

wwPDB EM Validation Summary Report (i)

Oct 5, 2022 - 01:26 pm BST

PDB ID	:	7Q66
EMDB ID	:	EMD-13853
Title	:	Cryo-em structure of the Nup98 fibril polymorph 3
Authors	:	Ibanez de Opakua, A.; Geraets, J.A.; Frieg, B.; Dienemann, C.; Savastano, A.;
		Rankovic, M.; Cima-Omori, MS.; Schroeder, G.F.; Zweckstetter, M.
Deposited on		
Resolution	:	2.79 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 (i) 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 (1)) were used in the production of this report:

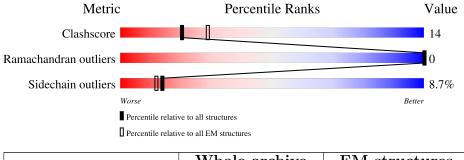
:	0.0.1. dev 43
:	4.02b-467
:	20191225.v01 (using entries in the PDB archive December 25th 2019)
:	1.9.9
:	Engh & Huber (2001)
:	Parkinson et al. (1996)
:	2.31.2
	::

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $ELECTRON\ MICROSCOPY$

The reported resolution of this entry is 2.79 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f EM} {f structures} \ (\#{f Entries})$
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	А	40	68%		18%	8%	8%
1	В	40	- 52%	10%	38%		
1	С	40	68%		18%	8%	8%
1	D	40	• 50%	12%	38%		
1	Е	40	62%		25%	5%	8%
1	F	40	- 50%	12%	38%	_	
1	G	40	65%		22%	5%	8%
1	Н	40	50%	12%	38%		

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Mol	Chain	Length	Quality of	chain
1	Ι	40	65%	22% 5% 8%
1	J	40	50% 12	2% 38%
1	Κ	40	65%	22% 5% 8%
1	L	40	• 50% 12	2% 38%
1	М	40	65%	22% 5% 8%
1	Ν	40	50% 12	2% 38%
1	0	40	65%	22% 5% 8%
1	Р	40	50% 12	2% 38%
1	Q	40	65%	20% 8% 8%
1	R	40	• 50% 12	2% 38%
1	S	40	70%	18% 5% 8%
1	Т	40	50% 12	2% 38%
1	U	40	68%	20% 5% 8%
1	V	40	<u>.</u>	2% 38%

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2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 4807 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.

Mol	Chain	Residues		Aton	ns		AltConf	Trace
1	٨	27	Total	С	Ν	0	0	0
1	А	37	262	162	45	55	0	0
1	П	25	Total	С	Ν	0	0	0
1	В	25	175	107	29	39	0	0
1	C	07	Total	С	Ν	0	0	0
1	С	37	262	162	45	55	0	0
1	р	95	Total	С	Ν	0	0	0
1	D	25	175	107	29	39	0	0
1	Е	27	Total	С	Ν	0	0	0
1	E	37	262	162	45	55	0	0
1	F	25	Total	С	Ν	0	0	0
	Г	20	175	107	29	39	0	0
1	G	37	Total	С	Ν	0	0	0
1	G	51	262	162	45	55	0	0
1	Н	25	Total	С	Ν	0	0	0
1	11	20	175	107	29	39		0
1	Ι	37	Total	С	Ν	0	0	0
1	L	51	262	162	45	55		0
1	J	25	Total	С	Ν	0	0	0
L	0	20	175	107	29	39	0	0
1	Κ	37	Total	С	Ν	Ο	0	0
1	17	51	262	162	45	55	0	0
1	L	25	Total	С	Ν	Ο	0	0
	Ľ	20	175	107	29	39	0	0
1	М	37	Total	С	Ν	Ο	0	0
	111		262	162	45	55	0	0
1	Ν	25	Total	С	Ν	Ο	0	0
1	11	20	175	107	29	39	0	0
1	Ο	37	Total	С	Ν	Ο	0	0
		01	262	162	45	55		0
1	Р	25	Total	С	Ν	Ο	0	0
	-	20	175	107	29	39		0
1	Q	37	Total	С	Ν	Ο	0	0
	ઝ	01	262	162	45	55		0

• Molecule 1 is a protein called Nuclear pore complex protein Nup98.

