



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:09 PM UTC

PDB ID : 9GKF / pdb_00009gkf
EMDB ID : EMD-51419
Title : Amyloid Fibril of Heterogeneous nuclear ribonucleoprotein A1A induced by RNA binding
Authors : Frey, L.; Riek, R.P.; Arosio, P.; Morelli, C.
Deposited on : 2024-08-23
Resolution : 3.21 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:

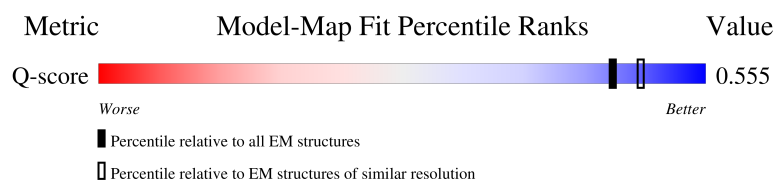
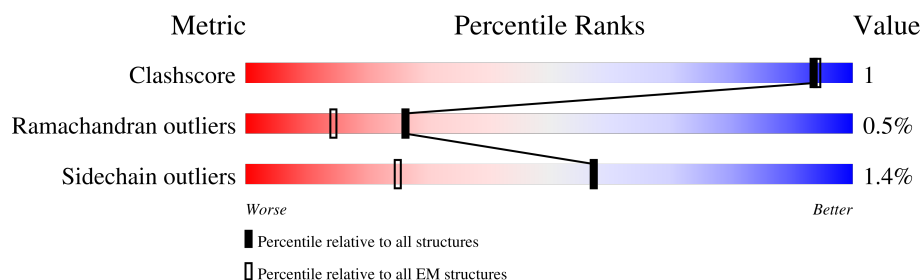
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.21 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14613 (2.71 - 3.71)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	320	
1	B	320	
1	C	320	
1	D	320	

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Mol	Chain	Length	Quality of chain	
1	E	320	<div><div></div></div> 18%	82%
1	F	320	<div><div></div></div> 18%	82%
1	G	320	<div><div></div></div> 18%	82%
1	H	320	<div><div></div></div> 17%	82%
1	I	320	<div><div></div></div> 17%	82%
1	J	320	<div><div></div></div> 17%	82%
1	K	320	<div><div></div></div> 17%	82%
1	L	320	<div><div></div></div> 17%	82%
1	M	320	<div><div></div></div> 17%	82%
1	N	320	<div><div></div></div> 17%	82%
1	O	320	<div><div></div></div> 18%	82%
1	P	320	<div><div></div></div> 17%	82%
1	Q	320	<div><div></div></div> 17%	82%
1	R	320	<div><div></div></div> 18%	82%
1	S	320	<div><div></div></div> 17%	82%
1	T	320	<div><div></div></div> 17%	82%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 8060 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 Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1.

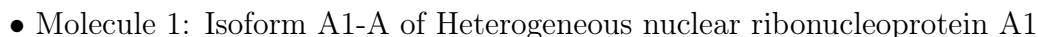
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	B	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	C	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	D	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	E	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	F	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	G	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	H	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	I	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	J	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	K	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	L	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	M	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	N	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	O	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	P	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	Q	57	Total 403	C 245	N 72	O 85	S 1	0	0

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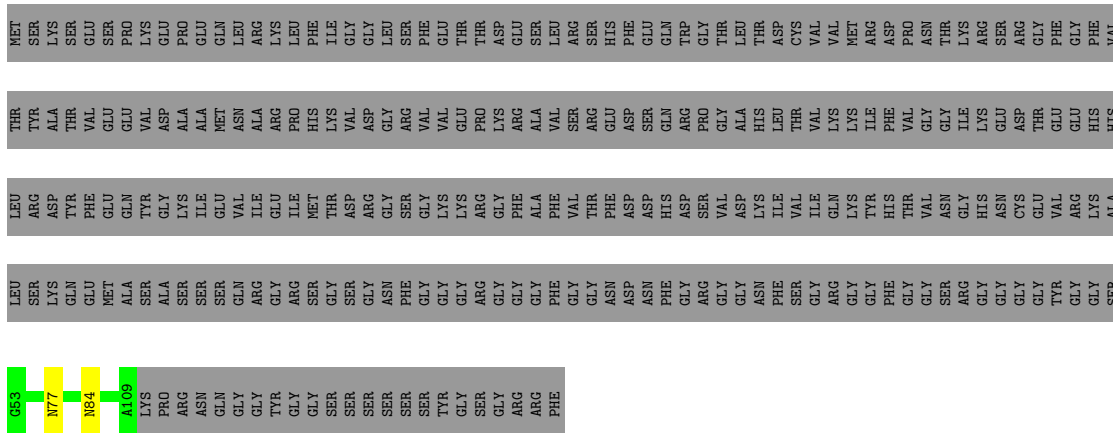
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	S	57	Total 403	C 245	N 72	O 85	S 1	0	0
1	T	57	Total 403	C 245	N 72	O 85	S 1	0	0

- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

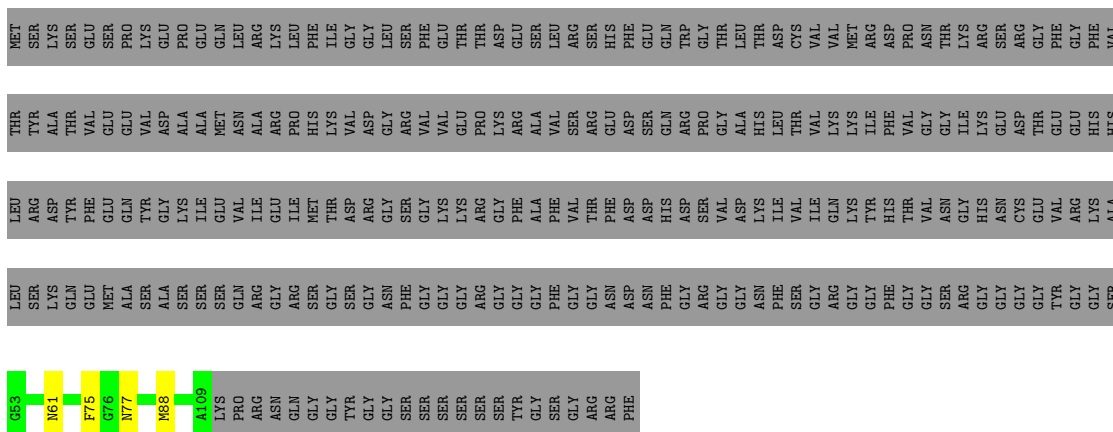






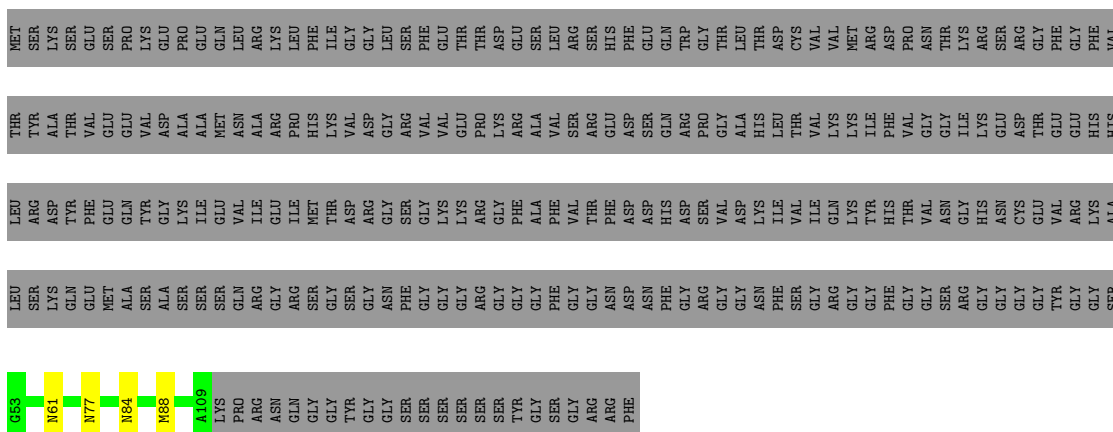
- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

