



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:51 PM UTC

PDB ID : 7NJV / pdb_00007njv
EMDB ID : EMD-12424
Title : Mycobacterium smegmatis ATP synthase Fo combined class 2
Authors : Montgomery, M.G.; Petri, J.; Spikes, T.E.; Walker, J.E.
Deposited on : 2021-02-17
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:

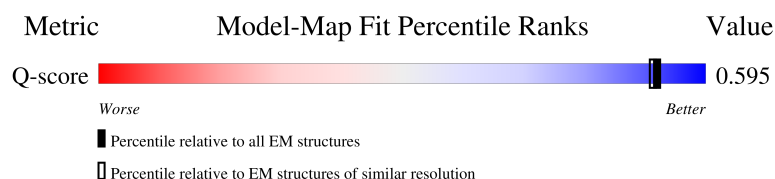
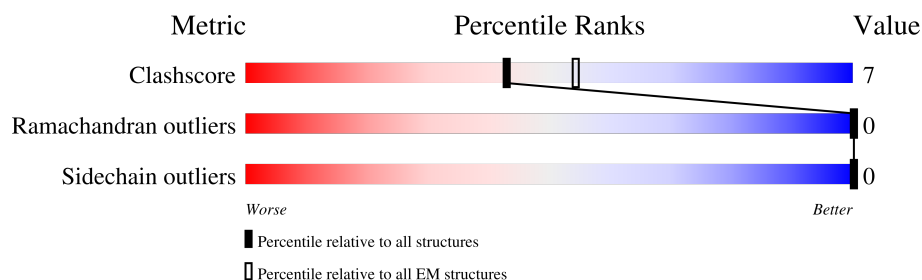
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 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	-
Sidechain outliers	223484	23102	-
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	L	86	 79% 19%
1	M	86	 77% 21%
1	N	86	 86% 12%
1	O	86	 85% 13%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	P	86	
1	Q	86	
1	R	86	
1	S	86	
1	T	86	
2	a	252	
3	b	180	
4	d	445	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 16494 atoms, of which 8368 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 ATP synthase subunit c.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	L	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
1	M	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
1	N	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
1	O	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
1	P	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
1	Q	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
1	R	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
1	S	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		
1	T	84	Total	C	H	N	O	S	0	0
			1192	387	603	96	104	2		

- Molecule 2 is a protein called ATP synthase subunit a.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	a	238	Total	C	H	N	O	S	0	0
			3767	1252	1916	292	301	6		

- Molecule 3 is a protein called ATP synthase subunit b.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	b	63	Total	C	H	N	O	S	0	0
			979	312	503	79	84	1		

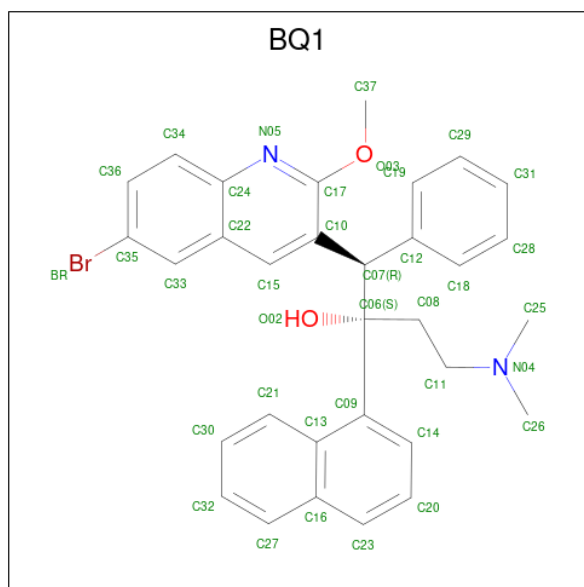
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	171	HIS	-	expression tag	UNP A0R204
b	172	HIS	-	expression tag	UNP A0R204
b	173	HIS	-	expression tag	UNP A0R204
b	174	HIS	-	expression tag	UNP A0R204
b	175	HIS	-	expression tag	UNP A0R204
b	176	HIS	-	expression tag	UNP A0R204
b	177	HIS	-	expression tag	UNP A0R204
b	178	HIS	-	expression tag	UNP A0R204
b	179	HIS	-	expression tag	UNP A0R204
b	180	HIS	-	expression tag	UNP A0R204

- Molecule 4 is a protein called ATP synthase subunit b-delta.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	d	61	Total	C	H	N	O	S	0	0
			952	299	491	81	78	3		

- Molecule 5 is Bedaquiline (CCD ID: BQ1) (formula: $C_{32}H_{31}BrN_2O_2$) (labeled as "Ligand of Interest" by depositor).

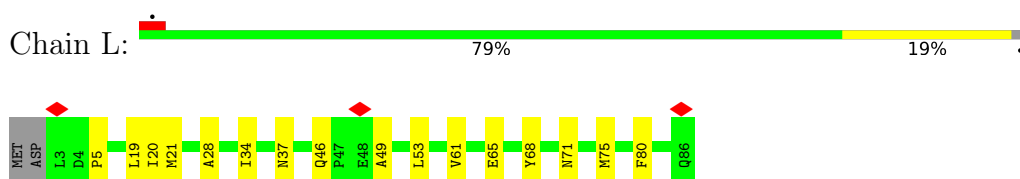


Mol	Chain	Residues	Atoms						AltConf
5	N	1	Total	Br	C	H	N	O	0
			68	1	32	31	2	2	

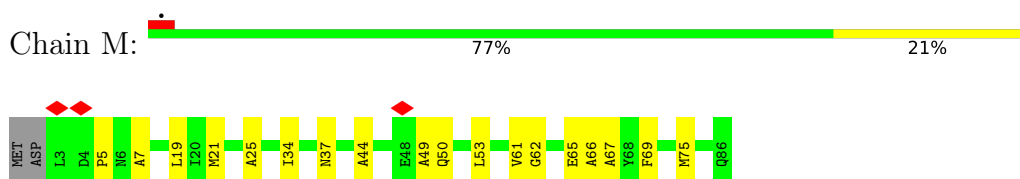
3 Residue-property plots [i](#)

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.

