W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

wwPDB EM Validation Summary Report (i)

Nov 20, 2022 – 03:29 PM JST

PDB ID	:	7BZW
EMDB ID	:	EMD-30261
Title	:	Structure of Hsp21
Authors	:	Lau, W.C.Y.
Deposited on	:	2020-04-28
Resolution	:	4.60 Å(reported)

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 4.60 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	Percentile Ranks	Value
Clashscore		28
Ramachandran outliers		0
Sidechain outliers		0

Worse　　　　　　　　　　　　　　　　　　*Better*

▮ Percentile relative to all structures
▯ Percentile relative to all EM structures
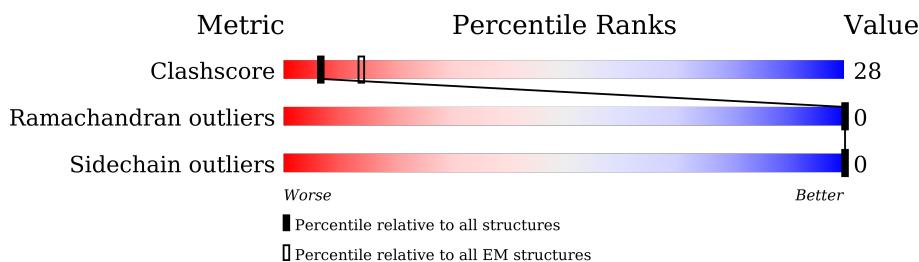
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	1	207	19% 29% 51%
1	10	207	25% 24% 51%
1	11	207	23% 26% 51%
1	12	207	23% 26% 51%
1	2	207	25% 24% 51%
1	3	207	23% 26% 51%
1	4	207	25% 24% 51%
1	5	207	24% 25% 51%

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Mol	Chain	Length	Quality of chain
1	6	207	24% 25% 51%
1	7	207	24% 25% 51%
1	8	207	22% 27% 51%
1	9	207	21% 28% 51%
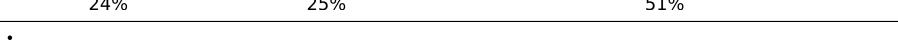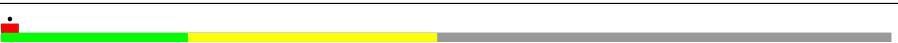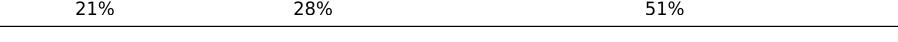
2 Entry composition ⓘ

There is only 1 type of molecule in this entry. The entry contains 9756 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 Heat shock protein 21, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	101	Total	C	N	O	S	0	0
			813	510	138	162	3		
1	2	101	Total	C	N	O	S	0	0
			813	510	138	162	3		
1	3	101	Total	C	N	O	S	0	0
			813	510	138	162	3		
1	4	101	Total	C	N	O	S	0	0
			813	510	138	162	3		
1	5	101	Total	C	N	O	S	0	0
			813	510	138	162	3		
1	6	101	Total	C	N	O	S	0	0
			813	510	138	162	3		
1	7	101	Total	C	N	O	S	0	0
			813	510	138	162	3		
1	8	101	Total	C	N	O	S	0	0
			813	510	138	162	3		
1	9	101	Total	C	N	O	S	0	0
			813	510	138	162	3		
1	10	101	Total	C	N	O	S	0	0
			813	510	138	162	3		
1	11	101	Total	C	N	O	S	0	0
			813	510	138	162	3		
1	12	101	Total	C	N	O	S	0	0
			813	510	138	162	3		

There are 276 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	21	MET	-	expression tag	UNP P31170
1	22	GLY	-	expression tag	UNP P31170
1	23	SER	-	expression tag	UNP P31170
1	24	SER	-	expression tag	UNP P31170
1	25	HIS	-	expression tag	UNP P31170
1	26	HIS	-	expression tag	UNP P31170

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Chain	Residue	Modelled	Actual	Comment	Reference
1	27	HIS	-	expression tag	UNP P31170
1	28	HIS	-	expression tag	UNP P31170
1	29	HIS	-	expression tag	UNP P31170
1	30	HIS	-	expression tag	UNP P31170
1	31	SER	-	expression tag	UNP P31170
1	32	GLN	-	expression tag	UNP P31170
1	33	ASP	-	expression tag	UNP P31170
1	34	PRO	-	expression tag	UNP P31170
1	35	ASN	-	expression tag	UNP P31170
1	36	SER	-	expression tag	UNP P31170
1	37	GLU	-	expression tag	UNP P31170
1	38	ASN	-	expression tag	UNP P31170
1	39	LEU	-	expression tag	UNP P31170
1	40	TYR	-	expression tag	UNP P31170
1	41	PHE	-	expression tag	UNP P31170
1	42	GLN	-	expression tag	UNP P31170
1	43	SER	-	expression tag	UNP P31170
2	21	MET	-	expression tag	UNP P31170
2	22	GLY	-	expression tag	UNP P31170
2	23	SER	-	expression tag	UNP P31170
2	24	SER	-	expression tag	UNP P31170
2	25	HIS	-	expression tag	UNP P31170
2	26	HIS	-	expression tag	UNP P31170
2	27	HIS	-	expression tag	UNP P31170
2	28	HIS	-	expression tag	UNP P31170
2	29	HIS	-	expression tag	UNP P31170
2	30	HIS	-	expression tag	UNP P31170
2	31	SER	-	expression tag	UNP P31170
2	32	GLN	-	expression tag	UNP P31170
2	33	ASP	-	expression tag	UNP P31170
2	34	PRO	-	expression tag	UNP P31170
2	35	ASN	-	expression tag	UNP P31170
2	36	SER	-	expression tag	UNP P31170
2	37	GLU	-	expression tag	UNP P31170
2	38	ASN	-	expression tag	UNP P31170
2	39	LEU	-	expression tag	UNP P31170
2	40	TYR	-	expression tag	UNP P31170
2	41	PHE	-	expression tag	UNP P31170
2	42	GLN	-	expression tag	UNP P31170
2	43	SER	-	expression tag	UNP P31170
3	21	MET	-	expression tag	UNP P31170
3	22	GLY	-	expression tag	UNP P31170

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Chain	Residue	Modelled	Actual	Comment	Reference
3	23	SER	-	expression tag	UNP P31170
3	24	SER	-	expression tag	UNP P31170
3	25	HIS	-	expression tag	UNP P31170
3	26	HIS	-	expression tag	UNP P31170
3	27	HIS	-	expression tag	UNP P31170
3	28	HIS	-	expression tag	UNP P31170
3	29	HIS	-	expression tag	UNP P31170
3	30	HIS	-	expression tag	UNP P31170
3	31	SER	-	expression tag	UNP P31170
3	32	GLN	-	expression tag	UNP P31170
3	33	ASP	-	expression tag	UNP P31170
3	34	PRO	-	expression tag	UNP P31170
3	35	ASN	-	expression tag	UNP P31170
3	36	SER	-	expression tag	UNP P31170
3	37	GLU	-	expression tag	UNP P31170
3	38	ASN	-	expression tag	UNP P31170
3	39	LEU	-	expression tag	UNP P31170
3	40	TYR	-	expression tag	UNP P31170
3	41	PHE	-	expression tag	UNP P31170
3	42	GLN	-	expression tag	UNP P31170
3	43	SER	-	expression tag	UNP P31170
4	21	MET	-	expression tag	UNP P31170
4	22	GLY	-	expression tag	UNP P31170
4	23	SER	-	expression tag	UNP P31170
4	24	SER	-	expression tag	UNP P31170
4	25	HIS	-	expression tag	UNP P31170
4	26	HIS	-	expression tag	UNP P31170
4	27	HIS	-	expression tag	UNP P31170
4	28	HIS	-	expression tag	UNP P31170
4	29	HIS	-	expression tag	UNP P31170
4	30	HIS	-	expression tag	UNP P31170
4	31	SER	-	expression tag	UNP P31170
4	32	GLN	-	expression tag	UNP P31170
4	33	ASP	-	expression tag	UNP P31170
4	34	PRO	-	expression tag	UNP P31170
4	35	ASN	-	expression tag	UNP P31170
4	36	SER	-	expression tag	UNP P31170
4	37	GLU	-	expression tag	UNP P31170
4	38	ASN	-	expression tag	UNP P31170
4	39	LEU	-	expression tag	UNP P31170
4	40	TYR	-	expression tag	UNP P31170
4	41	PHE	-	expression tag	UNP P31170