Chain J:  17% . 82%



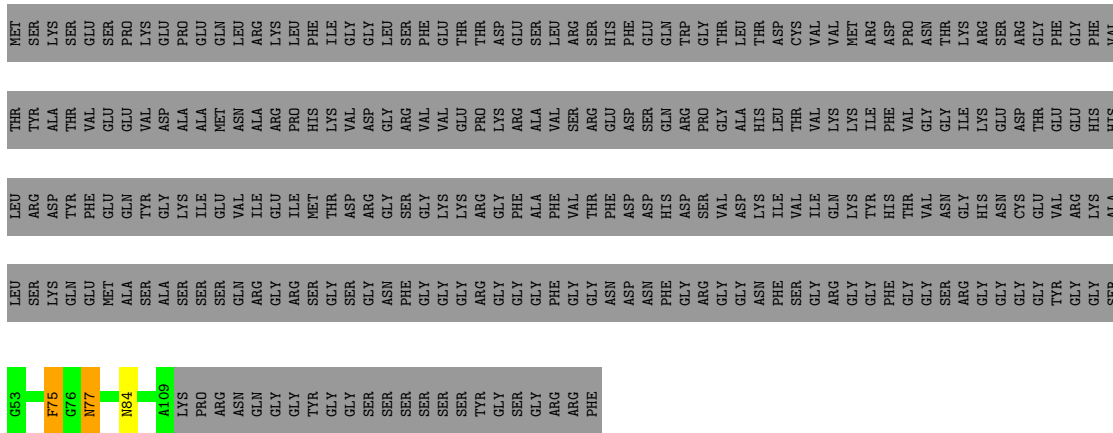
- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

