



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 06:27 PM UTC

PDB ID : 7MH2 / pdb_00007mh2
EMDB ID : EMD-23834
Title : T4GALA Engineered Protein Nanocage
Authors : Andreas, M.P.; Jones, J.A.; Cristie-David, A.S.; Giessen, T.W.
Deposited on : 2021-04-14
Resolution : 3.57 Å(reported)
Based on initial model : 6NJ8

This is a Full wwPDB EM Validation 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:

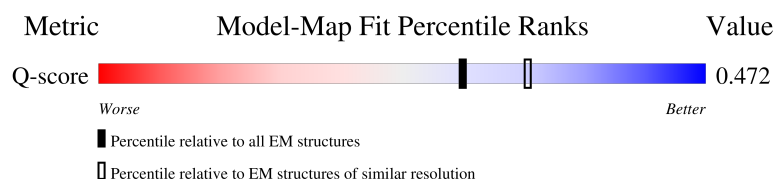
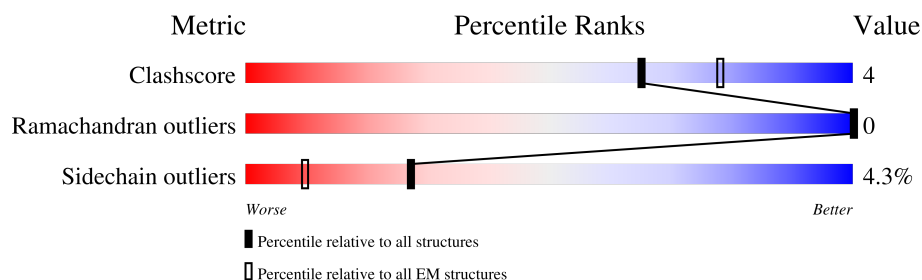
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.57 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	12682 (3.07 - 4.07)

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	316	
1	B	316	
1	C	316	
1	D	316	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8948 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 T4GALA Engineered Protein Nanocage.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	278	Total	C	N	O	S	0	0
			2235	1420	383	423	9		
1	B	279	Total	C	N	O	S	0	0
			2239	1422	384	424	9		
1	C	278	Total	C	N	O	S	0	0
			2235	1420	383	423	9		
1	D	279	Total	C	N	O	S	0	0
			2239	1422	384	424	9		

There are 136 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	62	GLY	-	insertion	UNP A0A0F5HPP7
A	63	GLY	-	insertion	UNP A0A0F5HPP7
A	64	GLY	-	insertion	UNP A0A0F5HPP7
A	65	GLU	-	insertion	UNP A0A0F5HPP7
A	66	ALA	-	insertion	UNP A0A0F5HPP7
A	67	LEU	-	insertion	UNP A0A0F5HPP7
A	68	ALA	-	insertion	UNP A0A0F5HPP7
A	69	GLU	-	insertion	UNP A0A0F5HPP7
A	70	ALA	-	insertion	UNP A0A0F5HPP7
A	71	LEU	-	insertion	UNP A0A0F5HPP7
A	72	ALA	-	insertion	UNP A0A0F5HPP7
A	73	GLU	-	insertion	UNP A0A0F5HPP7
A	74	ALA	-	insertion	UNP A0A0F5HPP7
A	75	LEU	-	insertion	UNP A0A0F5HPP7
A	76	ALA	-	insertion	UNP A0A0F5HPP7
A	77	GLU	-	insertion	UNP A0A0F5HPP7
A	78	ALA	-	insertion	UNP A0A0F5HPP7
A	79	LEU	-	insertion	UNP A0A0F5HPP7
A	80	ALA	-	insertion	UNP A0A0F5HPP7
A	81	GLY	-	insertion	UNP A0A0F5HPP7
A	82	GLY	-	insertion	UNP A0A0F5HPP7
A	83	GLY	-	insertion	UNP A0A0F5HPP7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	305	GLY	-	expression tag	UNP A0A0F5HPP7
A	306	GLY	-	expression tag	UNP A0A0F5HPP7
A	307	GLY	-	expression tag	UNP A0A0F5HPP7
A	308	GLY	-	expression tag	UNP A0A0F5HPP7
A	309	GLY	-	expression tag	UNP A0A0F5HPP7
A	310	GLY	-	expression tag	UNP A0A0F5HPP7
A	311	HIS	-	expression tag	UNP A0A0F5HPP7
A	312	HIS	-	expression tag	UNP A0A0F5HPP7
A	313	HIS	-	expression tag	UNP A0A0F5HPP7
A	314	HIS	-	expression tag	UNP A0A0F5HPP7
A	315	HIS	-	expression tag	UNP A0A0F5HPP7
A	316	HIS	-	expression tag	UNP A0A0F5HPP7
B	62	GLY	-	insertion	UNP A0A0F5HPP7
B	63	GLY	-	insertion	UNP A0A0F5HPP7
B	64	GLY	-	insertion	UNP A0A0F5HPP7
B	65	GLU	-	insertion	UNP A0A0F5HPP7
B	66	ALA	-	insertion	UNP A0A0F5HPP7
B	67	LEU	-	insertion	UNP A0A0F5HPP7
B	68	ALA	-	insertion	UNP A0A0F5HPP7
B	69	GLU	-	insertion	UNP A0A0F5HPP7
B	70	ALA	-	insertion	UNP A0A0F5HPP7
B	71	LEU	-	insertion	UNP A0A0F5HPP7
B	72	ALA	-	insertion	UNP A0A0F5HPP7
B	73	GLU	-	insertion	UNP A0A0F5HPP7
B	74	ALA	-	insertion	UNP A0A0F5HPP7
B	75	LEU	-	insertion	UNP A0A0F5HPP7
B	76	ALA	-	insertion	UNP A0A0F5HPP7
B	77	GLU	-	insertion	UNP A0A0F5HPP7
B	78	ALA	-	insertion	UNP A0A0F5HPP7
B	79	LEU	-	insertion	UNP A0A0F5HPP7
B	80	ALA	-	insertion	UNP A0A0F5HPP7
B	81	GLY	-	insertion	UNP A0A0F5HPP7
B	82	GLY	-	insertion	UNP A0A0F5HPP7
B	83	GLY	-	insertion	UNP A0A0F5HPP7
B	305	GLY	-	expression tag	UNP A0A0F5HPP7
B	306	GLY	-	expression tag	UNP A0A0F5HPP7
B	307	GLY	-	expression tag	UNP A0A0F5HPP7
B	308	GLY	-	expression tag	UNP A0A0F5HPP7
B	309	GLY	-	expression tag	UNP A0A0F5HPP7
B	310	GLY	-	expression tag	UNP A0A0F5HPP7
B	311	HIS	-	expression tag	UNP A0A0F5HPP7
B	312	HIS	-	expression tag	UNP A0A0F5HPP7

