



wwPDB EM Validation Summary Report ⓘ

Nov 27, 2022 – 05:11 PM EST

PDB ID : 7KEU
EMDB ID : EMD-22233
Title : Cryo-EM structure of the Caspase-1-CARD:ASC-CARD octamer
Authors : Hollingsworth, L.R.; David, L.; Li, Y.; Ruan, J.; Wu, H.
Deposited on : 2020-10-12
Resolution : 3.90 Å(reported)
Based on initial models : 6N1H, 5FNA

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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

PERCENTILES INFOmissingINFO

1 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5306 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 Caspase-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	85	Total	C	N	O	S	0	0
			666	417	112	131	6		
1	F	85	Total	C	N	O	S	0	0
			672	420	115	131	6		
1	G	85	Total	C	N	O	S	0	0
			666	417	112	131	6		
1	H	85	Total	C	N	O	S	0	0
			676	423	116	131	6		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	20	TRP	GLY	conflict	UNP P29466
F	20	TRP	GLY	conflict	UNP P29466
G	20	TRP	GLY	conflict	UNP P29466
H	20	TRP	GLY	conflict	UNP P29466

- Molecule 2 is a protein called Apoptosis-associated speck-like protein containing a CARD.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	82	Total	C	N	O	S	0	0
			648	411	113	122	2		
2	B	82	Total	C	N	O	S	0	0
			655	417	113	123	2		
2	C	82	Total	C	N	O	S	0	0
			662	421	117	122	2		
2	D	82	Total	C	N	O	S	0	0
			661	419	116	124	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	169	GLY	TRP	conflict	UNP Q9ULZ3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	169	GLY	TRP	conflict	UNP Q9ULZ3
C	169	GLY	TRP	conflict	UNP Q9ULZ3
D	169	GLY	TRP	conflict	UNP Q9ULZ3

SEQUENCE-PLOTS INFOmissingINFO

2 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	111053	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 ($e^-/\text{\AA}^2$)	57.12	Depositor
Minimum defocus (nm)	-800	Depositor
Maximum defocus (nm)	-2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.190	Depositor
Minimum map value	-0.080	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0439	Depositor
Map size (Å)	198.0, 198.0, 198.0	wwPDB
Map dimensions	120, 120, 120	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.65, 1.65, 1.65	Depositor

3 Model quality

3.1 Standard geometry

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	E	0.40	0/671	0.88	0/900
1	F	0.35	0/677	0.96	1/907 (0.1%)
1	G	0.35	0/671	0.84	0/900
1	H	0.35	0/681	0.91	2/911 (0.2%)
2	A	0.35	0/662	0.85	0/901
2	B	0.37	0/669	0.84	0/909
2	C	0.38	0/676	0.86	0/917
2	D	0.33	0/675	0.80	1/917 (0.1%)
All	All	0.36	0/5382	0.87	4/7262 (0.1%)

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
2	C	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	13	PHE	CB-CA-C	6.85	124.09	110.40
2	D	185	GLN	N-CA-CB	5.60	120.68	110.60
1	H	63	PRO	CB-CA-C	-5.50	98.26	112.00
1	H	53	LYS	CB-CA-C	-5.06	100.28	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	118	HIS	Mainchain

3.2 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	E	666	0	681	96	0
1	F	672	0	692	43	0
1	G	666	0	681	76	0
1	H	676	0	703	63	0
2	A	648	0	612	37	0
2	B	655	0	630	50	0
2	C	662	0	645	65	0
2	D	661	0	636	64	0
All	All	5306	0	5280	434	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 41.

The worst 5 of 434 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:G:11:LYS:NZ	1:G:58:ILE:HG23	1.07	1.36
1:G:11:LYS:NZ	1:G:58:ILE:CG2	1.88	1.35
1:E:11:LYS:NZ	1:E:61:VAL:CG2	1.90	1.33
1:G:11:LYS:HZ2	1:G:58:ILE:CG2	1.40	1.28
2:A:118:HIS:CD2	2:A:192:LEU:HD21	1.67	1.27

There are no symmetry-related clashes.

3.3 Torsion angles

3.3.1 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	E	83/85 (98%)	77 (93%)	5 (6%)	1 (1%)	13	49
1	F	83/85 (98%)	78 (94%)	5 (6%)	0	100	100
1	G	83/85 (98%)	75 (90%)	8 (10%)	0	100	100
1	H	83/85 (98%)	76 (92%)	7 (8%)	0	100	100
2	A	80/82 (98%)	76 (95%)	3 (4%)	1 (1%)	12	48
2	B	80/82 (98%)	77 (96%)	2 (2%)	1 (1%)	12	48
2	C	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
2	D	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
All	All	652/668 (98%)	610 (94%)	39 (6%)	3 (0%)	32	67

