Full wwPDB EM Validation Report

Sep 16, 2023 – 04:00 PM EDT

PDB ID	:	7T6E
EMDB ID	:	EMD-25714
Title	:	Cryo-EM of NBD-ffsy filaments (class 1)
Authors	:	Wang, F.; Guo, J.; Xu, B.; Egelman, E.H.
Deposited on	:	2021-12-13
Resolution	:	3.10 Å(reported)

This is a Full wwPDB EM Validation 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.dev50
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 3.10 Å.

There are no overall percentile quality scores available for this entry.

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	0	5	100%
1	1	5	100%
1	2	5	100%
1	3	5	100%
1	4	5	100%
1	5	5	100%
1	6	5	100%
1	7	5	100%
1	8	5	100%
1	9	5	100%
1	A	5	100%
1	B	5	100%
1	C	5	100%
1	D	5	100%
1	E	5	100%
1	F	5	100%
1	G	5	100%

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Mol	Chain	Length	Quality of chain
1	H	5	100%
1	I	5	100%
1	J	5	100%
1	K	5	100%
1	L	5	100%
1	M	5	100%
1	N	5	100%
1	O	5	100%
1	P	5	100%
1	Q	5	100%
1	R	5	100%
1	S	5	100%
1	T	5	100%
1	U	5	100%
1	V	5	100%
1	W	5	100%
1	X	5	100%
1	Y	5	100%
1	Z	5	100%
1	a	5	100%
1	b	5	100%
1	c	5	100%
1	d	5	100%
1	e	5	100%
1	f	5	100%

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Mol	Chain	Length	Quality of chain
1	g	5	100%
1	h	5	100%
1	i	5	100%
1	j	5	100%
1	k	5	100%
1	l	5	100%
1	m	5	100%
1	n	5	100%
1	o	5	100%
1	p	5	100%
1	q	5	100%
1	r	5	100%
1	s	5	100%
1	t	5	100%
1	u	5	100%
1	v	5	100%
1	w	5	100%
1	x	5	100%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 3480 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 (with D amino acids) called NBD-ffsy peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	5	Total	C	N	O	0	0
			58	39	8	11		
1	B	5	Total	C	N	O	0	0
			58	39	8	11		
1	C	5	Total	C	N	O	0	0
			58	39	8	11		
1	D	5	Total	C	N	O	0	0
			58	39	8	11		
1	E	5	Total	C	N	O	0	0
			58	39	8	11		
1	F	5	Total	C	N	O	0	0
			58	39	8	11		
1	G	5	Total	C	N	O	0	0
			58	39	8	11		
1	H	5	Total	C	N	O	0	0
			58	39	8	11		
1	I	5	Total	C	N	O	0	0
			58	39	8	11		
1	J	5	Total	C	N	O	0	0
			58	39	8	11		
1	K	5	Total	C	N	O	0	0
			58	39	8	11		
1	L	5	Total	C	N	O	0	0
			58	39	8	11		
1	M	5	Total	C	N	O	0	0
			58	39	8	11		
1	N	5	Total	C	N	O	0	0
			58	39	8	11		
1	O	5	Total	C	N	O	0	0
			58	39	8	11		
1	P	5	Total	C	N	O	0	0
			58	39	8	11		
1	Q	5	Total	C	N	O	0	0
			58	39	8	11		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	R	5	Total	C	N	O	0	0
			58	39	8	11		
1	S	5	Total	C	N	O	0	0
			58	39	8	11		
1	T	5	Total	C	N	O	0	0
			58	39	8	11		
1	U	5	Total	C	N	O	0	0
			58	39	8	11		
1	V	5	Total	C	N	O	0	0
			58	39	8	11		
1	W	5	Total	C	N	O	0	0
			58	39	8	11		
1	X	5	Total	C	N	O	0	0
			58	39	8	11		
1	Y	5	Total	C	N	O	0	0
			58	39	8	11		
1	Z	5	Total	C	N	O	0	0
			58	39	8	11		
1	0	5	Total	C	N	O	0	0
			58	39	8	11		
1	1	5	Total	C	N	O	0	0
			58	39	8	11		
1	2	5	Total	C	N	O	0	0
			58	39	8	11		
1	3	5	Total	C	N	O	0	0
			58	39	8	11		
1	4	5	Total	C	N	O	0	0
			58	39	8	11		
1	5	5	Total	C	N	O	0	0
			58	39	8	11		
1	6	5	Total	C	N	O	0	0
			58	39	8	11		
1	7	5	Total	C	N	O	0	0
			58	39	8	11		
1	8	5	Total	C	N	O	0	0
			58	39	8	11		
1	9	5	Total	C	N	O	0	0
			58	39	8	11		
1	a	5	Total	C	N	O	0	0
			58	39	8	11		
1	b	5	Total	C	N	O	0	0
			58	39	8	11		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	c	5	Total	C	N	O	0	0
			58	39	8	11		
1	d	5	Total	C	N	O	0	0
			58	39	8	11		
1	e	5	Total	C	N	O	0	0
			58	39	8	11		
1	f	5	Total	C	N	O	0	0
			58	39	8	11		
1	g	5	Total	C	N	O	0	0
			58	39	8	11		
1	h	5	Total	C	N	O	0	0
			58	39	8	11		
1	i	5	Total	C	N	O	0	0
			58	39	8	11		
1	j	5	Total	C	N	O	0	0
			58	39	8	11		
1	k	5	Total	C	N	O	0	0
			58	39	8	11		
1	l	5	Total	C	N	O	0	0
			58	39	8	11		
1	m	5	Total	C	N	O	0	0
			58	39	8	11		
1	n	5	Total	C	N	O	0	0
			58	39	8	11		
1	o	5	Total	C	N	O	0	0
			58	39	8	11		
1	p	5	Total	C	N	O	0	0
			58	39	8	11		
1	q	5	Total	C	N	O	0	0
			58	39	8	11		
1	r	5	Total	C	N	O	0	0
			58	39	8	11		
1	s	5	Total	C	N	O	0	0
			58	39	8	11		
1	t	5	Total	C	N	O	0	0
			58	39	8	11		
1	u	5	Total	C	N	O	0	0
			58	39	8	11		
1	v	5	Total	C	N	O	0	0
			58	39	8	11		
1	w	5	Total	C	N	O	0	0
			58	39	8	11		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	x	5	Total	C	N	O	0	0
			58	39	8	11		

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: NBD-ffsy peptide

Chain A: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: NBD-ffsy peptide

Chain B: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: NBD-ffsy peptide

Chain C: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: NBD-ffsy peptide

Chain D: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: NBD-ffsy peptide

Chain E: 100%

There are no outlier residues recorded for this chain.