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Chain	Residue	Modelled	Actual	Comment	Reference
4	42	GLN	-	expression tag	UNP P31170
4	43	SER	-	expression tag	UNP P31170
5	21	MET	-	expression tag	UNP P31170
5	22	GLY	-	expression tag	UNP P31170
5	23	SER	-	expression tag	UNP P31170
5	24	SER	-	expression tag	UNP P31170
5	25	HIS	-	expression tag	UNP P31170
5	26	HIS	-	expression tag	UNP P31170
5	27	HIS	-	expression tag	UNP P31170
5	28	HIS	-	expression tag	UNP P31170
5	29	HIS	-	expression tag	UNP P31170
5	30	HIS	-	expression tag	UNP P31170
5	31	SER	-	expression tag	UNP P31170
5	32	GLN	-	expression tag	UNP P31170
5	33	ASP	-	expression tag	UNP P31170
5	34	PRO	-	expression tag	UNP P31170
5	35	ASN	-	expression tag	UNP P31170
5	36	SER	-	expression tag	UNP P31170
5	37	GLU	-	expression tag	UNP P31170
5	38	ASN	-	expression tag	UNP P31170
5	39	LEU	-	expression tag	UNP P31170
5	40	TYR	-	expression tag	UNP P31170
5	41	PHE	-	expression tag	UNP P31170
5	42	GLN	-	expression tag	UNP P31170
5	43	SER	-	expression tag	UNP P31170
6	21	MET	-	expression tag	UNP P31170
6	22	GLY	-	expression tag	UNP P31170
6	23	SER	-	expression tag	UNP P31170
6	24	SER	-	expression tag	UNP P31170
6	25	HIS	-	expression tag	UNP P31170
6	26	HIS	-	expression tag	UNP P31170
6	27	HIS	-	expression tag	UNP P31170
6	28	HIS	-	expression tag	UNP P31170
6	29	HIS	-	expression tag	UNP P31170
6	30	HIS	-	expression tag	UNP P31170
6	31	SER	-	expression tag	UNP P31170
6	32	GLN	-	expression tag	UNP P31170
6	33	ASP	-	expression tag	UNP P31170
6	34	PRO	-	expression tag	UNP P31170
6	35	ASN	-	expression tag	UNP P31170
6	36	SER	-	expression tag	UNP P31170
6	37	GLU	-	expression tag	UNP P31170

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Chain	Residue	Modelled	Actual	Comment	Reference
6	38	ASN	-	expression tag	UNP P31170
6	39	LEU	-	expression tag	UNP P31170
6	40	TYR	-	expression tag	UNP P31170
6	41	PHE	-	expression tag	UNP P31170
6	42	GLN	-	expression tag	UNP P31170
6	43	SER	-	expression tag	UNP P31170
7	21	MET	-	expression tag	UNP P31170
7	22	GLY	-	expression tag	UNP P31170
7	23	SER	-	expression tag	UNP P31170
7	24	SER	-	expression tag	UNP P31170
7	25	HIS	-	expression tag	UNP P31170
7	26	HIS	-	expression tag	UNP P31170
7	27	HIS	-	expression tag	UNP P31170
7	28	HIS	-	expression tag	UNP P31170
7	29	HIS	-	expression tag	UNP P31170
7	30	HIS	-	expression tag	UNP P31170
7	31	SER	-	expression tag	UNP P31170
7	32	GLN	-	expression tag	UNP P31170
7	33	ASP	-	expression tag	UNP P31170
7	34	PRO	-	expression tag	UNP P31170
7	35	ASN	-	expression tag	UNP P31170
7	36	SER	-	expression tag	UNP P31170
7	37	GLU	-	expression tag	UNP P31170
7	38	ASN	-	expression tag	UNP P31170
7	39	LEU	-	expression tag	UNP P31170
7	40	TYR	-	expression tag	UNP P31170
7	41	PHE	-	expression tag	UNP P31170
7	42	GLN	-	expression tag	UNP P31170
7	43	SER	-	expression tag	UNP P31170
8	21	MET	-	expression tag	UNP P31170
8	22	GLY	-	expression tag	UNP P31170
8	23	SER	-	expression tag	UNP P31170
8	24	SER	-	expression tag	UNP P31170
8	25	HIS	-	expression tag	UNP P31170
8	26	HIS	-	expression tag	UNP P31170
8	27	HIS	-	expression tag	UNP P31170
8	28	HIS	-	expression tag	UNP P31170
8	29	HIS	-	expression tag	UNP P31170
8	30	HIS	-	expression tag	UNP P31170
8	31	SER	-	expression tag	UNP P31170
8	32	GLN	-	expression tag	UNP P31170
8	33	ASP	-	expression tag	UNP P31170

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Chain	Residue	Modelled	Actual	Comment	Reference
8	34	PRO	-	expression tag	UNP P31170
8	35	ASN	-	expression tag	UNP P31170
8	36	SER	-	expression tag	UNP P31170
8	37	GLU	-	expression tag	UNP P31170
8	38	ASN	-	expression tag	UNP P31170
8	39	LEU	-	expression tag	UNP P31170
8	40	TYR	-	expression tag	UNP P31170
8	41	PHE	-	expression tag	UNP P31170
8	42	GLN	-	expression tag	UNP P31170
8	43	SER	-	expression tag	UNP P31170
9	21	MET	-	expression tag	UNP P31170
9	22	GLY	-	expression tag	UNP P31170
9	23	SER	-	expression tag	UNP P31170
9	24	SER	-	expression tag	UNP P31170
9	25	HIS	-	expression tag	UNP P31170
9	26	HIS	-	expression tag	UNP P31170
9	27	HIS	-	expression tag	UNP P31170
9	28	HIS	-	expression tag	UNP P31170
9	29	HIS	-	expression tag	UNP P31170
9	30	HIS	-	expression tag	UNP P31170
9	31	SER	-	expression tag	UNP P31170
9	32	GLN	-	expression tag	UNP P31170
9	33	ASP	-	expression tag	UNP P31170
9	34	PRO	-	expression tag	UNP P31170
9	35	ASN	-	expression tag	UNP P31170
9	36	SER	-	expression tag	UNP P31170
9	37	GLU	-	expression tag	UNP P31170
9	38	ASN	-	expression tag	UNP P31170
9	39	LEU	-	expression tag	UNP P31170
9	40	TYR	-	expression tag	UNP P31170
9	41	PHE	-	expression tag	UNP P31170
9	42	GLN	-	expression tag	UNP P31170
9	43	SER	-	expression tag	UNP P31170
10	21	MET	-	expression tag	UNP P31170
10	22	GLY	-	expression tag	UNP P31170
10	23	SER	-	expression tag	UNP P31170
10	24	SER	-	expression tag	UNP P31170
10	25	HIS	-	expression tag	UNP P31170
10	26	HIS	-	expression tag	UNP P31170
10	27	HIS	-	expression tag	UNP P31170
10	28	HIS	-	expression tag	UNP P31170
10	29	HIS	-	expression tag	UNP P31170

