



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 04:56 AM UTC

PDB ID : 7CXM / pdb_00007cxm
EMDB ID : EMD-30492
Title : Architecture of a SARS-CoV-2 mini replication and transcription complex
Authors : Yan, L.; Zhang, Y.; Ge, J.; Zheng, L.; Gao, Y.; Wang, T.; Jia, Z.; Wang, H.;
Huang, Y.; Li, M.; Wang, Q.; Rao, Z.; Lou, Z.
Deposited on : 2020-09-02
Resolution : 2.90 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:

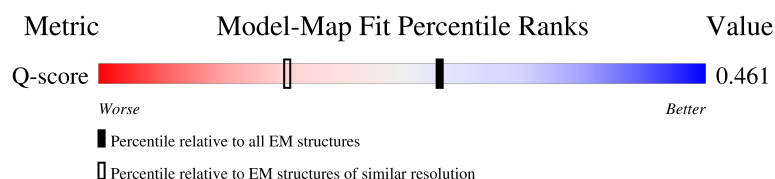
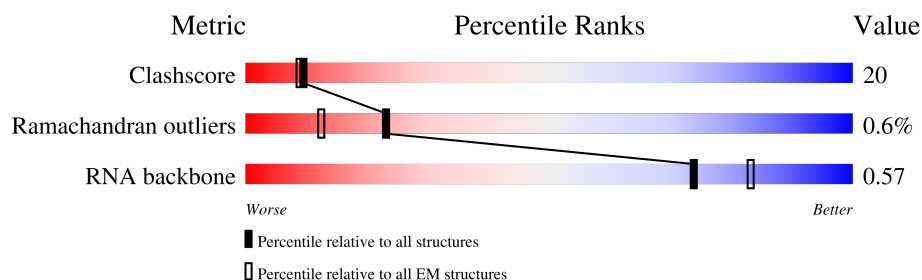
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.90 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	942	 77% 18%
2	B	198	 6% 65% 27% 6%
2	D	198	 58% 31% 5% 6%
3	C	83	 66% 19% 13%

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Mol	Chain	Length	Quality of chain
4	I	25	40% 52% 8%
5	J	58	28% 17% 55%
6	L	6	33% 83% 17%
7	E	601	6% 55% 42% ..
7	F	601	35% 41% 54% ..

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 21295 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 RNA-directed RNA polymerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	926	7458	4763	1252	1389	54	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	910	ASN	ASP	engineered mutation	UNP P0DTD1
A	933	HIS	-	expression tag	UNP P0DTD1
A	934	HIS	-	expression tag	UNP P0DTD1
A	935	HIS	-	expression tag	UNP P0DTD1
A	936	HIS	-	expression tag	UNP P0DTD1
A	937	HIS	-	expression tag	UNP P0DTD1
A	938	HIS	-	expression tag	UNP P0DTD1
A	939	HIS	-	expression tag	UNP P0DTD1
A	940	HIS	-	expression tag	UNP P0DTD1
A	941	HIS	-	expression tag	UNP P0DTD1
A	942	HIS	-	expression tag	UNP P0DTD1

- Molecule 2 is a protein called Non-structural protein 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	187	1396	872	240	273	11	0	0
2	D	186	1414	889	242	272	11	0	0

- Molecule 3 is a protein called Non-structural protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	72	553	349	91	107	6	0	0

- Molecule 4 is a RNA chain called RNA (25-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	25	Total	C	N	O	P	0	0
			545	242	105	173	25		

- Molecule 5 is a RNA chain called RNA (26-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	26	Total	C	N	O	P	0	0
			545	244	92	183	26		

- Molecule 6 is a RNA chain called RNA (5'-R(P*UP*UP*UP*UP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	6	Total	C	N	O	P	0	0
			128	58	24	40	6		

- Molecule 7 is a protein called Helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	596	Total	C	N	O	S	0	0
			4630	2940	787	869	34		
7	E	596	Total	C	N	O	S	0	0
			4618	2935	781	869	33		

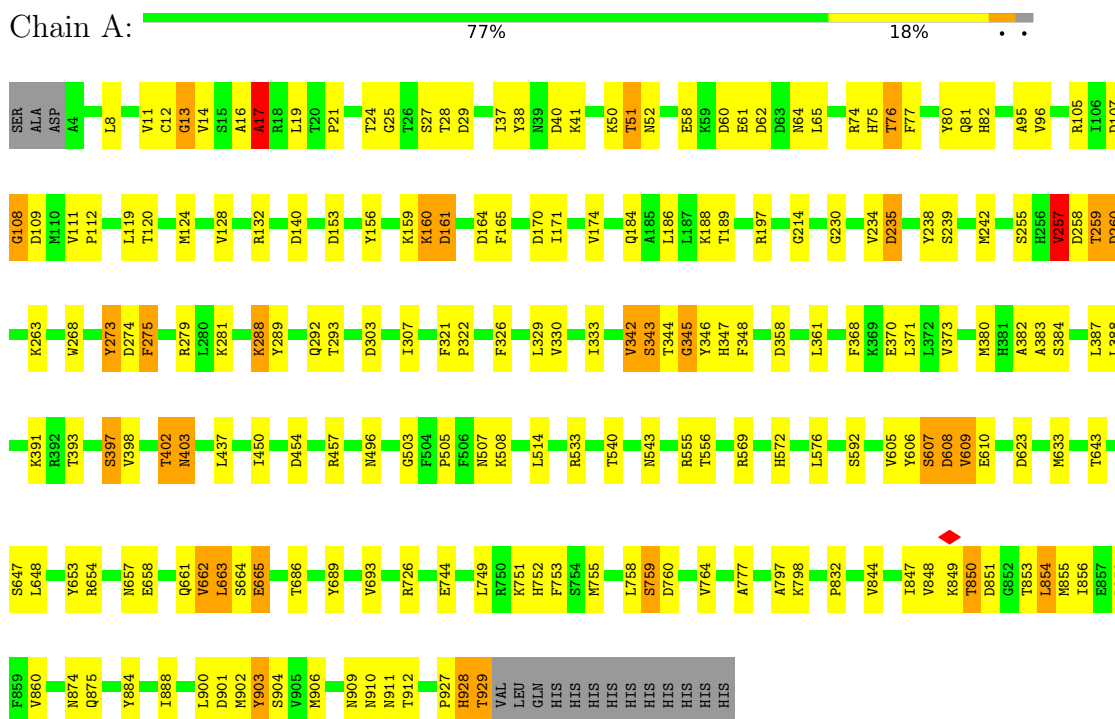
- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
8	A	2	Total	Zn	0
			2	2	
8	F	3	Total	Zn	0
			3	3	
8	E	3	Total	Zn	0
			3	3	