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	63	PRO
2	B	137	TYR
2	A	167	PRO

3.3.2 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	E	73/75 (97%)	71 (97%)	2 (3%)	44	67
1	F	74/75 (99%)	74 (100%)	0	100	100
1	G	73/75 (97%)	71 (97%)	2 (3%)	44	67
1	H	75/75 (100%)	73 (97%)	2 (3%)	44	67
2	A	67/72 (93%)	64 (96%)	3 (4%)	27	56
2	B	69/72 (96%)	69 (100%)	0	100	100
2	C	70/72 (97%)	67 (96%)	3 (4%)	29	57
2	D	70/72 (97%)	69 (99%)	1 (1%)	67	81
All	All	571/588 (97%)	558 (98%)	13 (2%)	53	71

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	130	GLU
2	A	170	ASN
2	D	188	LEU
2	C	127	THR
2	C	192	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	145	GLN
2	D	185	GLN
2	A	118	HIS
2	B	113	HIS
2	C	117	GLN

3.3.3 RNA [i](#)

There are no RNA molecules in this entry.

3.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

3.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

3.6 Ligand geometry [i](#)

There are no ligands in this entry.

3.7 Other polymers [i](#)

There are no such residues in this entry.

3.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

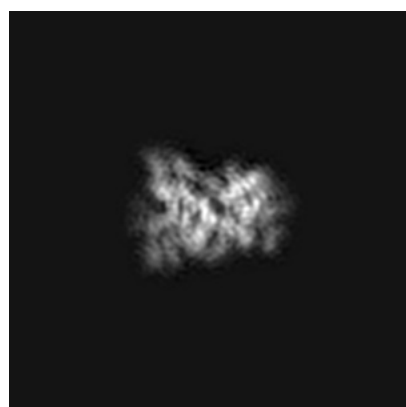
4 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22233. These allow visual inspection of the internal detail of the map and identification of artifacts.

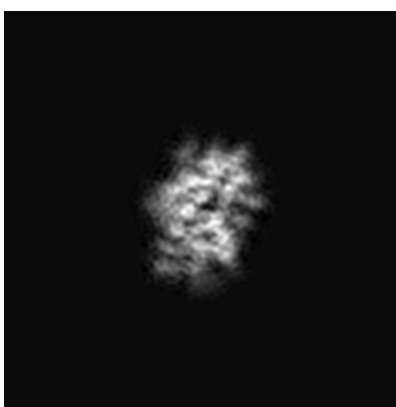
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