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Chain	Residue	Modelled	Actual	Comment	Reference
10	30	HIS	-	expression tag	UNP P31170
10	31	SER	-	expression tag	UNP P31170
10	32	GLN	-	expression tag	UNP P31170
10	33	ASP	-	expression tag	UNP P31170
10	34	PRO	-	expression tag	UNP P31170
10	35	ASN	-	expression tag	UNP P31170
10	36	SER	-	expression tag	UNP P31170
10	37	GLU	-	expression tag	UNP P31170
10	38	ASN	-	expression tag	UNP P31170
10	39	LEU	-	expression tag	UNP P31170
10	40	TYR	-	expression tag	UNP P31170
10	41	PHE	-	expression tag	UNP P31170
10	42	GLN	-	expression tag	UNP P31170
10	43	SER	-	expression tag	UNP P31170
11	21	MET	-	expression tag	UNP P31170
11	22	GLY	-	expression tag	UNP P31170
11	23	SER	-	expression tag	UNP P31170
11	24	SER	-	expression tag	UNP P31170
11	25	HIS	-	expression tag	UNP P31170
11	26	HIS	-	expression tag	UNP P31170
11	27	HIS	-	expression tag	UNP P31170
11	28	HIS	-	expression tag	UNP P31170
11	29	HIS	-	expression tag	UNP P31170
11	30	HIS	-	expression tag	UNP P31170
11	31	SER	-	expression tag	UNP P31170
11	32	GLN	-	expression tag	UNP P31170
11	33	ASP	-	expression tag	UNP P31170
11	34	PRO	-	expression tag	UNP P31170
11	35	ASN	-	expression tag	UNP P31170
11	36	SER	-	expression tag	UNP P31170
11	37	GLU	-	expression tag	UNP P31170
11	38	ASN	-	expression tag	UNP P31170
11	39	LEU	-	expression tag	UNP P31170
11	40	TYR	-	expression tag	UNP P31170
11	41	PHE	-	expression tag	UNP P31170
11	42	GLN	-	expression tag	UNP P31170
11	43	SER	-	expression tag	UNP P31170
12	21	MET	-	expression tag	UNP P31170
12	22	GLY	-	expression tag	UNP P31170
12	23	SER	-	expression tag	UNP P31170
12	24	SER	-	expression tag	UNP P31170
12	25	HIS	-	expression tag	UNP P31170

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Chain	Residue	Modelled	Actual	Comment	Reference
12	26	HIS	-	expression tag	UNP P31170
12	27	HIS	-	expression tag	UNP P31170
12	28	HIS	-	expression tag	UNP P31170
12	29	HIS	-	expression tag	UNP P31170
12	30	HIS	-	expression tag	UNP P31170
12	31	SER	-	expression tag	UNP P31170
12	32	GLN	-	expression tag	UNP P31170
12	33	ASP	-	expression tag	UNP P31170
12	34	PRO	-	expression tag	UNP P31170
12	35	ASN	-	expression tag	UNP P31170
12	36	SER	-	expression tag	UNP P31170
12	37	GLU	-	expression tag	UNP P31170
12	38	ASN	-	expression tag	UNP P31170
12	39	LEU	-	expression tag	UNP P31170
12	40	TYR	-	expression tag	UNP P31170
12	41	PHE	-	expression tag	UNP P31170
12	42	GLN	-	expression tag	UNP P31170
12	43	SER	-	expression tag	UNP P31170

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: Heat shock protein 21, chloroplastic

Chain 1:

- Molecule 1: Heat shock protein 21, chloroplastic

Chain 2:

- Molecule 1: Heat shock protein 21, chloroplastic

Chain 3:

• Molecule 1: Heat shock protein 21, chloroplastic

Chain 4:

• Molecule 1: Heat shock protein 21, chloroplastic

Chain 5:

• Molecule 1: Heat shock protein 21, chloroplastic

Chain 6:

• Molecule 1: Heat shock protein 21, chloroplastic

Chain 7:   24%   25%   51%

• Molecule 1: Heat shock protein 21, chloroplastic

Chain 8:   22%   27%   51%

• Molecule 1: Heat shock protein 21, chloroplastic

Chain 9:   21%   28%   51%

• Molecule 1: Heat shock protein 21, chloroplastic

Chain 10:   25%   24%   51%

• Molecule 1: Heat shock protein 21, chloroplastic

Chain 11:   23%   26%   51%

• Molecule 1: Heat shock protein 21, chloroplastic

Chain 12:   23%   26%   51%

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER GLN ASP PRO ASN SER GLU ASN LEU TYR PHE GLN SER ALA GLN ASP GLN ARG GLU ASN SER ILE ASP VAL VAL VAL GLN GLN GLY GLN GLN LYS GLY ASN GLN GLY SER SER VAL GLU LYS ARG PRO GLN GLN ARG LEU THR MET ASP VAL

SER PRO PHE GLY LEU LEU ASP PRO LEU SER PRO MET ARG THR MET ARG GLN MET LEU ASP THR MET ASP ARG MET PHE GLU ASP THR MET PRO VAL SER GLY ARG ASN ARG GLY GLY SER GLY VAL SER GLU ILE ARG **A127** **P128** **W129** **D130** **I131** **K132** **E133** **E134** **E137** **I138** **K139** **M140** **R141**

F142 **S148** **D151** **V152** **K153** **D158** **N159** **V160** **L161** **V162** **I163** **Q167** **K168** **D171** **S172** **D173** **D174** **S175** **W176** **R179** **S180** **V181** **Y184** **G185** **L188** **Q189** **L190** **P191** **D192** **D197** **K198** **I199** **E202** **L203** **K204** **N205** **L208** **F209** **I212** **P213** **K214** **T215** **K216** **V217** **E218** **R219** **K220** **V221**

I222 **D223** **V224** **Q225** **I226** **Q227**

4 Experimental information ⓘ

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, T	Depositor
Number of particles used	104126	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 $(e^-/\text{Å}^2)$	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.050	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0175	Depositor
Map size (Å)	254.4, 254.4, 254.4	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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	1	0.26	0/824	0.53	0/1105
1	10	0.25	0/824	0.54	0/1105
1	11	0.26	0/824	0.54	0/1105
1	12	0.26	0/824	0.53	0/1105
1	2	0.26	0/824	0.54	0/1105
1	3	0.26	0/824	0.53	0/1105
1	4	0.26	0/824	0.54	0/1105
1	5	0.26	0/824	0.54	0/1105
1	6	0.26	0/824	0.54	0/1105
1	7	0.26	0/824	0.54	0/1105
1	8	0.26	0/824	0.54	0/1105
1	9	0.26	0/824	0.54	0/1105
All	All	0.26	0/9888	0.54	0/13260

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 ⓘ

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	1	813	0	826	62	0
1	10	813	0	826	45	0
1	11	813	0	826	50	0
1	12	813	0	826	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	813	0	826	47	0
1	3	813	0	826	55	0
1	4	813	0	826	45	0
1	5	813	0	826	47	0
1	6	813	0	826	52	0
1	7	813	0	826	51	0
1	8	813	0	826	47	0
1	9	813	0	826	57	0
All	All	9756	0	9912	548	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 28.

