



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:17 PM UTC

PDB ID : 7W0E / pdb_00007w0e
EMDB ID : EMD-32240
Title : dmDicer2-LoqsPD-dsRNA Active-dicing status
Authors : Su, S.; Wang, J.; Wang, H.W.; Ma, J.
Deposited on : 2021-11-18
Resolution : 4.03 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

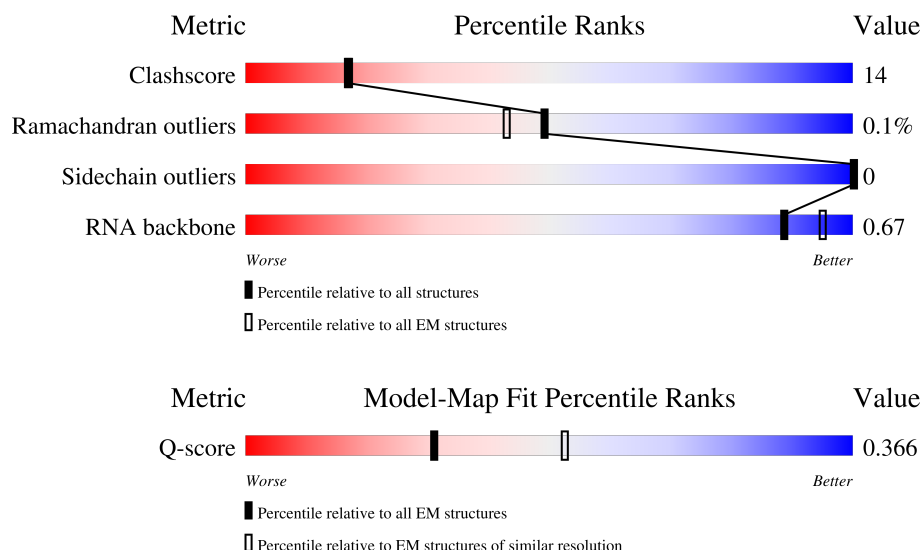
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.03 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.



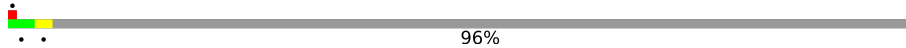
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	6618 (3.54 - 4.53)

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	C	53	6% 25% 72% .
1	D	53	6% 21% 74% .
2	A	1722	7% 63% 27% 11%

Continued on next page...

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Mol	Chain	Length	Quality of chain
3	B	359	 96%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14850 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 RNA chain called dsRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	53	Total	C	N	O	P	0	1
			1104	493	192	367	52		
1	D	52	Total	C	N	O	P	0	0
			1103	493	192	366	52		

- Molecule 2 is a protein called Dicer-2, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	1541	Total	C	N	O	S	0	0
			12470	7994	2131	2278	67		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1217	ASN	ASP	engineered mutation	UNP A1ZAW0
A	1476	ASN	ASP	engineered mutation	UNP A1ZAW0

- Molecule 3 is a protein called Loquacious, isoform D.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	B	16	Total	C	N	O	0	0
			143	94	22	27		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
4	A	3	Total	Mg	0
			3	3	

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
5	A	1	27	10	5	10	2	0

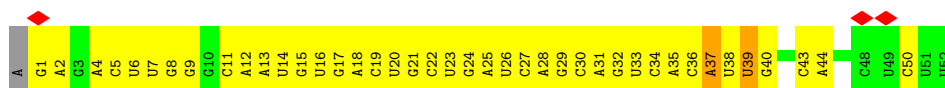
3 Residue-property plots

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.

