



wwPDB EM Validation Summary Report ⓘ

Dec 3, 2025 – 12:33 AM JST

PDB ID : 9WZI / pdb_00009wzi
EMDB ID : EMD-66403
Title : Full-length Caspase-1-CARD filament
Authors : Xue, D.; Ni, F.; Liu, S.; Yan, H.; Luo, Z.; Fu, G.; Wang, Q.; Ma, J.
Deposited on : 2025-09-29
Resolution : 4.00 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.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

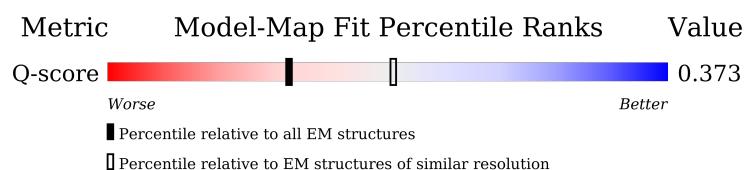
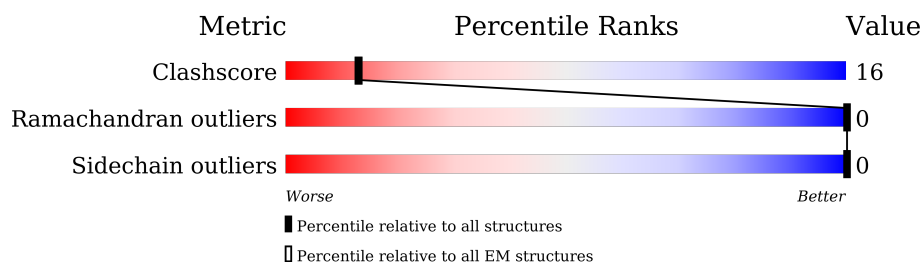
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	7587 (3.50 - 4.50)

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	404	<div> <div style="width: 11%; background-color: green;"></div> <div style="width: 11%; background-color: yellow;"></div> <div style="width: 78%; background-color: grey;"></div> </div> <div>11% 11% 78%</div>
1	B	404	<div> <div style="width: 14%; background-color: green;"></div> <div style="width: 8%; background-color: yellow;"></div> <div style="width: 78%; background-color: grey;"></div> </div> <div>14% 8% 78%</div>
1	C	404	<div> <div style="width: 15%; background-color: green;"></div> <div style="width: 7%; background-color: yellow;"></div> <div style="width: 78%; background-color: grey;"></div> </div> <div>15% 7% 78%</div>
1	D	404	<div> <div style="width: 14%; background-color: green;"></div> <div style="width: 8%; background-color: yellow;"></div> <div style="width: 78%; background-color: grey;"></div> </div> <div>14% 8% 78%</div>

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Mol	Chain	Length	Quality of chain
1	E	404	 14% 8% 78%
1	F	404	 15% 7% 78%
1	G	404	 16% 6% 78%
1	H	404	 15% 7% 78%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5544 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.

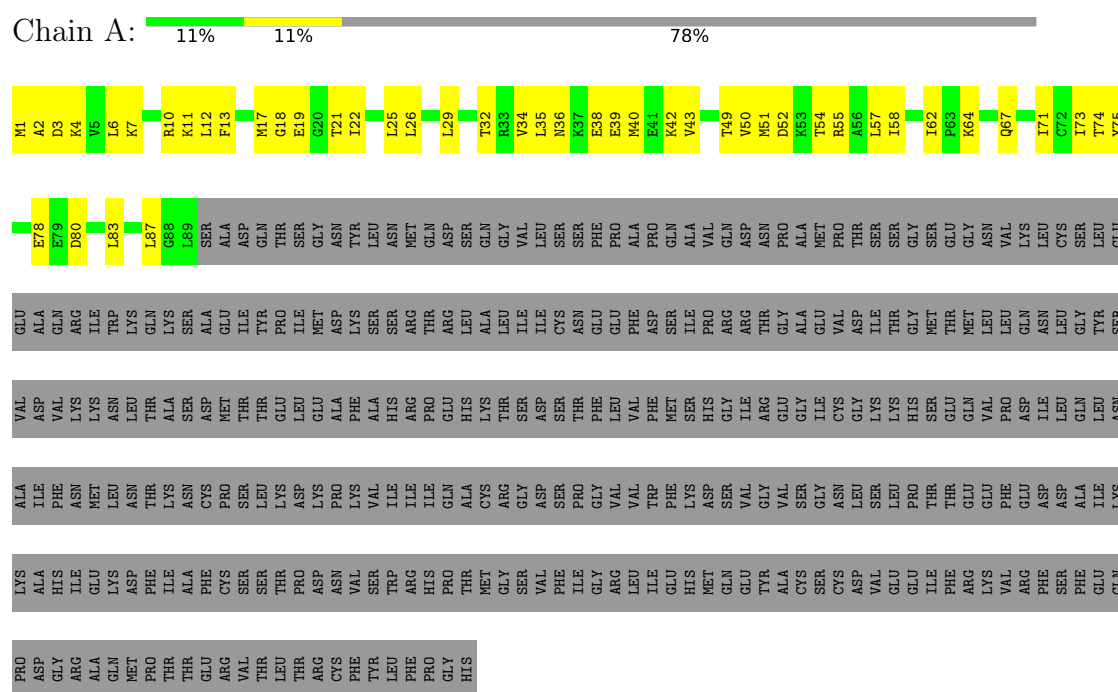
- Molecule 1 is a protein called Caspase-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	89	Total 693	C 433	N 119	O 134	S 7	0	0
1	B	89	Total 693	C 433	N 119	O 134	S 7	0	0
1	C	89	Total 693	C 433	N 119	O 134	S 7	0	0
1	D	89	Total 693	C 433	N 119	O 134	S 7	0	0
1	E	89	Total 693	C 433	N 119	O 134	S 7	0	0
1	F	89	Total 693	C 433	N 119	O 134	S 7	0	0
1	G	89	Total 693	C 433	N 119	O 134	S 7	0	0
1	H	89	Total 693	C 433	N 119	O 134	S 7	0	0