The worst 5 of 548 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)
1:7:163:ILE:O	1:7:185:GLY:HA2	1.75	0.87
1:8:156:VAL:HG22	1:11:222:ILE:H	1.40	0.87
1:9:163:ILE:O	1:9:185:GLY:HA2	1.75	0.87
1:3:163:ILE:O	1:3:185:GLY:HA2	1.75	0.87
1:8:163:ILE:O	1:8:185:GLY:HA2	1.75	0.87

There are no symmetry-related clashes.

5.3　Torsion angles ⓘ

5.3.1　Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	99/207 (48%)	80 (81%)	19 (19%)	0	100	100
1	10	99/207 (48%)	80 (81%)	19 (19%)	0	100	100
1	11	99/207 (48%)	80 (81%)	19 (19%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	12	99/207 (48%)	80 (81%)	19 (19%)	0	100	100
1	2	99/207 (48%)	80 (81%)	19 (19%)	0	100	100
1	3	99/207 (48%)	80 (81%)	19 (19%)	0	100	100
1	4	99/207 (48%)	79 (80%)	20 (20%)	0	100	100
1	5	99/207 (48%)	80 (81%)	19 (19%)	0	100	100
1	6	99/207 (48%)	79 (80%)	20 (20%)	0	100	100
1	7	99/207 (48%)	80 (81%)	19 (19%)	0	100	100
1	8	99/207 (48%)	80 (81%)	19 (19%)	0	100	100
1	9	99/207 (48%)	80 (81%)	19 (19%)	0	100	100
All	All	1188/2484 (48%)	958 (81%)	230 (19%)	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	1	94/190 (50%)	94 (100%)	0	100	100
1	10	94/190 (50%)	94 (100%)	0	100	100
1	11	94/190 (50%)	94 (100%)	0	100	100
1	12	94/190 (50%)	94 (100%)	0	100	100
1	2	94/190 (50%)	94 (100%)	0	100	100
1	3	94/190 (50%)	94 (100%)	0	100	100
1	4	94/190 (50%)	94 (100%)	0	100	100
1	5	94/190 (50%)	94 (100%)	0	100	100
1	6	94/190 (50%)	94 (100%)	0	100	100
1	7	94/190 (50%)	94 (100%)	0	100	100
1	8	94/190 (50%)	94 (100%)	0	100	100
1	9	94/190 (50%)	94 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1128/2280 (50%)	1128 (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 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	7	225	GLN
1	8	225	GLN
1	12	225	GLN
1	10	225	GLN
1	11	225	GLN

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 ⓘ

There are no monosaccharides in this entry.

5.6   Ligand geometry ⓘ

There are no ligands in this entry.

5.7   Other polymers ⓘ

There are no such residues in this entry.

5.8   Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-30261. 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 ⓘ

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   ⓘ

6.2.1   Primary map
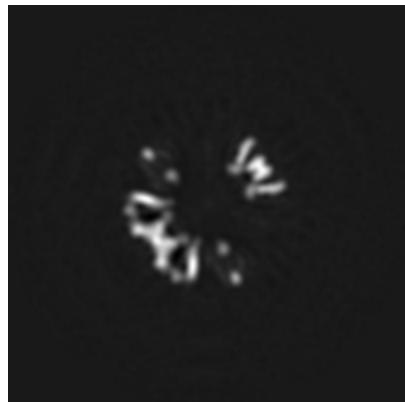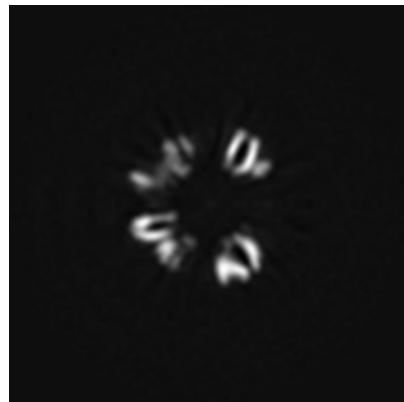
X Index: 120   Y Index: 120   Z Index: 120

6.2.2   Raw map
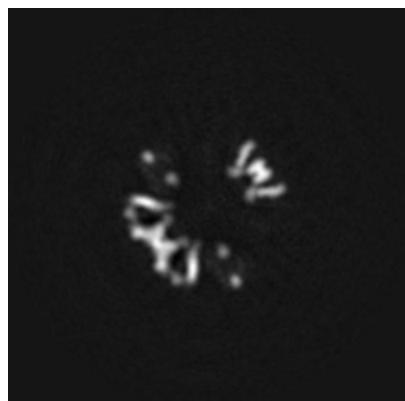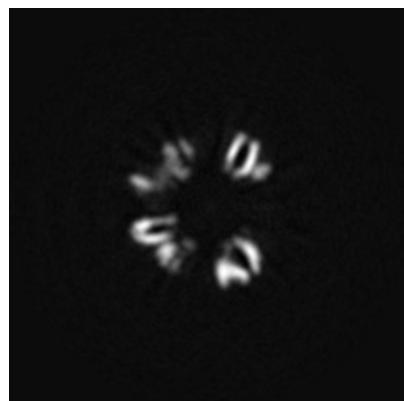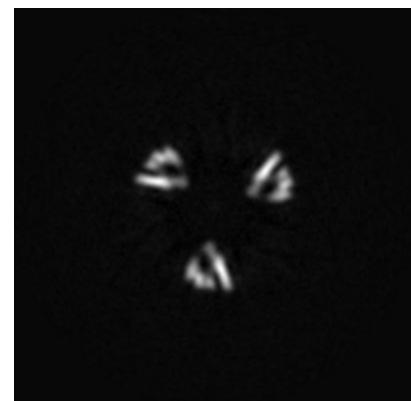
X Index: 120   Y Index: 120   Z Index: 120