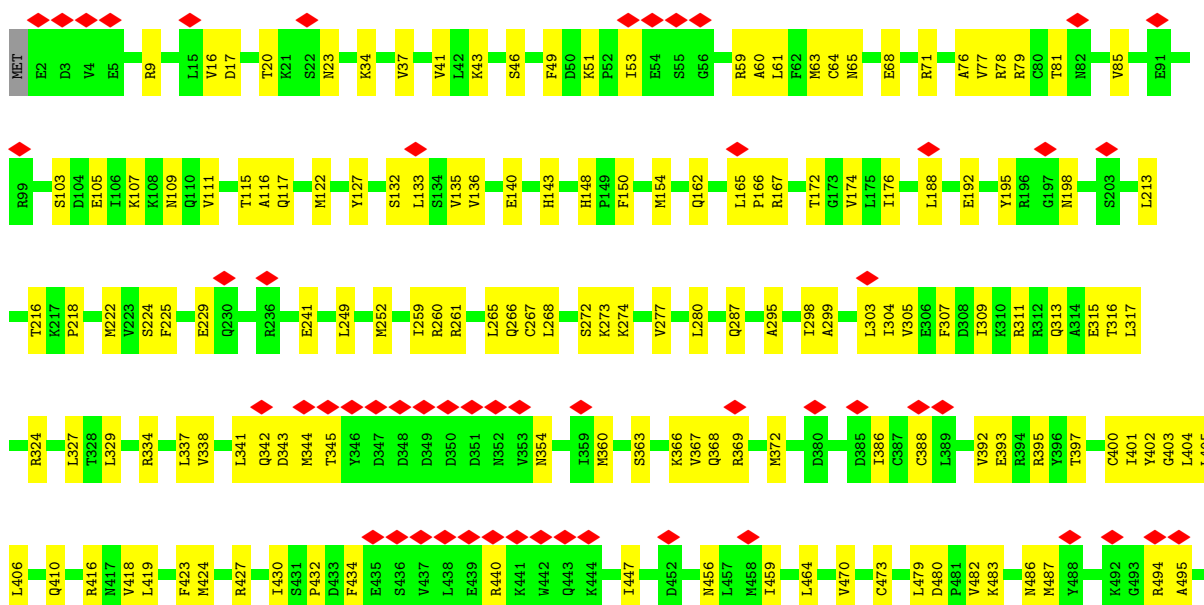
- Molecule 1: dsRNA

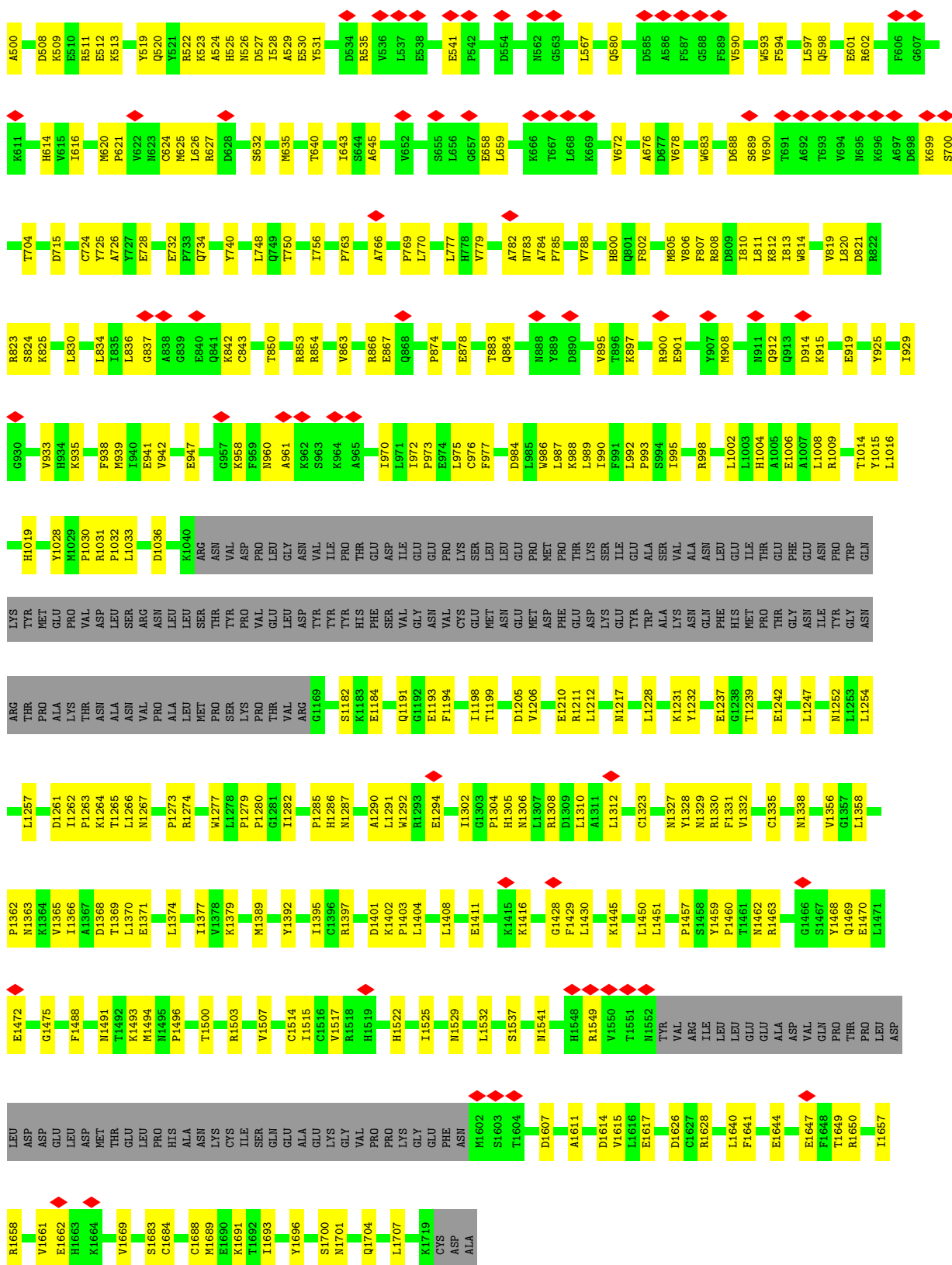


- Molecule 1: dsRNA



- Molecule 2: Dicer-2, isoform A





• Molecule 3: Loquacious, isoform D

Chain B: 96%

LYS	LYS	GLY	THR	LYS	MET
ASP	ASP	ASP	ALA	PHE	PRO
ILE	ILE	ALA	MET	VAL	GLN
ALA	ALA	SER	GLY	SER	GLU
ARG	ARG	LYS	GLY	THR	HIS
LEU	LEU	THR	ARG	ASP	VAL
ALA	ALA	VAL	SER	ALA	LYS
HIS	HIS	GLY	LYS	ASN	SER
ASN	ASN	ASN	LYS	GLY	LYS
ARG	ARG	PRO	GLU	LEU	LEU
MET	MET	ILE	ALA	ALA	GLU
TRP	TRP	GLY	LYS	MET	LYS
MET	MET	TRP	HIS	LYS	ILE
ARG	ARG	LEU	ALA	THR	SER
LEU	LEU	GLN	ALA	PRO	GLN
GLN	GLN	GLU	ALA	VAL	ALA
GLU	GLU	MET	ARG	SER	VAL
THR	THR	CYS	ALA	ILE	ALA
PRO	PRO	MET	LEU	LEU	ILE
ILE	ILE	GLN	ILE	GLN	GLN
ASP	ASP	ARG	ASP	GLU	SER
SER	SER	ARG	LYS	LEU	GLN
LYS	LYS	TRP	LEU	LEU	PRO
GLY	GLY	PRO	ILE	SER	GLY
ALA	ALA	PRO	GLY	ARG	ALA
SER	SER	PRO	GLN	GLY	SER
SER	SER	SER	GLN	ILE	ASN
ILE	ILE	TYR	LEU	ILE	PRO
GLY	GLY	GLU	PRO	THR	VAL
CYS	CYS	THR	GLU	PRO	GLN
GLY	GLY	GLU	SER	TYR	ASP
LEU	LEU	THR	GLU	GLY	GLY
GLU	GLU	VAL	SER	LEU	ALA
GLY	GLY	GLY	SER	VAL	PRO
GLU	GLU	LEU	ALA	GLN	ALA
VAL	VAL	PRO	GLY	ILE	ARG
SER	SER	HIS	PRO	GLU	ARG
ILE	ILE	GLU	SER	GLY	HIS
ILE	ILE	ARG	VAL	ALA	TYR
GLN	GLN	LEU	THR	ILE	ASN
ASP	ASP	PHE	GLY	HIS	ASN
I344	I344	THR	LEU	GLU	LEU
D345	D345	ILE	THR	PRO	VAL
R346	R346	ALA	VAL	THR	GLY
Y347	Y347	CYS	ALA	PHE	GLY
E348	E348	SER	GLY	ARG	ASN
		ILE	SER	PHE	GLY
		LEU	SER	PHE	LEU
S351	S351	ASN	GLY	ARG	MET
K352	K352	TYR	ASP	SER	ALA
D353	D353	ARG	GLY	PHE	VAL
F354	F354	GLU	ASN	LYS	ILE
		MET	ALA	ASP	LEU
		GLY	ASN	LYS	PRO
I359	I359	LYS	THR	ASP	SER
		GLY	THR	GLU	GLY
		SER	GLY	ALA	VAL
		THR	THR	PRO	GLY
		GLY	GLY	THR	ALA
		SER	GLY	PHE	THR

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	57679	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)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.399	Depositor
Minimum map value	-0.793	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	259.8, 259.8, 259.8	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0825, 1.0825, 1.0825	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: MG, ADP

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	C	0.12	0/1232	0.23	0/1918
1	D	0.12	0/1231	0.26	0/1915
2	A	0.13	0/12739	0.33	0/17233
3	B	0.09	0/145	0.27	0/192