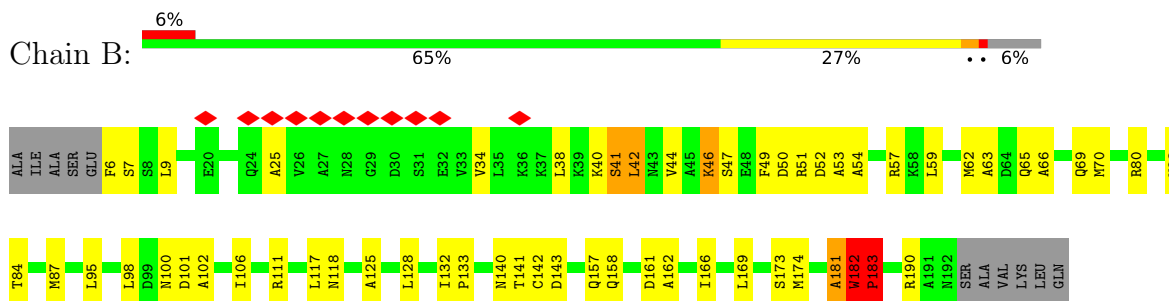
3 Residue-property plots [i](#)

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: RNA-directed RNA polymerase

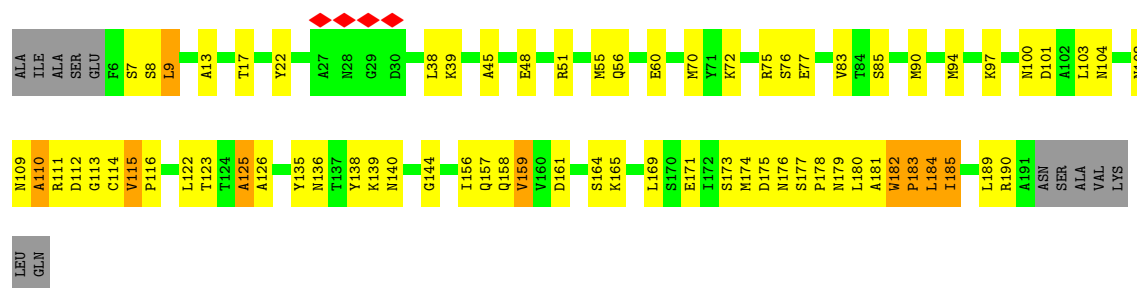


• Molecule 2: Non-structural protein 8



• Molecule 2: Non-structural protein 8

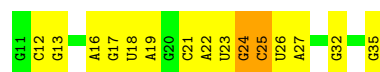




• Molecule 3: Non-structural protein 7



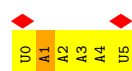
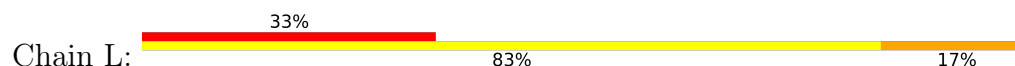
• Molecule 4: RNA (25-MER)



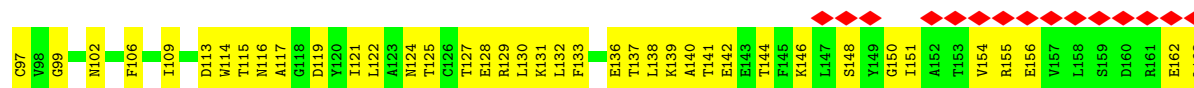
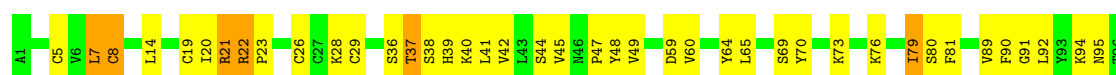
• Molecule 5: RNA (26-MER)