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

6.3 Largest variance slices ⓘ
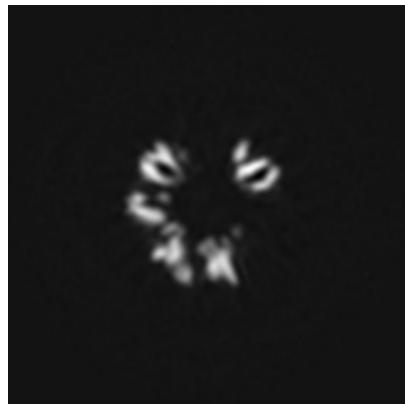
6.3.1 Primary map

X Index: 112	Y Index: 135	Z Index: 145

6.3.2 Raw map
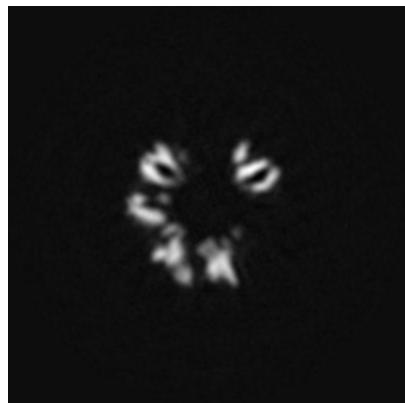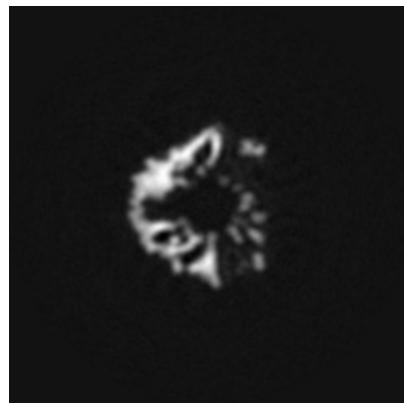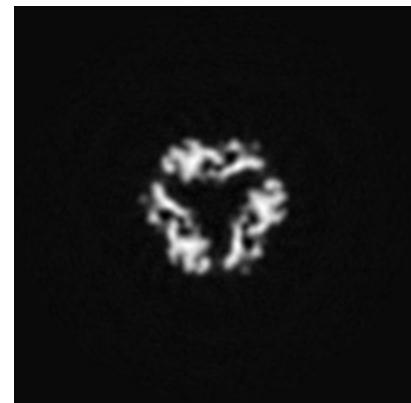
X Index: 112	Y Index: 135	Z Index: 145

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

6.4 Orthogonal surface views ⓘ
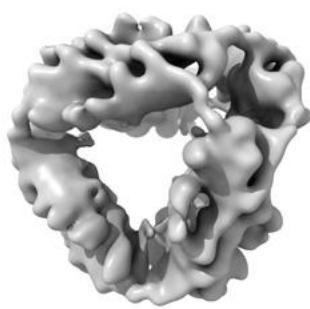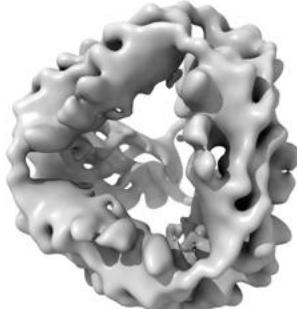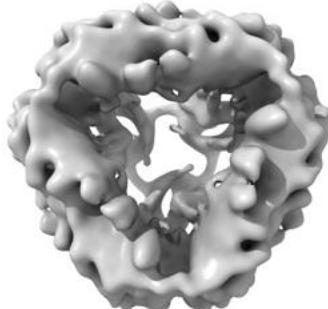
6.4.1 Primary map

| X | Y | Z |

The images above show the 3D surface view of the map at the recommended contour level 0.0175. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map
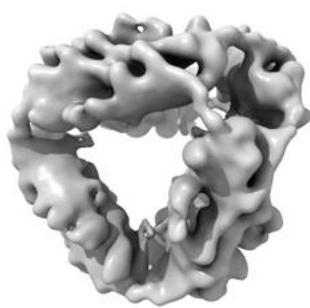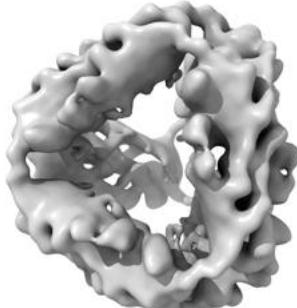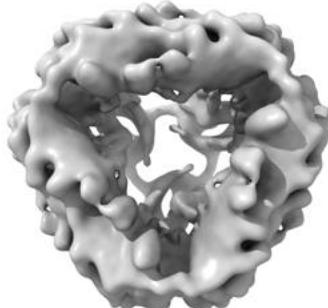
| X | Y | Z |

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.

