



wwPDB EM Validation Summary Report ⓘ

Apr 29, 2026 – 01:56 am BST

PDB ID : 9RST / pdb_00009rst
EMDB ID : EMD-54224
Title : Cryo-EM structure of the Target of Rapamycin Complex 2 (TORC2) in autophagy-inhibited conformation (monomer)
Authors : Tafur, L.; Zou, L.; Loewith, R.
Deposited on : 2025-07-01
Resolution : 2.93 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:

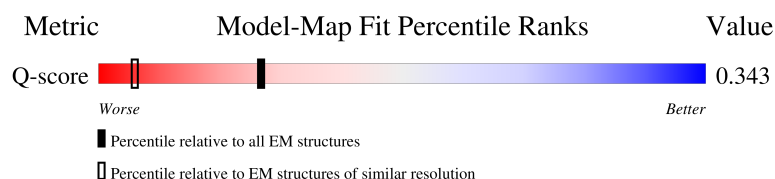
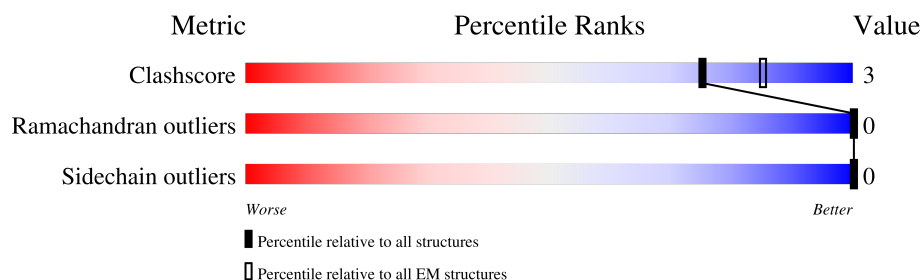
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.93 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.





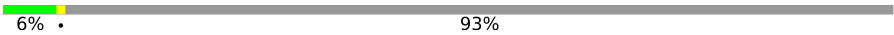
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13037 (2.43 - 3.43)

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	2474	 5% 83% 9% 8%
2	B	303	 1% 92% 7%
3	C	1430	 1% 68% 6% 26%
3	H	1430	 1% 97%

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Mol	Chain	Length	Quality of chain
4	D	426	 41% 56%
5	E	543	 37% 61%
6	G	1176	 6% 93%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 33546 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 Serine/threonine-protein kinase TOR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2272	Total	C	N	O	S	0	0
			18215	11676	3114	3340	85		

- Molecule 2 is a protein called Target of rapamycin complex subunit LST8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	302	Total	C	N	O	S	0	0
			2386	1476	435	464	11		

- Molecule 3 is a protein called Target of rapamycin complex 2 subunit TSC11.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	1059	Total	C	N	O	S	0	0
			8633	5565	1450	1571	47		
3	H	39	Total	C	N	O	S	0	0
			313	198	45	68	2		

- Molecule 4 is a protein called Target of rapamycin complex 2 subunit AVO2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	189	Total	C	N	O	S	0	0
			1518	969	270	267	12		

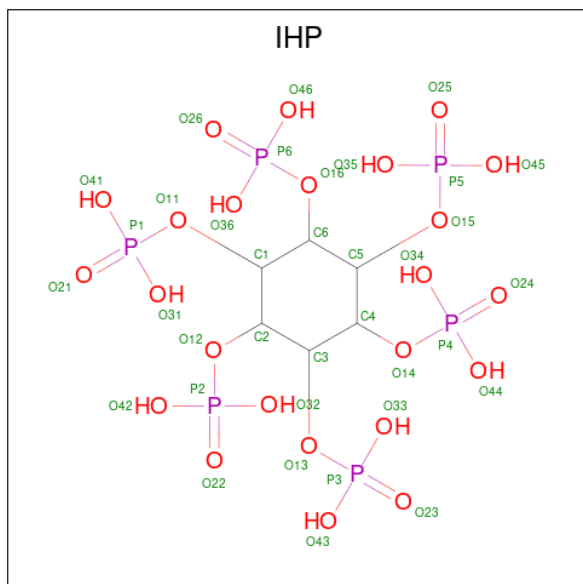
- Molecule 5 is a protein called Target of rapamycin complex 2 subunit BIT61.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	211	Total	C	N	O	S	0	0
			1749	1129	294	317	9		

- Molecule 6 is a protein called Target of rapamycin complex 2 subunit AVO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	88	Total	C	N	O	S	0	0
			696	443	114	133	6		

- Molecule 7 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total	C	O	P	0
			36	6	24	6	

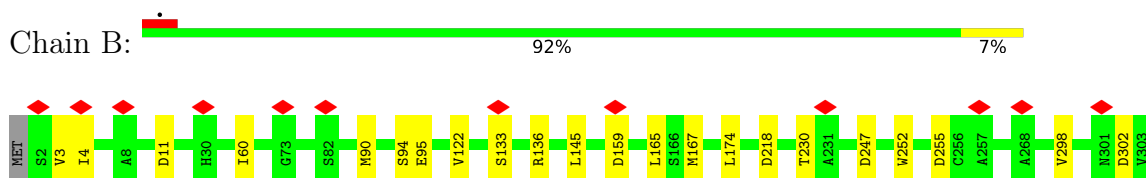
3 Residue-property plots

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.

