



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:07 AM UTC

PDB ID : 8AIX / pdb_00008aix
EMDB ID : EMD-15473
Title : Cryo-EM structure of crescentin filaments (wildtype, C2 symmetry and large box)
Authors : Liu, Y.; Lowe, J.
Deposited on : 2022-07-27
Resolution : 5.80 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

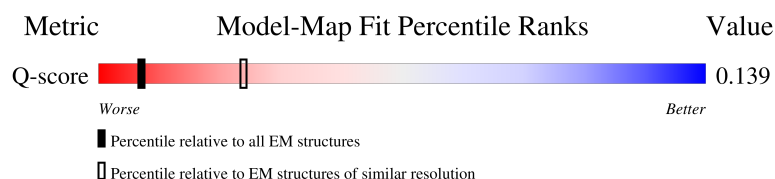
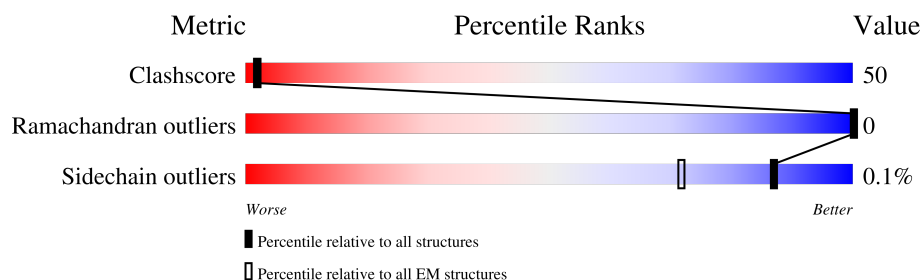
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.80 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.



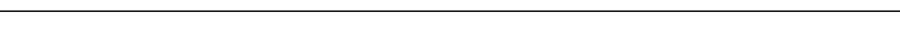
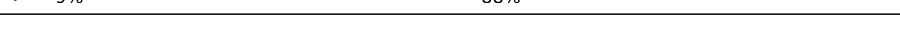
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	511 (5.30 - 6.30)

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	457	
1	B	457	
1	E	457	
1	F	457	

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Mol	Chain	Length	Quality of chain
1	G	457	 14% 26% 60%
1	H	457	 10% 30% 61%
1	K	457	 7% 9% 84%
1	L	457	 9% 9% 82%
1	M	457	 9% 24% 68%
1	N	457	 13% 21% 66%
1	Q	457	 14% 26% 60%
1	R	457	 10% 30% 61%
1	U	457	 6% 10% 84%
1	V	457	 9% 10% 82%
1	W	457	 9% 24% 68%
1	X	457	 14% 20% 66%
2	C	907	 7% 90%
2	D	907	 8% 88%
2	I	907	 9% 88%
2	J	907	 8% 88%
2	O	907	 7% 90%
2	P	907	 8% 88%
2	S	907	 9% 88%
2	T	907	 8% 88%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 21924 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	84	Total 655	C 390	N 134	O 130	S 1	0	0
1	B	85	Total 664	C 395	N 136	O 132	S 1	0	0
1	G	183	Total 1400	C 844	N 269	O 286	S 1	0	0
1	H	179	Total 1373	C 829	N 264	O 279	S 1	0	0
1	K	72	Total 556	C 341	N 104	O 110	S 1	0	0
1	L	84	Total 643	C 393	N 124	O 125	S 1	0	0
1	M	147	Total 1142	C 677	N 234	O 228	S 3	0	0
1	N	156	Total 1207	C 714	N 247	O 243	S 3	0	0
1	E	84	Total 655	C 390	N 134	O 130	S 1	0	0
1	F	85	Total 664	C 395	N 136	O 132	S 1	0	0
1	Q	183	Total 1400	C 844	N 269	O 286	S 1	0	0
1	R	179	Total 1373	C 829	N 264	O 279	S 1	0	0
1	U	72	Total 556	C 341	N 104	O 110	S 1	0	0
1	V	84	Total 643	C 393	N 124	O 125	S 1	0	0
1	W	147	Total 1142	C 677	N 234	O 228	S 3	0	0
1	X	156	Total 1207	C 714	N 247	O 243	S 3	0	0

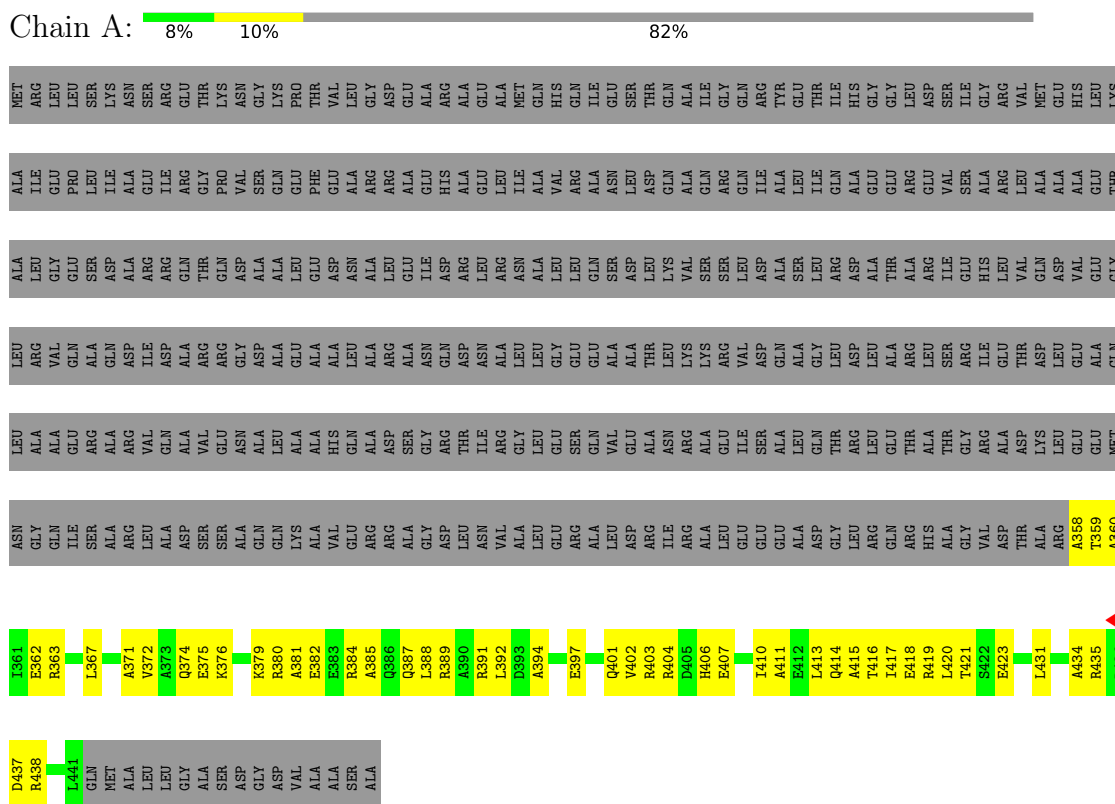
- Molecule 2 is a protein called Crescentin-specific megabody MB13.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	112	Total	C	N	O	S	0	0
			869	539	155	170	5		
2	J	111	Total	C	N	O	S	0	0
			860	534	154	167	5		
2	C	94	Total	C	N	O	S	0	0
			724	449	129	142	4		
2	I	112	Total	C	N	O	S	0	0
			869	539	155	170	5		
2	P	112	Total	C	N	O	S	0	0
			869	539	155	170	5		
2	T	111	Total	C	N	O	S	0	0
			860	534	154	167	5		
2	O	94	Total	C	N	O	S	0	0
			724	449	129	142	4		
2	S	112	Total	C	N	O	S	0	0
			869	539	155	170	5		

3 Residue-property plots

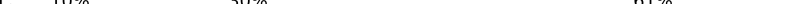
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Crescentin



• Molecule 1: Crescentin



Chain H:  10% 30% 61%



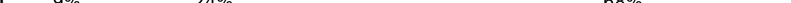
S125	D189	LEU	GLN	LYS	ARG	GLU	LYS	ARG	ARG	S126	LEU	ALA	VAL	LYS	ARG	GLU	LYS	ARG	ARG	S127	ALA	HIS	GLN	ALA	ASP	SER	GLY	ASP	ALA	GLN	VAL	ASP	GLY	THR	ASP	S128	ALA	ALA	ALA	ALA	ALA	S129	THR	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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● Molecule 1: Crescentin



ALA	ALA	GLN	GLY	LYS	ARG	ASP	ASP	GLY	ASN	ALA	GLY	ASP	ASP	GLY	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
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- Molecule 1: Crescentin