All	All	0.13	0/15347	0.32	0/21258

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	C	1104	0	559	41	0
1	D	1103	0	559	53	0
2	A	12470	0	12553	312	0
3	B	143	0	140	5	0
4	A	3	0	0	0	0
5	A	27	0	12	1	0
All	All	14850	0	13823	397	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 397 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)
2:A:1009:ARG:NH2	2:A:1028:TYR:OH	2.16	0.79
2:A:895:VAL:HA	2:A:942:VAL:HG12	1.65	0.78
1:D:43:C:H2'	1:D:44:A:H8	1.49	0.77
2:A:1257:LEU:HB2	2:A:1370:LEU:HD12	1.69	0.75
2:A:805:MET:HE2	2:A:854:ARG:HA	1.67	0.73

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	
2	A	1535/1722 (89%)	1460 (95%)	74 (5%)	1 (0%)	48	80
3	B	14/359 (4%)	13 (93%)	1 (7%)	0	100	100
All	All	1549/2081 (74%)	1473 (95%)	75 (5%)	1 (0%)	49	80

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	541	GLU

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	
2	A	1384/1549 (89%)	1384 (100%)	0	100	100
3	B	16/289 (6%)	16 (100%)	0	100	100
All	All	1400/1838 (76%)	1400 (100%)	0	100	100

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

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

Mol	Chain	Res	Type
2	A	1004	HIS
2	A	1529	ASN
2	A	1217	ASN
2	A	1656	HIS
2	A	1452	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C	51/53 (96%)	4 (7%)	0
1	D	51/53 (96%)	3 (5%)	0
All	All	102/106 (96%)	7 (6%)	0

5 of 7 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C	13	A
1	C	14	U
1	C	15	G
1	C	23	U
1	D	37	A

There are no RNA pucker outliers to report.

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 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
5	ADP	A	1804	4	28,29,29	1.41	4 (14%)	43,45,45	1.83	9 (20%)

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
5	ADP	A	1804	4	-	1/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1804	ADP	C5-C4	4.68	1.47	1.39
5	A	1804	ADP	C5-C6	2.70	1.48	1.41
5	A	1804	ADP	C8-N7	2.33	1.36	1.31
5	A	1804	ADP	C5-N7	-2.29	1.34	1.39

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1804	ADP	C5-C4-N3	-5.80	118.72	126.72
5	A	1804	ADP	N3-C4-N9	4.60	134.99	127.17
5	A	1804	ADP	C2-N3-C4	3.73	120.94	111.83
5	A	1804	ADP	C4-C5-N7	-3.44	106.65	110.58
5	A	1804	ADP	N3-C2-N1	-3.28	123.62	128.58

There are no chirality outliers.

All (1) torsion outliers are listed below:

