



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 02:52 AM UTC

PDB ID : 7ZT6 / pdb_00007zt6
EMDB ID : EMD-14955
Title : Cryo-EM structure of Ku 70/80 bound to inositol hexakisphosphate
Authors : Kefala Stavridi, A.; Chaplin, A.K.; Blundell, T.L.
Deposited on : 2022-05-09
Resolution : 3.50 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

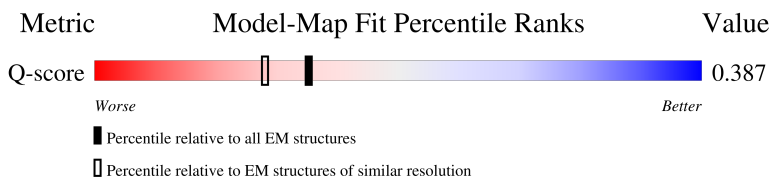
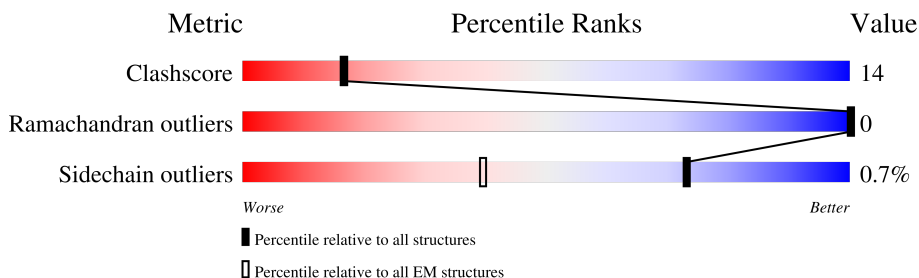
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	646	 53% 24% 22%
2	B	732	 49% 23% 28%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8073 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 X-ray repair cross-complementing protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	501	Total	C	N	O	S	0	0
			3863	2491	655	701	16		

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-36	MET	-	initiating methionine	UNP P12956
A	-35	ASN	-	expression tag	UNP P12956
A	-34	THR	-	expression tag	UNP P12956
A	-33	ILE	-	expression tag	UNP P12956
A	-32	HIS	-	expression tag	UNP P12956
A	-31	HIS	-	expression tag	UNP P12956
A	-30	HIS	-	expression tag	UNP P12956
A	-29	HIS	-	expression tag	UNP P12956
A	-28	HIS	-	expression tag	UNP P12956
A	-27	HIS	-	expression tag	UNP P12956
A	-26	ASN	-	expression tag	UNP P12956
A	-25	THR	-	expression tag	UNP P12956
A	-24	SER	-	expression tag	UNP P12956
A	-23	GLY	-	expression tag	UNP P12956
A	-22	SER	-	expression tag	UNP P12956
A	-21	GLY	-	expression tag	UNP P12956
A	-20	GLY	-	expression tag	UNP P12956
A	-19	GLY	-	expression tag	UNP P12956
A	-18	GLY	-	expression tag	UNP P12956
A	-17	GLY	-	expression tag	UNP P12956
A	-16	ARG	-	expression tag	UNP P12956
A	-15	LEU	-	expression tag	UNP P12956
A	-14	VAL	-	expression tag	UNP P12956
A	-13	PRO	-	expression tag	UNP P12956
A	-12	ARG	-	expression tag	UNP P12956
A	-11	GLY	-	expression tag	UNP P12956
A	-10	SER	-	expression tag	UNP P12956
A	-9	MET	-	expression tag	UNP P12956

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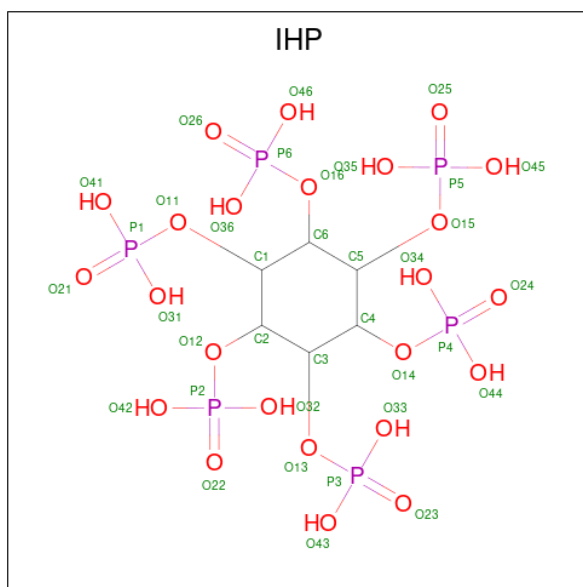
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Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	SER	-	expression tag	UNP P12956
A	-7	GLU	-	expression tag	UNP P12956
A	-6	ASN	-	expression tag	UNP P12956
A	-5	LEU	-	expression tag	UNP P12956
A	-4	TYR	-	expression tag	UNP P12956
A	-3	PHE	-	expression tag	UNP P12956
A	-2	GLN	-	expression tag	UNP P12956
A	-1	GLY	-	expression tag	UNP P12956
A	0	SER	-	expression tag	UNP P12956

- Molecule 2 is a protein called X-ray repair cross-complementing protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	530	Total	C	N	O	S	0	0
			4174	2678	708	766	22		

- Molecule 3 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$) (labeled as "Ligand of Interest" by depositor).