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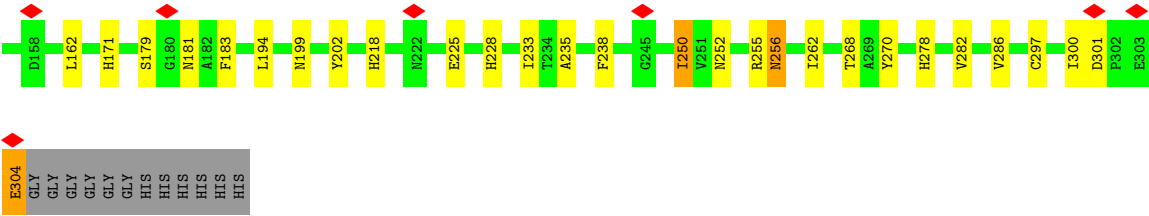
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Chain	Residue	Modelled	Actual	Comment	Reference
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B	314	HIS	-	expression tag	UNP A0A0F5HPP7
B	315	HIS	-	expression tag	UNP A0A0F5HPP7
B	316	HIS	-	expression tag	UNP A0A0F5HPP7
C	62	GLY	-	insertion	UNP A0A0F5HPP7
C	63	GLY	-	insertion	UNP A0A0F5HPP7
C	64	GLY	-	insertion	UNP A0A0F5HPP7
C	65	GLU	-	insertion	UNP A0A0F5HPP7
C	66	ALA	-	insertion	UNP A0A0F5HPP7
C	67	LEU	-	insertion	UNP A0A0F5HPP7
C	68	ALA	-	insertion	UNP A0A0F5HPP7
C	69	GLU	-	insertion	UNP A0A0F5HPP7
C	70	ALA	-	insertion	UNP A0A0F5HPP7
C	71	LEU	-	insertion	UNP A0A0F5HPP7
C	72	ALA	-	insertion	UNP A0A0F5HPP7
C	73	GLU	-	insertion	UNP A0A0F5HPP7
C	74	ALA	-	insertion	UNP A0A0F5HPP7
C	75	LEU	-	insertion	UNP A0A0F5HPP7
C	76	ALA	-	insertion	UNP A0A0F5HPP7
C	77	GLU	-	insertion	UNP A0A0F5HPP7
C	78	ALA	-	insertion	UNP A0A0F5HPP7
C	79	LEU	-	insertion	UNP A0A0F5HPP7
C	80	ALA	-	insertion	UNP A0A0F5HPP7
C	81	GLY	-	insertion	UNP A0A0F5HPP7
C	82	GLY	-	insertion	UNP A0A0F5HPP7
C	83	GLY	-	insertion	UNP A0A0F5HPP7
C	305	GLY	-	expression tag	UNP A0A0F5HPP7
C	306	GLY	-	expression tag	UNP A0A0F5HPP7
C	307	GLY	-	expression tag	UNP A0A0F5HPP7
C	308	GLY	-	expression tag	UNP A0A0F5HPP7
C	309	GLY	-	expression tag	UNP A0A0F5HPP7
C	310	GLY	-	expression tag	UNP A0A0F5HPP7
C	311	HIS	-	expression tag	UNP A0A0F5HPP7
C	312	HIS	-	expression tag	UNP A0A0F5HPP7
C	313	HIS	-	expression tag	UNP A0A0F5HPP7
C	314	HIS	-	expression tag	UNP A0A0F5HPP7
C	315	HIS	-	expression tag	UNP A0A0F5HPP7
C	316	HIS	-	expression tag	UNP A0A0F5HPP7
D	62	GLY	-	insertion	UNP A0A0F5HPP7
D	63	GLY	-	insertion	UNP A0A0F5HPP7
D	64	GLY	-	insertion	UNP A0A0F5HPP7
D	65	GLU	-	insertion	UNP A0A0F5HPP7

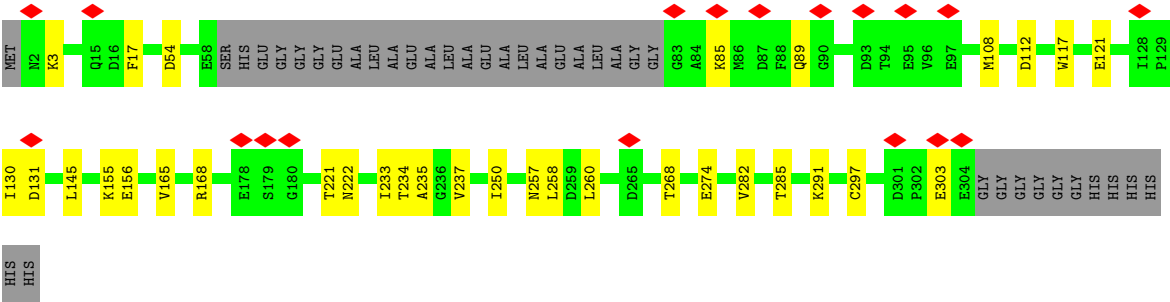
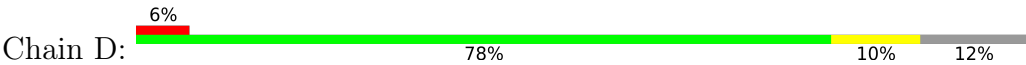
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Chain	Residue	Modelled	Actual	Comment	Reference
D	66	ALA	-	insertion	UNP A0A0F5HPP7
D	67	LEU	-	insertion	UNP A0A0F5HPP7
D	68	ALA	-	insertion	UNP A0A0F5HPP7
D	69	GLU	-	insertion	UNP A0A0F5HPP7
D	70	ALA	-	insertion	UNP A0A0F5HPP7
D	71	LEU	-	insertion	UNP A0A0F5HPP7
D	72	ALA	-	insertion	UNP A0A0F5HPP7
D	73	GLU	-	insertion	UNP A0A0F5HPP7
D	74	ALA	-	insertion	UNP A0A0F5HPP7
D	75	LEU	-	insertion	UNP A0A0F5HPP7
D	76	ALA	-	insertion	UNP A0A0F5HPP7
D	77	GLU	-	insertion	UNP A0A0F5HPP7
D	78	ALA	-	insertion	UNP A0A0F5HPP7
D	79	LEU	-	insertion	UNP A0A0F5HPP7
D	80	ALA	-	insertion	UNP A0A0F5HPP7
D	81	GLY	-	insertion	UNP A0A0F5HPP7
D	82	GLY	-	insertion	UNP A0A0F5HPP7
D	83	GLY	-	insertion	UNP A0A0F5HPP7
D	305	GLY	-	expression tag	UNP A0A0F5HPP7
D	306	GLY	-	expression tag	UNP A0A0F5HPP7
D	307	GLY	-	expression tag	UNP A0A0F5HPP7
D	308	GLY	-	expression tag	UNP A0A0F5HPP7
D	309	GLY	-	expression tag	UNP A0A0F5HPP7
D	310	GLY	-	expression tag	UNP A0A0F5HPP7
D	311	HIS	-	expression tag	UNP A0A0F5HPP7
D	312	HIS	-	expression tag	UNP A0A0F5HPP7
D	313	HIS	-	expression tag	UNP A0A0F5HPP7
D	314	HIS	-	expression tag	UNP A0A0F5HPP7
D	315	HIS	-	expression tag	UNP A0A0F5HPP7
D	316	HIS	-	expression tag	UNP A0A0F5HPP7



