



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:00 AM UTC

PDB ID : 6LXE / pdb_00006lxe
EMDB ID : EMD-30006
Title : DROSHA-DGCR8 complex
Authors : Jin, W.; Wang, J.; Liu, C.P.; Wang, H.W.; Xu, R.M.
Deposited on : 2020-02-10
Resolution : 4.20 Å(reported)
Based on initial model : 5B16

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

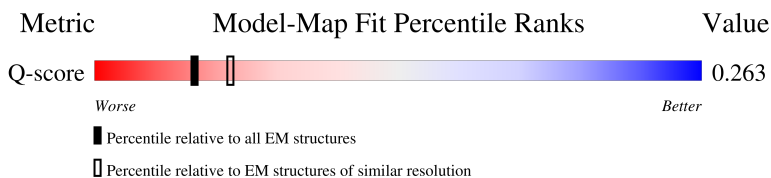
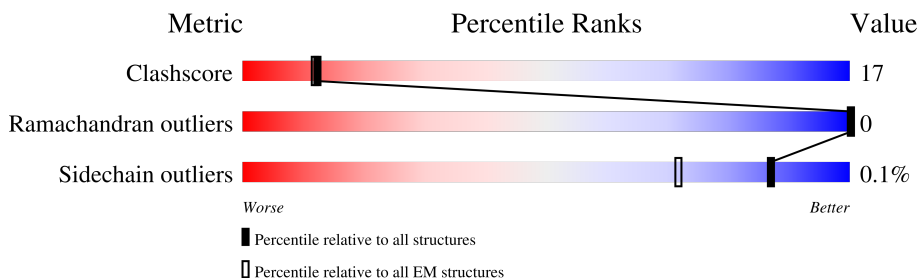
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5410 (3.70 - 4.70)

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	990	 51% 27% 22%
2	B	773	 97%
2	C	773	 97%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6519 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 Ribonuclease 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	768	Total	C	N	O	S	0	0
			6133	3910	1073	1111	39		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1045	GLN	GLU	engineered mutation	UNP Q9NRR4
A	1222	GLN	GLU	engineered mutation	UNP Q9NRR4
A	1375	HIS	-	expression tag	UNP Q9NRR4
A	1376	HIS	-	expression tag	UNP Q9NRR4
A	1377	HIS	-	expression tag	UNP Q9NRR4
A	1378	HIS	-	expression tag	UNP Q9NRR4
A	1379	HIS	-	expression tag	UNP Q9NRR4
A	1380	HIS	-	expression tag	UNP Q9NRR4

- Molecule 2 is a protein called Microprocessor complex subunit DGCR8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	24	Total	C	N	O	S	0	0
			205	125	39	40	1		
2	C	21	Total	C	N	O	S	0	0
			179	110	32	36	1		

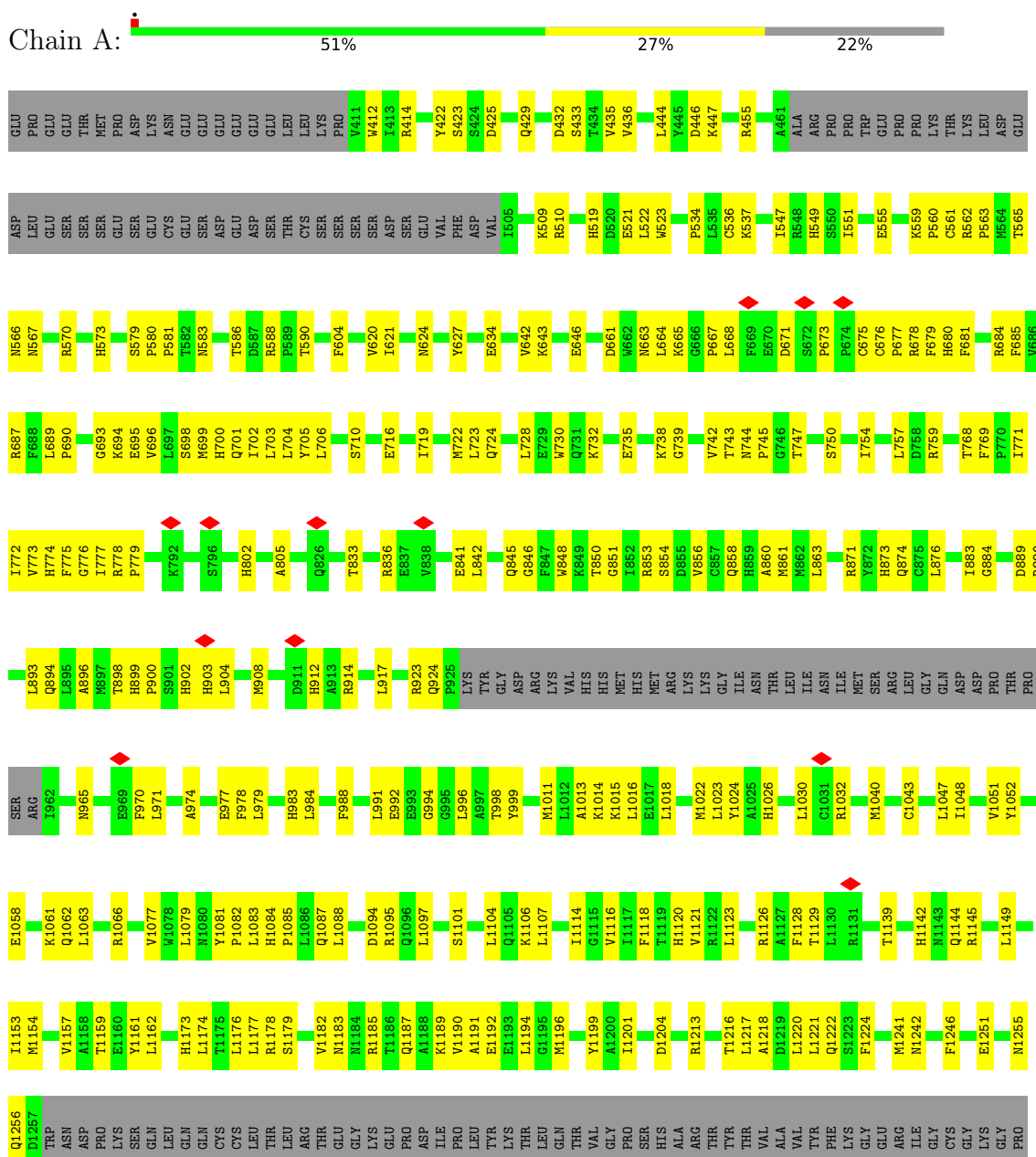
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Zn	0
			2	2	