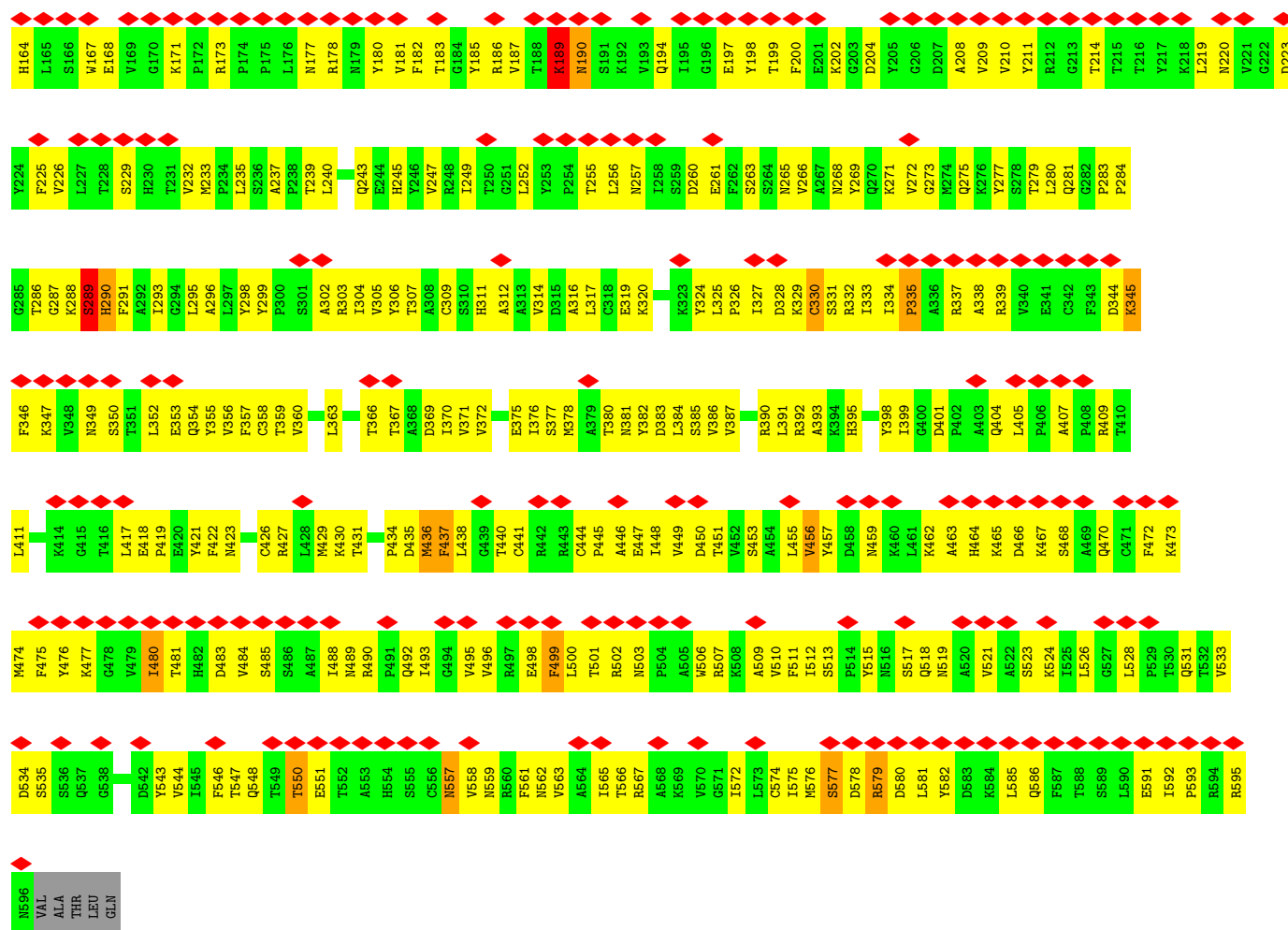


• Molecule 6: RNA (5'-R(P*UP*UP*UP*UP*UP*U)-3')

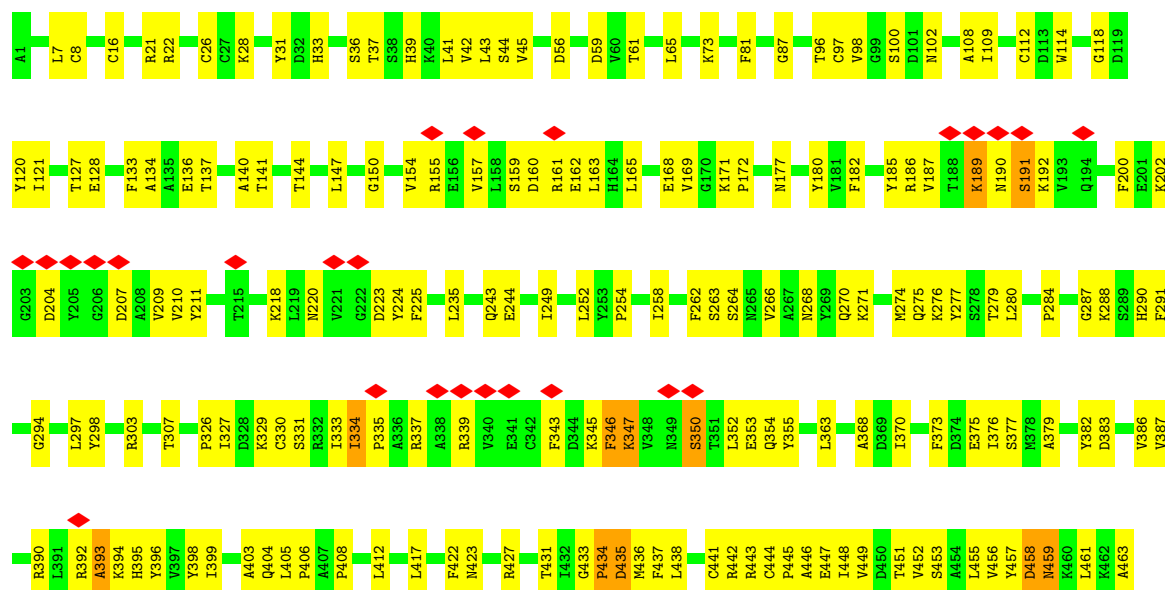


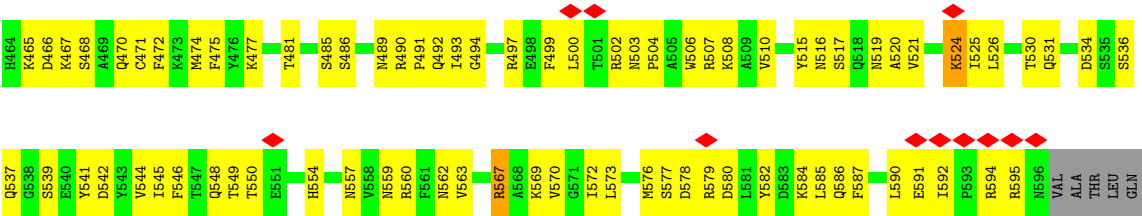
• Molecule 7: Helicase





Molecule 7: Helicase





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	384727	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.006	Depositor
Minimum map value	-0.890	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	0.25	Depositor
Map size ($\text{\AA}$)	367.36, 367.36, 367.36	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.82, 0.82, 0.82	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