- Molecule 1: NBD-ffsy peptide

Chain F: 100%

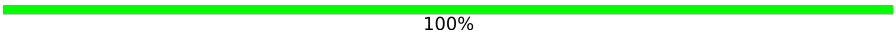
There are no outlier residues recorded for this chain.

- Molecule 1: NBD-ffsy peptide

Chain G: 100%

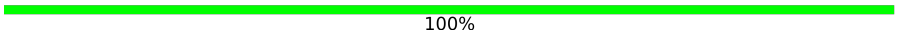
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain H: 

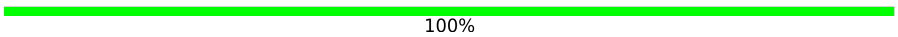
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain I: 

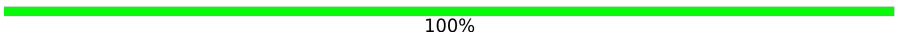
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain J: 

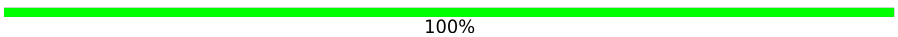
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain K: 

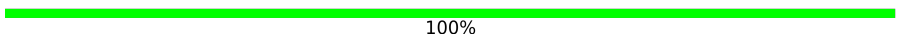
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain L: 

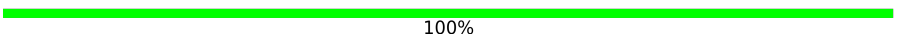
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain M: 

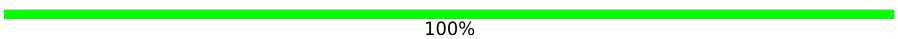
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain N: 

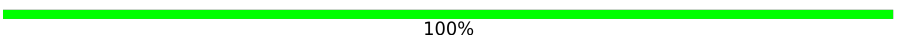
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain O: 

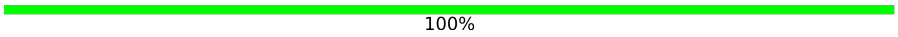
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain P: 

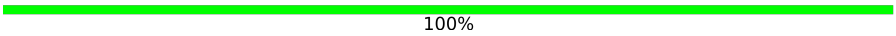
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain Q: 

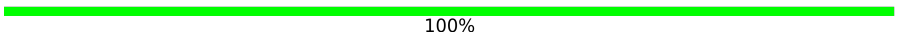
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain R: 

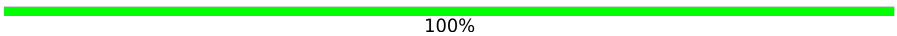
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain S: 

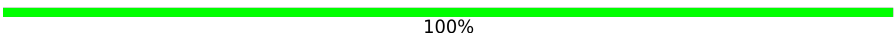
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain T: 

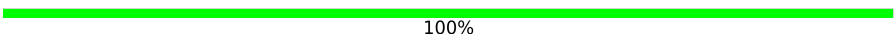
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain U: 

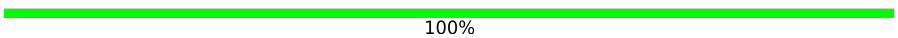
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain V: 

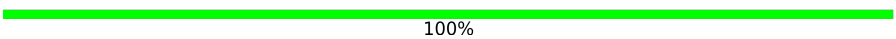
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain W: 

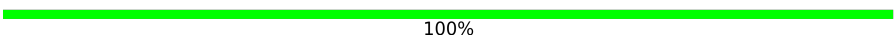
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain X: 

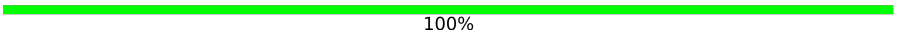
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain Y: 

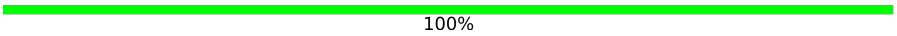
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain Z: 

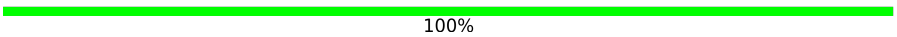
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain 0: 

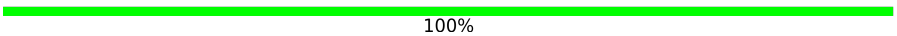
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain 1: 

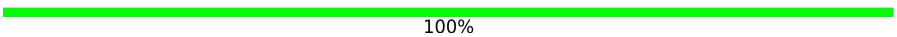
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain 2: 

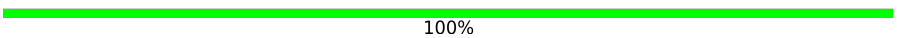
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain 3: 

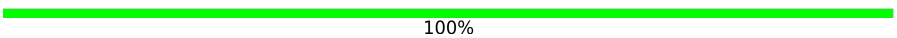
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain 4: 

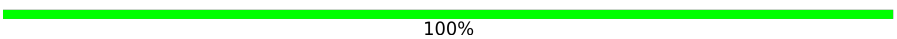
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain 5: 

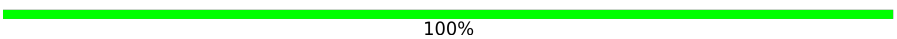
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain 6: 

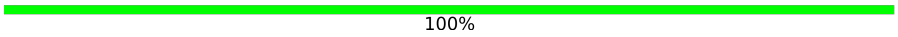
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain 7: 