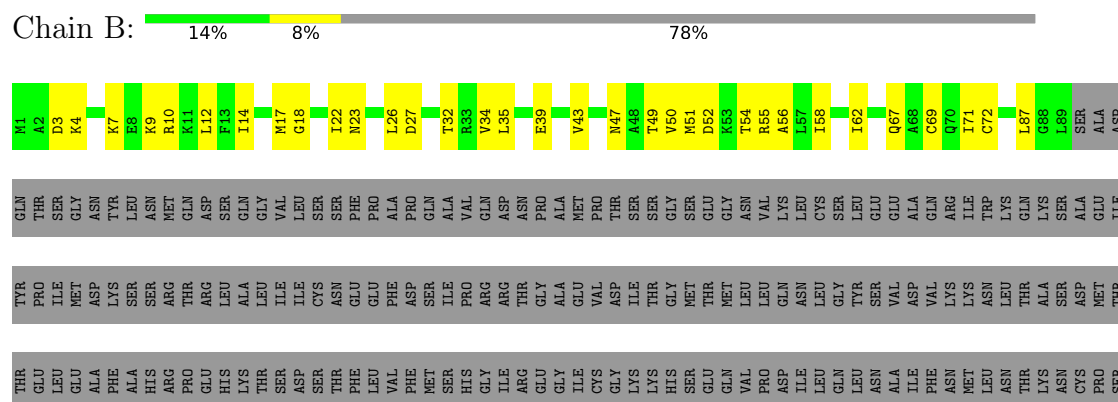
3 Residue-property plots

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: Caspase-1



• Molecule 1: Caspase-1



- Molecule 1: Caspase-1



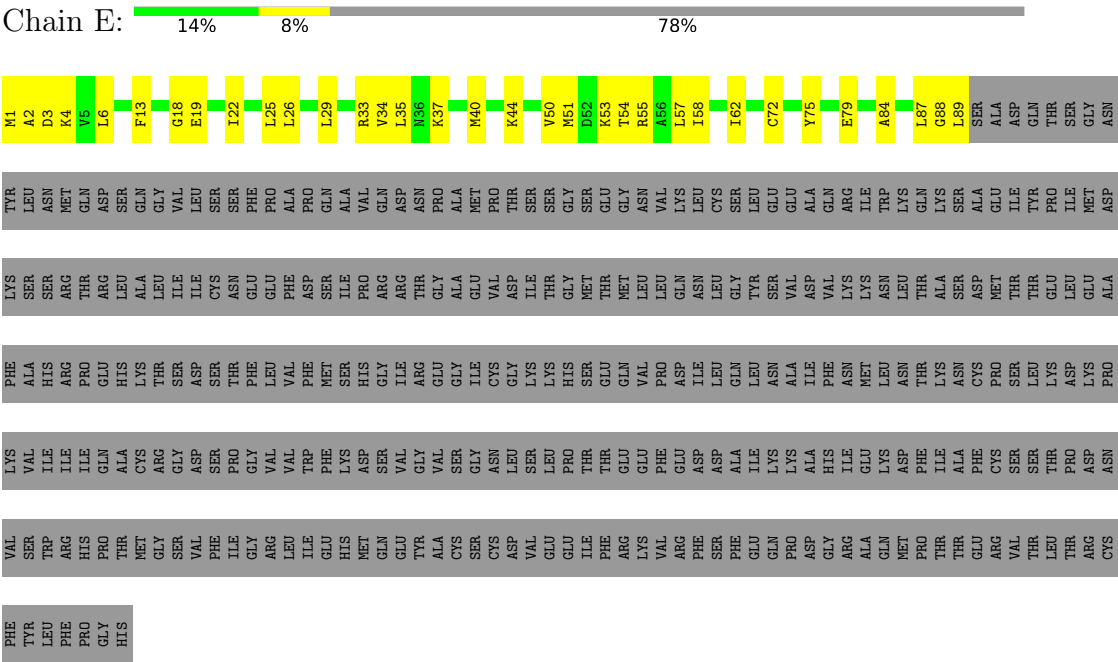
PHE	PRO	GLY	HIS	ARG	ILE	ARG	ARG	THR	MET	M1
				HIS	ILE	PRO	THR	GLN	A2	
HIS	HIS	GLY	PRO	THR	ALA	GLN	GLU	ARG	ASP	D3
				THR	ALA	THR	LEU	SER	K4	
HIS	GLY	SER	VAL	GLY	ARG	THR	LEU	GLY	VAL	K7
				GLY	ASP	ILE	VAL	GLY		
HIS	VAL	PHE	PHE	ILE	ASP	ASP	CYS	THR	SER	M17
				ILE	PRO	THR	ASN	SER	G18	
HIS	ARG	GLY	VAL	GLY	PHE	GLU	PHE	THR	ASN	I22
				VAL	GLU	PRO	ALA			
HIS	LEU	VAL	THR	VAL	VAL	PHE	ASP	PRO	GLN	L26
				THR	PHE	ASP	GLN			
HIS	ILE	PHE	PHE	THR	THR	THR	GLN	VAL	ALA	T32
				THR	THR	GLN	ALA			
HIS	HIS	MET	HIS	THR	ASP	THR	VAL	VAL	VAL	R33
				THR	THR	VAL	VAL			
HIS	GLN	SER	GLY	VAL	SER	GLY	ARG	GLN	ASP	L35
				VAL	GLY	ARG	GLN			
HIS	TYR	ALA	CYS	GLY	GLY	THR	THR	ASN	SER	M40
				GLY	GLY	THR	GLY			
HIS	CYS	VAL	SER	GLY	GLY	ALA	ALA	ALA	MET	V43
				GLY	GLY	ALA	ALA			
HIS	CYS	ASP	CYS	ASN	GLY	VAL	VAL	PRO	THR	K44
				ASN	GLY	ASP	THR			
HIS	VAL	GLU	SER	LEU	LEU	ILE	ILE	SER	SER	M47
				LEU	LEU	ILE	SER			
HIS	GLU	GLU	GLU	SER	LEU	THR	THR	SER	SER	D52
				THR	THR	THR	GLY			
HIS	ILE	PHE	ARG	THR	THR	SER	MET	SER	SER	T54
				THR	THR	SER	GLU			
HIS	ARG	VAL	VAL	GLY	GLY	LEU	LEU	ASN	GLY	R55
				GLY	GLY	LEU	VAL			
HIS	ARG	GLU	GLU	ASP	ASP	GLN	GLN	LYS	LYS	L57
				ASP	ASP	ASN	LEU			
HIS	SER	PHE	PHE	ASP	ASP	LEU	LEU	CYS	CYS	V61
				ASP	ASP	LEU	GLY			
HIS	GLU	GLN	GLN	ILE	ILE	TYR	TYR	GLY	GLY	I62
				ILE	ILE	SER	GLY			
HIS	PRO	PRO	LYS	LYS	LYS	VAL	VAL	GLU	GLU	Q67
				LYS	LYS	VAL	GLU			
HIS	ASP	ALA	HIS	ASP	ASP	ALA	ALA	ASP	ALA	I71
				ASP	ASP	ALA	ALA			
HIS	GLY	ARG	ALA	ILE	ILE	PHE	VAL	VAL	GLN	C72
				ILE	ILE	ASN	ARG			
HIS	GLN	GLN	GLN	LYS	LYS	LYS	LYS	ILE	ILE	I73
				LYS	LYS	TRP	TRP			
HIS	MET	MET	MET	ASP	ASP	LEU	LEU	LYS	LYS	L83
				ASP	ASP	LEU	GLN			
HIS	THR	THR	ALA	THR	THR	THR	THR	GLN	LYS	L87
				THR	THR	THR	LYS			
HIS	THR	PHE	PHE	ALA	ALA	ASN	SER	SER	SER	Q88
				ALA	ALA	ASN	ALA			
HIS	ARG	ARG	VAL	GLY	GLY	THR	THR	ILE	GLU	ALA
				GLY	GLY	THR	ILE			
HIS	VAL	SER	SER	LEU	LEU	THR	THR	TVR	GLN	ASP
				LEU	LEU	THR	GLN			
HIS	LEU	THR	THR	LEU	LEU	GLU	PRO	PRO	THR	THR
				THR	THR	ILE	ILE			
HIS	THR	ARG	ARG	THR	THR	GLU	GLU	GLU	MET	GLY
				THR	THR	LEU	LEU			
HIS	PHE	PHE	VAL	VAL	VAL	PHE	PHE	LYS	LYS	ASN
				VAL	VAL	VAL	VAL			
HIS	TYR	SER	SER	THR	THR	THR	THR	THR	THR	TYR
				THR	THR	THR	THR			
HIS	LEU	SER	SER	THR	THR	THR	THR	THR	THR	ASN
				THR	THR	THR	THR			
HIS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR