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	R	25	Total	С	Ν	0	0	0
1	п	20	175	107	29	39	0	0
1	S	37	Total	С	Ν	0	0	0
1	G	51	262	162	45	55	0	0
1	Т	25	Total	С	Ν	0	0	0
1	T	20	175	107	29	39	0	0
1	U	37	Total	С	Ν	0	0	0
1	U	51	262	162	45	55	0	0
1	V	25	Total	С	Ν	0	0	0
	v	20	175	107	29	39	U	0

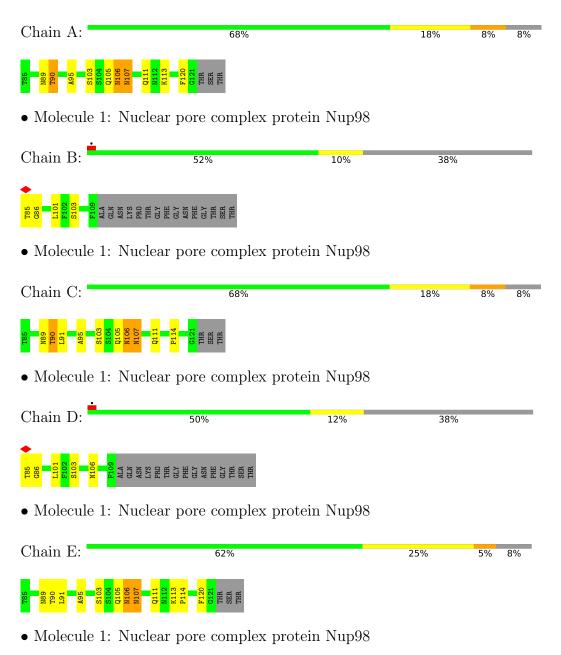
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3 Residue-property plots (i)

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: Nuclear pore complex protein Nup98





Chain F:	50%	12%	38%	
T85 C86 C86 C86 C80 C90 C90 C90 C100	ASN LYS PRO THR GLY GLY GLY GLY THR THR THR THR THR			
• Molecule 1: Nu	ıclear pore complex p	orotein Nup98		
Chain G:	65%		22%	5% 8%
185 190 190 190 106 106 106 106 106 106 106 106 106	0111 114 114 114 114 114 114 1120 1120 1			
• Molecule 1: Nu	ıclear pore complex p	orotein Nup98		
Chain H:	50%	12%	38%	
T85 686 686 1101 F102 F103 N106 A1A ALA ALA ALA	ASN LYS PRO GLY GLY GLY ASN PHE GLY THR THR THR THR THR			
• Molecule 1: Nu	ıclear pore complex p	orotein Nup98		
Chain I:	65%		22%	5% 8%
T85 T90 N89 8103 S103 8104 N107 N107	0111 N112 F114 F120 G121 THR SER THR			
• Molecule 1: Nu	ıclear pore complex p	orotein Nup98		
Chain J:	50%	12%	38%	
T85 686 5101 5103 8103 8103 7109 7109 614	L ASN PRO CITHR CILY CILY PHE ASN ASN CILY FHR SIER THR SIER THR			
• Molecule 1: Nu	iclear pore complex p	orotein Nup98		
Chain K:	65%		22%	5% 8%
185 190 190 190 190 190 190 100 810 8100 810	N107 Q111 F114 F114 F120 G121 THR SER THR THR			
• Molecule 1: Nu	ıclear pore complex p	orotein Nup98		
Chain L:	50%	12%	38%	
T85 686 101 101 8103 8103 8103 ALA ALA GLA	ASN LYS PRO THR GLY GLY ASN ASN THR THR STR THR			