Chain M:  9% 24% 68%

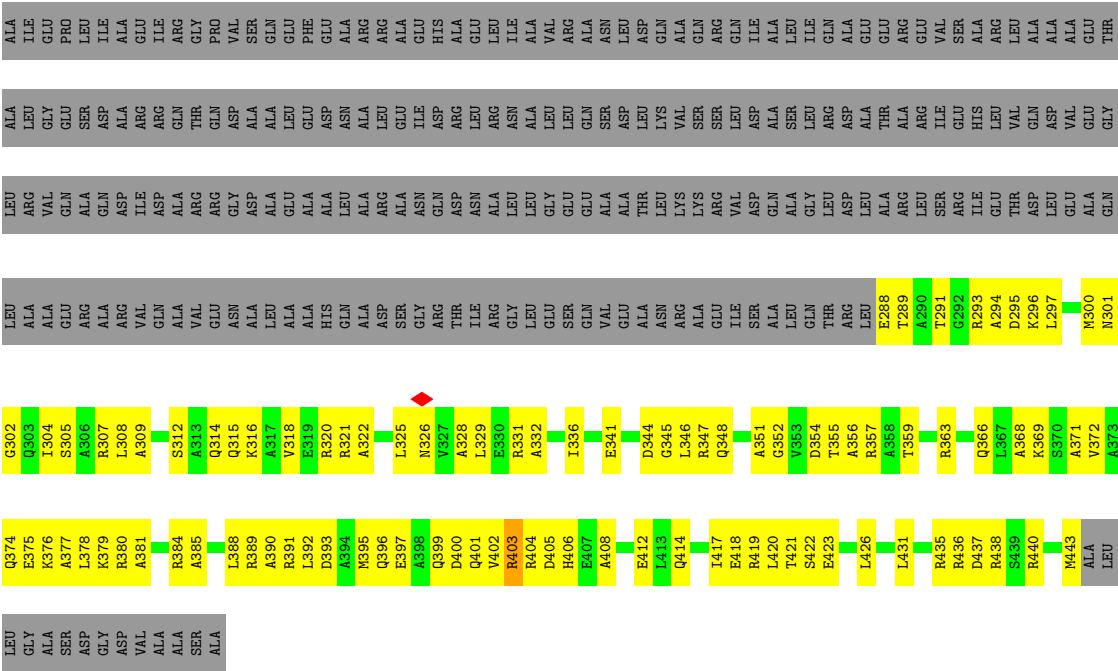
[illegible]

A433	A434	R435	R436	D437	R438	S439	R440	L441	Q442	M443	ALA	LEU	LEU	GLY	ALA	SER	ASP	GLY	ASP	VAL	ALA	ALA	SER	ALA
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- Molecule 1: Crescentin

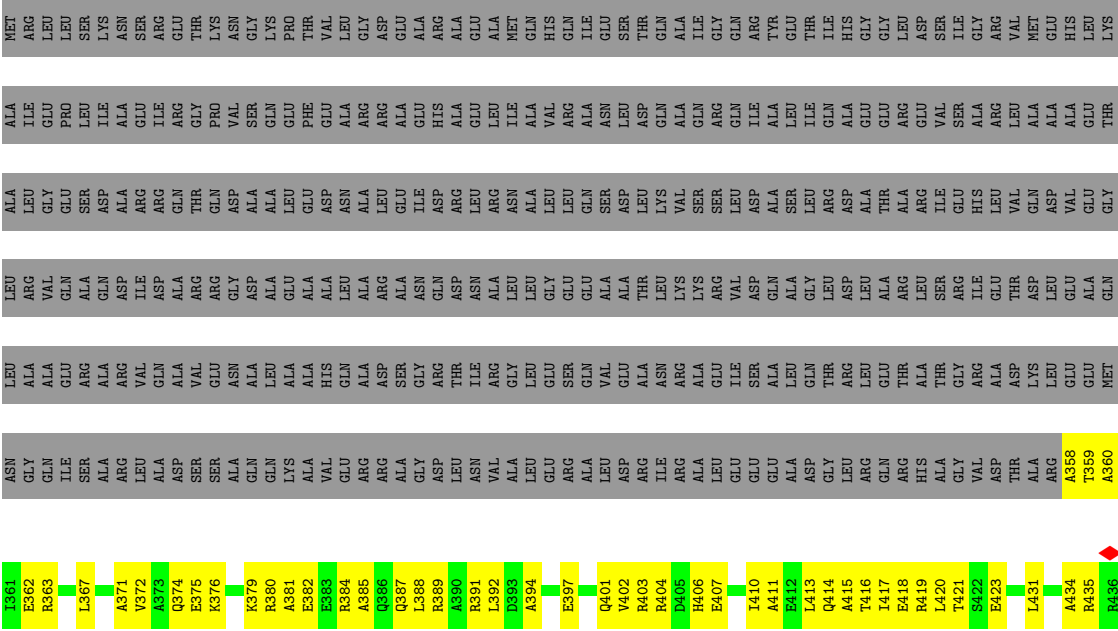
Chain N: 13% 21% 66%

MET	ARG	LEU	LEU	LEU	LEU	LYS	ASN	ASN	ARG	GLU	THR	THR	LYS	ASN	GLY	LYS	PRO	THR	THR	VAL	LEU	GLY	GLY	ASP	GLU	GLU	ALA	ALA	ARG	ALA	GLU	GLN	MET	MET	HIS	GLN	GLN	ILE	GLN	GLU	GLY	GLY	GLY	GLN	GLN	ARG	TYR	GLU	THR	THR	ILE	ILE	HIS	HIS	GLY	GLY	GLY	GLY	LEU	ASP	SER	SER	ILE	ILE	ILE	GLY	GLY	GLY	ARG	VAL	VAL	MET	MET	GLU	GLU	HIS	HIS	LEU	LEU	LYS
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● Molecule 1: Crescentin

Chain E: 8% 11% 82%



● Molecule 1: Crescentin

Chain F: 7% 11% 81%

R436	R437	R438	S439	R440	L441	Q442	MET	ALA	LEU	LEU	GLY	ALA	SER	ASP	GLY	ASP	VAL	ALA	ALA	SER	ALA
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Chain R: 10% 30% 61%

ARG	LEU	VAL	HIS	ALA	ASP	E63
SER	LYS	GLU	GLN	ALA	ASN	P64
ARG	ARG	ARG	ALA	ALA	ALA	P65
LEU	ALA	ARG	ASP	ALA	LEU	I66
GLN	GLU	ALA	SER	ALA	GLU	A67
MET	GLU	GLY	GLY	ASN	ILE	E68
ALA	ARG	ASP	ARG	GLN	ASP	I69
LEU	ALA	LEU	THR	ASP	ARG	R70
LEU	ALA	ASN	ILE	ASN	LEU	G71
GLY	GLN	VAL	ARG	ALA	ARG	P72
ALA	LEU	ALA	GLY	LEU	ASN	V73
SER	ARG	LEU	LEU	GLY	LEU	S74
ASP	ALA	GLU	GLU	GLY	LEU	Q75
GLY	ARG	ARG	SER	GLU	LEU	
ASP	LEU	ALA	GLN	GLU	GLN	E78
VAL	ASP	LEU	VAL	ALA	SER	A79
ALA	ALA	ASP	GLU	ALA	ASP	R80
ALA	MET	ARG	ALA	THR	LEU	
SER	GLN	ILE	ASN	LEU	LYS	H84
ALA	GLU	ARG	ARG	LEU	VAL	A85
SER	ALA	ALA	ALA	LYS	SER	E86
ALA	ALA	ALA	GLU	ARG	SER	L87
ASP	ASP	GLU	ILE	VAL	LEU	
GLN	GLN	GLU	SER	ASP	ASP	V90
VAL	VAL	GLU	ALA	GLN	ALA	R91
ARG	ARG	ALA	LEU	ALA	SER	A92
ARG	ARG	ASP	GLN	GLY	LEU	
HIS	HIS	GLY	THR	LEU	ARG	D95
GLU	GLU	LEU	ARG	LEU	ASP	Q96
ALA	ALA	ARG	LEU	ALA	ALA	A97
LYS	LYS	GLN	GLU	ARG	ALA	
ILE	ILE	HIS	THR	LEU	ALA	Q100
GLU	GLU	ALA	LEU	ARG	ILE	I101
SER	SER	THR	LEU	ILE	GLU	
THR	THR	GLY	ARG	GLY	HIS	I104
GLN	GLN	VAL	ARG	ILE	GLY	Q105
ILE	ILE	ASP	ALA	THR	LEU	A106
GLY	GLY	THR	ASP	ASP	VAL	E107
ARG	ARG	ALA	LYS	GLN	GLN	E108
THR	THR	ARG	LEU	LEU	ASP	R109
LEU	LEU	ALA	GLU	GLU	VAL	E110
THR	THR	ALA	GLU	ALA	GLU	V111
THR	THR	ILE	MET	GLN	GLY	
SER	SER	ASN	ASN	LEU	LEU	R114
GLU	GLU	GLY	GLY	ALA	ARG	
ALA	ALA	GLN	GLN	VAL	VAL	A117
ALA	ALA	ILE	ILE	GLU	GLN	A118
LEU	LEU	ASP	SER	ARG	ALA	E119
ALA	ALA	GLN	ALA	ALA	GLN	T120
ALA	ALA	ARG	ALA	ARG	ASP	
GLU	GLU	LEU	LEU	VAL	ILE	R128
GLY	GLY	LYS	ASP	GLN	ASP	ARG
LEU	LEU	ALA	ASP	ALA	GLN	G53
LEU	LEU	ALA	SER	VAL	ARG	R54
ALA	ALA	VAL	SER	GLU	ARG	
ALA	ALA	ALA	ALA	ASN	GLY	ASP
ARG	ARG	GLN	GLN	ALA	ASP	ALA
ASP	ASP	LYS	LYS	LEU	ALA	L59
					GLU	X60
					ALA	A61