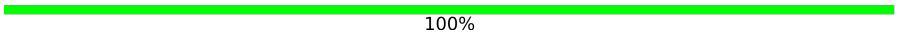
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain 8: 

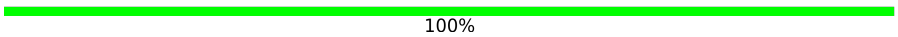
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain 9: 

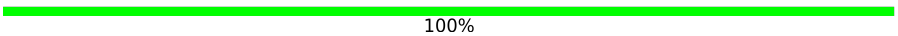
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain a: 

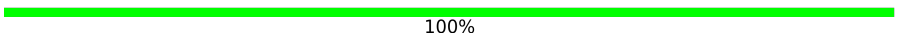
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain b: 

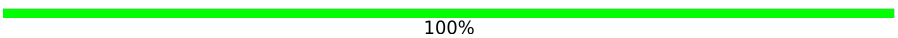
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain c: 

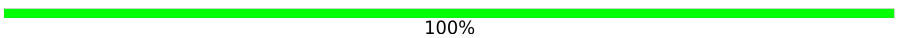
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain d: 

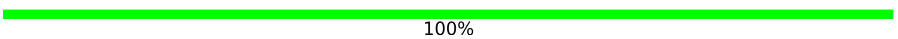
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain e: 

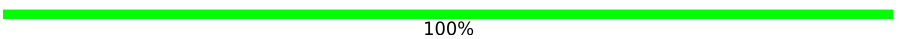
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain f: 

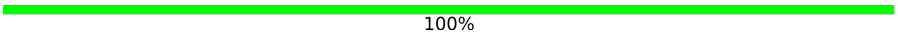
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain g: 

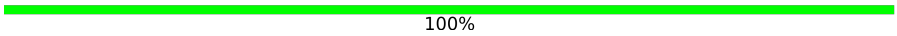
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain h: 

There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain i: 

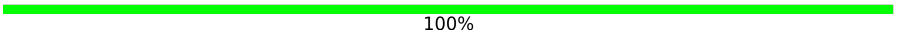
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain j: 

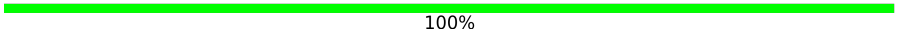
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain k: 

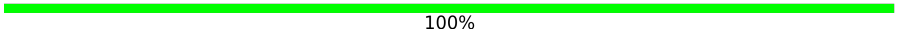
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain l: 

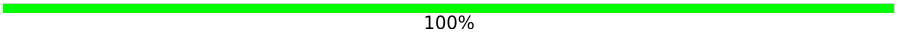
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain m: 

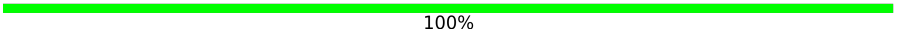
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain n: 

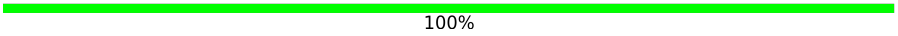
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain o: 

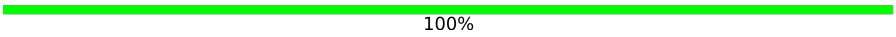
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain p: 

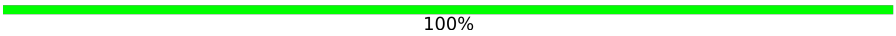
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain q: 

There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain r: 

There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain s: 

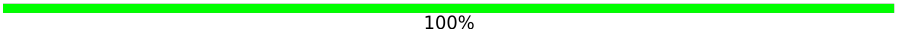
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain t: 

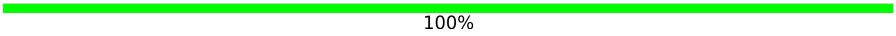
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain u: 

There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain v: 

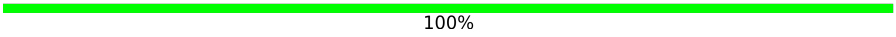
There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain w: 

There are no outlier residues recorded for this chain.

• Molecule 1: NBD-ffsy peptide

Chain x: 

There are no outlier residues recorded for this chain.

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=35.77°, rise=0.483 Å, axial sym=C1	Depositor
Number of segments used	677537	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.800	Depositor
Minimum map value	-0.902	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.053	Depositor
Recommended contour level	0.582	Depositor
Map size (Å)	345.6, 345.6, 345.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UQ4, DSN, DPN, DTY

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein molecules in this entry.

5.3.2 Protein sidechains

There are no protein molecules in this entry.

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

240 non-standard protein/DNA/RNA residues are modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

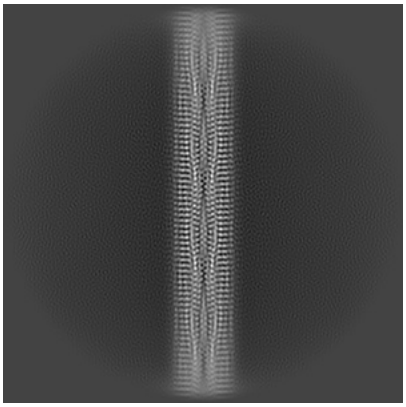
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-25714. These allow visual inspection of the internal detail of the map and identification of artifacts.