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	0.74	19/7647 (0.2%)	1.06	84/10379 (0.8%)
2	B	0.47	2/1414 (0.1%)	1.10	19/1922 (1.0%)
2	D	0.68	4/1433 (0.3%)	1.31	28/1944 (1.4%)
3	C	0.40	0/556	0.72	3/749 (0.4%)
4	I	0.28	0/611	0.29	0/953
5	J	0.31	0/606	0.28	0/940
6	L	0.13	0/143	0.23	0/220
7	E	0.26	0/4722	0.96	31/6430 (0.5%)
7	F	0.23	0/4734	0.96	41/6443 (0.6%)
All	All	0.52	25/21866 (0.1%)	1.00	206/29980 (0.7%)

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
1	A	0	1
7	F	0	1
All	All	0	2

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	343	SER	CA-C	-7.61	1.42	1.52
1	A	348	PHE	C-O	-7.30	1.15	1.23
1	A	342	VAL	C-O	-7.09	1.16	1.23
1	A	346	TYR	C-O	-7.02	1.15	1.23
2	D	109	ASN	CA-C	-6.75	1.44	1.52

The worst 5 of 206 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	E	458	ASP	N-CA-C	-21.53	78.65	110.52
7	F	36	SER	N-CA-C	20.45	140.69	114.31
2	B	142	CYS	N-CA-C	-19.53	74.01	107.80
1	A	344	THR	N-CA-C	-19.04	79.88	109.96
2	D	126	ALA	N-CA-CB	-18.21	85.25	110.38

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	17	ALA	Peptide
7	F	189	LYS	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	7458	0	7193	150	0
2	B	1396	0	1365	50	0
2	D	1414	0	1416	51	0
3	C	553	0	585	11	0
4	I	545	0	272	20	0
5	J	545	0	281	10	0
6	L	128	0	65	4	0
7	E	4618	0	4564	225	0
7	F	4630	0	4585	324	0
8	A	2	0	0	0	0
8	E	3	0	0	0	0
8	F	3	0	0	0	0
All	All	21295	0	20326	822	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 20.

The worst 5 of 822 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:75:HIS:CD2	1:A:76:THR:CG2	1.84	1.58
1:A:75:HIS:CD2	1:A:76:THR:HG23	1.53	1.35
7:F:434:PRO:HB2	7:F:436:MET:O	1.22	1.30
1:A:260:ASP:OD2	1:A:263:LYS:NZ	1.71	1.22
2:D:182:TRP:HE3	2:D:182:TRP:O	1.31	1.14

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	924/942 (98%)	863 (93%)	53 (6%)	8 (1%)	14	41
2	B	185/198 (93%)	168 (91%)	15 (8%)	2 (1%)	11	36
2	D	184/198 (93%)	168 (91%)	14 (8%)	2 (1%)	11	36
3	C	70/83 (84%)	67 (96%)	3 (4%)	0	100	100
7	E	594/601 (99%)	524 (88%)	69 (12%)	1 (0%)	43	72
7	F	594/601 (99%)	516 (87%)	75 (13%)	3 (0%)	24	54
All	All	2551/2623 (97%)	2306 (90%)	229 (9%)	16 (1%)	23	51

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	76	THR
1	A	161	ASP
1	A	259	THR
1	A	607	SER
7	F	289	SER

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	I	24/25 (96%)	1 (4%)	1 (4%)
5	J	25/58 (43%)	0	0
6	L	5/6 (83%)	4 (80%)	0
All	All	54/89 (60%)	5 (9%)	1 (1%)

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	I	25	C
6	L	1	A
6	L	3	A
6	L	4	A
6	L	5	U

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	I	24	G

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 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

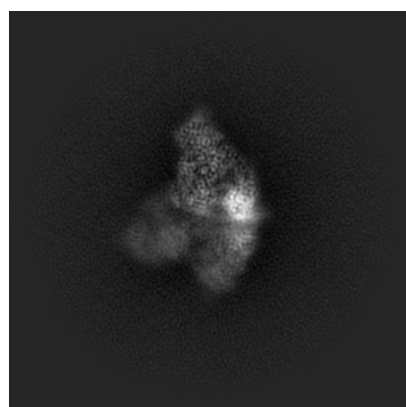
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30492. These allow visual inspection of the internal detail of the map and identification of artifacts.

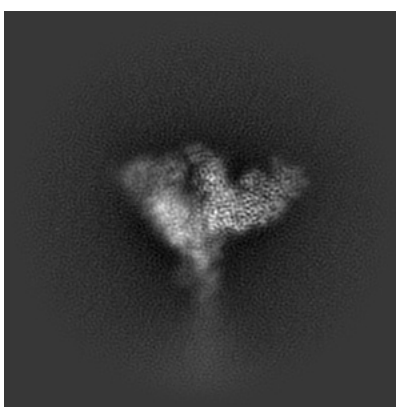
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

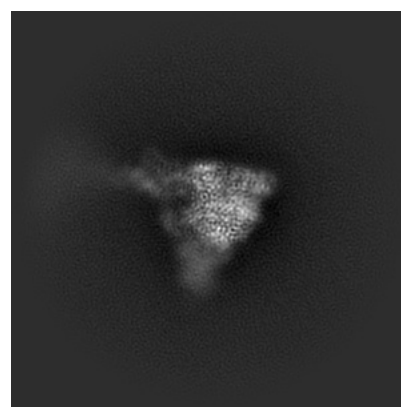
6.1.1 Primary map



X



Y

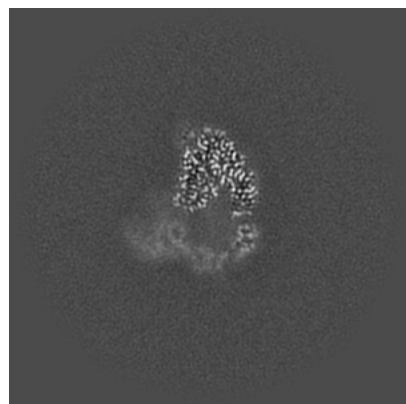


Z

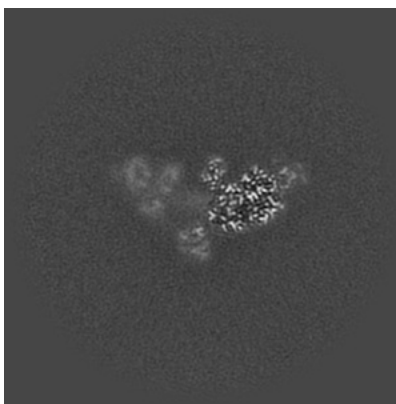
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