• Molecule 1: Nuclear pore complex protein Nup98



Chain M:	65%		22%	5%	8%
186 189 190 190 190 103 103 104 105 105 105	q111 N112 F114 F114 F120 G121 THR SER THR				
• Molecule 1: Nu	clear pore complex j	protein Nup98			
Chain N:	50%	12%	38%		
T85 686 1101 1101 1100 8103 8103 8103 8103 8109 8109 8109 8109 8109 8109 8109 8109	LYS LYS PRO PHE CLY PHE PHE PHE CLY THR THR THR				
• Molecule 1: Nu	clear pore complex j	protein Nup98			
Chain O:	65%		22%	5%	8%
T85 N89 A95 S103 S103 S104 Q105 N106 N106	0111 N112 K113 F114 F120 F120 G121 THR SER THR				
• Molecule 1: Nu	clear pore complex j	protein Nup98			
Chain P:	50%	12%	38%		_
T85 686 686 1101 1101 8103 8103 8103 8103 810 810 810 810 810 810 810 810 810 810	LYS LYS PRO THR GLY GLY ASN PHE GLY THR THR THR THR THR				
• Molecule 1: Nu	clear pore complex j	protein Nup98			
Chain Q:	65%		20%	8%	8%
T85 N89 A95 S103 S103 S104 Q105 N106	0111 N112 F114 F114 F120 F120 G121 THR SER THR				
• Molecule 1: Nu	clear pore complex j	protein Nup98			
Chain R:	50%	12%	38%		
T85	L YS L YS PRO CLY CLY PHE ASN PHE ASN THR SER THR				
• Molecule 1: Nu	clear pore complex j	protein Nup98			
Chain S:	70%		18%	5%	8%
185 190 190 190 190 191 191 110 111	P114 P120 C121 THR SER THR				
• Molecule 1: Nu	clear pore complex j	protein Nup98			



Chain T:	50%	12%	38%		_			
185 686 1101 102 8103 8103 8103 810 810 811 811	ASN LYS PRO CLY GLY GLY GLY GLY GLY THR THR THR THR							
• Molecule 1: Nuclear pore complex protein Nup98								
Chain U:	68%		20%	5%	8%			
185 190 191 191 191 191 191 190 100 100 100	K113 P114 F120 F120 THR SER THR							
• Molecule 1: Nuclear pore complex protein Nup98								
Chain V:	50%	12%	38%		_			
T85 686 1101 101 102 103 100 110 610 610	LASN LASN THR PRO GLY CLY CLY CLY CLY THR SER THR SER THR							



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-3.29°, rise=4.67 Å, axial	Depositor
	sym=C1	
Number of segments used	28360	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	41	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 $(6k \ge 4k)$	Depositor
Maximum map value	0.214	Depositor
Minimum map value	-0.097	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	262.5, 262.5, 262.5	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor



5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 5 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles		
	Unain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.89	1/267~(0.4%)	0.91	1/361~(0.3%)	
1	В	0.67	0/177	0.76	0/240	
1	С	0.89	1/267~(0.4%)	0.91	0/361	
1	D	0.67	0/177	0.76	0/240	
1	Е	0.89	0/267	0.91	0/361	
1	F	0.67	0/177	0.76	0/240	
1	G	0.89	0/267	0.91	0/361	
1	Н	0.67	0/177	0.76	0/240	
1	Ι	0.89	0/267	0.91	0/361	
1	J	0.67	0/177	0.76	0/240	
1	Κ	0.89	0/267	0.91	0/361	
1	L	0.67	0/177	0.76	0/240	
1	М	0.89	0/267	0.90	0/361	
1	Ν	0.67	0/177	0.76	0/240	
1	0	0.89	0/267	0.91	0/361	
1	Р	0.67	0/177	0.76	0/240	
1	Q	0.89	0/267	0.91	1/361~(0.3%)	
1	R	0.67	0/177	0.76	0/240	
1	S	0.89	0/267	0.91	0/361	
1	Т	0.67	0/177	0.76	0/240	
1	U	0.89	0/267	0.91	0/361	
1	V	0.67	0/177	0.76	0/240	
All	All	0.81	2/4884~(0.0%)	0.85	$2/6611 \ (0.0\%)$	