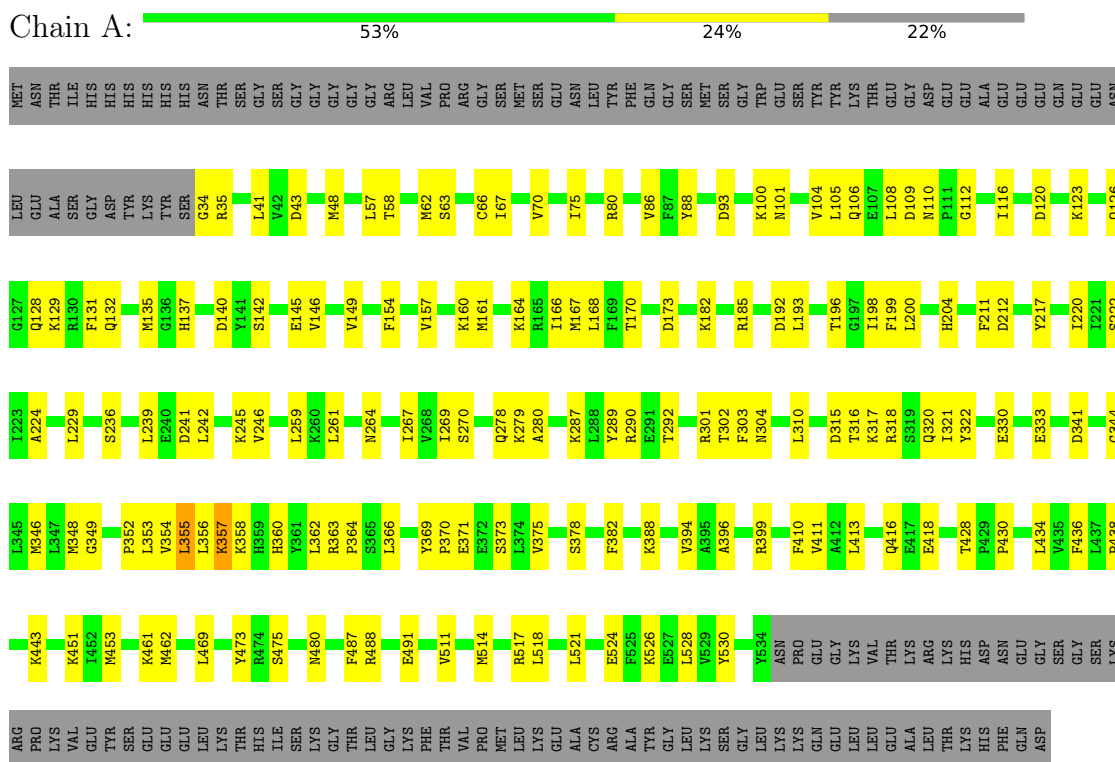


Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	O	P	0
			36	6	24	6	

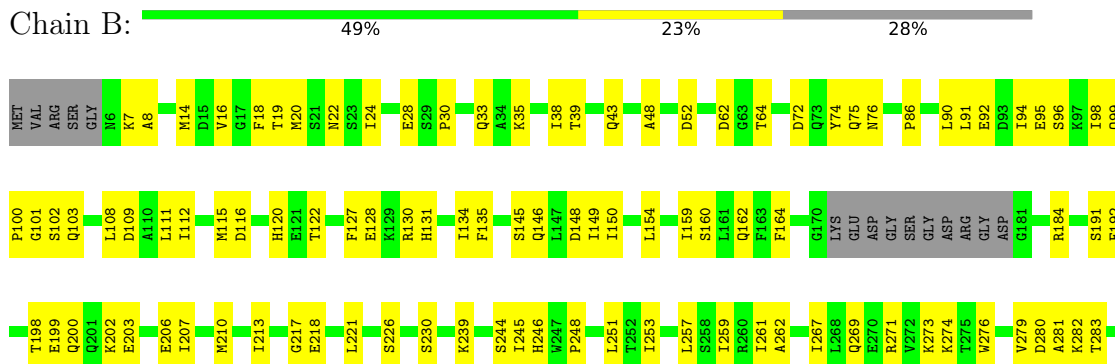
3 Residue-property plots

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: X-ray repair cross-complementing protein 6



- Molecule 2: X-ray repair cross-complementing protein 5



PHE	ASN	PHE	Y421	K286
TRP	GLN	GLN	Y422	
GLU	LEU	ASP	Q423	Q290
ILE	ILE	ASN	L424	K291
VAL	ASN	HIS	K425	E292
VAL	HIS	GLU	F426	
GLN	ILE	ASP	M427	Y295
ASP	GLU	GLY	E428	
GLY	GLN	PRO	D429	V305
ILE	PHE	THR	L430	
THR	LEU	ALA	R431	E308
THR	ASP	LYS		D309
ILE	THR	LYS	E448	I310
LYS	THR	LEU		
GLY	GLU	LYS	N452	S318
GLU	THR	THR		
GLU	PRO	GLU	L457	Q330
ALA	TYR	GLN		M331
ALA	PHE	GLY		
SER	GLY	GLY	M461	S335
SER	MET	GLY		E336
SER	LYS	HIS	D475	G337
SER	SER	ALA	L476	
VAL	ILE	PHE	F477	K338
THR	ASP	SER	F478	
ALA	CYS	VAL	T479	V342
ALA	ILE	SER		
GLU	ARG	SER		K347
GLU	ALA	LEU	R497	S348
LYS	PHE	ALA		S349
LYS	ARG	GLU	H500	Q350
PHE	ARG	GLY	P501	
LEU	GLU	SER	R502	K351
ALA	ALA	VAL	E503	Q352
PRO	ILE	THR		R353
LYS	LYS	SER	Q509	K354
ASP	PHE	VAL	Q510	
LYS	SER	GLY	H511	M357
PRO	GLU	SER		G358
SER	GLU	VAL	M514	
GLY	GLN	ASN	M515	V361
ASP	ARG	PRO	L516	
THR	PHE	ALA		E371
ALA	ASN	GLU	P519	L380
ALA	ASN	ASN	E520	
VAL	PHE	PHE	E521	D388
PHE	LEU	ARG	V522	M389
GLU	LYS	VAL		
GLU	ALA	LEU	I528	D398
GLY	LEU	VAL	P529	K399
GLY	GLN	VAL		
ASP	GLU	LYS	K534	
VAL	LYS	LYS		A408
ASP	VAL	LYS	K545	I412
ASP	GLU	ALA	ASP	K413
LEU	ILE	SER	GLN	
LEU	LYS	PHE	THR	Y416
ASP	GLN	GLU	THR	E417
MET	LEU	GLU	GLN	C418
ILE	ASN	GLU	ILE	L419
	HIS	SER	GLU	U420

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	93175	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 ($e^-/\text{\AA}^2$)	49.43	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.157	Depositor
Minimum map value	-0.051	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0308	Depositor
Map size (Å)	195.6, 195.6, 195.6	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.652, 0.652, 0.652	Depositor

5 Model quality

5.1 Standard geometry

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	0.30	0/3942	0.40	0/5335
2	B	0.27	0/4261	0.39	0/5754
All	All	0.28	0/8203	0.39	0/11089

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

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	3863	0	3825	119	0
2	B	4174	0	4168	129	0
3	A	36	0	6	0	0
All	All	8073	0	7999	225	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 225 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:B:347:LYS:HD2	2:B:389:MET:HE1	1.50	0.92
2:B:347:LYS:HB2	2:B:350:GLN:HG3	1.64	0.80
1:A:57:LEU:HB3	1:A:62:MET:HE3	1.67	0.76
1:A:43:ASP:HB3	1:A:48:MET:HE3	1.69	0.74
1:A:48:MET:HE1	1:A:170:THR:HA	1.68	0.74

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	499/646 (77%)	483 (97%)	16 (3%)	0	100	100
2	B	526/732 (72%)	502 (95%)	24 (5%)	0	100	100
All	All	1025/1378 (74%)	985 (96%)	40 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	405/577 (70%)	400 (99%)	5 (1%)	63	73
2	B	455/649 (70%)	454 (100%)	1 (0%)	87	85
All	All	860/1226 (70%)	854 (99%)	6 (1%)	73	78

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	358	LYS
1	A	443	LYS
2	B	479	THR
1	A	355	LEU
1	A	354	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	293	ASN
1	A	360	HIS
1	A	416	GLN
2	B	45	GLN
2	B	527	GLN

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
3	IHP	A	701	-	36,36,36	0.62	2 (5%)	60,60,60	0.94	4 (6%)

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
3	IHP	A	701	-	-	7/30/54/54	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	701	IHP	P4-O14	2.01	1.63	1.59
3	A	701	IHP	P3-O13	2.01	1.63	1.59

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	701	IHP	P2-O12-C2	2.78	130.84	123.43
3	A	701	IHP	C6-C5-C4	-2.47	105.01	110.43
3	A	701	IHP	C5-C4-C3	-2.08	105.86	110.43
3	A	701	IHP	O14-C4-C3	2.00	113.02	108.76