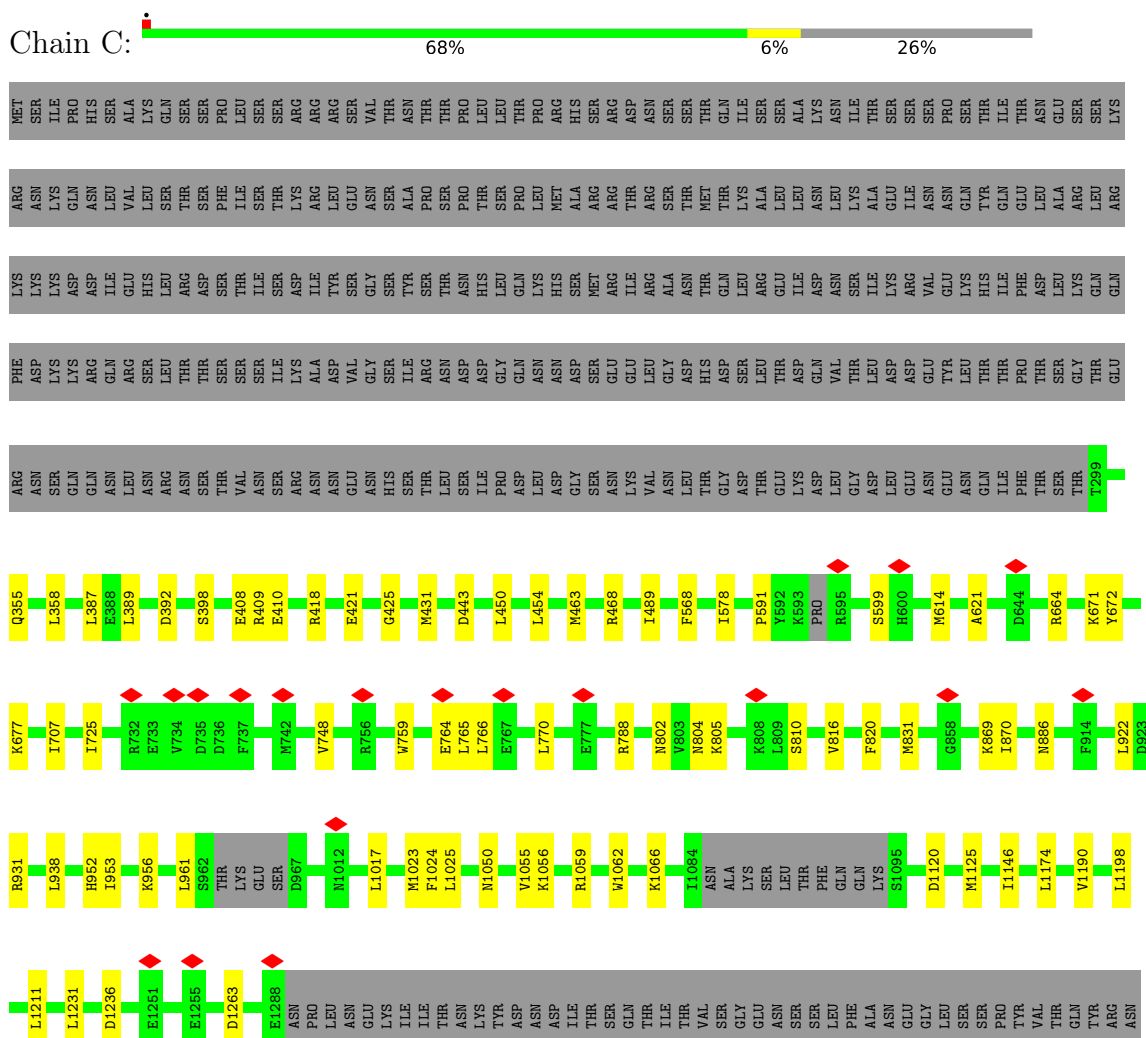
- Molecule 1: Serine/threonine-protein kinase TOR2



- Molecule 2: Target of rapamycin complex subunit LST8



- Molecule 3: Target of rapamycin complex 2 subunit TSC11



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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	125785	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.106	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.0339	Depositor
Map size (\AA)	464.896, 464.896, 464.896	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.908, 0.908, 0.908	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: IHP

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	0.14	0/18580	0.33	0/25157
2	B	0.12	0/2442	0.38	0/3327
3	C	0.12	0/8792	0.29	0/11840
3	H	0.12	0/316	0.32	0/422
4	D	0.11	0/1550	0.29	0/2095
5	E	0.10	0/1779	0.26	0/2401
6	G	0.14	0/705	0.36	0/950
All	All	0.13	0/34164	0.32	0/46192

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	18215	0	18558	125	0
2	B	2386	0	2276	17	0
3	C	8633	0	8811	53	0
3	H	313	0	303	0	0
4	D	1518	0	1537	8	0
5	E	1749	0	1768	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	G	696	0	726	11	0
7	A	36	0	6	0	0
All	All	33546	0	33985	207	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 3.

The worst 5 of 207 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:1970:GLY:HA3	1:A:1994:LEU:HD11	1.75	0.69
3:C:450:LEU:HD21	3:C:489:ILE:HD11	1.79	0.64
1:A:1877:GLU:O	1:A:2141:GLN:NE2	2.33	0.61
3:C:591:PRO:HB2	3:C:599:SER:HB2	1.83	0.61
4:D:155:ILE:HA	4:D:158:MET:HE3	1.82	0.59

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	2248/2474 (91%)	2203 (98%)	45 (2%)	0	100	100
2	B	300/303 (99%)	281 (94%)	19 (6%)	0	100	100
3	C	1049/1430 (73%)	1029 (98%)	20 (2%)	0	100	100
3	H	37/1430 (3%)	36 (97%)	1 (3%)	0	100	100
4	D	185/426 (43%)	179 (97%)	6 (3%)	0	100	100
5	E	201/543 (37%)	198 (98%)	3 (2%)	0	100	100
6	G	82/1176 (7%)	78 (95%)	4 (5%)	0	100	100
All	All	4102/7782 (53%)	4004 (98%)	98 (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	A	2034/2219 (92%)	2034 (100%)	0	100	100
2	B	266/267 (100%)	266 (100%)	0	100	100
3	C	971/1320 (74%)	971 (100%)	0	100	100
3	H	36/1320 (3%)	36 (100%)	0	100	100
4	D	168/378 (44%)	168 (100%)	0	100	100
5	E	199/499 (40%)	199 (100%)	0	100	100
6	G	84/1066 (8%)	84 (100%)	0	100	100
All	All	3758/7069 (53%)	3758 (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 42 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	1367	ASN
5	E	391	GLN
3	C	1413	ASN
4	D	87	HIS
5	E	498	GLN

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 [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
7	IHP	A	2501	-	36,36,36	1.49	6 (16%)	54,60,60	0.85	3 (5%)

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
7	IHP	A	2501	-	-	7/30/54/54	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	2501	IHP	P3-O13	3.17	1.65	1.59
7	A	2501	IHP	P1-O11	3.13	1.65	1.59
7	A	2501	IHP	P5-O15	3.13	1.65	1.59
7	A	2501	IHP	P6-O16	3.11	1.65	1.59
7	A	2501	IHP	P4-O14	3.08	1.65	1.59

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	2501	IHP	C5-C4-C3	3.47	118.02	110.41
7	A	2501	IHP	C6-C5-C4	2.69	116.29	110.41
7	A	2501	IHP	C4-C3-C2	2.35	115.56	110.41

There are no chirality outliers.

