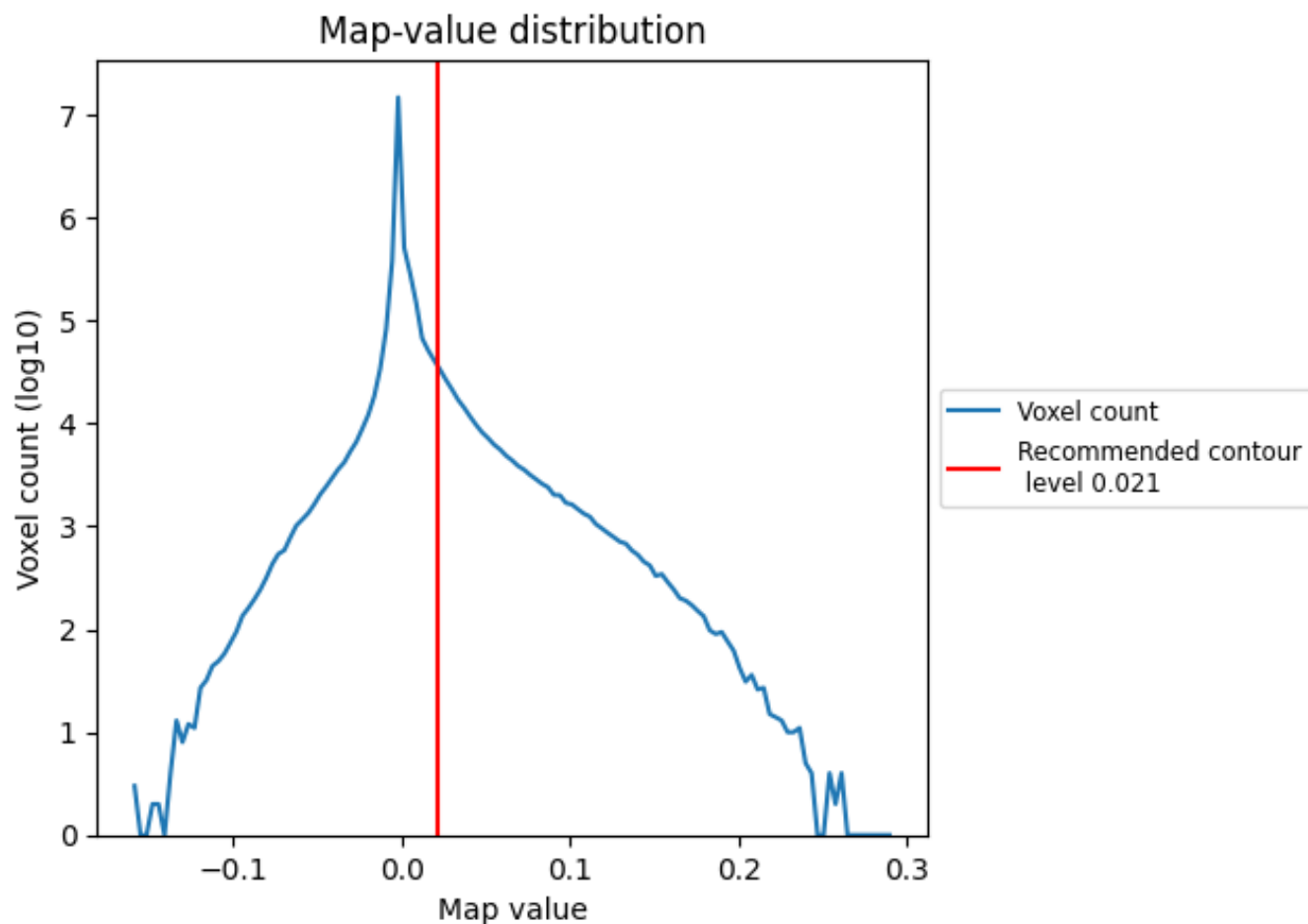
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