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

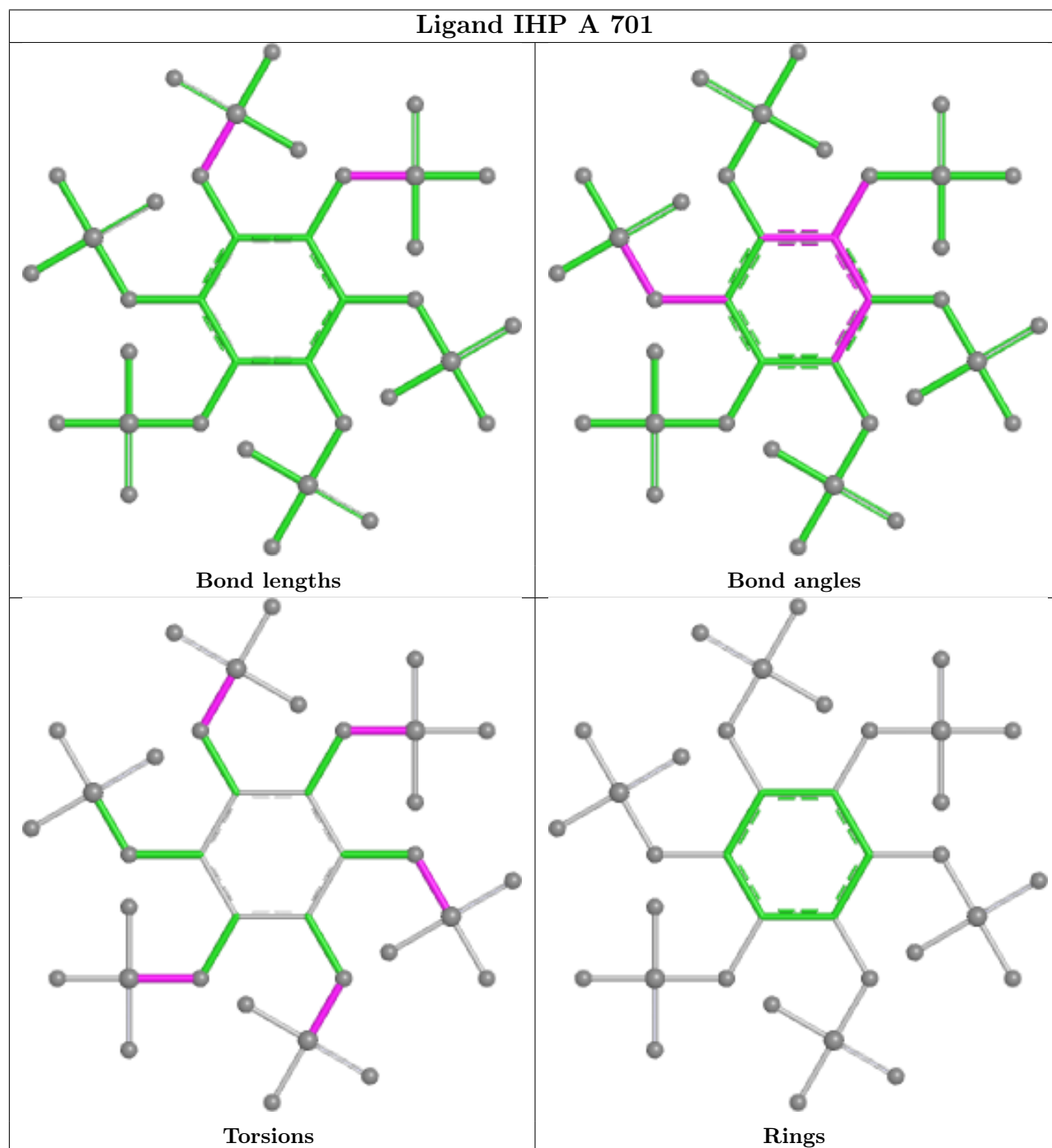
Mol	Chain	Res	Type	Atoms
3	A	701	IHP	C3-O13-P3-O33
3	A	701	IHP	C5-O15-P5-O25
3	A	701	IHP	C6-O16-P6-O26
3	A	701	IHP	C1-O11-P1-O31
3	A	701	IHP	C4-O14-P4-O34

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.

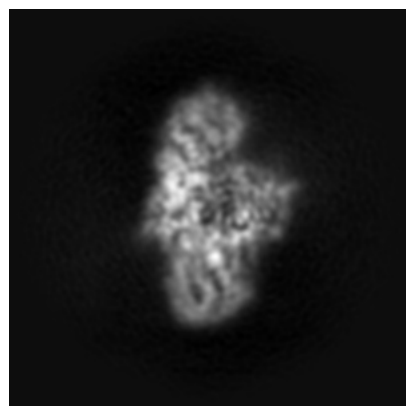
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14955. These allow visual inspection of the internal detail of the map and identification of artifacts.

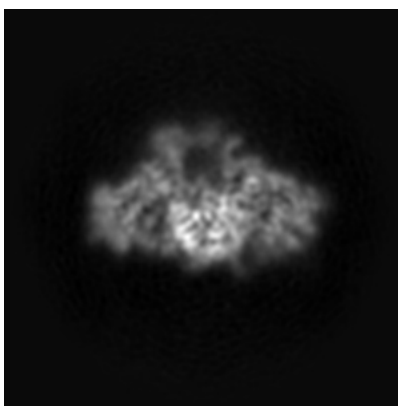
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

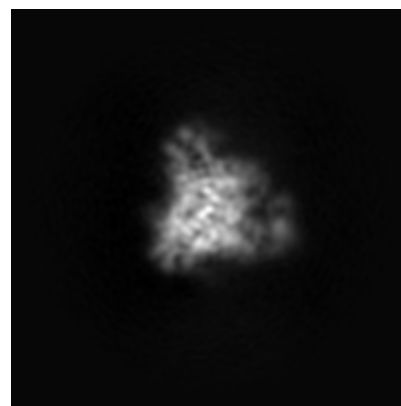
6.1.1 Primary map



X

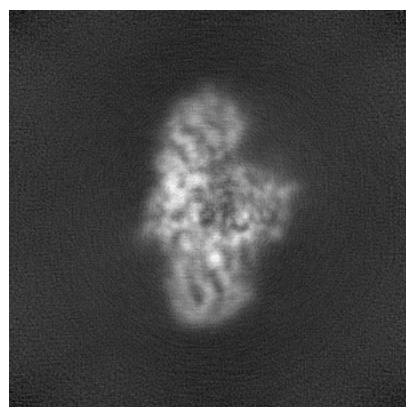


Y

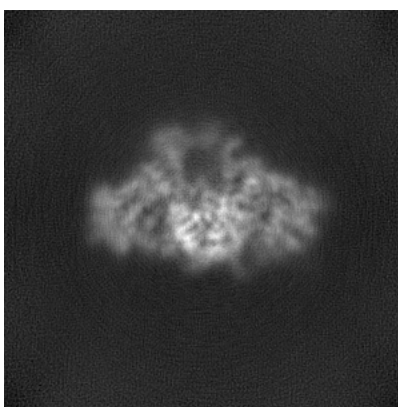


Z

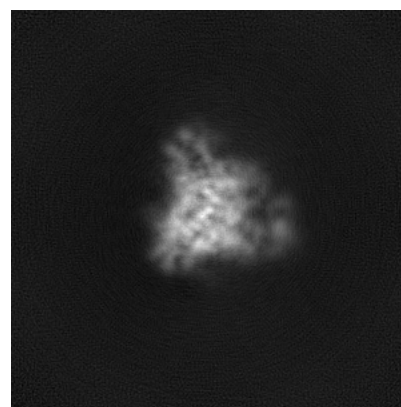
6.1.2 Raw map



X



Y

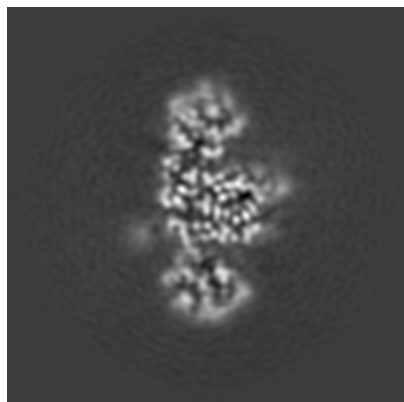


Z

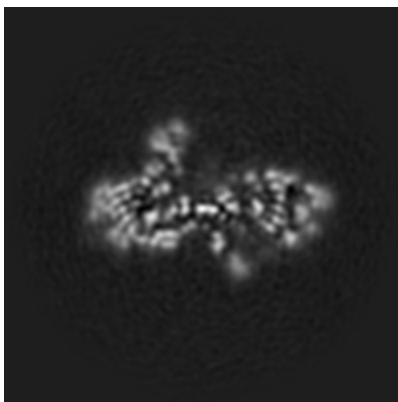
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