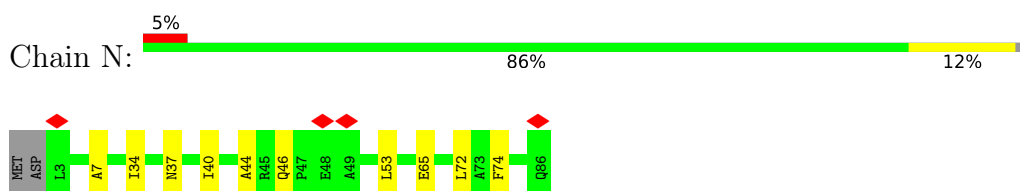
- Molecule 1: ATP synthase subunit c



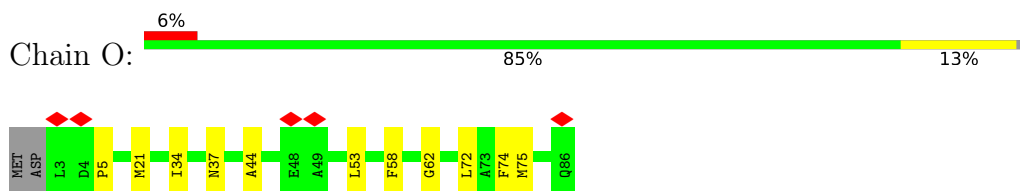
- Molecule 1: ATP synthase subunit c



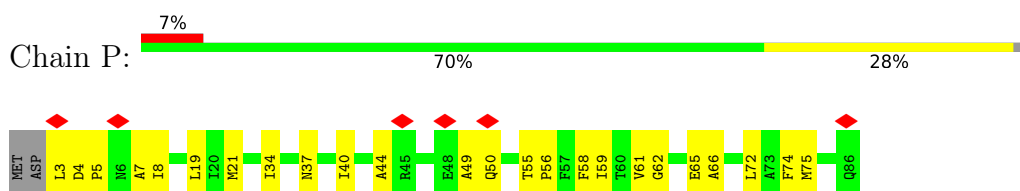
- Molecule 1: ATP synthase subunit c



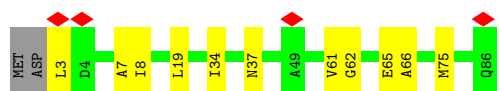
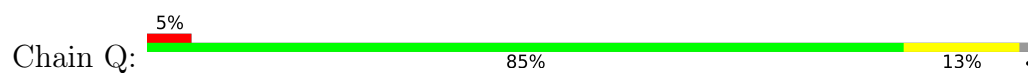
- Molecule 1: ATP synthase subunit c



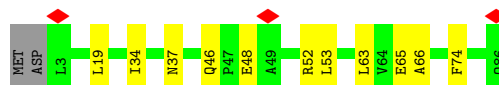
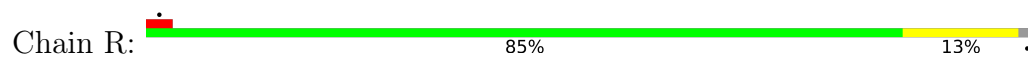
- Molecule 1: ATP synthase subunit c



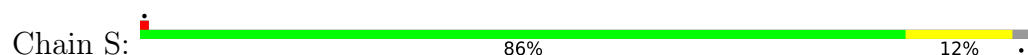
- Molecule 1: ATP synthase subunit c



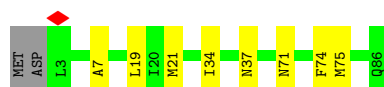
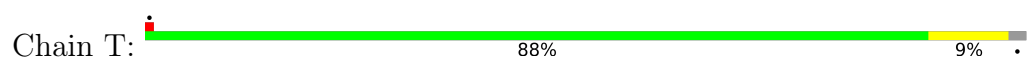
- Molecule 1: ATP synthase subunit c



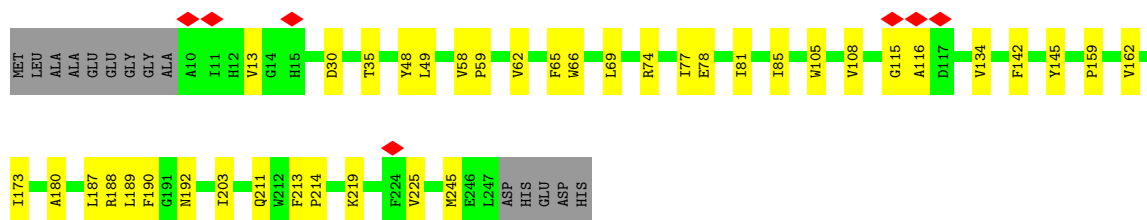
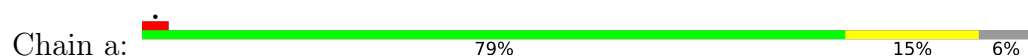
- Molecule 1: ATP synthase subunit c



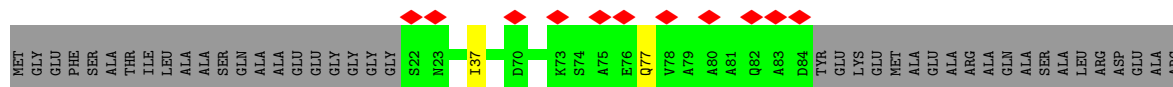
- Molecule 1: ATP synthase subunit c



- Molecule 2: ATP synthase subunit a



- Molecule 3: ATP synthase subunit b



ASN
SER
GLY
GLY
THR
GLN
HIS
HIS
HIS
HIS
HIS
HIS
HIS
HIS
HIS
HIS

- Molecule 4: ATP synthase subunit b-delta



H1	I14	R31	V37	A42	A45	E46	K49	X50	L51	A52	D53	A54	D55	A56	M57	H58	A59	K60	A61	LEU	ALA	ASP	ALA	LYS	ALA	ALA	GLU	SER	GLU	LYS	VAL	THR	GLU	GLU	ALA	LYS	GLN	ASP	SER	SER	GLU	ARG	TLE	ALA	ALA	GLN	LEU	SER	GLU	GLN	ALA	GLY	SER	GLU
----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLU	ARG	ILE	LYS	ALA	GLN	GLY	ALA	GLN	ILE	GLN	LEU	MET	ARG	ARG	GLN	GLN	LEU	ILE	ARG	THR	GLY	LEU	GLY	ALA	GLU	GLU	GLU	ILE	VAL	ASN	LYS	ALA	ALA	VAL	ASP	ALA	PRO	ARG	ARG	HIS	ALA	VAL	VAL	THR	ALA	SER	GLN	ALA	GLN	ARG	PHE	LEU	LEU	SER	GLU	LEU	ILE
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

[illegible][illegible]

ARG	LEU	ALA	ALA	LEU	LEU	LYS	ARG	ALA	ALA	GLU	VAL	ASP	GLU	VAL	GLU	GLN	LEU	PHE	ARG	PHE	GLY	ARG	VAL	LEU	ASP	ALA	GLU	PRO	ARG	LEU	SER	LEU	ALA	LEU	SER	SER	THR	THR	PRO	ALA	GLU	GLY	GLY	ARG	VAL	LYS	LEU	LEU	THR	GLY	ARG	PRO
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLY VAL ASN ASN GLN THR ALA ALA ALA LEU LEU SER SER GLN THR VAL GLY GLU LEU LEU ARG GLY GLU GLU ASP ASP ASP ASP LEU LEU VAL VAL VAL VAL VAL HIS VAL SER SER ALA ALA ALA GLU LEU SER ASP ALA ALA GLN ARG THR ARG LEU THR

VAL	LEU	SER	ARG	ILE	TYR	GLY	ARG	PRO	VAL	SER	VAL	GLN	LEU	HIS	VAL	ASP	GLU	LEU	LEU	GLY	GLY	SER	ILE	THR	VAL	GLY	ASP	GLU	VAL	ILE	ASP	GLY	SER	ILE	ALA	SER	ARG	LEU	ALA	ALA	ALA	GLN	THR	GLY	LEU	PRO	ASP
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	46961	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 ($e^-/\text{\AA}^2$)	59.86	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.074	Depositor
Minimum map value	-0.030	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	415.0, 415.0, 415.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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: BQ1