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: Ribonuclease 3



[illegible]

- Molecule 2: Microprocessor complex subunit DGCR8

Chain B: 97%

Tyr	Ala	Thr	Ile	Pro	Pro	Pro	Gly	Asn	Glu	Asp	Lys	Ser	Ser	Leu	Met	
	Lys	Arg	Ile	Gly	Leu	Lys	Val	Glu	Pro	Asp	Lys	Val	Ser	Pro	Thr	
	Asn	Gly	Asp	Ser	Ala	Ala	Lys	Arg	Glu	Pro	Lys	Thr	Glu	Ala	Ala	
	Lys	Cys	Ser	Val	Val	Val	Lys	Gln	Gly	Gly	Asn	Glu	Ser	Pro	Ser	
	P727	Lys	Arg	Thr	Gln	Lys	Val	Ser	Trp	Val	Glu	Ser	Phe	Pro	Ser	
		Asn	Val	Ile	Lys	Glu	Ser	Gly	Ile	Trp	Asp	Leu	Asn	Ser	Ser	
	H730	Thr	Gly	Asp	Lys	Val	Asp	Asp	Met	Met	Ala	Asp	Arg	Phe	Pro	
		Arg	Trp	Glu	Ile	Cys	Leu	Leu	Thr	Phe	Leu	Gln	Ser	Tyr	Leu	
	K734	Val	Val	Val	Thr	Lys	Thr	Pro	His	Glu	Lys	Lys	Lys	Gly	Pro	Cys
		Lys	Thr	Ser	Ser	Glu	Ser	Asn	Asn	Val	Glu	Arg	Arg	Ser	Ala	Gly
Lys	E738	Gln	Lys	Ser	Tyr	Thr	Glu	Ser	Pro	Val	Pro	Val	Thr	Gly	Val	Ala
	H739	Leu	Ala	Lys	Gly	Val	Ser	Gly	Ser	Gly	Val	Lys	Lys	Lys	Leu	Pro
	K740	Leu	Ala	Ser	Ser	Gln	Ser	Asp	Gln	Leu	Glu	Val	Val	Val	Leu	Ala
	R741	Ala	Gly	Thr	Ala	Ala	Leu	Val	Pro	Ala	Cys	Tyr	Gly	Ser	Gly	Ala
	L742	Ser	Ser	Thr	Thr	Ala	Leu	Ser	Pro	Ala	Lys	Val	Thr	Lys	Glu	Gly
	A743	Gln	Leu	Ser	Ala	Pro	Glu	Arg	Ser	Glu	Asp	Val	Arg	Ala	Arg	Ala
	E744	Lys	Ser	Ser	Thr	Thr	Glu	Ser	Val	Thr	Lys	Val	Val	Val	Leu	Pro
	E745	Ile	Leu	Pro	Ser	Lys	Phe	Arg	Glu	Trp	Lys	Arg	Arg	Leu	Leu	Arg
	R746	Gln	Gln	Thr	Lys	Lys	Ser	Leu	Leu	Arg	Glu	Asp	Val	Val	Arg	Ala
		Leu	Leu	Ile	Leu	Ile	Val	Ser	Ser	Ser	Leu	Asp	Val	Val	Arg	Ala
Lys	R750	His	His	Lys	Lys	Ile	Glu	Ser	Arg	Thr	Lys	Arg	Arg	Leu	Arg	Ala
	Lys	Pro	Pro	Arg	Asn	Lys	Arg	Pro	Ala	Val	Lys	Thr	Ala	Leu	Pro	Pro
	Pro	His	Cys	Thr	Lys	Pro	Lys	Glu	Val	Val	Asp	Glu	Glu	Ile	Leu	Phe
	Met	Val	Met	Ala	Ala	Asn	Phe	Leu	Leu	Thr	Gly	Asn	Cys	Asp	Gln	Gln
	Ser	Lys	Lys	Arg	Lys	Gly	Lys	Glu	Trp	Arg	Gly	Val	Val	Gly	Pro	Ala