Chain K: 17% 82%

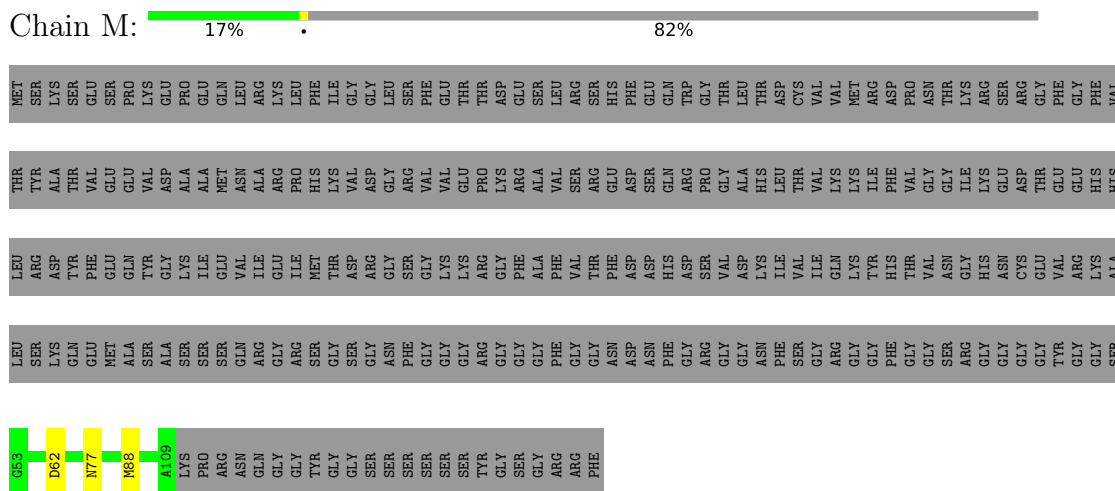


- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

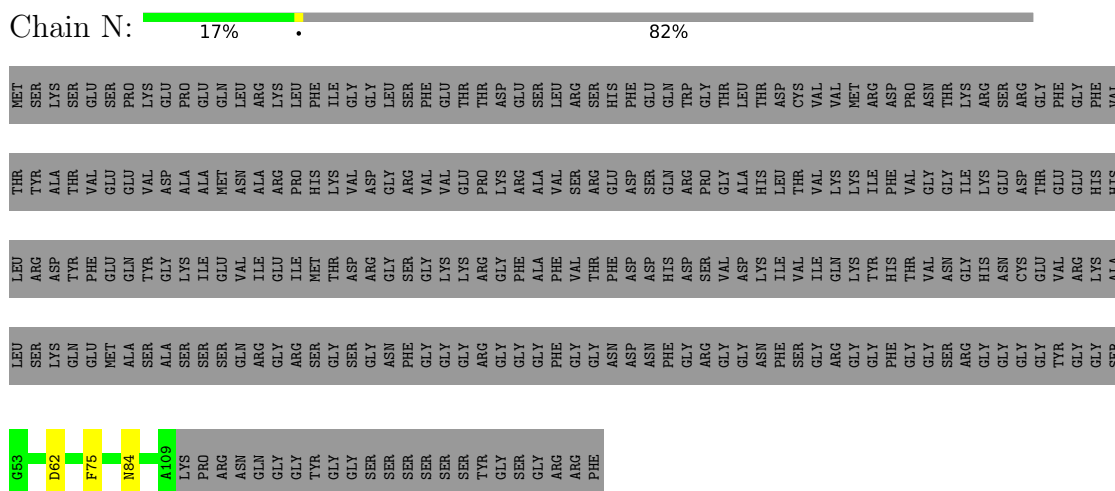
Chain L: 17% 82%



- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

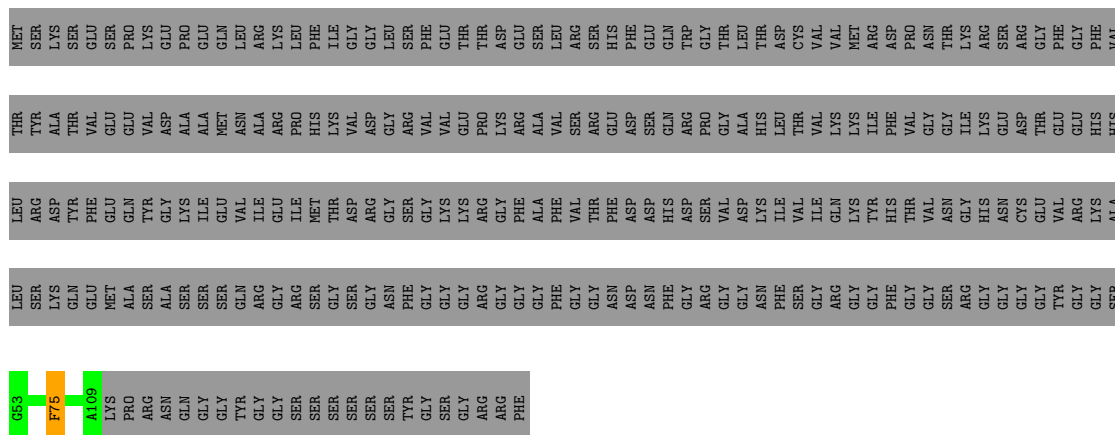


- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

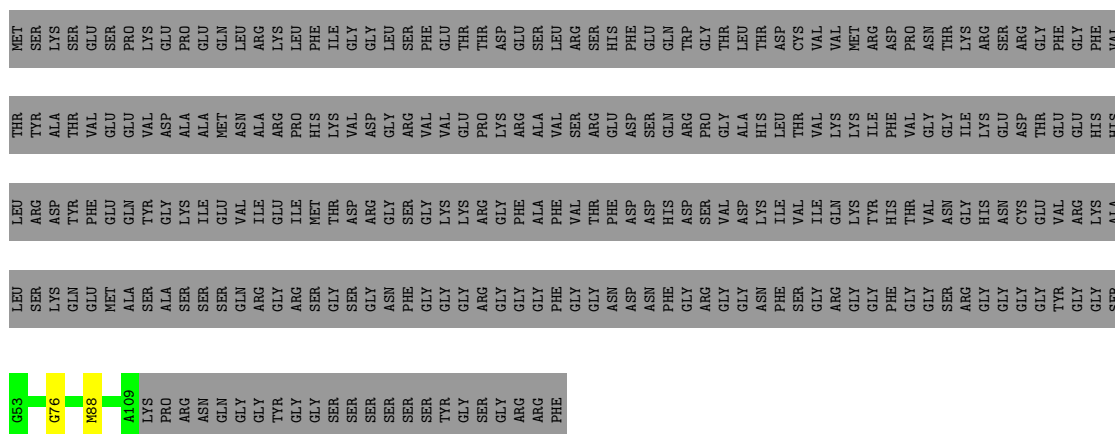


- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

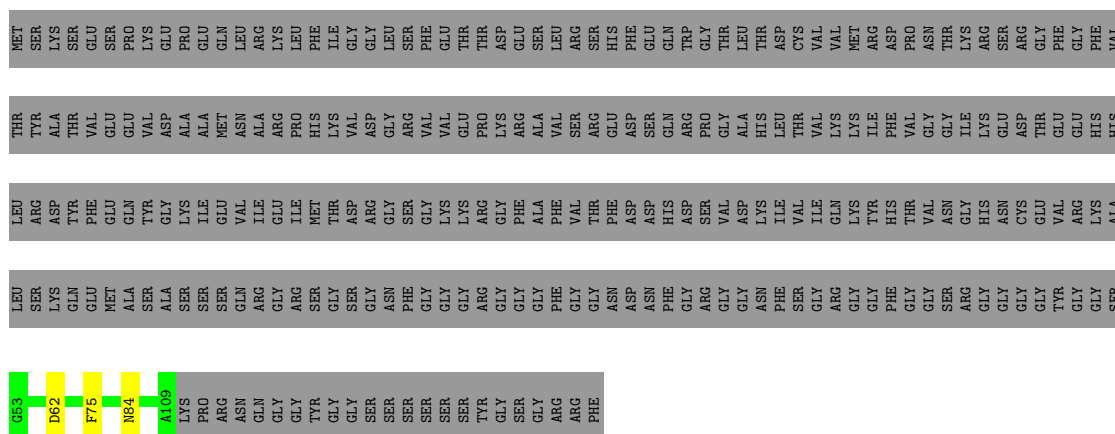




- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1



- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1



- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1



G5S	LEU	LEU	LEU	THR	MET
	SER	SER	ASP	TYR	SER
F7S	LYS	LYS	ASP	ALA	LYS
	GLN	GLN	TYR	THR	SER
A1G9	GLU	GLU	PHE	VAL	GLU
LYS	MET	GLN	GLU	GLU	SER
PRO	ALA	GLN	TYR	VAL	PRO
ARG	SER	ARG	GLY	ASP	LYS
ASN	ALA	GLY	GLY	ASP	GLU
GLN	SER	LYS	LYS	ALA	PRO
GLY	SER	ILE	ILE	ALA	GLU
GLY	SER	GLU	GLU	MET	GLN
TYR	GLN	VAL	VAL	ASN	LEU
GLY	ARG	ILE	ILE	ALA	ARG
GLY	GLY	GLU	GLU	LYS	ARG
SER	ARG	ILE	ILE	PRO	LEU
SER	SER	MET	THR	HIS	PHE
SER	GLY	THR	ASP	LYS	ILE
SER	SER	ASP	VAL	VAL	GLY
SER	GLY	ARG	ASP	ASP	GLY
SER	ASN	GLY	GLY	ARG	LEU
TYR	PHE	SER	SER	ARG	PHE
GLY	GLY	GLY	VAL	VAL	GLY
SER	GLY	LYS	VAL	GLU	THR
GLY	GLY	LYS	GLU	ALA	GLU
ARG	ARG	ARG	ASP	ALA	LEU
ARG	GLY	ILE	LYS	HIS	THR
PHE	PHE	VAL	ILE	LEU	ASP
	GLY	VAL	VAL	THR	CYS
	GLY	GLY	LYS	VAL	VAL
	ARG	GLN	LYS	LYS	VAL
	GLY	LYS	LYS	MET	ARG
	GLY	TYR	ILE	ARG	ARG
	PHE	HIS	PHE	ASP	ASP
	GLY	THR	THR	PRO	THR
	GLY	VAL	GLY	GLY	ASN
	SER	ASN	ILE	LYS	THR
	ARG	HIS	GLY	LYS	ARG
	GLY	ASN	GLU	SER	SER
	GLY	CYS	ASP	ARG	ARG
	TYR	VAL	GLY	THR	PHE
	GLY	VAL	GLY	GLU	GLY
	GLY	ARG	ARG	GLU	PHE
	SER	LYS	VAL	HIS	VAL

- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

Chain S:  17% 82%

G53	LEU	LEU	LEU	THR	MET
	SER	ARG	TYR	SER	
	LYS	ASP	ALA	ALA	
	GLN	TYR	THR	SER	
	MET	PHE	VAL	GLU	
	ALA	GLU	GLU	PRO	
	SER	TYR	VAL	LYS	
	ALA	GLY	ASP	GLU	
	ALA	LYS	ALA	PRO	
	GLN	ILE	ALA	GLU	
A169	SER	ILE	ALA	ALA	
	SER	GLU	MET	GLN	
	ARG	VAL	ASN	LEU	
	ASN	ILE	ALA	ARG	
	GLN	GLU	ARG	LYS	
	GLY	ILE	PRO	LEU	
	TYR	MET	HIS	PHE	
	GLY	THR	LYS	ILE	
	GLY	ASP	VAL	GLY	
	GLY	ARG	ASP	GLY	
Y56	SER	ARG	GLY	LEU	
	ASN	GLY	GLY	SER	
	SER	PHE	SER	ARG	
	SER	GLY	GLY	VAL	
	SER	GLY	LYS	VAL	
	TYR	ARG	GLY	PRO	
	GLY	PHE	ALA	GLU	
	GLY	PHE	VAL	LEU	
	ARG	GLY	VAL	LEU	
	PHE	THR	ARG	ARG	
N61	ASN	PHE	THR	SER	
	ASP	ASP	GLU	HIS	
	ASN	ASP	SER	GLU	
	PHE	HIS	GLN	GLN	
	GLY	ASP	ARG	TRP	
	GLY	VAL	GLY	THR	
	ASN	LYS	ALA	LEU	
	GLY	LYS	HIS	THR	
	PHE	ILE	LEU	ASP	
	SER	VAL	THR	CYS	
W88	GLY	ILE	VAL	VAL	
	ARG	GLN	LYS	VAL	
	GLY	LYS	MET	LYS	
	PHE	TYR	ILE	ARG	
	GLY	HIS	PHE	ASP	
	GLY	THR	VAL	PRO	
	SER	VAL	GLY	ASN	
	ARG	GLY	ILE	LYS	
	GLY	HIS	LYS	ARG	
	GLY	ASN	GLU	SER	
A169	GLY	CYS	ASP	ARG	
	GLY	VAL	THR	PHE	
	TYR	VAL	GLU	GLY	
	GLY	ARG	GLU	GLY	
	SER	LYS	HIS	PHE	
	GLY	ALA	THR	VAL	
	GLY	THR	GLY	THR	
	GLY	ASN	GLY	ASN	
	GLY	GLY	ILE	LYS	
	GLY	GLY	LYS	ARG	

- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

Chain T:  17% 82%

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-2.94, -2.94°, rise=4.83, 4.83 Å, axial sym=C1, C1	Depositor
Number of segments used	100000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	0.171	Depositor
Minimum map value	-0.087	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.007	Depositor
Map size (Å)	332.8, 332.8, 332.8	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	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	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.13	0/415	0.41	0/553
1	B	0.15	0/415	0.46	0/553
1	C	0.16	0/415	0.45	0/553
1	D	0.15	0/415	0.43	0/553
1	E	0.16	0/415	0.44	0/553
1	F	0.16	0/415	0.45	0/553
1	G	0.15	0/415	0.44	0/553
1	H	0.15	0/415	0.46	0/553
1	I	0.15	0/415	0.43	0/553
1	J	0.15	0/415	0.43	0/553
1	K	0.15	0/415	0.43	0/553
1	L	0.16	0/415	0.44	0/553
1	M	0.15	0/415	0.44	0/553
1	N	0.15	0/415	0.45	0/553
1	O	0.15	0/415	0.44	0/553
1	P	0.15	0/415	0.46	0/553
1	Q	0.16	0/415	0.45	0/553
1	R	0.15	0/415	0.40	0/553
1	S	0.15	0/415	0.39	0/553
1	T	0.15	0/415	0.38	0/553
All	All	0.15	0/8300	0.43	0/11060

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 [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	A	403	0	324	1	0
1	B	403	0	324	1	0
1	C	403	0	324	1	0
1	D	403	0	324	0	0
1	E	403	0	324	0	0
1	F	403	0	324	1	0
1	G	403	0	324	1	0
1	H	403	0	324	3	0
1	I	403	0	324	1	0
1	J	403	0	324	2	0
1	K	403	0	324	3	0
1	L	403	0	324	3	0
1	M	403	0	324	2	0
1	N	403	0	324	2	0
1	O	403	0	324	1	0
1	P	403	0	324	1	0
1	Q	403	0	324	2	0
1	R	403	0	324	0	0
1	S	403	0	324	3	0
1	T	403	0	324	3	0
All	All	8060	0	6480	19	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 1.