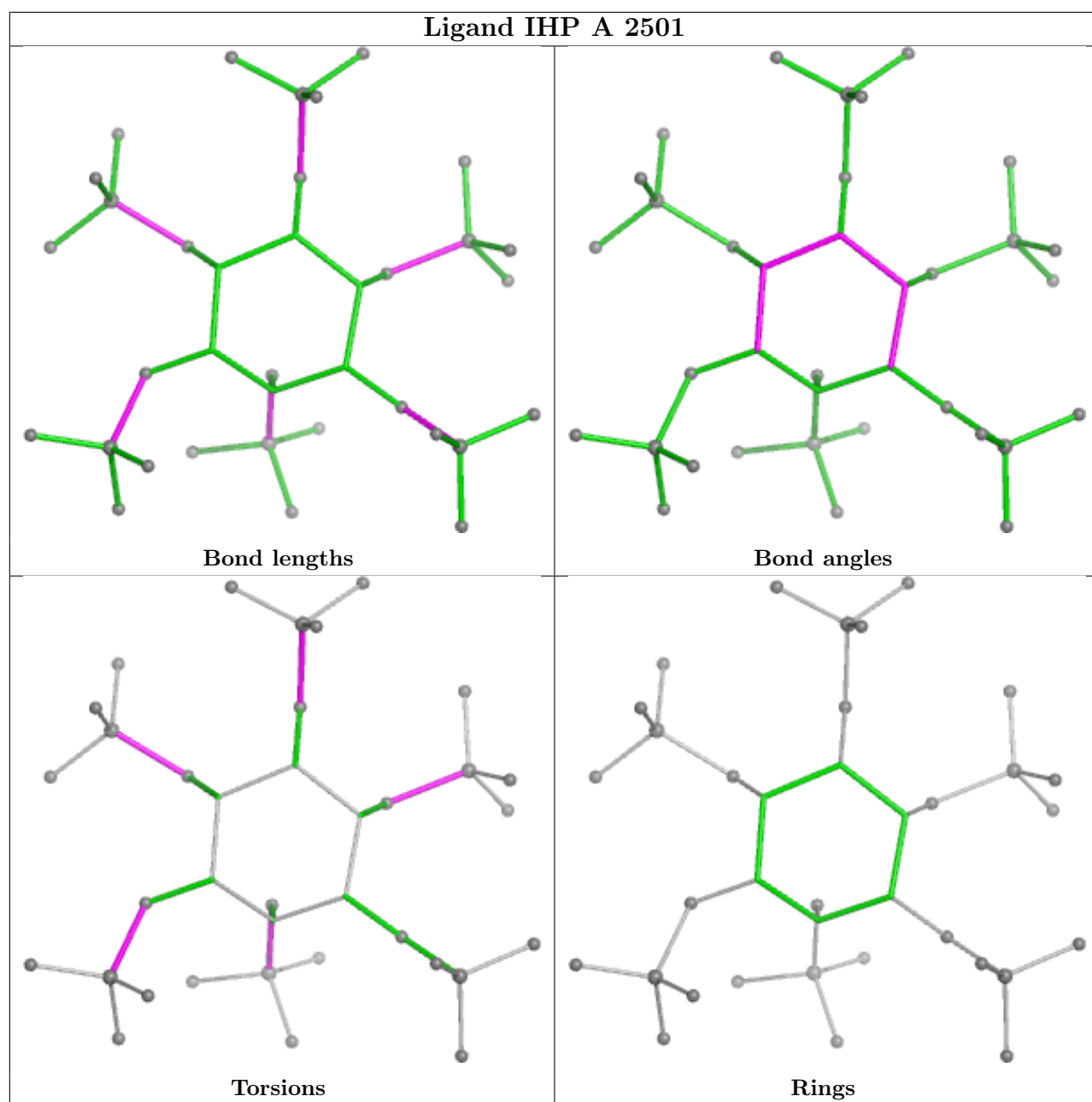
5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	2501	IHP	C3-O13-P3-O23
7	A	2501	IHP	C4-O14-P4-O24
7	A	2501	IHP	C1-O11-P1-O21
7	A	2501	IHP	C5-O15-P5-O25
7	A	2501	IHP	C6-O16-P6-O26

There are no ring outliers.

No monomer is involved in short contacts.

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.

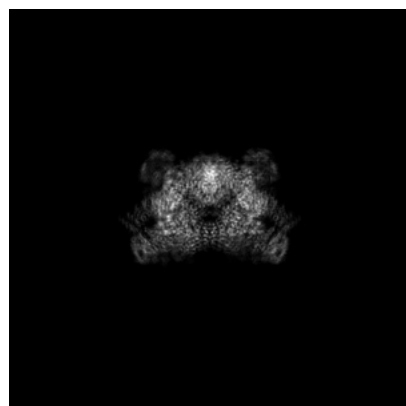
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-54224. These allow visual inspection of the internal detail of the map and identification of artifacts.

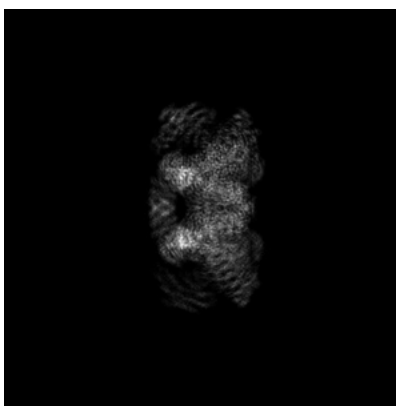
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