	Ile	Asn	Arg	Arg	Lys	Lys	Phe	Pro	Ser	Thr	Ala	Ala	Leu	Asn	Pro	Ala
	Val	Trp	His	Ala	Ser	Glu	Glu	Pro	Pro	Thr	Gly	Leu	Leu	Cys	Thr	Arg
	Ala	Gly	His	His	Thr	Lys	Gln	Leu	Arg	Glu	Asp	Leu	Leu	Leu	Leu	Pro
	Ser	Ser	Met	Leu	Leu	Val	Val	Asp	Pro	Phe	Thr	Thr	Phe	Val	Val	Pro
	Ala	Leu	Met	Ala	Gly	Cys	Thr	Glu	Leu	Leu	Ser	Ser	His	Arg	Arg	Leu
Cys	Thr	Ser	Glu	Lys	Lys	Pro	Thr	Arg	Pro	Lys	Gln	Lys	Cys	Ala	Ala	Thr
	Thr	Ser	Val	Lys	Val	Val	Arg	Gly	Gly	His	Pro	Ala	Phe	Ala	Pro	Ser
	Val	Met	Pro	Ser	Lys	Pro	Arg	Met	Met	Ile	Met	Val	Gly	Val	Ala	Ser
	Asp	Val	Gly	Glu	Glu	Lys	Gln	Asp	Pro	Val	Thr	Lys	Arg	Arg	Lys	Val
	Val	Lys	Lys	Glu	Glu	Pro	Phe	Glu	Ser	Leu	Thr	Arg	Ser	Phe	Val	Met
	Gln	Glu	Gln	Pro	Lys	Val	Asn	Lys	Ser	Ser	Ile	Asp	Val	Gly	Val	Ser
	Glu	Glu	Gln	Val	Pro	Val	Arg	Asp	Ser	Leu	Thr	Arg	Gly	Ser	Ser	Met
	Thr	Ser	Val	Thr	Lys	Thr	Glu	Pro	Asn	Ile	Thr	Val	Val	Asp	Val	Ser
	Val	Met	Pro	Ser	Lys	Thr	Glu	Pro	Asn	Ile	Thr	Val	Val	Asp	Val	Ser
	Asp	Val	Gly	Glu	Glu	Lys	Gln	Lys	Gly	Val	Thr	Gly	Gly	Val	Val	Ser
Val	Lys	Lys	Glu	Glu	Pro	Phe	Glu	Ser	Leu	Thr	Arg	Ser	Phe	Val	Met	

- Molecule 2: Microprocessor complex subunit DGCR8

Chain C: 97%

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	109333	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.071	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	174.56, 174.56, 174.56	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.091, 1.091, 1.091	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.12	0/6284	0.34	0/8521
2	B	0.11	0/206	0.30	0/272
2	C	0.10	0/179	0.36	0/236
All	All	0.12	0/6669	0.34	0/9029

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	6133	0	5916	208	0
2	B	205	0	210	8	0
2	C	179	0	183	5	0
3	A	2	0	0	1	0
All	All	6519	0	6309	218	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 17.