All (19) 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:S:88:MET:HE1	1:T:84:ASN:HB3	1.85	0.57
1:L:77:ASN:OD1	1:M:77:ASN:ND2	2.36	0.55
1:A:88:MET:HE1	1:B:84:ASN:HB3	1.90	0.53
1:S:61:ASN:OD1	1:T:61:ASN:ND2	2.35	0.51
1:P:88:MET:HE1	1:Q:84:ASN:HB3	1.94	0.50
1:M:88:MET:HE1	1:N:84:ASN:HB3	1.94	0.49
1:J:61:ASN:OD1	1:K:61:ASN:ND2	2.41	0.46
1:G:88:MET:HE1	1:H:84:ASN:HB3	1.99	0.44
1:H:88:MET:HE1	1:I:84:ASN:HB3	2.00	0.43
1:Q:75:PHE:CD1	1:Q:75:PHE:N	2.87	0.42
1:H:75:PHE:CD1	1:H:75:PHE:N	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:75:PHE:CD1	1:C:75:PHE:N	2.88	0.41
1:F:75:PHE:CD1	1:F:75:PHE:N	2.87	0.41
1:J:88:MET:HE1	1:K:84:ASN:HB3	2.02	0.41
1:N:75:PHE:N	1:N:75:PHE:CD1	2.88	0.41
1:S:56:TYR:OH	1:T:61:ASN:ND2	2.53	0.41
1:L:75:PHE:CD1	1:L:75:PHE:N	2.88	0.41
1:K:88:MET:HE1	1:L:84:ASN:HB3	2.02	0.41
1:O:75:PHE:N	1:O:75:PHE:CD1	2.89	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	55/320 (17%)	54 (98%)	0	1 (2%)	6	33
1	B	55/320 (17%)	51 (93%)	4 (7%)	0	100	100
1	C	55/320 (17%)	52 (94%)	3 (6%)	0	100	100
1	D	55/320 (17%)	51 (93%)	4 (7%)	0	100	100
1	E	55/320 (17%)	51 (93%)	4 (7%)	0	100	100
1	F	55/320 (17%)	51 (93%)	4 (7%)	0	100	100
1	G	55/320 (17%)	52 (94%)	3 (6%)	0	100	100
1	H	55/320 (17%)	50 (91%)	4 (7%)	1 (2%)	6	33
1	I	55/320 (17%)	52 (94%)	3 (6%)	0	100	100
1	J	55/320 (17%)	53 (96%)	2 (4%)	0	100	100
1	K	55/320 (17%)	51 (93%)	4 (7%)	0	100	100
1	L	55/320 (17%)	52 (94%)	3 (6%)	0	100	100
1	M	55/320 (17%)	52 (94%)	2 (4%)	1 (2%)	6	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	N	55/320 (17%)	51 (93%)	3 (6%)	1 (2%)	6	33
1	O	55/320 (17%)	52 (94%)	3 (6%)	0	100	100
1	P	55/320 (17%)	50 (91%)	4 (7%)	1 (2%)	6	33
1	Q	55/320 (17%)	52 (94%)	2 (4%)	1 (2%)	6	33
1	R	55/320 (17%)	53 (96%)	2 (4%)	0	100	100
1	S	55/320 (17%)	53 (96%)	2 (4%)	0	100	100
1	T	55/320 (17%)	54 (98%)	1 (2%)	0	100	100
All	All	1100/6400 (17%)	1037 (94%)	57 (5%)	6 (0%)	26	58

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	N	62	ASP
1	Q	62	ASP
1	H	62	ASP
1	M	62	ASP
1	P	76	GLY
1	A	62	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	36/244 (15%)	36 (100%)	0	100	100
1	B	36/244 (15%)	36 (100%)	0	100	100
1	C	36/244 (15%)	35 (97%)	1 (3%)	38	65
1	D	36/244 (15%)	36 (100%)	0	100	100
1	E	36/244 (15%)	36 (100%)	0	100	100
1	F	36/244 (15%)	35 (97%)	1 (3%)	38	65
1	G	36/244 (15%)	36 (100%)	0	100	100
1	H	36/244 (15%)	36 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	36/244 (15%)	35 (97%)	1 (3%)	38	65
1	J	36/244 (15%)	34 (94%)	2 (6%)	19	50
1	K	36/244 (15%)	35 (97%)	1 (3%)	38	65
1	L	36/244 (15%)	34 (94%)	2 (6%)	19	50
1	M	36/244 (15%)	36 (100%)	0	100	100
1	N	36/244 (15%)	36 (100%)	0	100	100
1	O	36/244 (15%)	35 (97%)	1 (3%)	38	65
1	P	36/244 (15%)	36 (100%)	0	100	100
1	Q	36/244 (15%)	36 (100%)	0	100	100
1	R	36/244 (15%)	35 (97%)	1 (3%)	38	65
1	S	36/244 (15%)	36 (100%)	0	100	100
1	T	36/244 (15%)	36 (100%)	0	100	100
All	All	720/4880 (15%)	710 (99%)	10 (1%)	57	75

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	75	PHE
1	F	75	PHE
1	I	77	ASN
1	J	75	PHE
1	J	77	ASN
1	K	77	ASN
1	L	75	PHE
1	L	77	ASN
1	O	75	PHE
1	R	75	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	92	ASN
1	B	57	ASN
1	B	61	ASN
1	B	77	ASN
1	B	92	ASN

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Mol	Chain	Res	Type
1	C	57	ASN
1	C	61	ASN
1	C	77	ASN
1	D	57	ASN
1	D	61	ASN
1	D	77	ASN
1	E	57	ASN
1	E	61	ASN
1	E	77	ASN
1	E	106	GLN
1	F	57	ASN
1	F	61	ASN
1	F	77	ASN
1	G	57	ASN
1	G	61	ASN
1	G	77	ASN
1	H	57	ASN
1	H	61	ASN
1	H	77	ASN
1	I	57	ASN
1	I	61	ASN
1	J	57	ASN
1	J	61	ASN
1	K	57	ASN
1	K	61	ASN
1	L	57	ASN
1	L	61	ASN
1	M	57	ASN
1	M	61	ASN
1	N	57	ASN
1	N	61	ASN
1	N	77	ASN
1	O	57	ASN
1	O	61	ASN
1	P	57	ASN
1	P	61	ASN
1	Q	57	ASN
1	Q	61	ASN
1	Q	77	ASN
1	R	57	ASN
1	R	61	ASN
1	R	77	ASN

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Mol	Chain	Res	Type
1	S	57	ASN
1	S	61	ASN
1	S	77	ASN
1	T	61	ASN
1	T	65	ASN
1	T	77	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

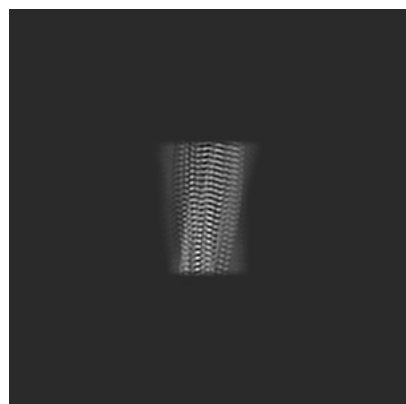
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51419. These allow visual inspection of the internal detail of the map and identification of artifacts.

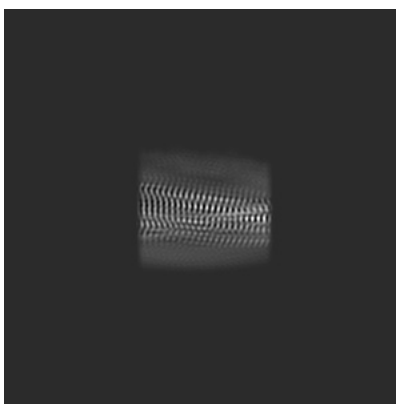
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