Chain W: 9% 24% 68%

[illegible]

WORLDWIDE
PDB
PROTEIN DATA BANK

[illegible]

Chain D: 8% 88%

[illegible]

[illegible]

- Molecule 2: Crescentin-specific megabody MB13

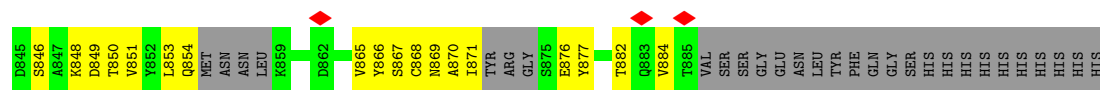
Chain J: 8% 88%

[illegible]

[illegible]

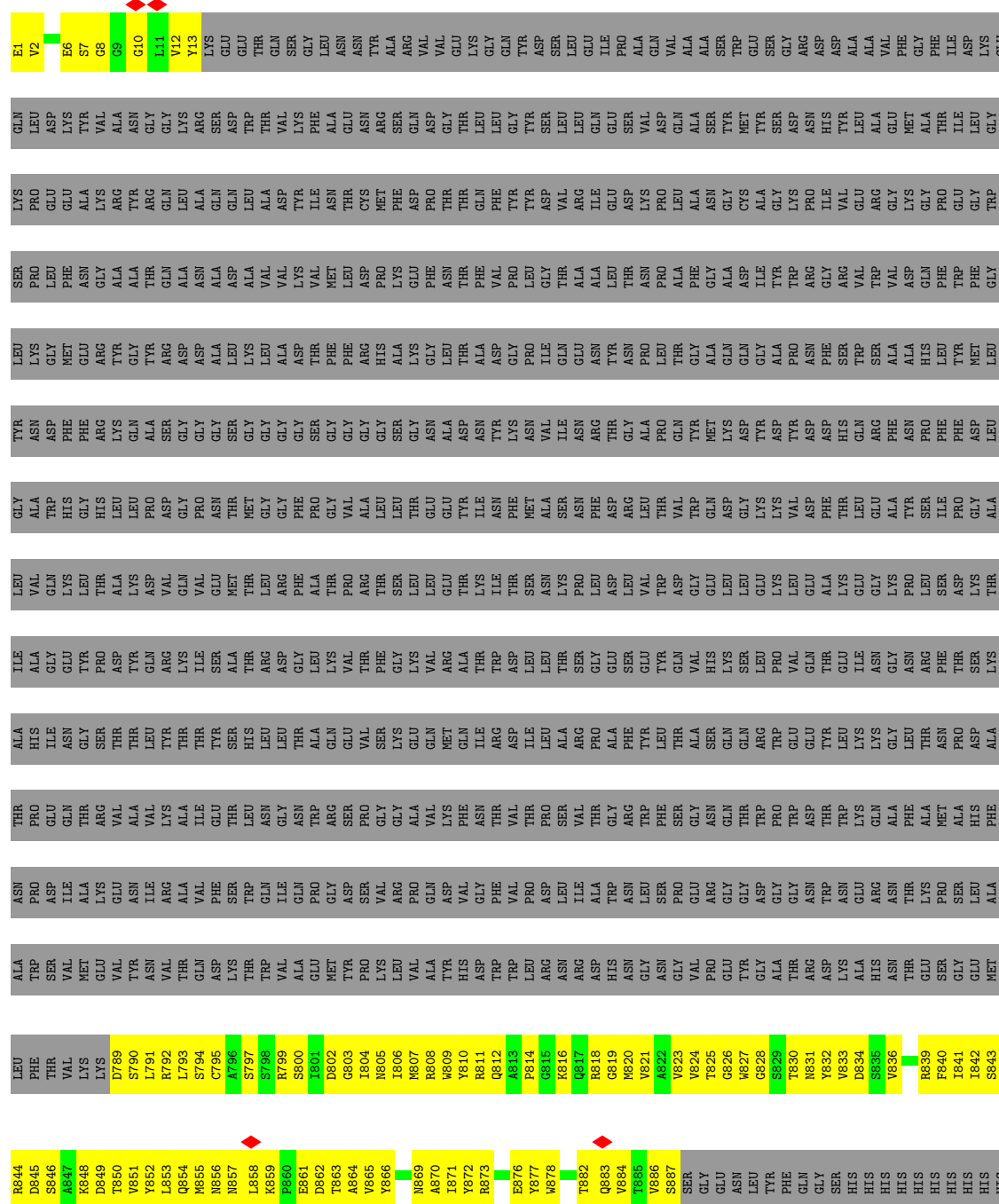
Chain C: 7% 90%





• Molecule 2: Crescentin-specific megabody MB13

Chain I: 9% 88%



• Molecule 2: Crescentin-specific megabody MB13

Chain P: 8% 88%



Chain T: 8%



B844	D845	S846	A847	K848	D849	T850	V851	Y852	L853	Q854	M855	N856	N857	L858	K859	P860	E861	D862	T863	A864	V865	Y866		N869	A870	I871	Y872	B873		E876	Y877	W878		T882	Q883	V884	T885	V886	S887	SER	GLY	GLU	ASN	LEU	TYR	PHE	GLN	GLY	SER	HIS	HIS	HIS	HIS	HIS	HIS	HIS																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
LEU	PHE	THR	VAL	LYS	D789	S790	L791	R792	L793	S794	C795	A796	S797	S798	R799	S800	I801	D802	G803	I804	N805	I806	M807	R808	W809	Y810	R811	Q812	A813	P814	G815	K816	R817	R818	G819	M820	V821	A822	V823	V824	T825	G826	W827	S828	S829	T830	N831	Y832	V833	D834	S835	V836		R839	F840	I841	I842	S843																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
ALA	TRP	SER	VAL	MET	GLU	VAL	ASN	VAL	THR	GLN	ASP	LYS	THR	TRP	GLN	VAL	ALA	GLU	MET	TYR	PRO	LYS	LEU	VAL	ALA	THR	ASP	TRP	TRP	LEU	ARG	ASN	ARG	ASN	GLY	ASN	GLY	VAL	PRO	GLU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	550574	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 ($e^-/\text{\AA}^2$)	34	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.942	Depositor
Minimum map value	-0.003	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	972.0, 972.0, 972.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.944, 1.944, 1.944	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	0.35	0/655	0.75	0/875
1	B	0.41	0/664	0.89	0/887
1	E	0.35	0/655	0.75	0/875
1	F	0.41	0/664	0.88	0/887
1	G	0.28	0/1407	0.65	0/1899
1	H	0.30	0/1380	0.64	0/1862
1	K	0.21	0/560	0.49	0/755
1	L	0.25	0/648	0.55	0/872
1	M	0.29	0/1143	0.63	0/1528
1	N	0.35	0/1208	0.78	1/1615 (0.1%)
1	Q	0.28	0/1407	0.65	0/1899
1	R	0.31	0/1380	0.64	0/1862
1	U	0.21	0/560	0.49	0/755
1	V	0.24	0/648	0.55	0/872
1	W	0.29	0/1143	0.63	0/1528
1	X	0.35	0/1208	0.78	1/1615 (0.1%)
2	C	0.46	0/734	0.75	1/988 (0.1%)
2	D	0.34	0/883	0.61	0/1192
2	I	0.43	0/883	0.73	0/1192
2	J	0.37	0/874	0.67	0/1180
2	O	0.46	0/734	0.75	1/988 (0.1%)
2	P	0.34	0/883	0.60	0/1192
2	S	0.43	0/883	0.73	0/1192
2	T	0.38	0/874	0.67	0/1180
All	All	0.34	0/22078	0.68	4/29690 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	403	ARG	CB-CG-CD	6.24	125.66	111.30
1	X	403	ARG	CB-CG-CD	6.21	125.59	111.30
2	O	798	SER	N-CA-C	-5.43	107.20	113.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	798	SER	N-CA-C	-5.43	107.20	113.88