The worst 5 of 218 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:433:SER:OG	1:A:565:THR:HG21	1.32	1.26
1:A:435:VAL:O	1:A:565:THR:HG23	1.49	1.09
1:A:562:ARG:O	1:A:642:VAL:HG21	1.52	1.07
1:A:560:PRO:HA	1:A:676:CYS:HB2	1.30	1.06
1:A:433:SER:OG	1:A:565:THR:CG2	2.03	1.06

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	762/990 (77%)	692 (91%)	70 (9%)	0	100	100
2	B	22/773 (3%)	22 (100%)	0	0	100	100
2	C	19/773 (2%)	19 (100%)	0	0	100	100
All	All	803/2536 (32%)	733 (91%)	70 (9%)	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	651/894 (73%)	650 (100%)	1 (0%)	87	85
2	B	23/673 (3%)	23 (100%)	0	100	100
2	C	20/673 (3%)	20 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	694/2240 (31%)	693 (100%)	1 (0%)	87	88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	561	CYS

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

Mol	Chain	Res	Type
1	A	859	HIS
1	A	1173	HIS
1	A	868	HIS
1	A	1222	GLN
1	A	1142	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

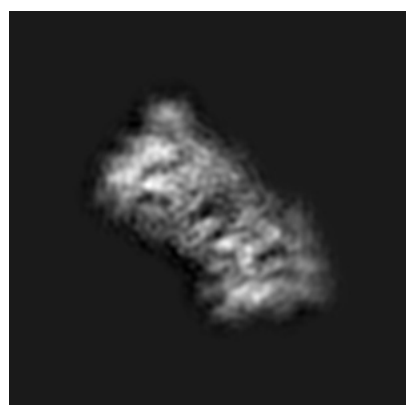
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30006. These allow visual inspection of the internal detail of the map and identification of artifacts.

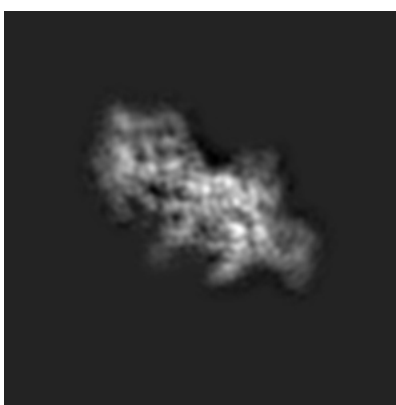
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

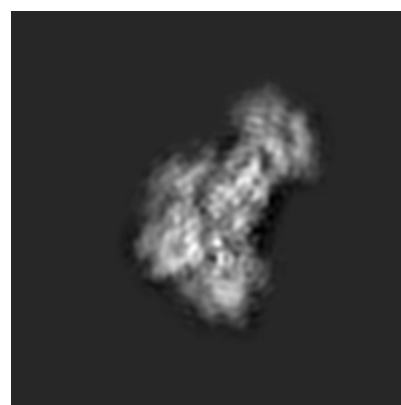
6.1.1 Primary map



X



Y

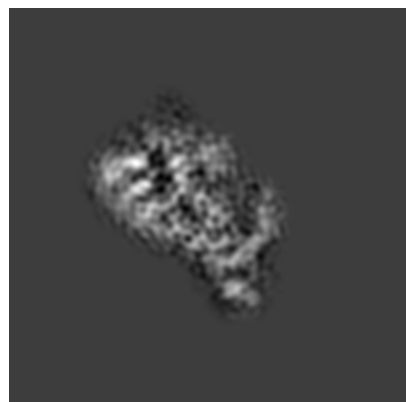


Z

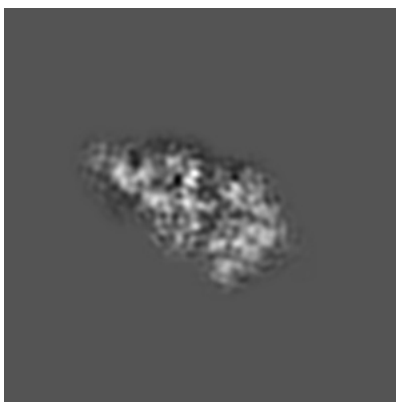
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 80