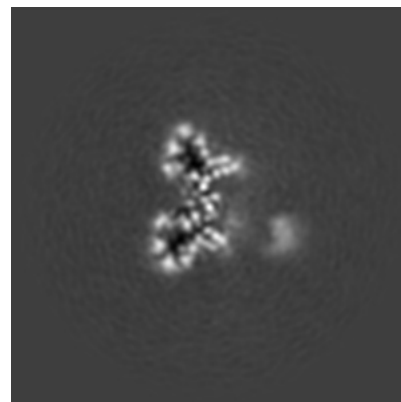
6.2.1 Primary map



X Index: 150

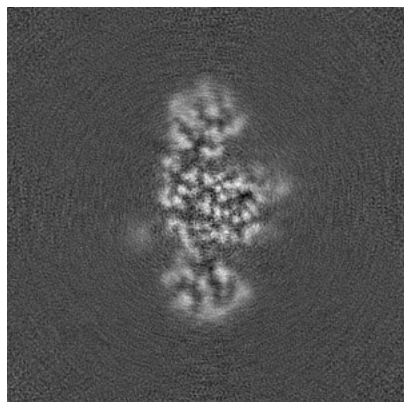


Y Index: 150

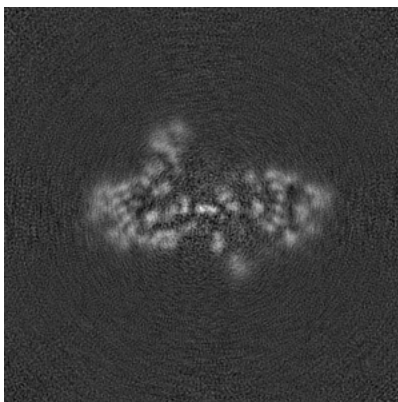


Z Index: 150

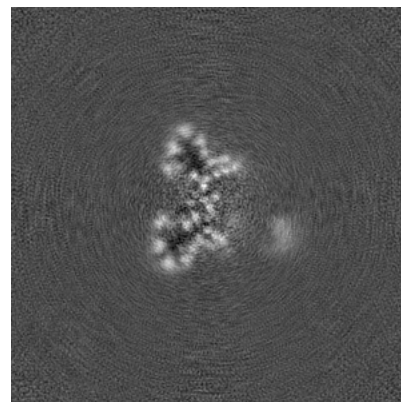
6.2.2 Raw map



X Index: 150



Y Index: 150

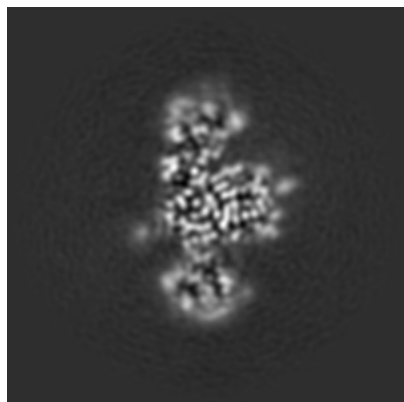


Z Index: 150

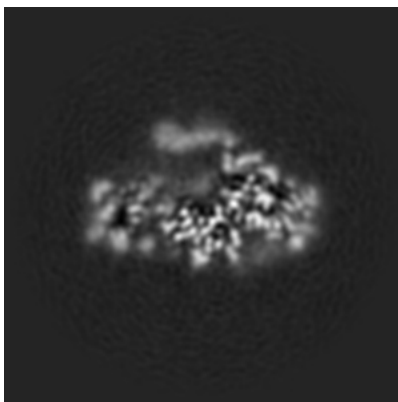
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

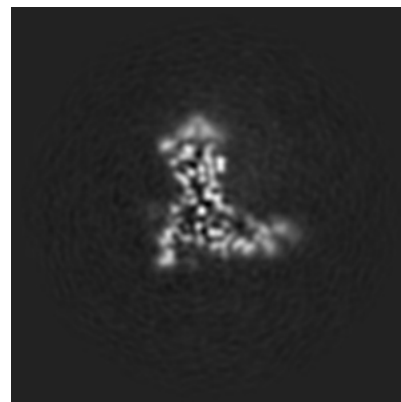
6.3.1 Primary map



X Index: 146

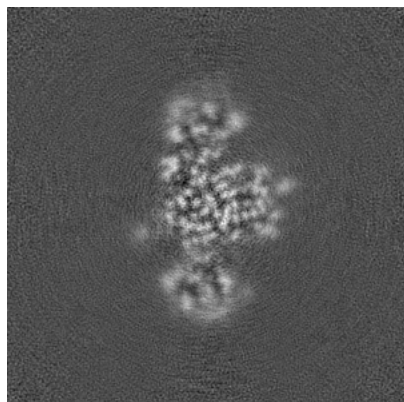


Y Index: 137

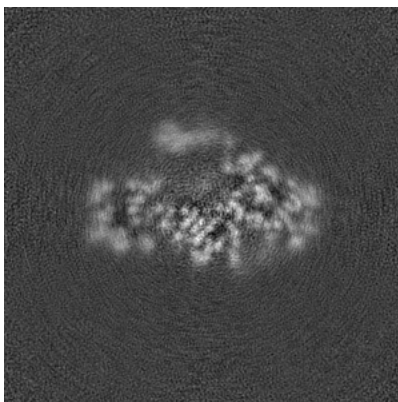


Z Index: 164

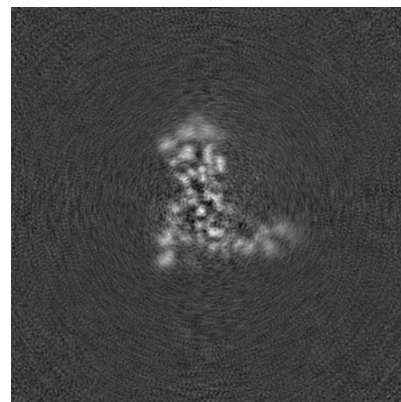
6.3.2 Raw map



X Index: 146



Y Index: 139

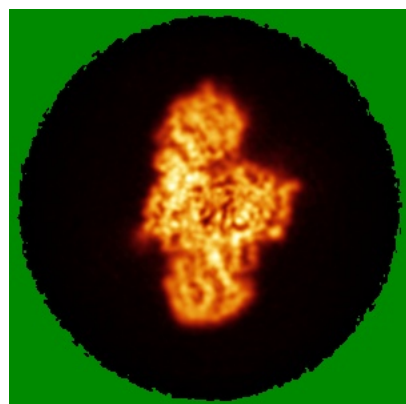


Z Index: 163

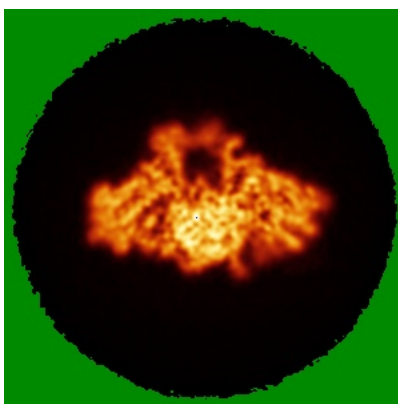
The images above show the largest variance slices of the map in three orthogonal directions.