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	655	0	667	72	0
1	B	664	0	674	70	0
1	E	655	0	667	71	0
1	F	664	0	674	71	0
1	G	1400	0	1389	138	0
1	H	1373	0	1364	179	0
1	K	556	0	557	44	0
1	L	643	0	646	49	0
1	M	1142	0	1151	145	0
1	N	1207	0	1214	119	0
1	Q	1400	0	1389	139	0
1	R	1373	0	1364	179	0
1	U	556	0	557	47	0
1	V	643	0	646	51	0
1	W	1142	0	1151	141	0
1	X	1207	0	1214	118	0
2	C	724	0	697	106	0
2	D	869	0	846	95	0
2	I	869	0	846	130	0
2	J	860	0	837	103	0
2	O	724	0	697	103	0
2	P	869	0	846	92	0
2	S	869	0	846	127	0
2	T	860	0	837	99	0
All	All	21924	0	21776	2187	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 50.

The worst 5 of 2187 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:O:802:ASP:OD1	2:O:844:ARG:HD3	1.52	1.09
2:C:802:ASP:OD1	2:C:844:ARG:HD3	1.52	1.08
2:J:832:TYR:HB2	2:J:836:VAL:HG21	1.42	1.01
1:A:404:ARG:NH2	1:X:320:ARG:HD2	1.76	1.01
2:I:805:ASN:HD21	2:I:872:TYR:HD1	1.01	1.01

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	82/457 (18%)	76 (93%)	6 (7%)	0	100	100
1	B	83/457 (18%)	72 (87%)	11 (13%)	0	100	100
1	E	82/457 (18%)	76 (93%)	6 (7%)	0	100	100
1	F	83/457 (18%)	72 (87%)	11 (13%)	0	100	100
1	G	181/457 (40%)	166 (92%)	15 (8%)	0	100	100
1	H	177/457 (39%)	166 (94%)	11 (6%)	0	100	100
1	K	70/457 (15%)	67 (96%)	3 (4%)	0	100	100
1	L	82/457 (18%)	77 (94%)	5 (6%)	0	100	100
1	M	145/457 (32%)	139 (96%)	6 (4%)	0	100	100
1	N	154/457 (34%)	151 (98%)	3 (2%)	0	100	100
1	Q	181/457 (40%)	166 (92%)	15 (8%)	0	100	100
1	R	177/457 (39%)	166 (94%)	11 (6%)	0	100	100
1	U	70/457 (15%)	67 (96%)	3 (4%)	0	100	100
1	V	82/457 (18%)	77 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	W	145/457 (32%)	139 (96%)	6 (4%)	0	100	100
1	X	154/457 (34%)	151 (98%)	3 (2%)	0	100	100
2	C	86/907 (10%)	70 (81%)	16 (19%)	0	100	100
2	D	108/907 (12%)	88 (82%)	20 (18%)	0	100	100
2	I	108/907 (12%)	81 (75%)	27 (25%)	0	100	100
2	J	107/907 (12%)	80 (75%)	27 (25%)	0	100	100
2	O	86/907 (10%)	70 (81%)	16 (19%)	0	100	100
2	P	108/907 (12%)	88 (82%)	20 (18%)	0	100	100
2	S	108/907 (12%)	81 (75%)	27 (25%)	0	100	100
2	T	107/907 (12%)	80 (75%)	27 (25%)	0	100	100
All	All	2766/14568 (19%)	2466 (89%)	300 (11%)	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	62/345 (18%)	62 (100%)	0	100	100
1	B	63/345 (18%)	63 (100%)	0	100	100
1	E	62/345 (18%)	62 (100%)	0	100	100
1	F	63/345 (18%)	63 (100%)	0	100	100
1	G	140/345 (41%)	140 (100%)	0	100	100
1	H	137/345 (40%)	137 (100%)	0	100	100
1	K	55/345 (16%)	55 (100%)	0	100	100
1	L	63/345 (18%)	63 (100%)	0	100	100
1	M	110/345 (32%)	110 (100%)	0	100	100
1	N	116/345 (34%)	116 (100%)	0	100	100
1	Q	140/345 (41%)	140 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	R	137/345 (40%)	137 (100%)	0	100	100
1	U	55/345 (16%)	55 (100%)	0	100	100
1	V	63/345 (18%)	63 (100%)	0	100	100
1	W	110/345 (32%)	110 (100%)	0	100	100
1	X	116/345 (34%)	116 (100%)	0	100	100
2	C	78/749 (10%)	77 (99%)	1 (1%)	61	73
2	D	94/749 (13%)	94 (100%)	0	100	100
2	I	94/749 (13%)	94 (100%)	0	100	100
2	J	93/749 (12%)	93 (100%)	0	100	100
2	O	78/749 (10%)	77 (99%)	1 (1%)	61	73
2	P	94/749 (13%)	94 (100%)	0	100	100
2	S	94/749 (13%)	94 (100%)	0	100	100
2	T	93/749 (12%)	93 (100%)	0	100	100
All	All	2210/11512 (19%)	2208 (100%)	2 (0%)	87	89

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

Mol	Chain	Res	Type
2	C	808	ARG
2	O	808	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	W	387	GLN
1	X	301	ASN
2	O	3	GLN
1	N	387	GLN
1	N	315	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.

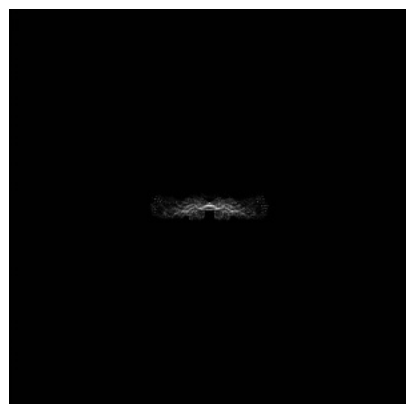
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15473. These allow visual inspection of the internal detail of the map and identification of artifacts.

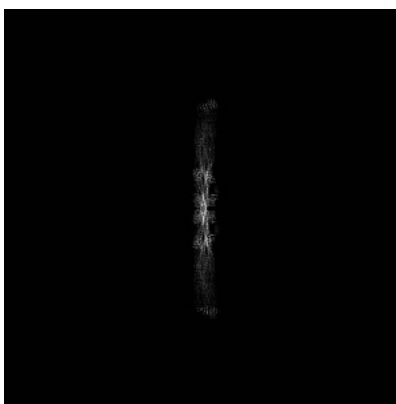
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

