



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 11:27 AM UTC

PDB ID : 6UTI / pdb_00006uti
EMDB ID : EMD-20880
Title : Allosteric coupling between alpha-rings of 20S proteasome, 20S proteasome with singly capped PAN complex
Authors : Cheng, Y.; Yu, Z.
Deposited on : 2019-10-29
Resolution : 3.40 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
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

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Mol	Chain	Length	Quality of chain
1	F	227	5% 91% 8%
1	G	227	91% 7%
2	O	227	87% 13%
2	P	227	87% 13%
2	Q	227	86% 14%
2	R	227	87% 13%
2	S	227	86% 14%
2	T	227	88% 12%
2	U	227	86% 14%
3	H	203	94% 6%
3	I	203	95% 5%
3	J	203	95% 5%
3	K	203	96% 5%
3	L	203	96% 5%
3	M	203	96% 5%
3	N	203	95% 5%
3	V	203	96% 5%
3	W	203	95% 5%
3	X	203	94% 6%
3	Y	203	95% 5%
3	Z	203	95% 5%
3	a	203	94% 6%
3	b	203	94% 6%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 46396 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 Proteasome subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	225	1748	1108	296	341	3	0	0
1	B	225	1748	1108	296	341	3	0	0
1	C	225	1748	1108	296	341	3	0	0
1	D	225	1748	1108	296	341	3	0	0
1	E	225	1748	1108	296	341	3	0	0
1	F	225	1748	1108	296	341	3	0	0
1	G	225	1748	1108	296	341	3	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	66	ALA	LYS	conflict	UNP P25156
B	66	ALA	LYS	conflict	UNP P25156
C	66	ALA	LYS	conflict	UNP P25156
D	66	ALA	LYS	conflict	UNP P25156
E	66	ALA	LYS	conflict	UNP P25156
F	66	ALA	LYS	conflict	UNP P25156
G	66	ALA	LYS	conflict	UNP P25156

- Molecule 2 is a protein called Proteasome subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	O	227	1766	1123	296	344	3	0	0
2	P	227	1766	1123	296	344	3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Q	227	Total	C	N	O	S	0	0
			1766	1123	296	344	3		
2	R	227	Total	C	N	O	S	0	0
			1766	1123	296	344	3		
2	S	227	Total	C	N	O	S	0	0
			1766	1123	296	344	3		
2	T	227	Total	C	N	O	S	0	0
			1766	1123	296	344	3		
2	U	227	Total	C	N	O	S	0	0
			1766	1123	296	344	3		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	28	LEU	ARG	engineered mutation	UNP P25156
P	28	LEU	ARG	engineered mutation	UNP P25156
Q	28	LEU	ARG	engineered mutation	UNP P25156
R	28	LEU	ARG	engineered mutation	UNP P25156
S	28	LEU	ARG	engineered mutation	UNP P25156
T	28	LEU	ARG	engineered mutation	UNP P25156
U	28	LEU	ARG	engineered mutation	UNP P25156

- Molecule 3 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		
3	I	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		
3	J	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		
3	K	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		
3	L	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		
3	M	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		
3	N	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		
3	V	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		
3	W	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		

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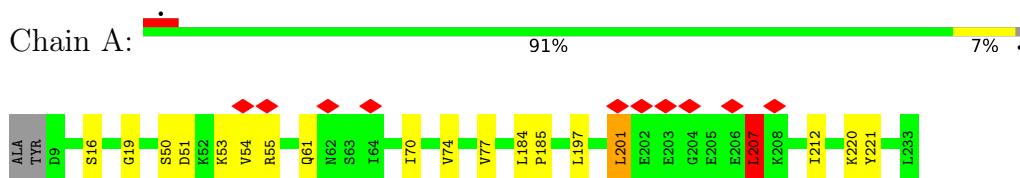
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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	X	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		
3	Y	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		
3	Z	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		
3	a	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		
3	b	203	Total	C	N	O	S	0	0
			1557	985	264	297	11		

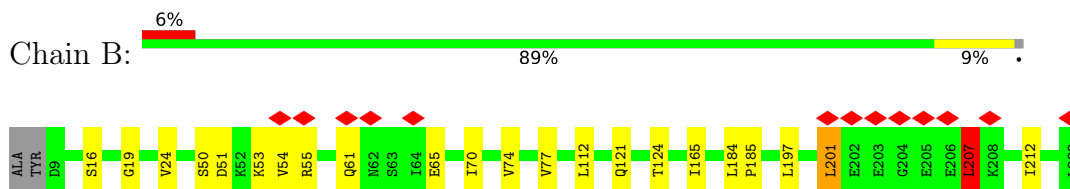
3 Residue-property plots [i](#)

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.

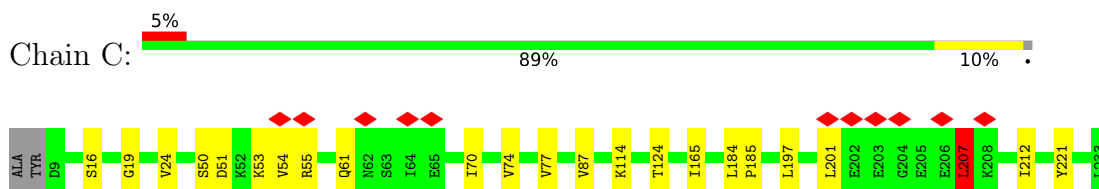
- Molecule 1: Proteasome subunit alpha



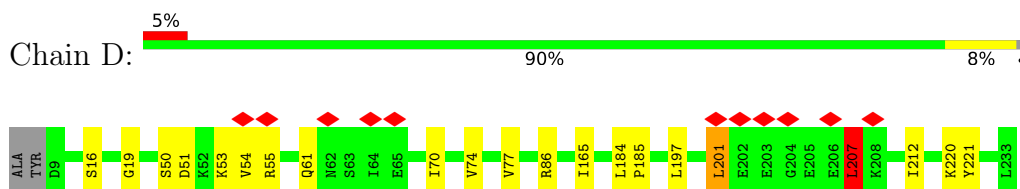
- Molecule 1: Proteasome subunit alpha



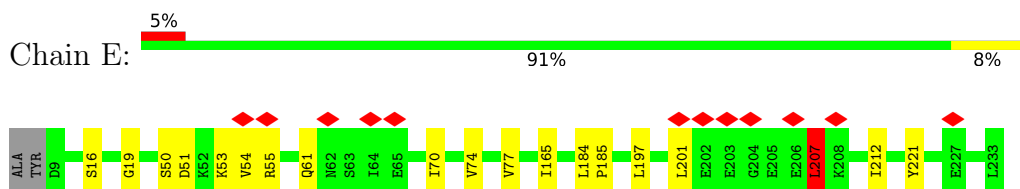
- Molecule 1: Proteasome subunit alpha



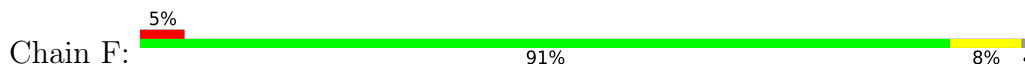
- Molecule 1: Proteasome subunit alpha



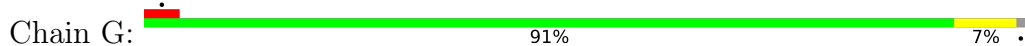
- Molecule 1: Proteasome subunit alpha



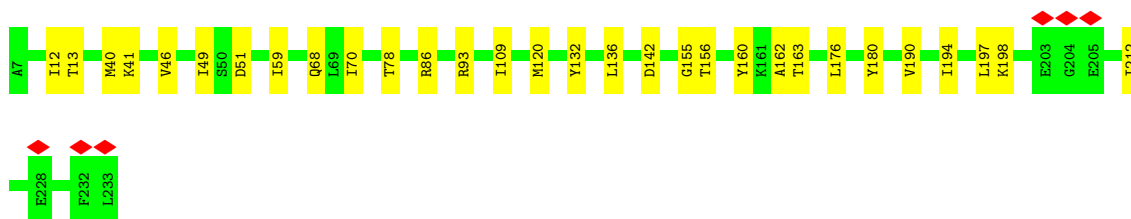
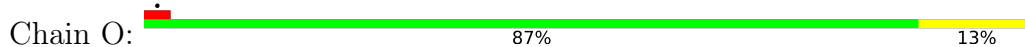
• Molecule 1: Proteasome subunit alpha