Y Index: 80

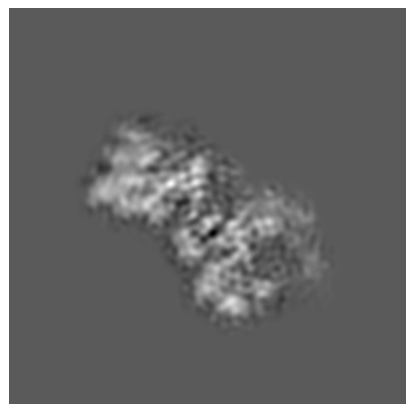


Z Index: 80

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

6.3 Largest variance slices [i](#)

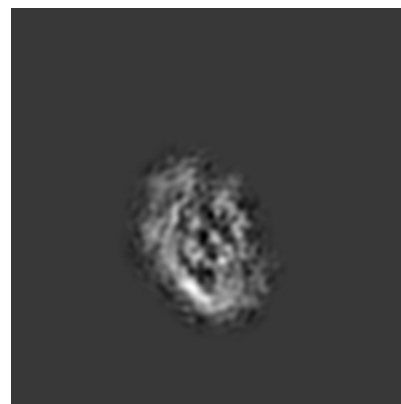
6.3.1 Primary map



X Index: 91



Y Index: 59



Z Index: 93

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

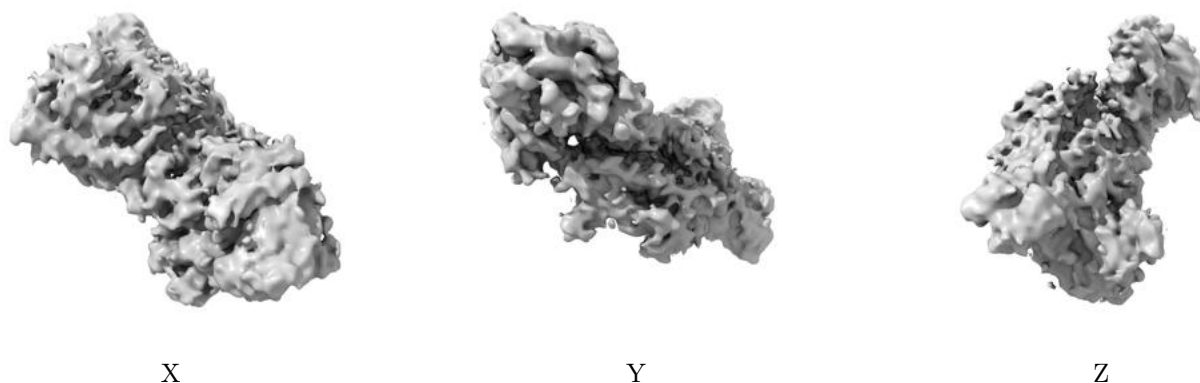


Z

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

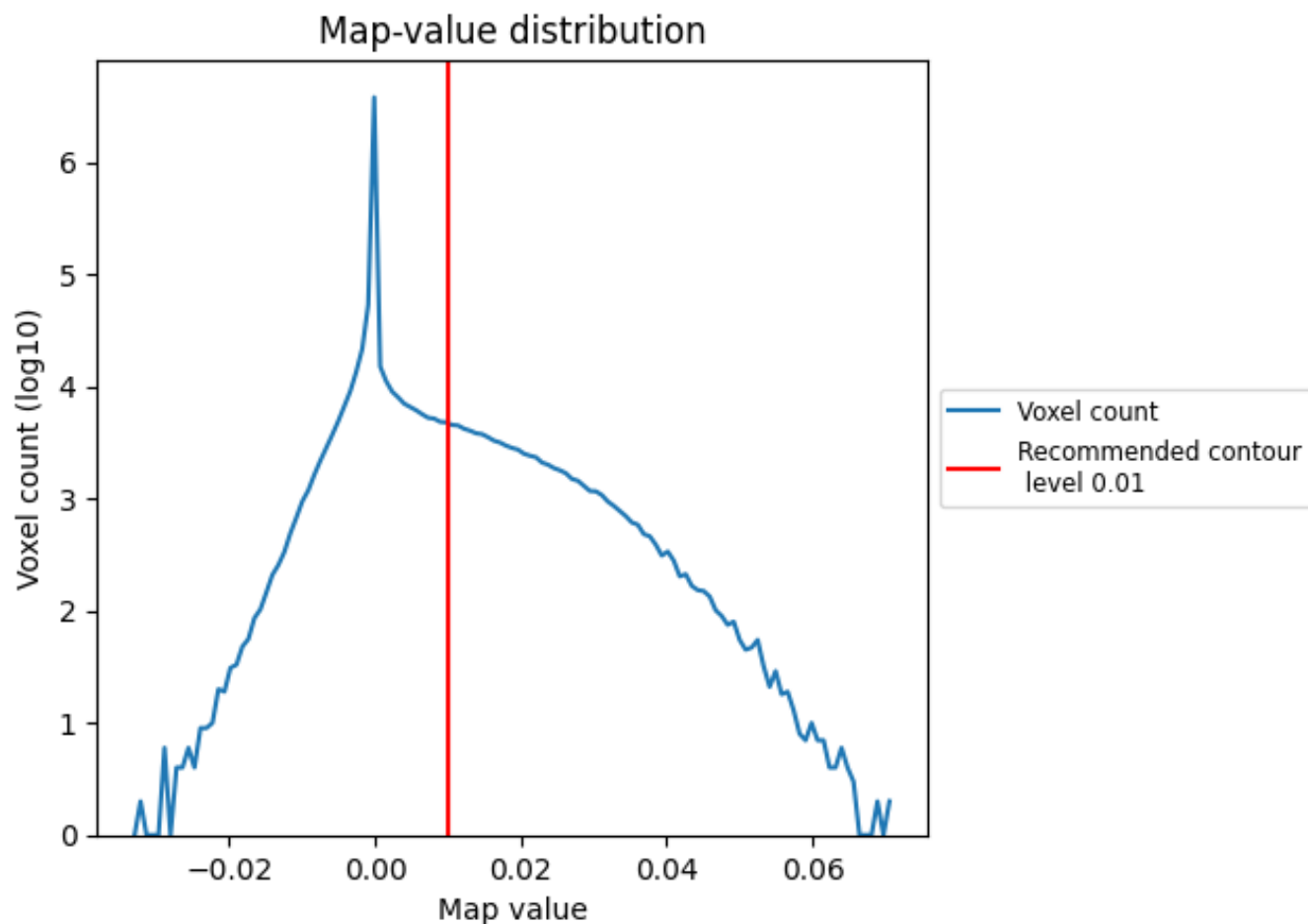
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