- Molecule 1: Caspase-1

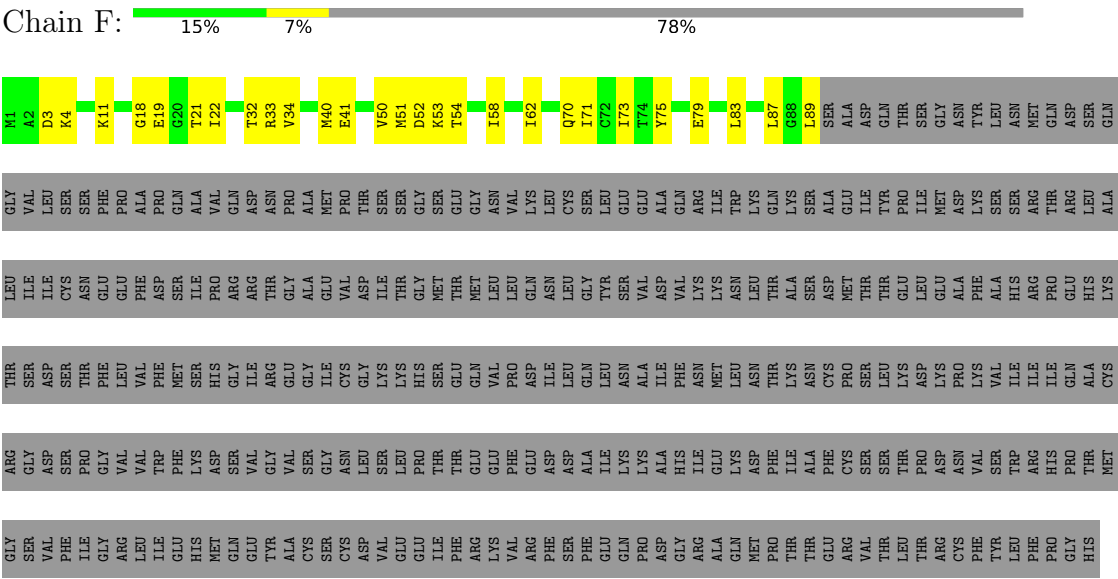


CYS	PHE	VAL	ASN	PRO	ALA	ASP	ASN	M1
	TYR	SER	VAL	LYS	PHE	LYS	TYR	A2
	LEU	TRP	ILE	VAL	ALA	SER	LEU	D3
	PHE	ARG	ILE	ILE	HIS	SER	ASN	K4
	PRO	HIS	ILE	ILE	PRO	THR	GLN	V5
	GLY	PRO	GLN	GLN	GLU	ARG	ASP	L6
	HIS	THR	ALA	HIS	HIS	LEU	SER	
		MET	CYS	CYS	LYS	ALA	GLN	R10
		GLY	ARG	VAL	THR	LEU	GLY	K11
		SER	GLY	ASP	SER	ILE	VAL	L12
HIS	VAL	VAL	ASN	ASP	ASP	ILE	LEU	F13
	PHE	PHE	SER	SER	SER	CYS	SER	I14
	ILE	ILE	PRO	PRO	THR	ASN	SER	M17
	GLY	ARG	GLY	VAL	PHE	GLU	PHE	G18
	LEU	VAL	VAL	VAL	VAL	GLU	PRO	E19
	THR	TRP	PHE	THR	PHE	ASP	ALA	G20
	GLU	HIS	LYS	LYS	MET	SER	GLN	T21
	HIS	ASN	MET	ASP	HIS	ILE	VAL	I22
	GLN	GLN	GLN	SER	GLY	ARG	GLN	L25
	TYR	GLY	VAL	VAL	ILE	ARG	ASP	L29
ALA	ALA	ALA	TYR	GLY	ARG	THR	ASN	
	CYS	SER	VAL	VAL	GLY	GLY	PRO	T32
	SER	SER	GLY	SER	GLY	ALA	ALA	R33
	CYS	CYS	ASN	ASN	CYS	VAL	MET	V34
	ASP	ASP	LEU	GLY	GLY	ASP	THR	L35
	VAL	VAL	SER	LYS	LYS	ILE	SER	V43
	GLU	GLU	LEU	LYS	HIS	THR	SER	
	ILE	ILE	THR	THR	GLY	MET	GLY	V50
	PHE	ARG	THR	THR	GLU	THR	GLU	M51
	LYS	GLY	GLY	GLY	GLN	MET	GLY	D52
ARG	VAL	VAL	LYS	GLY	VAL	LEU	ASN	K53
	VAL	PHE	GLY	PHE	PRO	LEU	VAL	T54
	ARG	ARG	GLY	GLY	ASP	GLN	LYS	R55
	SER	PHE	ASP	ASP	ILE	ASN	LEU	A56
	PHE	SER	ASP	ASP	LEU	CYS	CYS	L57
	GLY	PHE	ALA	ALA	GLN	GLY	SER	I58
	GLN	GLY	ILE	ILE	LEU	TYR	LEU	V61
	PRO	PRO	LYS	LYS	ASN	SER	GLY	I62
	ASP	GLY	THR	THR	ILE	VAL	GLY	C69
	ALA	ALA	HIS	HIS	PHE	VAL	GLN	
THR	ARG	ARG	ILE	ILE	ASN	LYS	ARG	C72
	ALA	ALA	GLY	GLY	MET	LYS	ILE	
	GLN	GLN	LYS	LYS	ASN	ASN	TRP	L83
	PRO	PRO	ASP	ASP	ASN	LEU	LYS	
	THR	THR	ILE	ILE	LYS	ALA	GLN	L87
	THR	THR	ALA	ALA	ASN	LYS	SER	G88
	GLY	GLY	PHE	PHE	CYS	ASP	ALA	L89
	ARG	ARG	THR	THR	PRO	THR	GLY	SER
	VAL	VAL	SER	CYS	PRO	GLY	ALA	ALA
	THR	THR	SER	SER	THR	ILE	THR	ASP
LEU	LEU	LEU	THR	THR	LEU	GLU	PRO	GLN
	THR	THR	THR	PRO	LYS	LEU	ILE	THR
	ARG	ARG	ASP	ASP	LYS	LEU	THR	SER
	GLY	GLY	THR	THR	THR	GLY	GLY	CYS
	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ALA
	THR	THR	THR	THR	THR	THR	THR	ALA
	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA
	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ALA
	THR	THR	THR	THR	THR	THR	THR	ALA
	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ALA

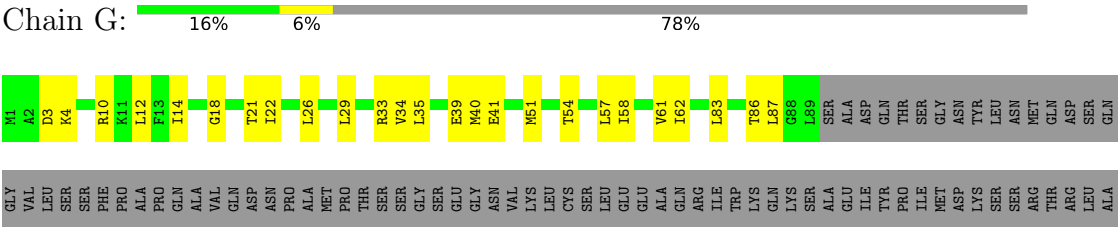
● Molecule 1: Caspase-1



● Molecule 1: Caspase-1



● Molecule 1: Caspase-1



- Molecule 1: Caspase-1

GLY
HIS

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-100.2°, rise=5.1 Å, axial sym=C3	Depositor
Number of segments used	194125	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 ($e^-/\text{Å}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.232	Depositor
Minimum map value	-0.092	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	217.6, 217.6, 217.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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	0.21	0/696	0.59	0/930
1	B	0.18	0/696	0.55	0/930
1	C	0.16	0/696	0.47	0/930
1	D	0.18	0/696	0.49	0/930
1	E	0.17	0/696	0.47	0/930
1	F	0.16	0/696	0.44	0/930
1	G	0.16	0/696	0.42	0/930
1	H	0.16	0/696	0.43	0/930
All	All	0.17	0/5568	0.49	0/7440

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	693	0	733	37	0
1	B	693	0	733	26	0
1	C	693	0	733	16	0
1	D	693	0	733	24	0
1	E	693	0	733	28	0
1	F	693	0	733	20	0
1	G	693	0	733	20	0
1	H	693	0	733	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5544	0	5864	185	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 16.

The worst 5 of 185 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:38:GLU:OE1	1:A:42:LYS:NZ	2.07	0.88
1:E:34:VAL:HG13	1:E:35:LEU:HD12	1.62	0.82
1:B:35:LEU:HD11	1:B:39:GLU:HB2	1.61	0.80
1:E:6:LEU:HD12	1:E:13:PHE:HE2	1.51	0.76
1:D:29:LEU:HD21	1:D:35:LEU:HD13	1.71	0.71

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	87/404 (22%)	85 (98%)	2 (2%)	0	100	100
1	B	87/404 (22%)	86 (99%)	1 (1%)	0	100	100
1	C	87/404 (22%)	84 (97%)	3 (3%)	0	100	100
1	D	87/404 (22%)	87 (100%)	0	0	100	100
1	E	87/404 (22%)	85 (98%)	2 (2%)	0	100	100
1	F	87/404 (22%)	85 (98%)	2 (2%)	0	100	100
1	G	87/404 (22%)	86 (99%)	1 (1%)	0	100	100
1	H	87/404 (22%)	86 (99%)	1 (1%)	0	100	100
All	All	696/3232 (22%)	684 (98%)	12 (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	77/356 (22%)	77 (100%)	0	100	100
1	B	77/356 (22%)	77 (100%)	0	100	100
1	C	77/356 (22%)	77 (100%)	0	100	100
1	D	77/356 (22%)	77 (100%)	0	100	100
1	E	77/356 (22%)	77 (100%)	0	100	100
1	F	77/356 (22%)	77 (100%)	0	100	100
1	G	77/356 (22%)	77 (100%)	0	100	100
1	H	77/356 (22%)	77 (100%)	0	100	100
All	All	616/2848 (22%)	616 (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 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	47	ASN
1	D	47	ASN
1	F	47	ASN
1	D	70	GLN
1	B	23	ASN

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](#)

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.

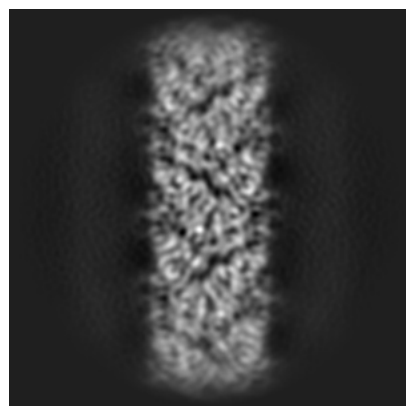
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66403. These allow visual inspection of the internal detail of the map and identification of artifacts.

