



wwPDB EM Validation Summary Report ⓘ

Mar 15, 2026 – 10:20 AM UTC

PDB ID : 8AJB / pdb_00008ajb
EMDB ID : EMD-15476
Title : Cryo-EM structure of crescentin filaments (stutter mutant, C2 symmetry and large box)
Authors : Liu, Y.; Lowe, J.
Deposited on : 2022-07-28
Resolution : 4.30 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

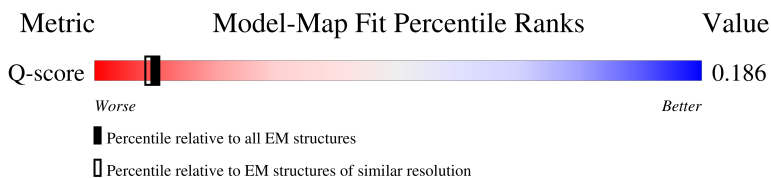
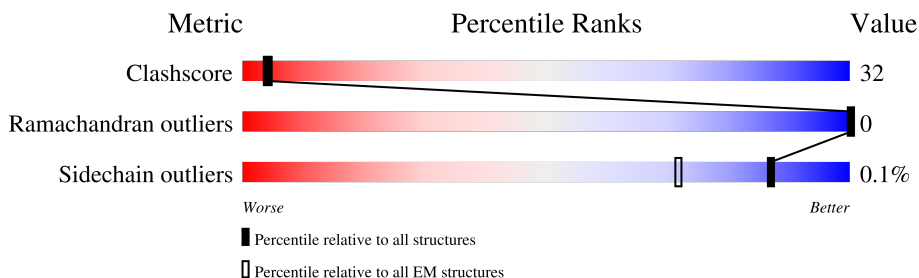
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

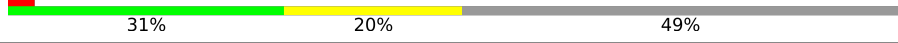
The reported resolution of this entry is 4.30 Å.

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.



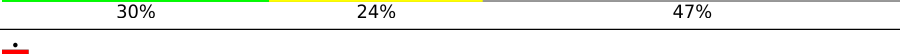
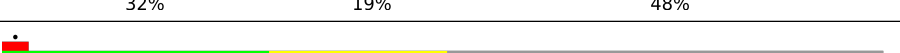
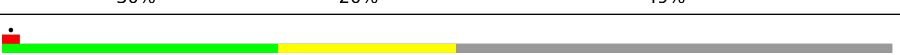
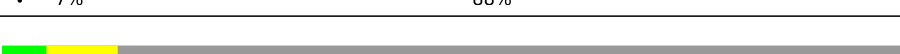
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	4585 (3.80 - 4.80)

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	460	
1	B	460	
1	C	460	
1	D	460	

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Mol	Chain	Length	Quality of chain
1	G	460	 17% 16% 66%
1	H	460	 18% 17% 65%
1	I	460	 12% 15% 74%
1	J	460	 15% 11% 74%
1	M	460	 30% 24% 47%
1	N	460	 32% 19% 48%
1	O	460	 30% 20% 49%
1	P	460	 31% 20% 49%
1	S	460	 17% 17% 66%
1	T	460	 18% 17% 65%
1	U	460	 12% 14% 74%
1	V	460	 15% 11% 74%
2	E	907	 5% 8% 88%
2	F	907	 5% 7% 88%
2	K	907	 5% 8% 88%
2	L	907	 5% 7% 88%
2	Q	907	 5% 8% 88%
2	R	907	 5% 8% 88%
2	W	907	 5% 8% 88%
2	X	907	 5% 7% 88%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 30088 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 Crescentin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	245	Total	C	N	O	S	0	0
			1876	1127	366	382	1		
1	B	238	Total	C	N	O	S	0	0
			1828	1099	358	370	1		
1	C	234	Total	C	N	O	S	0	0
			1793	1065	364	361	3		
1	D	234	Total	C	N	O	S	0	0
			1793	1065	364	361	3		
1	G	155	Total	C	N	O	S	0	0
			1203	727	234	241	1		
1	H	163	Total	C	N	O	S	0	0
			1264	764	244	255	1		
1	I	120	Total	C	N	O	S	0	0
			934	555	192	185	2		
1	J	120	Total	C	N	O	S	0	0
			934	555	192	185	2		
1	M	245	Total	C	N	O	S	0	0
			1876	1127	366	382	1		
1	N	238	Total	C	N	O	S	0	0
			1828	1099	358	370	1		
1	O	234	Total	C	N	O	S	0	0
			1793	1065	364	361	3		
1	P	234	Total	C	N	O	S	0	0
			1793	1065	364	361	3		
1	S	155	Total	C	N	O	S	0	0
			1203	727	234	241	1		
1	T	163	Total	C	N	O	S	0	0
			1264	764	244	255	1		
1	U	120	Total	C	N	O	S	0	0
			934	555	192	185	2		
1	V	120	Total	C	N	O	S	0	0
			934	555	192	185	2		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	406	SER	-	insertion	UNP A0A8F8EC09
A	407	ALA	-	insertion	UNP A0A8F8EC09
A	408	THR	-	insertion	UNP A0A8F8EC09
B	406	SER	-	insertion	UNP A0A8F8EC09
B	407	ALA	-	insertion	UNP A0A8F8EC09
B	408	THR	-	insertion	UNP A0A8F8EC09
C	406	SER	-	insertion	UNP A0A8F8EC09
C	407	ALA	-	insertion	UNP A0A8F8EC09
C	408	THR	-	insertion	UNP A0A8F8EC09
D	406	SER	-	insertion	UNP A0A8F8EC09
D	407	ALA	-	insertion	UNP A0A8F8EC09
D	408	THR	-	insertion	UNP A0A8F8EC09
G	406	SER	-	insertion	UNP A0A8F8EC09
G	407	ALA	-	insertion	UNP A0A8F8EC09
G	408	THR	-	insertion	UNP A0A8F8EC09
H	406	SER	-	insertion	UNP A0A8F8EC09
H	407	ALA	-	insertion	UNP A0A8F8EC09
H	408	THR	-	insertion	UNP A0A8F8EC09
I	406	SER	-	insertion	UNP A0A8F8EC09
I	407	ALA	-	insertion	UNP A0A8F8EC09
I	408	THR	-	insertion	UNP A0A8F8EC09
J	406	SER	-	insertion	UNP A0A8F8EC09
J	407	ALA	-	insertion	UNP A0A8F8EC09
J	408	THR	-	insertion	UNP A0A8F8EC09
M	406	SER	-	insertion	UNP A0A8F8EC09
M	407	ALA	-	insertion	UNP A0A8F8EC09
M	408	THR	-	insertion	UNP A0A8F8EC09
N	406	SER	-	insertion	UNP A0A8F8EC09
N	407	ALA	-	insertion	UNP A0A8F8EC09
N	408	THR	-	insertion	UNP A0A8F8EC09
O	406	SER	-	insertion	UNP A0A8F8EC09
O	407	ALA	-	insertion	UNP A0A8F8EC09
O	408	THR	-	insertion	UNP A0A8F8EC09
P	406	SER	-	insertion	UNP A0A8F8EC09
P	407	ALA	-	insertion	UNP A0A8F8EC09
P	408	THR	-	insertion	UNP A0A8F8EC09
S	406	SER	-	insertion	UNP A0A8F8EC09
S	407	ALA	-	insertion	UNP A0A8F8EC09
S	408	THR	-	insertion	UNP A0A8F8EC09
T	406	SER	-	insertion	UNP A0A8F8EC09
T	407	ALA	-	insertion	UNP A0A8F8EC09
T	408	THR	-	insertion	UNP A0A8F8EC09
U	406	SER	-	insertion	UNP A0A8F8EC09

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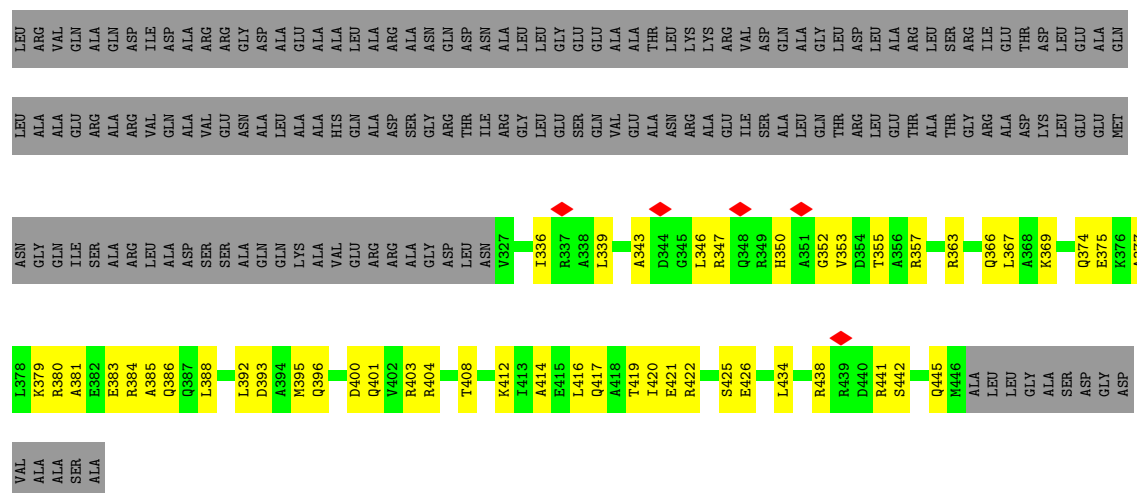
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Chain	Residue	Modelled	Actual	Comment	Reference
U	407	ALA	-	insertion	UNP A0A8F8EC09
U	408	THR	-	insertion	UNP A0A8F8EC09
V	406	SER	-	insertion	UNP A0A8F8EC09
V	407	ALA	-	insertion	UNP A0A8F8EC09
V	408	THR	-	insertion	UNP A0A8F8EC09