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	90	THR	CB-CG2	-5.00	1.35	1.52
1	С	90	THR	CB-CG2	-5.00	1.35	1.52

All (2) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
1	Q	120	PHE	CB-CG-CD1	5.03	124.32	120.80
1	А	120	PHE	CB-CG-CD1	5.01	124.31	120.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	262	0	239	9	0
1	В	175	0	160	4	0
1	С	262	0	239	11	0
1	D	175	0	160	6	0
1	Е	262	0	239	14	0
1	F	175	0	160	6	0
1	G	262	0	239	13	0
1	Н	175	0	160	6	0
1	Ι	262	0	239	13	0
1	J	175	0	160	6	0
1	Κ	262	0	239	13	0
1	L	175	0	160	6	0
1	М	262	0	239	13	0
1	Ν	175	0	160	6	0
1	0	262	0	239	13	0
1	Р	175	0	160	6	0
1	Q	262	0	239	13	0
1	R	175	0	160	6	0
1	S	262	0	239	10	0
1	Т	175	0	160	6	0
1	U	262	0	239	10	0
1	V	175	0	160	4	0
All	All	4807	0	4389	125	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 14.

The worst 5 of 125 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:ASN:ND2	1:B:103:SER:OG	2.28	0.67
1:E:106:ASN:ND2	1:F:103:SER:OG	2.28	0.67
1:I:106:ASN:ND2	1:J:103:SER:OG	2.28	0.67
1:K:106:ASN:ND2	1:L:103:SER:OG	2.28	0.67
1:O:106:ASN:ND2	1:P:103:SER:OG	2.28	0.67

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	А	35/40~(88%)	35~(100%)	0	0	100 100
1	В	23/40~(58%)	23~(100%)	0	0	100 100
1	С	35/40~(88%)	35~(100%)	0	0	100 100
1	D	23/40~(58%)	23~(100%)	0	0	100 100
1	Е	35/40~(88%)	35~(100%)	0	0	100 100
1	F	23/40~(58%)	23~(100%)	0	0	100 100
1	G	35/40~(88%)	35~(100%)	0	0	100 100
1	Η	23/40~(58%)	23~(100%)	0	0	100 100
1	Ι	35/40~(88%)	35~(100%)	0	0	100 100
1	J	23/40~(58%)	23~(100%)	0	0	100 100
1	Κ	35/40~(88%)	35~(100%)	0	0	100 100
1	L	23/40~(58%)	23~(100%)	0	0	100 100
1	М	35/40~(88%)	35~(100%)	0	0	100 100
1	Ν	23/40~(58%)	23 (100%)	0	0	100 100
1	О	35/40~(88%)	35 (100%)	0	0	100 100
1	Р	23/40~(58%)	23~(100%)	0	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	\mathbf{ntiles}
1	Q	35/40~(88%)	35~(100%)	0	0	100	100
1	R	23/40~(58%)	23 (100%)	0	0	100	100
1	S	35/40~(88%)	35~(100%)	0	0	100	100
1	Т	23/40~(58%)	23 (100%)	0	0	100	100
1	U	35/40~(88%)	35~(100%)	0	0	100	100
1	V	23/40~(58%)	23 (100%)	0	0	100	100
All	All	638/880~(72%)	638 (100%)	0	0	100	100