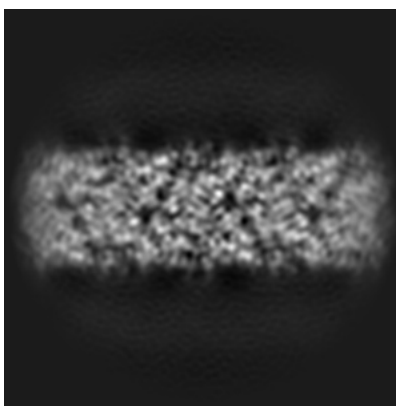
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

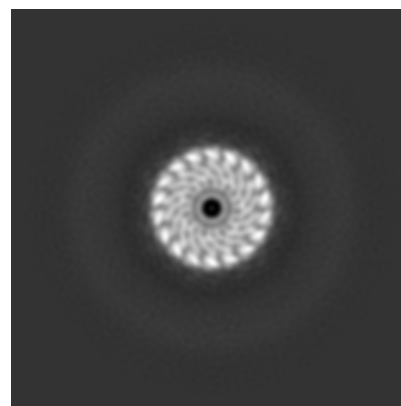
6.1.1 Primary map



X

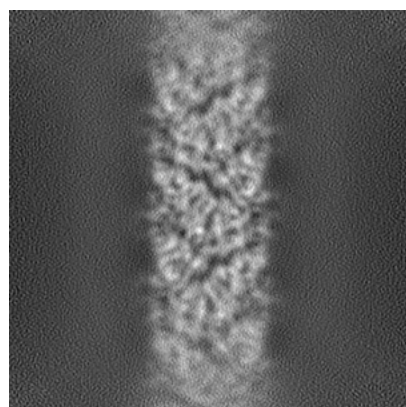


Y

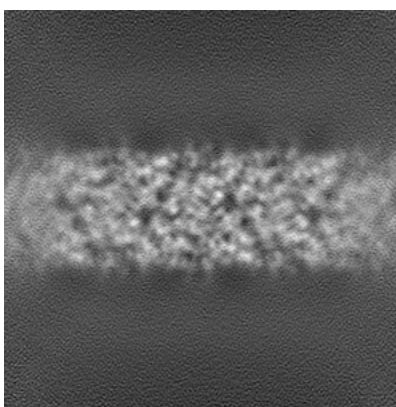


Z

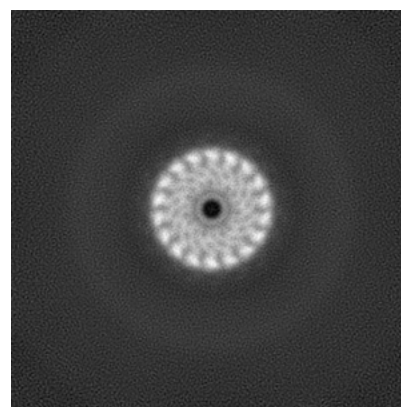
6.1.2 Raw map



X



Y

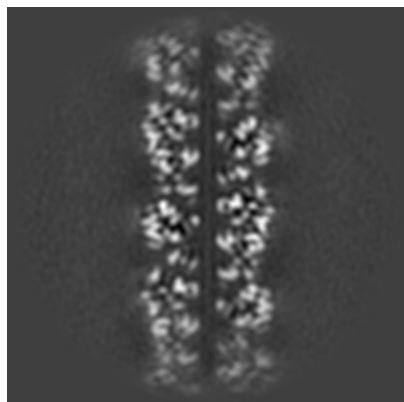


Z

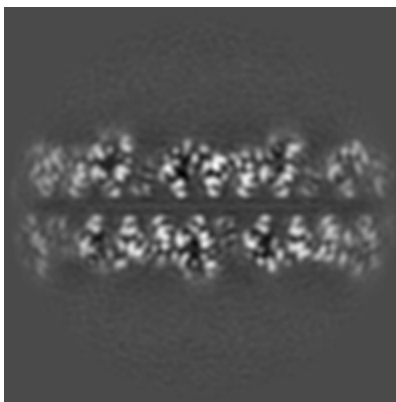
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

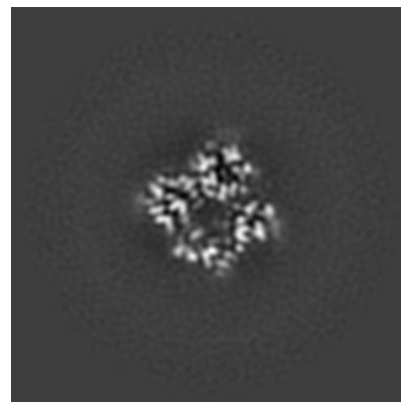
6.2.1 Primary map



X Index: 128

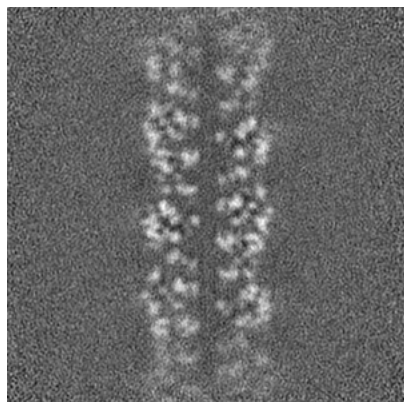


Y Index: 128

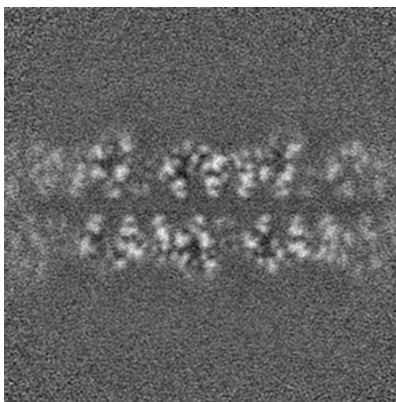


Z Index: 128

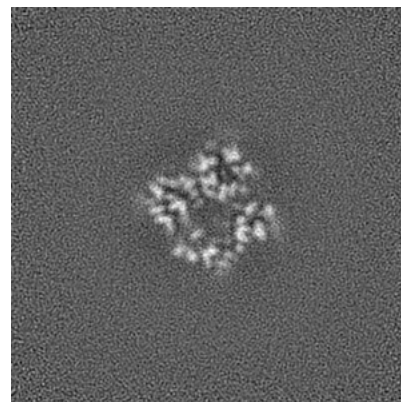
6.2.2 Raw map



X Index: 128



Y Index: 128

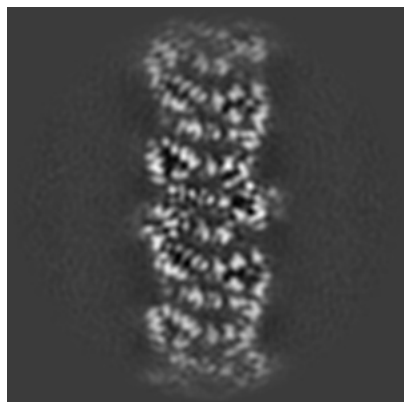


Z Index: 128

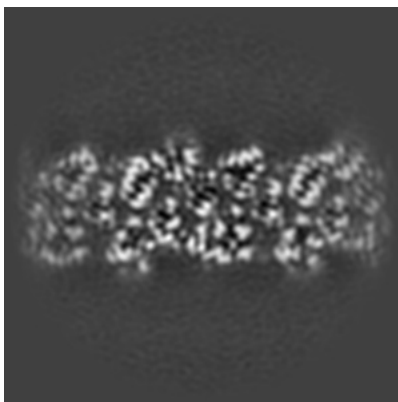
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