4.1 Orthogonal projections [i](#)

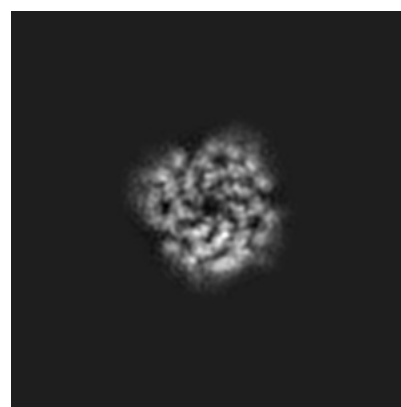
4.1.1 Primary map



X



Y

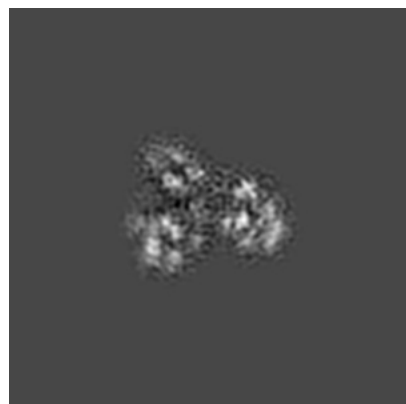


Z

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

4.2 Central slices [i](#)

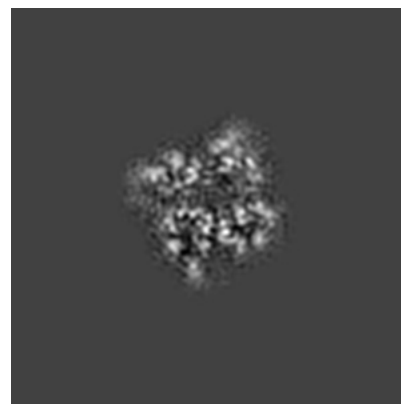
4.2.1 Primary map



X Index: 60



Y Index: 60

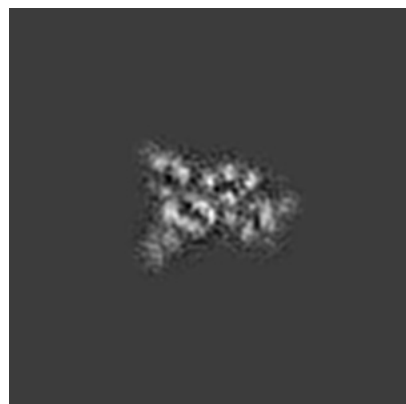


Z Index: 60

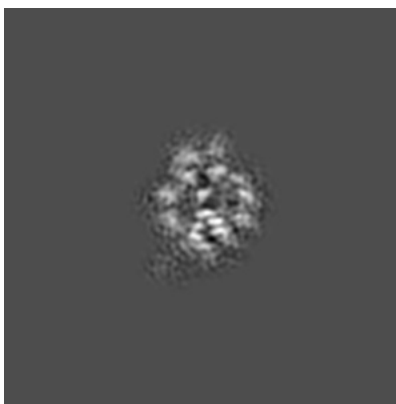
The images above show central slices of the map in three orthogonal directions.

4.3 Largest variance slices [i](#)

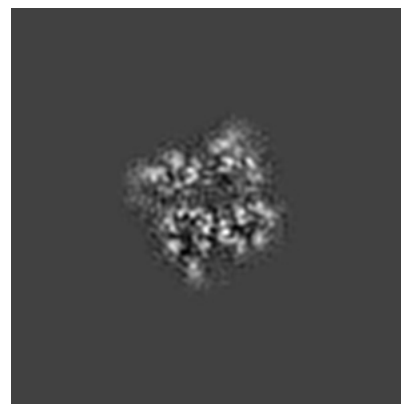
4.3.1 Primary map



X Index: 68



Y Index: 53

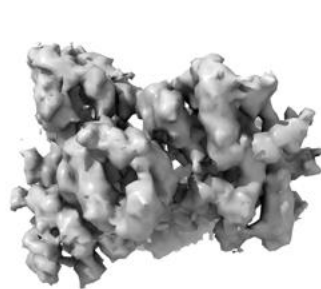


Z Index: 60

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

4.4 Orthogonal surface views [i](#)

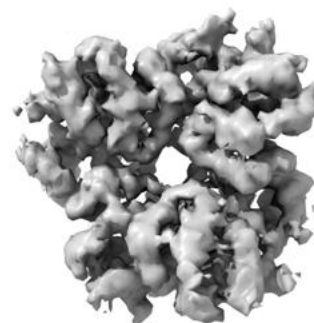
4.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0439. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