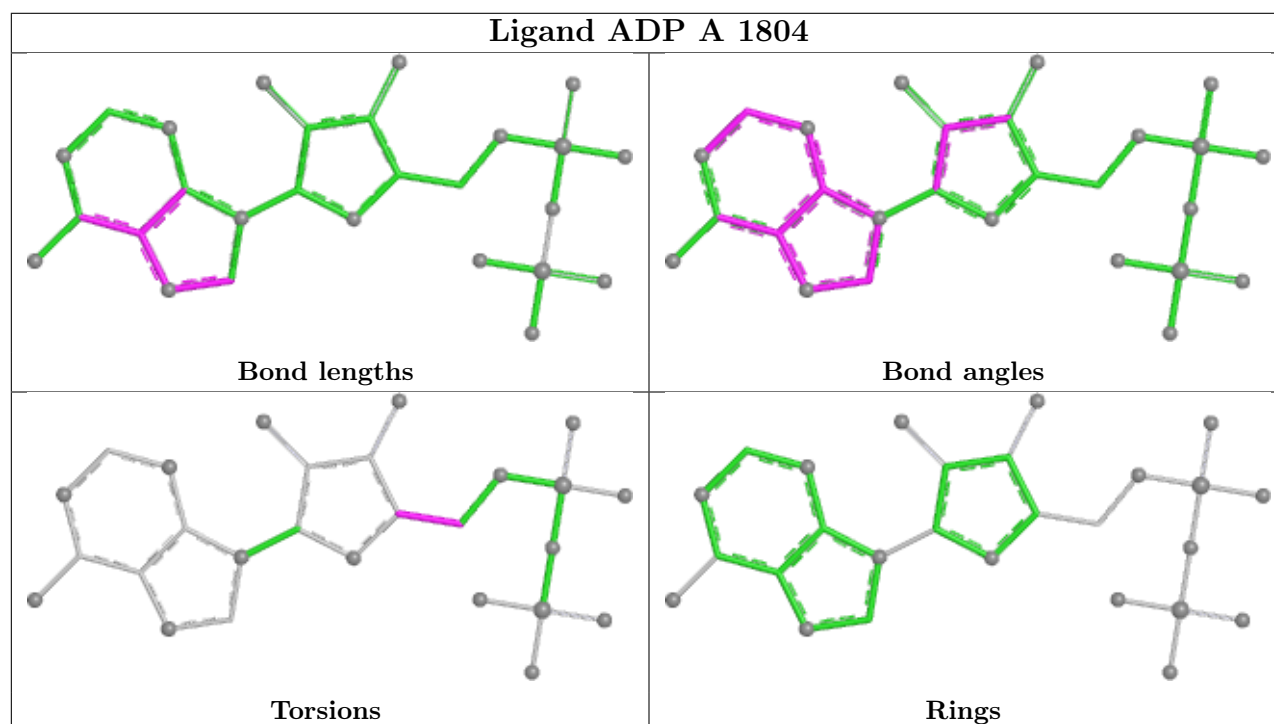
Mol	Chain	Res	Type	Atoms
5	A	1804	ADP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1804	ADP	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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

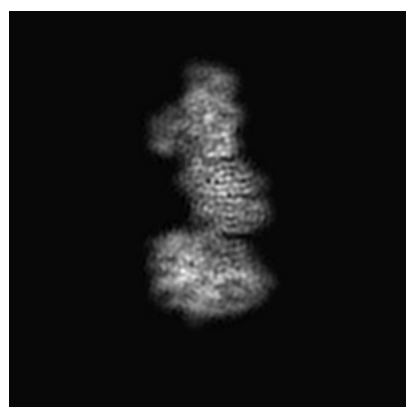
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32240. These allow visual inspection of the internal detail of the map and identification of artifacts.

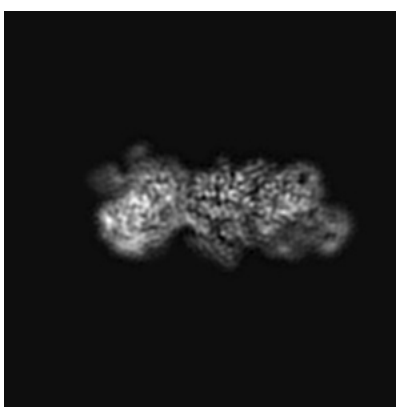
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

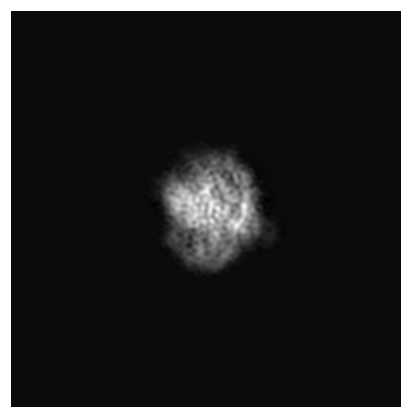
6.1.1 Primary map



X



Y

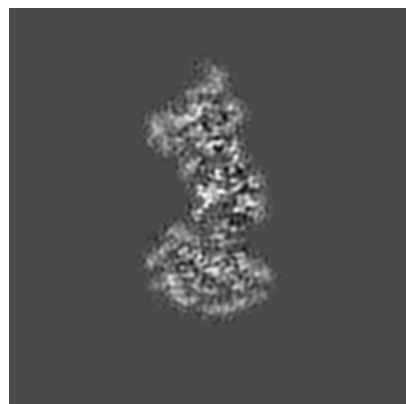


Z

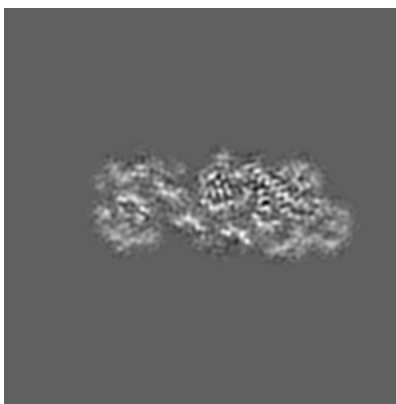
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 120



Y Index: 120

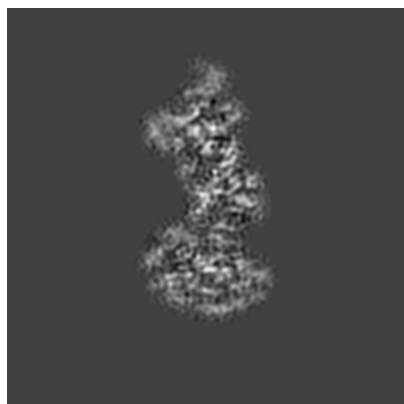


Z Index: 120

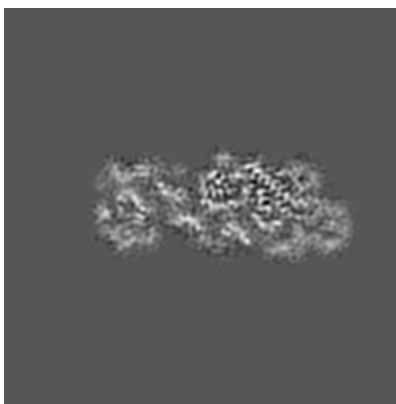
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 119