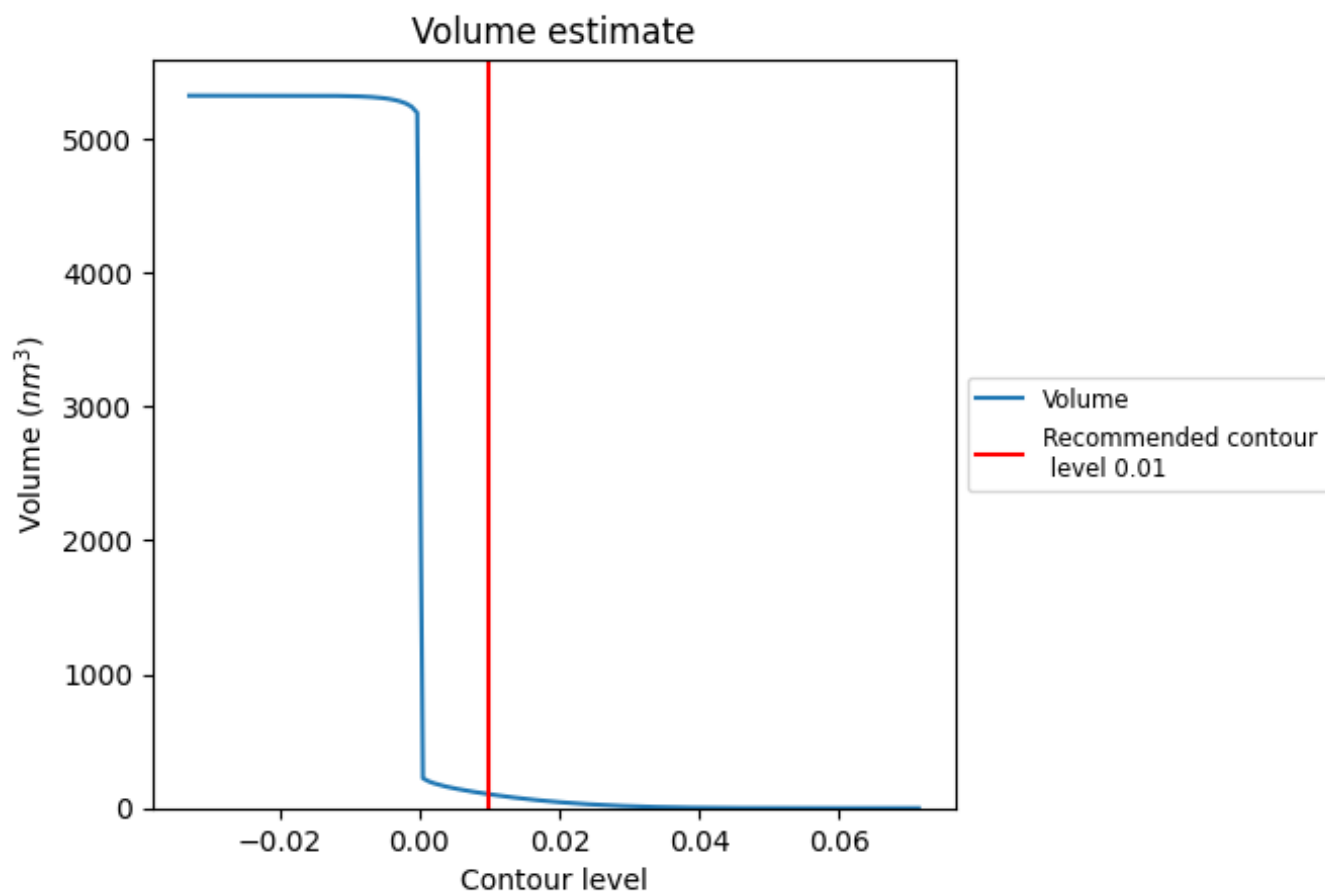
This section contains the results of statistical analysis of the map.

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.