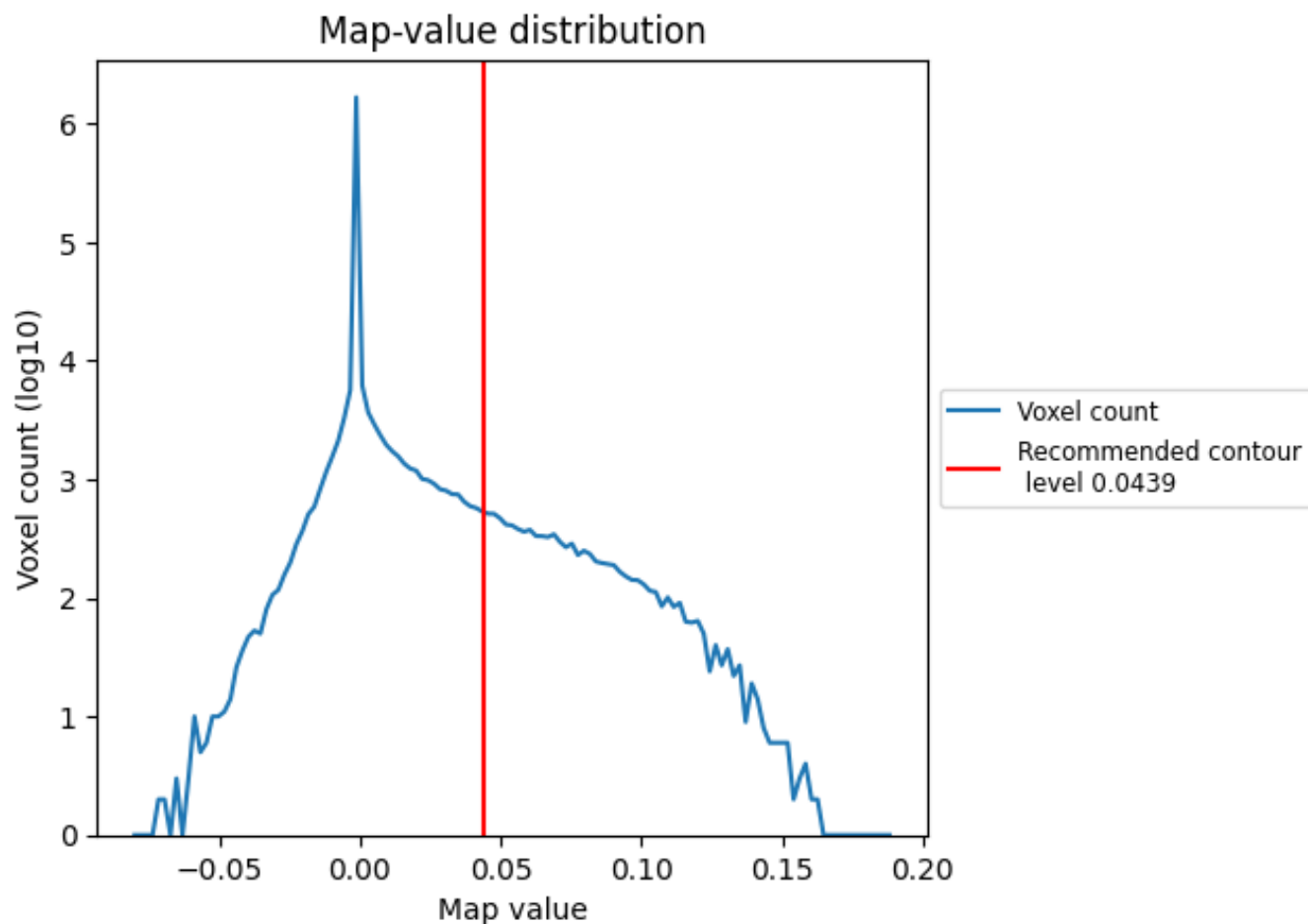
4.5 Mask visualisation

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

5 Map analysis [i](#)

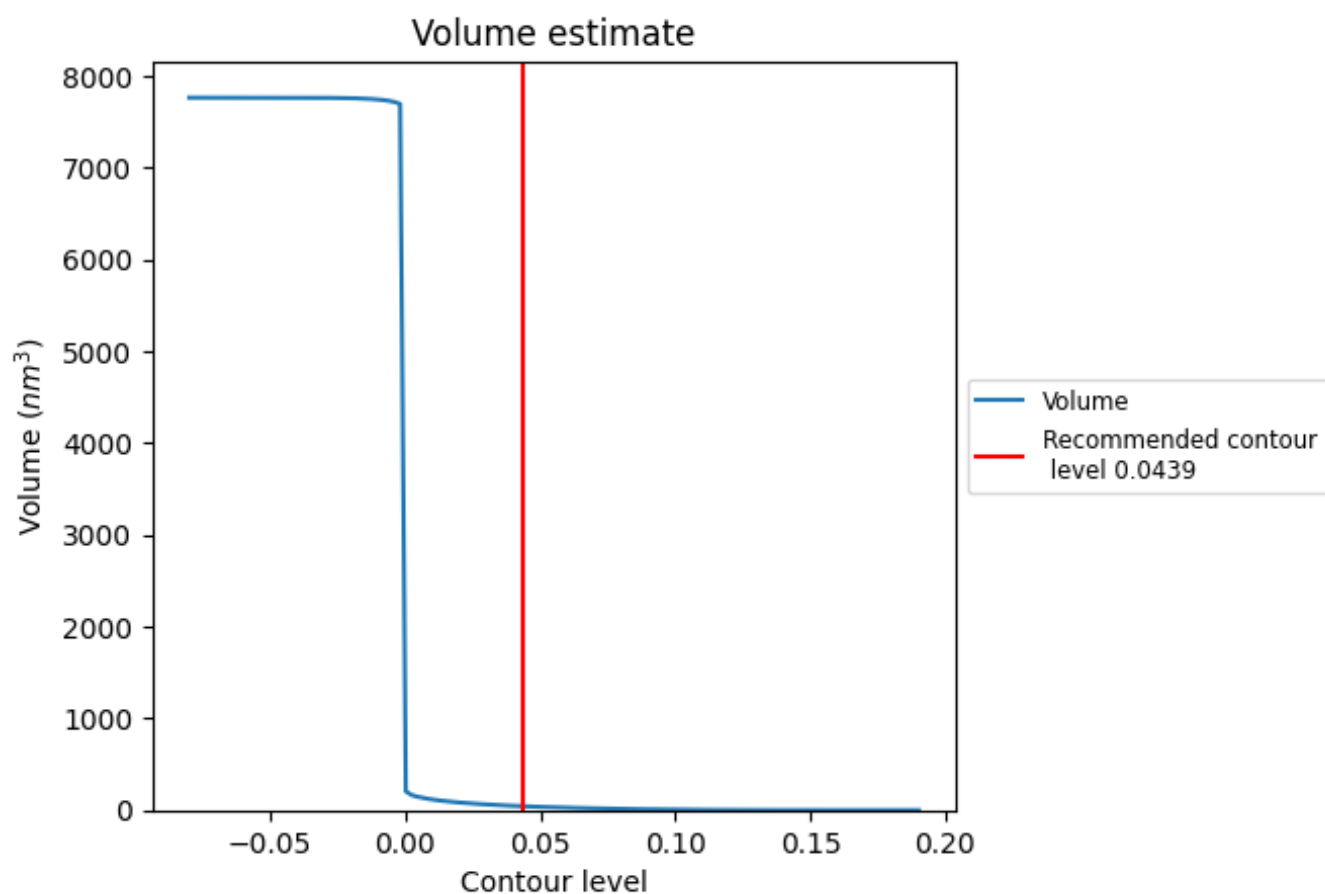
This section contains the results of statistical analysis of the map.