• Molecule 1: T4GALA Engineered Protein Nanocage



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	6707	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	62	Depositor
Minimum defocus (nm)	-1300	Depositor
Maximum defocus (nm)	-1800	Depositor
Magnification	45000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.597	Depositor
Minimum map value	-0.560	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	0.45	Depositor
Map size (Å)	617.39996, 617.39996, 617.39996	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.4031818, 1.4031818, 1.4031818	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	0.15	0/2281	0.33	0/3087
1	B	0.14	0/2285	0.33	0/3092
1	C	0.14	0/2281	0.32	0/3087
1	D	0.14	0/2285	0.33	0/3092
All	All	0.14	0/9132	0.33	0/12358

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	2235	0	2192	20	0
1	B	2239	0	2195	23	0
1	C	2235	0	2192	17	0
1	D	2239	0	2195	12	0
All	All	8948	0	8774	70	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 4.

All (70) 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:D:221:THR:O	1:D:222:ASN:ND2	2.22	0.73
1:C:255:ARG:O	1:C:256:ASN:ND2	2.21	0.72
1:A:268:THR:HG22	1:A:282:VAL:HG12	1.77	0.67
1:B:268:THR:HG22	1:B:282:VAL:HG12	1.77	0.66
1:B:163:MET:O	1:B:168:ARG:NH1	2.33	0.62
1:C:270:TYR:HE1	1:C:278:HIS:HB3	1.65	0.61
1:B:271:LEU:HB3	1:B:279:PRO:HG2	1.83	0.61
1:B:255:ARG:O	1:B:256:ASN:ND2	2.35	0.59
1:B:87:ASP:OD1	1:B:88:PHE:N	2.37	0.58
1:C:268:THR:HG22	1:C:282:VAL:HG12	1.85	0.57
1:D:268:THR:HG22	1:D:282:VAL:HG12	1.86	0.57
1:B:84:ALA:HB3	1:C:145:LEU:HD22	1.87	0.57
1:A:270:TYR:HE1	1:A:278:HIS:HB3	1.71	0.56
1:A:224:LEU:HG	1:A:226:ILE:HG22	1.89	0.55
1:A:50:SER:OG	1:A:103:ASN:OD1	2.19	0.54
1:C:25:ILE:O	1:C:29:ARG:HG3	2.08	0.52
1:C:250:ILE:HG23	1:C:297:CYS:HB3	1.92	0.52
1:D:250:ILE:HG23	1:D:297:CYS:HB3	1.90	0.52
1:D:233:ILE:HG22	1:D:235:ALA:H	1.75	0.52
1:B:128:ILE:HG12	1:B:129:PRO:HD2	1.92	0.50
1:D:117:TRP:O	1:D:121:GLU:HG2	2.14	0.48
1:B:117:TRP:O	1:B:121:GLU:HG2	2.14	0.48
1:B:255:ARG:HG2	1:B:256:ASN:H	1.78	0.47
1:C:301:ASP:HB3	1:C:304:GLU:HB2	1.95	0.47
1:A:11:PRO:HG3	1:A:278:HIS:CE1	2.49	0.47
1:B:221:THR:HG21	1:B:228:HIS:NE2	2.30	0.47
1:A:18:ASN:O	1:A:22:GLN:HG2	2.15	0.47
1:D:108:MET:HA	1:D:285:THR:HG22	1.97	0.46
1:D:131:ASP:OD1	1:D:131:ASP:N	2.49	0.46
1:A:85:LYS:HD3	1:A:86:MET:N	2.31	0.46
1:A:197:ASN:O	1:A:197:ASN:ND2	2.48	0.46
1:B:18:ASN:OD1	1:B:19:GLN:N	2.49	0.46
1:B:250:ILE:HG23	1:B:297:CYS:HB3	1.98	0.46
1:C:199:ASN:O	1:C:252:ASN:ND2	2.44	0.46
1:C:262:ILE:HG22	1:C:286:VAL:HG23	1.97	0.46
1:B:175:ASN:O	1:B:181:ASN:ND2	2.48	0.45
1:D:165:VAL:O	1:D:168:ARG:NH1	2.50	0.45
1:A:233:ILE:O	1:A:234:THR:HG22	2.16	0.45
1:B:233:ILE:O	1:B:234:THR:HG22	2.17	0.45
1:C:183:PHE:CE1	1:C:228:HIS:HB3	2.52	0.45
1:C:179:SER:OG	1:C:181:ASN:OD1	2.21	0.45
1:D:257:ASN:C	1:D:258:LEU:HD12	2.42	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:86:MET:HB2	1:D:145:LEU:HD21	2.00	0.44
1:A:164:ASN:C	1:A:168:ARG:HH21	2.26	0.43
1:D:112:ASP:OD1	1:D:112:ASP:N	2.52	0.43
1:B:22:GLN:O	1:B:26:GLU:HG2	2.18	0.43
1:A:303:GLU:H	1:A:303:GLU:CD	2.26	0.43
1:B:32:LEU:HD23	1:B:32:LEU:HA	1.89	0.43
1:D:54:ASP:OD1	1:D:54:ASP:N	2.52	0.42
1:A:259:ASP:N	1:A:259:ASP:OD1	2.52	0.42
1:B:258:LEU:HG	1:B:290:ILE:HG22	2.01	0.42
1:C:218:HIS:HB2	1:C:225:GLU:HG2	2.02	0.42
1:B:24:VAL:HG22	1:B:135:ALA:HB1	2.00	0.42
1:B:219:LYS:H	1:B:219:LYS:HG3	1.72	0.42
1:A:32:LEU:HD23	1:A:32:LEU:HA	1.90	0.42
1:C:199:ASN:HA	1:C:202:TYR:OH	2.19	0.42
1:A:281:ARG:HG2	1:A:282:VAL:N	2.35	0.42
1:B:267:GLU:HB3	1:B:283:TYR:CZ	2.54	0.42
1:B:192:LYS:O	1:B:195:GLU:HG3	2.20	0.41
1:A:117:TRP:C	1:A:119:ASP:H	2.29	0.41
1:A:164:ASN:OD1	1:A:164:ASN:N	2.53	0.41
1:A:272:GLY:O	1:A:279:PRO:HD2	2.20	0.41
1:A:304:GLU:H	1:A:304:GLU:HG3	1.59	0.41
1:A:284:GLU:HG2	1:A:285:THR:N	2.36	0.41
1:B:22:GLN:HA	1:B:25:ILE:HG12	2.03	0.41
1:B:112:ASP:N	1:B:112:ASP:OD1	2.53	0.41
1:C:33:VAL:HG23	1:C:36:ARG:NH1	2.36	0.41
1:C:171:HIS:O	1:C:300:ILE:HG22	2.20	0.40
1:C:233:ILE:HG22	1:C:235:ALA:H	1.85	0.40
1:A:2:ASN:HB2	1:A:5:GLN:NE2	2.37	0.40