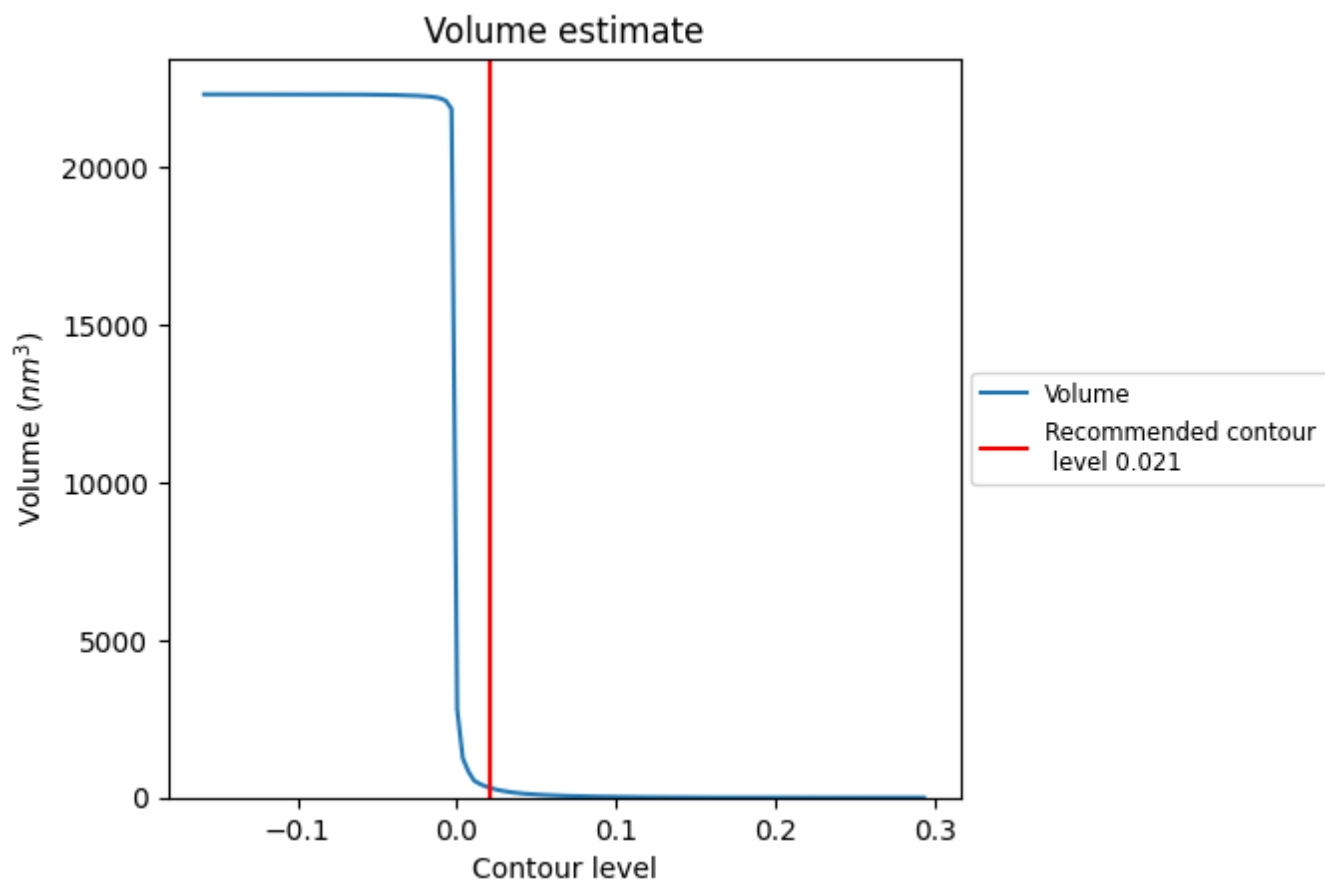
This section contains the results of statistical analysis of the map.

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.