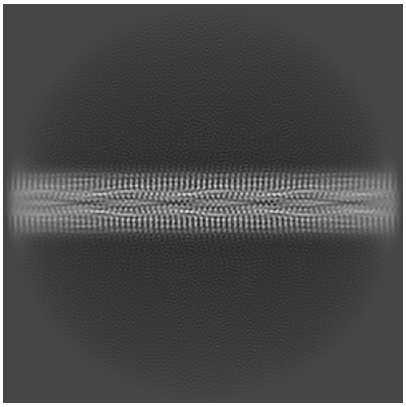
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

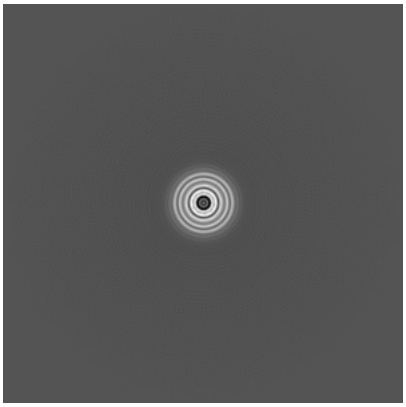
6.1.1 Primary map



X



Y

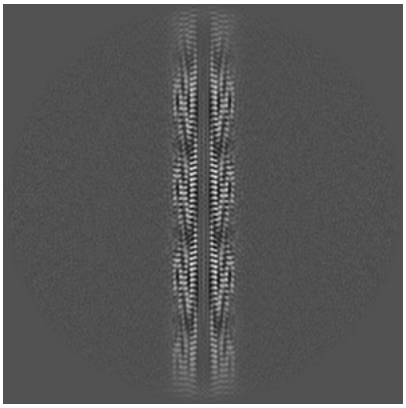


Z

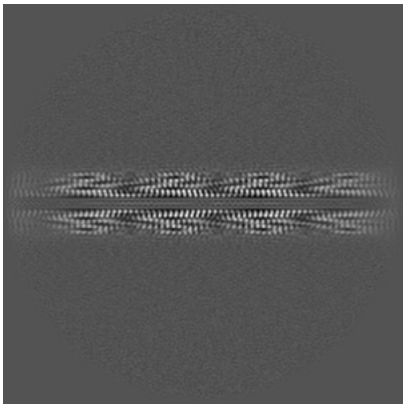
The images above show the map projected in three orthogonal directions.

6.2 Central slices

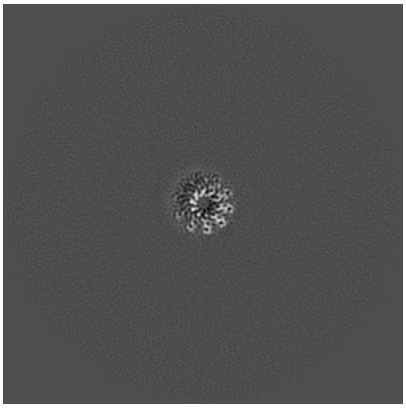
6.2.1 Primary map



X Index: 160



Y Index: 160

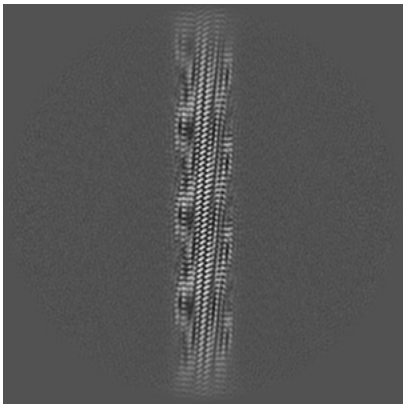


Z Index: 160

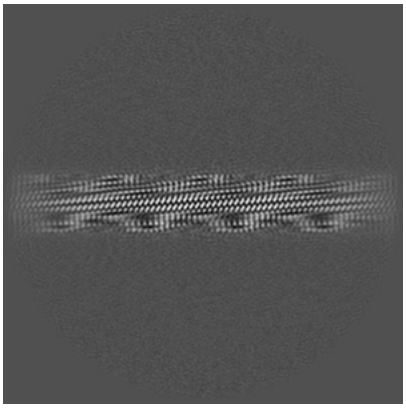
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

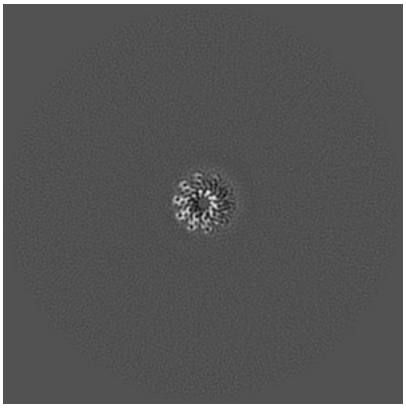
6.3.1 Primary map



X Index: 151



Y Index: 169

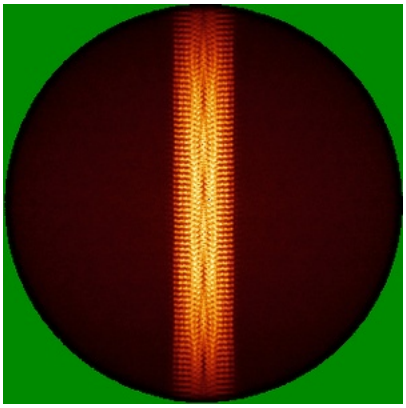


Z Index: 154

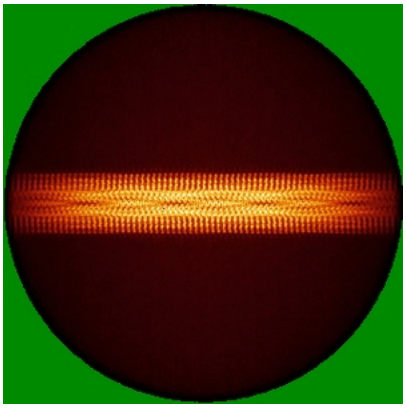
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