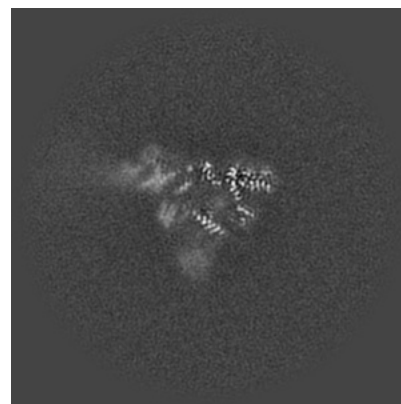
6.2.1 Primary map



X Index: 224



Y Index: 224

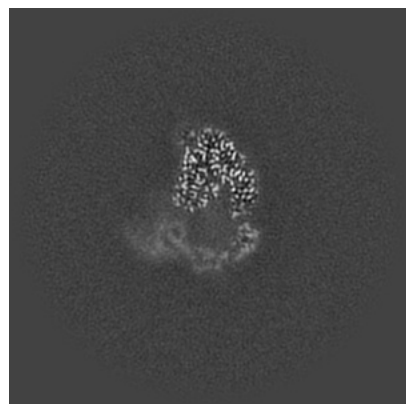


Z Index: 224

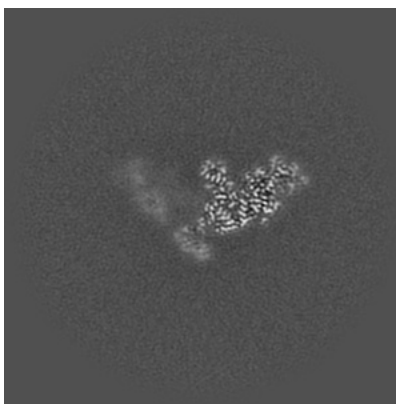
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

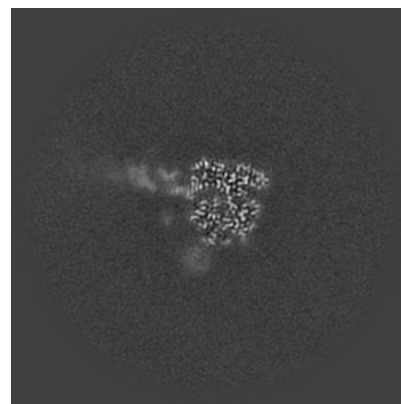
6.3.1 Primary map



X Index: 225



Y Index: 217

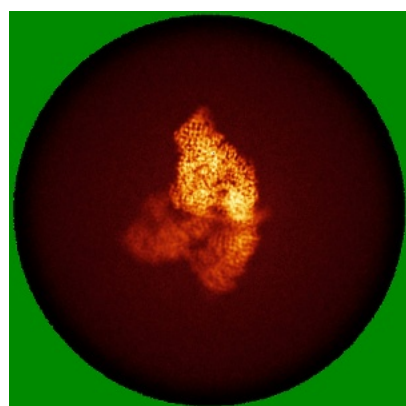


Z Index: 234

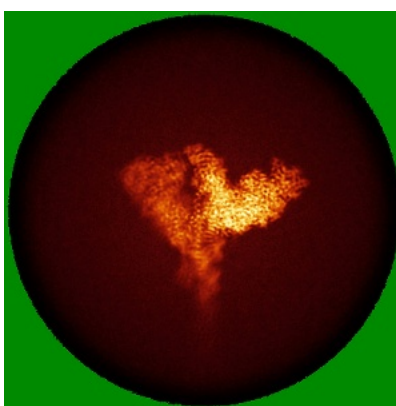
The images above show the largest variance slices of the map in three orthogonal directions.

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

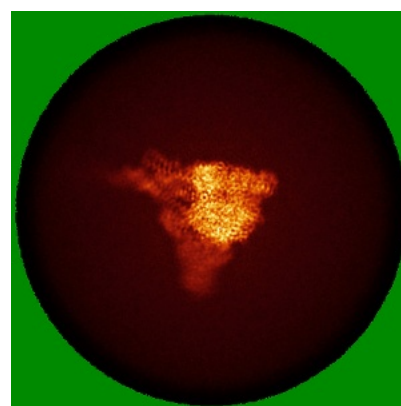
6.4.1 Primary map



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

This section was not generated.