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There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	А	27/30~(90%)	24 (89%)	3 (11%)	6 19
1	В	19/30~(63%)	18 (95%)	1 (5%)	22 54
1	С	27/30~(90%)	24 (89%)	3(11%)	6 19
1	D	19/30~(63%)	18 (95%)	1 (5%)	22 54
1	Ε	27/30~(90%)	24 (89%)	3(11%)	6 19
1	F	19/30~(63%)	18 (95%)	1 (5%)	22 54
1	G	27/30~(90%)	24 (89%)	3(11%)	6 19
1	Н	19/30~(63%)	18 (95%)	1 (5%)	22 54
1	Ι	27/30~(90%)	24 (89%)	3 (11%)	6 19
1	J	19/30~(63%)	18 (95%)	1 (5%)	22 54
1	K	27/30~(90%)	24 (89%)	3 (11%)	6 19
1	L	19/30~(63%)	18 (95%)	1 (5%)	22 54
1	М	27/30~(90%)	24 (89%)	3 (11%)	6 19
1	Ν	19/30~(63%)	18 (95%)	1 (5%)	22 54
1	Ο	27/30~(90%)	24 (89%)	3 (11%)	6 19

Continued on next page...



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	Р	19/30~(63%)	18 (95%)	1 (5%)	22 54
1	Q	27/30~(90%)	24 (89%)	3(11%)	6 19
1	R	19/30~(63%)	18 (95%)	1 (5%)	22 54
1	S	27/30~(90%)	24~(89%)	3 (11%)	6 19
1	Т	19/30~(63%)	18 (95%)	1 (5%)	22 54
1	U	27/30~(90%)	24~(89%)	3(11%)	6 19
1	V	19/30~(63%)	$18 \ (95\%)$	1 (5%)	22 54
All	All	506/660~(77%)	462 (91%)	44 (9%)	14 30

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5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	105	GLN
1	R	101	LEU
1	0	106	ASN
1	Q	105	GLN
1	S	106	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	0	106	ASN
1	Q	106	ASN
1	U	106	ASN
1	S	106	ASN
1	Ι	106	ASN

5.3.3 RNA (i)

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 monosaccharides 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.



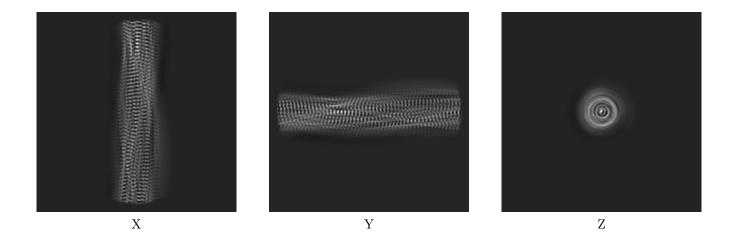
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-13853. These allow visual inspection of the internal detail of the map and identification of artifacts.

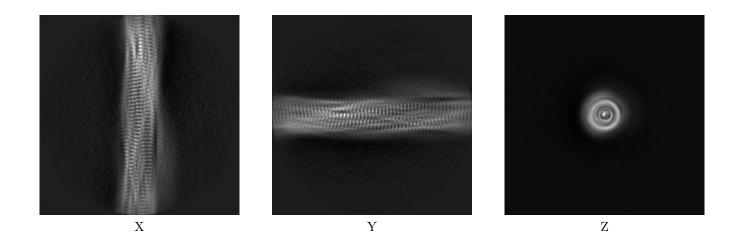
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

6.1.1 Primary map



6.1.2 Raw map

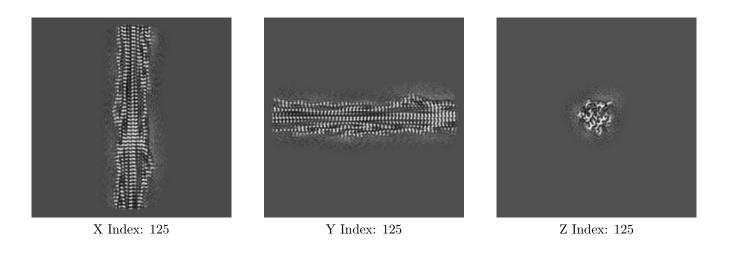


The images above show the map projected in three orthogonal directions.