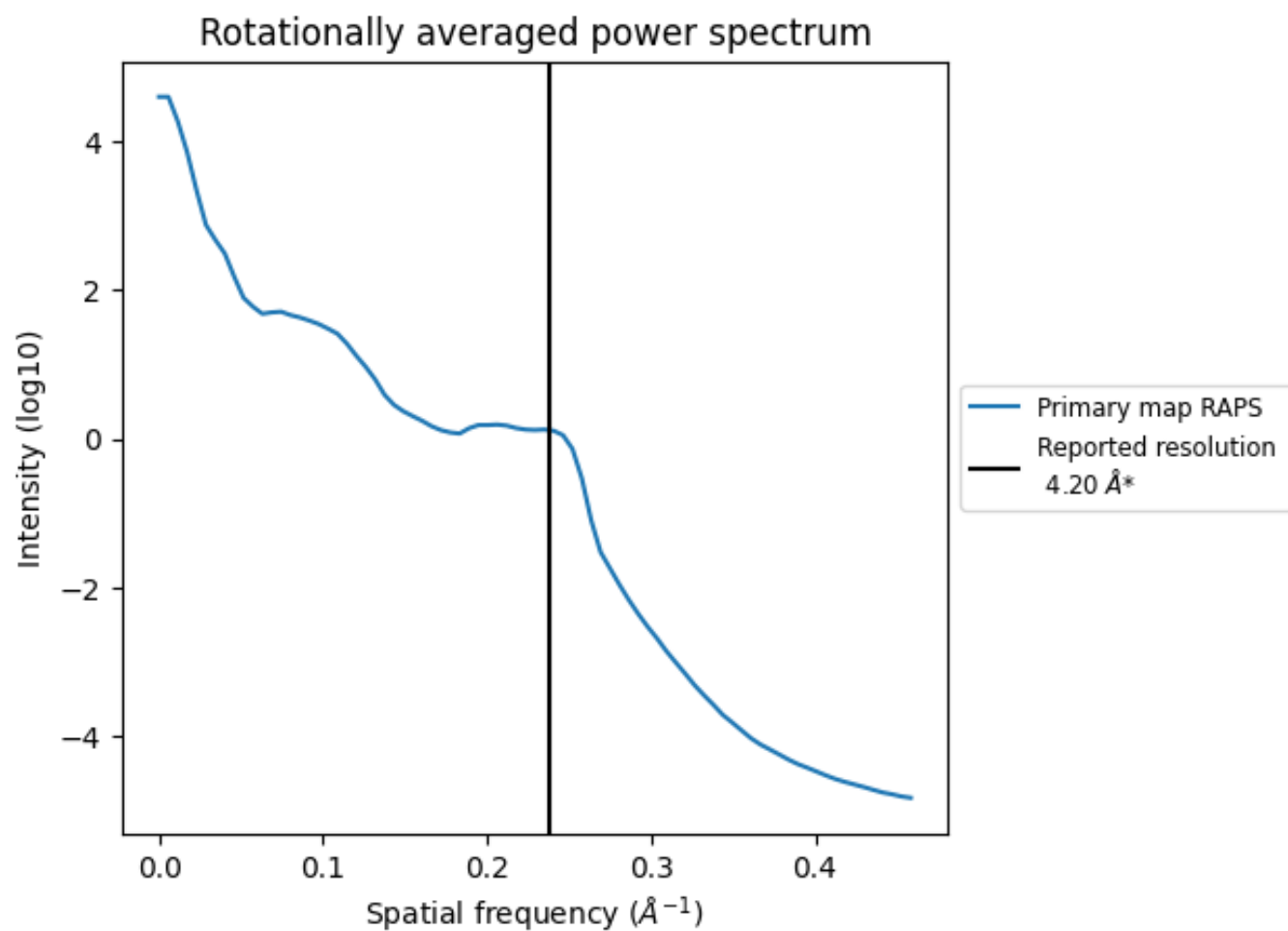
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 104 nm³; this corresponds to an approximate mass of 94 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 0.238 Å⁻¹

8 Fourier-Shell correlation

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

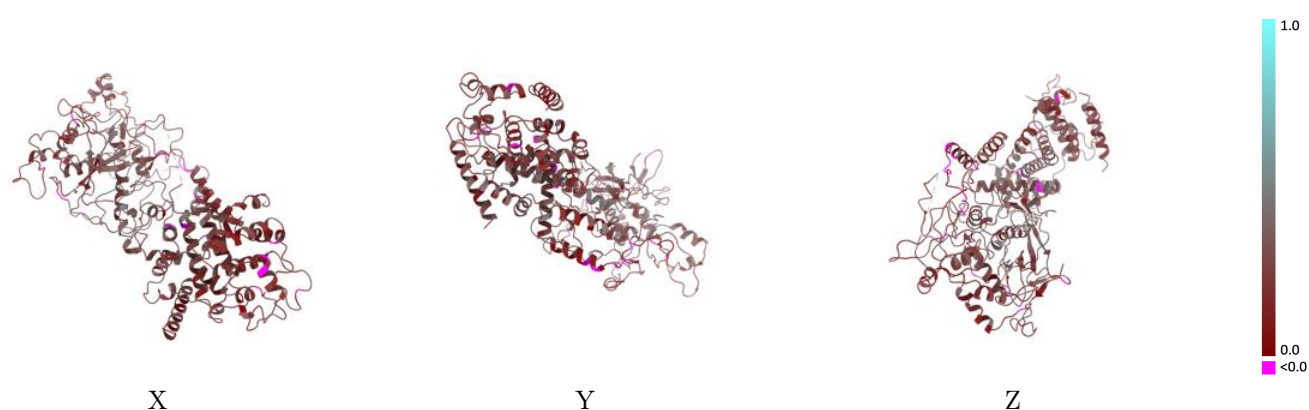
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30006 and PDB model 6LXE. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