Y Index: 121

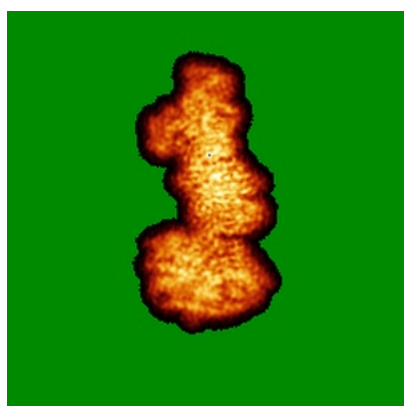


Z Index: 80

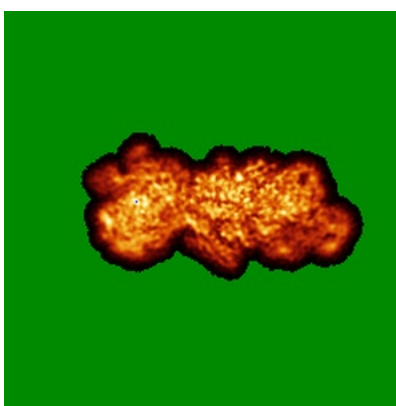
The images above show the largest variance slices of the map in three orthogonal directions.

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

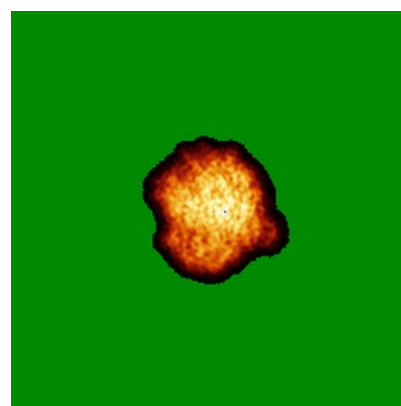
6.4.1 Primary map



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.