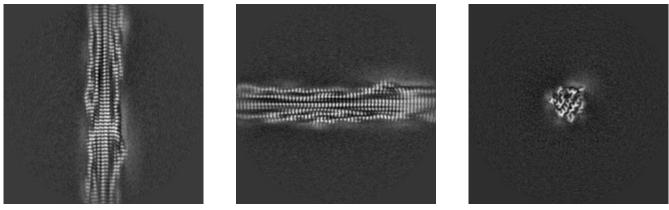


6.2 Central slices (i)

6.2.1 Primary map



6.2.2 Raw map



X Index: 125

Y Index: 125

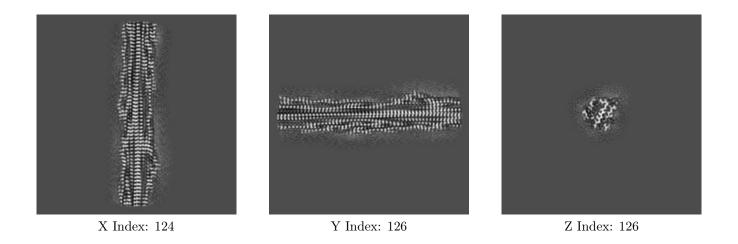


The images above show central slices of the map in three orthogonal directions.

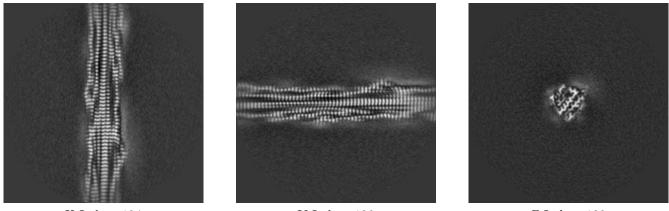


6.3 Largest variance slices (i)

6.3.1 Primary map



6.3.2 Raw map



X Index: 124

Y Index: 126

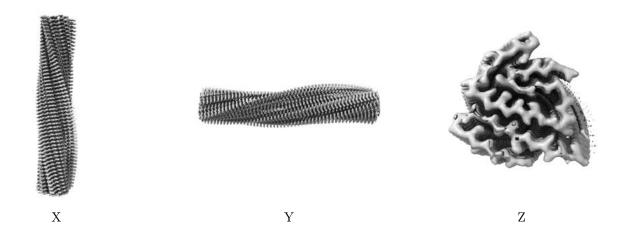


The images above show the largest variance slices of the map in three orthogonal directions.



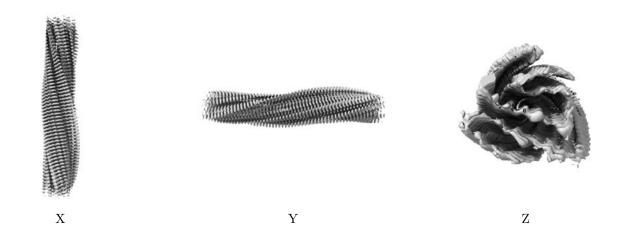
6.4 Orthogonal surface views (i)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. 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



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 (i)

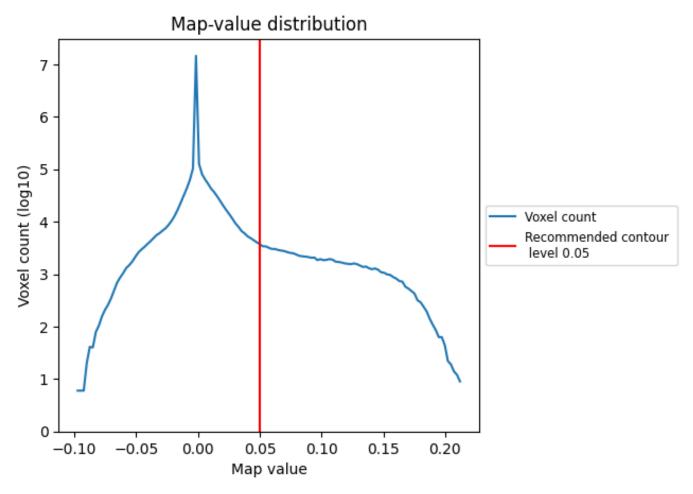
This section was not generated. No masks/segmentation were deposited.