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	274/316 (87%)	266 (97%)	8 (3%)	0	100	100
1	B	275/316 (87%)	264 (96%)	11 (4%)	0	100	100
1	C	274/316 (87%)	262 (96%)	12 (4%)	0	100	100
1	D	275/316 (87%)	258 (94%)	17 (6%)	0	100	100
All	All	1098/1264 (87%)	1050 (96%)	48 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	244/262 (93%)	235 (96%)	9 (4%)	30	56
1	B	244/262 (93%)	235 (96%)	9 (4%)	30	56
1	C	244/262 (93%)	233 (96%)	11 (4%)	24	51
1	D	244/262 (93%)	231 (95%)	13 (5%)	20	47
All	All	976/1048 (93%)	934 (96%)	42 (4%)	27	52

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	LYS
1	A	137	ASN
1	A	155	LYS
1	A	156	GLU
1	A	234	THR
1	A	256	ASN
1	A	258	LEU
1	A	301	ASP
1	A	304	GLU
1	B	17	PHE
1	B	22	GLN
1	B	117	TRP
1	B	128	ILE

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Mol	Chain	Res	Type
1	B	172	LEU
1	B	234	THR
1	B	250	ILE
1	B	262	ILE
1	B	274	GLU
1	C	17	PHE
1	C	88	PHE
1	C	92	PHE
1	C	96	VAL
1	C	145	LEU
1	C	162	LEU
1	C	194	LEU
1	C	238	PHE
1	C	250	ILE
1	C	256	ASN
1	C	304	GLU
1	D	3	LYS
1	D	17	PHE
1	D	85	LYS
1	D	89	GLN
1	D	130	ILE
1	D	155	LYS
1	D	156	GLU
1	D	234	THR
1	D	237	VAL
1	D	260	LEU
1	D	274	GLU
1	D	291	LYS
1	D	303	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	53	ASN
1	A	152	HIS
1	A	199	ASN
1	B	2	ASN
1	B	199	ASN
1	C	53	ASN
1	C	198	HIS
1	C	218	HIS

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Mol	Chain	Res	Type
1	D	103	ASN
1	D	184	GLN
1	D	252	ASN

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 oligosaccharides 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.

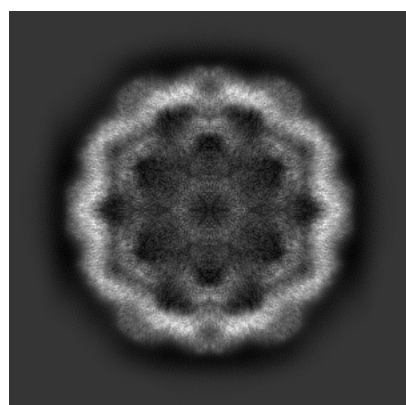
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23834. These allow visual inspection of the internal detail of the map and identification of artifacts.

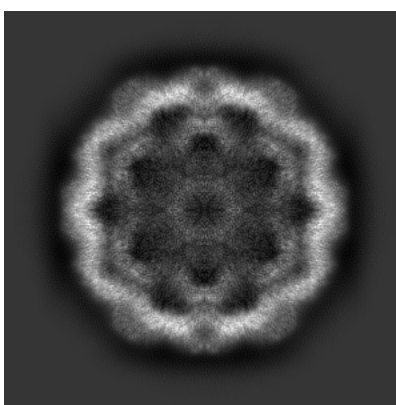
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

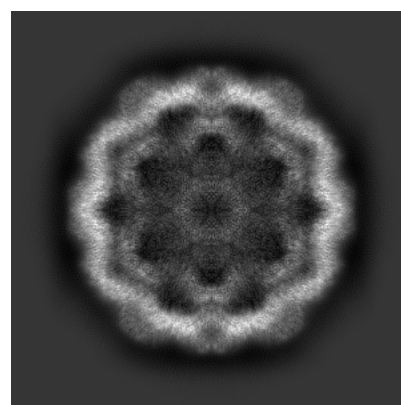
6.1.1 Primary map



X



Y

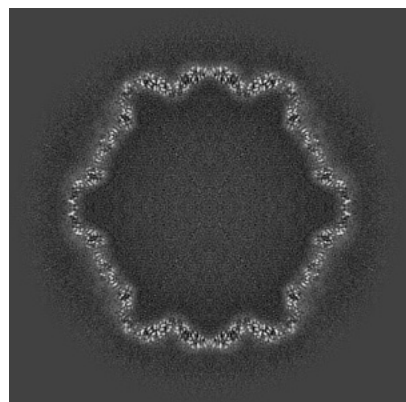


Z

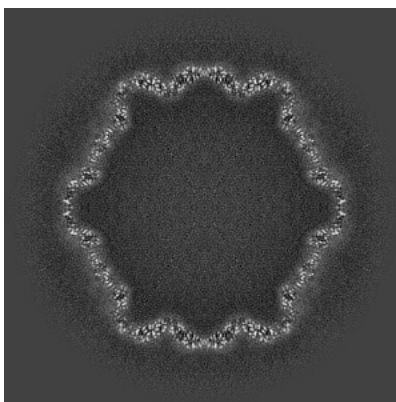
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