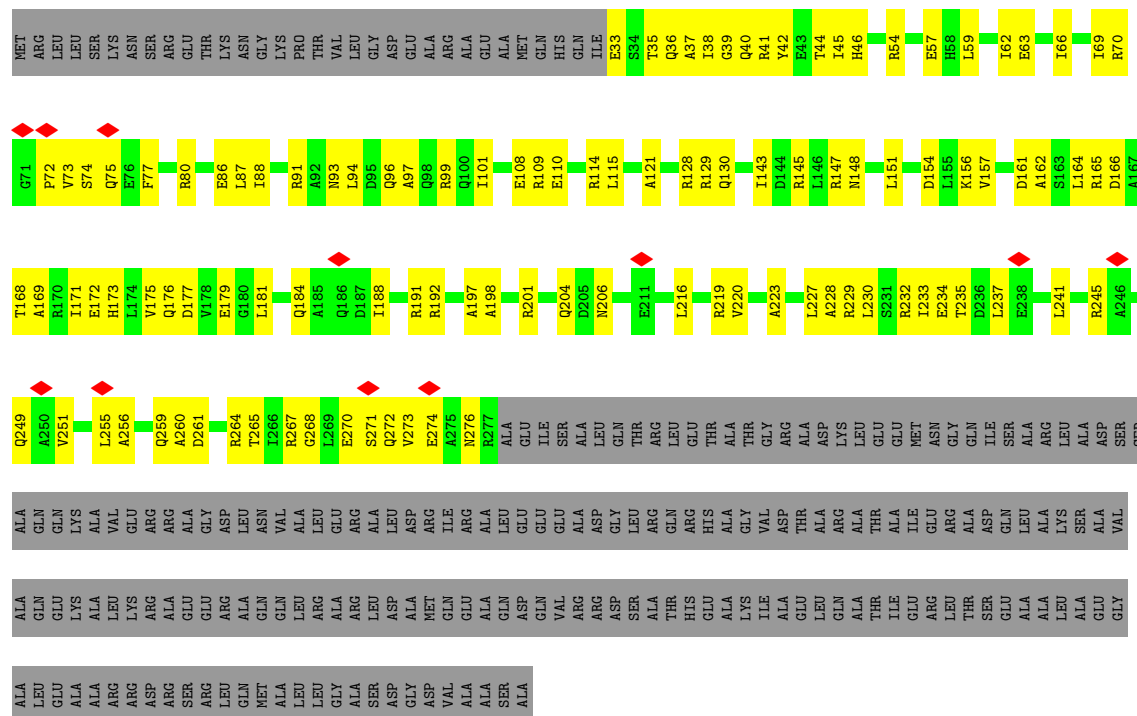
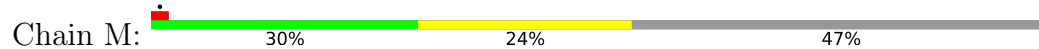
- Molecule 2 is a protein called Crescentin-specific megabody MB13.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	112	Total	C	N	O	S	0	0
			869	539	155	170	5		
2	F	111	Total	C	N	O	S	0	0
			861	535	154	167	5		
2	K	112	Total	C	N	O	S	0	0
			869	539	155	170	5		
2	L	105	Total	C	N	O	S	0	0
			820	508	148	159	5		
2	Q	112	Total	C	N	O	S	0	0
			869	539	155	170	5		
2	R	111	Total	C	N	O	S	0	0
			861	535	154	167	5		
2	W	112	Total	C	N	O	S	0	0
			869	539	155	170	5		
2	X	105	Total	C	N	O	S	0	0
			820	508	148	159	5		

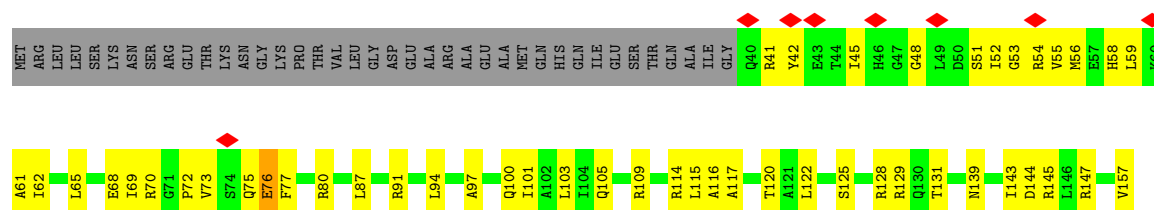
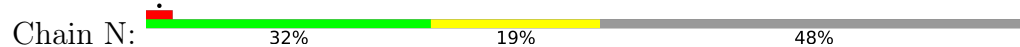