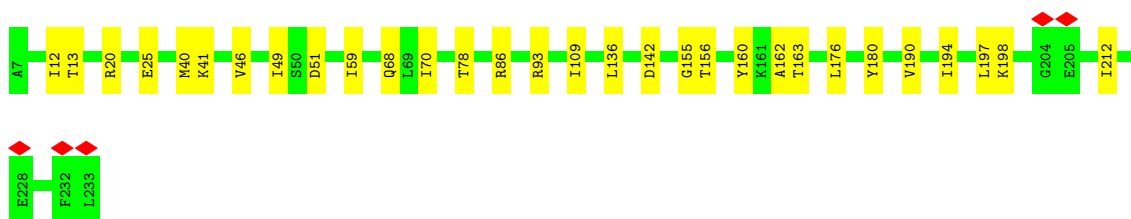
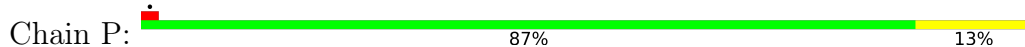
• Molecule 1: Proteasome subunit alpha



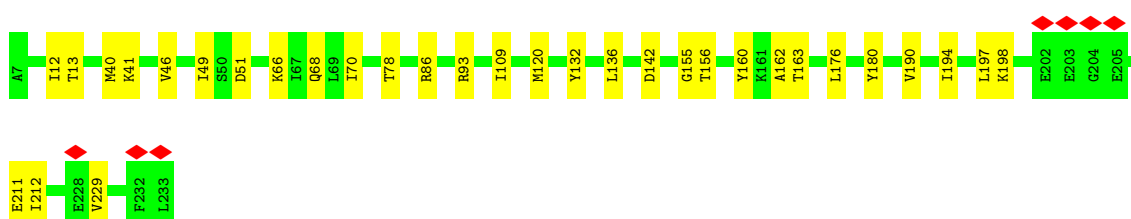
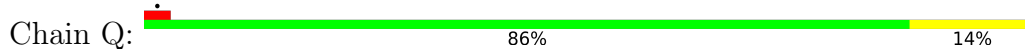
• Molecule 2: Proteasome subunit alpha