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	L	0.13	0/600	0.26	0/814
1	M	0.14	0/600	0.29	0/814
1	N	0.13	0/600	0.27	0/814
1	O	0.13	0/600	0.27	0/814
1	P	0.15	0/600	0.31	0/814
1	Q	0.13	0/600	0.25	0/814
1	R	0.13	0/600	0.26	0/814
1	S	0.12	0/600	0.24	0/814
1	T	0.13	0/600	0.25	0/814
2	a	0.11	0/1905	0.27	0/2602
3	b	0.13	0/484	0.29	0/658
4	d	0.12	0/468	0.26	0/632
All	All	0.13	0/8257	0.27	0/11218

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	L	589	603	603	18	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	M	589	603	603	16	0
1	N	589	603	603	12	0
1	O	589	603	603	12	0
1	P	589	603	603	20	0
1	Q	589	603	603	9	0
1	R	589	603	603	10	0
1	S	589	603	603	12	0
1	T	589	603	603	13	0
2	a	1851	1916	1916	27	0
3	b	476	503	503	2	0
4	d	461	491	491	5	0
5	N	37	31	31	3	0
All	All	8126	8368	8368	108	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 7.

The worst 5 of 108 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:R:46:GLN:NE2	1:R:48:GLU:OE2	2.18	0.77
1:N:65:GLU:OE1	5:N:101:BQ1:N04	2.26	0.69
1:R:53:LEU:HD21	1:S:44:ALA:HB2	1.76	0.66
1:P:74:PHE:CE1	1:Q:75:MET:HE1	2.33	0.64
1:L:21:MET:HG3	1:L:75:MET:HE2	1.80	0.63

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	L	82/86 (95%)	82 (100%)	0	0	100	100
1	M	82/86 (95%)	78 (95%)	4 (5%)	0	100	100
1	N	82/86 (95%)	79 (96%)	3 (4%)	0	100	100
1	O	82/86 (95%)	81 (99%)	1 (1%)	0	100	100
1	P	82/86 (95%)	80 (98%)	2 (2%)	0	100	100
1	Q	82/86 (95%)	78 (95%)	4 (5%)	0	100	100
1	R	82/86 (95%)	81 (99%)	1 (1%)	0	100	100
1	S	82/86 (95%)	81 (99%)	1 (1%)	0	100	100
1	T	82/86 (95%)	80 (98%)	2 (2%)	0	100	100
2	a	236/252 (94%)	232 (98%)	4 (2%)	0	100	100
3	b	61/180 (34%)	57 (93%)	4 (7%)	0	100	100
4	d	59/445 (13%)	58 (98%)	1 (2%)	0	100	100
All	All	1094/1651 (66%)	1067 (98%)	27 (2%)	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	L	54/56 (96%)	54 (100%)	0	100	100
1	M	54/56 (96%)	54 (100%)	0	100	100
1	N	54/56 (96%)	54 (100%)	0	100	100
1	O	54/56 (96%)	54 (100%)	0	100	100
1	P	54/56 (96%)	54 (100%)	0	100	100
1	Q	54/56 (96%)	54 (100%)	0	100	100
1	R	54/56 (96%)	54 (100%)	0	100	100
1	S	54/56 (96%)	54 (100%)	0	100	100
1	T	54/56 (96%)	54 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	a	191/200 (96%)	191 (100%)	0	100	100
3	b	50/134 (37%)	50 (100%)	0	100	100
4	d	45/347 (13%)	45 (100%)	0	100	100
All	All	772/1185 (65%)	772 (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. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	86	GLN
1	T	46	GLN
1	T	71	ASN
2	a	192	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](#)

1 ligand is modelled in this entry.

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	BQ1	N	101	-	41,41,41	1.36	6 (14%)	58,59,59	5.88	16 (27%)

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	BQ1	N	101	-	-	4/28/28/28	0/5/5/5

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	N	101	BQ1	O03-C17	3.50	1.40	1.35
5	N	101	BQ1	C06-C07	-3.24	1.53	1.57
5	N	101	BQ1	C22-C24	-3.00	1.37	1.42
5	N	101	BQ1	C13-C16	-2.70	1.38	1.43
5	N	101	BQ1	C17-N05	2.48	1.35	1.30

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	N	101	BQ1	C14-C09-C06	-26.96	106.61	117.96
5	N	101	BQ1	O03-C17-C10	19.94	138.72	115.05
5	N	101	BQ1	C06-C09-C13	19.02	134.30	123.76
5	N	101	BQ1	O03-C17-N05	-14.59	101.21	119.93
5	N	101	BQ1	C17-C10-C07	-8.81	108.06	119.77

There are no chirality outliers.

All (4) torsion outliers are listed below:

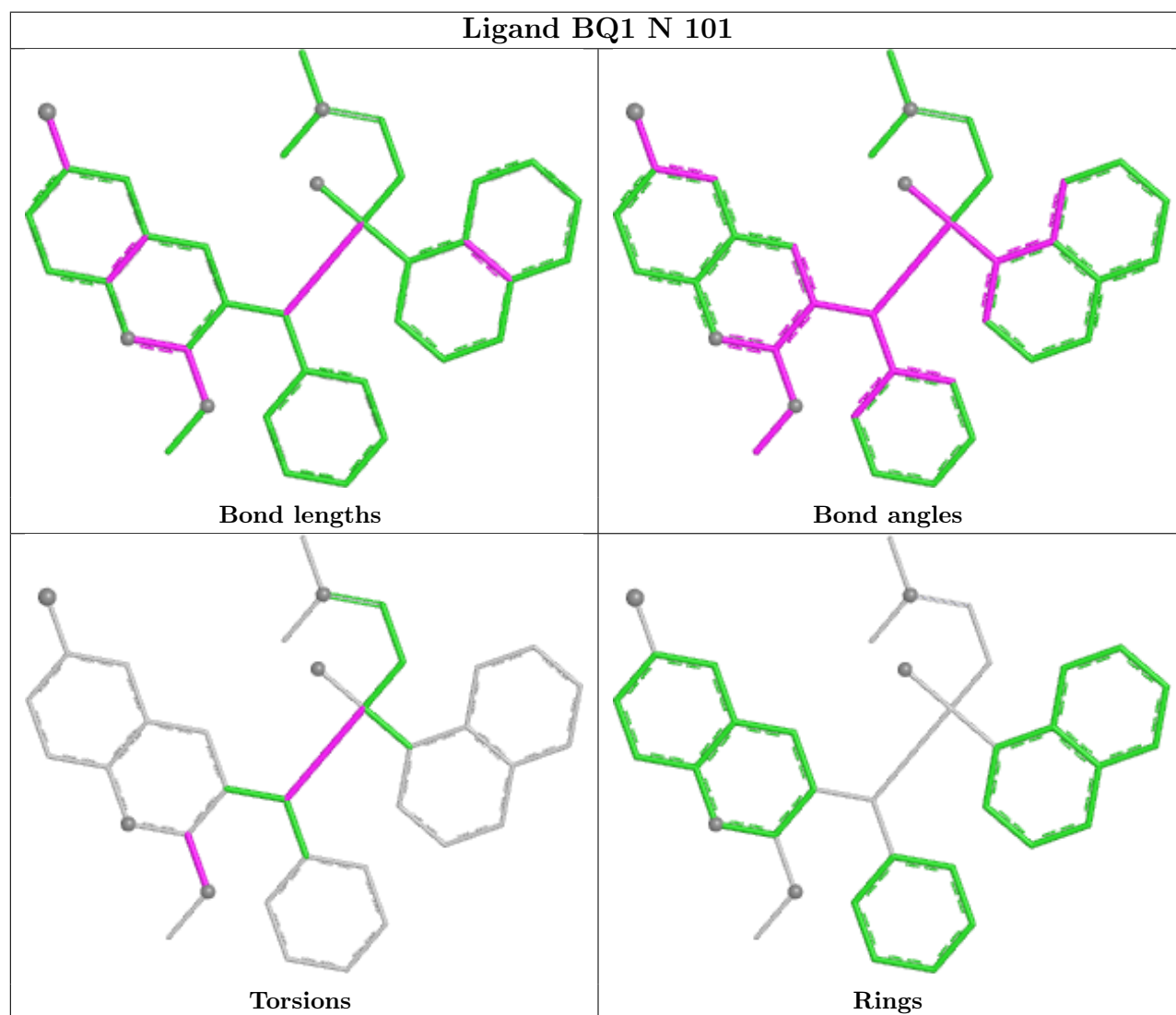
Mol	Chain	Res	Type	Atoms
5	N	101	BQ1	N05-C17-O03-C37
5	N	101	BQ1	C10-C17-O03-C37
5	N	101	BQ1	O02-C06-C07-C10
5	N	101	BQ1	C08-C06-C07-C10