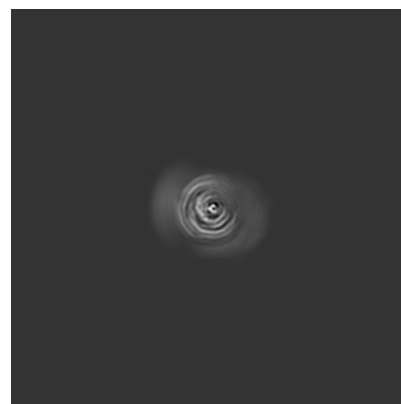
6.1.1 Primary map



X

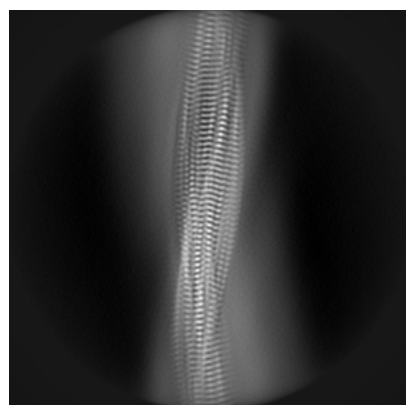


Y

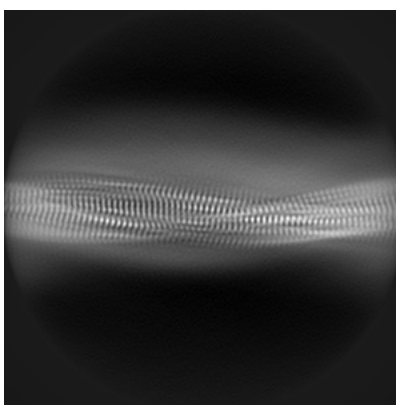


Z

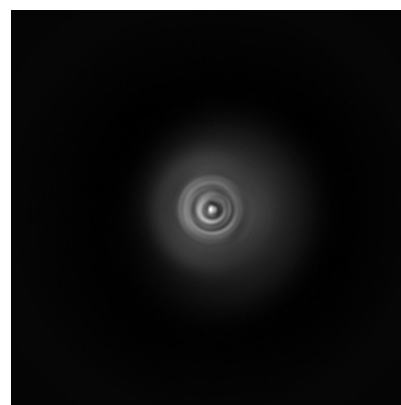
6.1.2 Raw map



X



Y

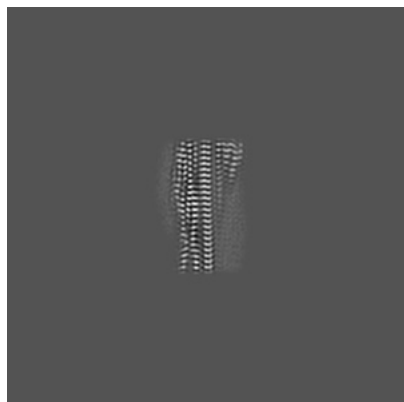


Z

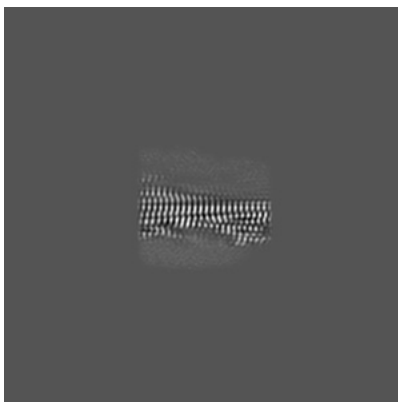
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

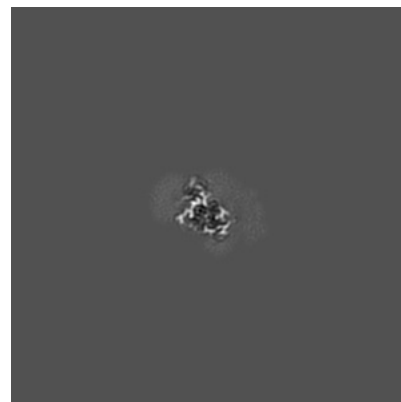
6.2.1 Primary map



X Index: 128

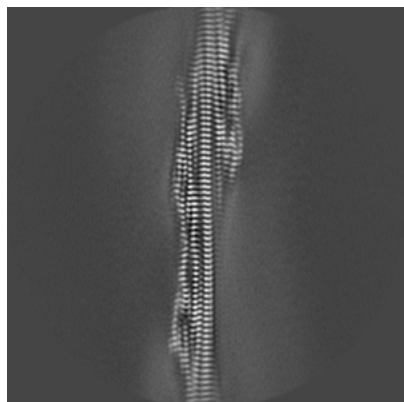


Y Index: 128

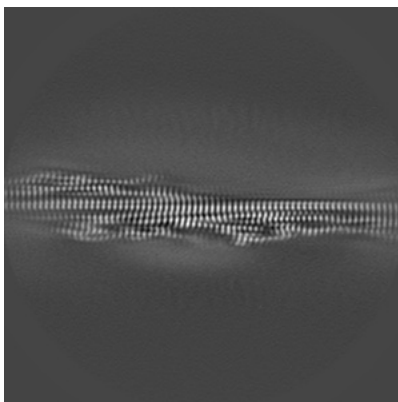


Z Index: 128

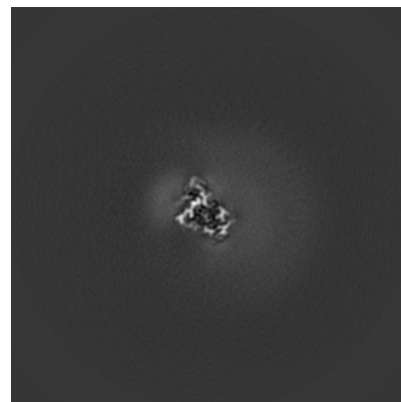
6.2.2 Raw map



X Index: 128



Y Index: 128

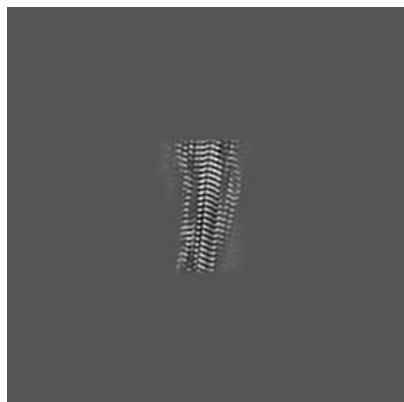


Z Index: 128

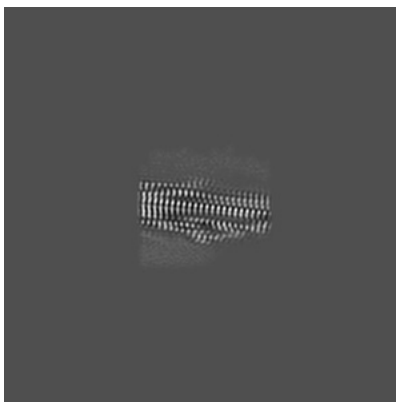
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

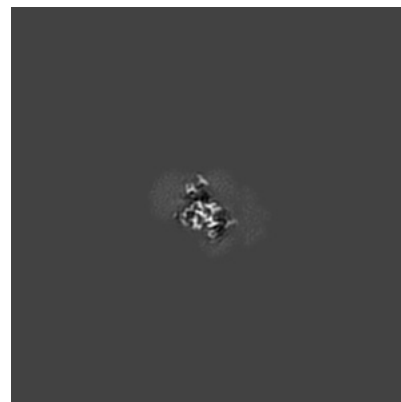
6.3.1 Primary map



X Index: 121

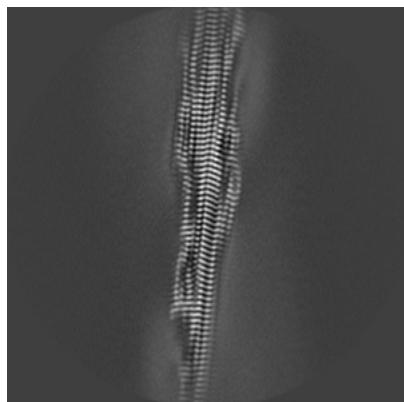


Y Index: 120

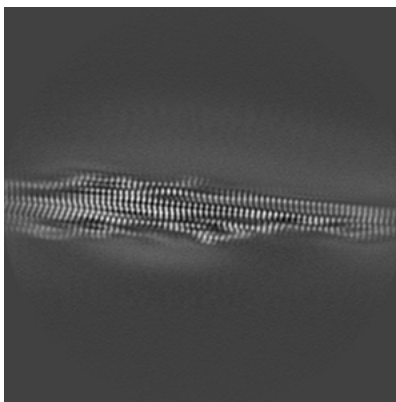


Z Index: 133

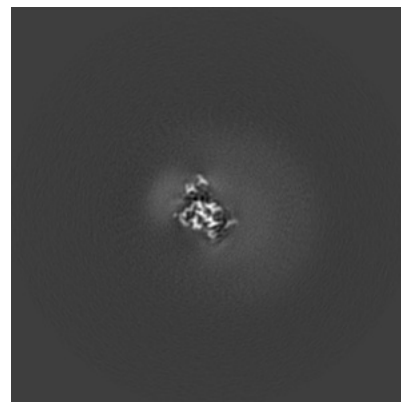
6.3.2 Raw map



X Index: 121



Y Index: 121

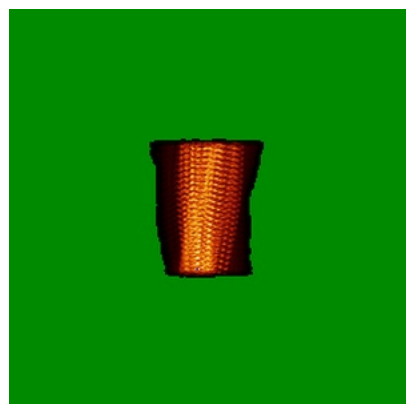


Z Index: 133

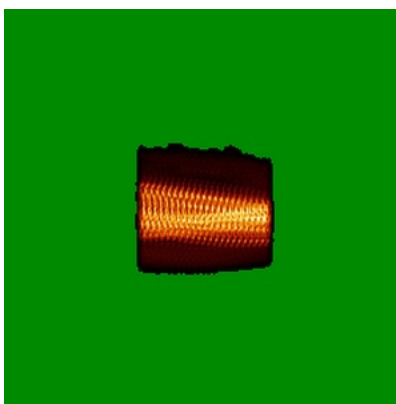
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