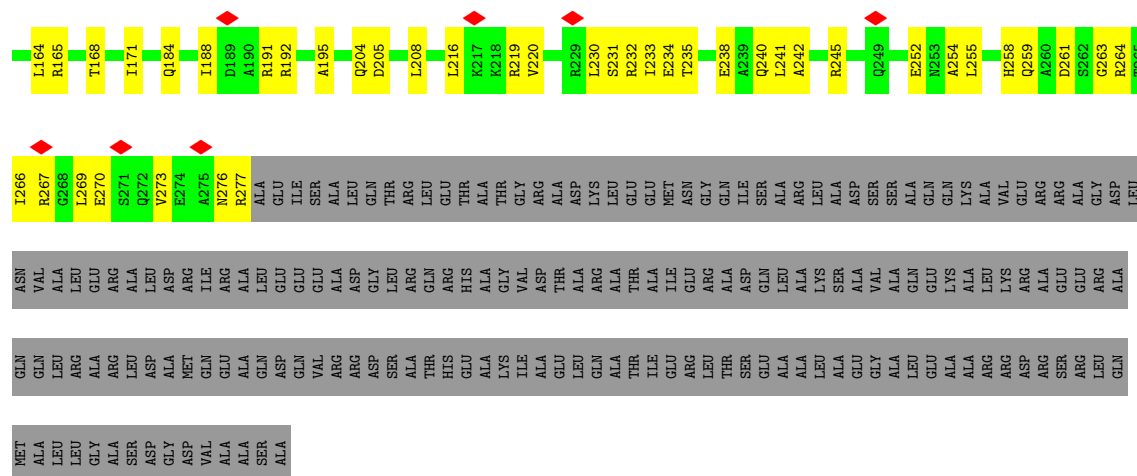


• Molecule 1: Crescentin

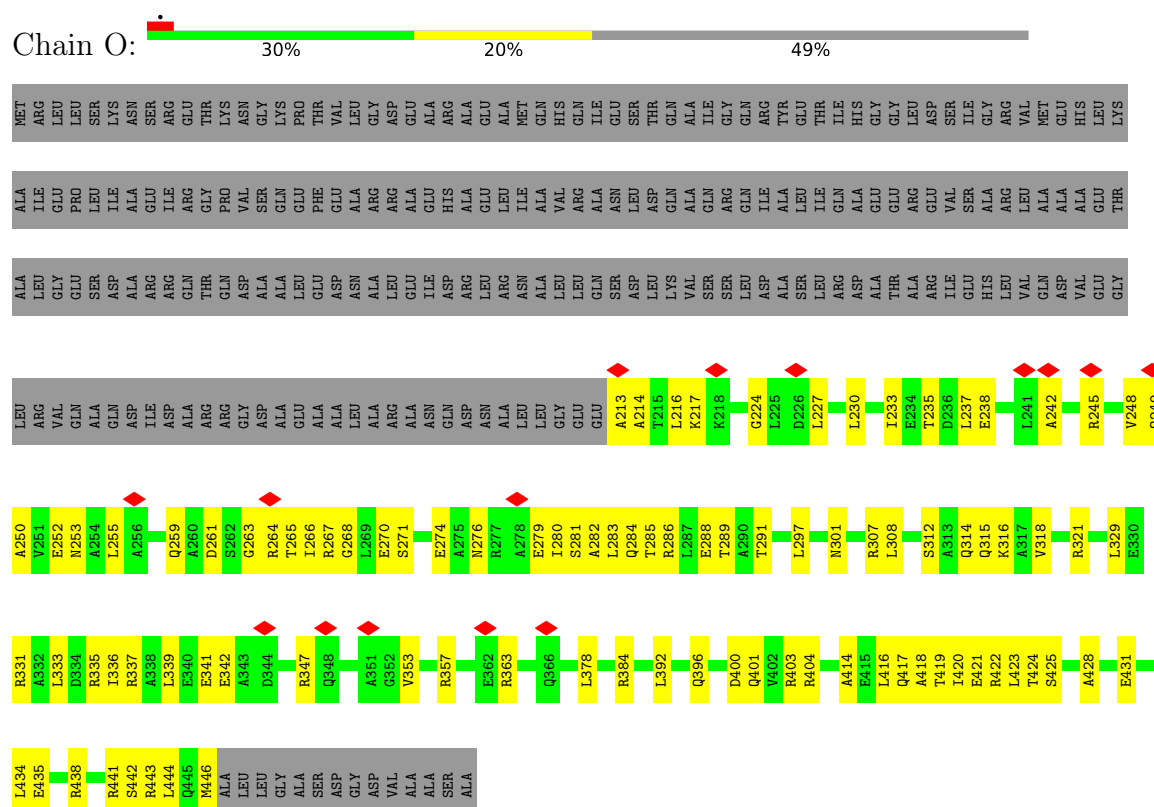


• Molecule 1: Crescentin

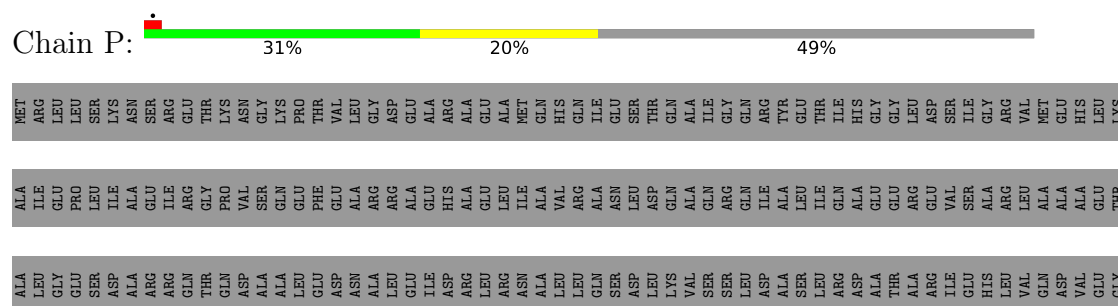


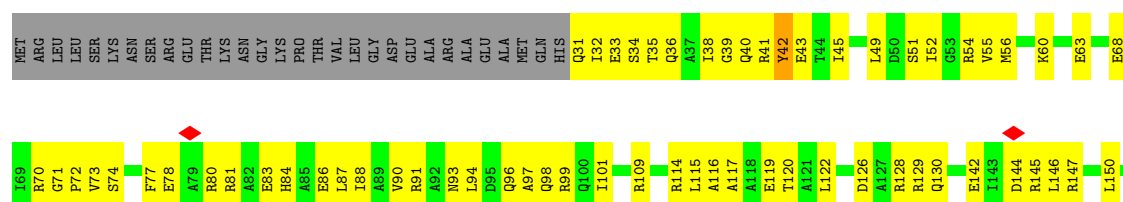


• Molecule 1: Crescentin

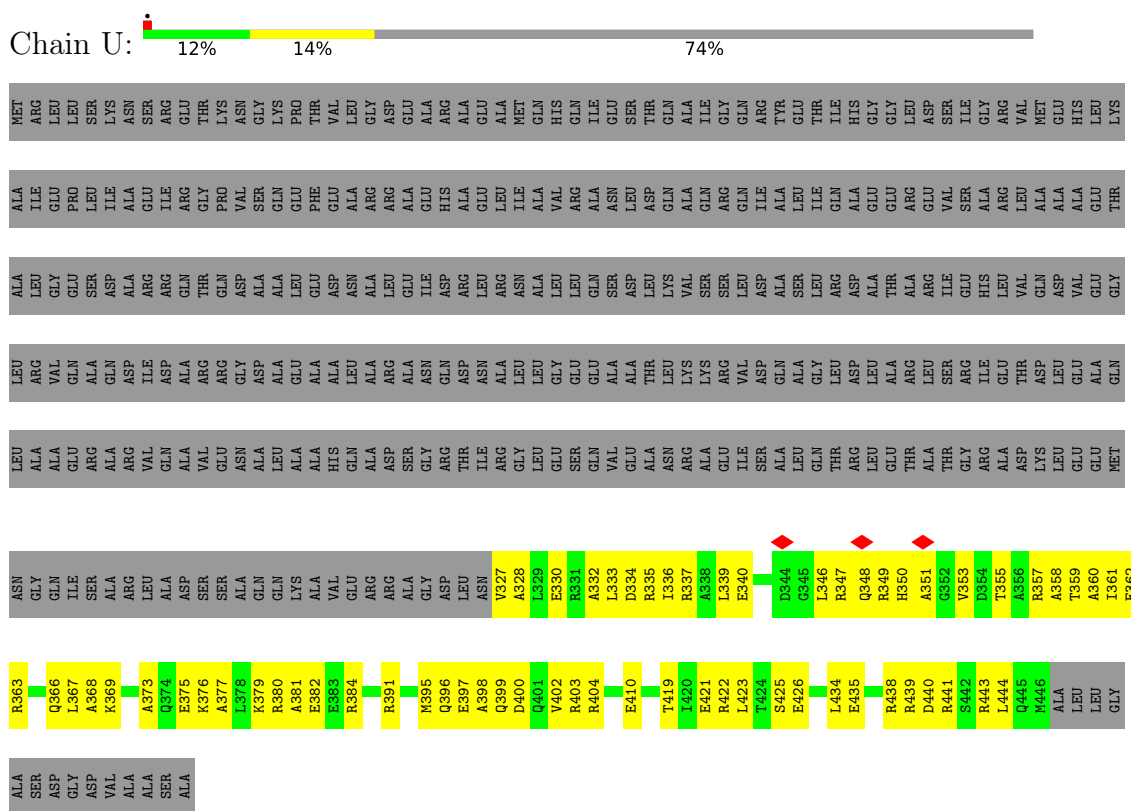


• Molecule 1: Crescentin

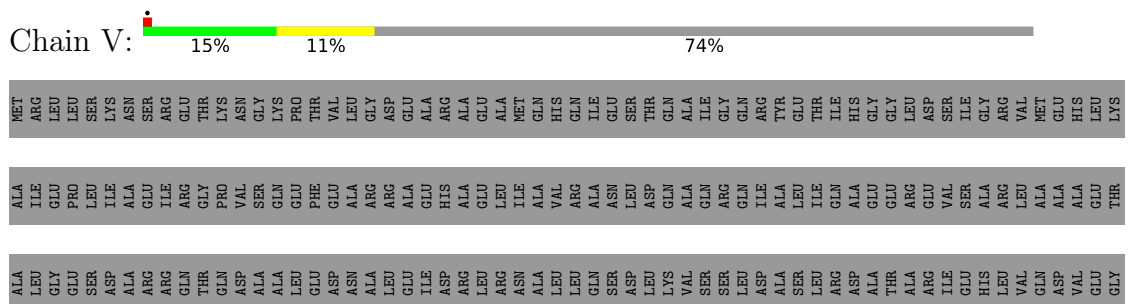




- Molecule 1: Crescentin



- Molecule 1: Crescentin



Y851	Y852	Y853	Q854	Y855	Y856	Y857	Y858	Y859	P860	Y861	Y862	Y863	Y864	Y865	Y866	Y867	Y868	Y869	A870	Y871	Y872	Y873	Y874	Y875	Y876	Y877	Y878	Y879	Y880	Y881	Y882	Y883	Y884	Y885	Y886	Y887	Y888	Y889	Y890	Y891	Y892	Y893	Y894	Y895	Y896	Y897	Y898	Y899	Y900	Y901	Y902	Y903	Y904	Y905	Y906	Y907	Y908	Y909	Y910	Y911	Y912	Y913	Y914	Y915	Y916	Y917	Y918	Y919	Y920	Y921	Y922	Y923	Y924	Y925	Y926	Y927	Y928	Y929	Y930	Y931	Y932	Y933	Y934	Y935	Y936	Y937	Y938	Y939	Y940	Y941	Y942	Y943	Y944	Y945	Y946	Y947	Y948	Y949	Y950	Y951	Y952	Y953	Y954	Y955	Y956	Y957	Y958	Y959	Y960	Y961	Y962	Y963	Y964	Y965	Y966	Y967	Y968	Y969	Y970	Y971	Y972	Y973	Y974	Y975	Y976	Y977	Y978	Y979	Y980	Y981	Y982	Y983	Y984	Y985	Y986	Y987	Y988	Y989	Y990	Y991	Y992	Y993	Y994	Y995	Y996	Y997	Y998	Y999	Y1000
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Chain F: 5% 7% 88%







[illegible]

- Molecule 2: Crescentin-specific megabody MB13

Chain X: 7% 88%

[illegible]

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	585252	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 ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.736	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.022	Depositor
Map size (Å)	954.0, 954.0, 954.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.59, 1.59, 1.59	Depositor