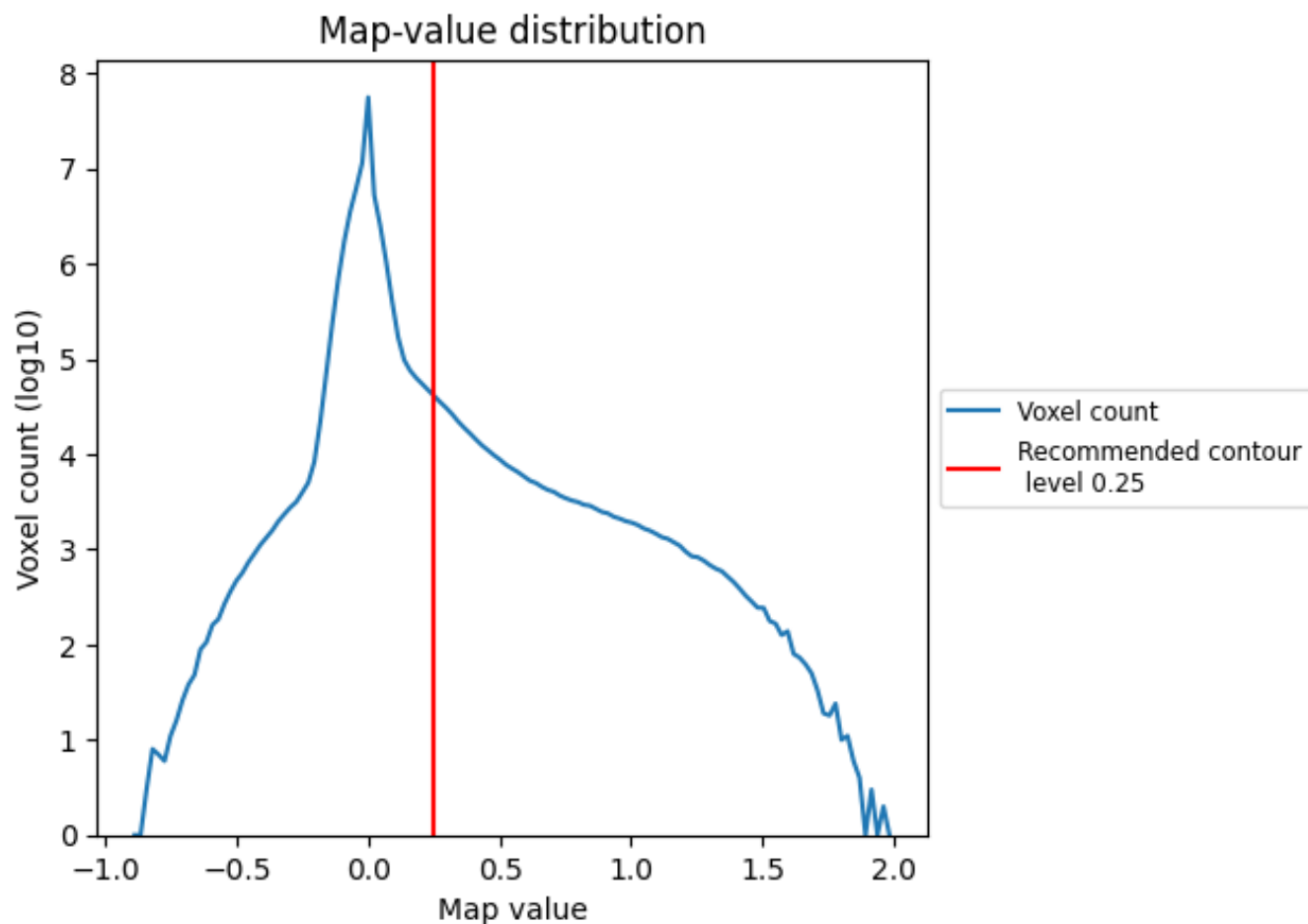
6.6 Mask visualisation

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

7 Map analysis [i](#)

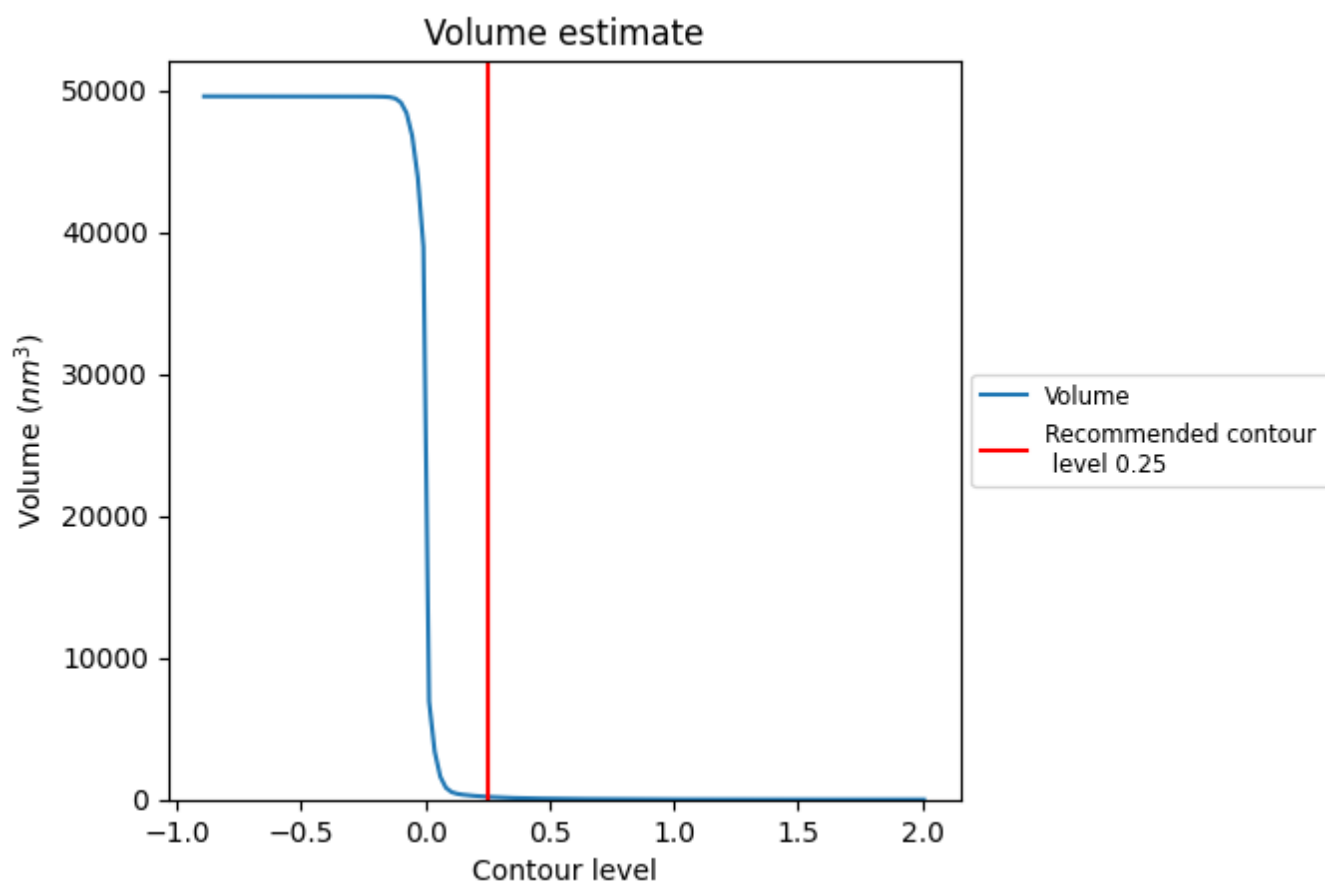
This section contains the results of statistical analysis of the map.