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	N	101	BQ1	3	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

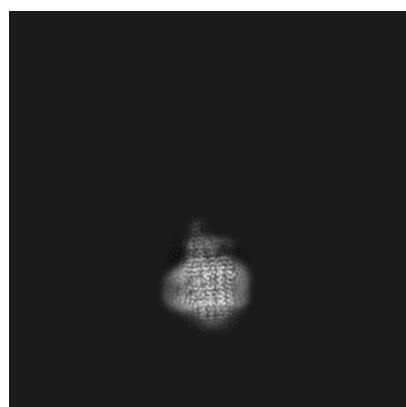
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12424. These allow visual inspection of the internal detail of the map and identification of artifacts.

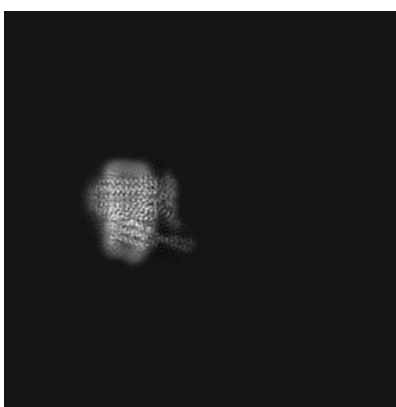
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

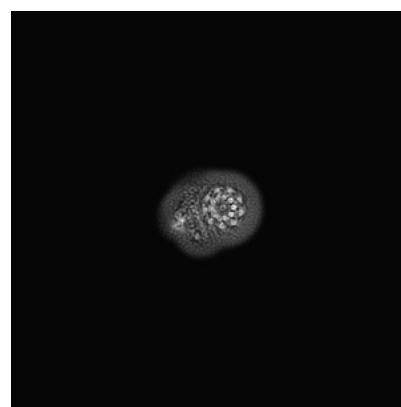
6.1.1 Primary map



X



Y

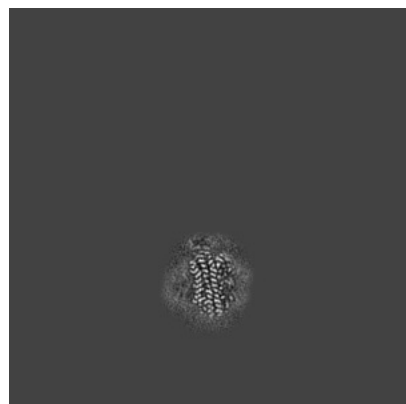


Z

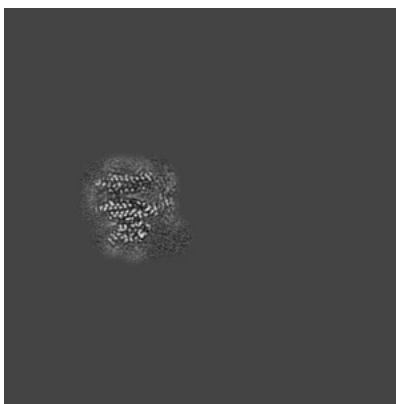
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

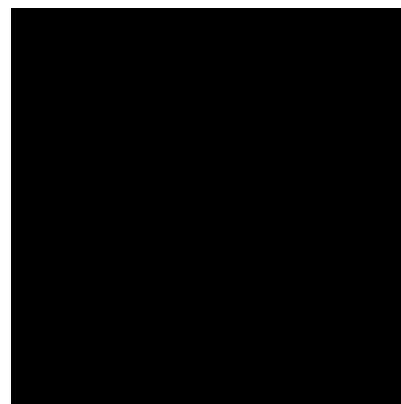
6.2.1 Primary map



X Index: 250



Y Index: 250

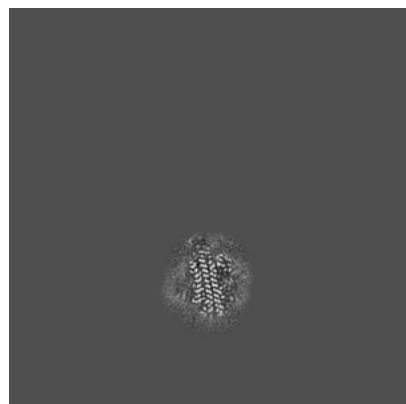


Z Index: 250

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

6.3 Largest variance slices [i](#)

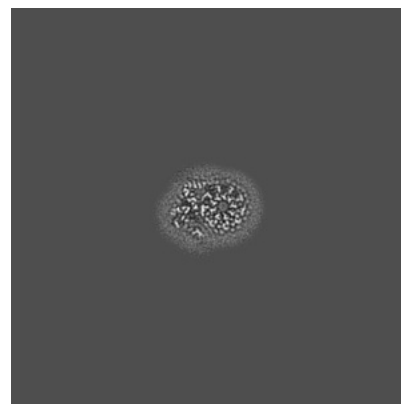
6.3.1 Primary map



X Index: 251



Y Index: 243

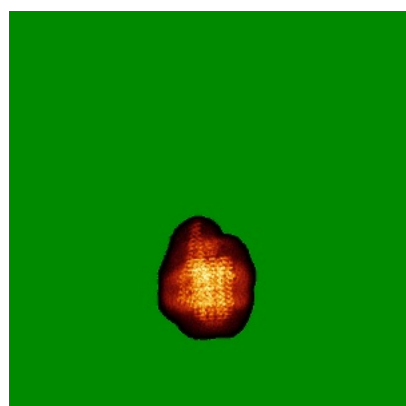


Z Index: 170

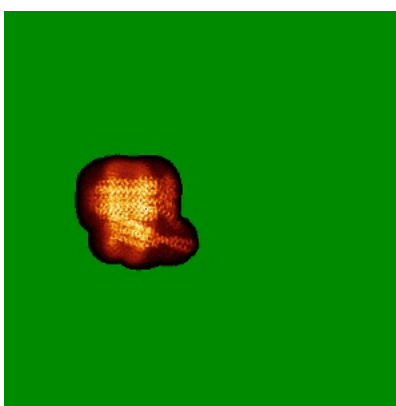
The images above show the largest variance slices of the map in three orthogonal directions.