5 Model quality ⓘ

5.1 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	A	0.31	0/1884	0.61	0/2540
1	B	0.31	0/1836	0.63	1/2475 (0.0%)
1	C	0.29	0/1795	0.61	0/2407
1	D	0.30	0/1795	0.59	0/2407
1	G	0.29	0/1210	0.67	0/1630
1	H	0.30	0/1271	0.68	2/1713 (0.1%)
1	I	0.34	0/935	0.60	0/1251
1	J	0.29	0/935	0.62	0/1251
1	M	0.31	0/1884	0.61	0/2540
1	N	0.31	0/1836	0.63	1/2475 (0.0%)
1	O	0.29	0/1795	0.61	0/2407
1	P	0.30	0/1795	0.59	0/2407
1	S	0.29	0/1210	0.66	0/1630
1	T	0.30	0/1271	0.68	2/1713 (0.1%)
1	U	0.34	0/935	0.60	0/1251
1	V	0.29	0/935	0.62	0/1251
2	E	0.44	0/883	0.69	0/1192
2	F	0.39	0/875	0.73	1/1181 (0.1%)
2	K	0.37	0/883	0.55	0/1192
2	L	0.35	0/833	0.65	0/1124
2	Q	0.43	0/883	0.69	0/1192
2	R	0.39	0/875	0.73	1/1181 (0.1%)
2	W	0.37	0/883	0.55	0/1192
2	X	0.35	0/833	0.65	0/1124
All	All	0.33	0/30270	0.63	8/40726 (0.0%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	42	TYR	CA-C-N	-5.71	112.63	120.28
1	H	42	TYR	C-N-CA	-5.71	112.63	120.28
1	T	42	TYR	CA-C-N	-5.70	112.64	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	42	TYR	C-N-CA	-5.70	112.64	120.28
2	R	885	THR	N-CA-C	5.67	115.90	108.07

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	1876	0	1869	140	0
1	B	1828	0	1824	131	0
1	C	1793	0	1815	111	0
1	D	1793	0	1813	104	0
1	G	1203	0	1200	104	0
1	H	1264	0	1261	107	0
1	I	934	0	946	84	0
1	J	934	0	946	71	0
1	M	1876	0	1869	142	0
1	N	1828	0	1824	128	0
1	O	1793	0	1815	109	0
1	P	1793	0	1813	107	0
1	S	1203	0	1200	104	0
1	T	1264	0	1261	105	0
1	U	934	0	946	81	0
1	V	934	0	946	73	0
2	E	869	0	846	83	0
2	F	861	0	842	74	0
2	K	869	0	846	121	0
2	L	820	0	802	79	0
2	Q	869	0	846	83	0
2	R	861	0	842	79	0
2	W	869	0	846	122	0
2	X	820	0	802	78	0
All	All	30088	0	30020	1926	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 32.

The worst 5 of 1926 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:K:804:ILE:HB	2:K:872:TYR:CZ	1.30	1.66
2:K:804:ILE:HD13	2:K:872:TYR:CD2	1.28	1.64
2:W:804:ILE:HD13	2:W:872:TYR:CD2	1.28	1.63
2:W:804:ILE:HB	2:W:872:TYR:CZ	1.29	1.62
2:W:804:ILE:CB	2:W:872:TYR:CE1	1.85	1.60

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	243/460 (53%)	239 (98%)	4 (2%)	0	100	100
1	B	236/460 (51%)	231 (98%)	5 (2%)	0	100	100
1	C	232/460 (50%)	230 (99%)	2 (1%)	0	100	100
1	D	232/460 (50%)	229 (99%)	3 (1%)	0	100	100
1	G	153/460 (33%)	152 (99%)	1 (1%)	0	100	100
1	H	161/460 (35%)	159 (99%)	2 (1%)	0	100	100
1	I	118/460 (26%)	117 (99%)	1 (1%)	0	100	100
1	J	118/460 (26%)	116 (98%)	2 (2%)	0	100	100
1	M	243/460 (53%)	239 (98%)	4 (2%)	0	100	100
1	N	236/460 (51%)	231 (98%)	5 (2%)	0	100	100
1	O	232/460 (50%)	230 (99%)	2 (1%)	0	100	100
1	P	232/460 (50%)	229 (99%)	3 (1%)	0	100	100
1	S	153/460 (33%)	152 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	T	161/460 (35%)	159 (99%)	2 (1%)	0	100	100
1	U	118/460 (26%)	117 (99%)	1 (1%)	0	100	100
1	V	118/460 (26%)	116 (98%)	2 (2%)	0	100	100
2	E	108/907 (12%)	90 (83%)	18 (17%)	0	100	100
2	F	107/907 (12%)	81 (76%)	26 (24%)	0	100	100
2	K	108/907 (12%)	92 (85%)	16 (15%)	0	100	100
2	L	101/907 (11%)	89 (88%)	12 (12%)	0	100	100
2	Q	108/907 (12%)	90 (83%)	18 (17%)	0	100	100
2	R	107/907 (12%)	81 (76%)	26 (24%)	0	100	100
2	W	108/907 (12%)	92 (85%)	16 (15%)	0	100	100
2	X	101/907 (11%)	90 (89%)	11 (11%)	0	100	100
All	All	3834/14616 (26%)	3651 (95%)	183 (5%)	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	187/347 (54%)	187 (100%)	0	100	100
1	B	182/347 (52%)	182 (100%)	0	100	100
1	C	174/347 (50%)	174 (100%)	0	100	100
1	D	174/347 (50%)	174 (100%)	0	100	100
1	G	122/347 (35%)	122 (100%)	0	100	100
1	H	129/347 (37%)	128 (99%)	1 (1%)	73	77
1	I	89/347 (26%)	89 (100%)	0	100	100
1	J	89/347 (26%)	89 (100%)	0	100	100
1	M	187/347 (54%)	187 (100%)	0	100	100
1	N	182/347 (52%)	182 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	O	174/347 (50%)	174 (100%)	0	100	100
1	P	174/347 (50%)	174 (100%)	0	100	100
1	S	122/347 (35%)	122 (100%)	0	100	100
1	T	129/347 (37%)	128 (99%)	1 (1%)	73	77
1	U	89/347 (26%)	89 (100%)	0	100	100
1	V	89/347 (26%)	89 (100%)	0	100	100
2	E	94/749 (13%)	94 (100%)	0	100	100
2	F	93/749 (12%)	93 (100%)	0	100	100
2	K	94/749 (13%)	94 (100%)	0	100	100
2	L	89/749 (12%)	89 (100%)	0	100	100
2	Q	94/749 (13%)	94 (100%)	0	100	100
2	R	93/749 (12%)	93 (100%)	0	100	100
2	W	94/749 (13%)	94 (100%)	0	100	100
2	X	89/749 (12%)	89 (100%)	0	100	100
All	All	3032/11544 (26%)	3030 (100%)	2 (0%)	87	88

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	93	ASN
1	T	93	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
1	T	93	ASN
1	T	132	GLN
2	W	880	GLN
1	H	40	GLN
1	H	31	GLN

5.3.3 RNA ⓘ

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.

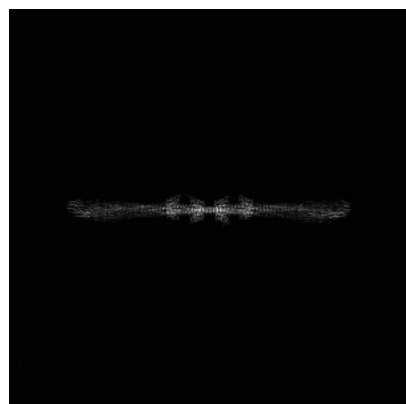
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15476. These allow visual inspection of the internal detail of the map and identification of artifacts.

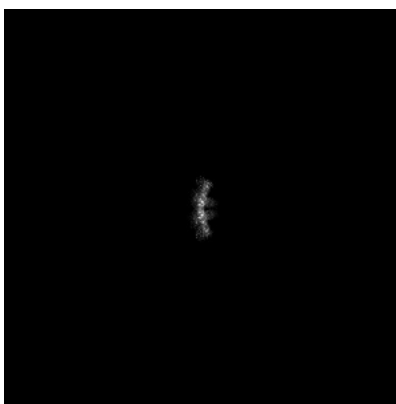
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