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

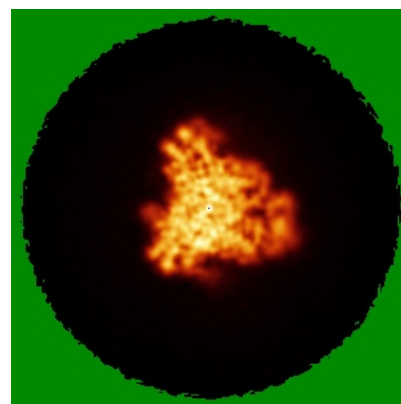
6.4.1 Primary map



X

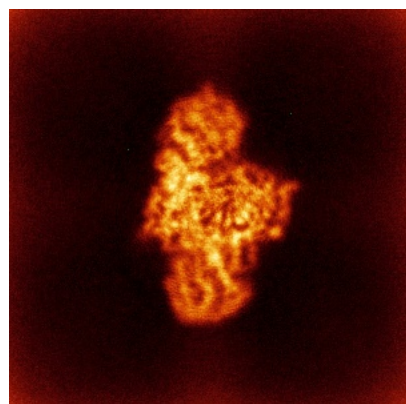


Y

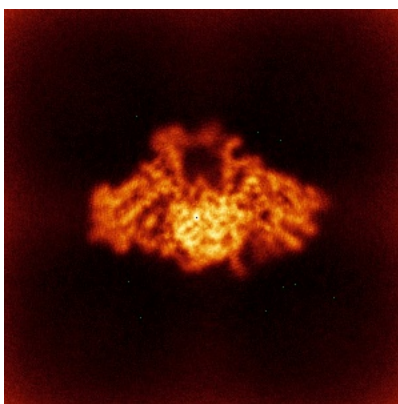


Z

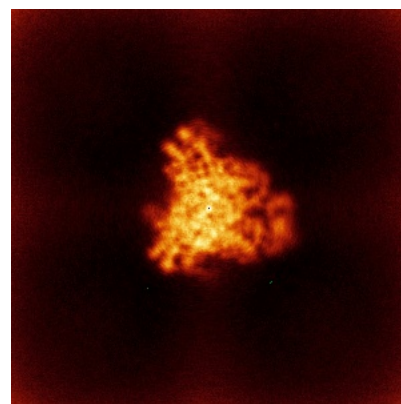
6.4.2 Raw map



X



Y

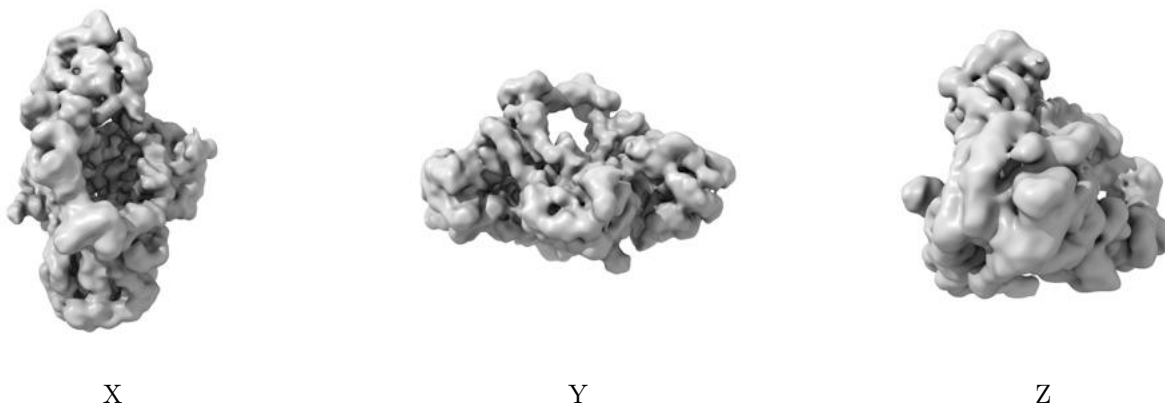


Z

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.

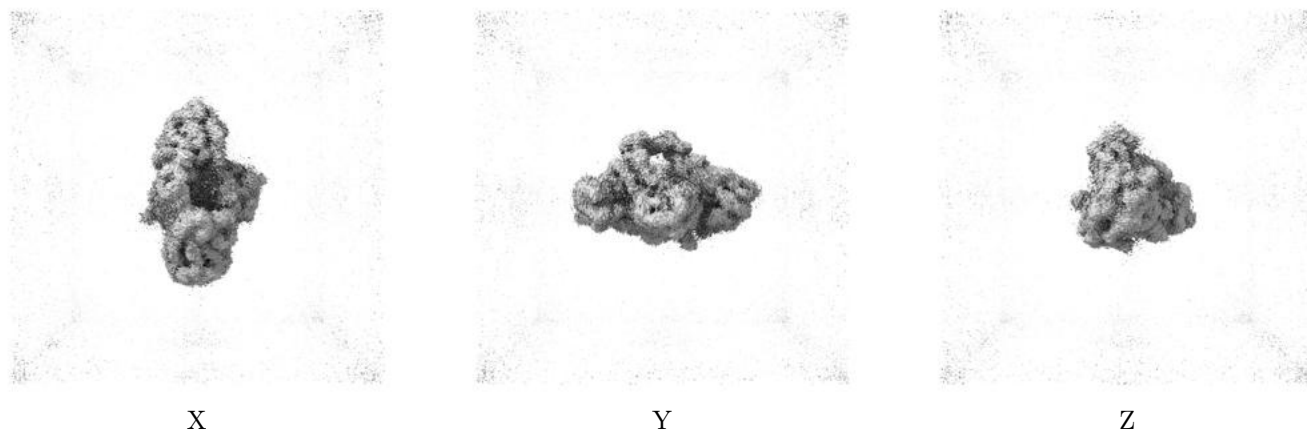
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0308. 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



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.

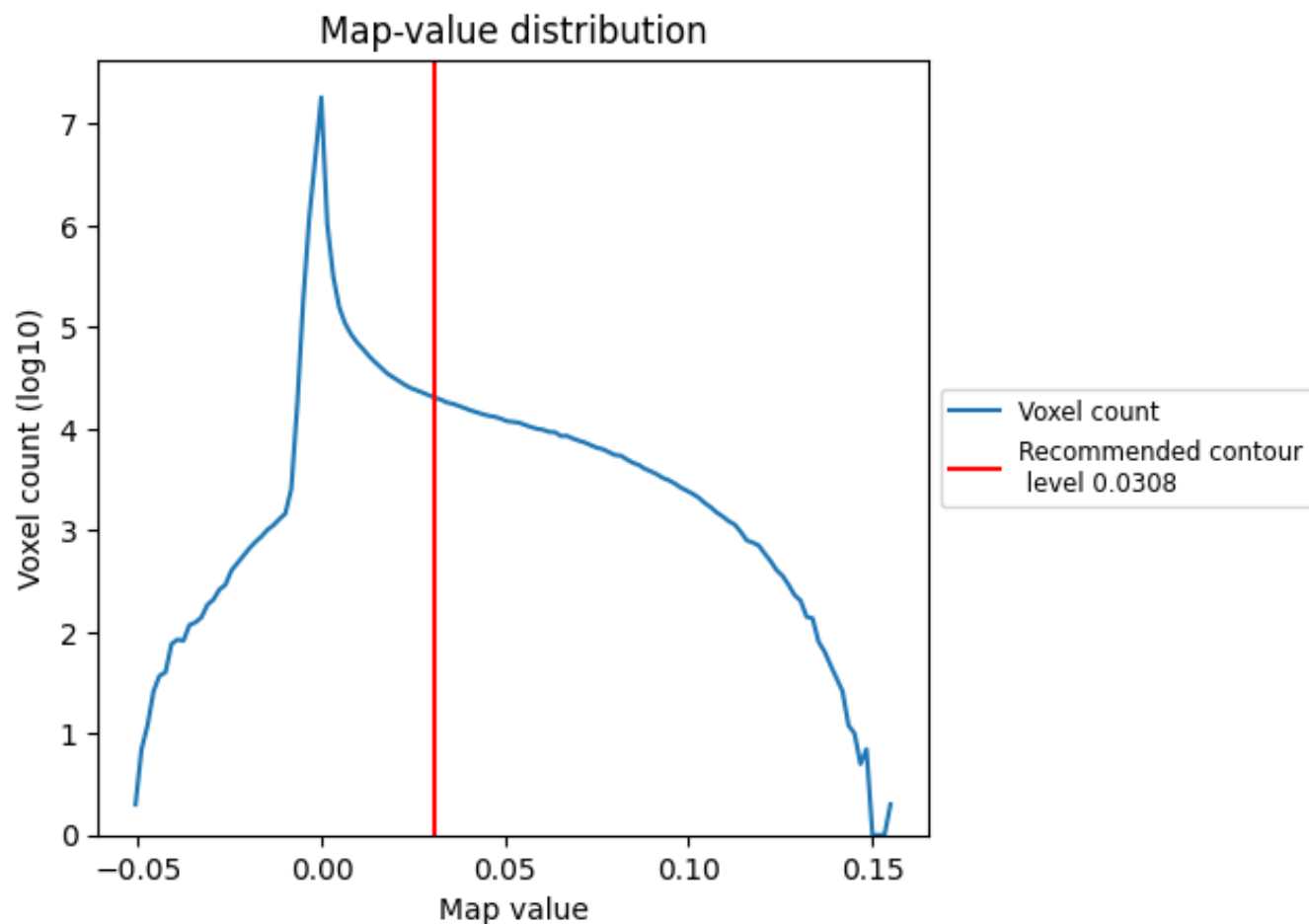
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