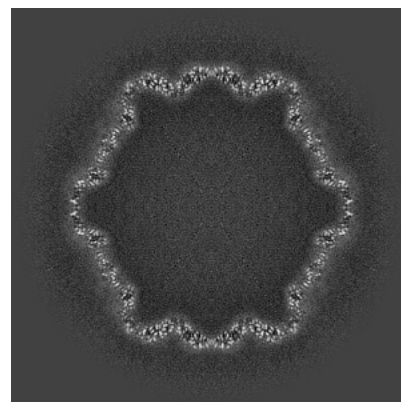
6.2.1 Primary map



X Index: 220



Y Index: 220

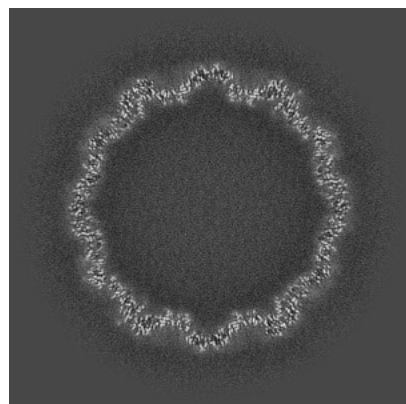


Z Index: 220

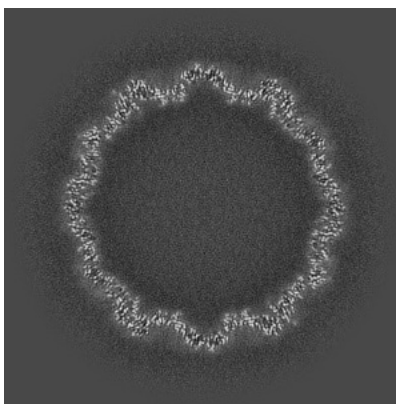
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

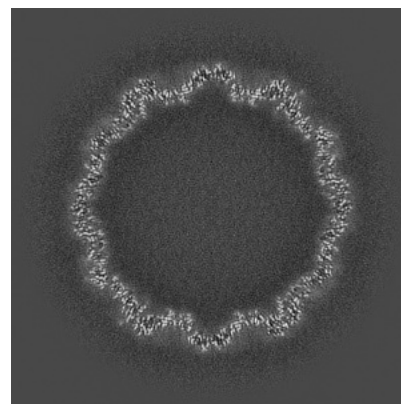
6.3.1 Primary map



X Index: 239



Y Index: 201

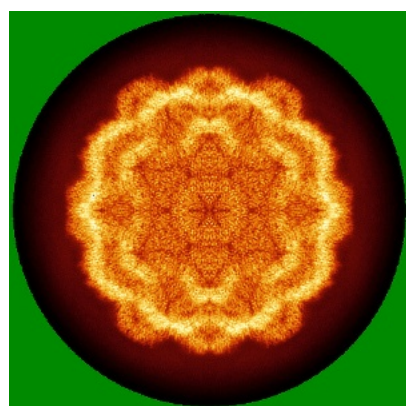


Z Index: 239

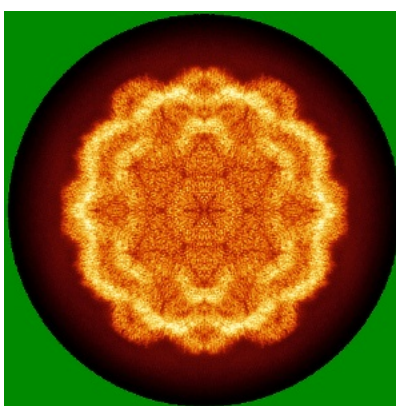
The images above show the largest variance slices of the map in three orthogonal directions.