6.5 Mask visualisation ⓘ

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

7　Map analysis ⓘ

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

7.1　Map-value distribution ⓘ
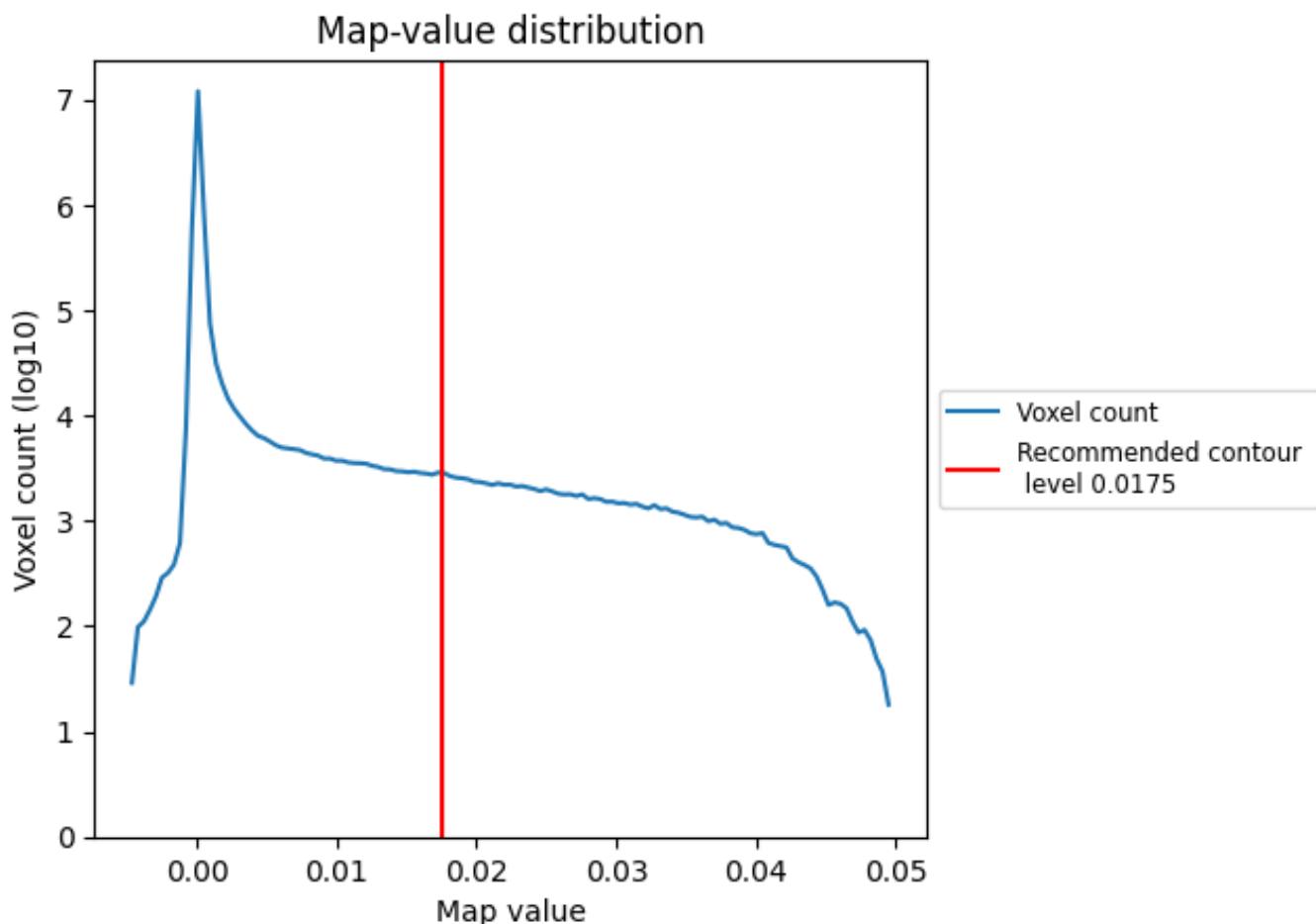
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate ⓘ
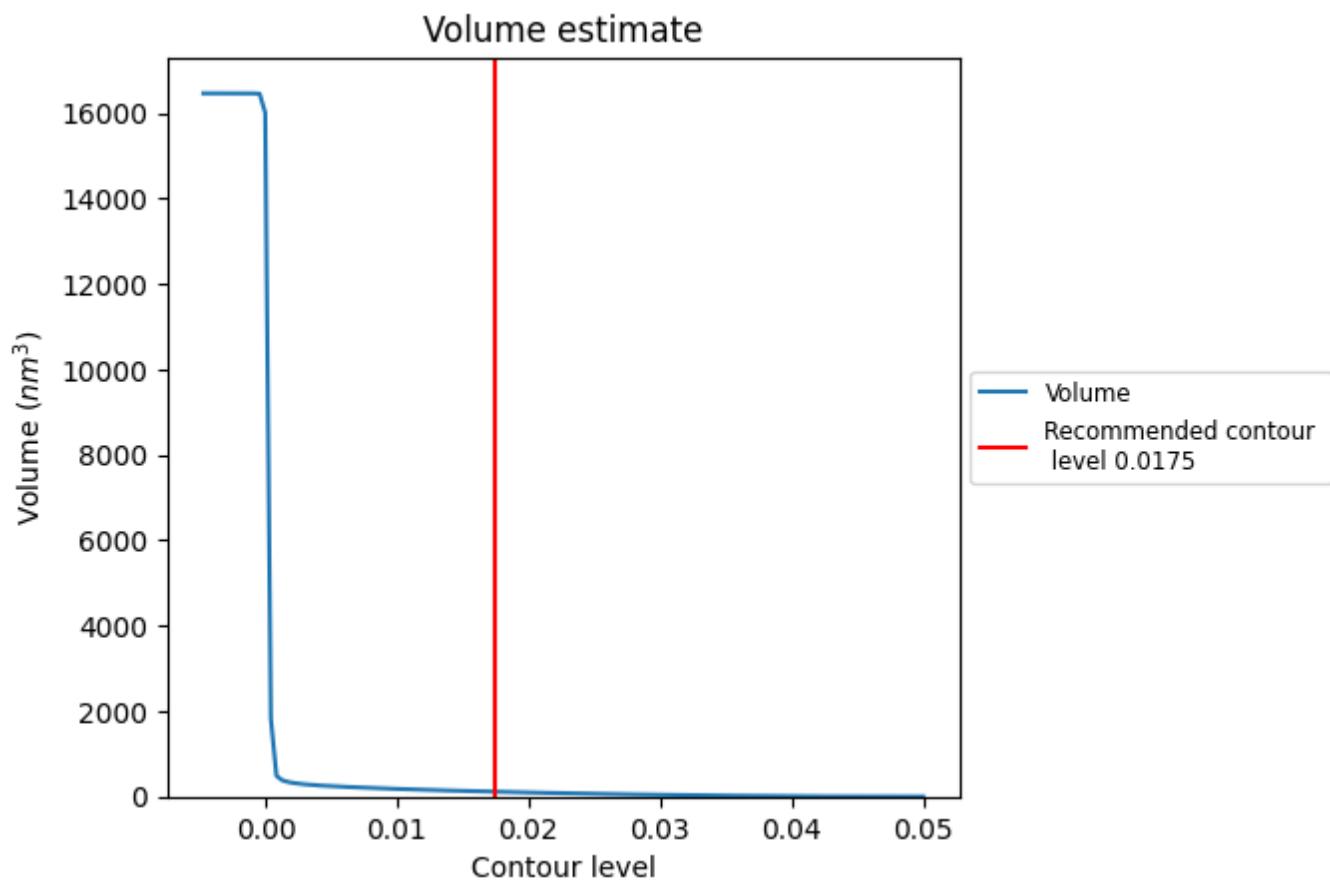
The volume at the recommended contour level is 113 nm^3; this corresponds to an approximate mass of 102 kDa.

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 ⓘ
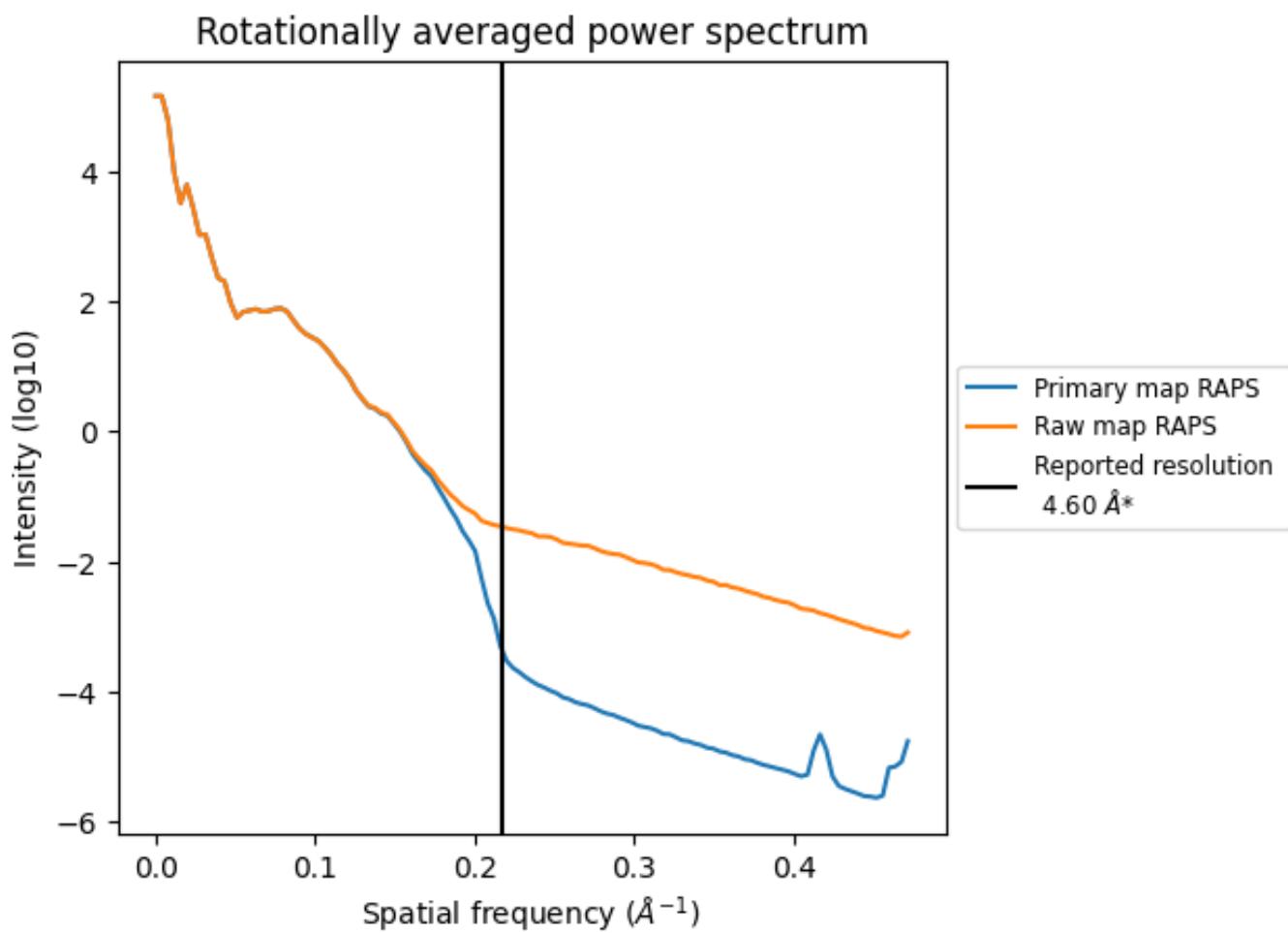
*Reported resolution corresponds to spatial frequency of 0.217 $\mathring{A}^{-1}$