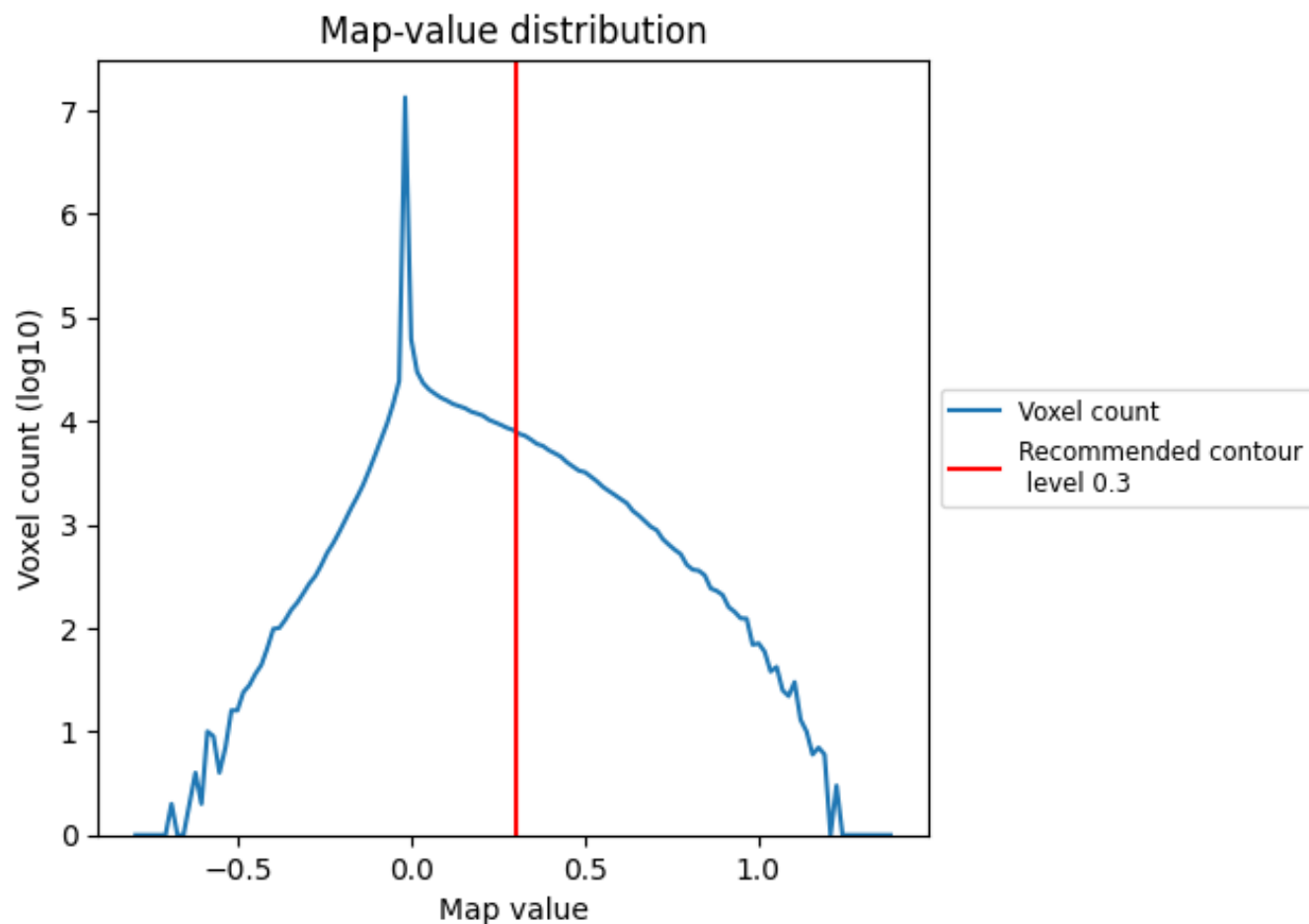
6.6 Mask visualisation

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

7 Map analysis [i](#)

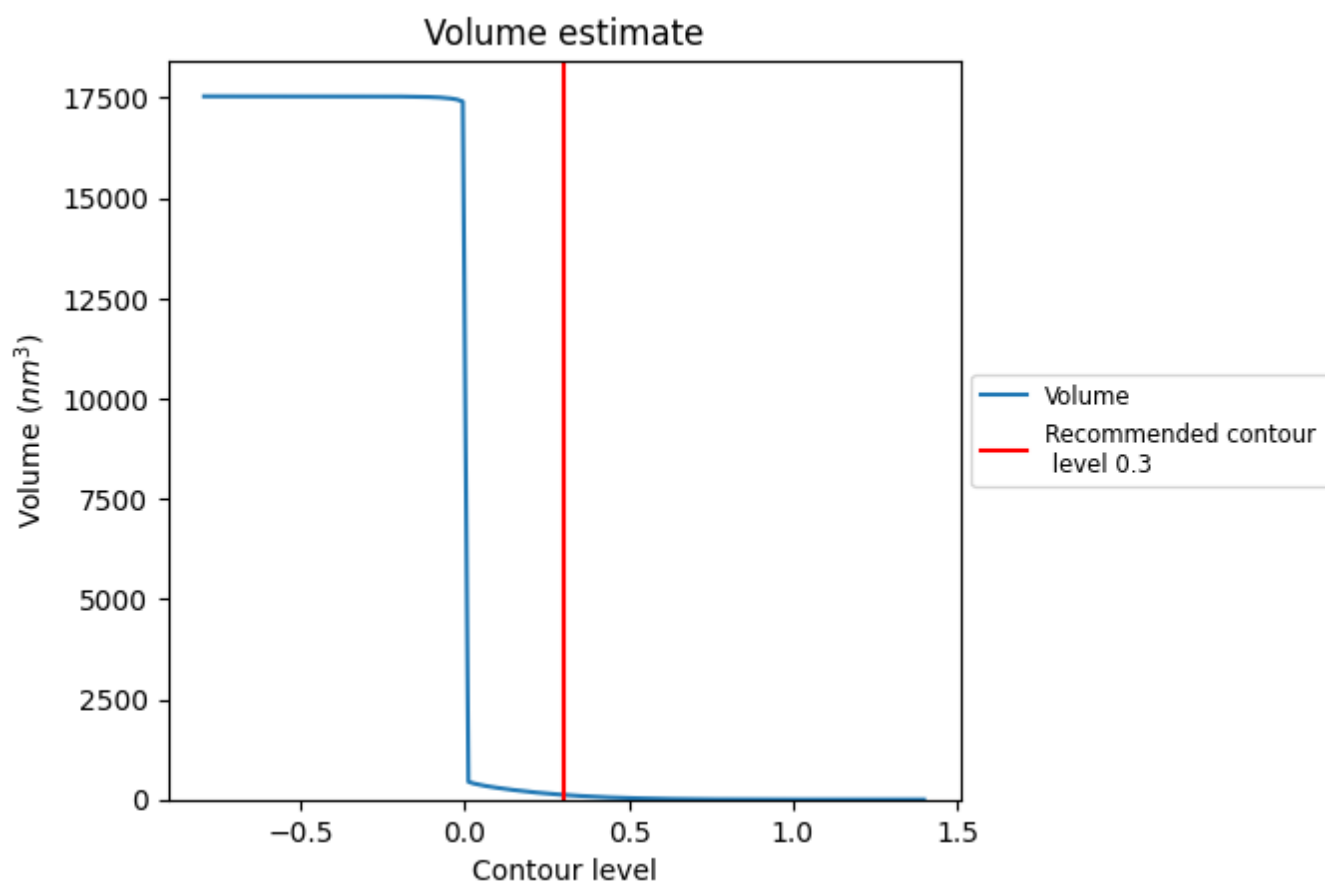
This section contains the results of statistical analysis of the map.

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.