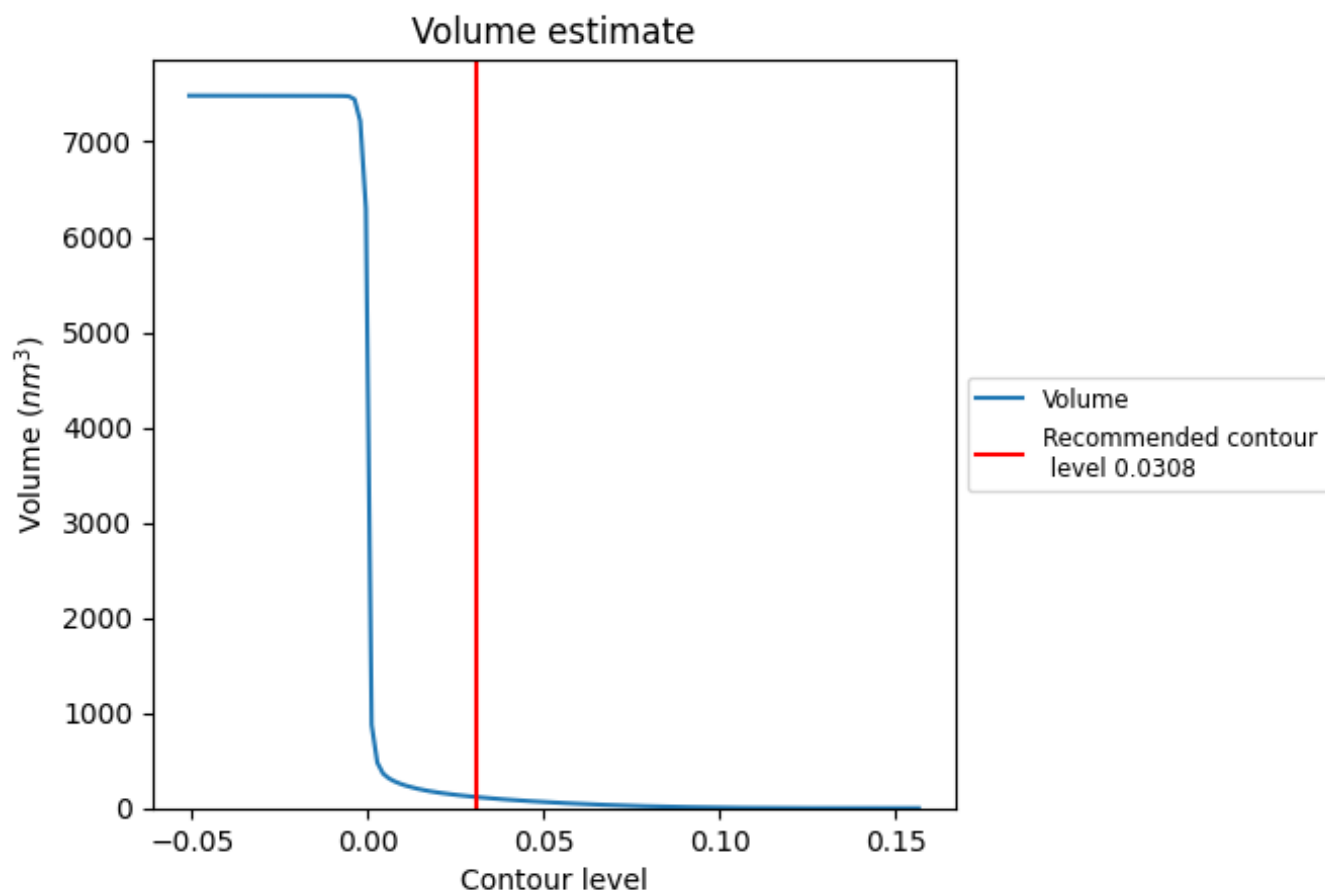
This section contains the results of statistical analysis of the map.

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.