7 Map analysis (i)

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

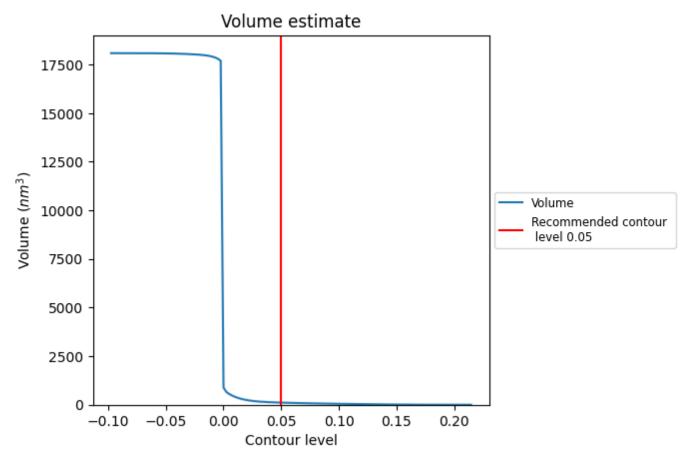
7.1 Map-value distribution (i)



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)

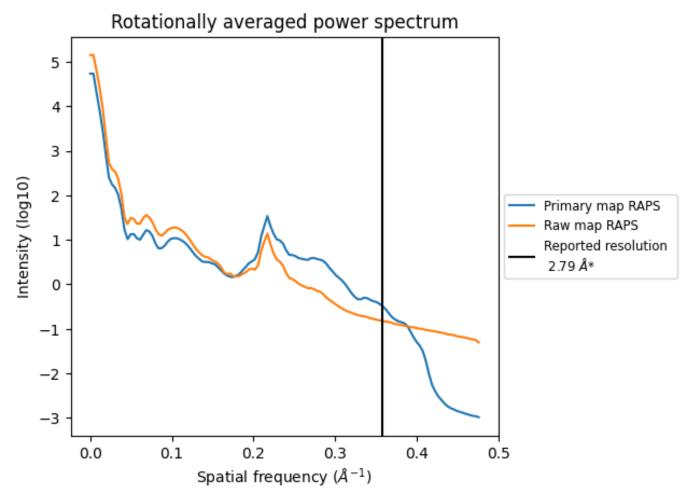


The volume at the recommended contour level is 111 nm^3 ; this corresponds to an approximate mass of 100 kDa.

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 (i)



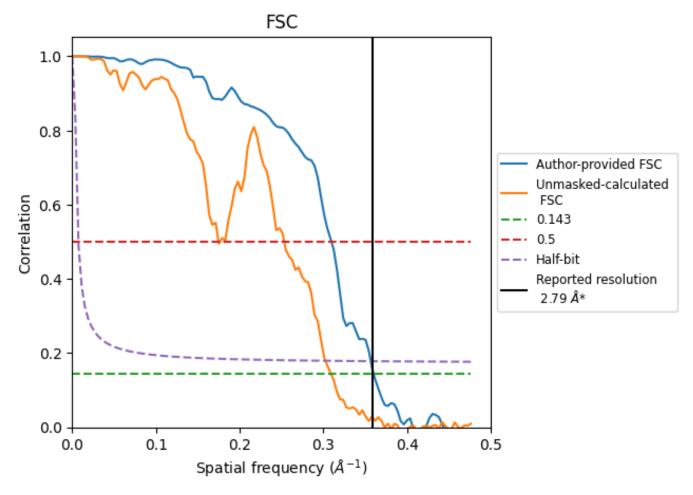
*Reported resolution corresponds to spatial frequency of 0.358 ${\rm \AA^{-1}}$