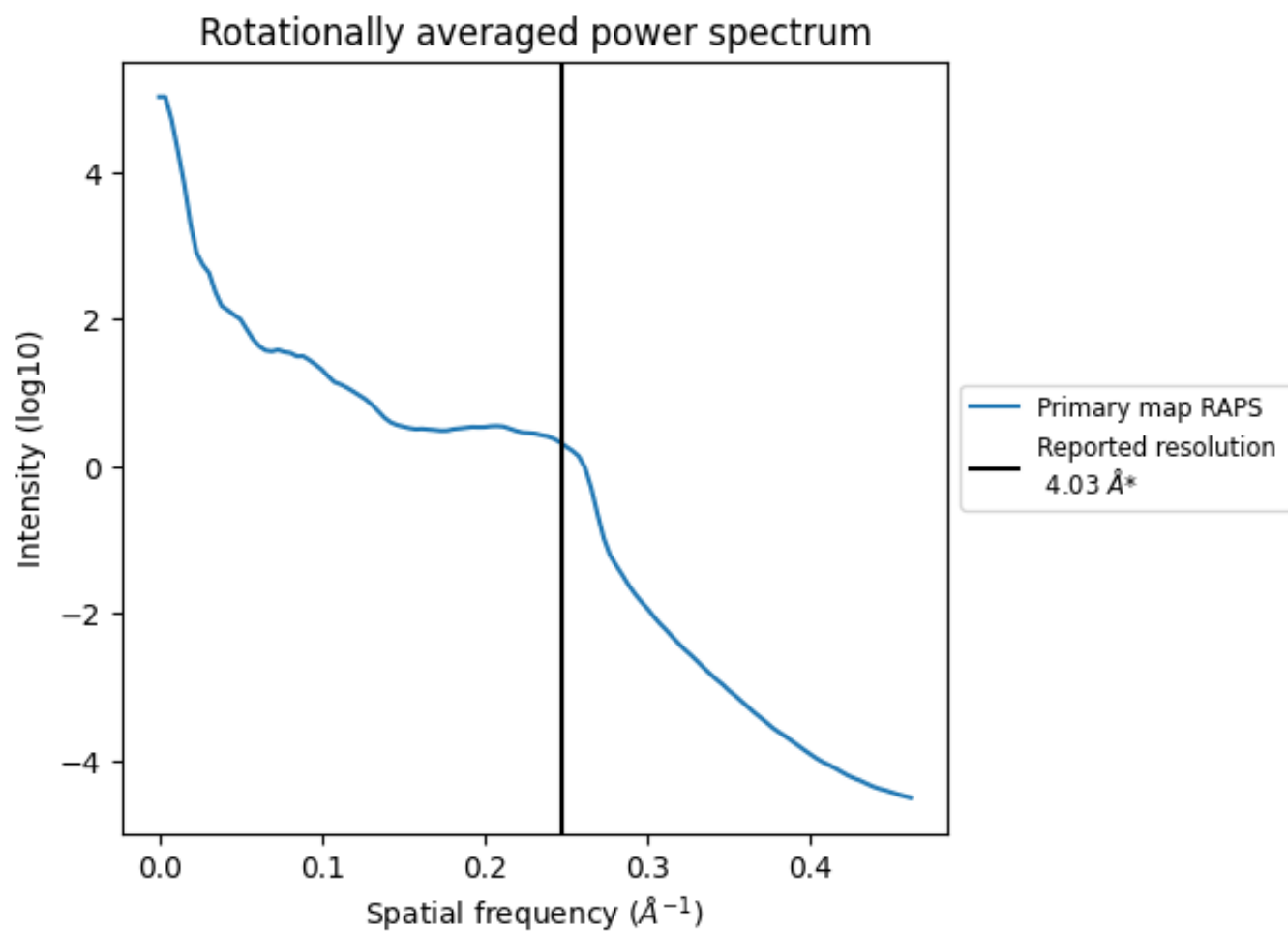
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 118 nm^3 ; this corresponds to an approximate mass of 107 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 0.248 Å⁻¹

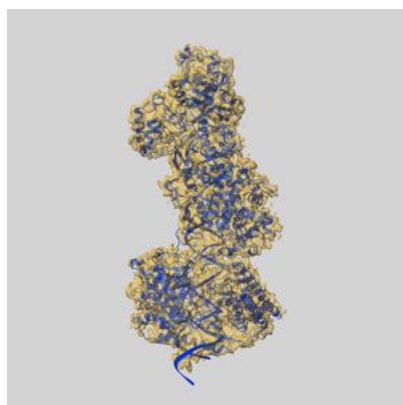
8 Fourier-Shell correlation

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

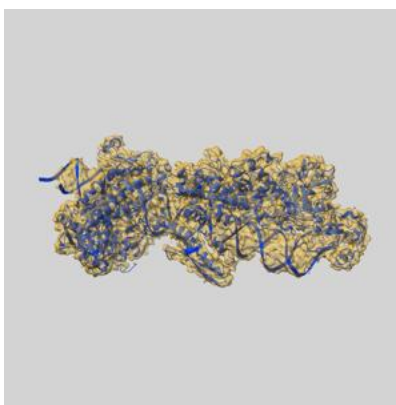
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32240 and PDB model 7W0E. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

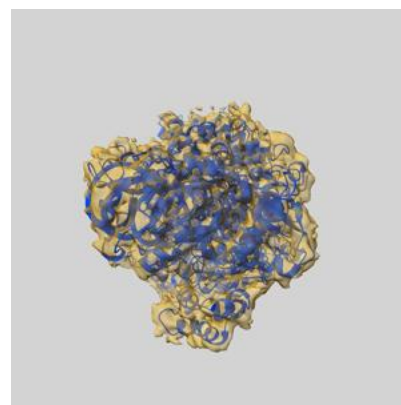
9.1 Map-model overlay [i](#)