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

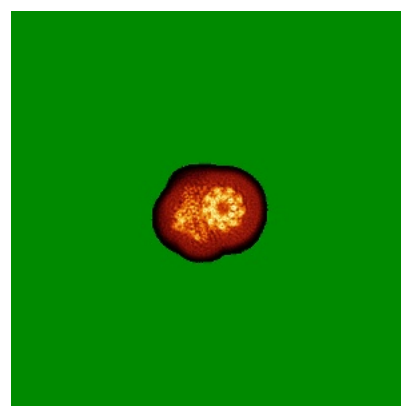
6.4.1 Primary map



X



Y

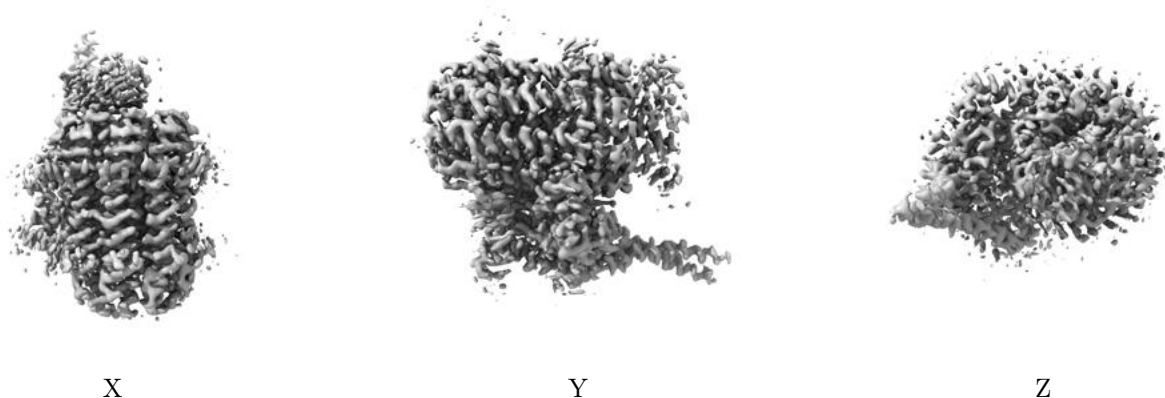


Z

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

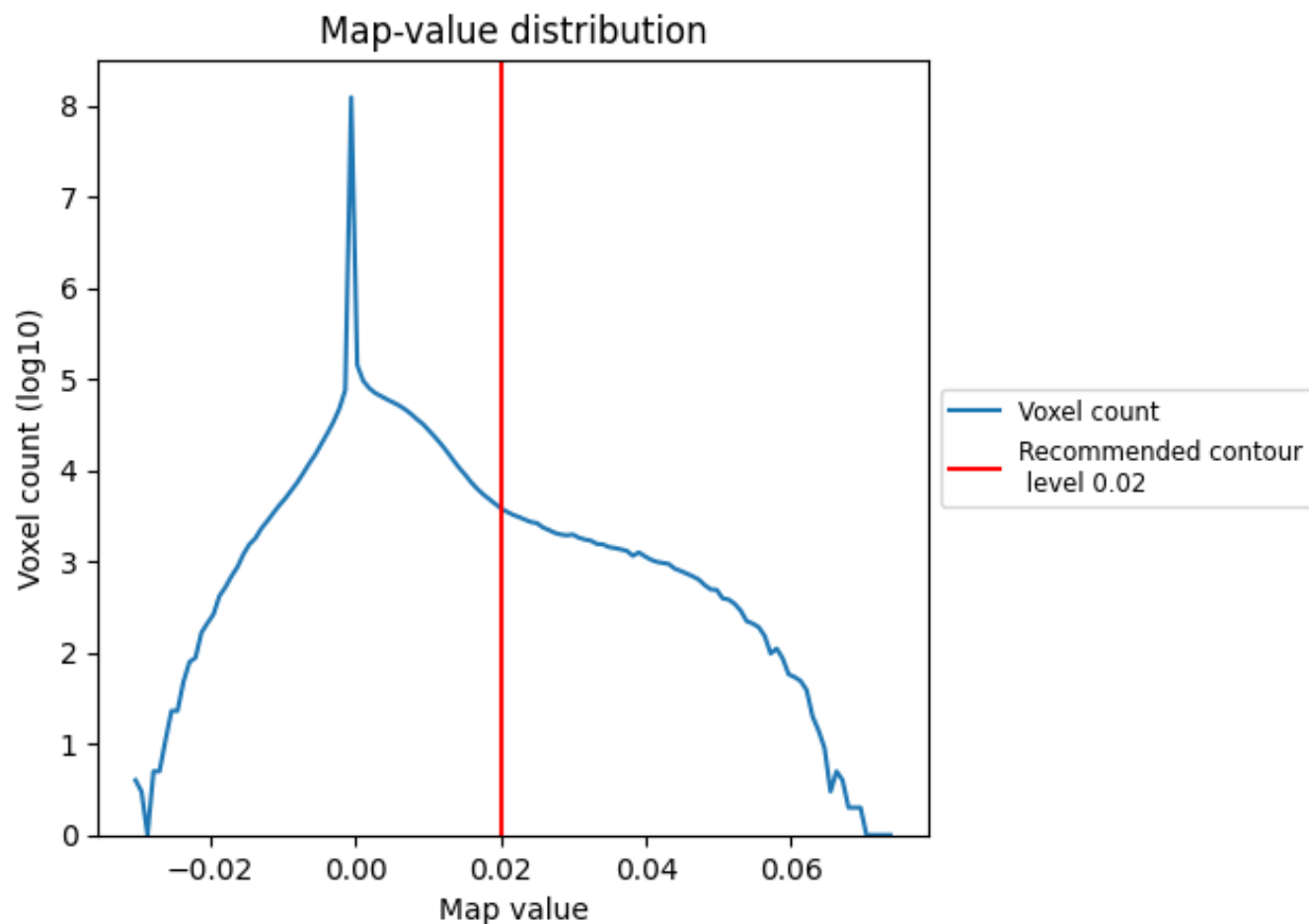
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