5.1 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.

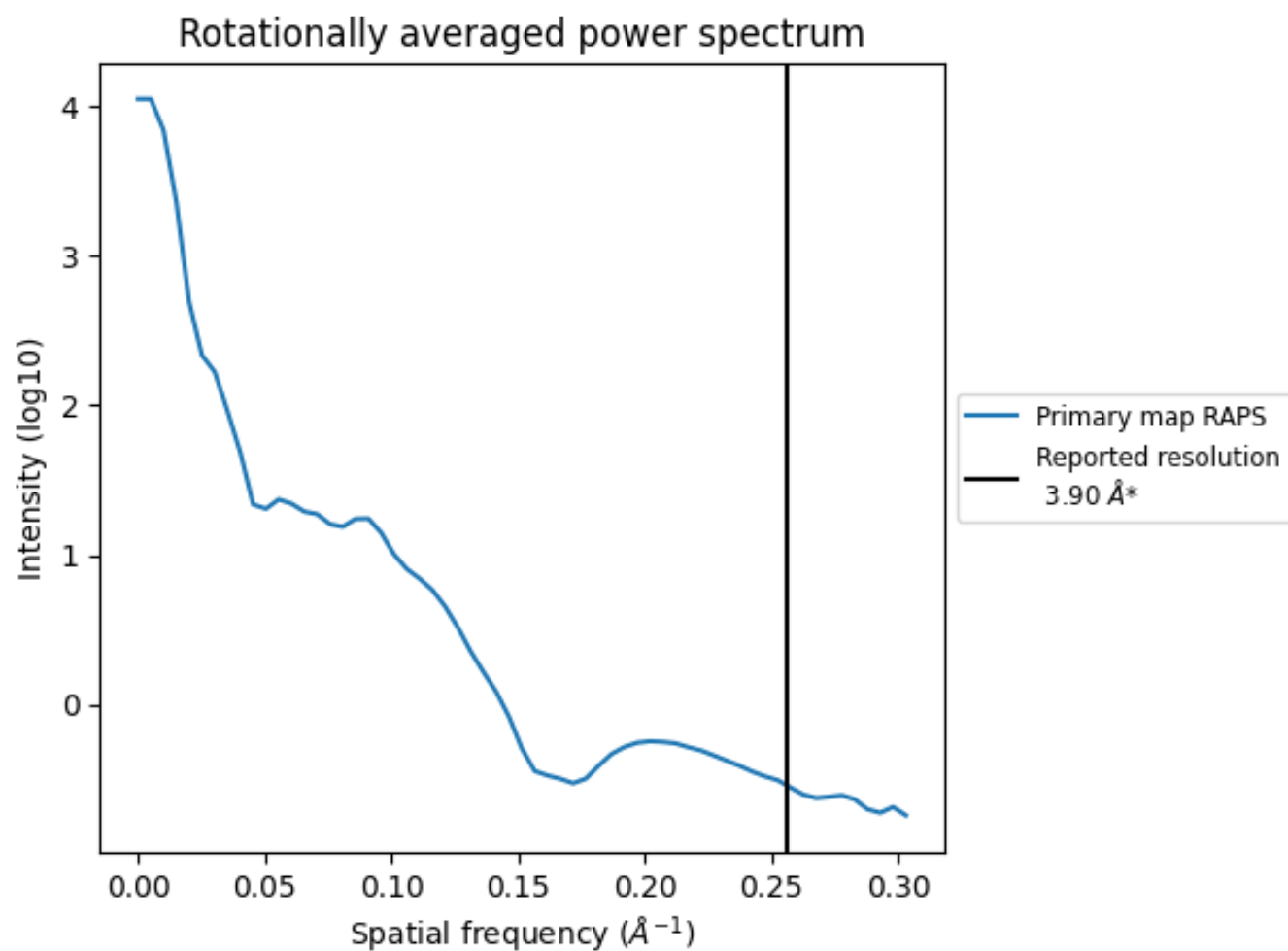
5.2 Volume estimate [i](#)



The volume at the recommended contour level is 42 nm³; this corresponds to an approximate mass of 38 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.