• Molecule 2: Proteasome subunit alpha

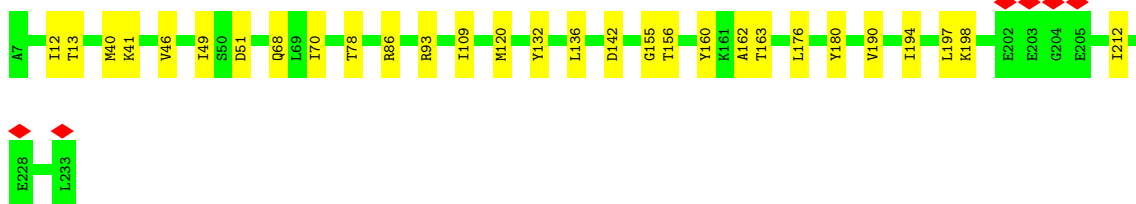


• Molecule 2: Proteasome subunit alpha




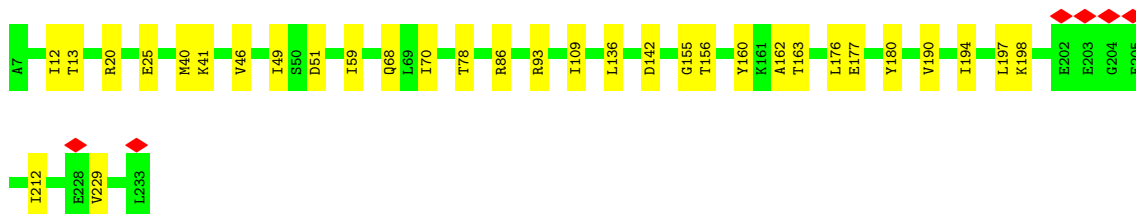
• Molecule 2: Proteasome subunit alpha

Chain R:  87% 13%




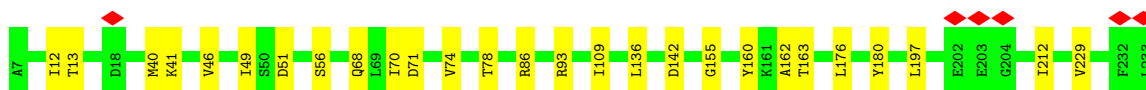
- Molecule 2: Proteasome subunit alpha

Chain S:  86% 14%




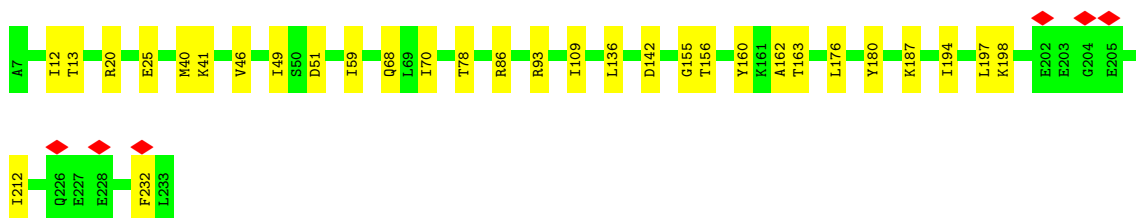
- Molecule 2: Proteasome subunit alpha

Chain T:  88% 12%



- Molecule 2: Proteasome subunit alpha

Chain U:  86% 14%



- Molecule 3: Proteasome subunit beta

Chain H:  94% 6%



- Molecule 3: Proteasome subunit beta

Chain I:  95% 5%



- Molecule 3: Proteasome subunit beta



- Molecule 3: Proteasome subunit beta



- Molecule 3: Proteasome subunit beta



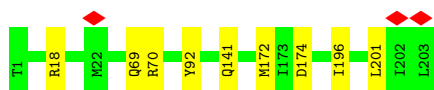
- Molecule 3: Proteasome subunit beta



- Molecule 3: Proteasome subunit beta



- Molecule 3: Proteasome subunit beta



- Molecule 3: Proteasome subunit beta



● Molecule 3: Proteasome subunit beta



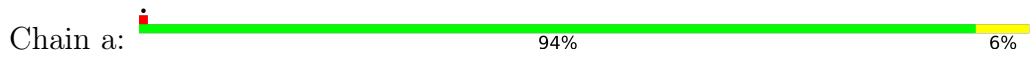
● Molecule 3: Proteasome subunit beta



● Molecule 3: Proteasome subunit beta



● Molecule 3: Proteasome subunit beta



● Molecule 3: Proteasome subunit beta



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	33000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	8.774	Depositor
Minimum map value	-5.580	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.255	Depositor
Recommended contour level	0.836	Depositor
Map size (\AA)	414.72003, 414.72003, 414.72003	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	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	0.35	0/1771	0.78	2/2387 (0.1%)
1	B	0.36	0/1771	0.79	2/2387 (0.1%)
1	C	0.36	0/1771	0.78	2/2387 (0.1%)
1	D	0.35	0/1771	0.78	2/2387 (0.1%)
1	E	0.36	0/1771	0.78	2/2387 (0.1%)
1	F	0.35	0/1771	0.78	2/2387 (0.1%)
1	G	0.35	0/1771	0.78	2/2387 (0.1%)
2	O	0.33	0/1790	0.73	0/2413
2	P	0.33	0/1790	0.74	0/2413
2	Q	0.33	0/1790	0.72	0/2413
2	R	0.32	0/1790	0.72	0/2413
2	S	0.32	0/1790	0.72	0/2413
2	T	0.32	0/1790	0.72	0/2413
2	U	0.33	0/1790	0.74	0/2413
3	H	0.27	0/1576	0.64	0/2129
3	I	0.27	0/1576	0.64	0/2129
3	J	0.27	0/1576	0.64	0/2129
3	K	0.27	0/1576	0.64	0/2129
3	L	0.27	0/1576	0.64	0/2129
3	M	0.27	0/1576	0.64	0/2129
3	N	0.27	0/1576	0.64	0/2129
3	V	0.27	0/1576	0.64	0/2129
3	W	0.27	0/1576	0.64	0/2129
3	X	0.27	0/1576	0.64	0/2129
3	Y	0.27	0/1576	0.64	0/2129
3	Z	0.27	0/1576	0.64	0/2129
3	a	0.27	0/1576	0.64	0/2129
3	b	0.27	0/1576	0.64	0/2129
All	All	0.31	0/46991	0.70	14/63406 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
All	All	0	7

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	207	LEU	CA-C-N	8.03	136.89	121.54
1	A	207	LEU	C-N-CA	8.03	136.89	121.54
1	F	207	LEU	CA-C-N	8.01	136.85	121.54
1	F	207	LEU	C-N-CA	8.01	136.85	121.54
1	C	207	LEU	CA-C-N	8.01	136.83	121.54

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	207	LEU	Peptide
1	B	207	LEU	Peptide
1	C	207	LEU	Peptide
1	D	207	LEU	Peptide
1	E	207	LEU	Peptide

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	1748	0	1778	12	0
1	B	1748	0	1778	16	0
1	C	1748	0	1778	16	0
1	D	1748	0	1778	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1748	0	1778	13	0
1	F	1748	0	1778	10	0
1	G	1748	0	1778	12	0
2	O	1766	0	1798	21	0
2	P	1766	0	1798	20	0
2	Q	1766	0	1798	21	0
2	R	1766	0	1798	20	0
2	S	1766	0	1798	23	0
2	T	1766	0	1798	19	0
2	U	1766	0	1798	20	0
3	H	1557	0	1609	8	0
3	I	1557	0	1609	7	0
3	J	1557	0	1609	8	0
3	K	1557	0	1609	6	0
3	L	1557	0	1609	6	0
3	M	1557	0	1609	5	0
3	N	1557	0	1609	7	0
3	V	1557	0	1609	6	0
3	W	1557	0	1609	7	0
3	X	1557	0	1609	8	0
3	Y	1557	0	1609	8	0
3	Z	1557	0	1609	7	0
3	a	1557	0	1609	8	0
3	b	1557	0	1609	8	0
All	All	46396	0	47558	299	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 299 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:16:SER:HG	1:A:19:GLY:H	1.39	0.69
3:H:141:GLN:HE21	3:a:141:GLN:HE21	1.46	0.64
1:C:16:SER:OG	1:C:19:GLY:N	2.32	0.63
1:B:16:SER:OG	1:B:19:GLY:N	2.32	0.62
1:E:16:SER:OG	1:E:19:GLY:N	2.31	0.62

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	186/187 (100%)	184 (99%)	2 (1%)	65	74
1	B	186/187 (100%)	184 (99%)	2 (1%)	65	74
1	C	186/187 (100%)	185 (100%)	1 (0%)	81	81
1	D	186/187 (100%)	184 (99%)	2 (1%)	65	74
1	E	186/187 (100%)	185 (100%)	1 (0%)	81	81
1	F	186/187 (100%)	184 (99%)	2 (1%)	65	74
1	G	186/187 (100%)	185 (100%)	1 (0%)	81	81
2	O	188/188 (100%)	188 (100%)	0	100	100
2	P	188/188 (100%)	188 (100%)	0	100	100
2	Q	188/188 (100%)	188 (100%)	0	100	100
2	R	188/188 (100%)	188 (100%)	0	100	100
2	S	188/188 (100%)	188 (100%)	0	100	100
2	T	188/188 (100%)	188 (100%)	0	100	100
2	U	188/188 (100%)	188 (100%)	0	100	100
3	H	170/170 (100%)	170 (100%)	0	100	100
3	I	170/170 (100%)	170 (100%)	0	100	100
3	J	170/170 (100%)	170 (100%)	0	100	100
3	K	170/170 (100%)	170 (100%)	0	100	100
3	L	170/170 (100%)	170 (100%)	0	100	100
3	M	170/170 (100%)	170 (100%)	0	100	100
3	N	170/170 (100%)	170 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	V	170/170 (100%)	170 (100%)	0	100	100
3	W	170/170 (100%)	170 (100%)	0	100	100
3	X	170/170 (100%)	170 (100%)	0	100	100
3	Y	170/170 (100%)	170 (100%)	0	100	100
3	Z	170/170 (100%)	170 (100%)	0	100	100
3	a	170/170 (100%)	170 (100%)	0	100	100
3	b	170/170 (100%)	170 (100%)	0	100	100
All	All	4998/5005 (100%)	4987 (100%)	11 (0%)	85	85

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	212	ILE
1	F	201	LEU
1	G	212	ILE
1	F	212	ILE
1	C	212	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	121	GLN
2	R	68	GLN
3	Z	141	GLN
1	G	125	GLN
2	P	68	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](#)

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.

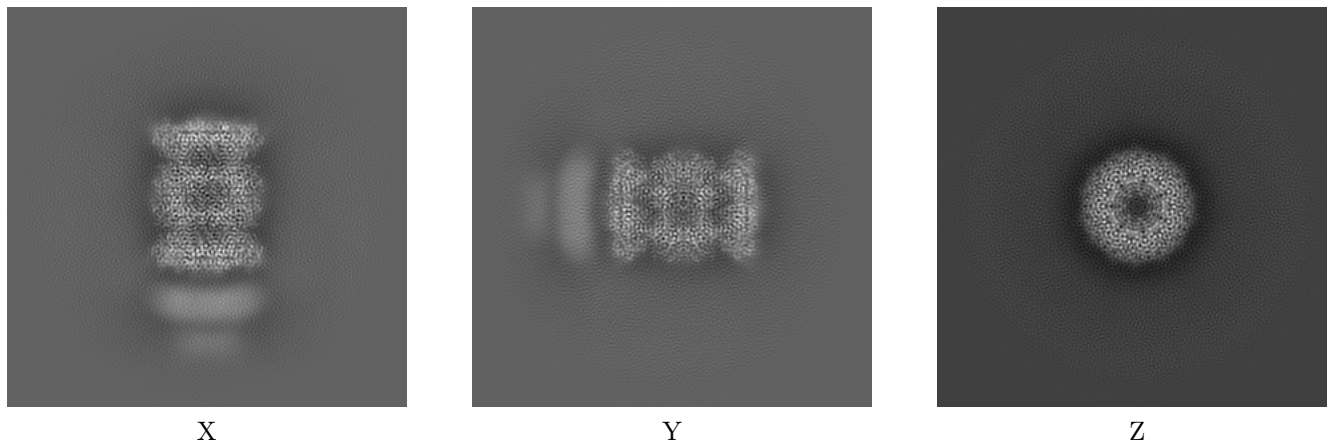
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20880. These allow visual inspection of the internal detail of the map and identification of artifacts.