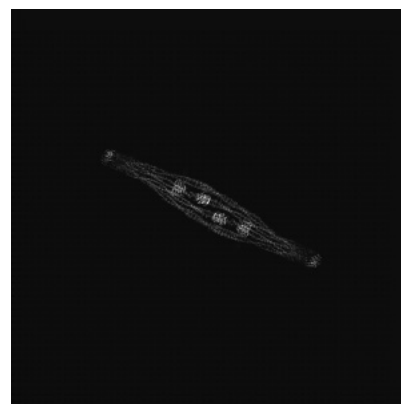
6.1.1 Primary map



X

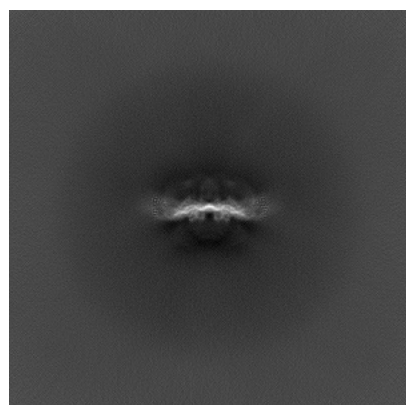


Y

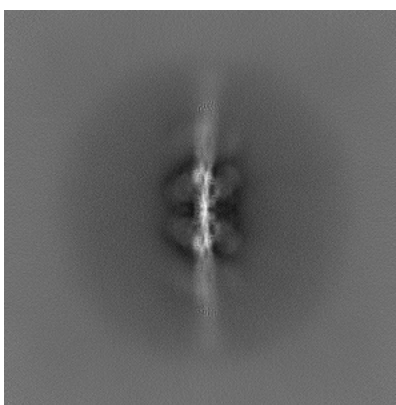


Z

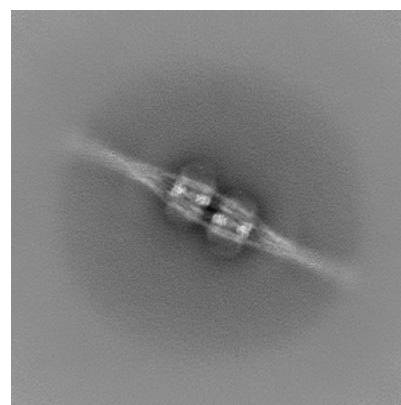
6.1.2 Raw map



X



Y

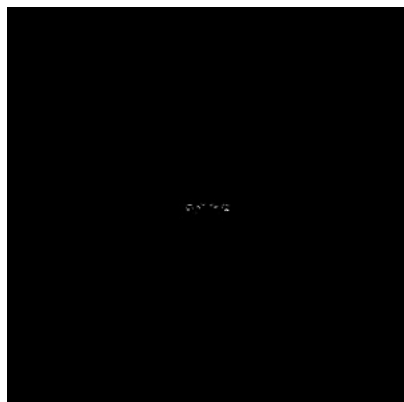


Z

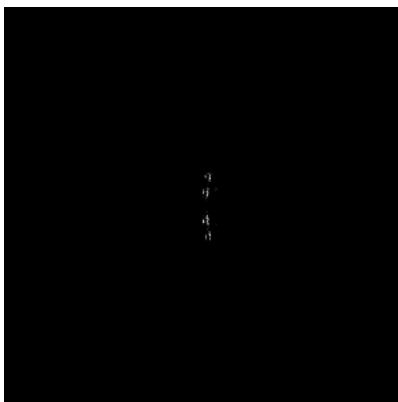
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 250

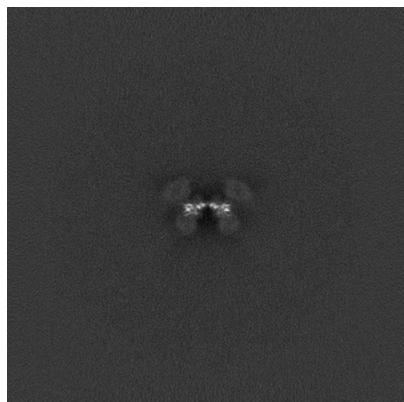


Y Index: 250

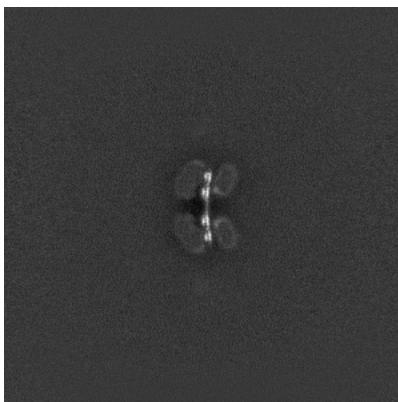


Z Index: 250

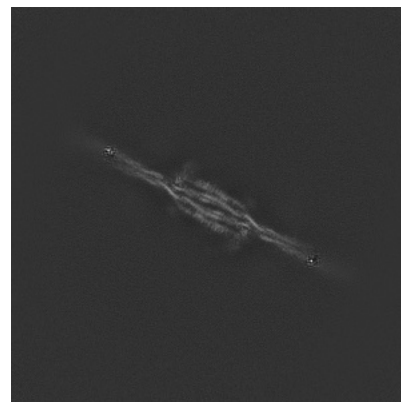
6.2.2 Raw map



X Index: 250



Y Index: 250

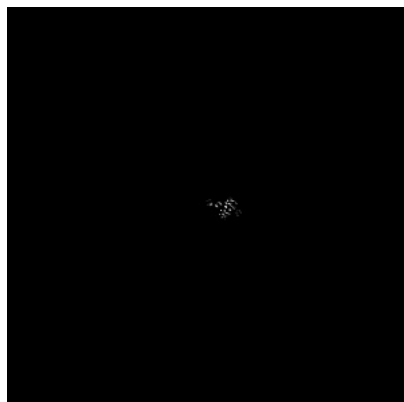


Z Index: 250

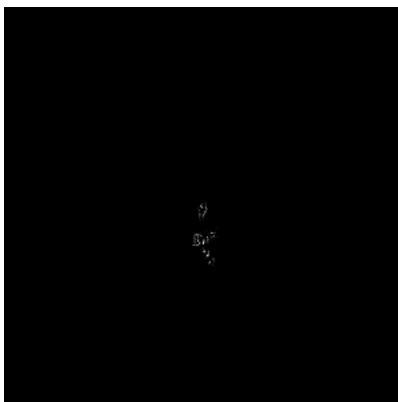
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 208

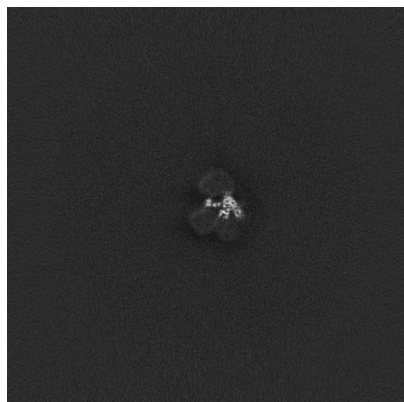


Y Index: 274

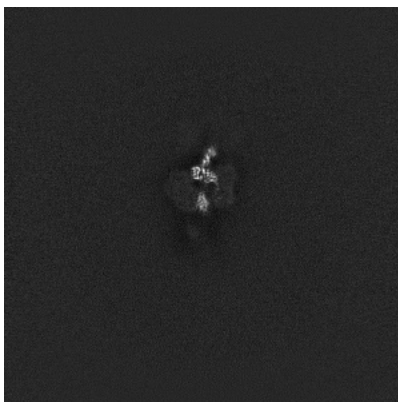


Z Index: 254

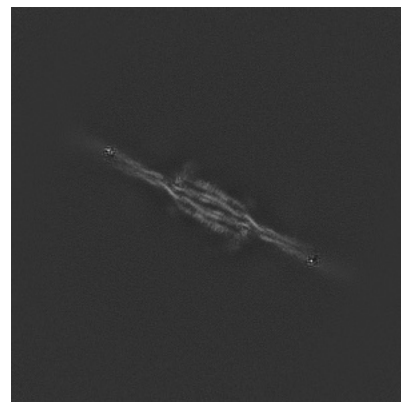
6.3.2 Raw map



X Index: 211



Y Index: 226



Z Index: 250

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

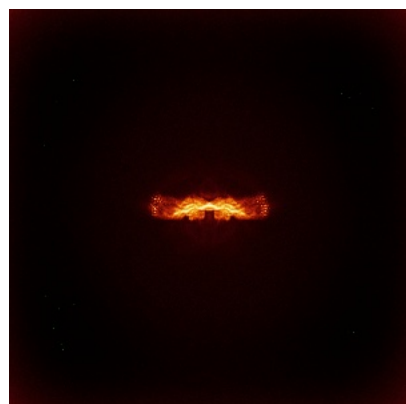


Y

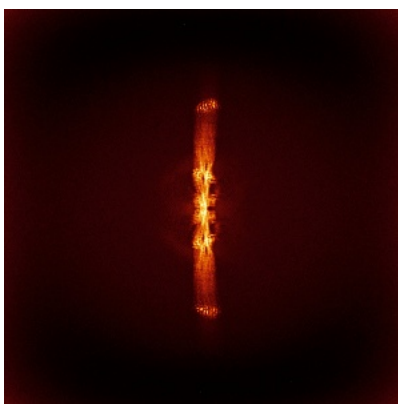


Z

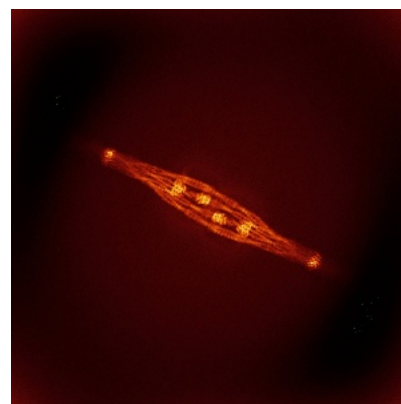
6.4.2 Raw map



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 0.017. 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.