5.3 Rotationally averaged power spectrum ⓘ

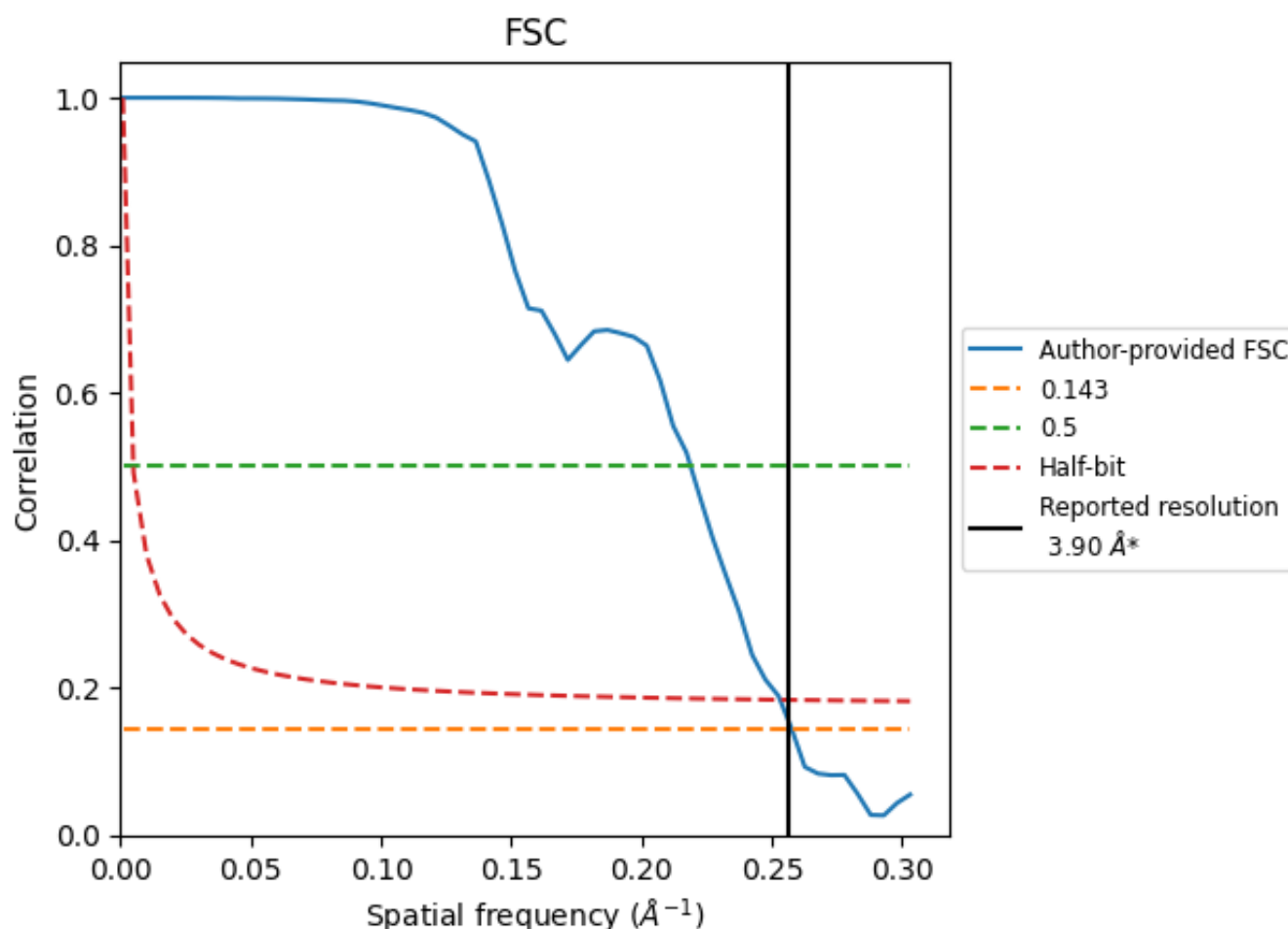


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

6 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.

6.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

6.2 Resolution estimates

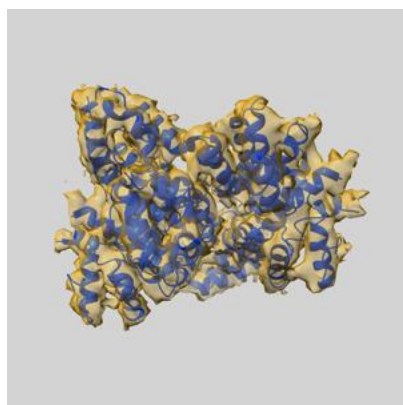
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.88	4.57	3.95
Unmasked-calculated*	-	-	-

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

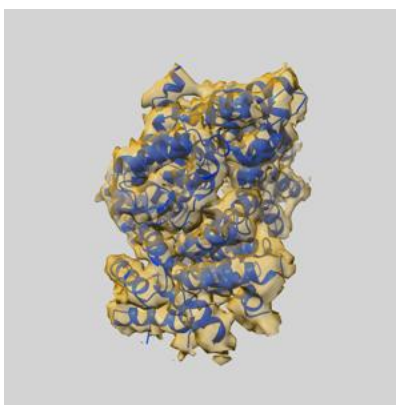
7 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22233 and PDB model 7KEU. Per-residue inclusion information can be found in section ?? on page ??.