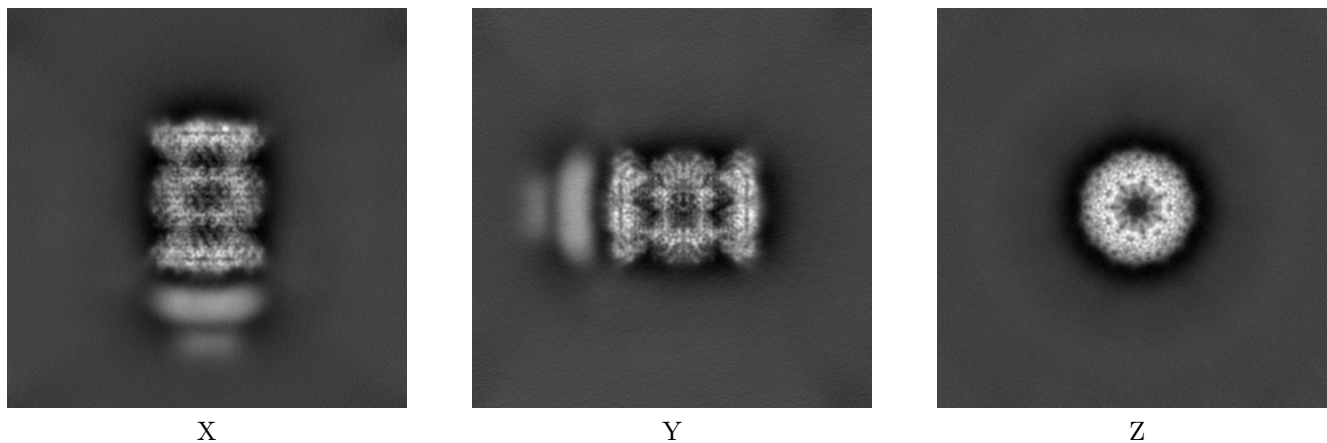
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



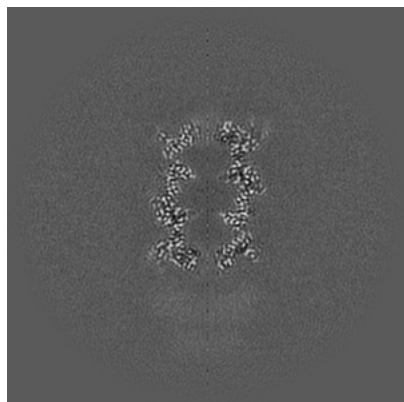
6.1.2 Raw map



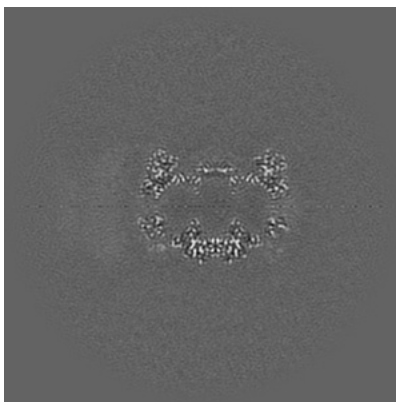
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

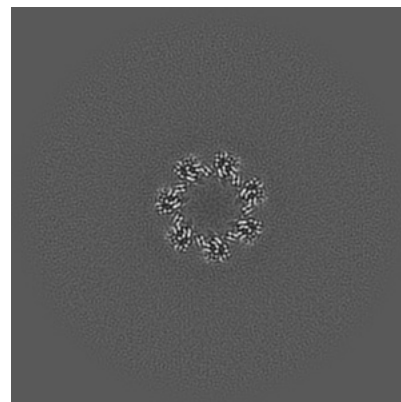
6.2.1 Primary map



X Index: 192

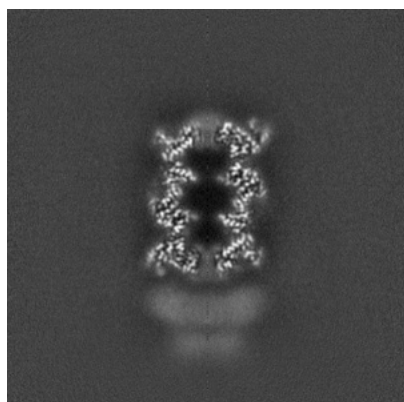


Y Index: 192

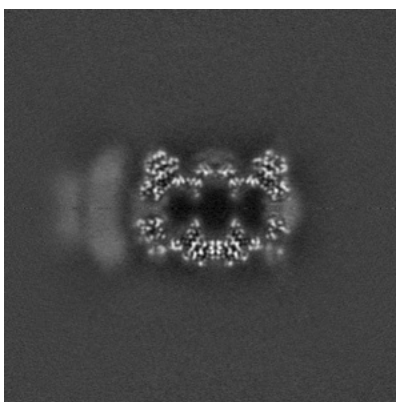


Z Index: 192

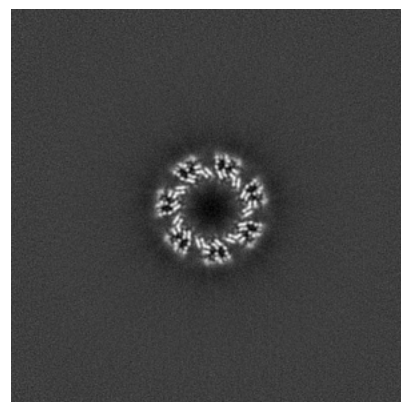
6.2.2 Raw map



X Index: 192



Y Index: 192

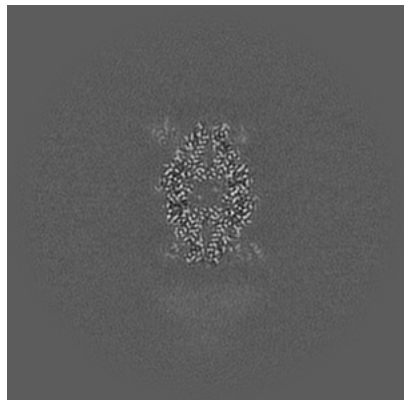


Z Index: 192

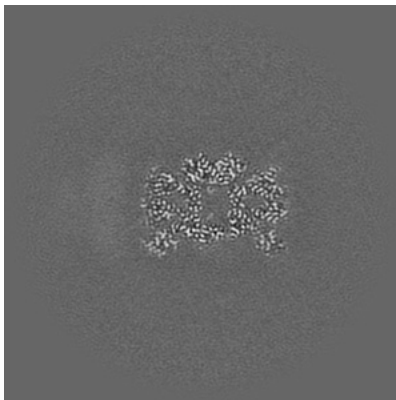
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