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

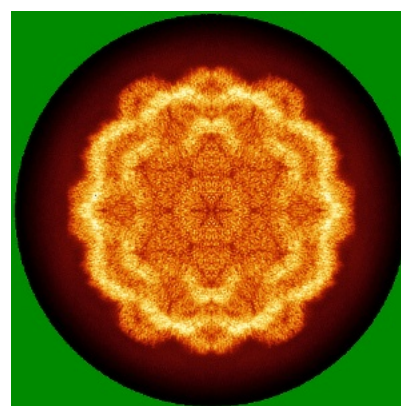
6.4.1 Primary map



X



Y

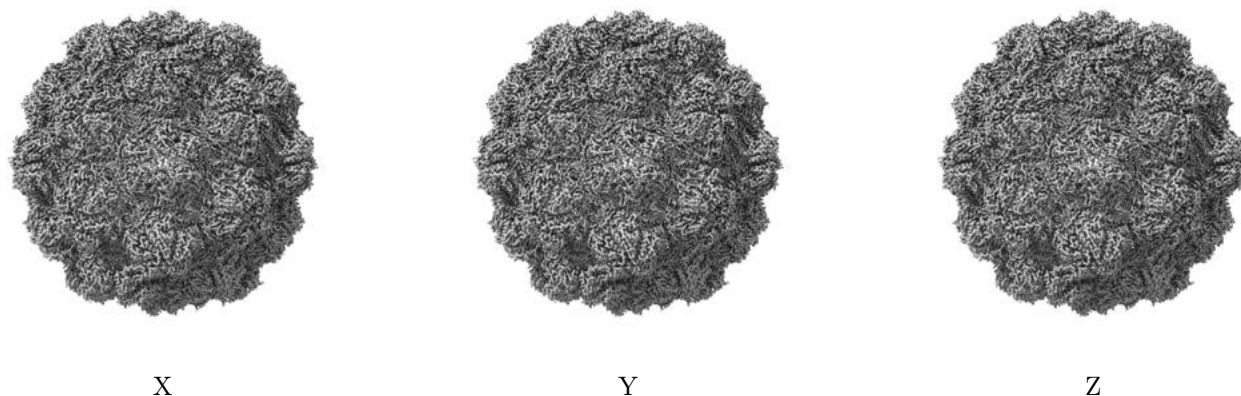


Z

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

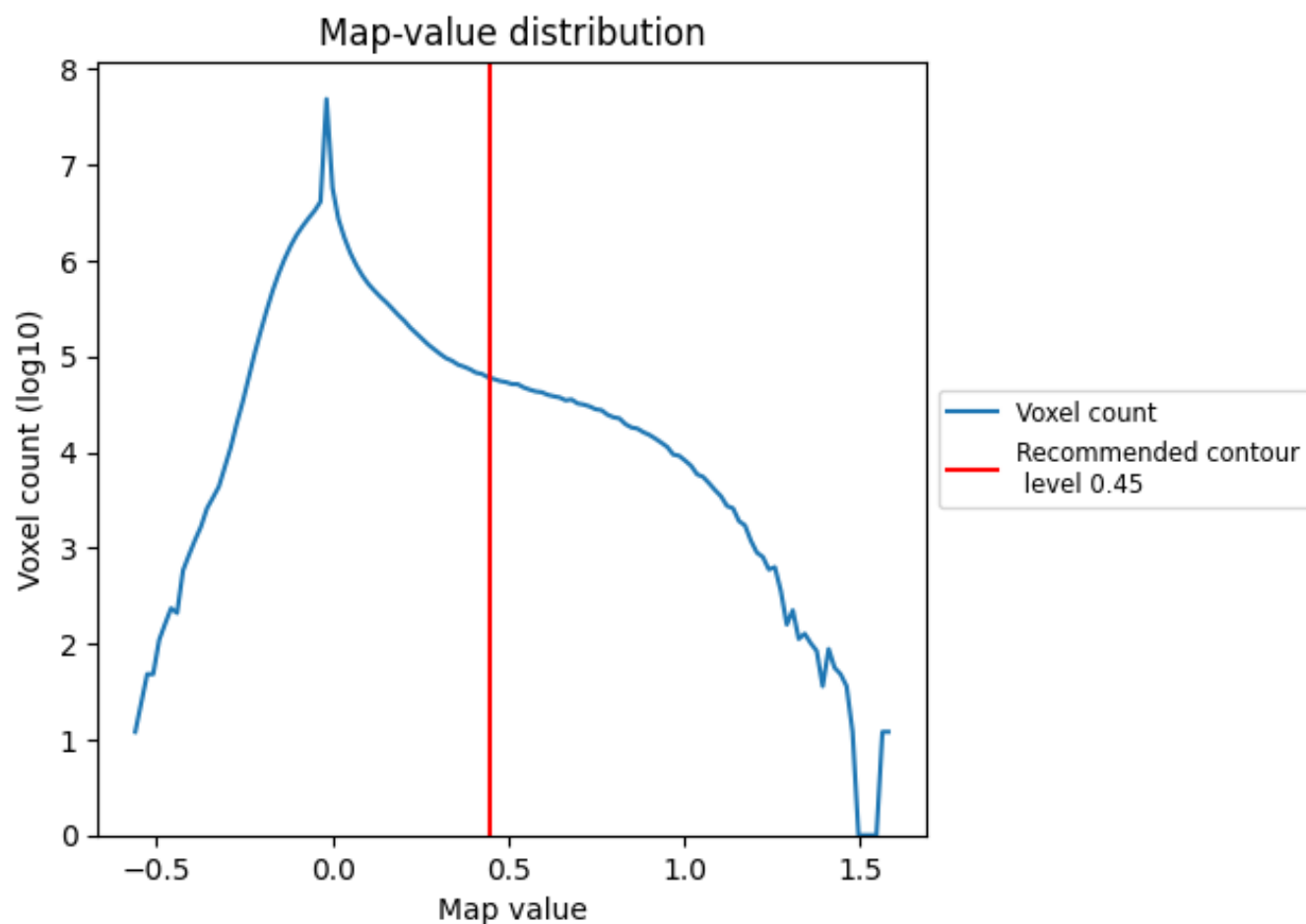
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

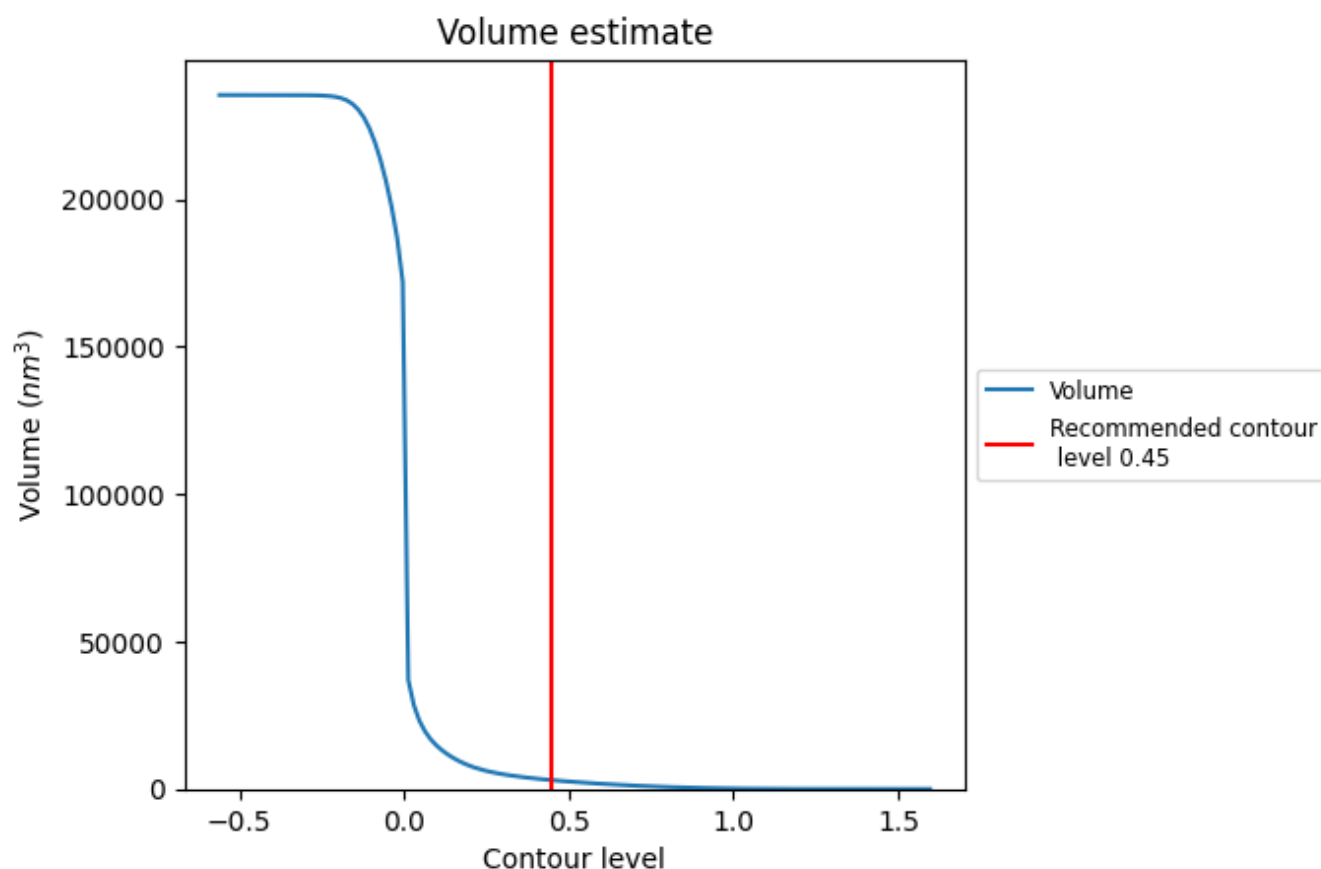
This section contains the results of statistical analysis of the map.

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.