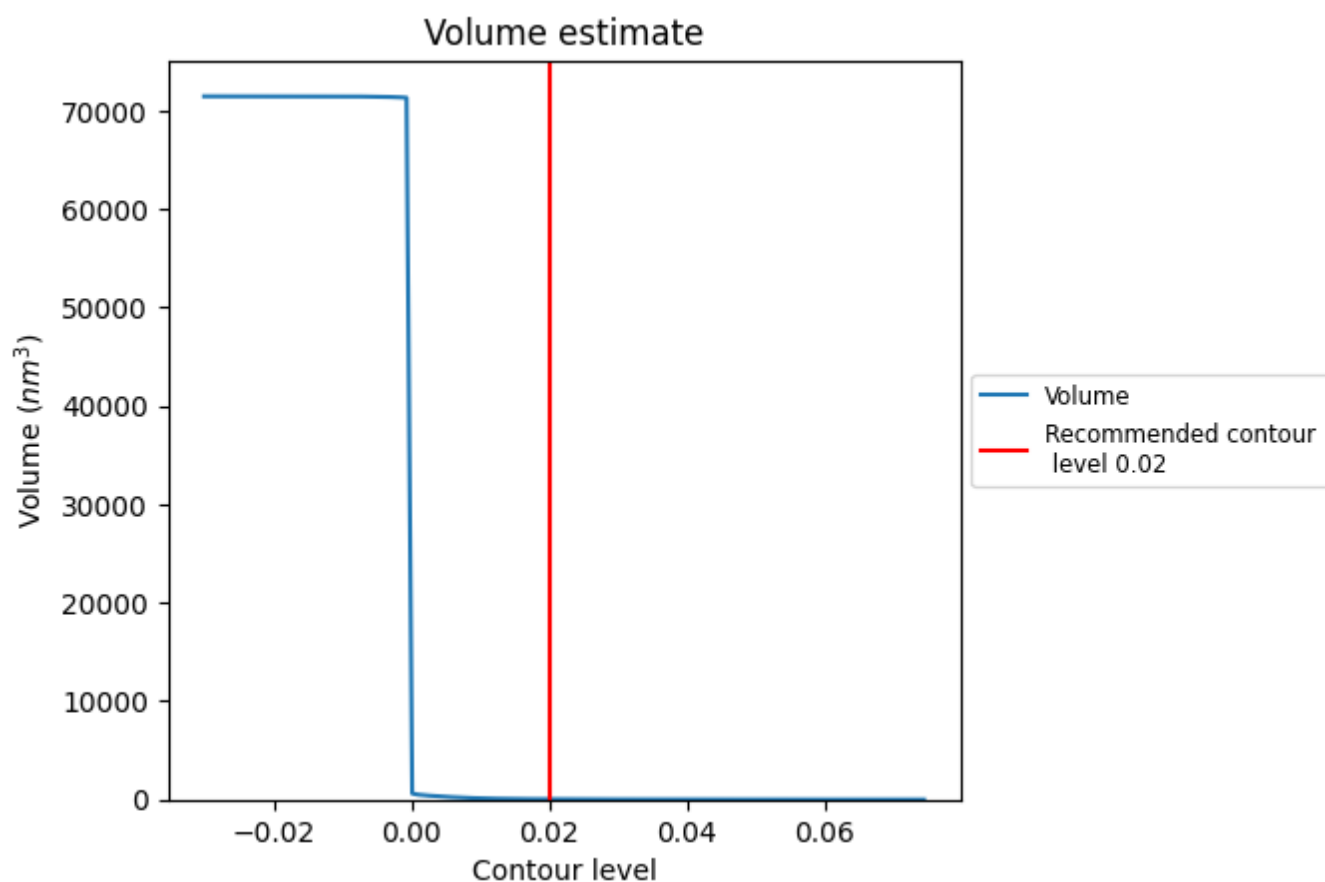
This section contains the results of statistical analysis of the map.

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.

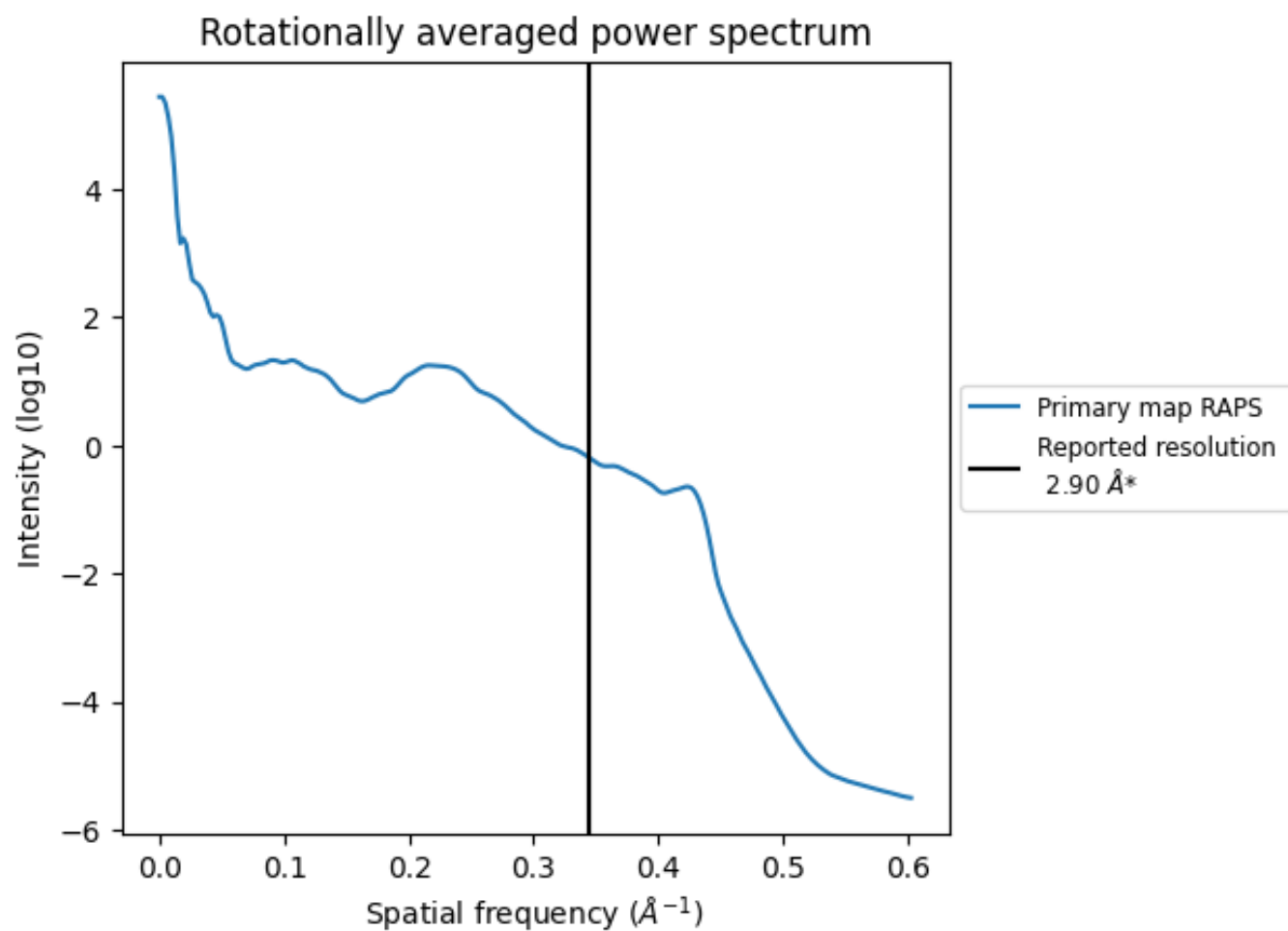
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 37 nm³; this corresponds to an approximate mass of 33 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 ⓘ