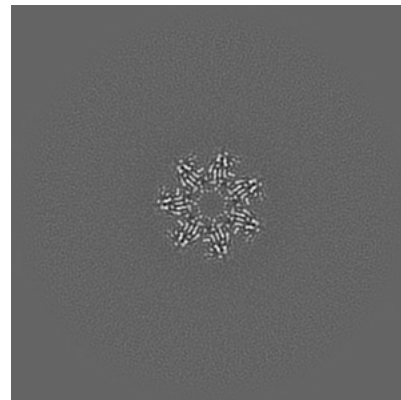
6.3.1 Primary map



X Index: 168

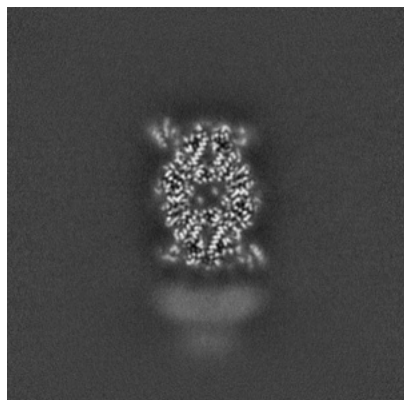


Y Index: 169

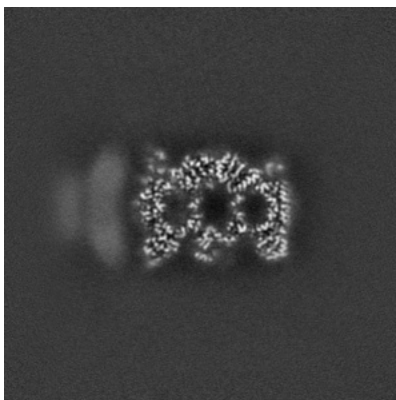


Z Index: 186

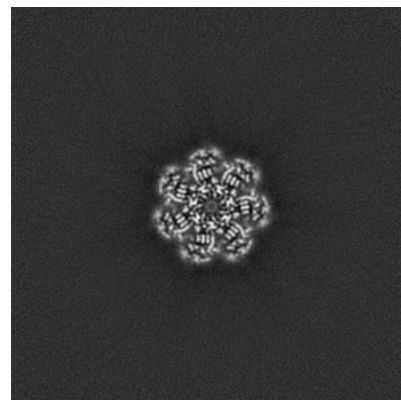
6.3.2 Raw map



X Index: 168



Y Index: 208

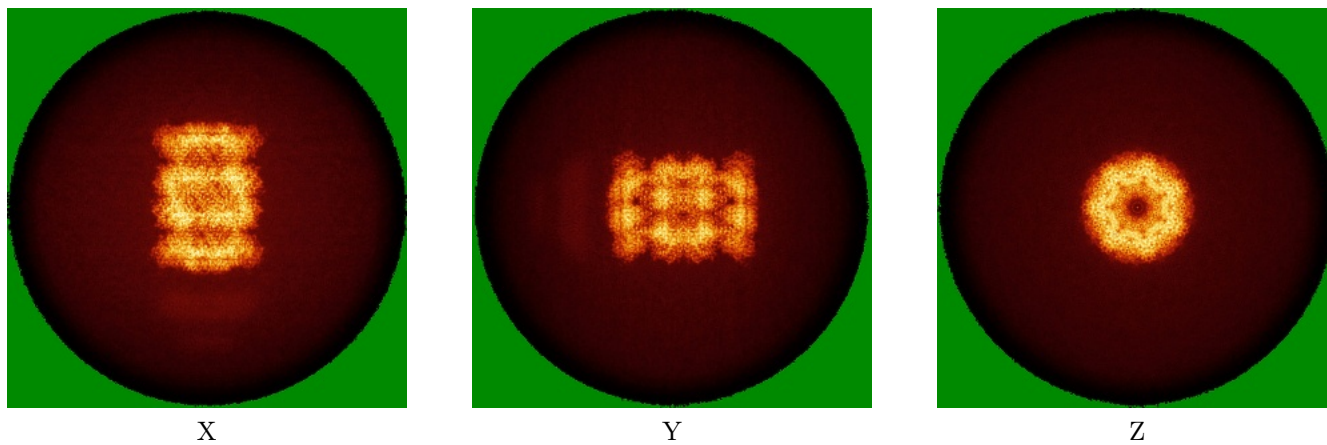


Z Index: 256

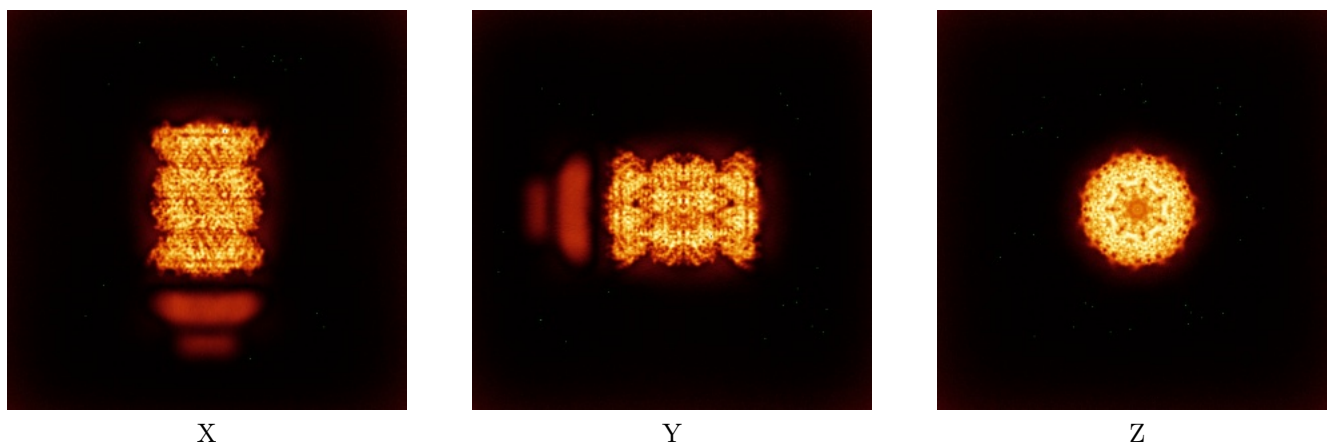
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

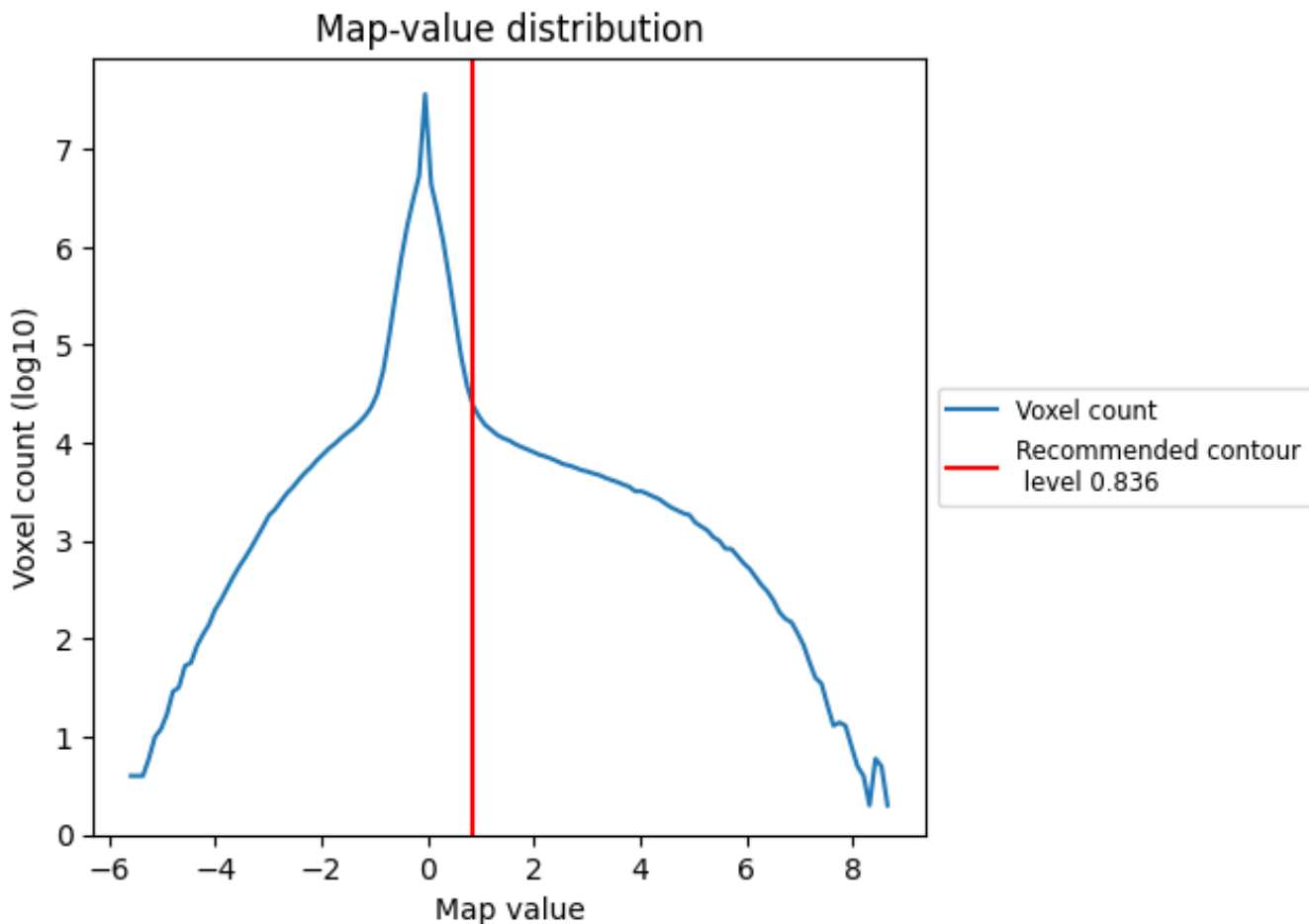
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