8   Fourier-Shell correlation ⓘ

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 ⓘ
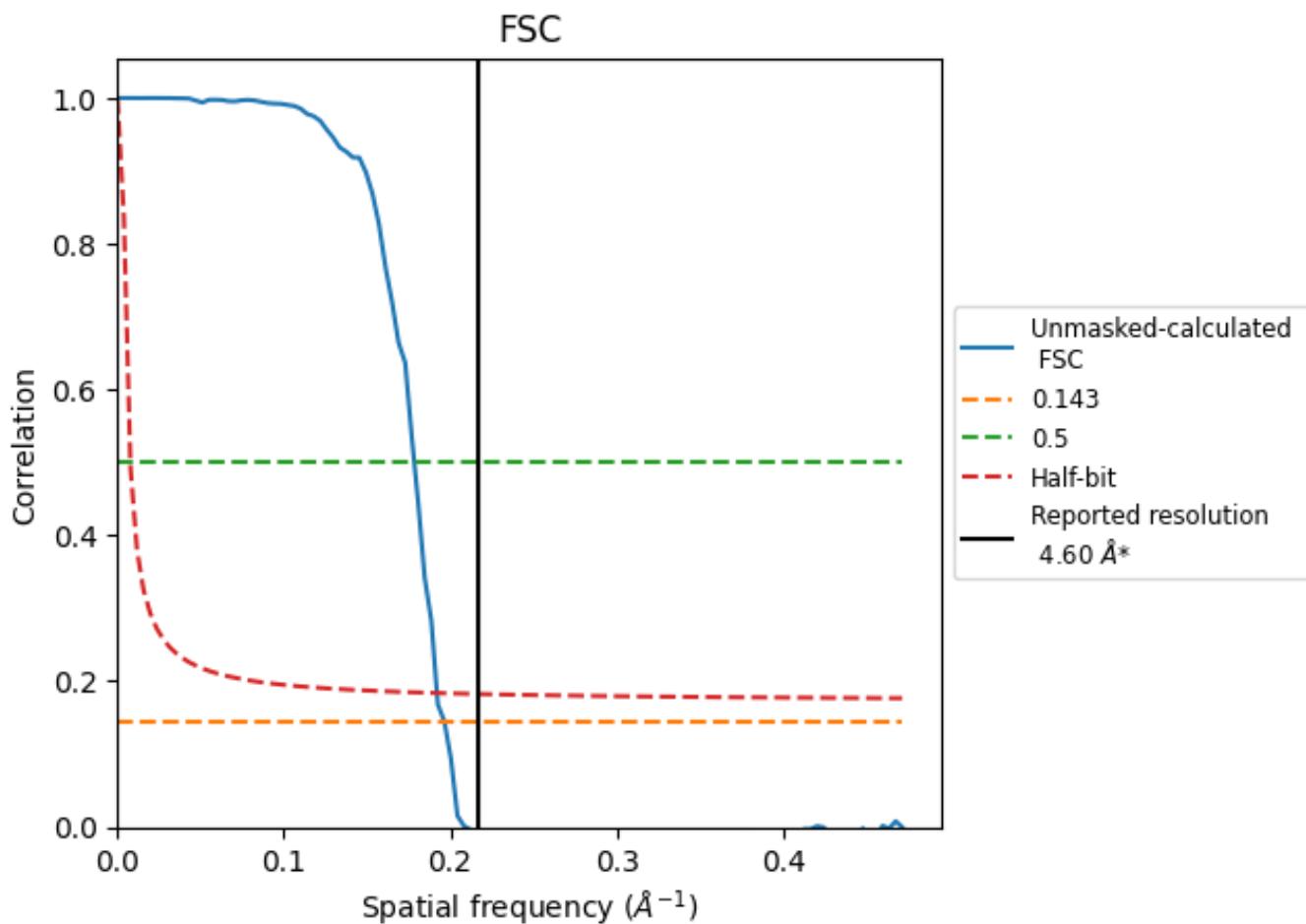
*Reported resolution corresponds to spatial frequency of 0.217 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.08	5.61	5.21

*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 5.08 differs from the reported value 4.6 by more than 10 %

9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-30261 and PDB model 7BZW. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay ⓘ
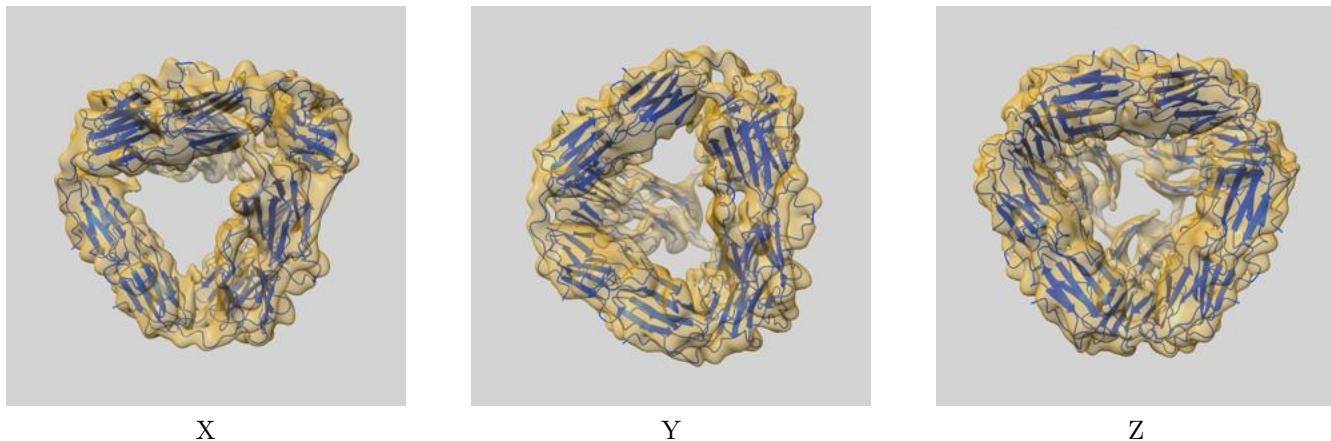
X   Y   Z

The images above show the 3D surface view of the map at the recommended contour level 0.0175 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 ⓘ