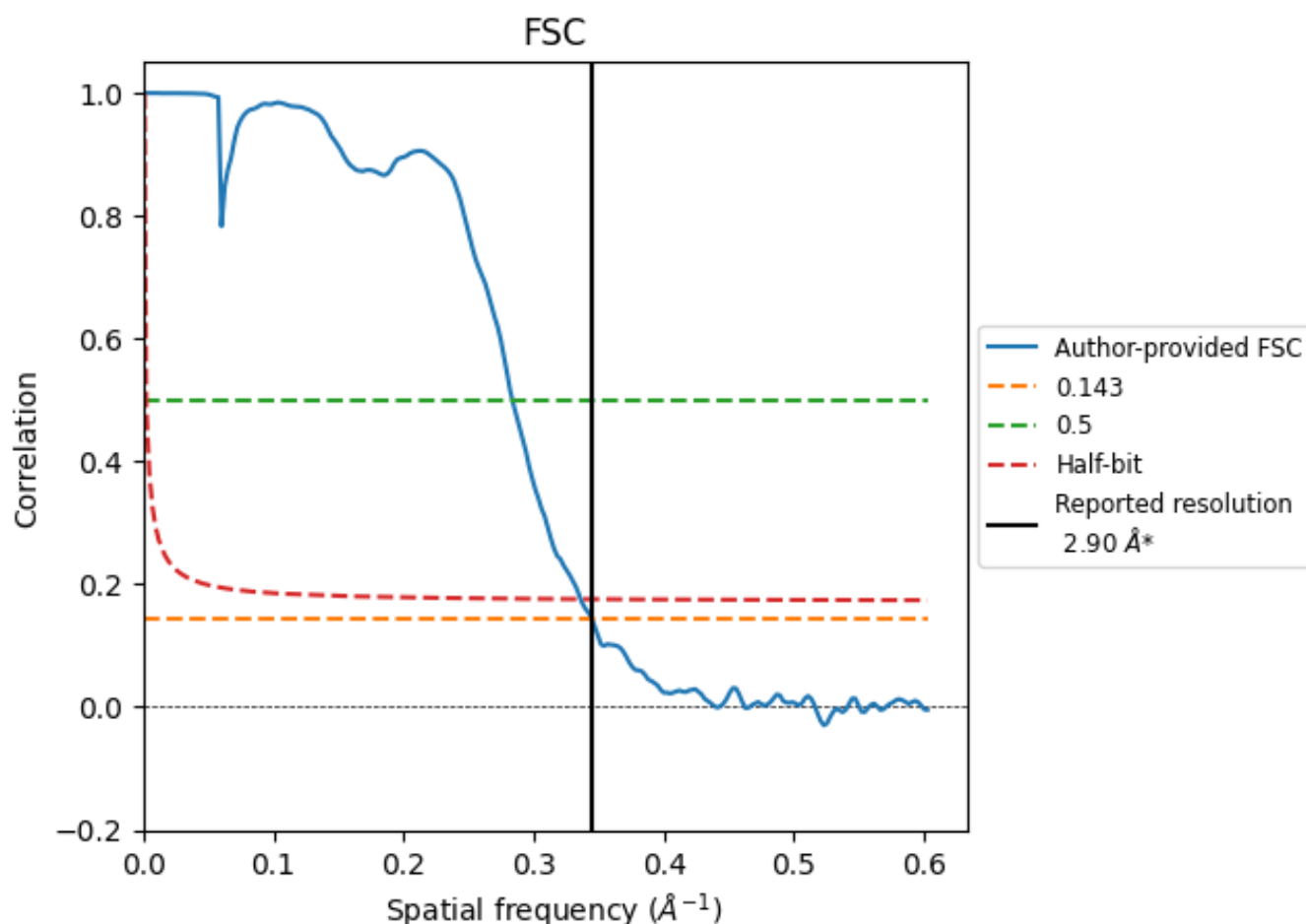


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

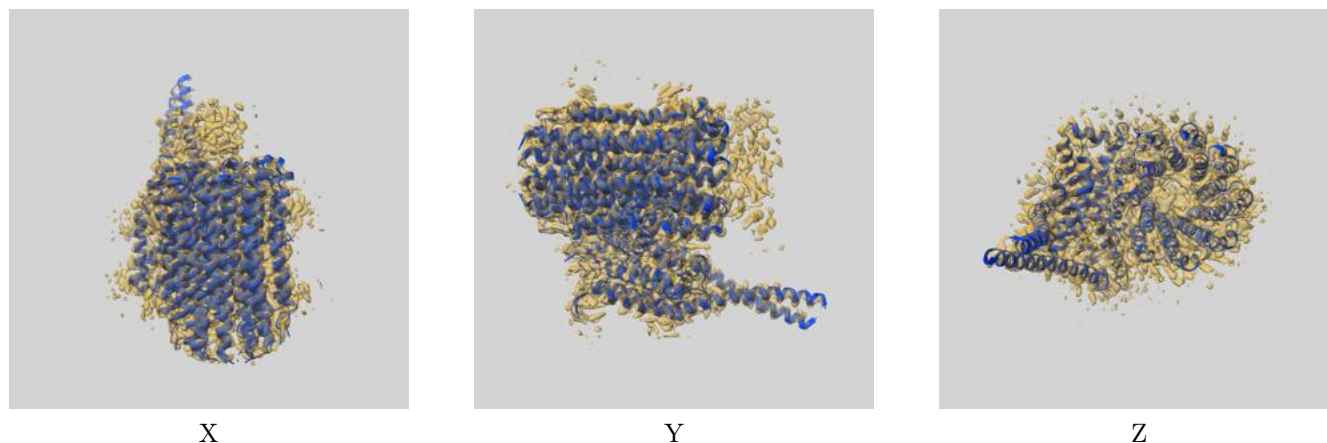
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.90	3.52	2.98
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