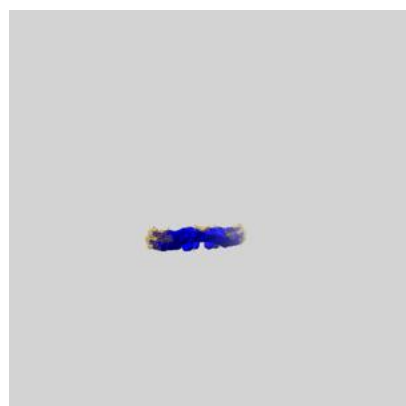
6.6 Mask visualisation [i](#)

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

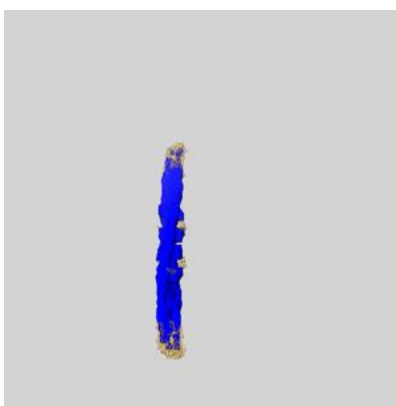
A mask typically either:

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

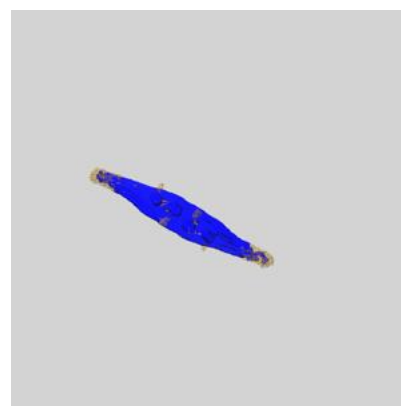
6.6.1 emd_15473_msk_1.map [i](#)



X



Y

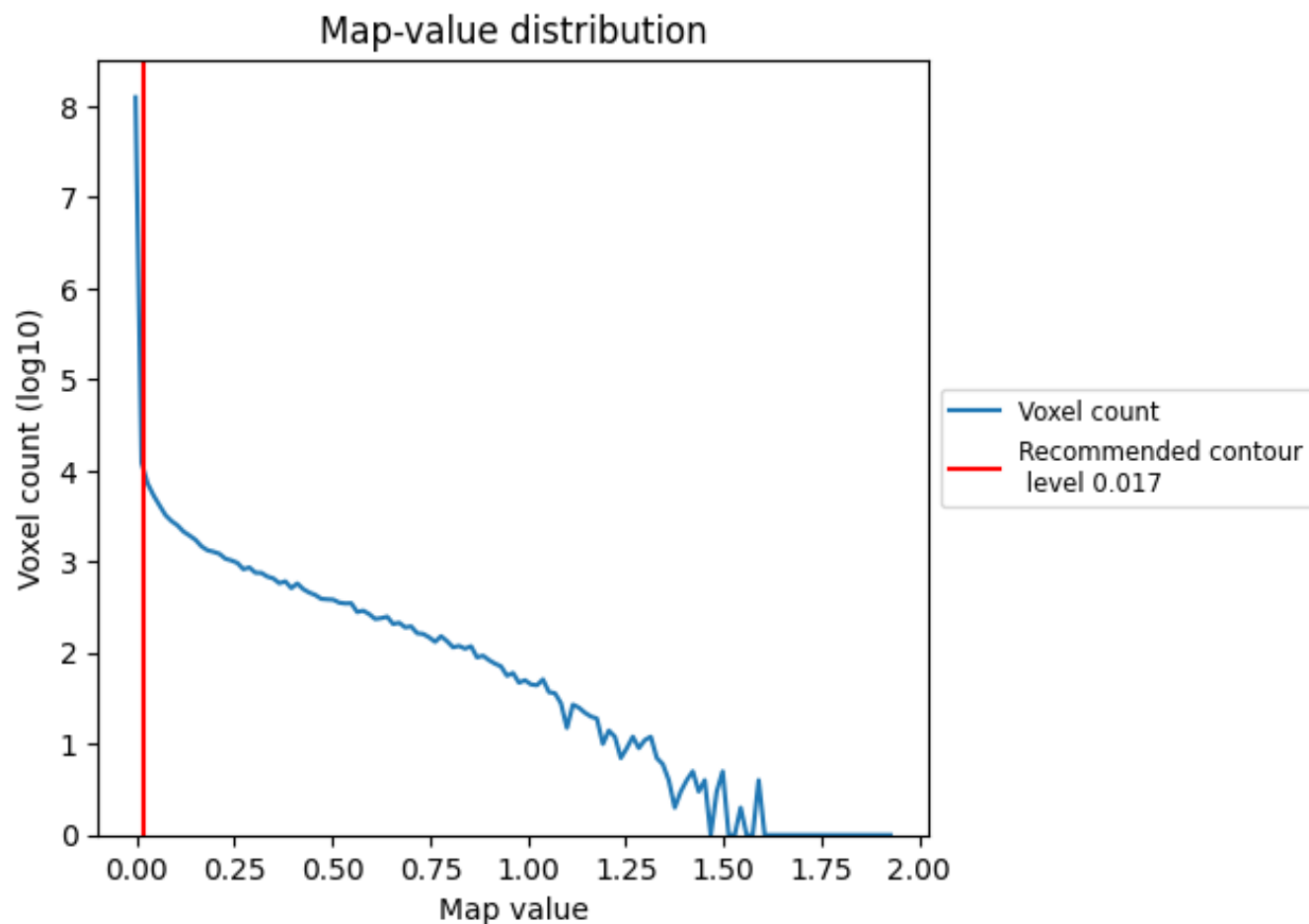


Z

7 Map analysis [i](#)

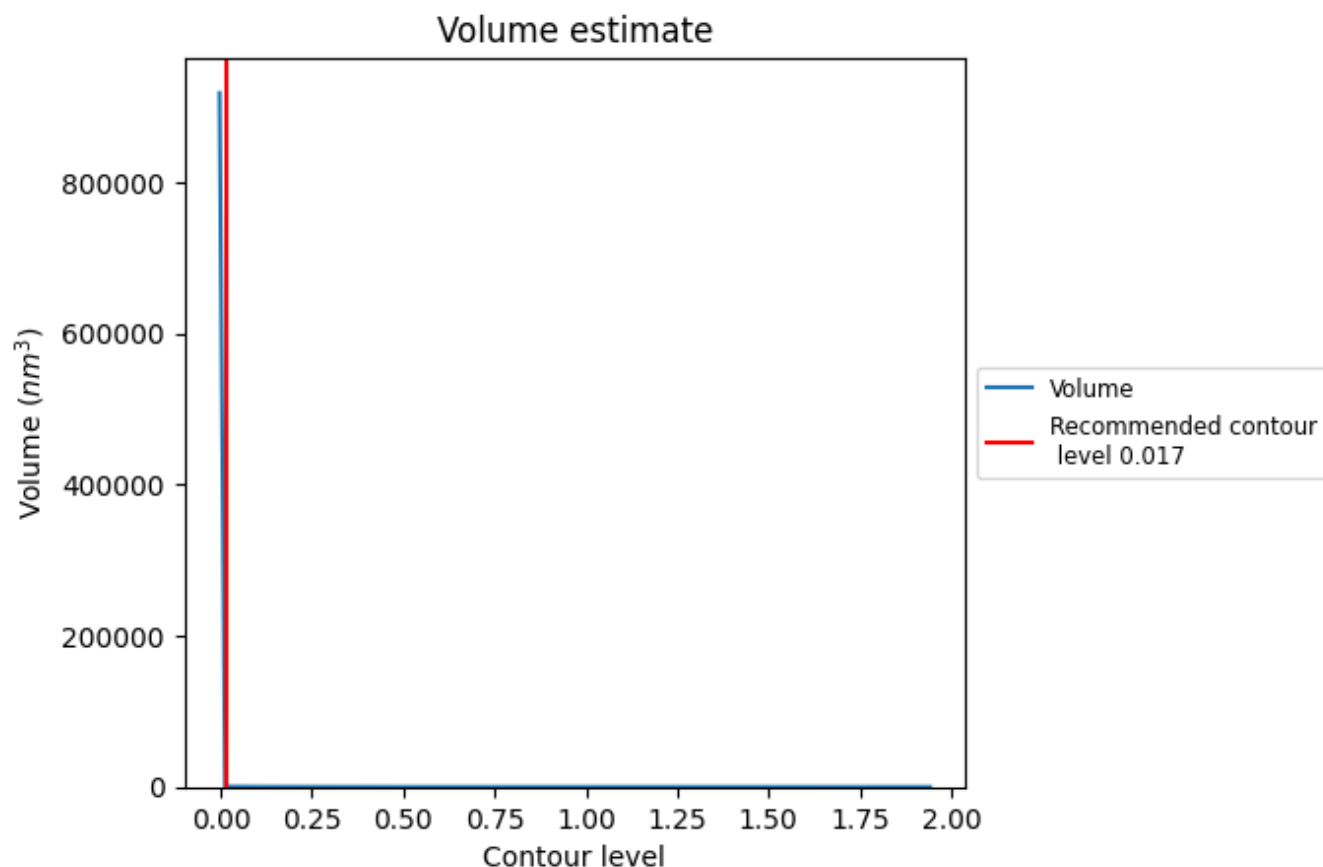
This section contains the results of statistical analysis of the map.