X



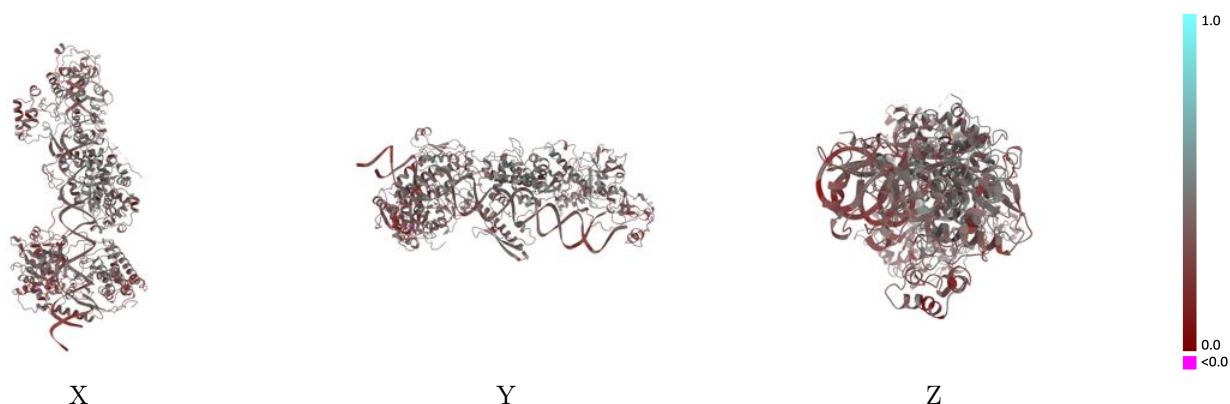
Y



Z

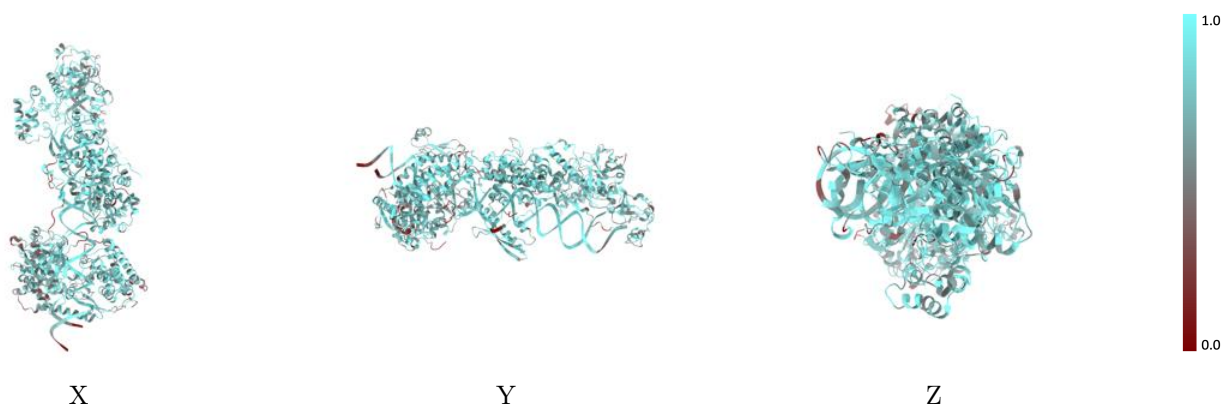
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



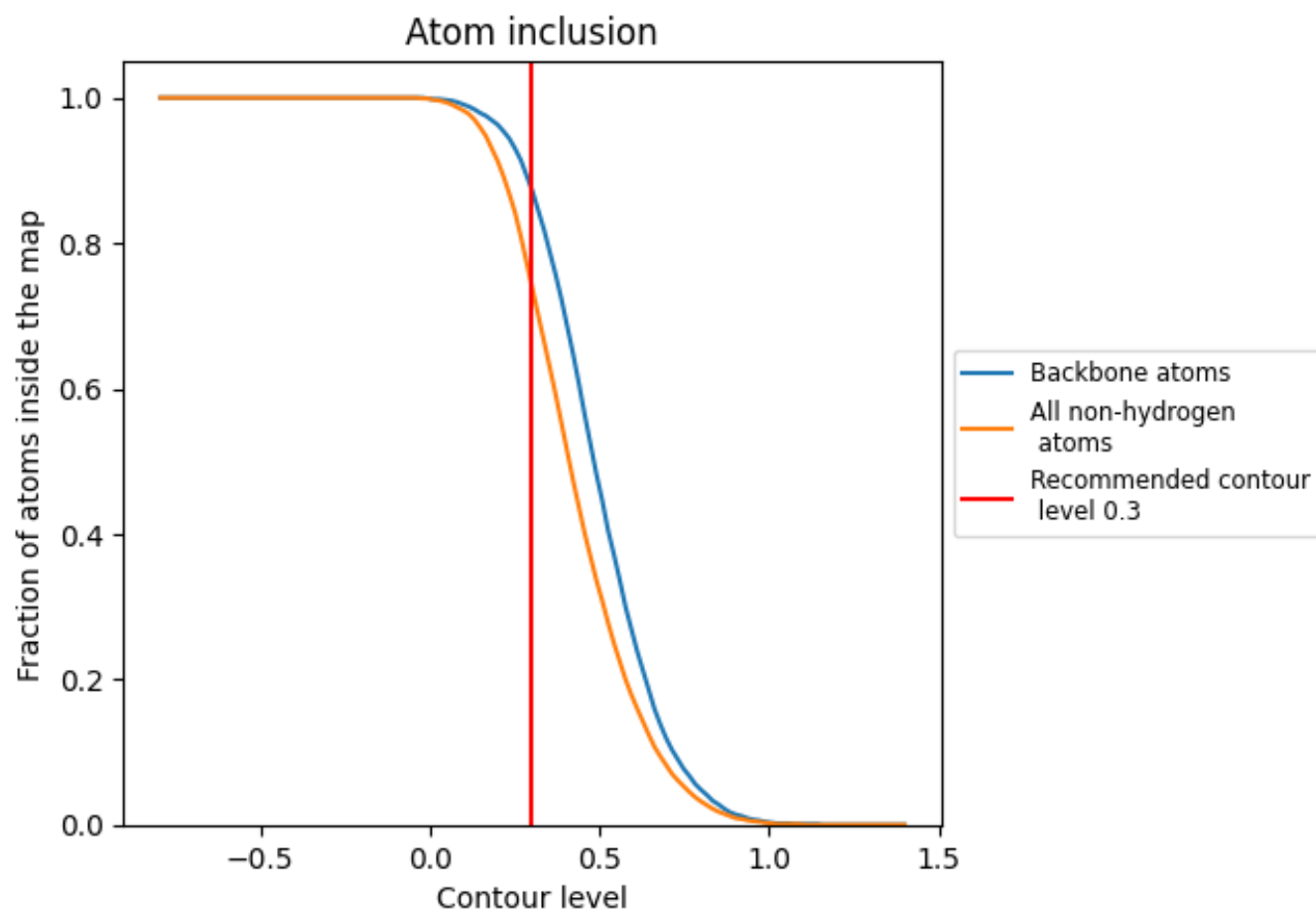
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 74% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7430	0.3660
A	0.7290	0.3730
B	0.6570	0.3440
C	0.8240	0.3280
D	0.8310	0.3290