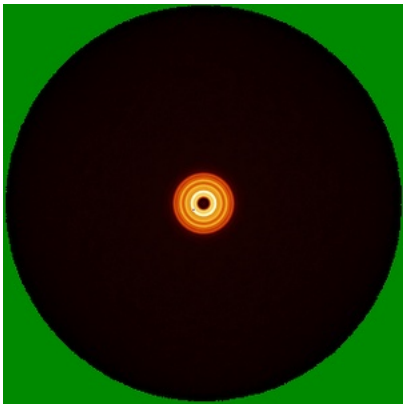
6.4.1 Primary map



X



Y

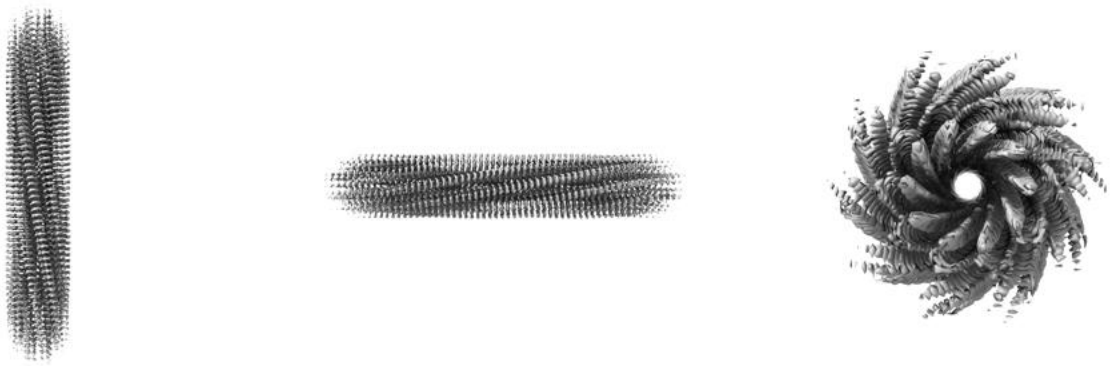


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.582. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

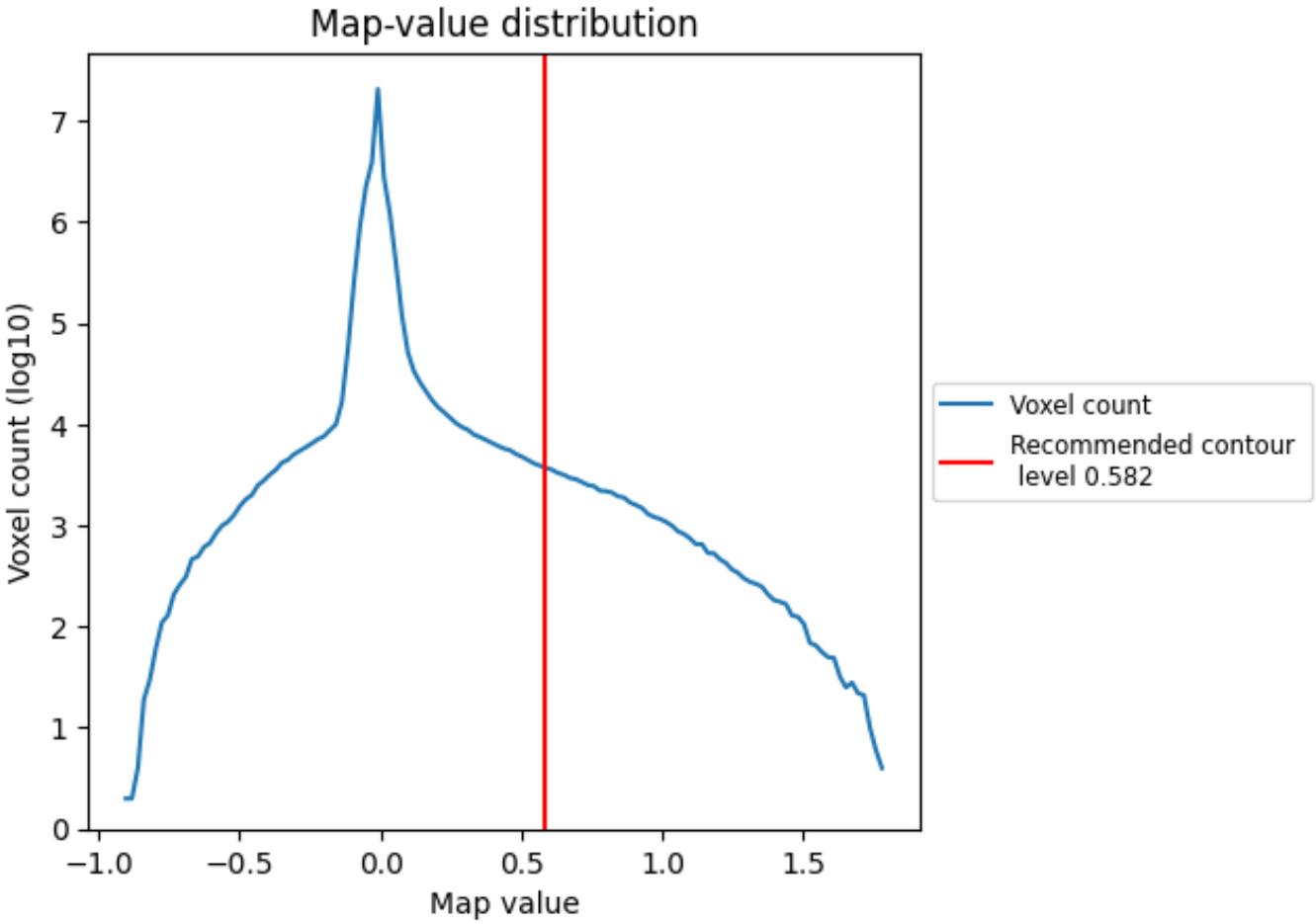
6.6 Mask visualisation (i)