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.

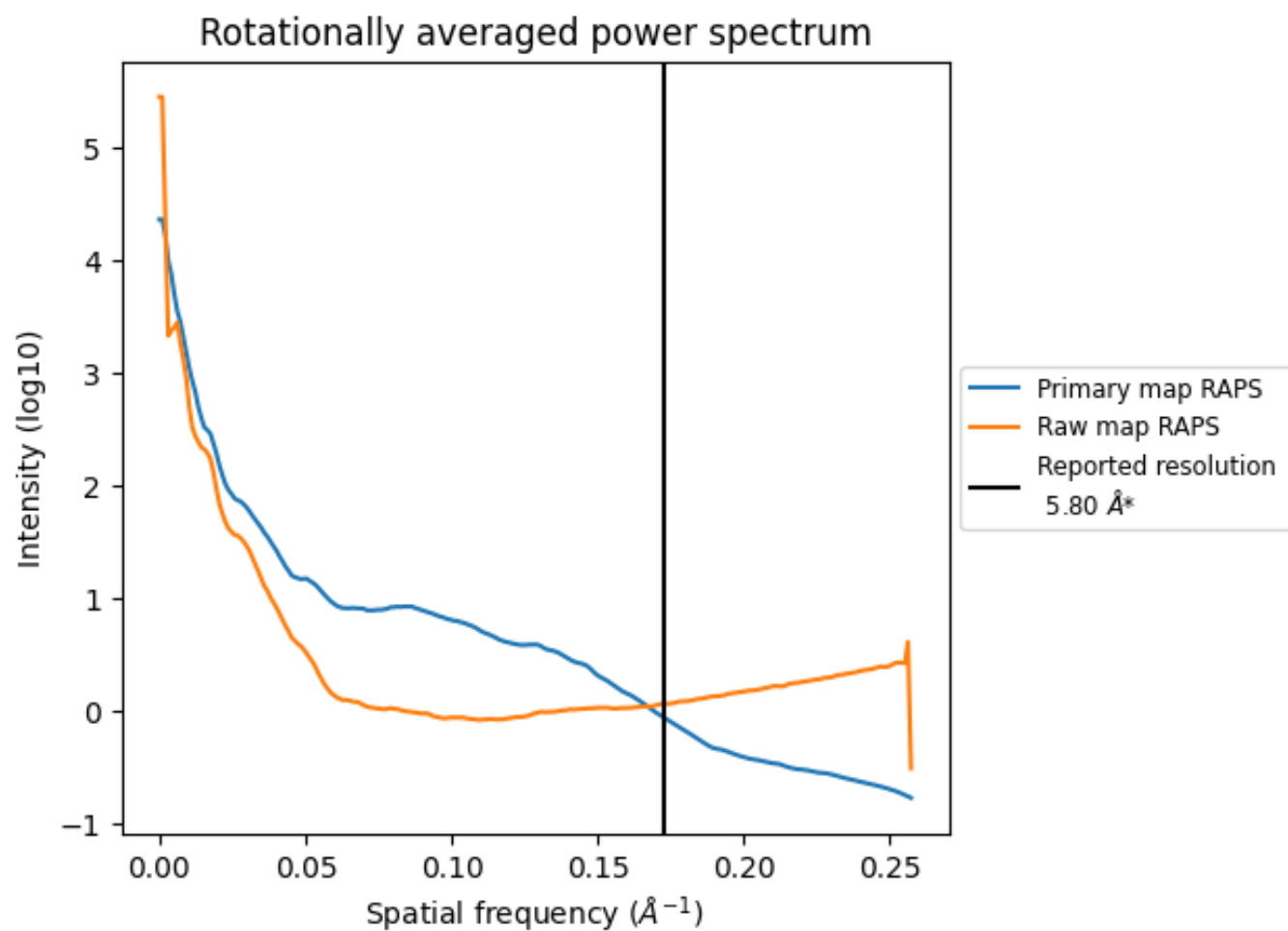
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 465 nm³; this corresponds to an approximate mass of 420 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 ⓘ

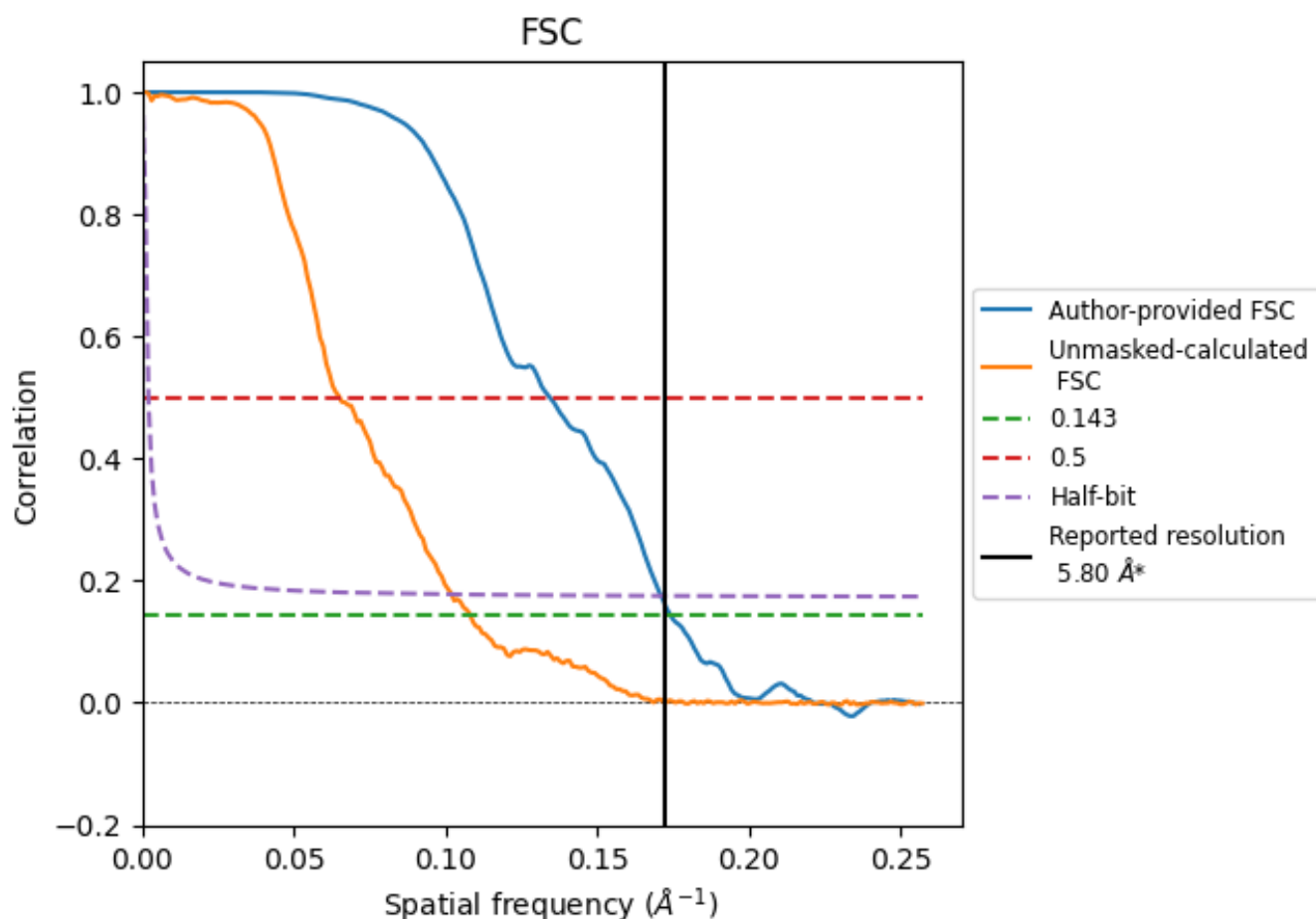


*Reported resolution corresponds to spatial frequency of 0.172 $\text{\AA}^{-1}$

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 0.172 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.80	-	-
Author-provided FSC curve	5.74	7.44	5.84
Unmasked-calculated*	9.24	15.36	9.80