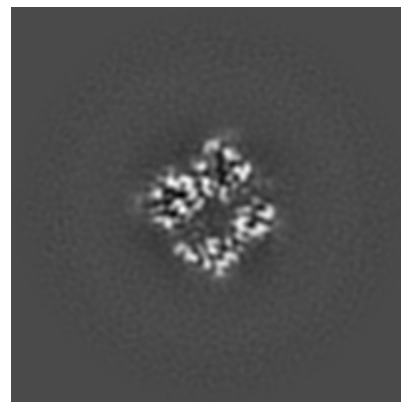
6.3.1 Primary map



X Index: 140

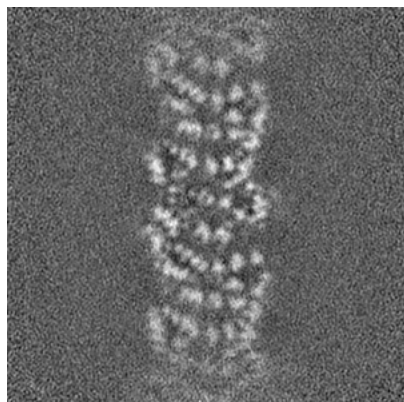


Y Index: 144

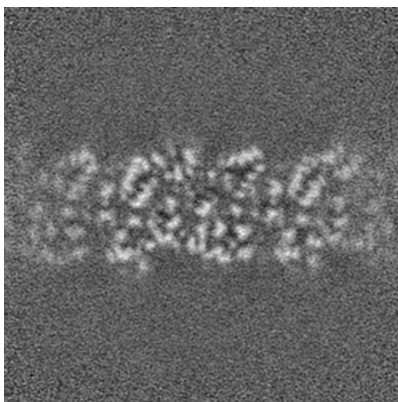


Z Index: 126

6.3.2 Raw map



X Index: 141



Y Index: 144

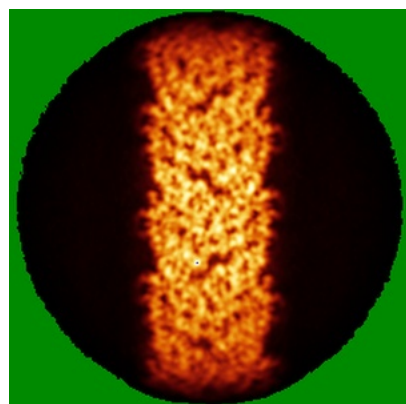


Z Index: 0

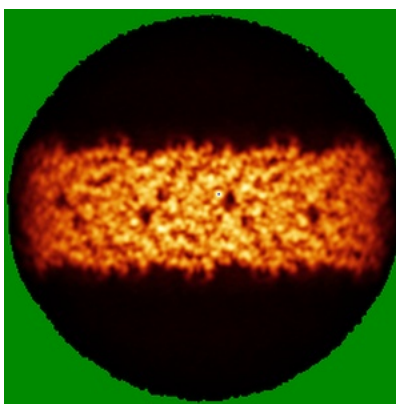
The images above show the largest variance slices of the map in three orthogonal directions.

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

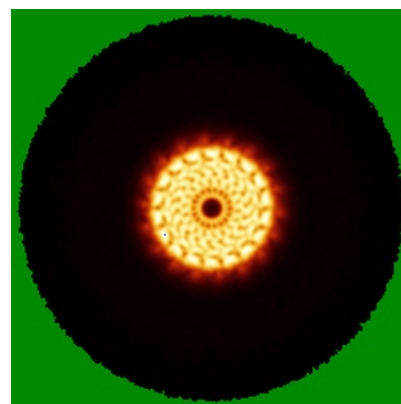
6.4.1 Primary map



X

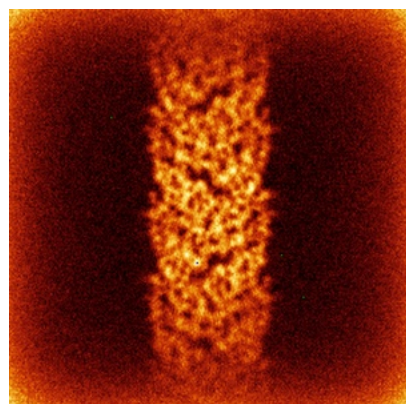


Y

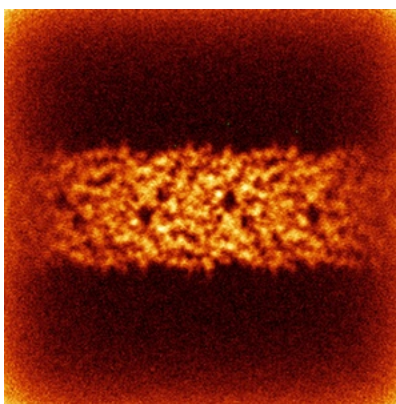


Z

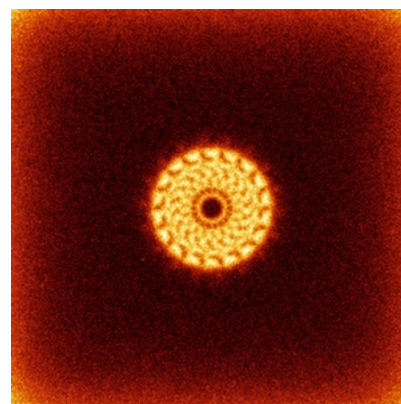
6.4.2 Raw map



X



Y



Z

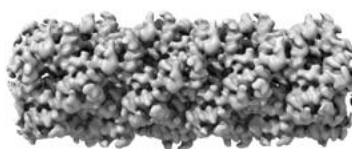
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

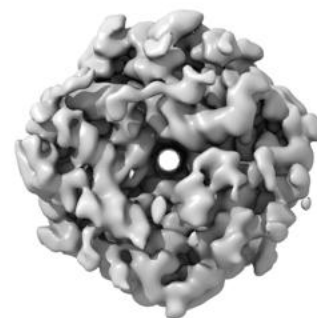
6.5.1 Primary map



X



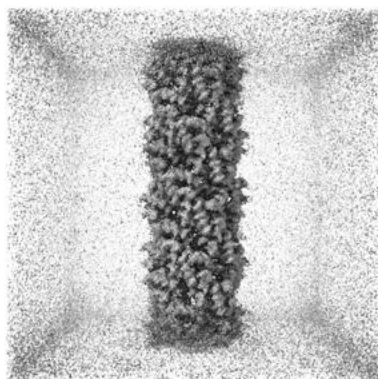
Y



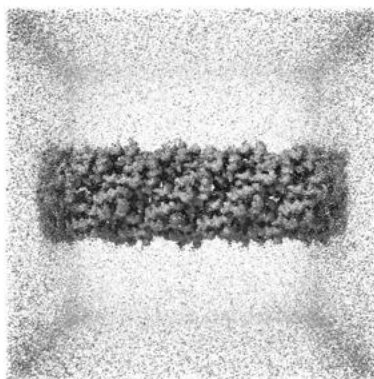
Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

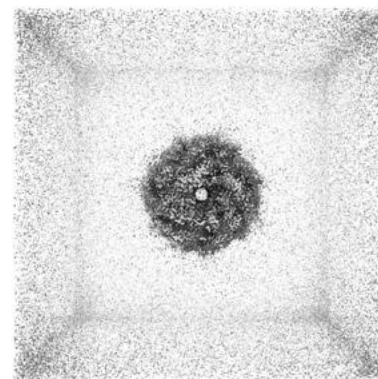
6.5.2 Raw map



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.

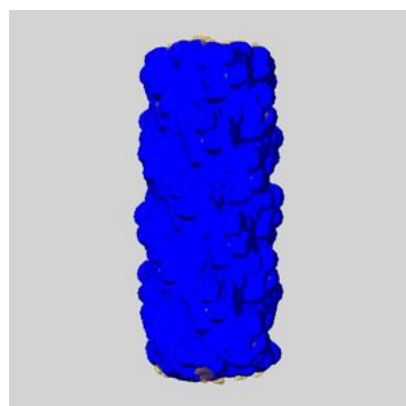
6.6 Mask visualisation [i](#)

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

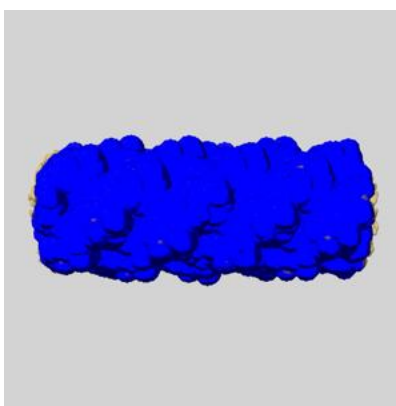
A mask typically either:

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

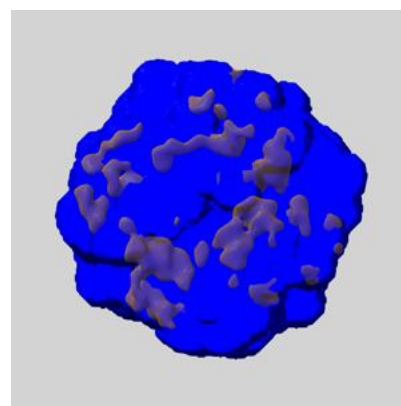
6.6.1 emd_66403_msk_1.map [i](#)