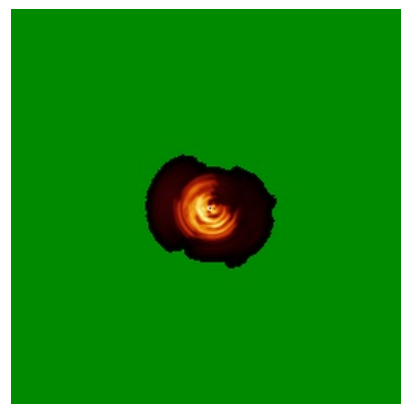
6.4.1 Primary map



X

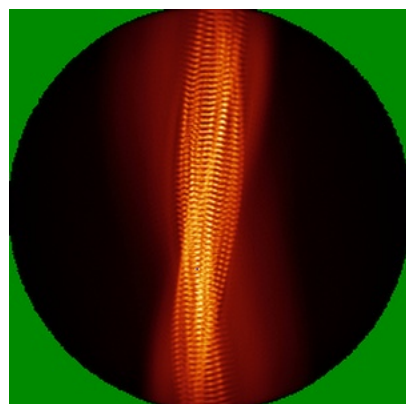


Y

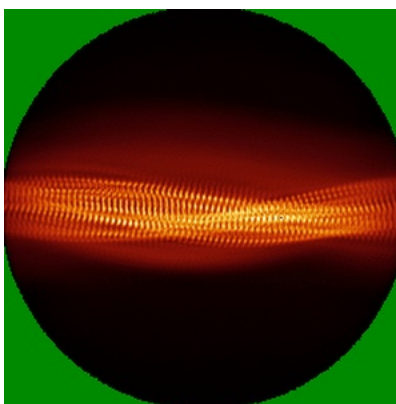


Z

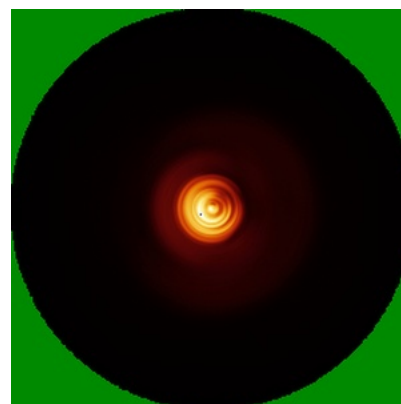
6.4.2 Raw map



X



Y

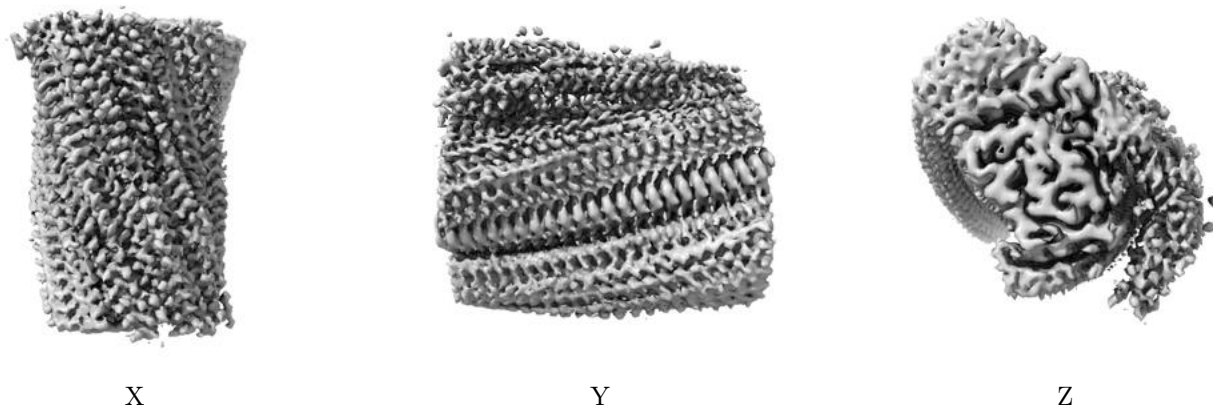


Z

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

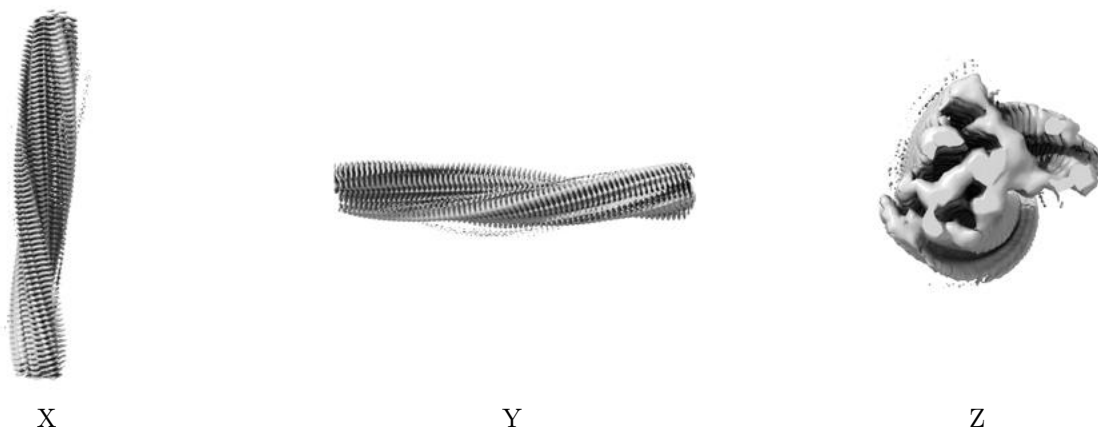
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

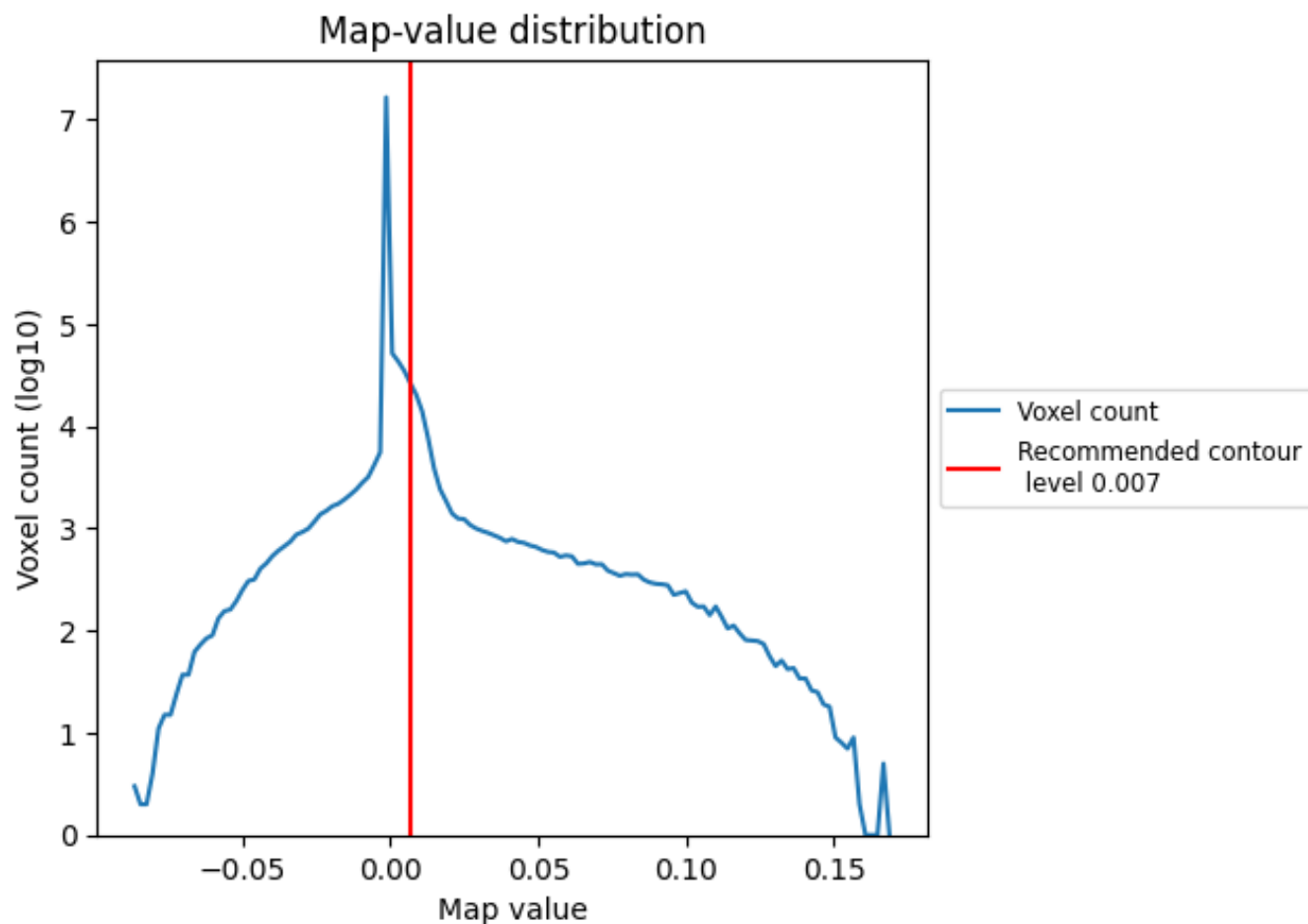
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