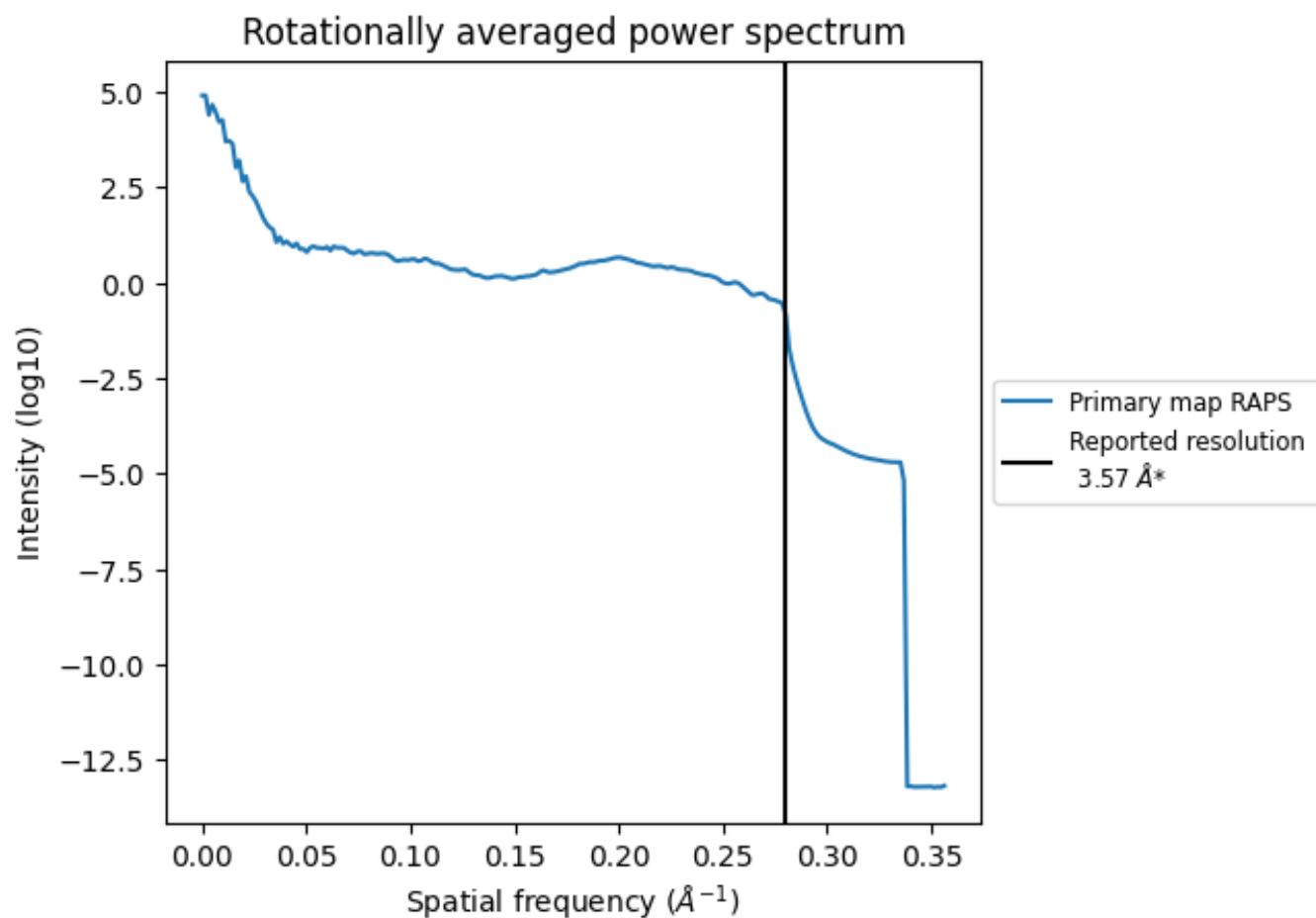
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2977 nm³; this corresponds to an approximate mass of 2689 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 0.280 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

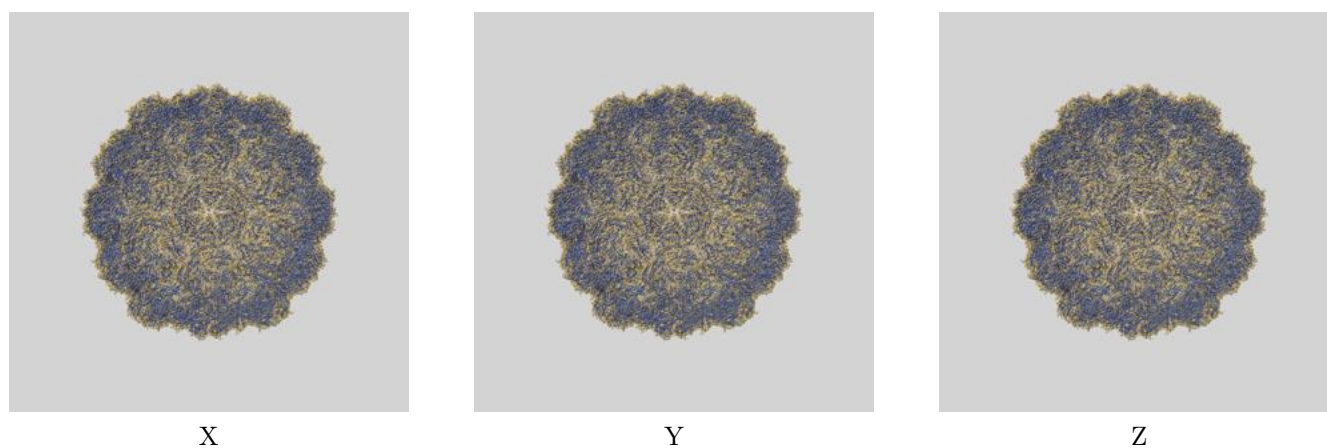
This section contains information regarding the fit between EMDB map EMD-23834 and PDB model 7MH2. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