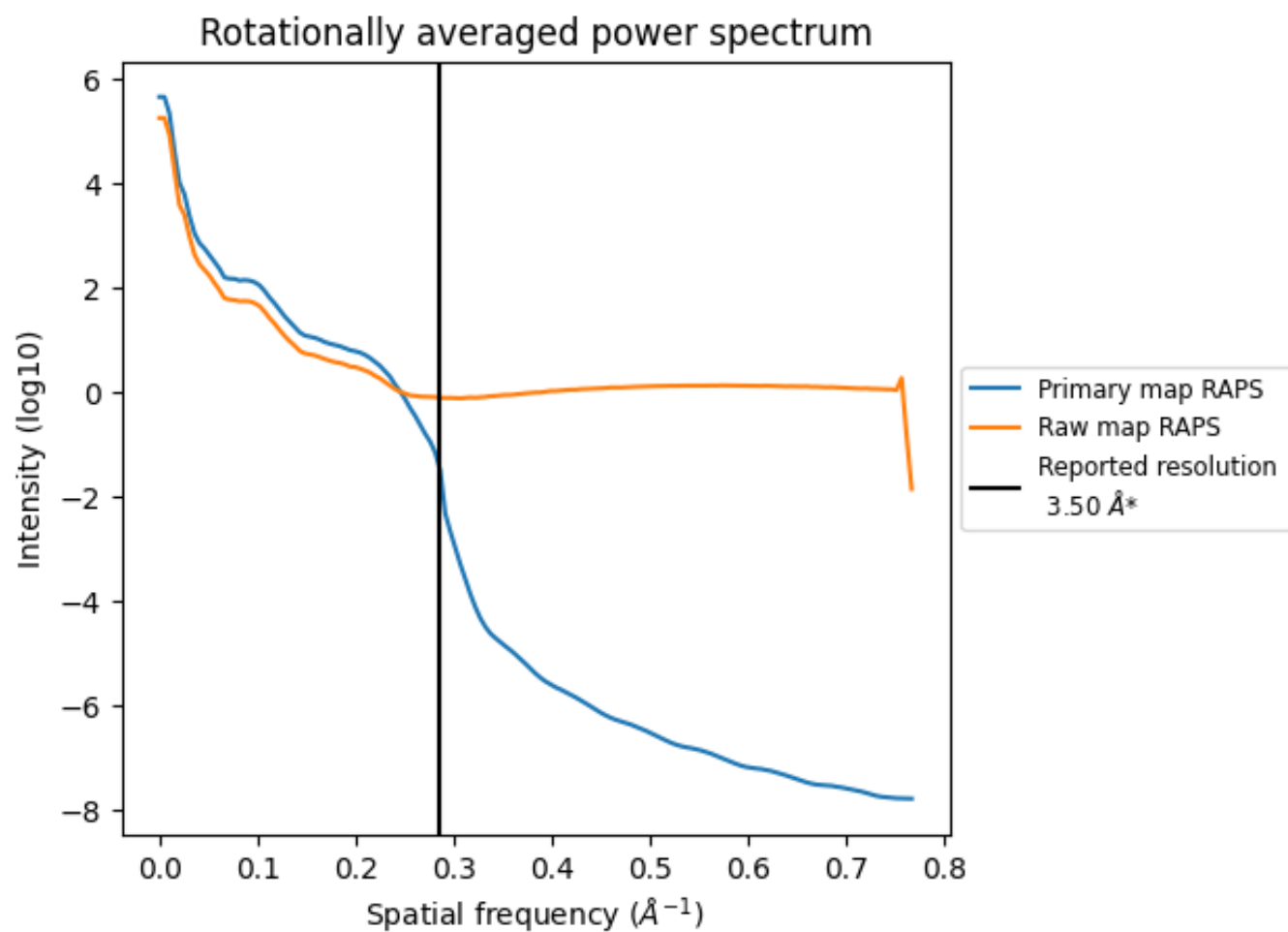
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 117 nm³; this corresponds to an approximate mass of 106 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 ⓘ

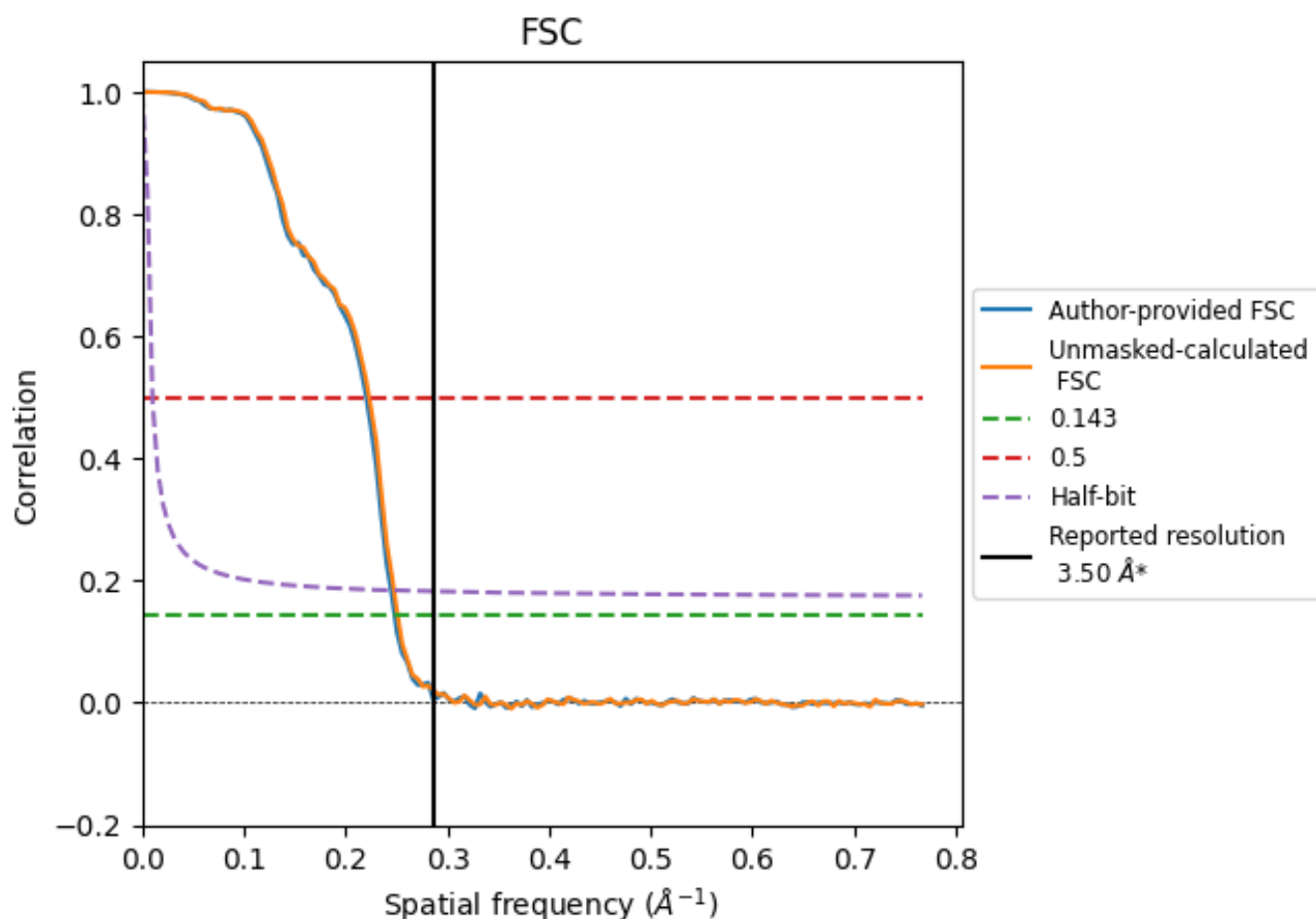


*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

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 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	4.03	4.54	4.08
Unmasked-calculated*	3.98	4.48	4.04

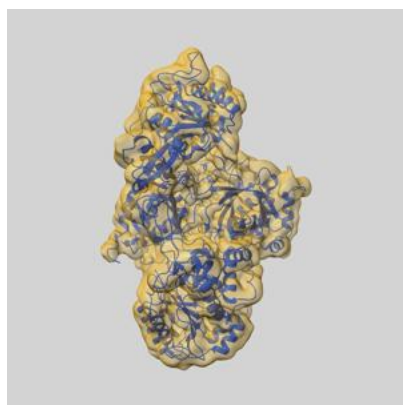
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.03 differs from the reported value 3.5 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.98 differs from the reported value 3.5 by more than 10 %

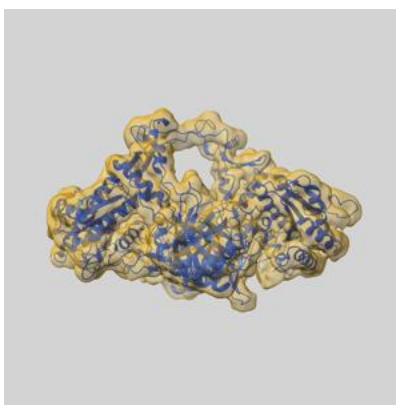
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14955 and PDB model 7ZT6. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

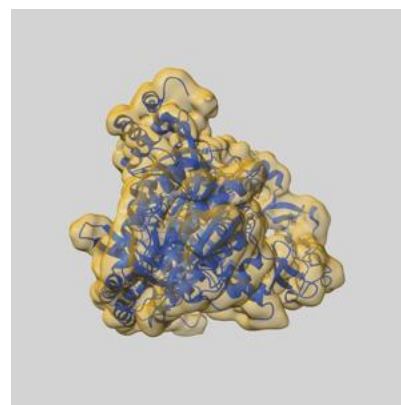
9.1 Map-model overlay [i](#)