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.

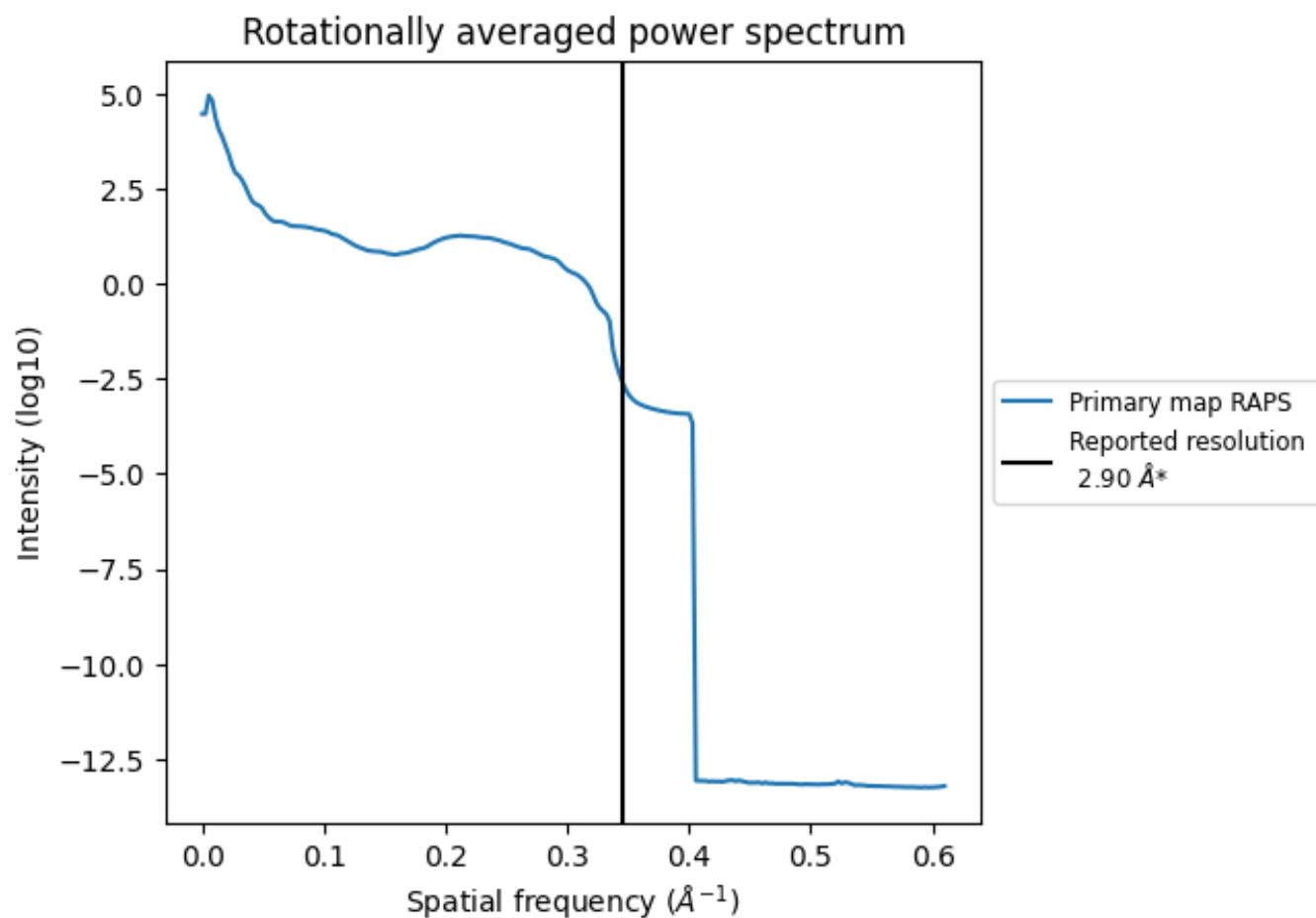
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 194 nm³; this corresponds to an approximate mass of 176 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 0.345 Å⁻¹

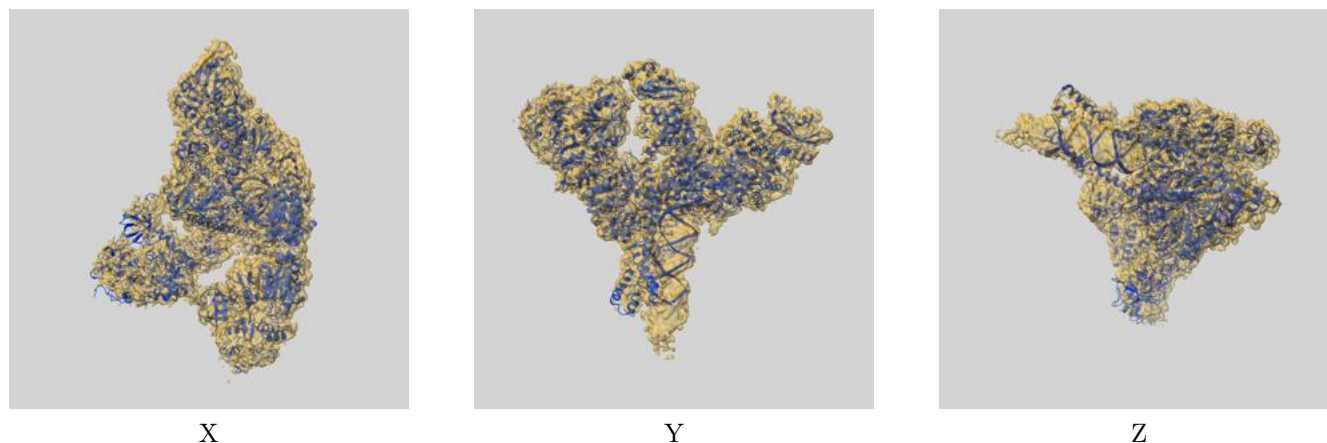
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