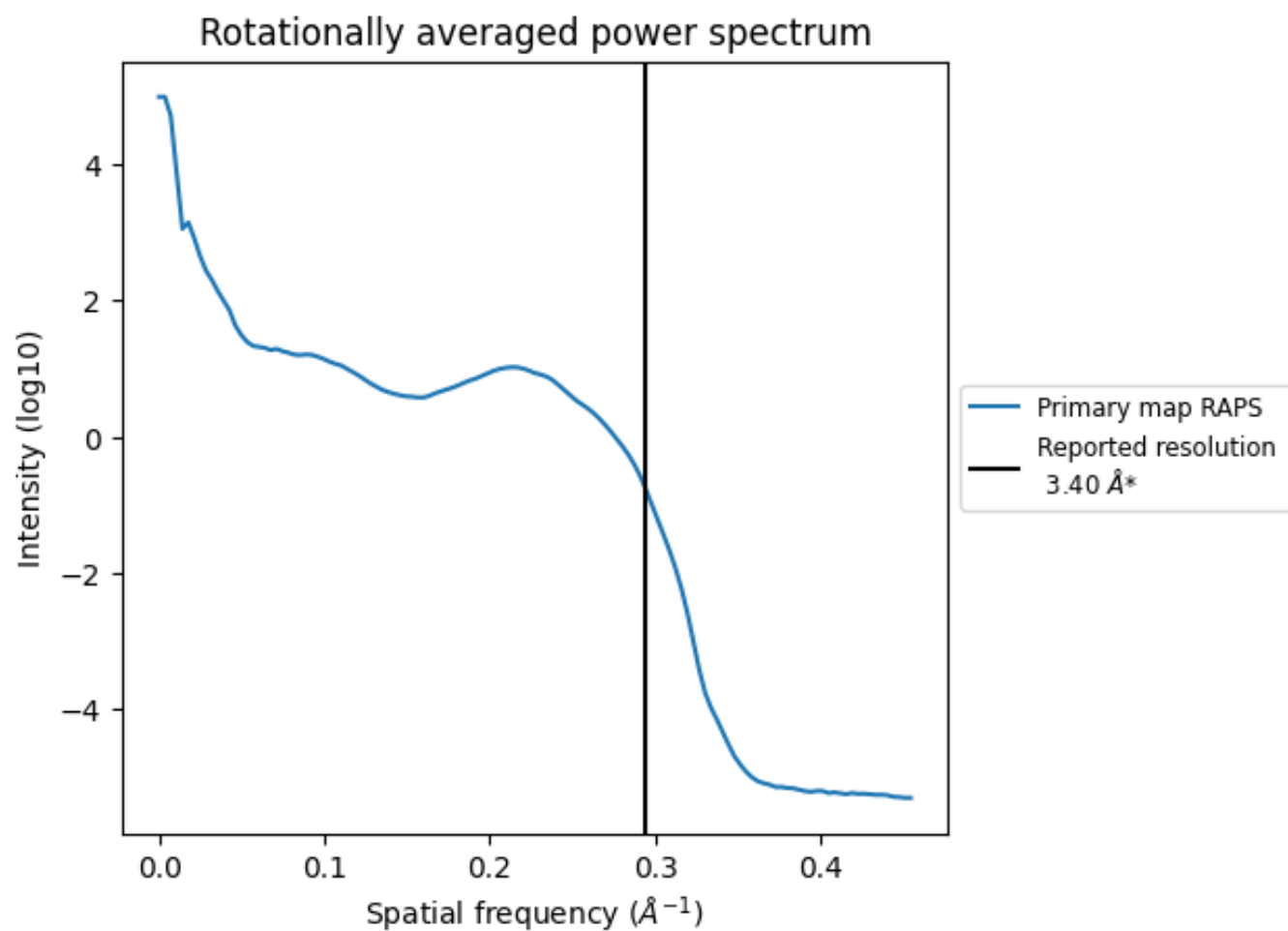
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 306 nm³; this corresponds to an approximate mass of 277 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 0.294 Å⁻¹

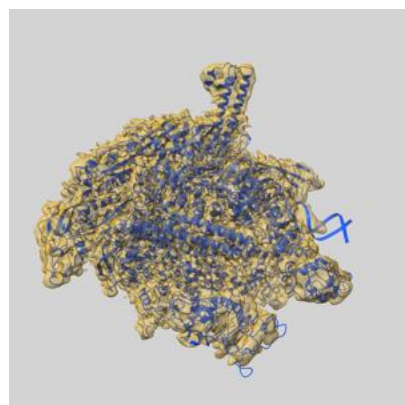
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

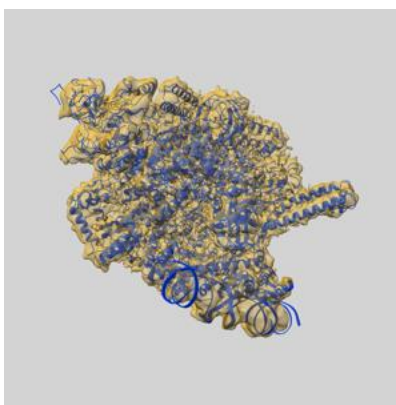
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14190 and PDB model 7QWP. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