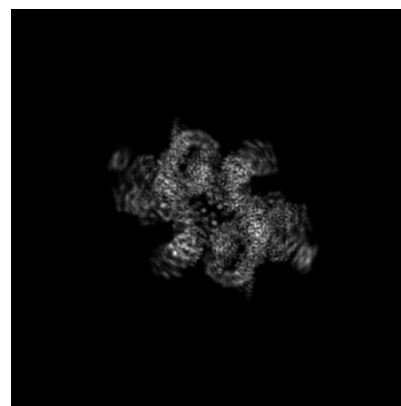
6.1.1 Primary map



X

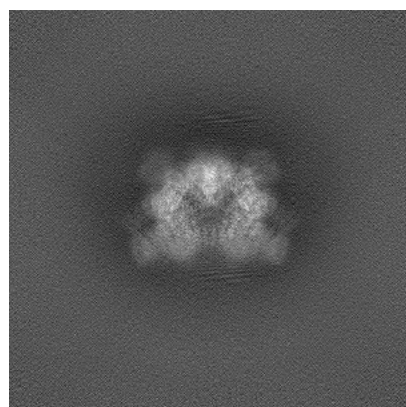


Y

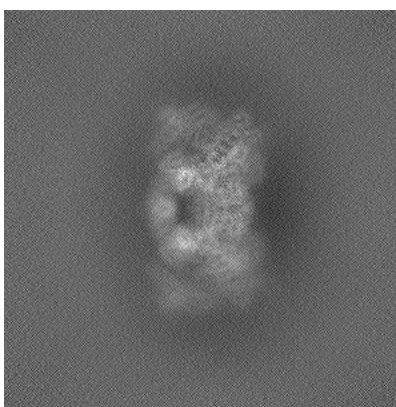


Z

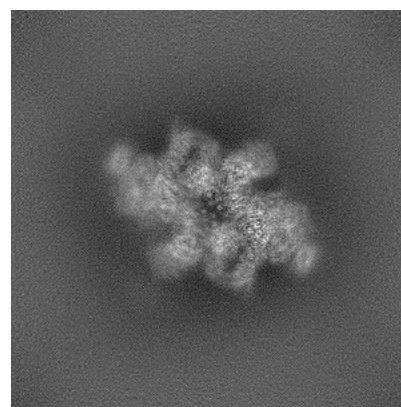
6.1.2 Raw map



X



Y

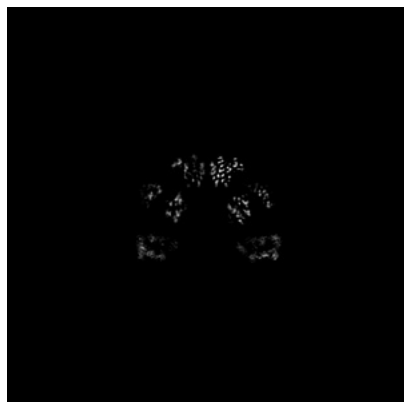


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 256

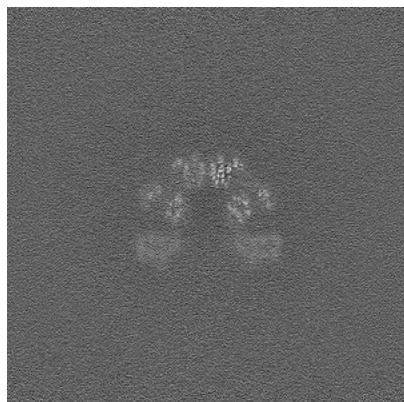


Y Index: 256



Z Index: 256

6.2.2 Raw map



X Index: 256



Y Index: 256



Z Index: 256

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: 209

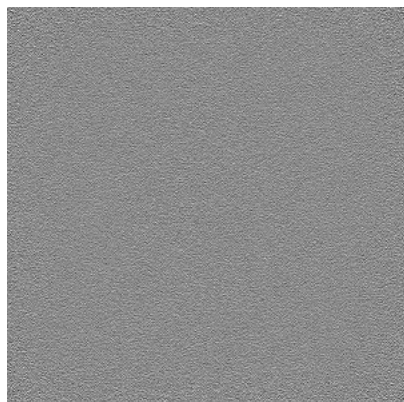


Y Index: 261

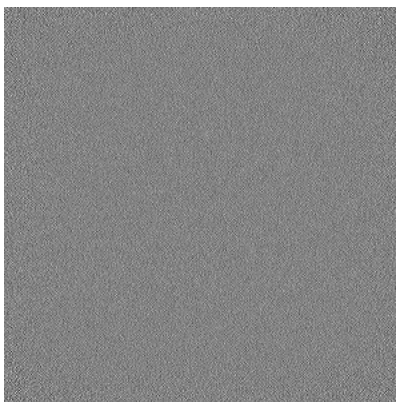


Z Index: 227

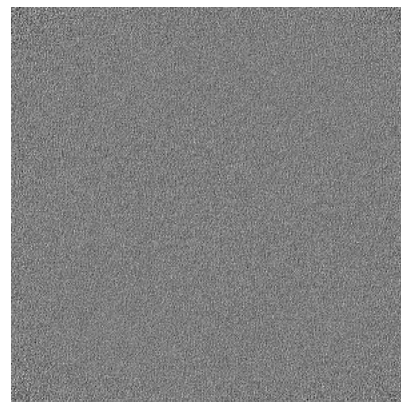
6.3.2 Raw map



X Index: 0



Y Index: 0

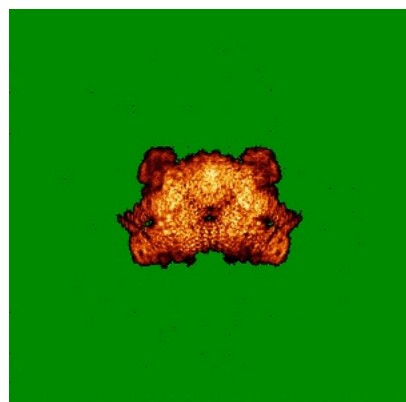


Z Index: 0

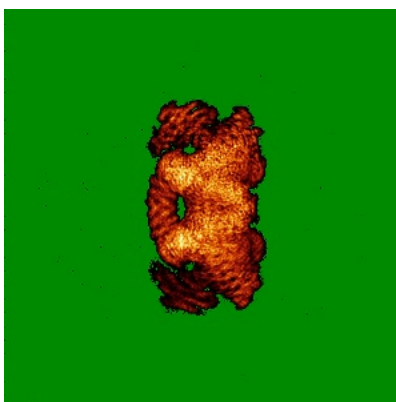
The images above show the largest variance slices of the map in three orthogonal directions.

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

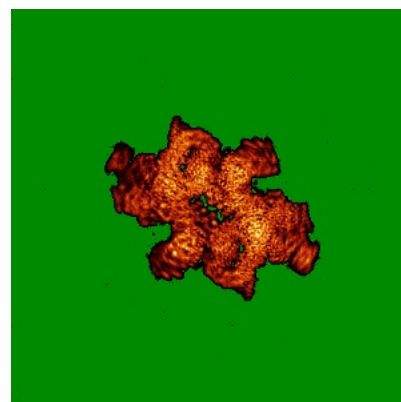
6.4.1 Primary map



X

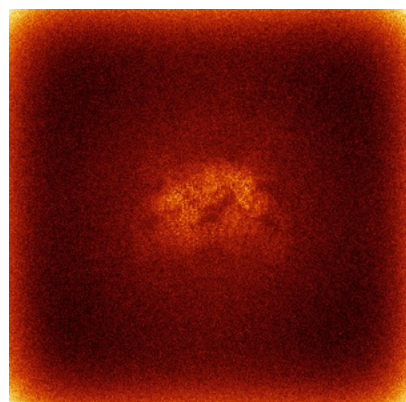


Y

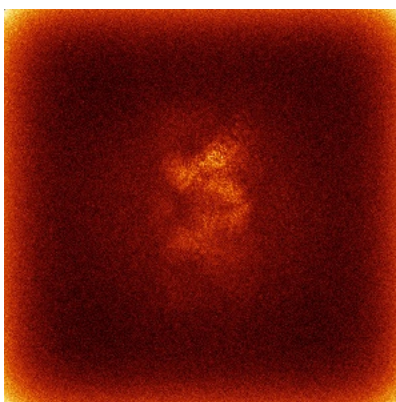


Z

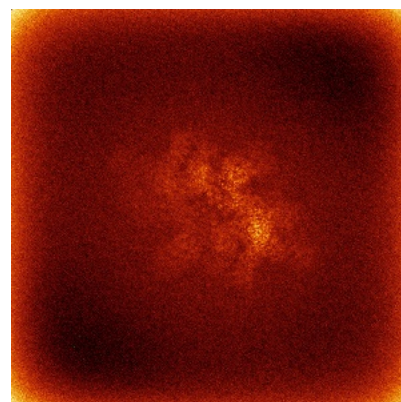
6.4.2 Raw map



X



Y

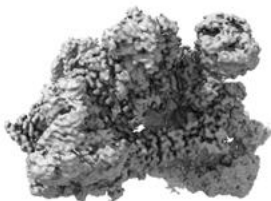


Z

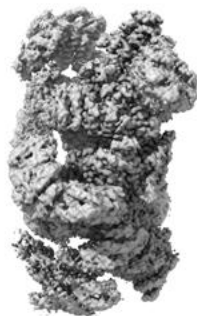
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



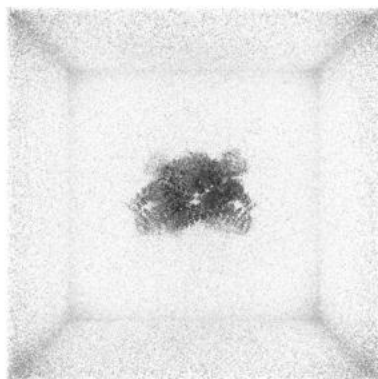
Y



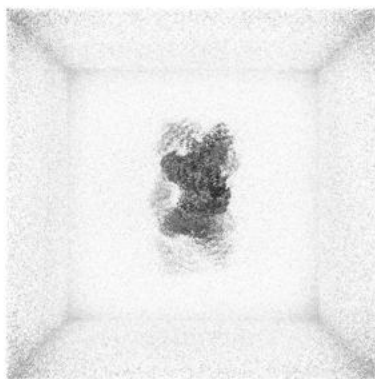
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0339. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