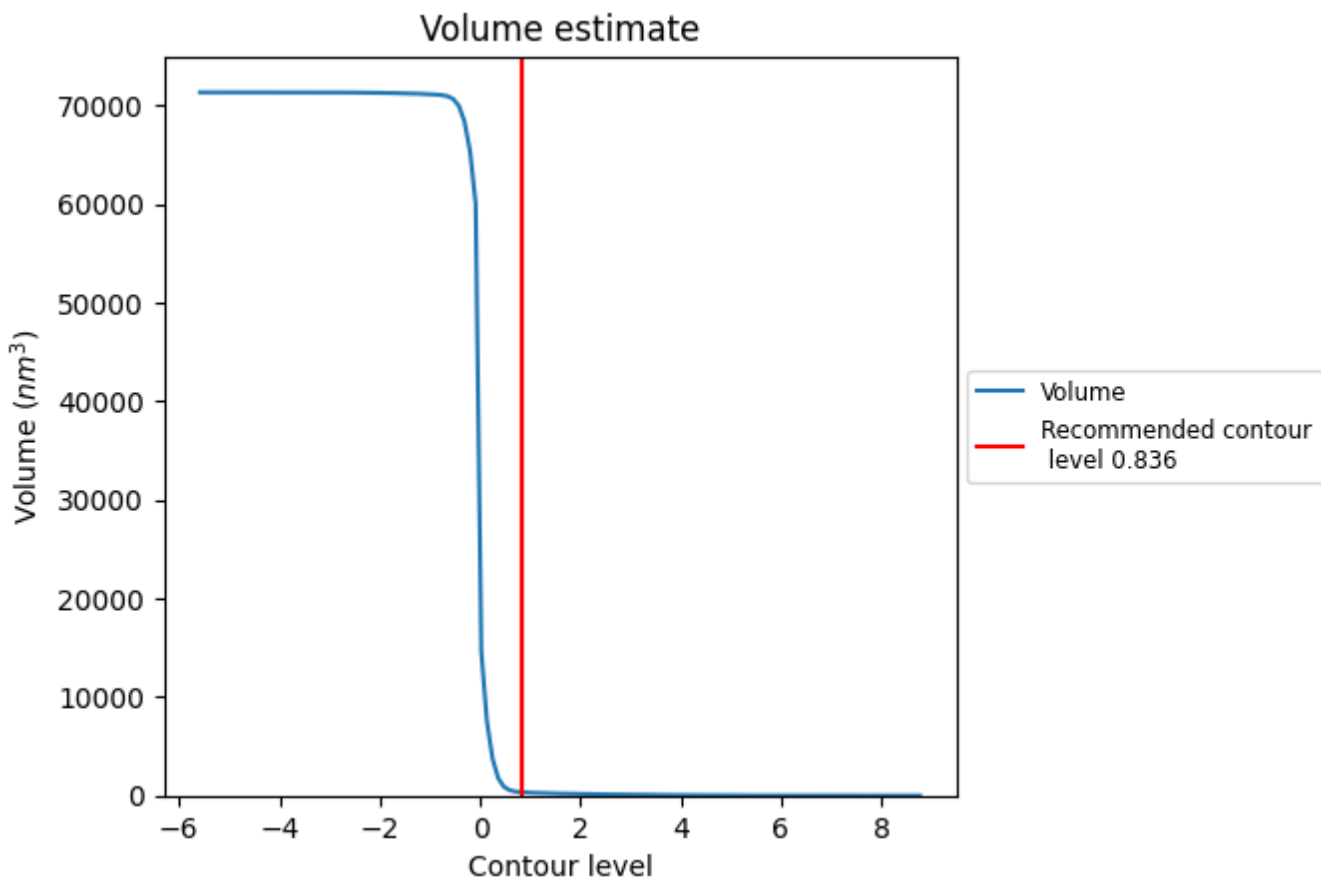
This section contains the results of statistical analysis of the map.

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.

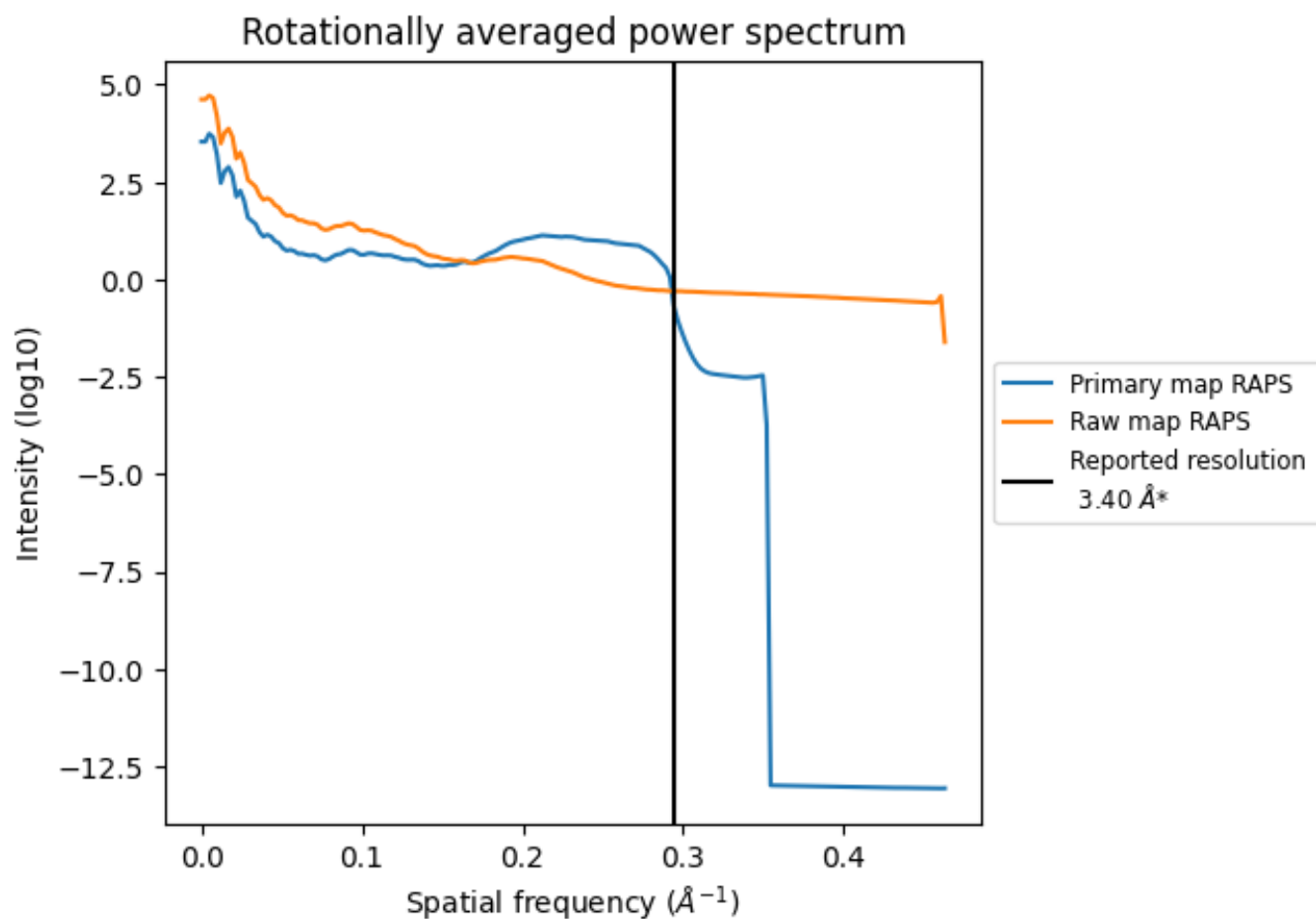
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 343 nm³; this corresponds to an approximate mass of 310 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 [i](#)