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

7 Map analysis

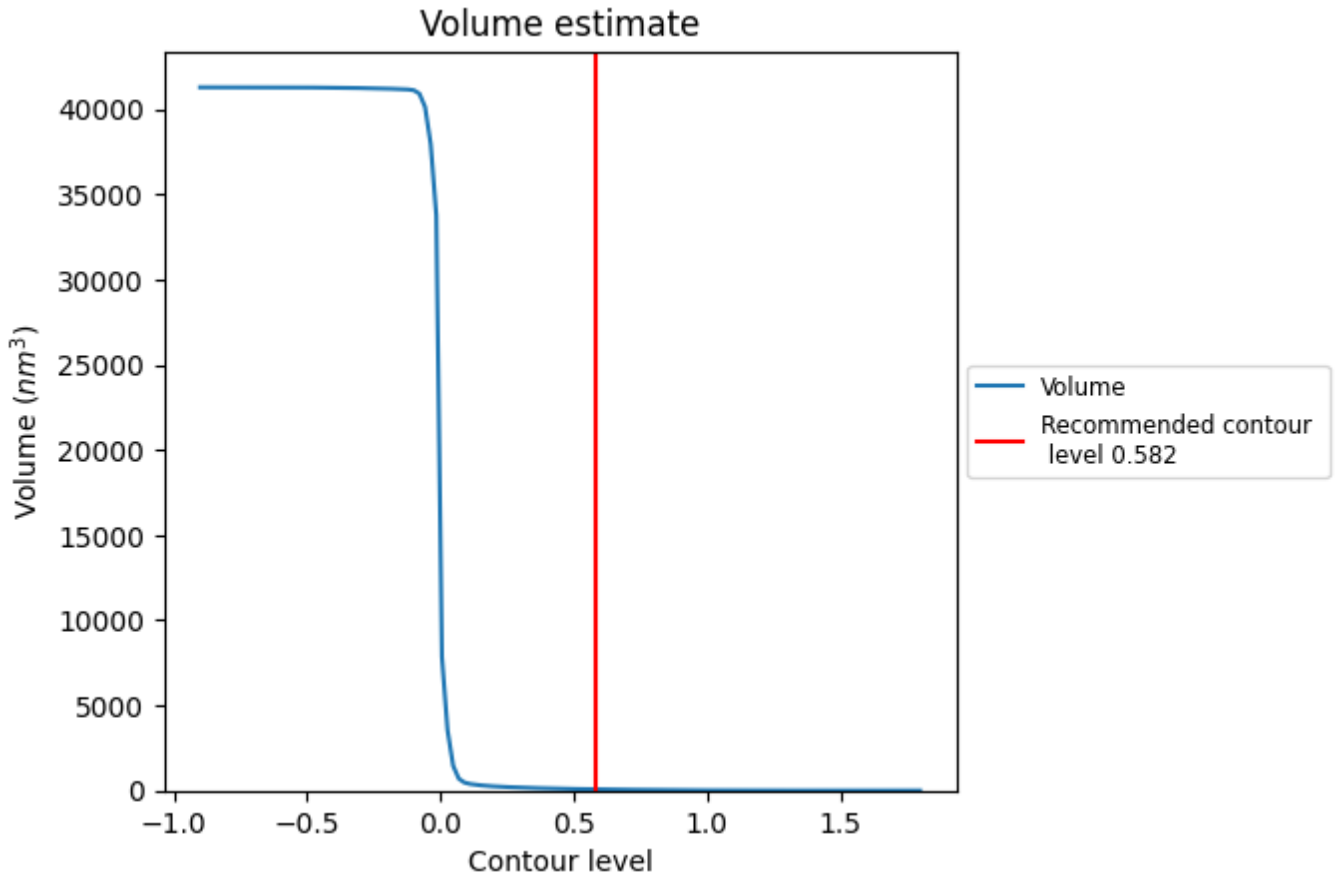
This section contains the results of statistical analysis of the map.

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.

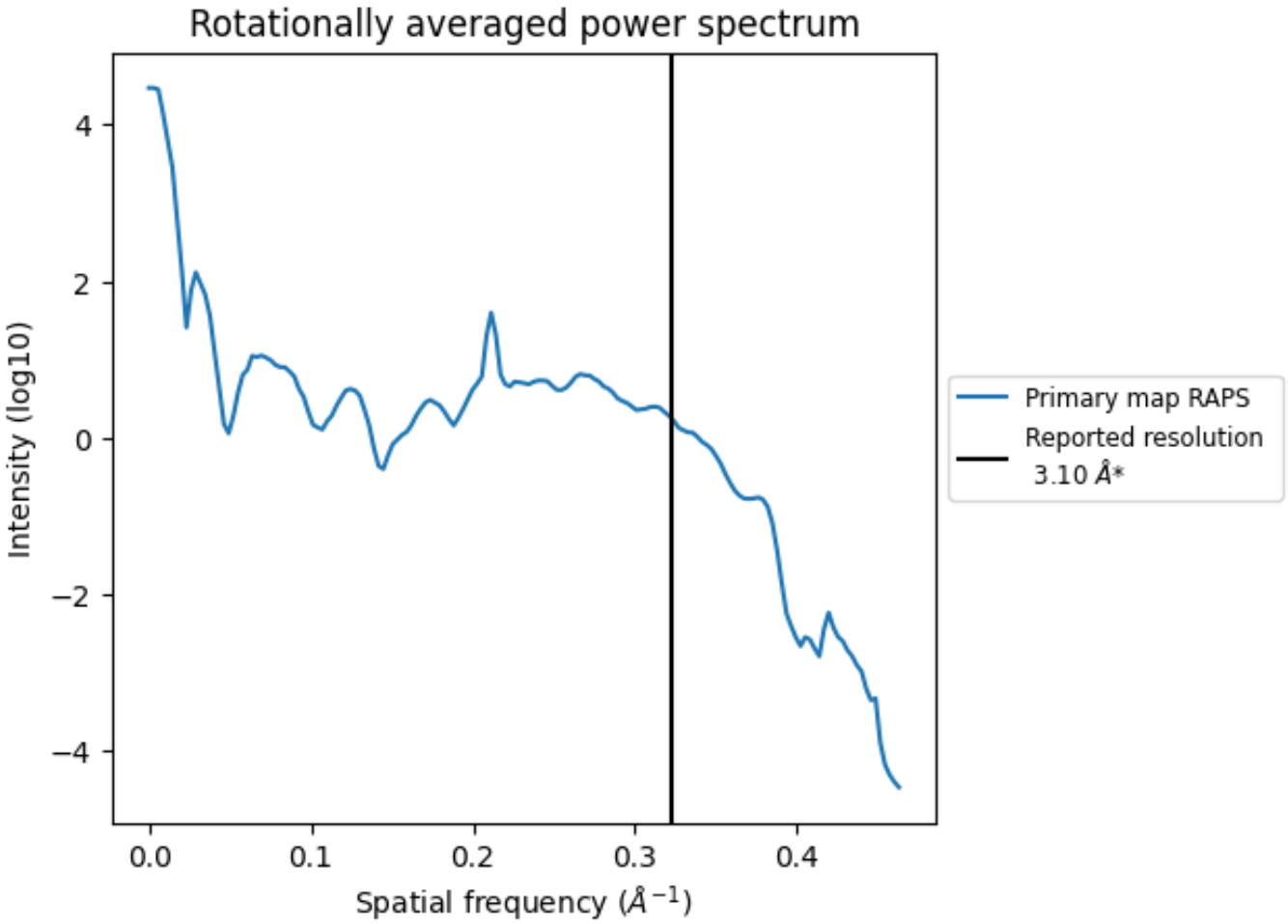
7.2 Volume estimate



The volume at the recommended contour level is 73 nm^3; this corresponds to an approximate mass of 66 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 0.323 $Å^{-1}$