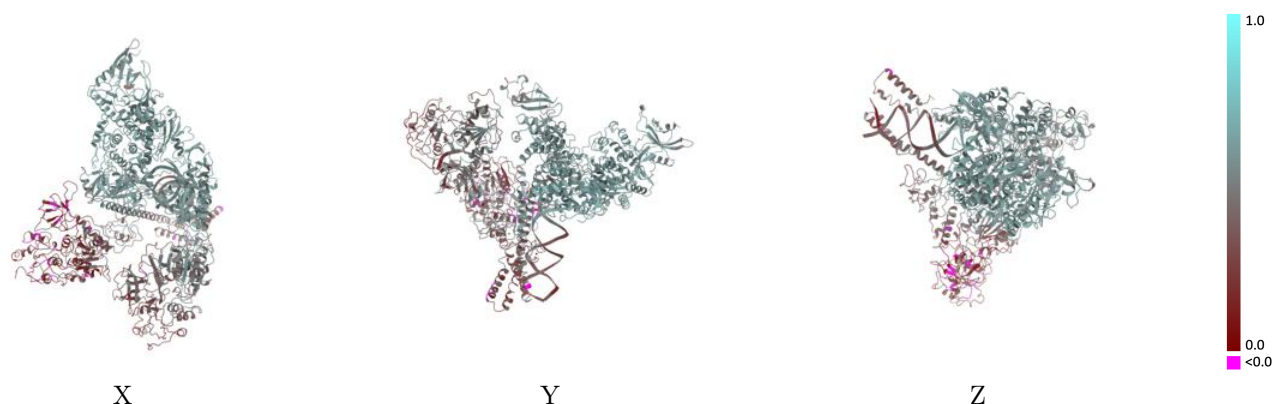
This section contains information regarding the fit between EMDB map EMD-30492 and PDB model 7CXM. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.25 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](#)

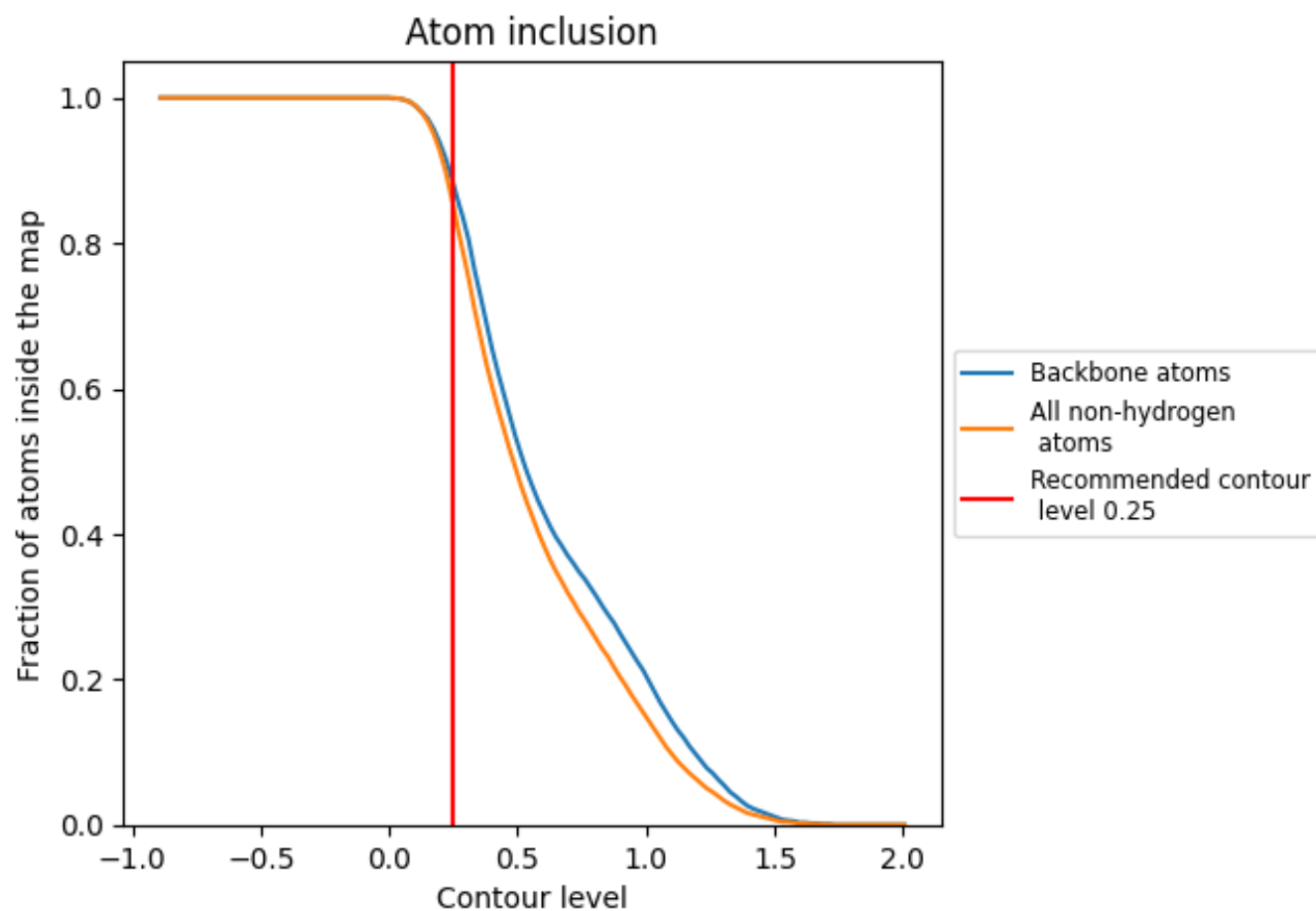


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 85% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8510	0.4610
A	0.9840	0.5870
B	0.9010	0.4860
C	0.9600	0.5650
D	0.9390	0.5040
E	0.8340	0.4250
F	0.5770	0.2670
I	0.9740	0.4270
J	0.9850	0.4670
L	0.4920	0.3520

1.0

0.0

<0.0