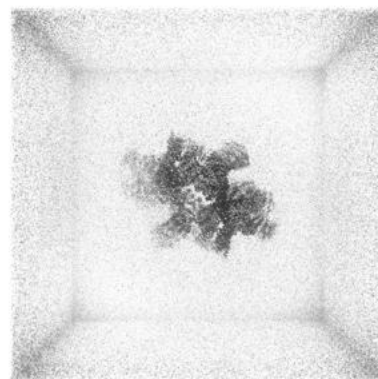
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

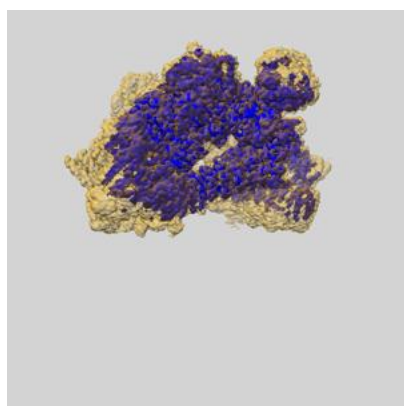
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

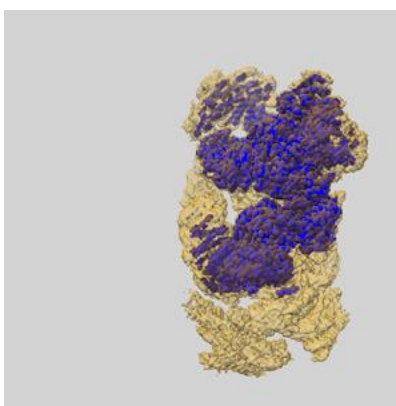
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

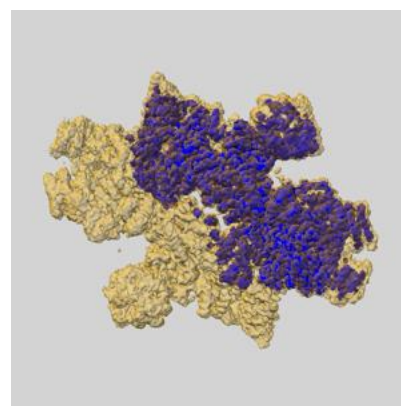
6.6.1 emd_54224_msk_1.map [i](#)