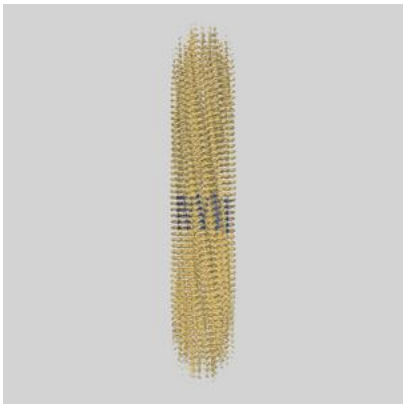
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

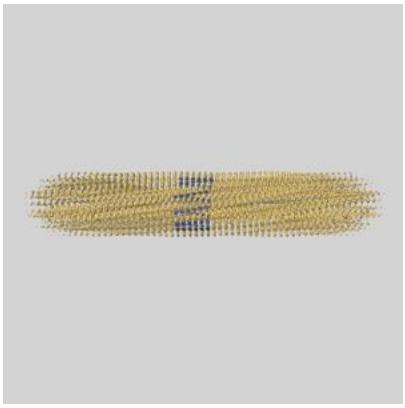
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-25714 and PDB model 7T6E. Per-residue inclusion information can be found in section 3 on page 9.

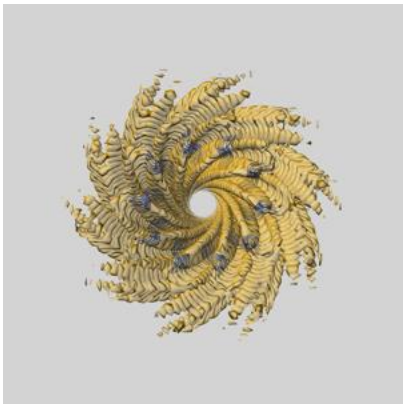
9.1 Map-model overlay



X



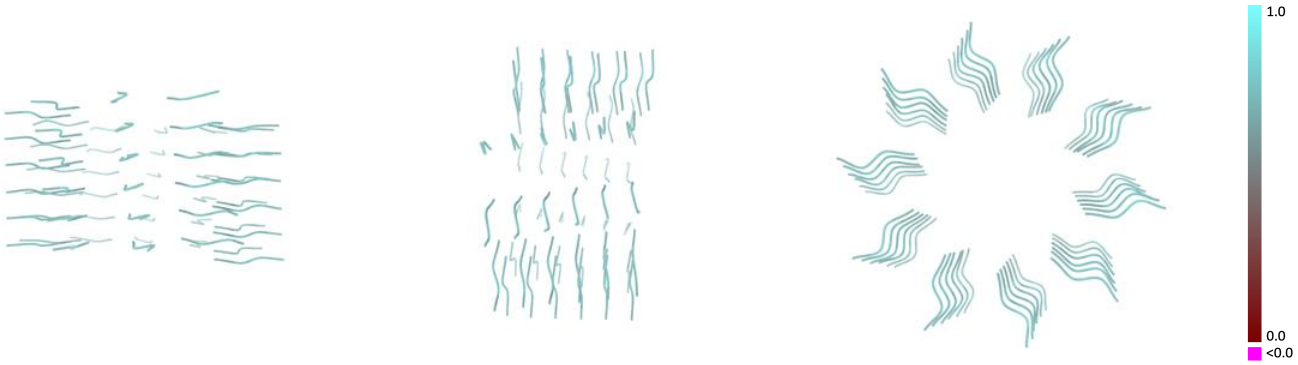
Y



Z

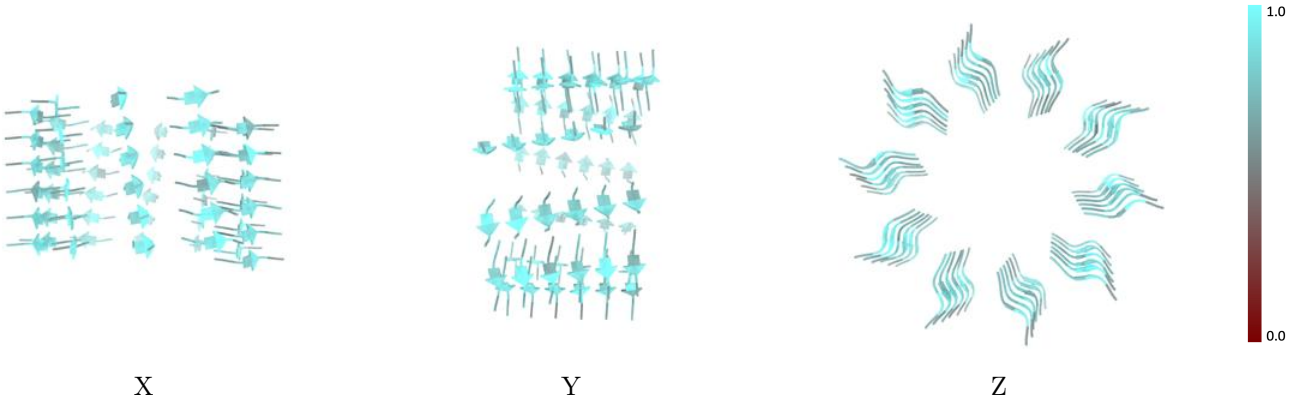
The images above show the 3D surface view of the map at the recommended contour level 0.582 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