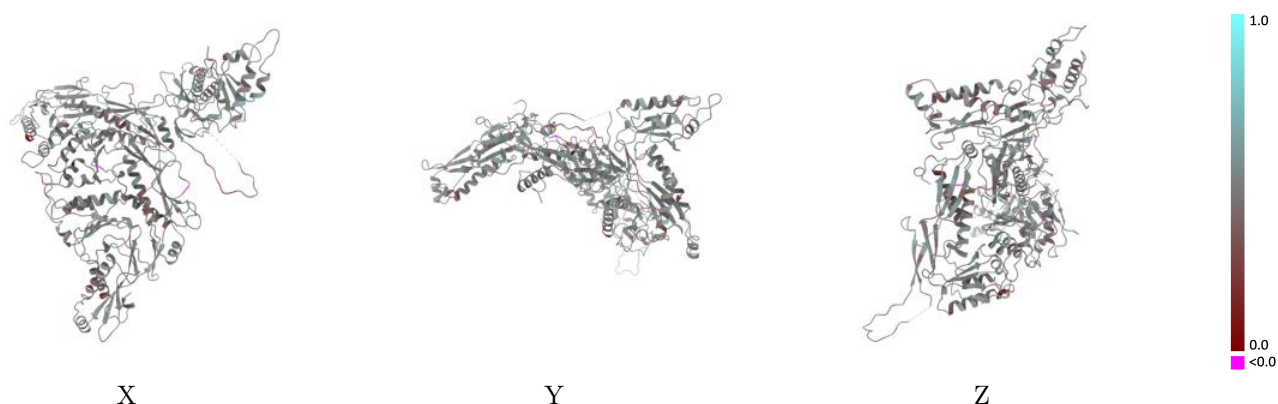


9.1.2 Map-model assembly overlay [i](#)



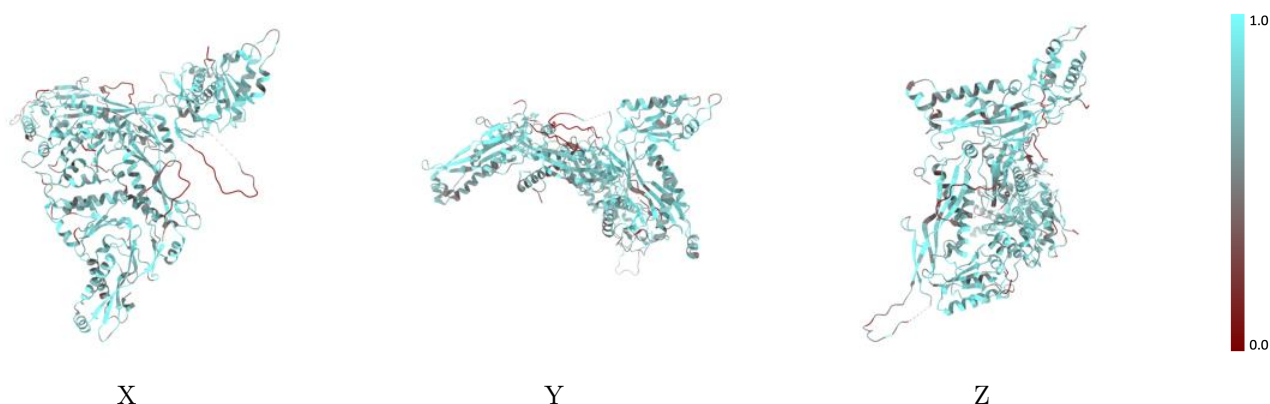
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



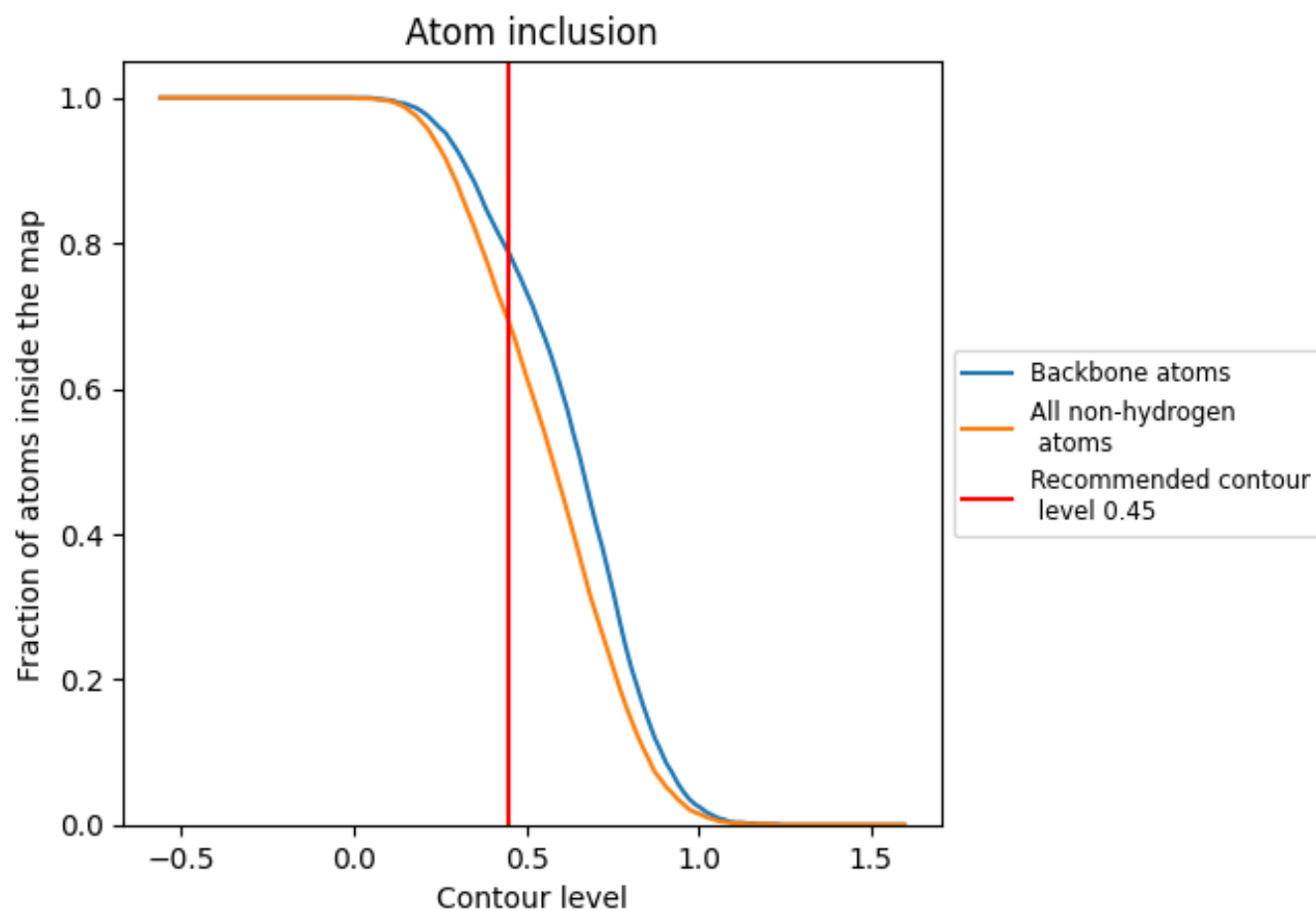
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 69% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6910	0.4720
A	0.6930	0.4770
B	0.6880	0.4680
C	0.6730	0.4670
D	0.7110	0.4750