X



Y

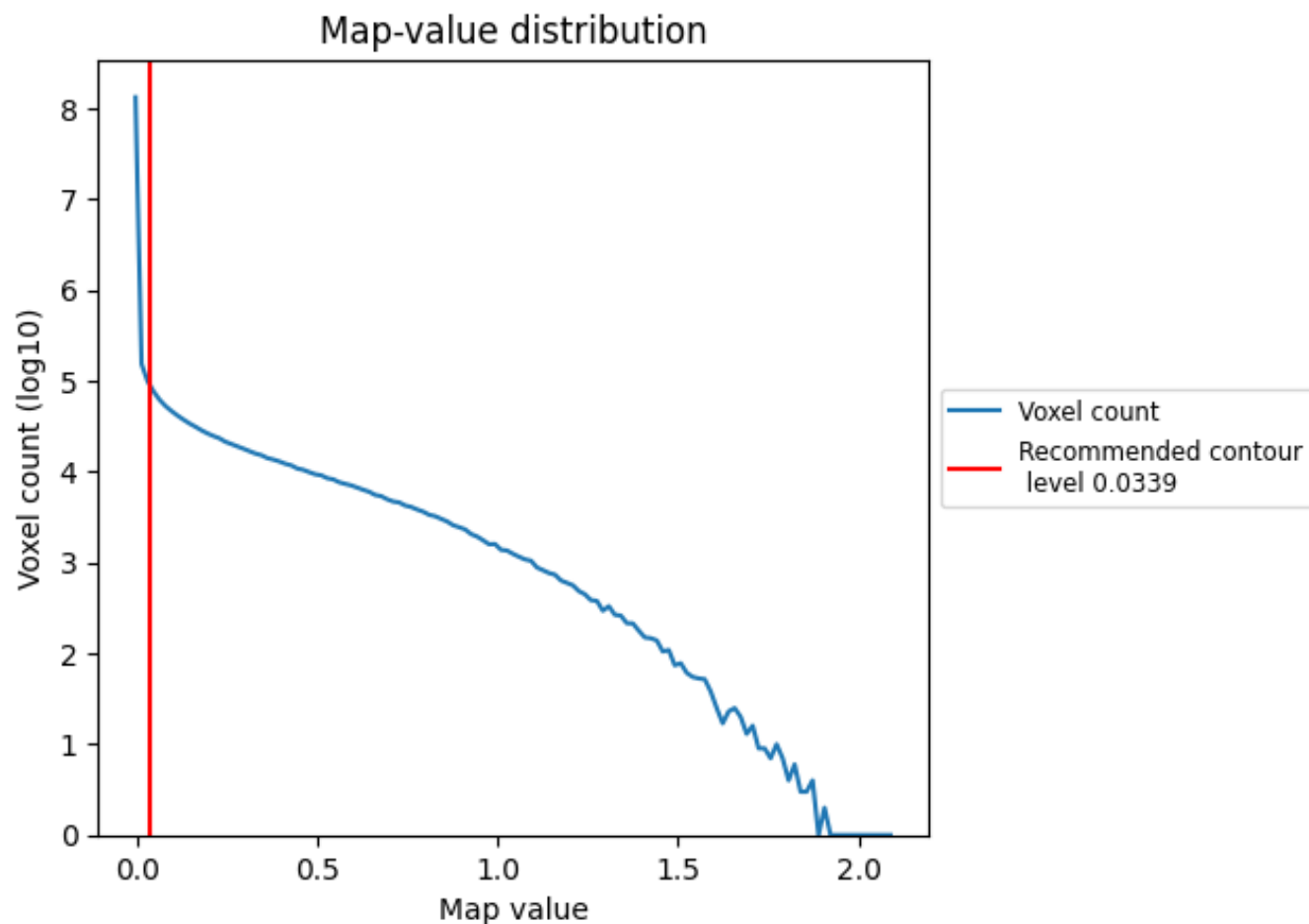


Z

7 Map analysis [i](#)

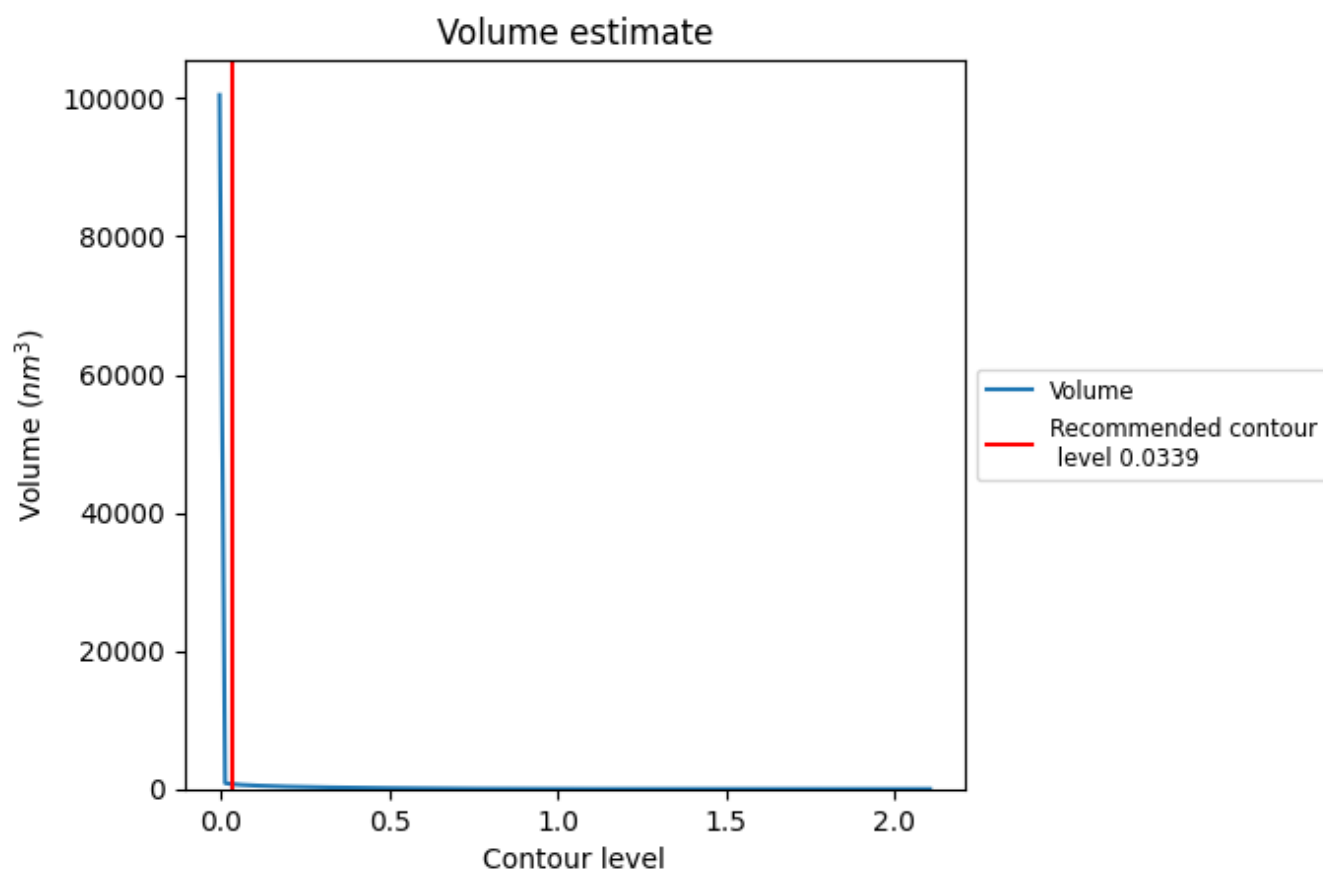
This section contains the results of statistical analysis of the map.

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.

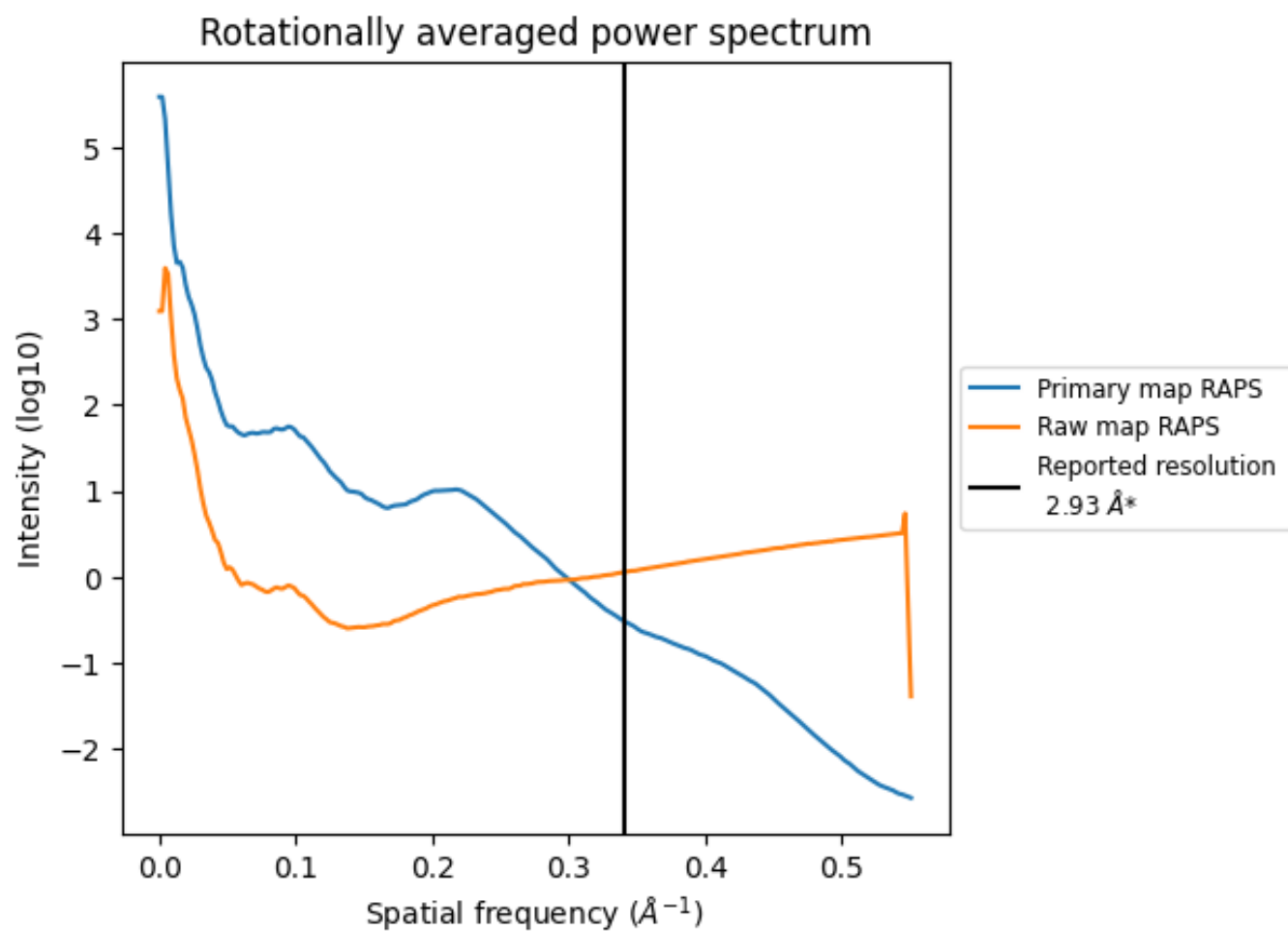
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 709 nm³; this corresponds to an approximate mass of 640 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 ⓘ