X



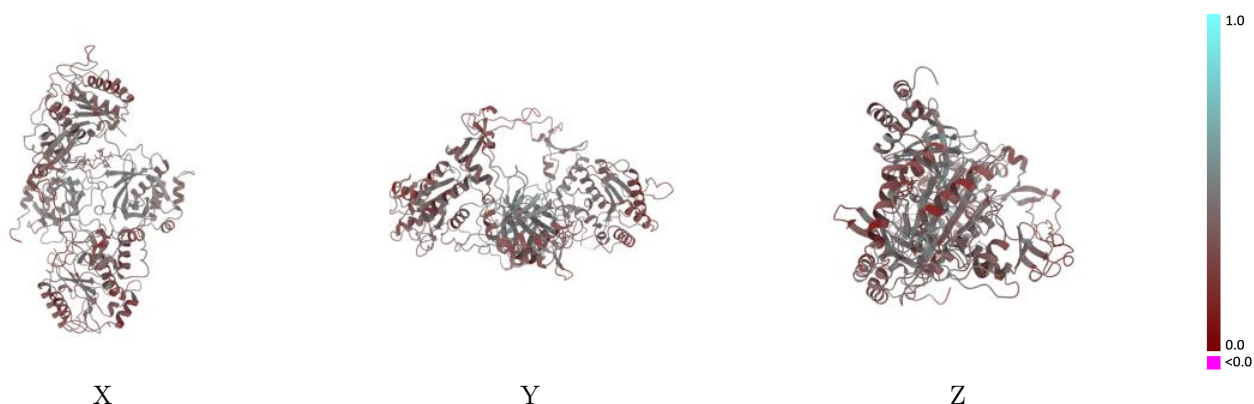
Y



Z

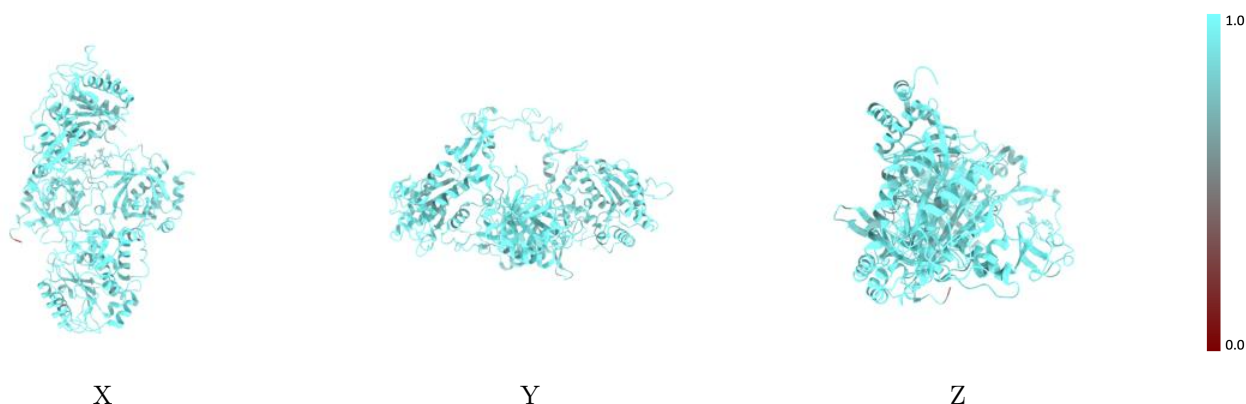
The images above show the 3D surface view of the map at the recommended contour level 0.0308 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



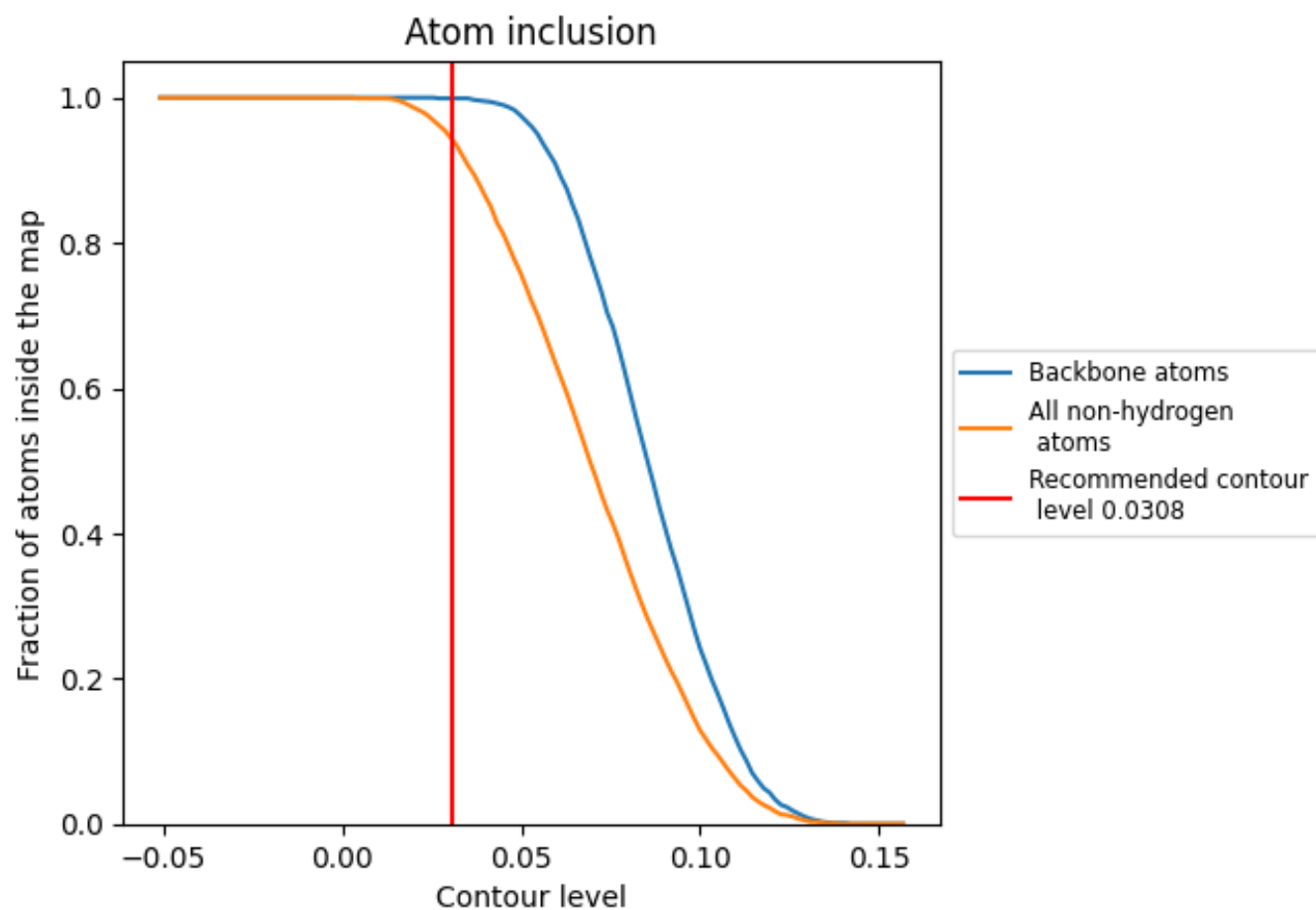
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0308).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 94% 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 (0.0308) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9420	0.3870
A	0.9480	0.3840
B	0.9370	0.3900