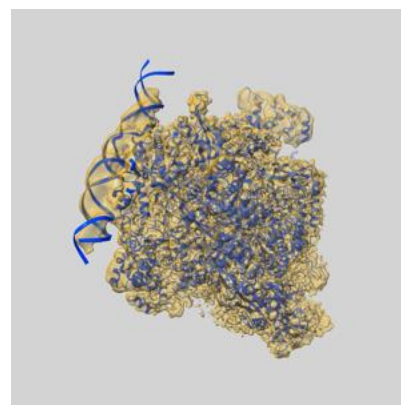
9.1 Map-model overlay [i](#)



X



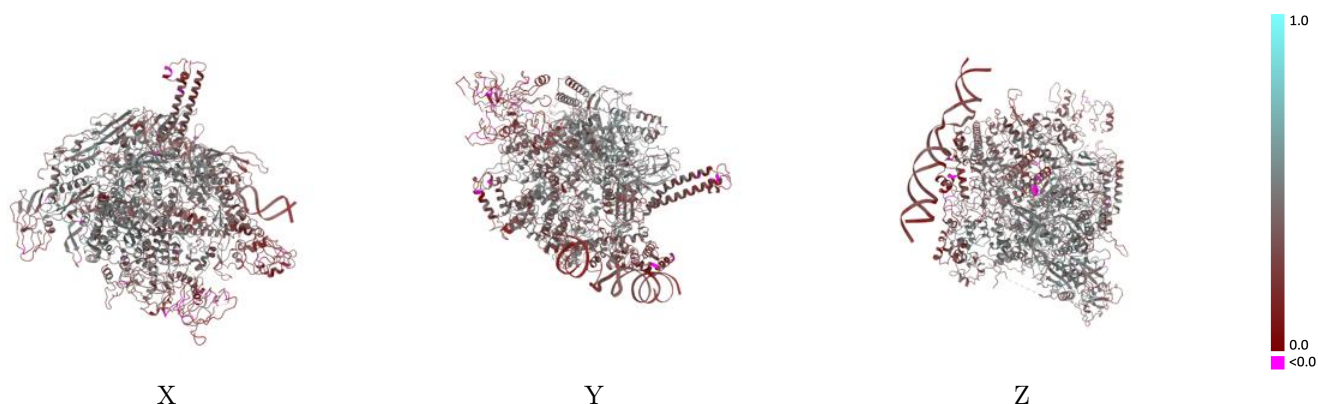
Y



Z

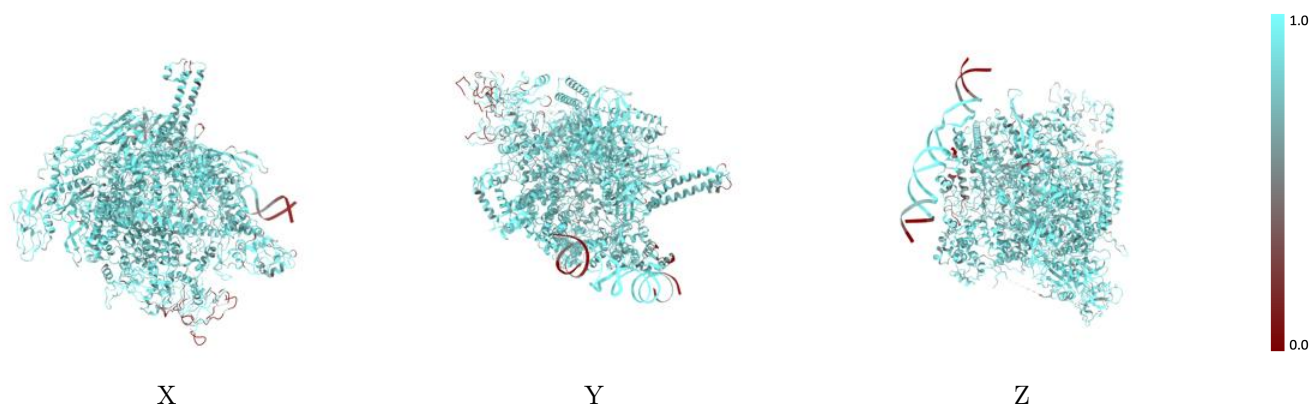
The images above show the 3D surface view of the map at the recommended contour level 0.021 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