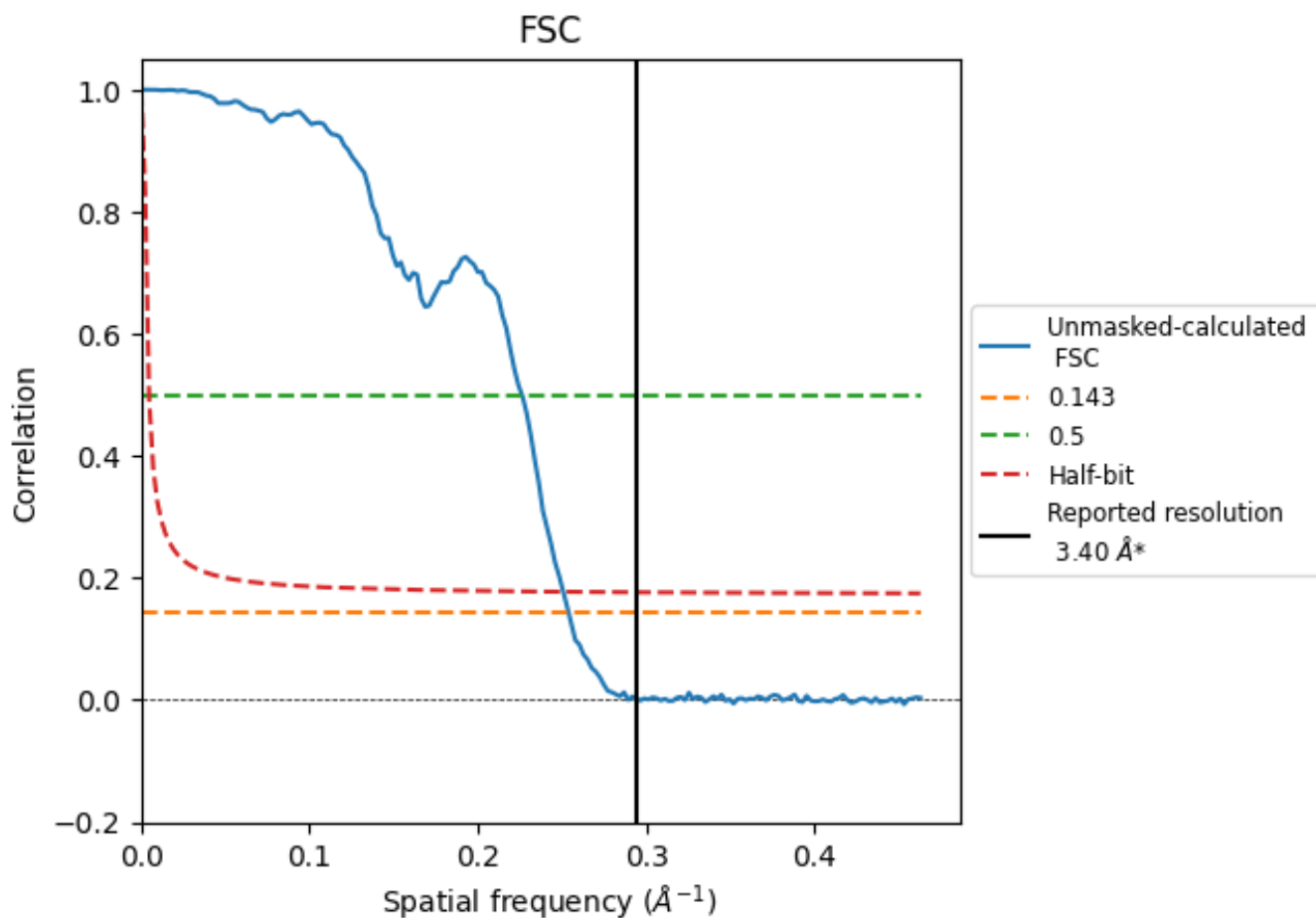


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

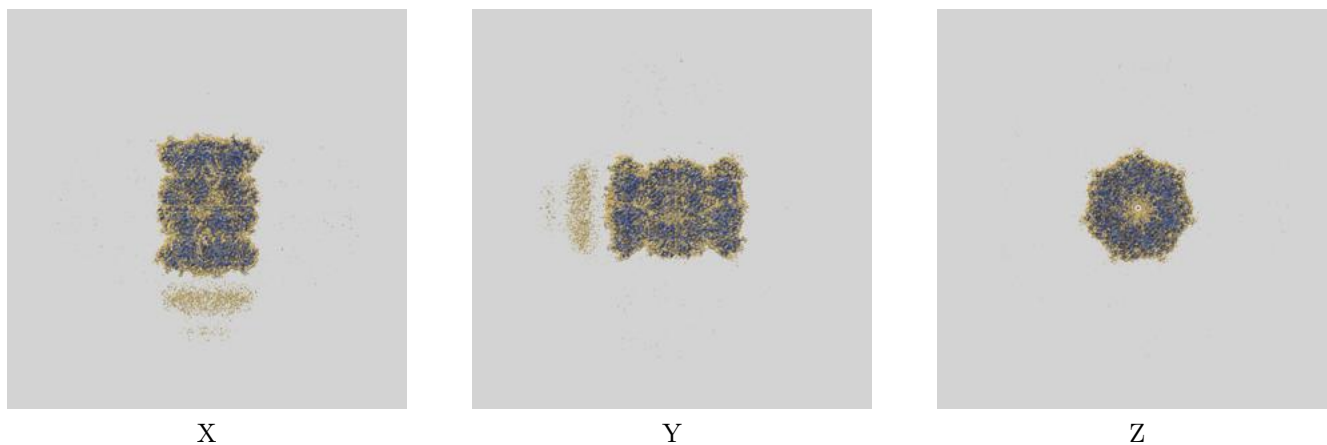
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.94	4.42	3.99

*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 3.94 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