*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 9.24 differs from the reported value 5.8 by more than 10 %

9 Map-model fit [i](#)

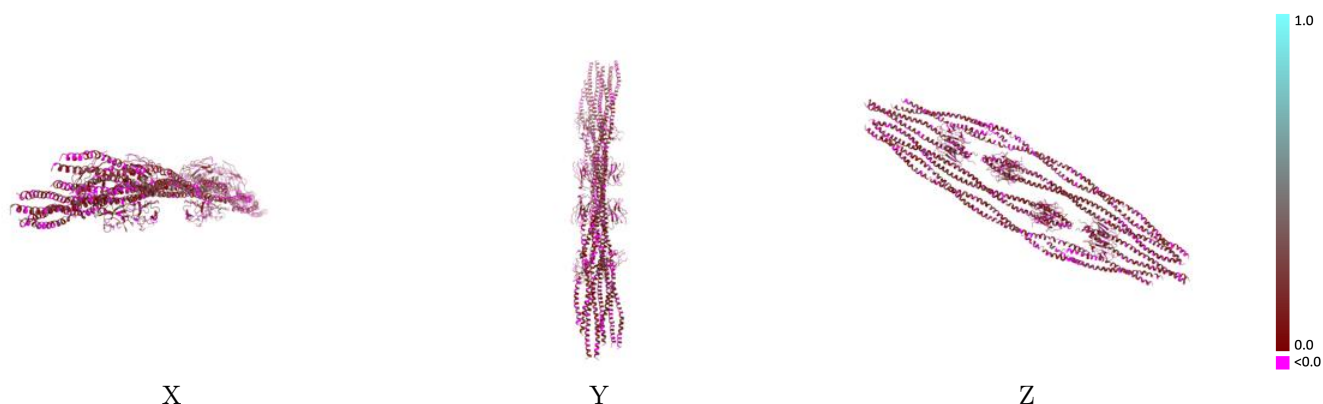
This section contains information regarding the fit between EMDB map EMD-15473 and PDB model 8AIX. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



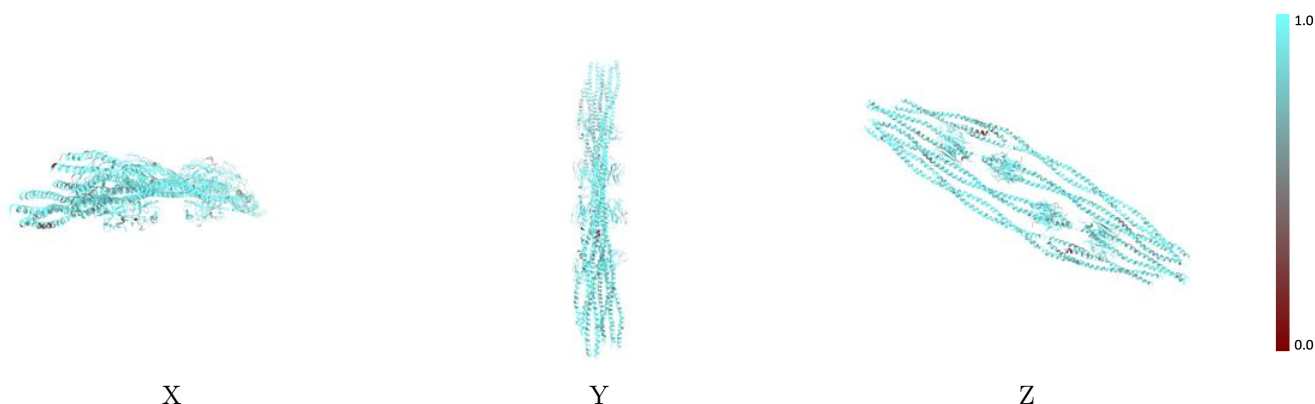
The images above show the 3D surface view of the map at the recommended contour level 0.017 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



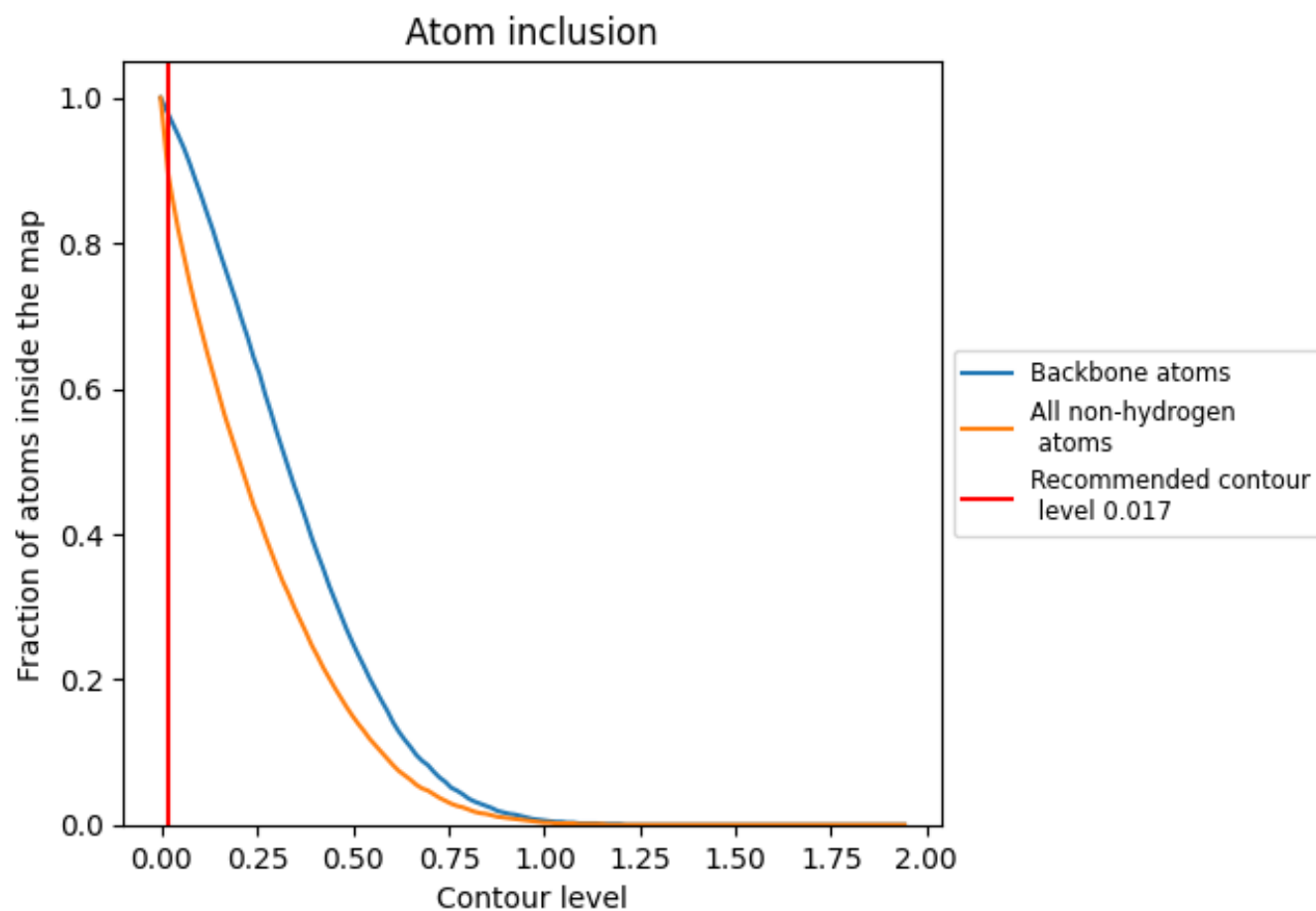
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.017).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 90% 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 (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8950	 0.1390
A	 0.8860	 0.1330
B	 0.9190	 0.1380
C	 0.8810	 0.1620
D	 0.8810	 0.1690
E	 0.8730	 0.1210
F	 0.9280	 0.1550
G	 0.9100	 0.1400
H	 0.9140	 0.1320
I	 0.8840	 0.1320
J	 0.8960	 0.1600
K	 0.7510	 0.0560
L	 0.8670	 0.1160
M	 0.9340	 0.1560
N	 0.9200	 0.1390
O	 0.8620	 0.1580
P	 0.9060	 0.1630
Q	 0.9050	 0.1390
R	 0.9170	 0.1240
S	 0.9090	 0.1630
T	 0.8670	 0.1560
U	 0.7730	 0.0570
V	 0.8930	 0.1130
W	 0.9200	 0.1670
X	 0.9070	 0.1250