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 0.358 $\mathrm{\AA^{-1}}$



8.2 Resolution estimates (i)

Resolution estimate (Å)	Estim	Estimation criterion (FSC cut-off)			
Resolution estimate (A)	0.143	0.5	Half-bit		
Reported by author	2.79	-	-		
Author-provided FSC curve	2.78	3.23	2.80		
Unmasked-calculated*	3.23	5.72	3.31		

*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 3.23 differs from the reported value 2.79 by more than 10 %



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-13853 and PDB model 7Q66. Per-residue inclusion information can be found in section 3 on page 6.

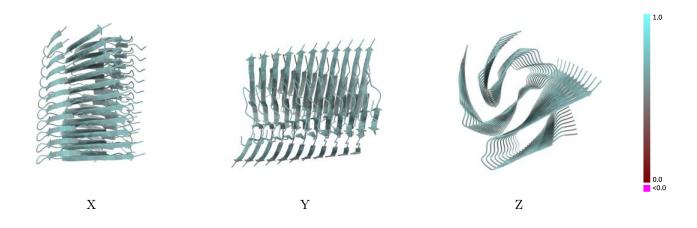
9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.05 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.

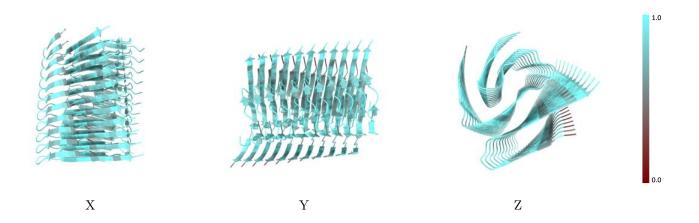


9.2 Q-score mapped to coordinate model (i)



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.

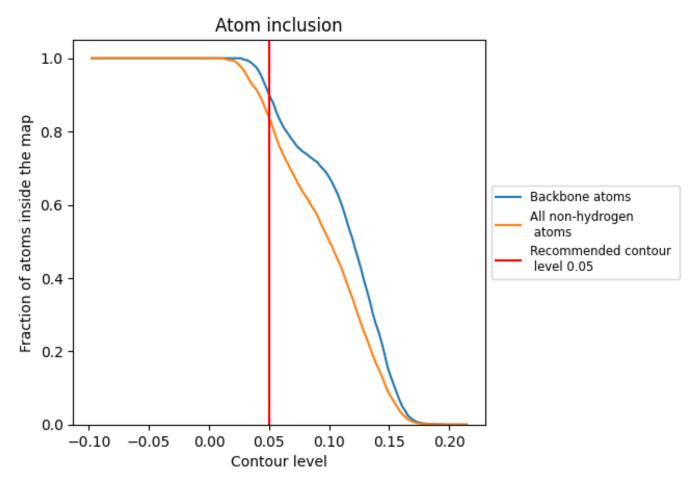
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.05).



9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.



1.0

0.0 <0.0

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8390	0.6070
А	0.8550	0.6030
В	0.8400	0.6250
С	0.8550	0.6010
D	0.8171	0.6170
Е	0.8664	0.6040
F	0.8400	0.6250
G	0.8321	0.5970
Н	0.8114	0.6150
Ι	0.8473	0.6000
J	0.8343	0.6200
Κ	0.8435	0.5960
L	0.8171	0.6190
М	0.8550	0.5970
Ν	0.8171	0.6160
0	0.8359	0.5960
Р	0.8286	0.6180
Q	0.8473	0.5990
R	0.8171	0.6120
S	0.8511	0.6000
Т	0.8286	0.6230
U	0.8550	0.5950
V	0.8057	0.6080