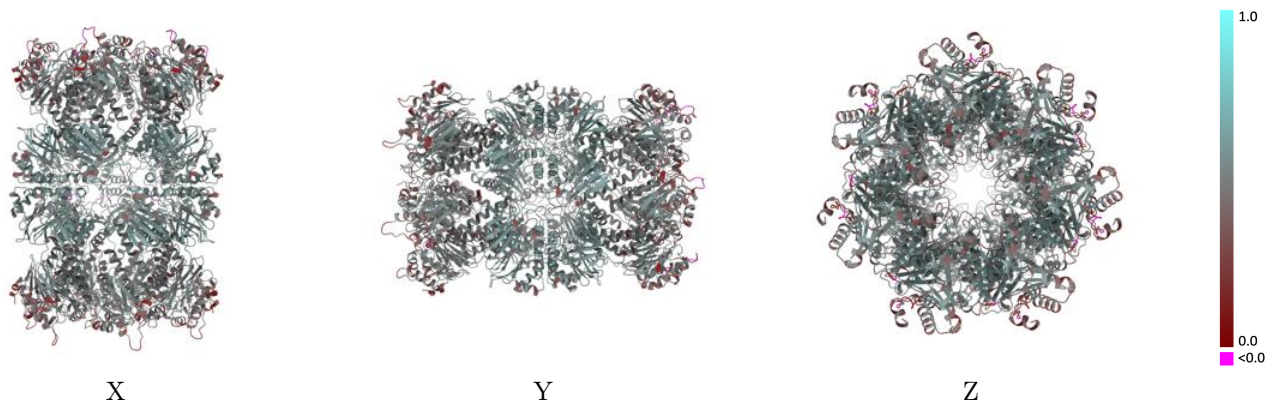
This section contains information regarding the fit between EMDB map EMD-20880 and PDB model 6UTI. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



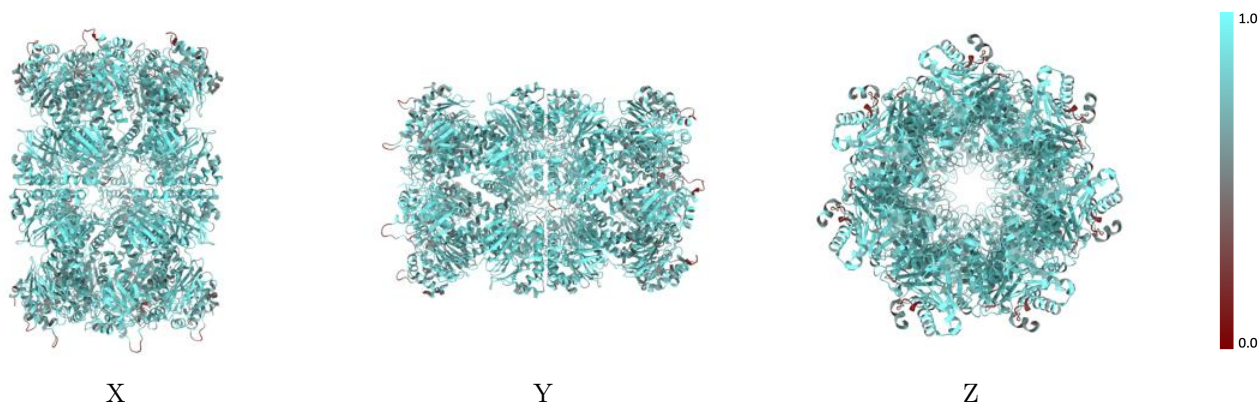
The images above show the 3D surface view of the map at the recommended contour level 0.836 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



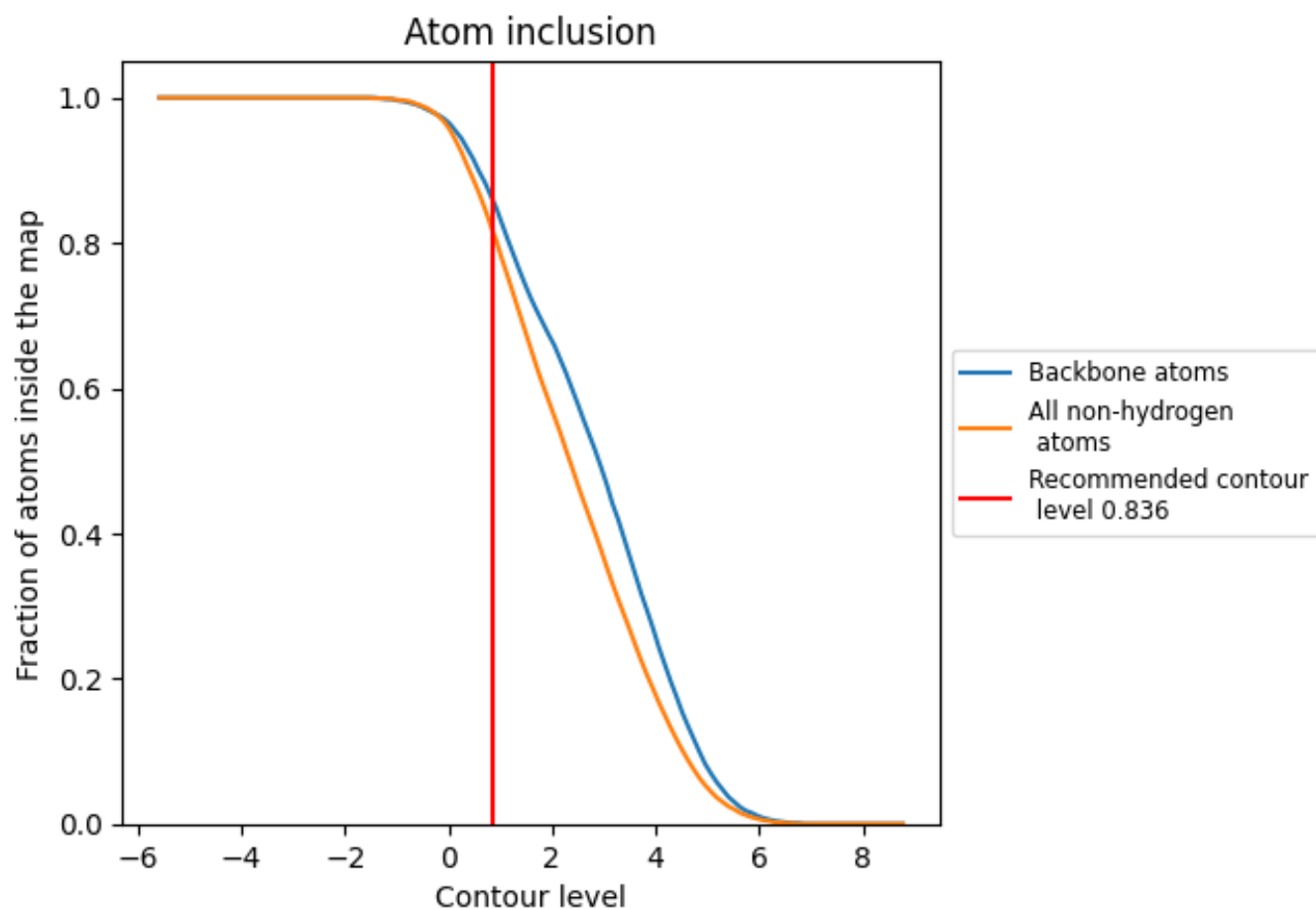
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.836).



























































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 82% 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 (0.836) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8200	 0.4810
A	 0.7690	 0.4340
B	 0.7620	 0.4230
C	 0.7680	 0.4300
D	 0.7710	 0.4350
E	 0.7700	 0.4330
F	 0.7680	 0.4340
G	 0.7720	 0.4370
H	 0.8690	 0.5280
I	 0.8680	 0.5310
J	 0.8700	 0.5290
K	 0.8680	 0.5290
L	 0.8680	 0.5280
M	 0.8710	 0.5290
N	 0.8700	 0.5280
O	 0.7810	 0.4470
P	 0.7840	 0.4500
Q	 0.7800	 0.4490
R	 0.7950	 0.4510
S	 0.7920	 0.4520
T	 0.7870	 0.4380
U	 0.7840	 0.4480
V	 0.8680	 0.5270
W	 0.8700	 0.5250
X	 0.8670	 0.5260
Y	 0.8660	 0.5270
Z	 0.8680	 0.5280
a	 0.8700	 0.5290
b	 0.8680	 0.5250