X



Y

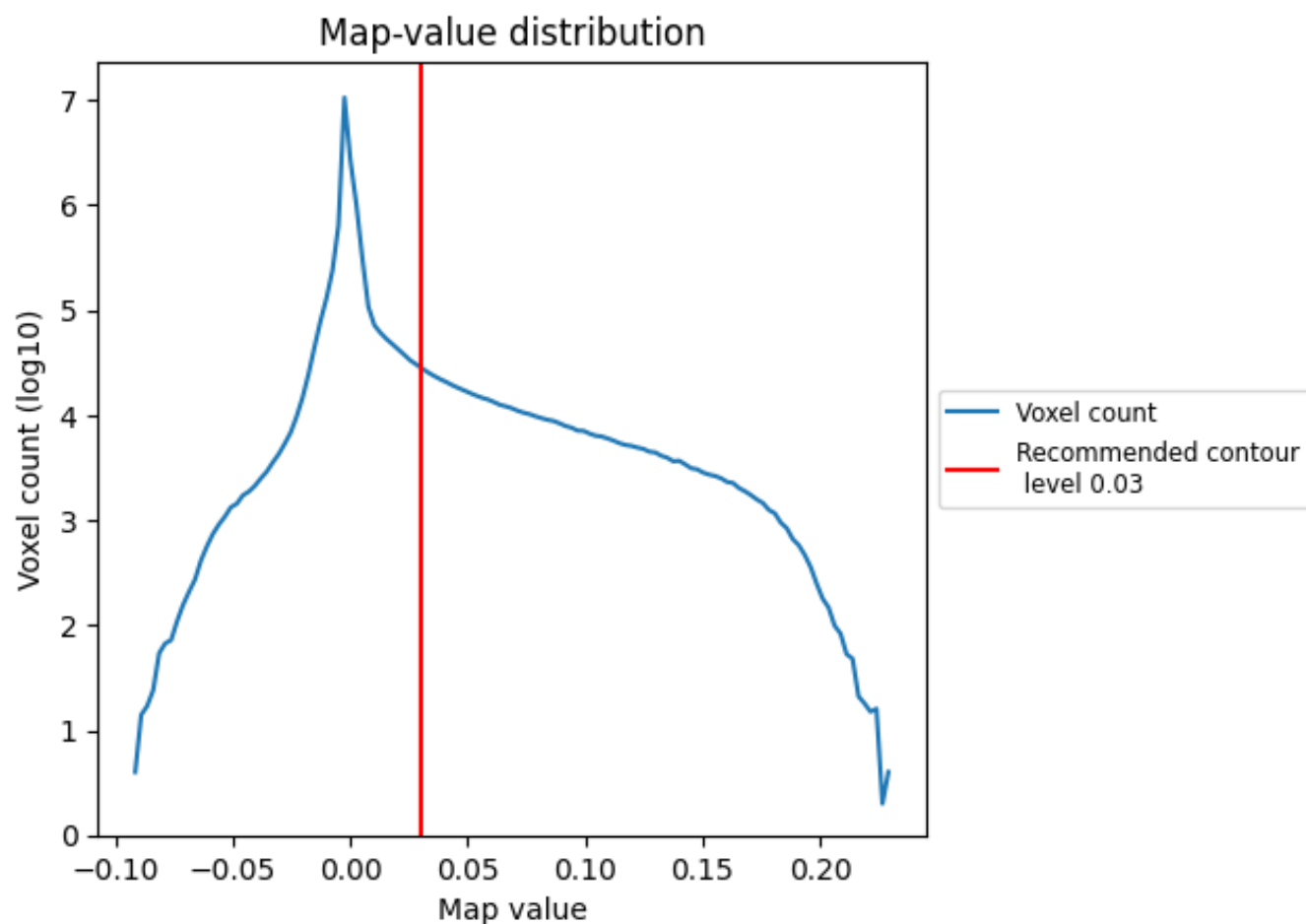


Z

7 Map analysis [i](#)

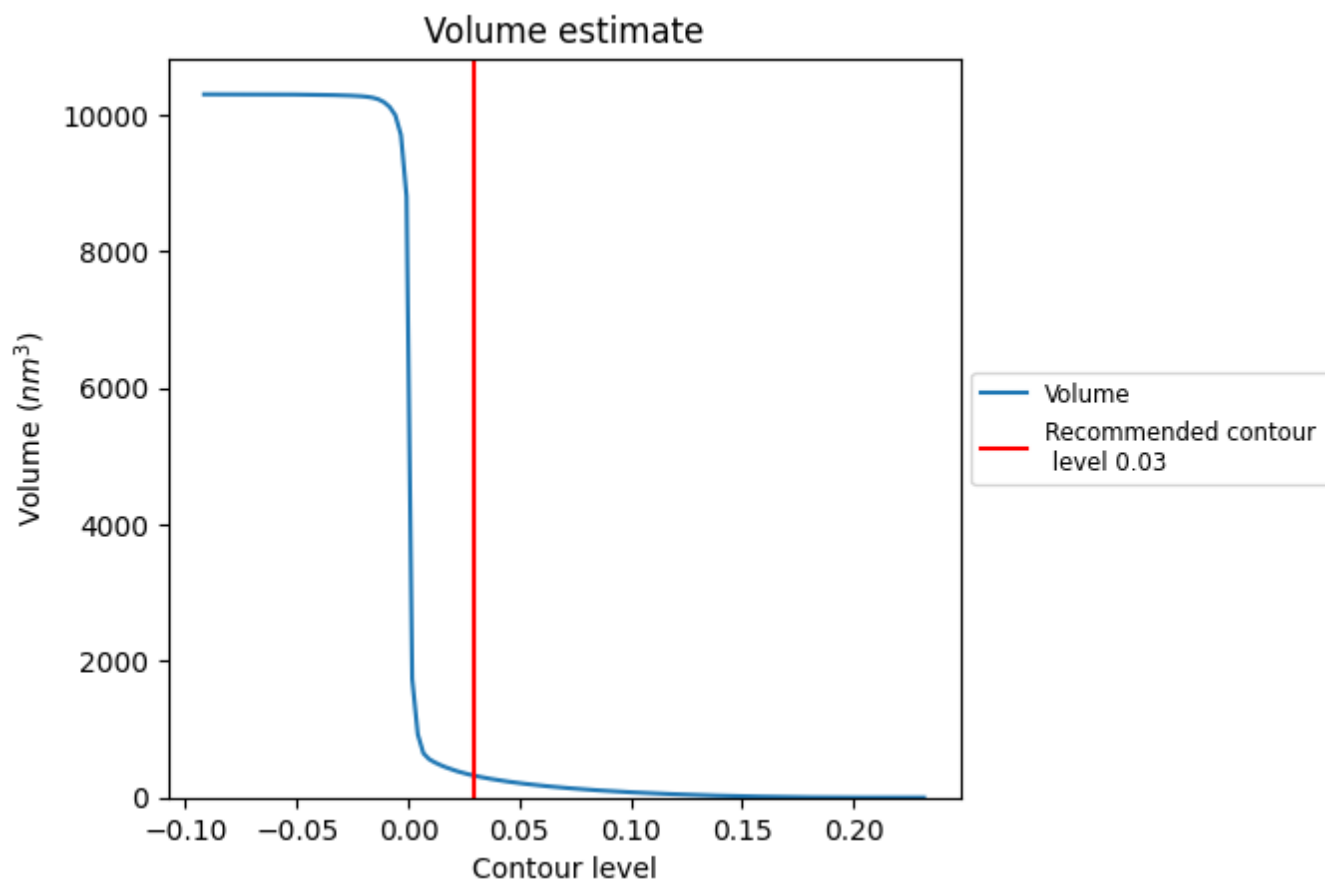
This section contains the results of statistical analysis of the map.

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.