This section was not generated.

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



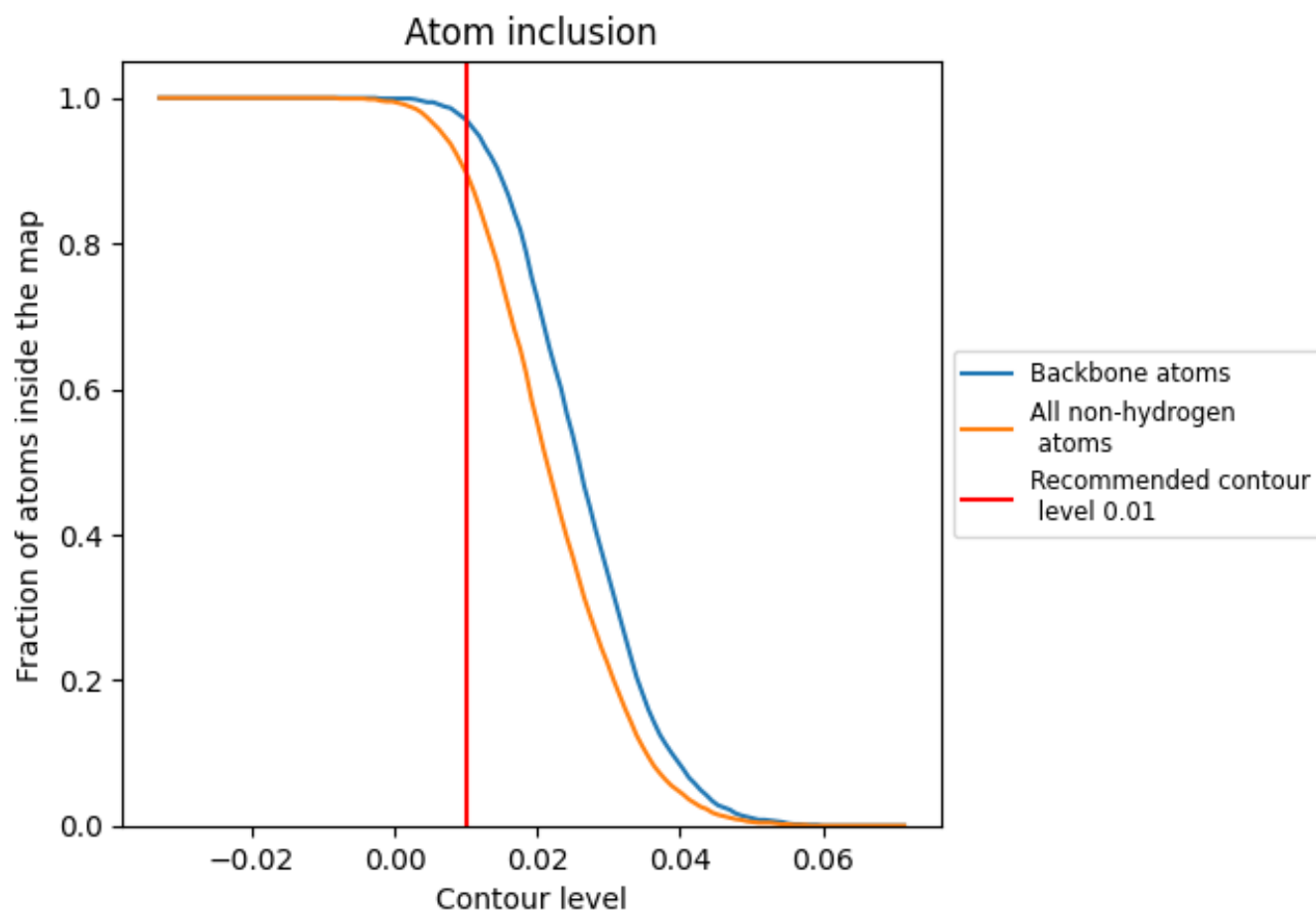
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 90% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8970	0.2630
A	0.9000	0.2660
B	0.9090	0.2440
C	0.7660	0.1980