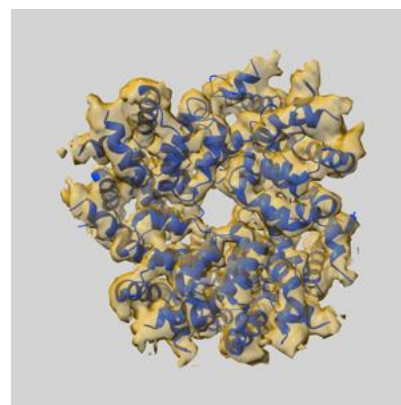
7.1 Map-model overlay [i](#)



X



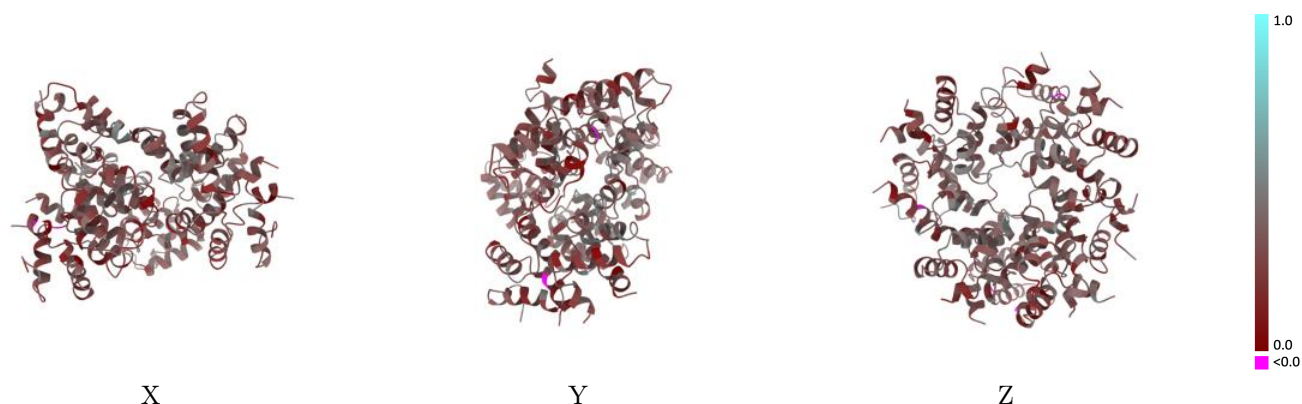
Y



Z

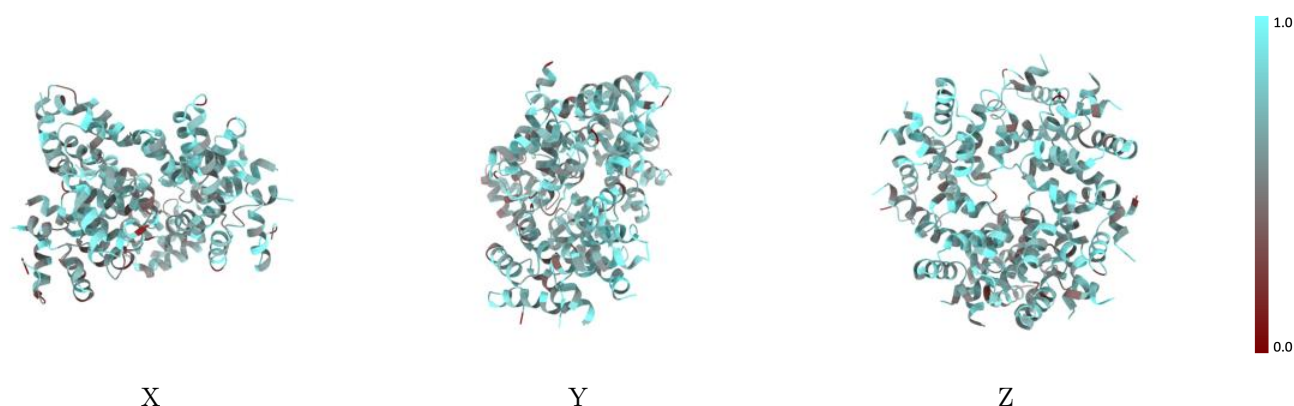
The images above show the 3D surface view of the map at the recommended contour level 0.0439 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