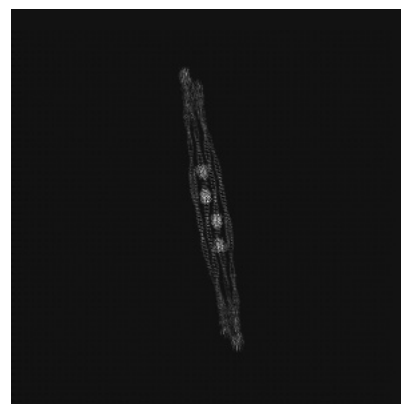
6.1.1 Primary map



X

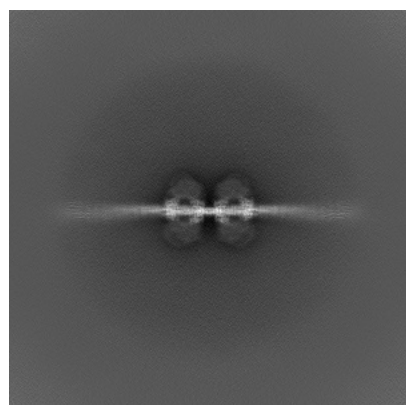


Y

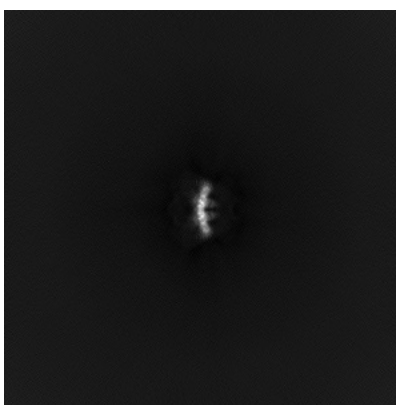


Z

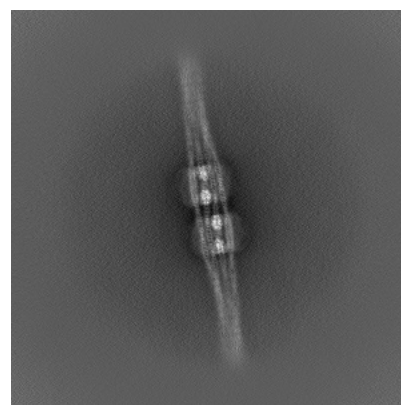
6.1.2 Raw map



X



Y

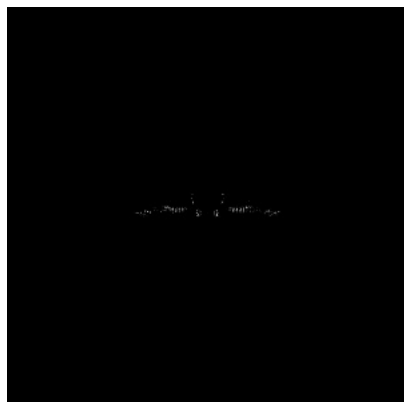


Z

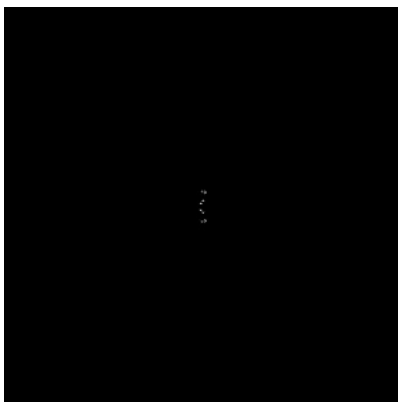
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 300

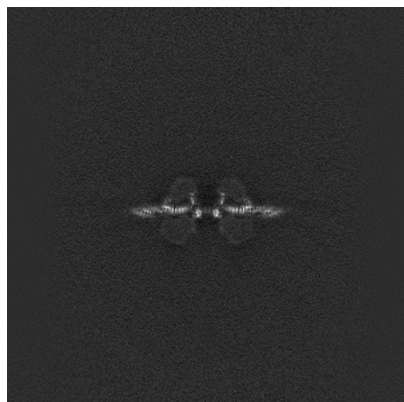


Y Index: 300

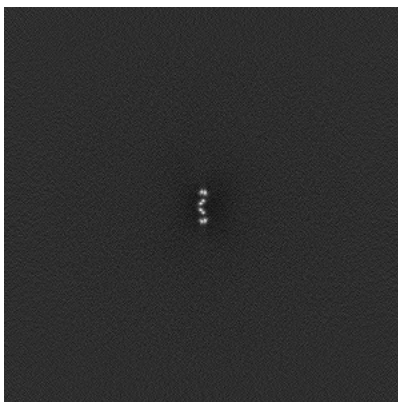


Z Index: 300

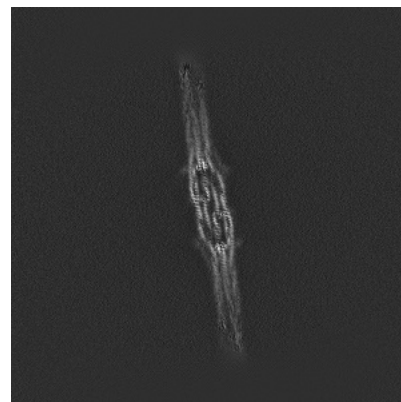
6.2.2 Raw map



X Index: 300



Y Index: 300



Z Index: 300

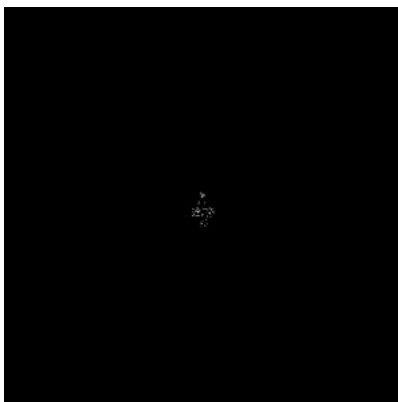
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 310

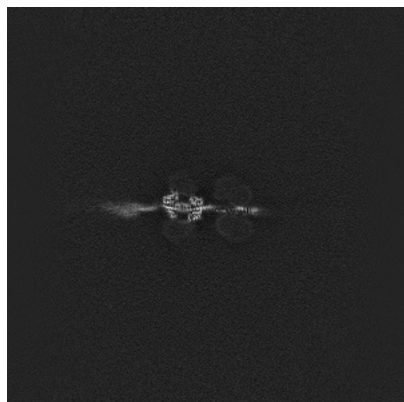


Y Index: 318

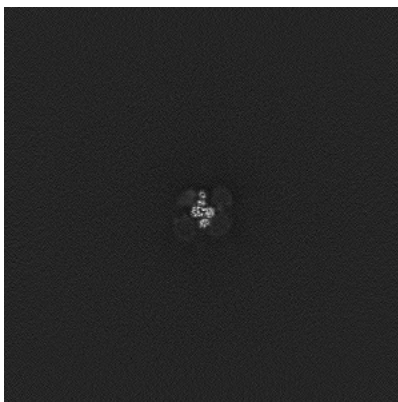


Z Index: 299

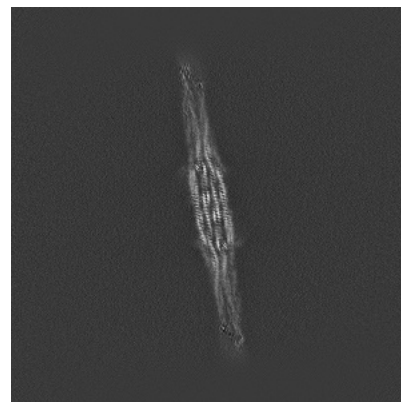
6.3.2 Raw map



X Index: 310



Y Index: 317

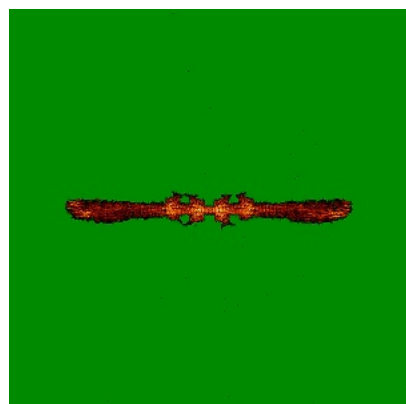


Z Index: 298

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

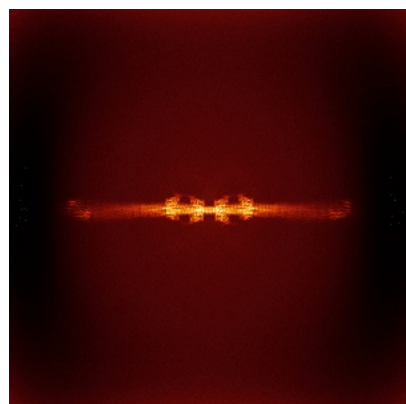


Y

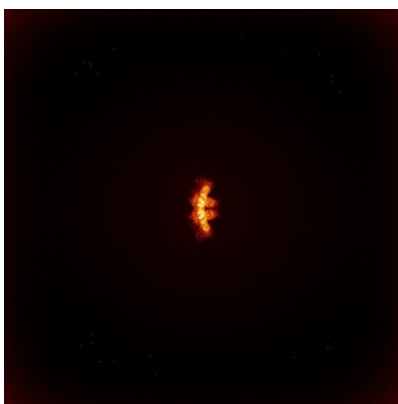


Z

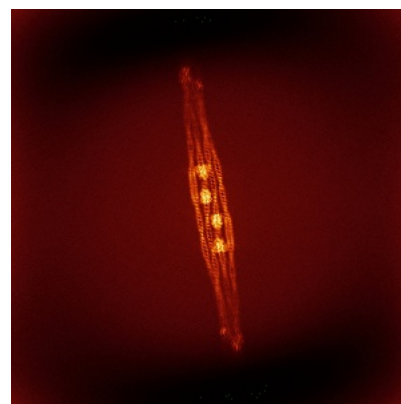
6.4.2 Raw map



X



Y

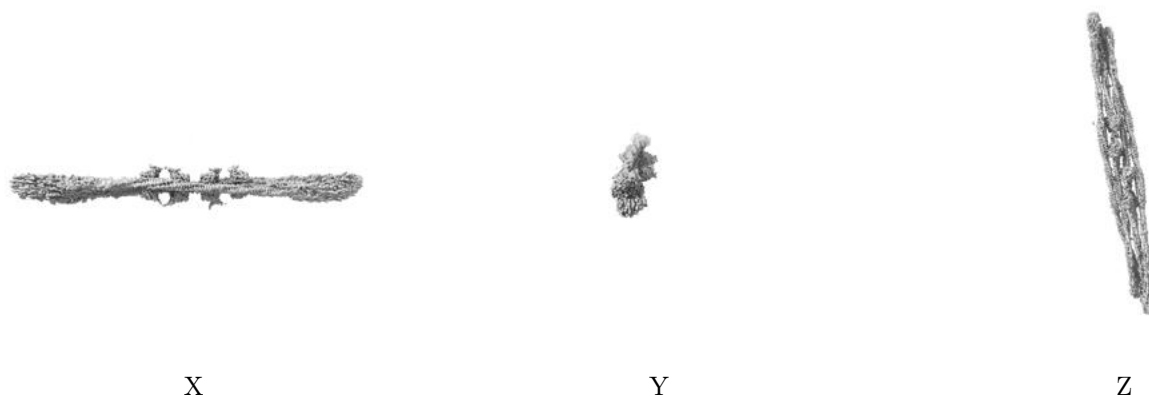


Z

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.