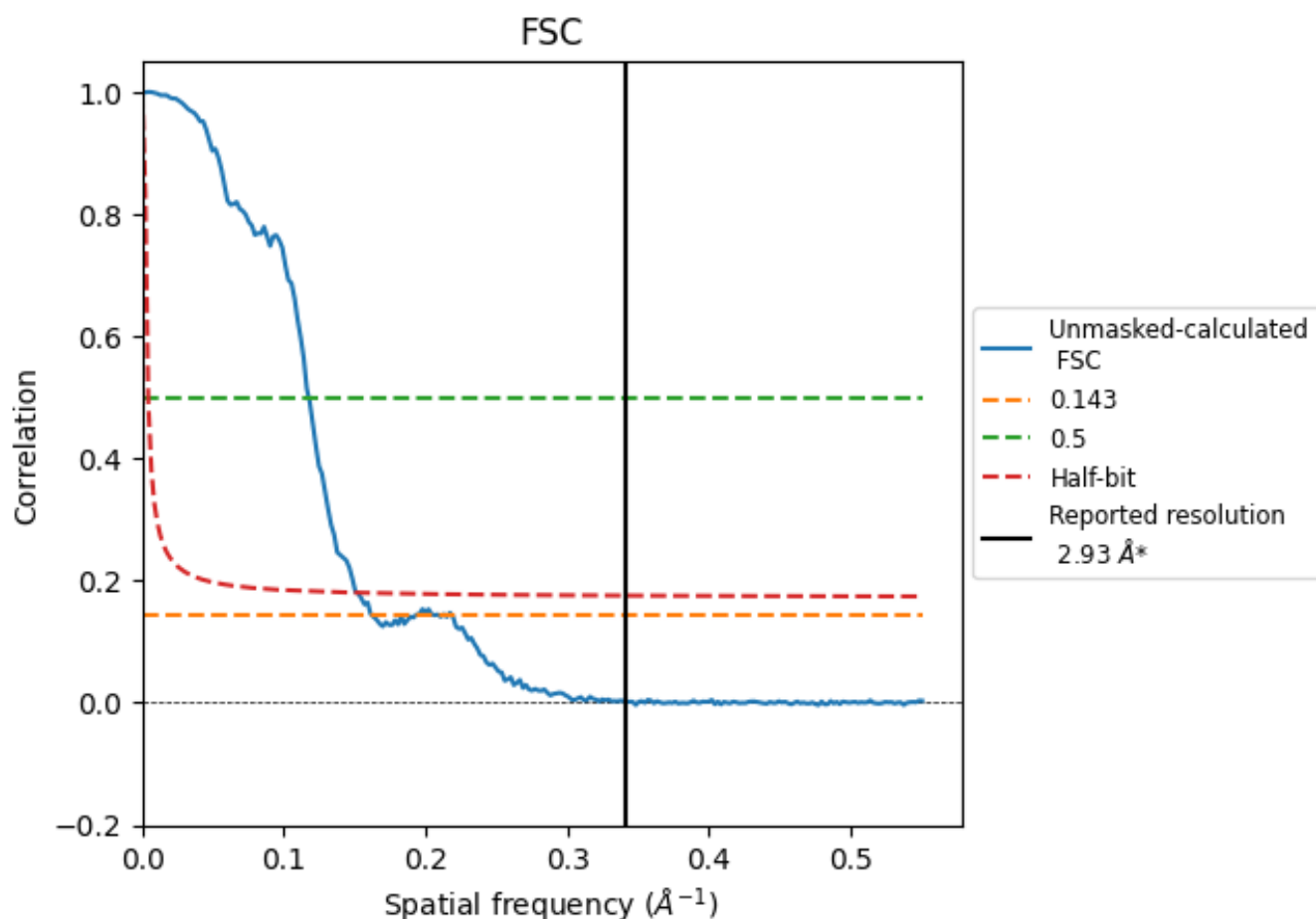


*Reported resolution corresponds to spatial frequency of 0.341 Å⁻¹

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 0.341 Å⁻¹

8.2 Resolution estimates [i](#)

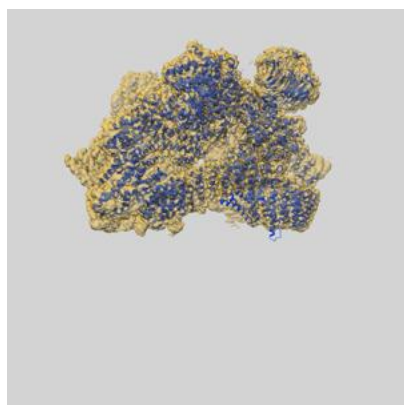
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.93	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.17	8.51	6.60

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.17 differs from the reported value 2.93 by more than 10 %

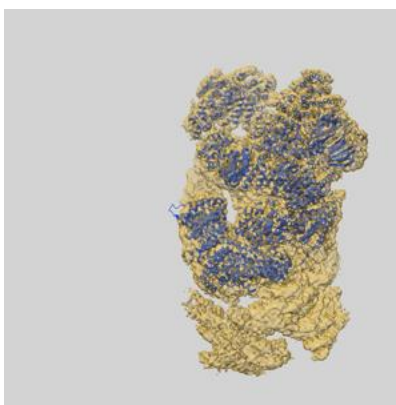
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-54224 and PDB model 9RST. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

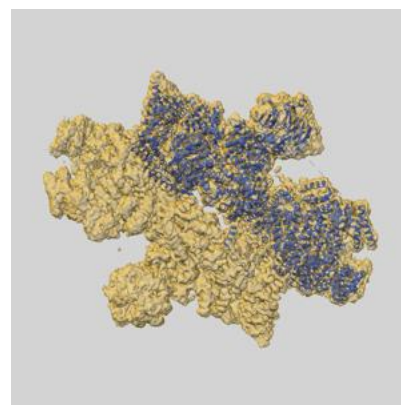
9.1 Map-model overlay [i](#)