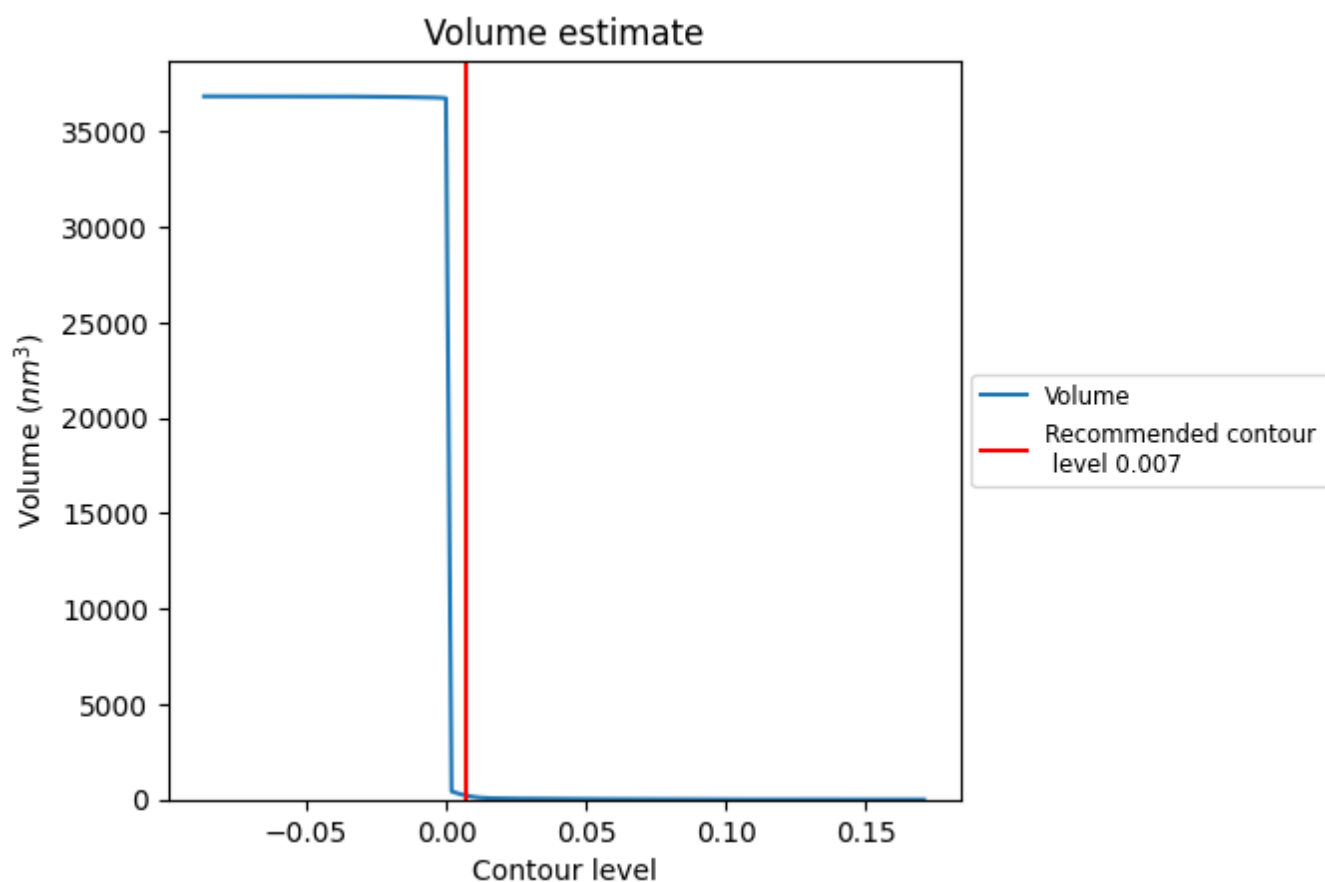
This section contains the results of statistical analysis of the map.

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.

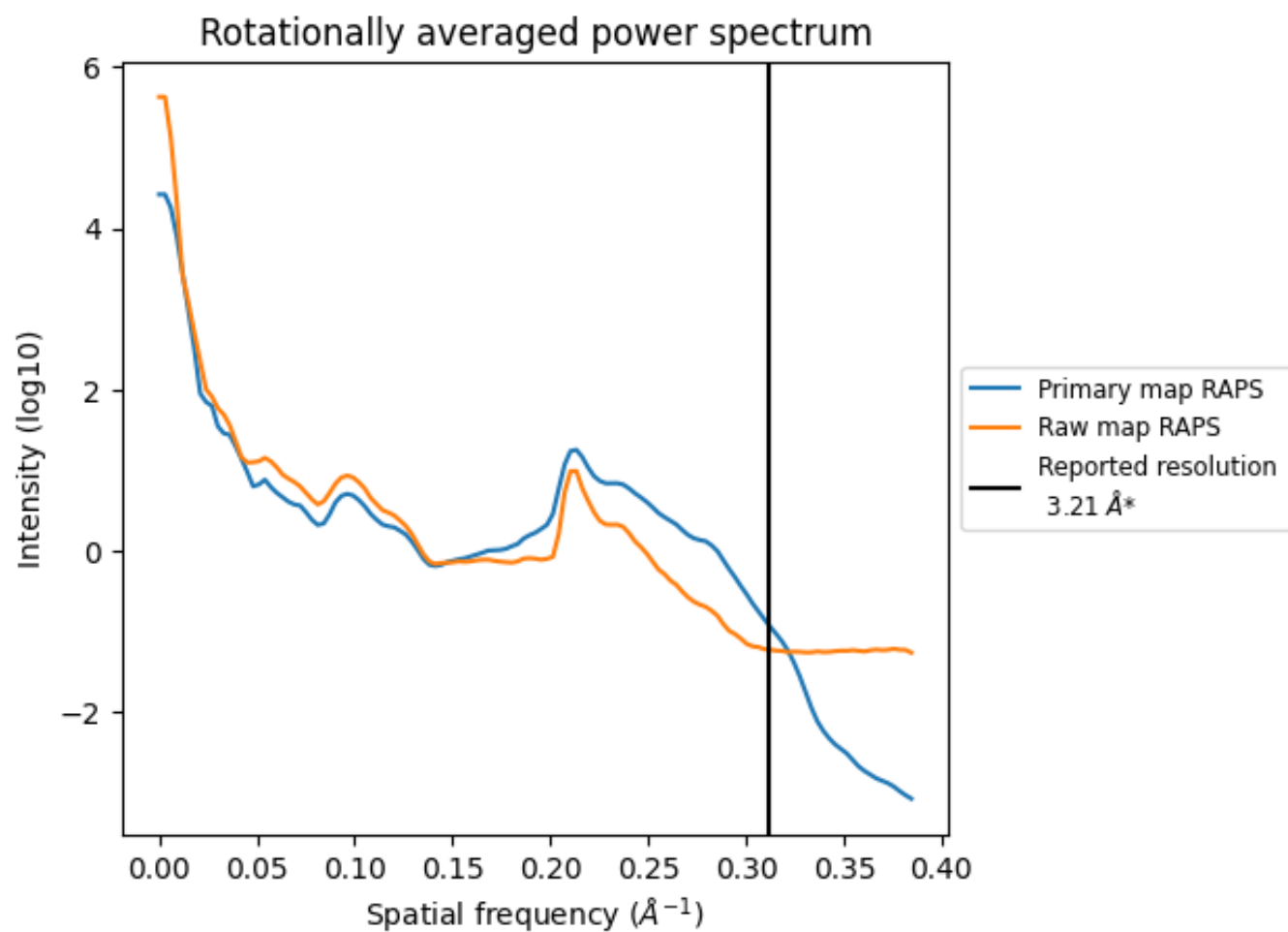
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 217 nm^3 ; this corresponds to an approximate mass of 196 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 ⓘ