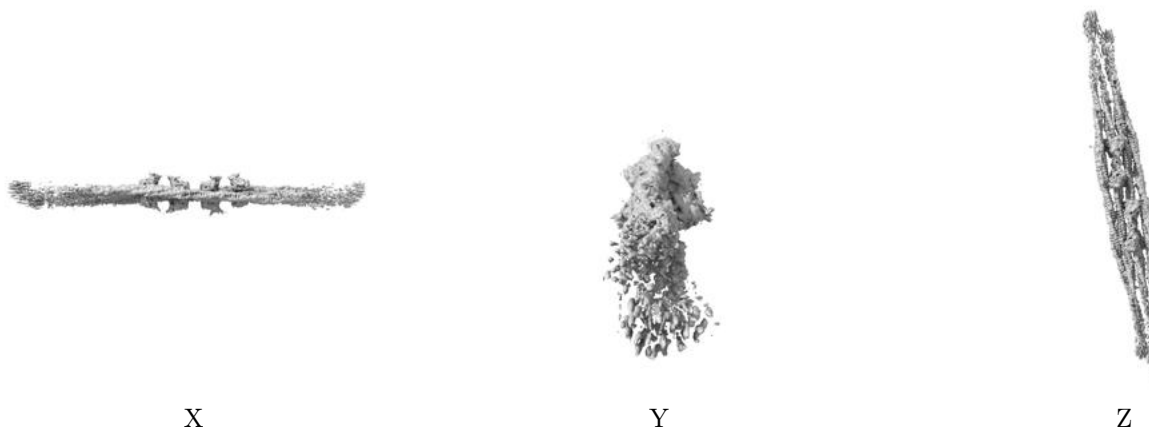
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.022. 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.

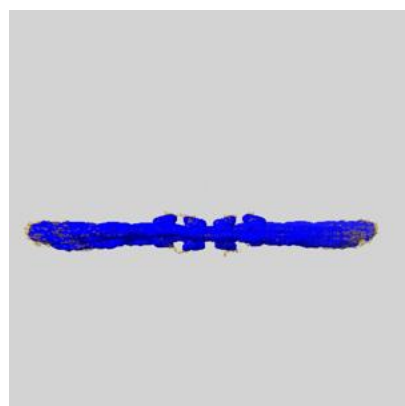
6.6 Mask visualisation [i](#)

This section 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

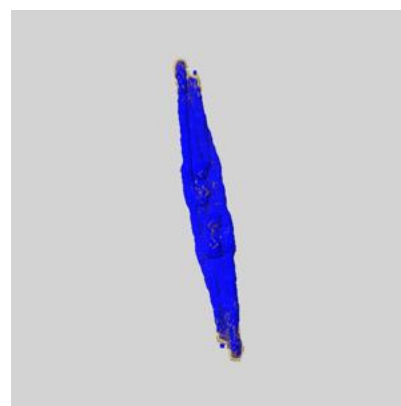
6.6.1 emd_15476_msk_1.map [i](#)