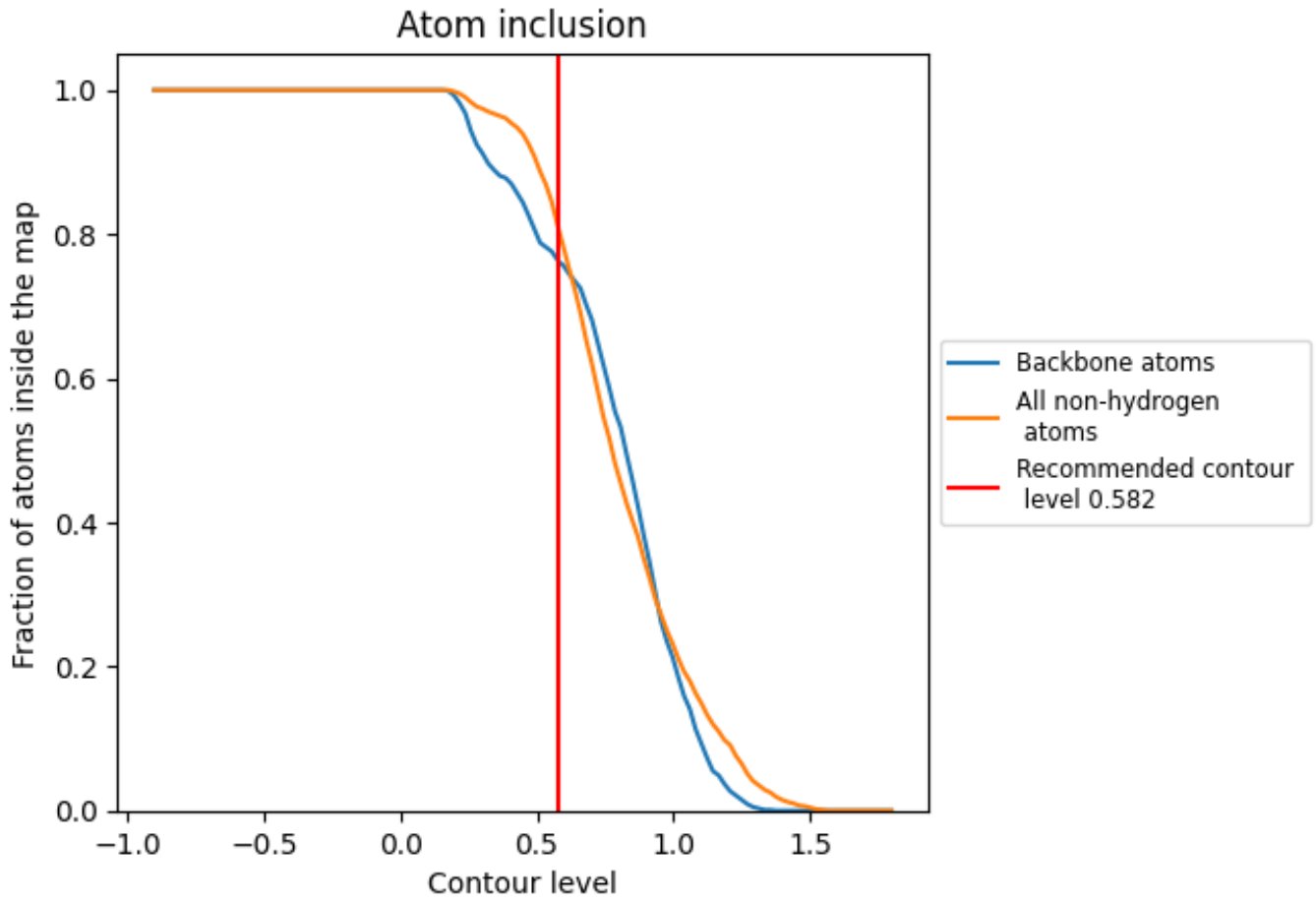
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.582).

9.4 Atom inclusion (i)



At the recommended contour level, 76% of all backbone atoms, 80% 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 (0.582) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8040	0.6740
0	0.7720	0.6730
1	0.7890	0.6700
2	0.8070	0.6710
3	0.7890	0.6780
4	0.7540	0.6710
5	0.7890	0.6720
6	0.8070	0.6680
7	0.8070	0.6790
8	0.7720	0.6780
9	0.8070	0.6760
A	0.7890	0.6720
B	0.7720	0.6690
C	0.8420	0.6700
D	0.8070	0.6700
E	0.8070	0.6760
F	0.8250	0.6730
G	0.8250	0.6770
H	0.8420	0.6790
I	0.7890	0.6710
J	0.8250	0.6740
K	0.8420	0.6700
L	0.8070	0.6800
M	0.8250	0.6770
N	0.8420	0.6730
O	0.7890	0.6720
P	0.8070	0.6680
Q	0.8250	0.6750
R	0.7890	0.6750
S	0.8420	0.6790
T	0.8250	0.6720
U	0.8250	0.6770
V	0.8070	0.6770
W	0.7720	0.6730
X	0.7720	0.6670

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Chain	Atom inclusion	Q-score
Y	0.7720	0.6750
Z	0.8420	0.6720
a	0.8070	0.6720
b	0.8250	0.6830
c	0.8250	0.6760
d	0.8420	0.6810
e	0.7890	0.6760
f	0.8070	0.6760
g	0.8770	0.6780
h	0.7890	0.6810
i	0.8420	0.6790
j	0.7890	0.6730
k	0.7890	0.6840
l	0.8250	0.6800
m	0.7890	0.6790
n	0.8250	0.6710
o	0.7540	0.6690
p	0.7540	0.6720
q	0.7540	0.6640
r	0.8420	0.6690
s	0.8070	0.6710
t	0.7890	0.6710
u	0.7540	0.6780
v	0.7720	0.6770
w	0.7720	0.6730
x	0.8070	0.6830