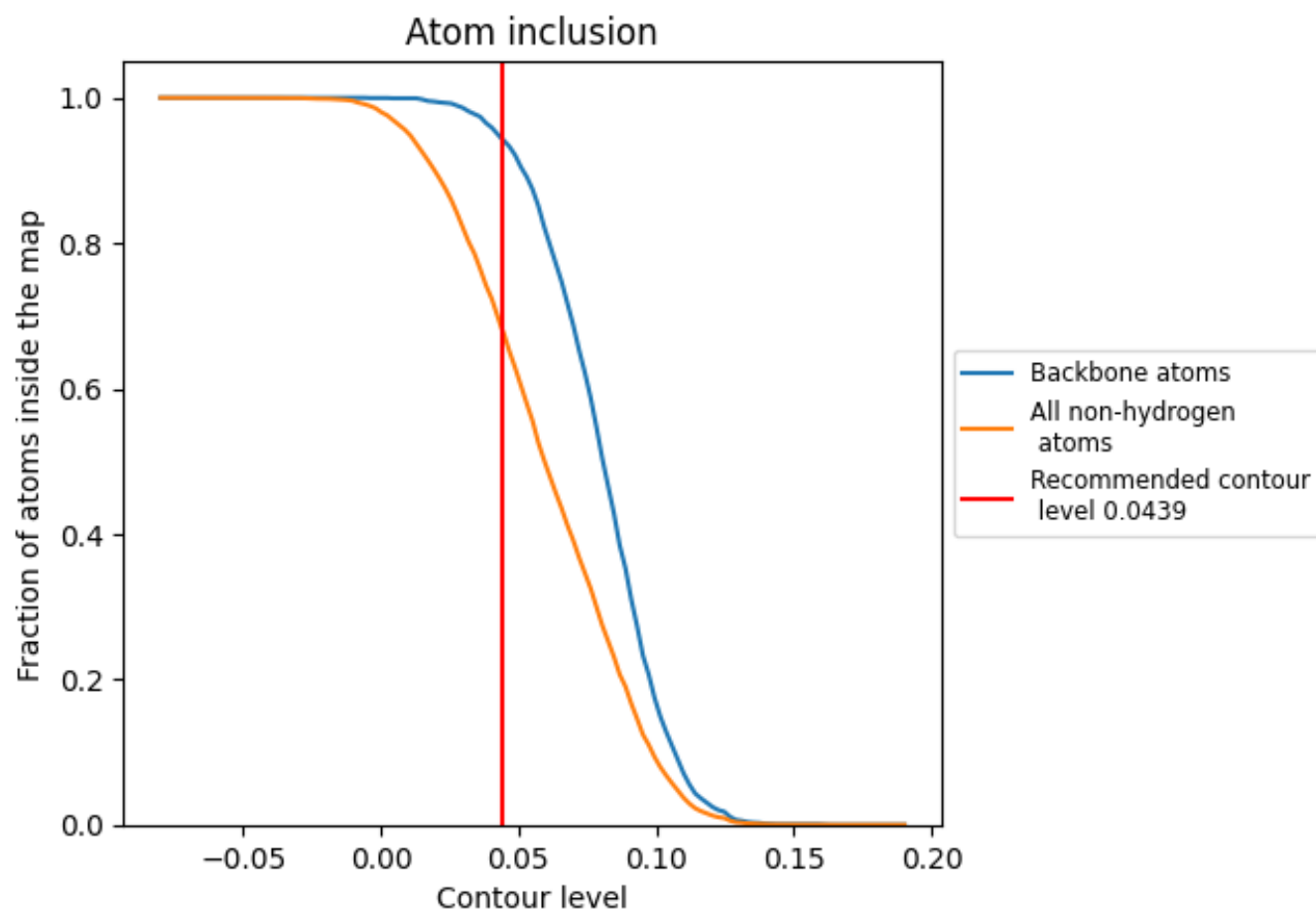
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

7.3 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 (0.0439).

7.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 68% of all non-hydrogen atoms, are inside the map.

7.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0439) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.6823	<div><div></div></div> 0.3010
A	<div><div></div></div> 0.6840	<div><div></div></div> 0.3210
B	<div><div></div></div> 0.7391	<div><div></div></div> 0.3340
C	<div><div></div></div> 0.7597	<div><div></div></div> 0.3240
D	<div><div></div></div> 0.7267	<div><div></div></div> 0.3400
E	<div><div></div></div> 0.5679	<div><div></div></div> 0.2500
F	<div><div></div></div> 0.6525	<div><div></div></div> 0.2810
G	<div><div></div></div> 0.6702	<div><div></div></div> 0.2770
H	<div><div></div></div> 0.6621	<div><div></div></div> 0.2870

1.0

0.0

<0.0