X



Y

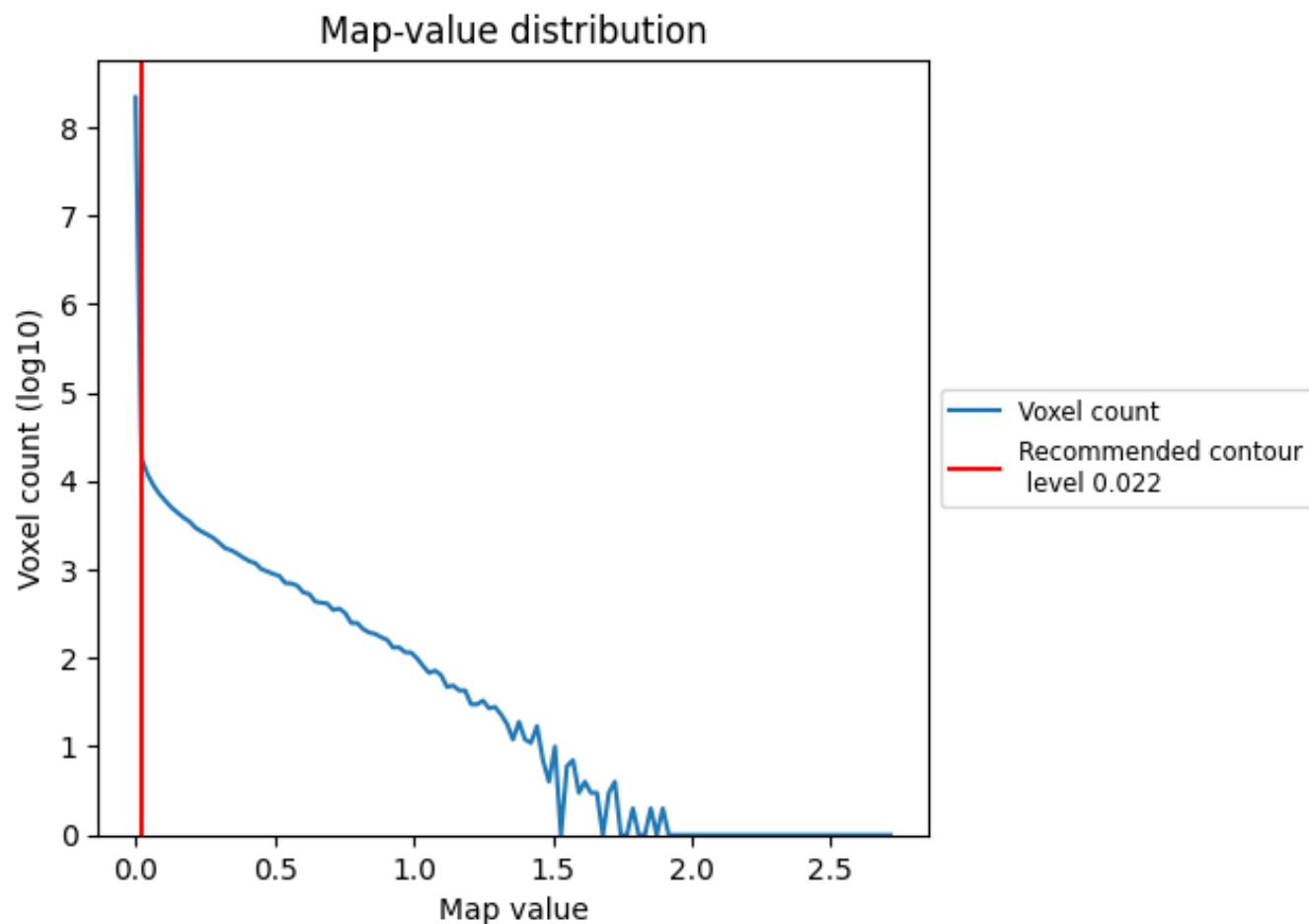


Z

7 Map analysis [i](#)

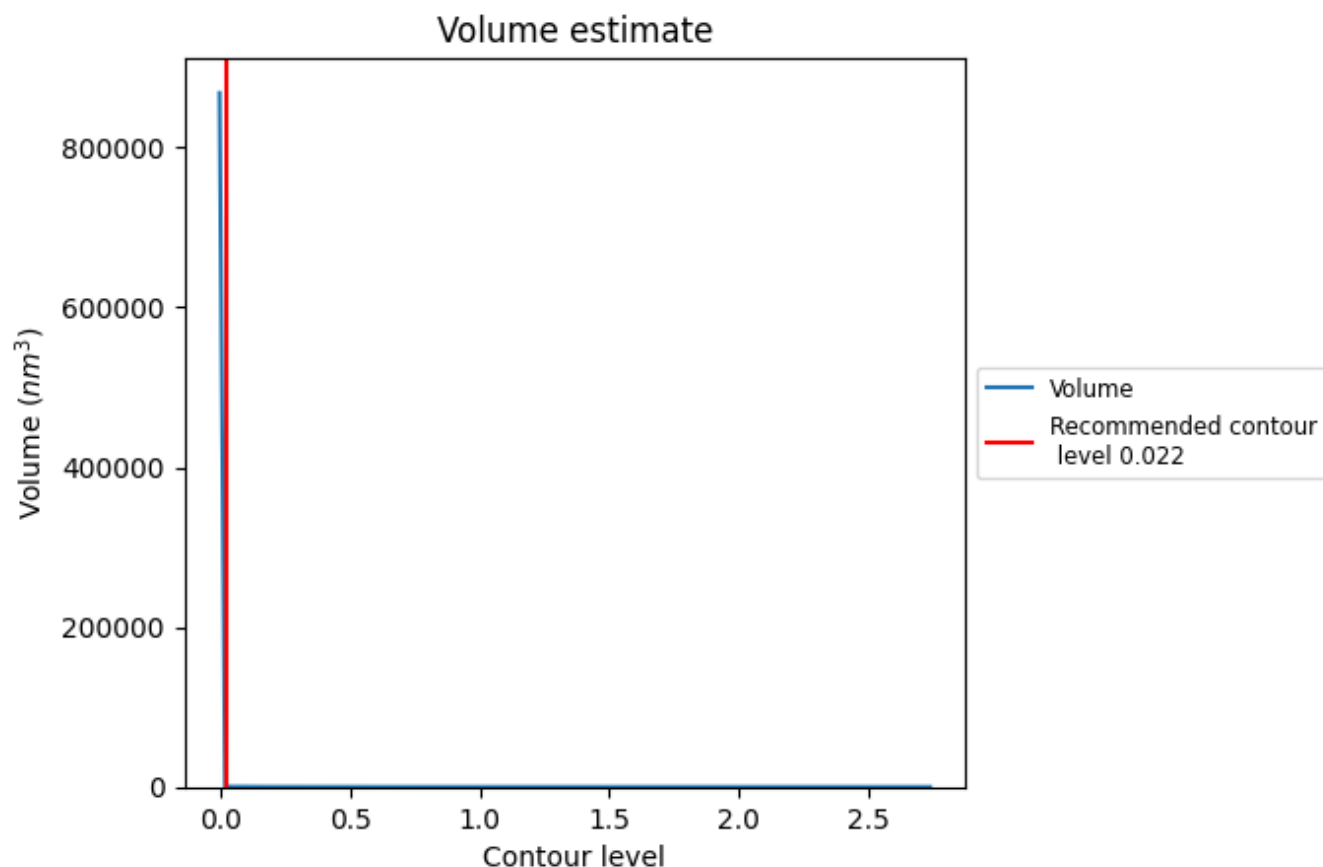
This section contains the results of statistical analysis of the map.

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.

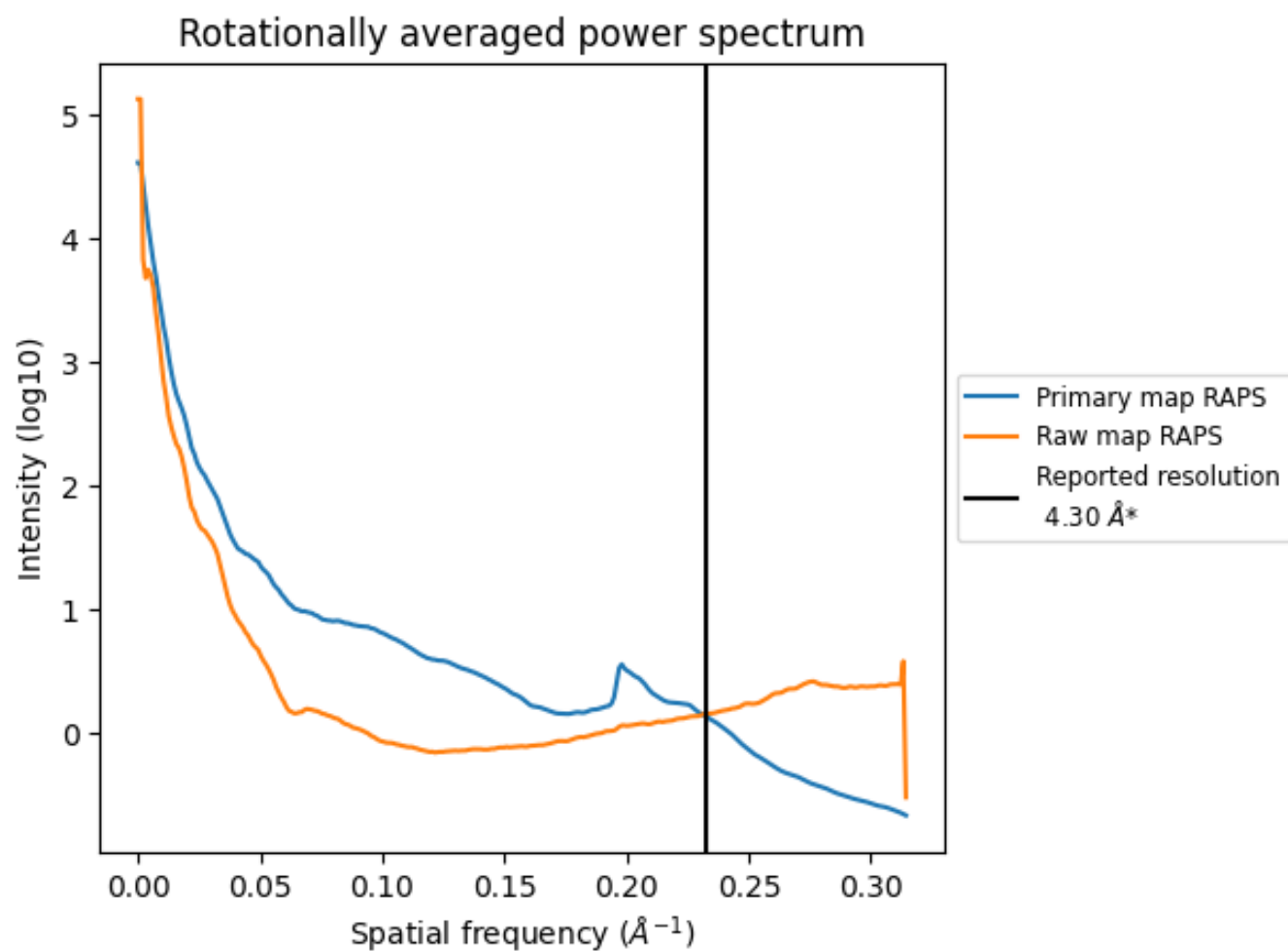
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 401 nm^3 ; this corresponds to an approximate mass of 362 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 ⓘ

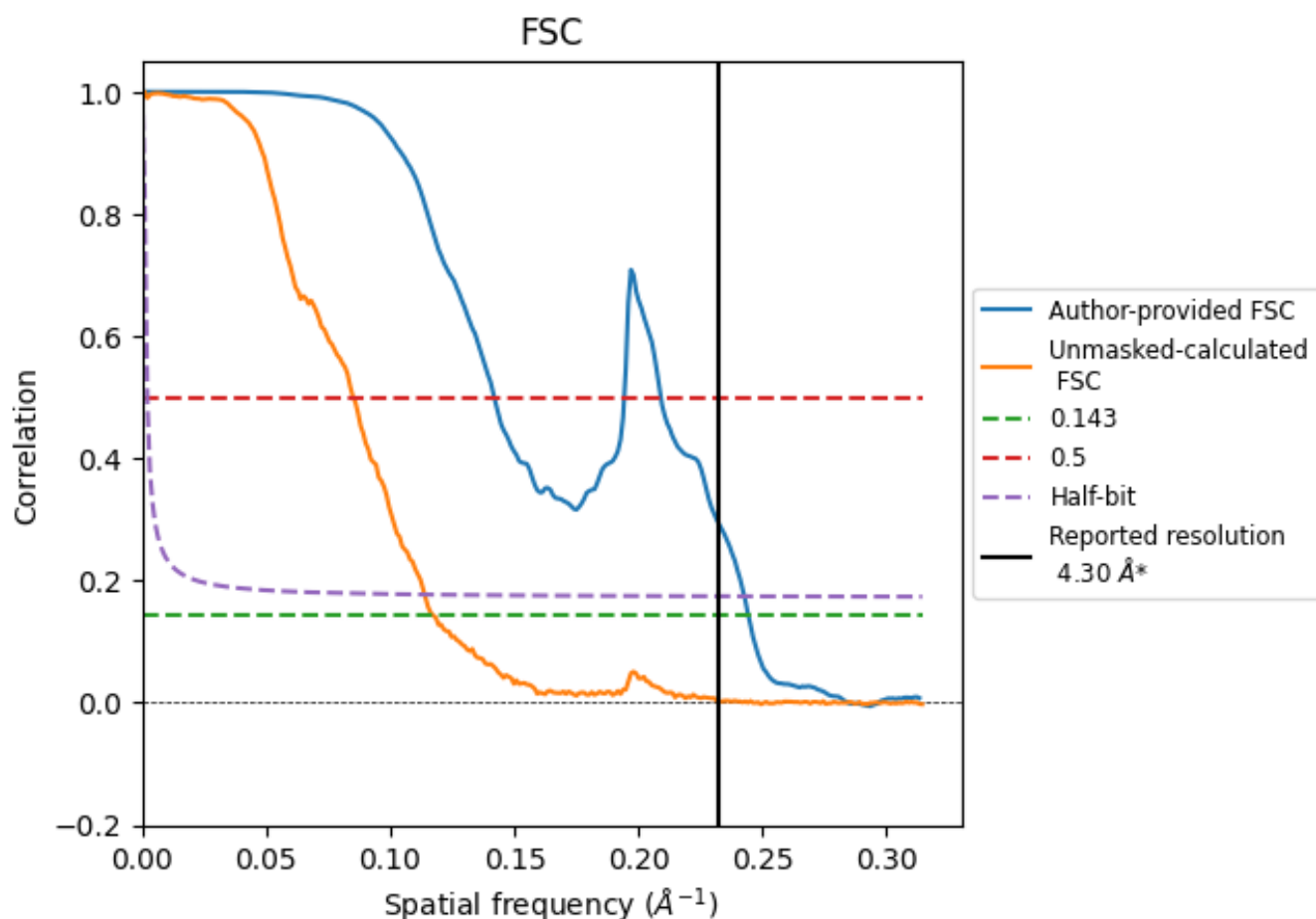


*Reported resolution corresponds to spatial frequency of 0.233 $\text{\AA}^{-1}$

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 $0.233 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