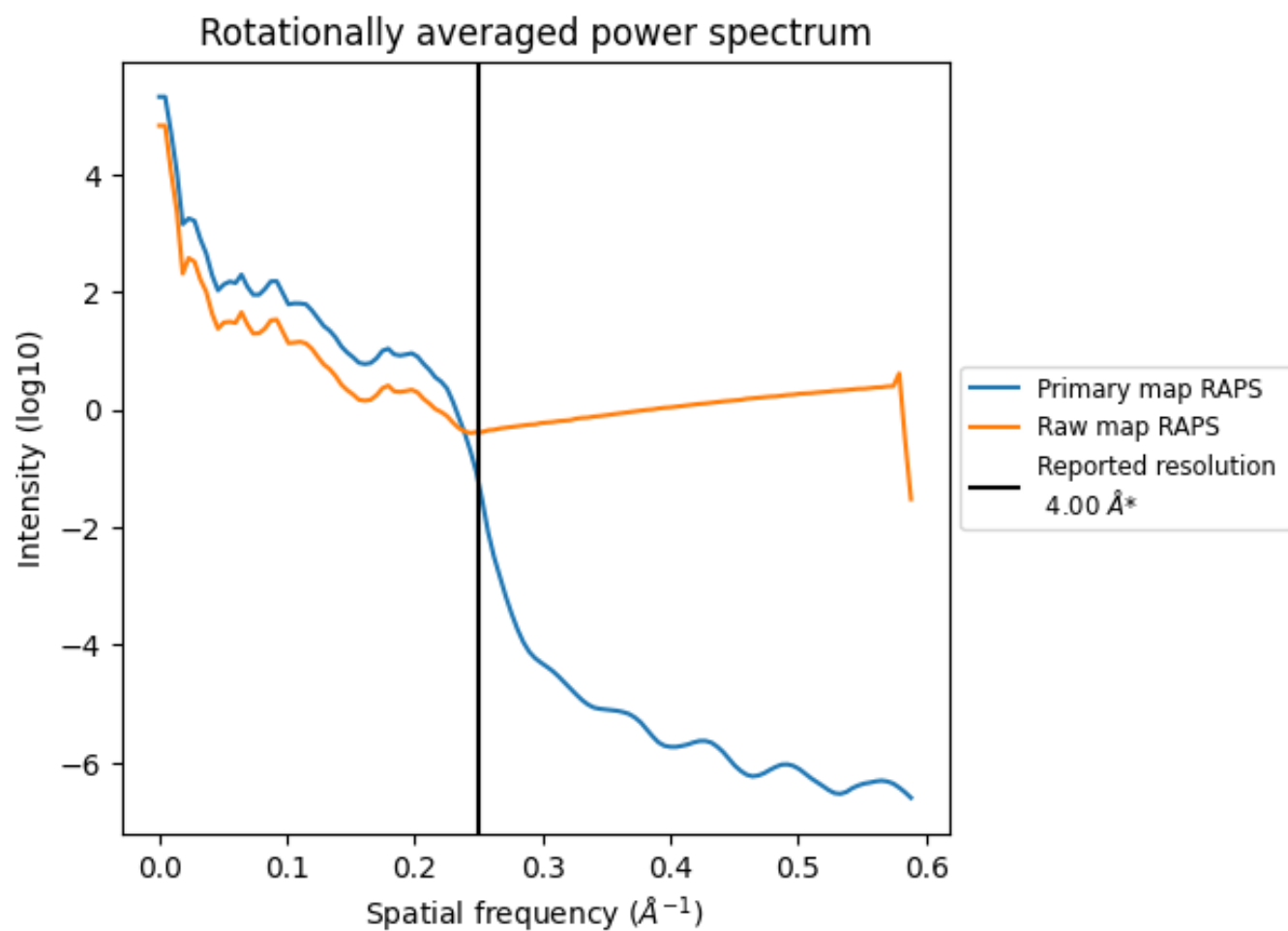
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 319 nm³; this corresponds to an approximate mass of 288 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 ⓘ

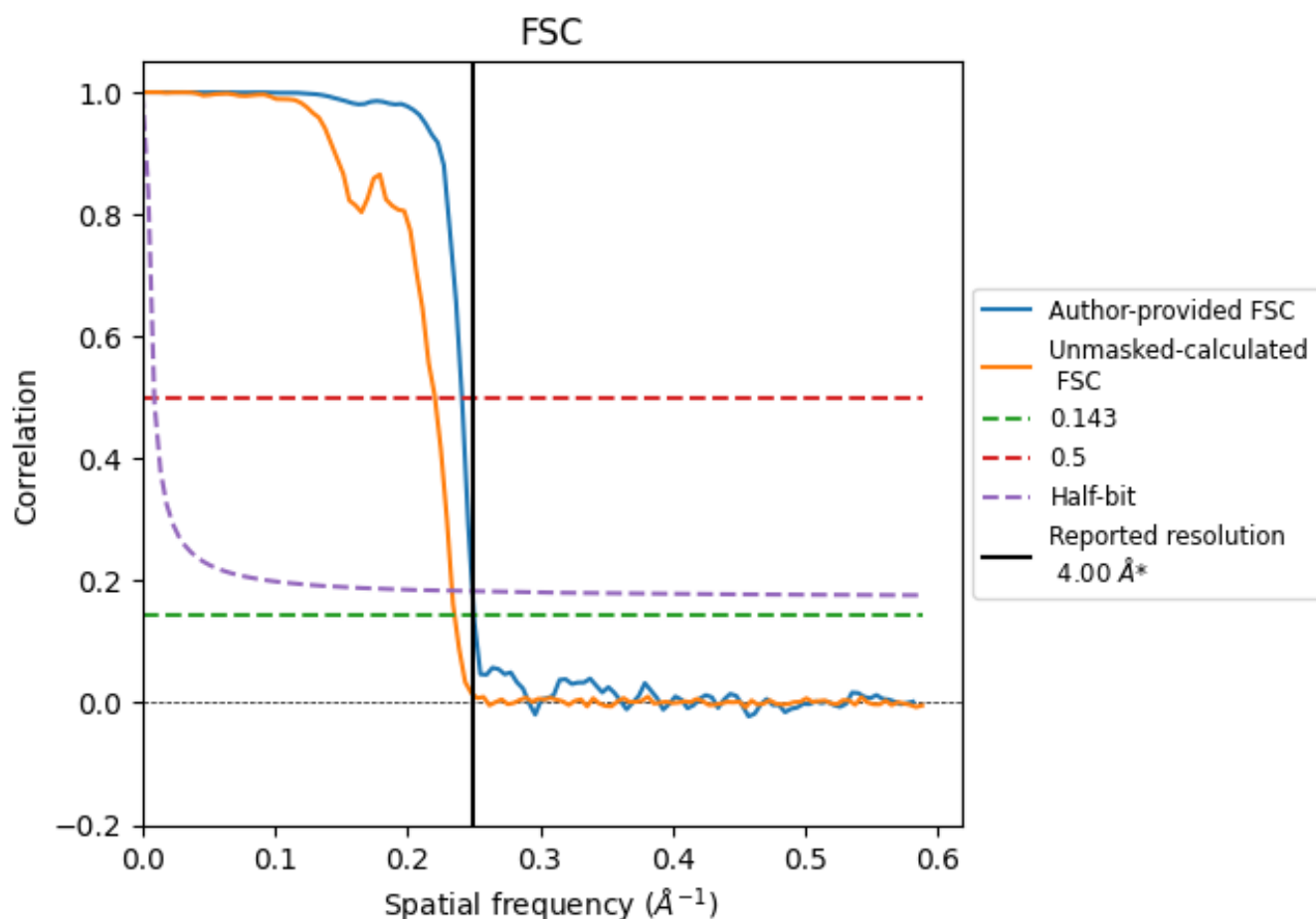


*Reported resolution corresponds to spatial frequency of 0.250 \AA^{-1}

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

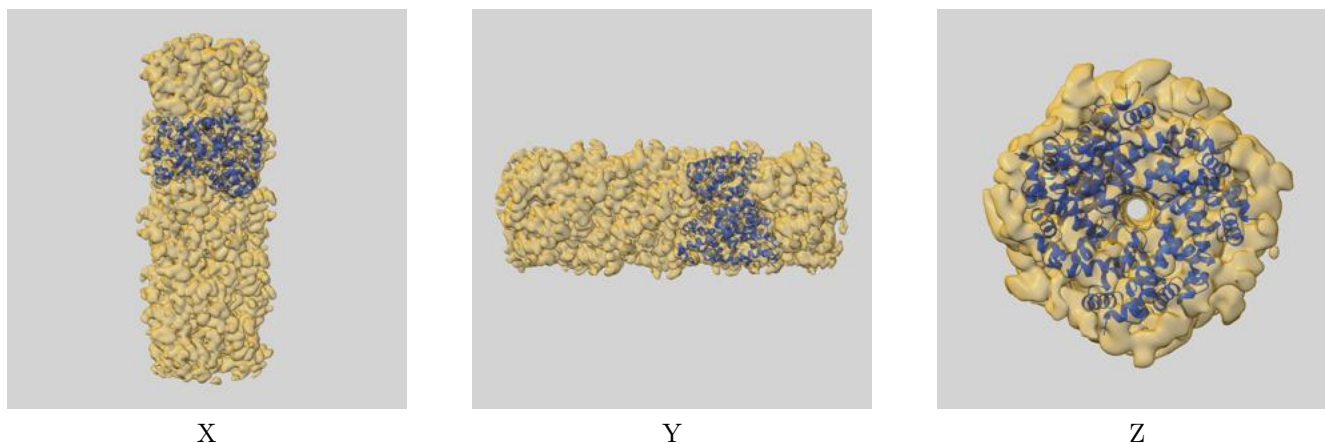
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	4.00	4.15	4.02
Unmasked-calculated*	4.24	4.53	4.28