X



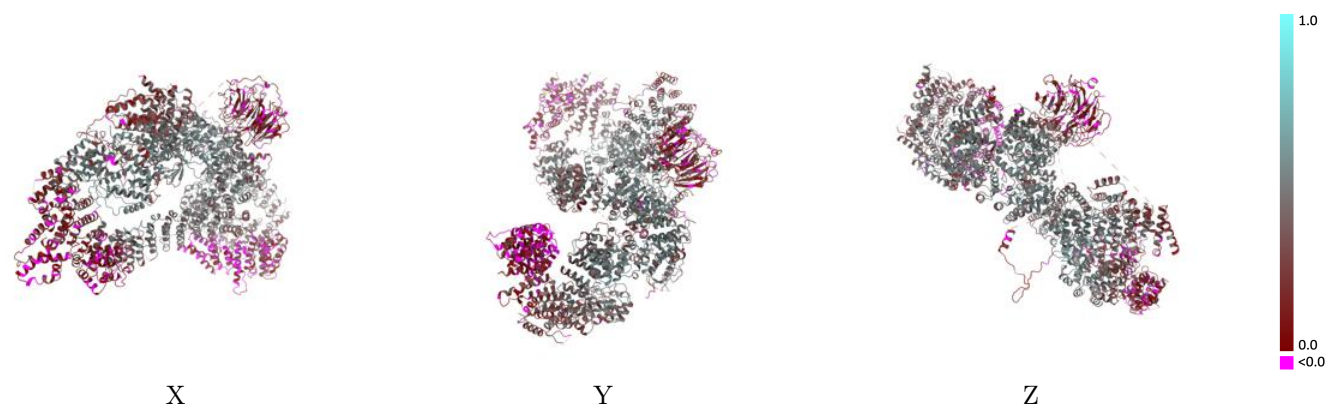
Y



Z

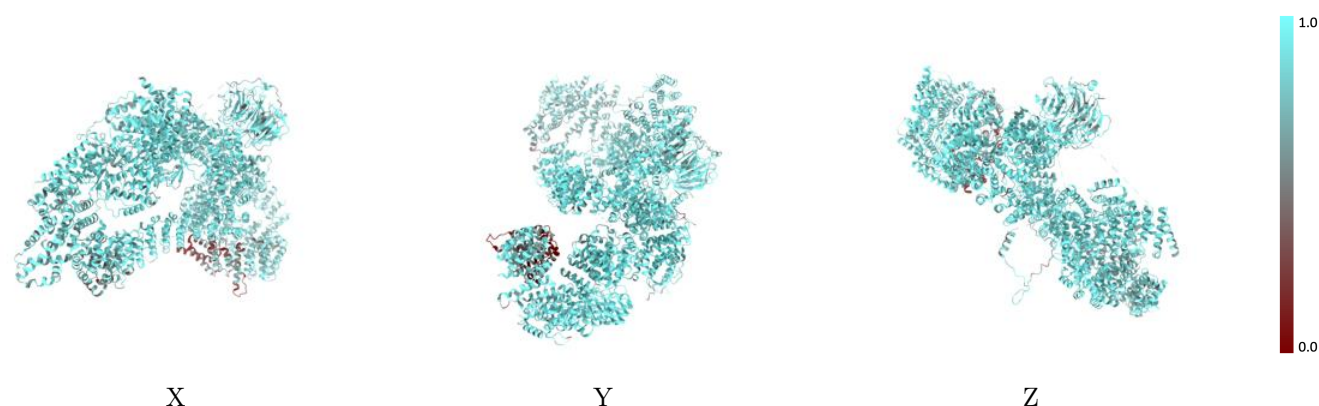
The images above show the 3D surface view of the map at the recommended contour level 0.0339 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



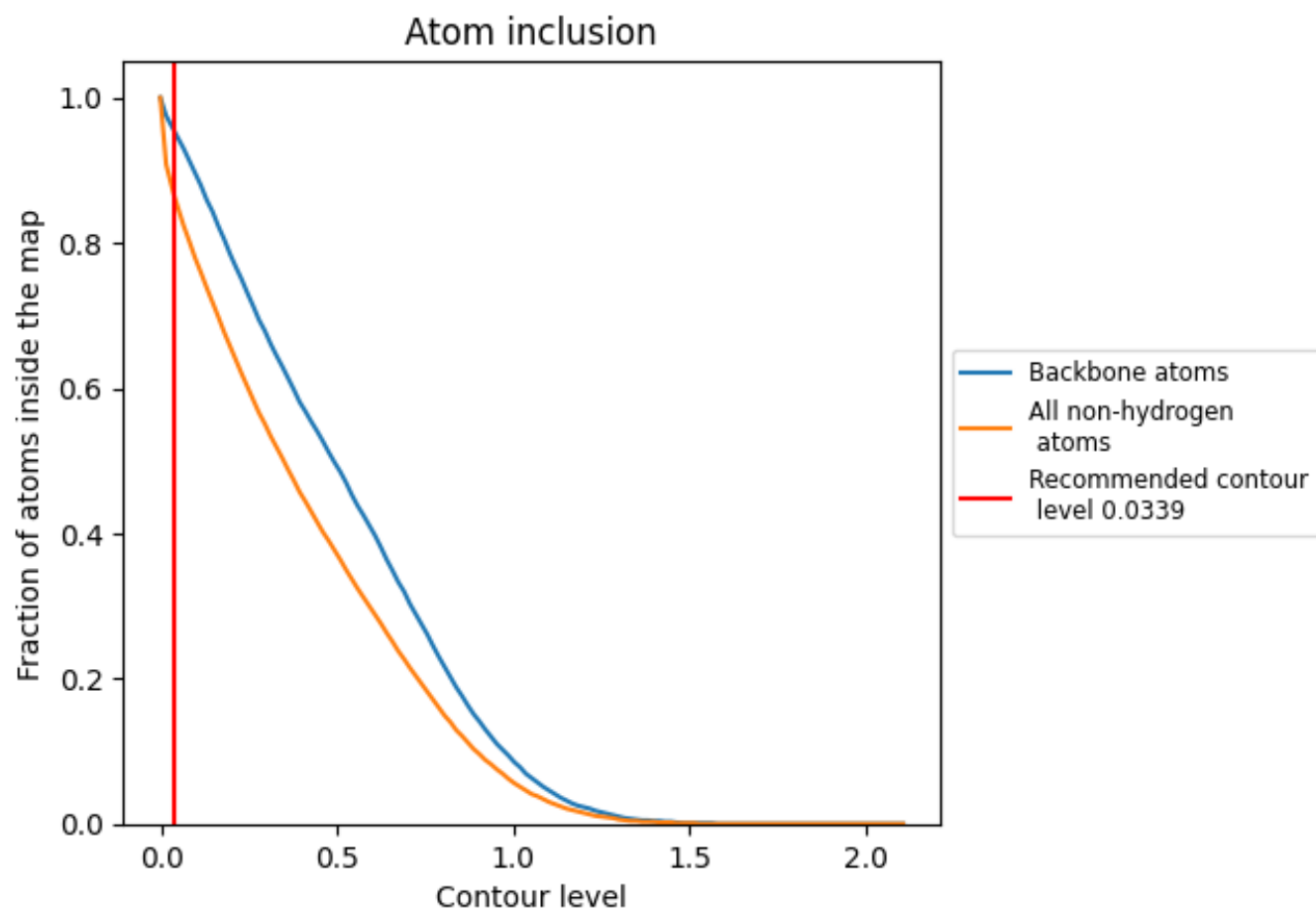
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0339).

9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 87% 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 (0.0339) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8680</div>	<div><div></div>0.3430</div>
A	<div><div></div>0.8770</div>	<div><div></div>0.3830</div>
B	<div><div></div>0.8460</div>	<div><div></div>0.1800</div>
C	<div><div></div>0.8620</div>	<div><div></div>0.3440</div>
D	<div><div></div>0.9240</div>	<div><div></div>0.4060</div>
E	<div><div></div>0.8170</div>	<div><div></div>0.1160</div>
G	<div><div></div>0.8100</div>	<div><div></div>0.2700</div>
H	<div><div></div>0.8040</div>	<div><div></div>0.3360</div>

1.0

0.0

<0.0