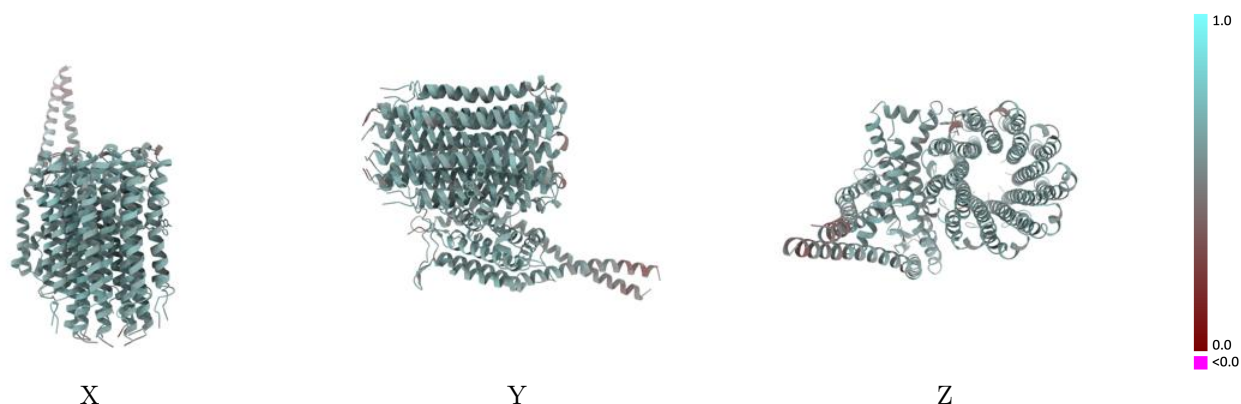
This section contains information regarding the fit between EMDB map EMD-12424 and PDB model 7NJV. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



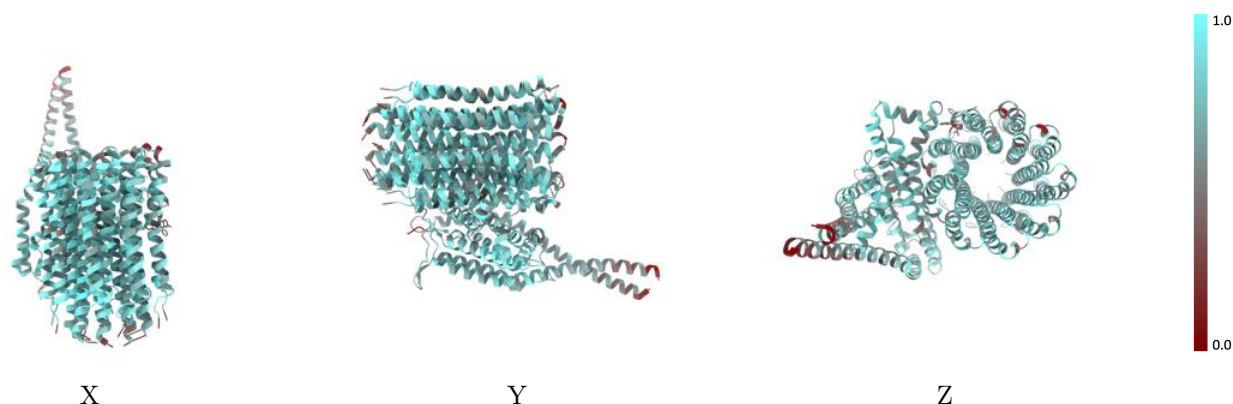
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



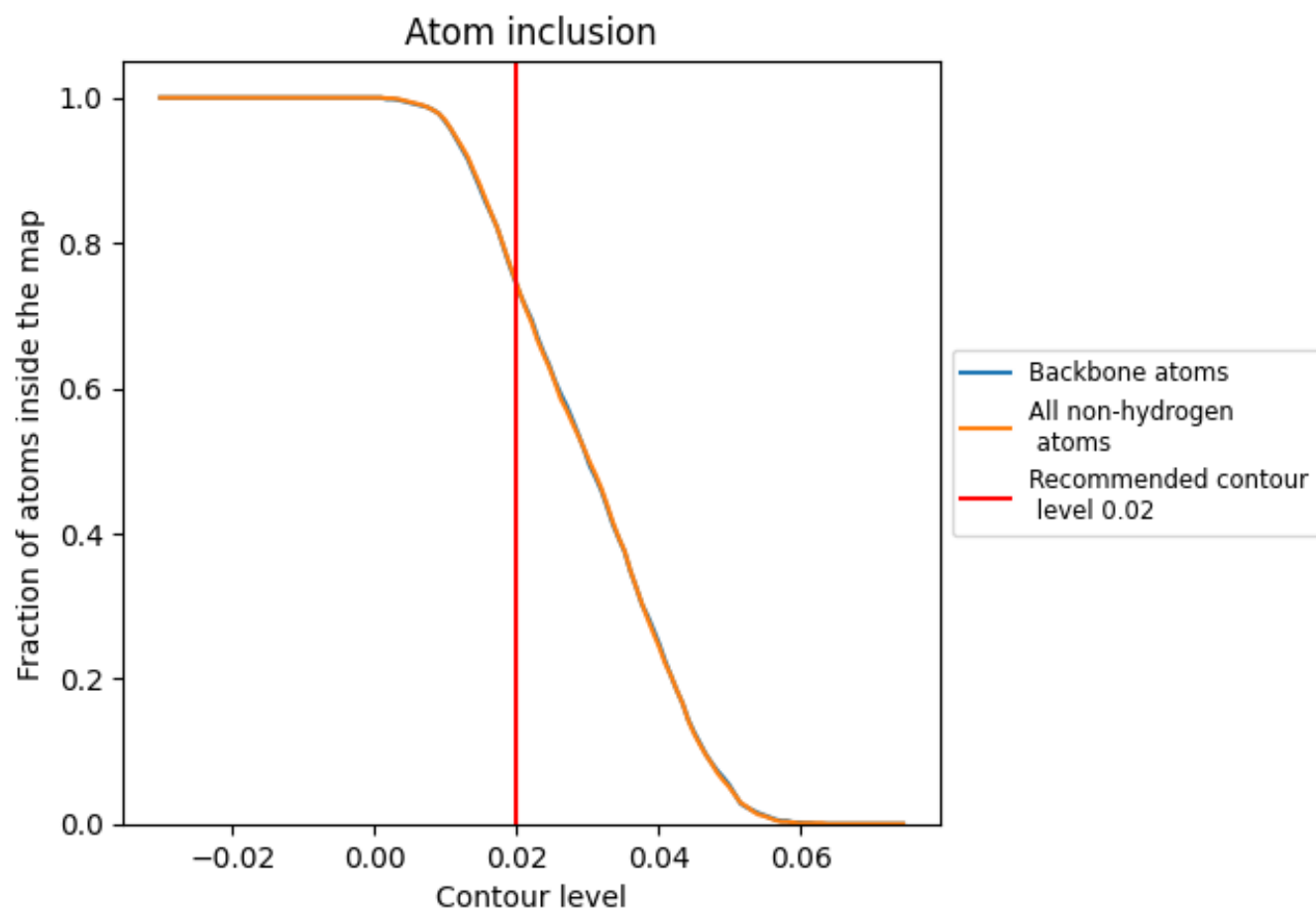
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7440	0.5950
L	0.7910	0.6110
M	0.7940	0.6090
N	0.7260	0.5970
O	0.7180	0.5920
P	0.7280	0.5930
Q	0.7480	0.5970
R	0.7860	0.6080
S	0.7890	0.6070
T	0.7890	0.6130
a	0.7620	0.6020
b	0.6160	0.5380
d	0.5990	0.5380