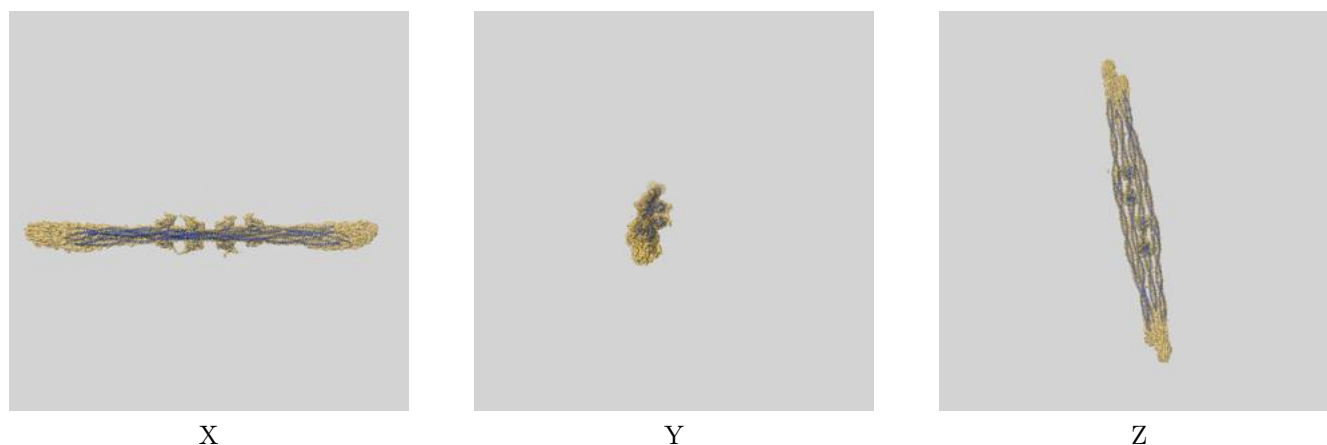
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.09	7.05	4.12
Unmasked-calculated*	8.53	11.75	8.78

*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 8.53 differs from the reported value 4.3 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15476 and PDB model 8AJB. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



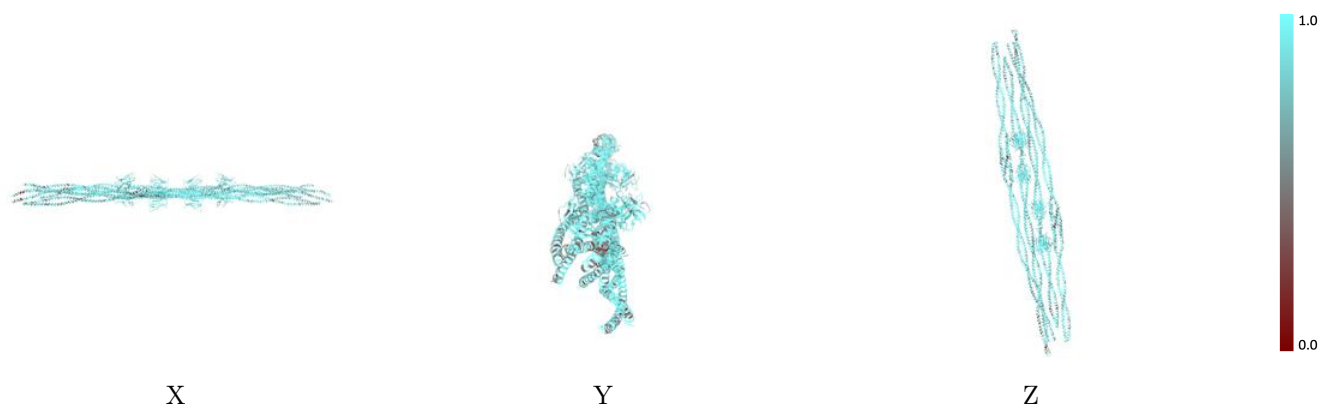
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



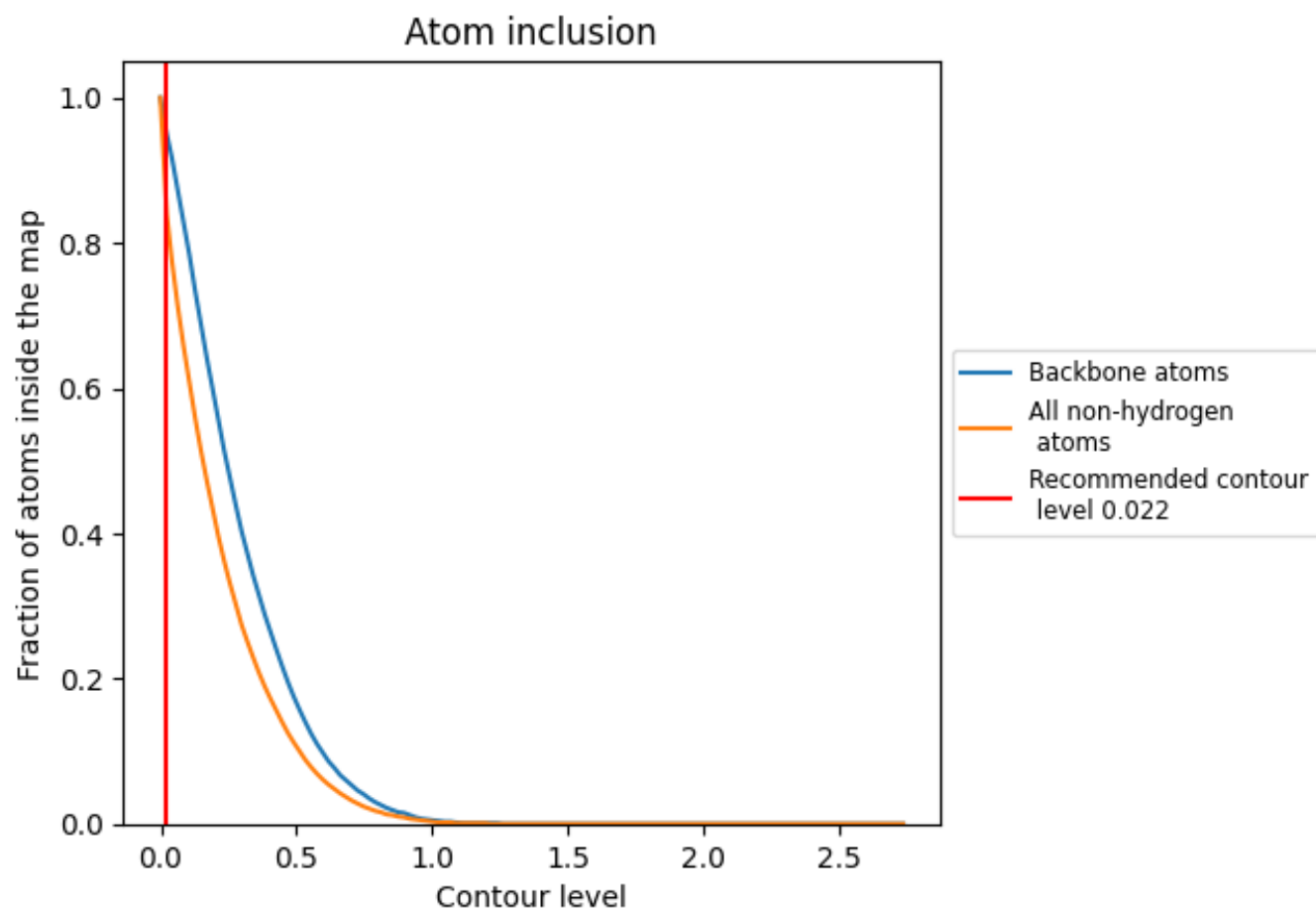
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.022).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 84% 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 (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8400	 0.1860
A	 0.8330	 0.1630
B	 0.8260	 0.1630
C	 0.8050	 0.1570
D	 0.8420	 0.1700
E	 0.9230	 0.3140
F	 0.9030	 0.2830
G	 0.7630	 0.0640
H	 0.8310	 0.0980
I	 0.8450	 0.1850
J	 0.8430	 0.1680
K	 0.9000	 0.2960
L	 0.8880	 0.3160
M	 0.8200	 0.1590
N	 0.8150	 0.1620
O	 0.8080	 0.1660
P	 0.8600	 0.1950
Q	 0.9050	 0.2970
R	 0.8990	 0.2710
S	 0.7620	 0.0650
T	 0.8280	 0.1230
U	 0.8440	 0.1940
V	 0.8330	 0.1830
W	 0.8920	 0.2850
X	 0.8960	 0.3280