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

9 Map-model fit [i](#)

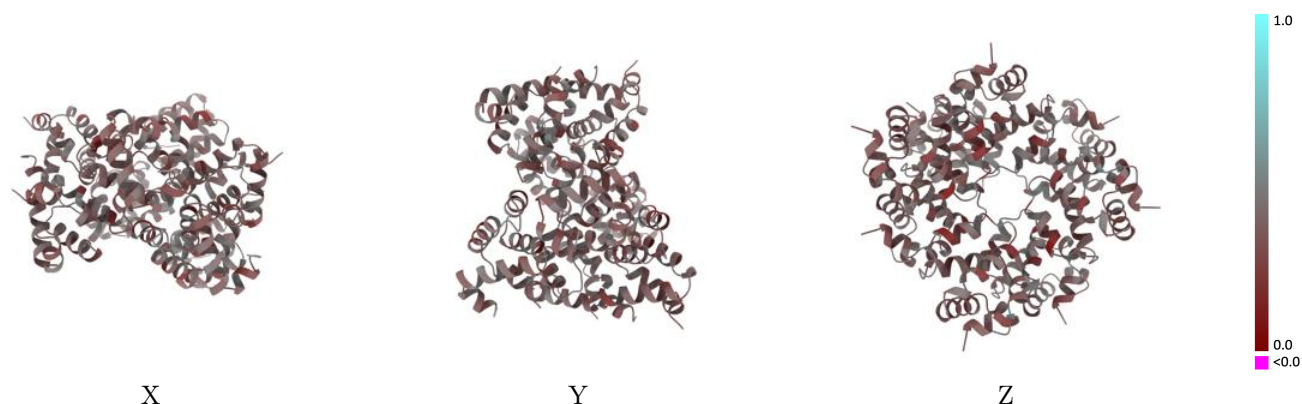
This section contains information regarding the fit between EMDB map EMD-66403 and PDB model 9WZI. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



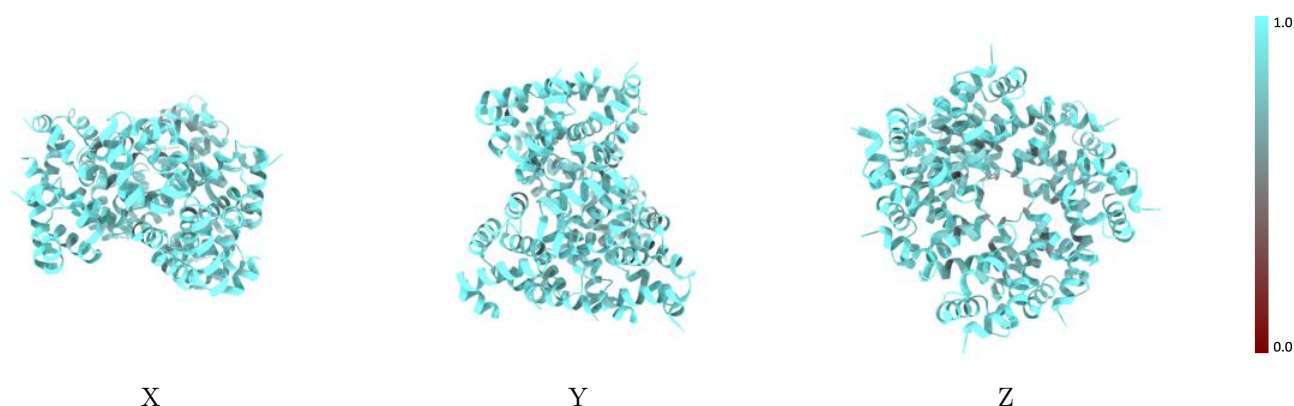
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



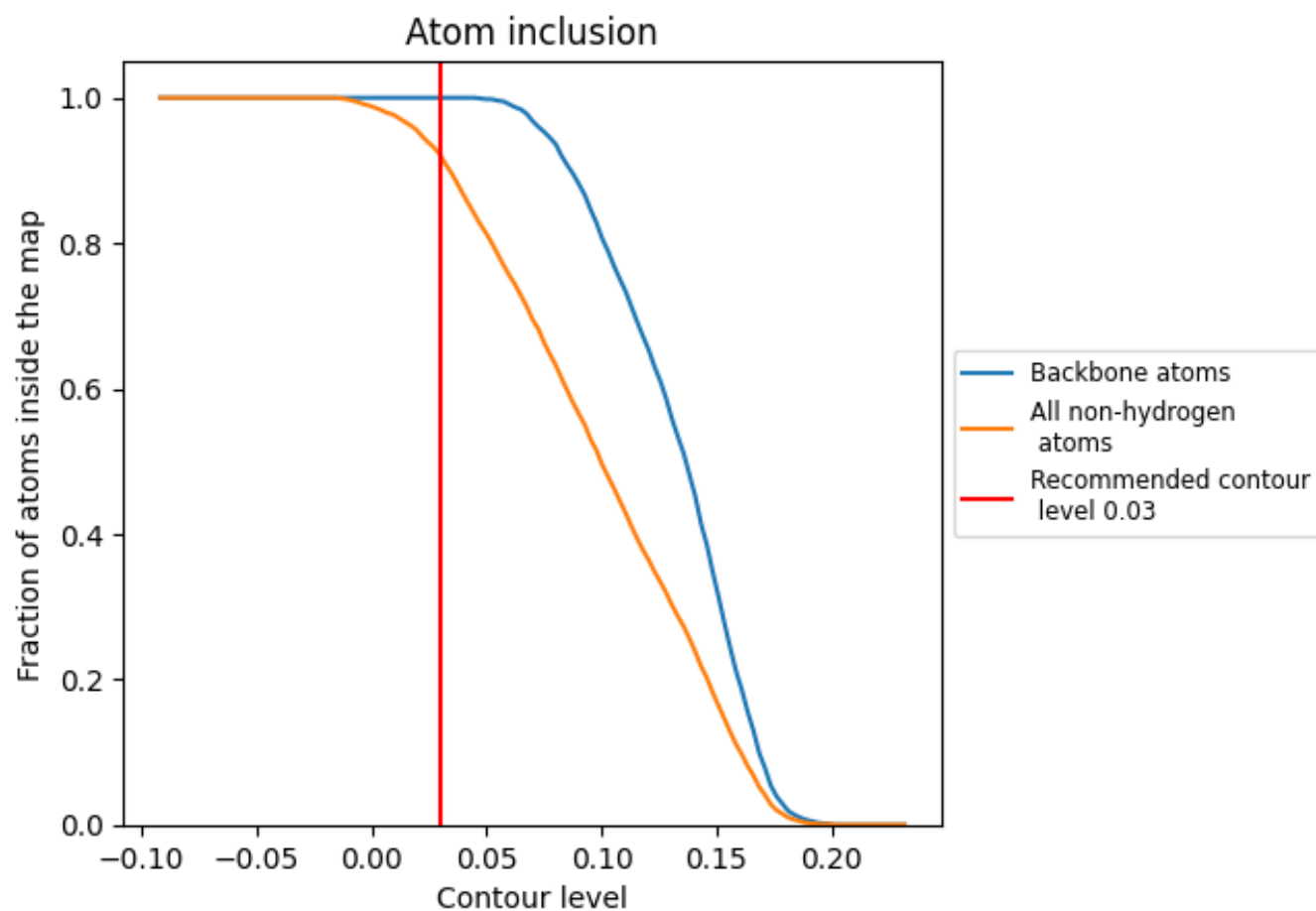
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 92% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.9210	<div><div></div></div> 0.3730
A	<div><div></div></div> 0.9180	<div><div></div></div> 0.3490
B	<div><div></div></div> 0.9180	<div><div></div></div> 0.3640
C	<div><div></div></div> 0.9150	<div><div></div></div> 0.3700
D	<div><div></div></div> 0.9120	<div><div></div></div> 0.3730
E	<div><div></div></div> 0.9280	<div><div></div></div> 0.3740
F	<div><div></div></div> 0.9280	<div><div></div></div> 0.3770
G	<div><div></div></div> 0.9310	<div><div></div></div> 0.3900
H	<div><div></div></div> 0.9190	<div><div></div></div> 0.3900

1.0

0.0

<0.0