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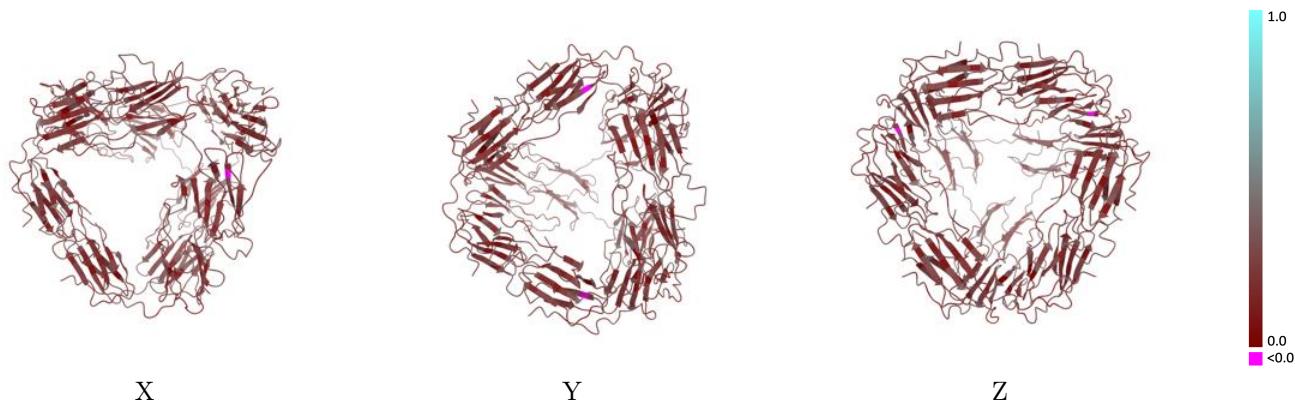
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

X   Y   Z
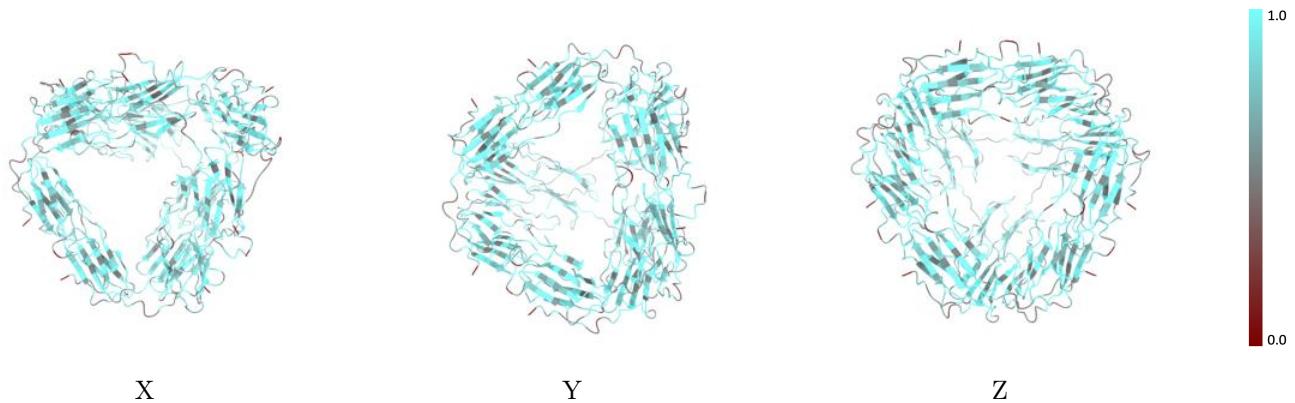
The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0175).

9.4   Atom inclusion ⓘ
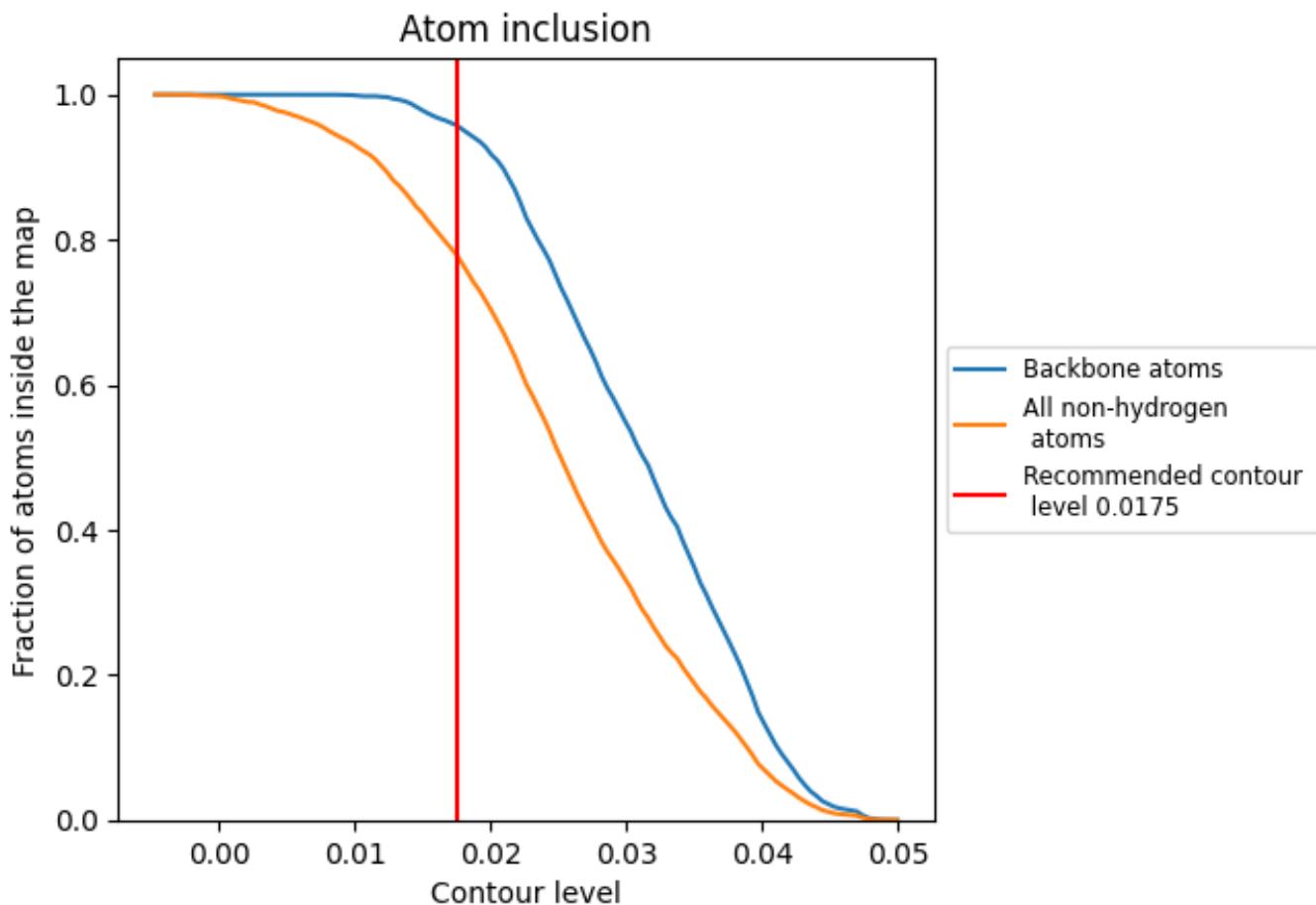
At the recommended contour level, 96% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0175) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7786	0.2420
1	0.7718	0.2370
10	0.7781	0.2380
11	0.7805	0.2490
12	0.7830	0.2470
2	0.7718	0.2370
3	0.7793	0.2410
4	0.7868	0.2420
5	0.7781	0.2450
6	0.7830	0.2420
7	0.7731	0.2400
8	0.7868	0.2440
9	0.7706	0.2380

1.0

0.0
<0.0