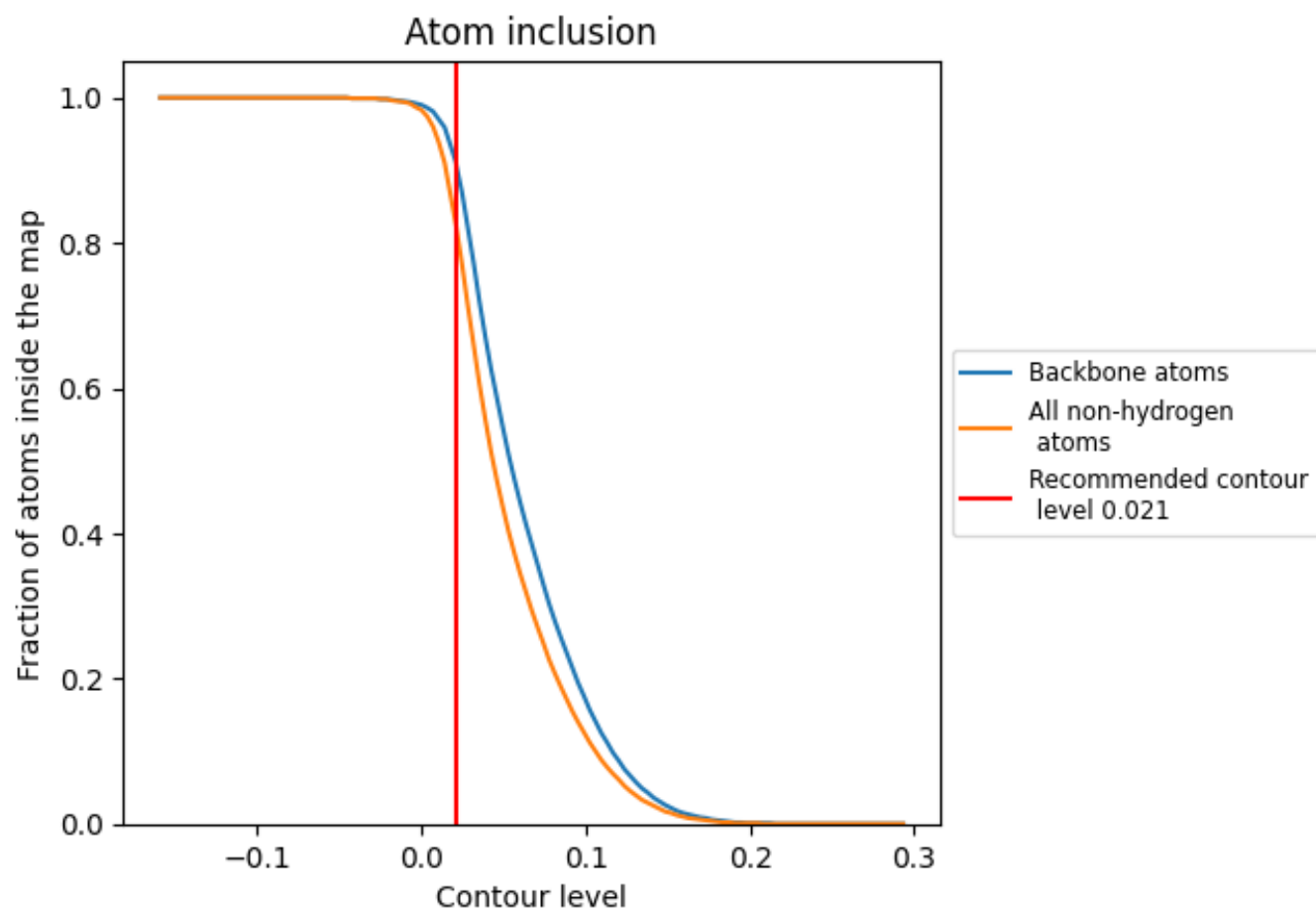
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.021).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 83% 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 (0.021) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8280	<div><div></div></div> 0.3780
A	<div><div></div></div> 0.8590	<div><div></div></div> 0.4250
B	<div><div></div></div> 0.8410	<div><div></div></div> 0.3820
C	<div><div></div></div> 0.8470	<div><div></div></div> 0.3970
D	<div><div></div></div> 0.8300	<div><div></div></div> 0.3780
E	<div><div></div></div> 0.8690	<div><div></div></div> 0.4290
M	<div><div></div></div> 0.7900	<div><div></div></div> 0.3390
N	<div><div></div></div> 0.7180	<div><div></div></div> 0.2390
T	<div><div></div></div> 0.6580	<div><div></div></div> 0.2340

1.0

0.0

<0.0