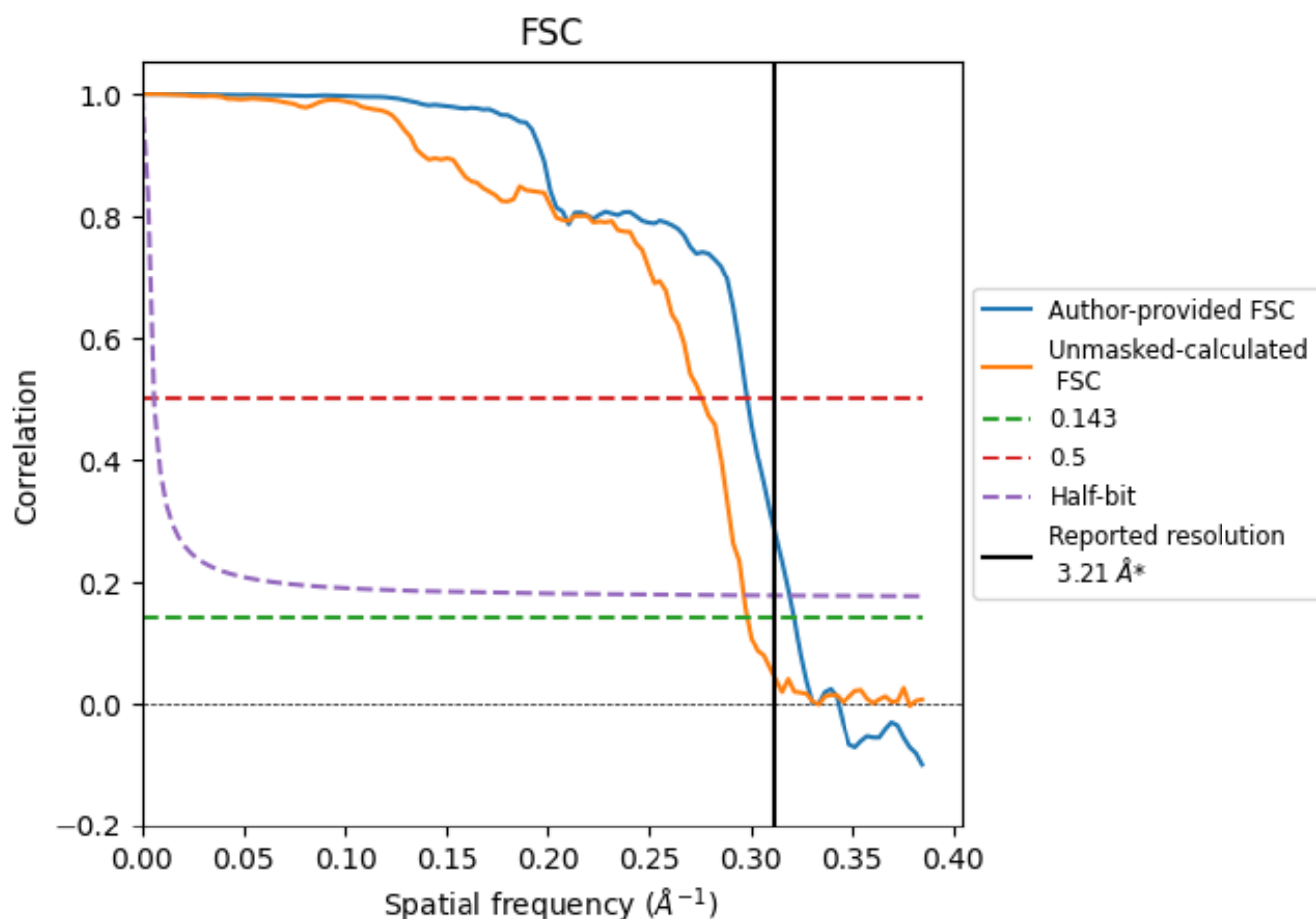


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 \AA^{-1}

8.2 Resolution estimates [i](#)

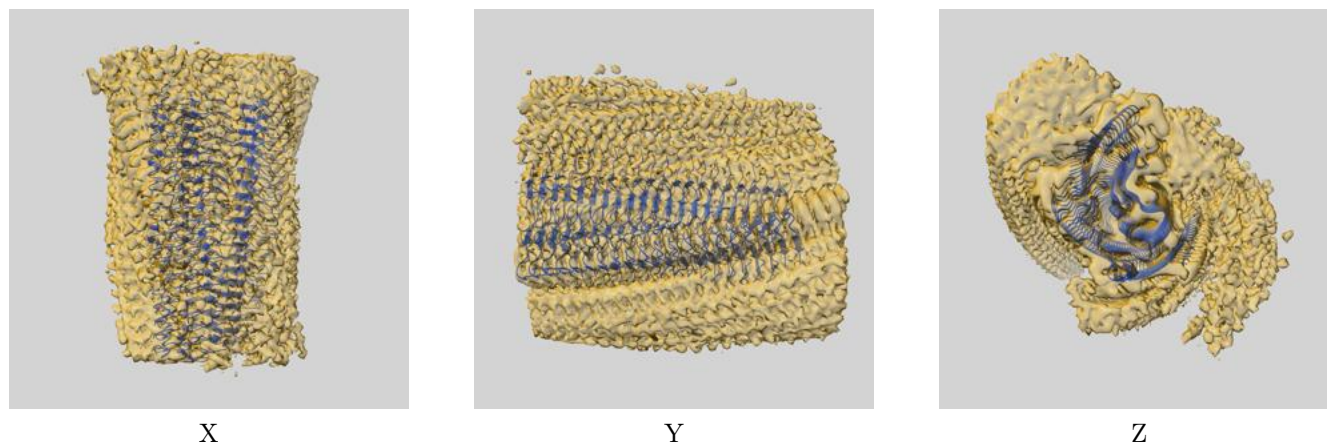
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.21	-	-
Author-provided FSC curve	3.11	3.35	3.13
Unmasked-calculated*	3.35	3.62	3.37

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

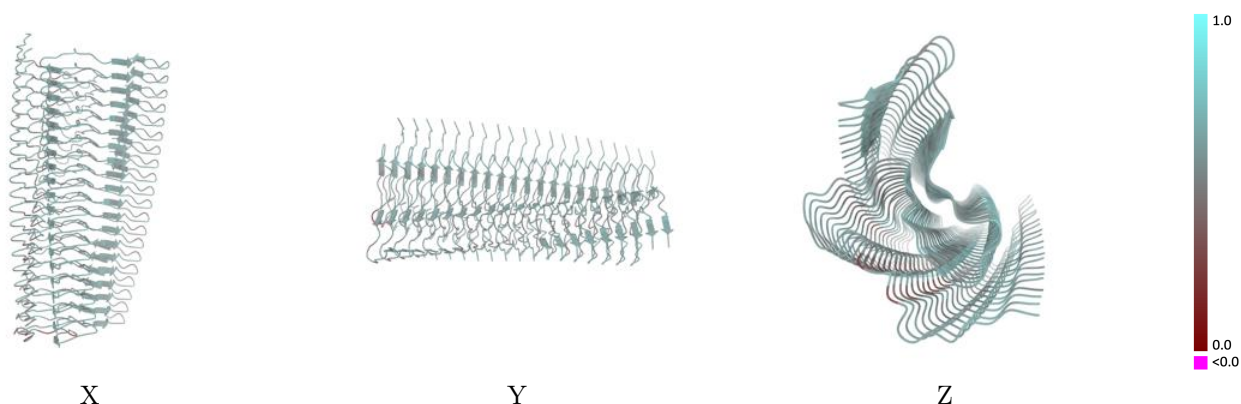
This section contains information regarding the fit between EMDB map EMD-51419 and PDB model 9GKF. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

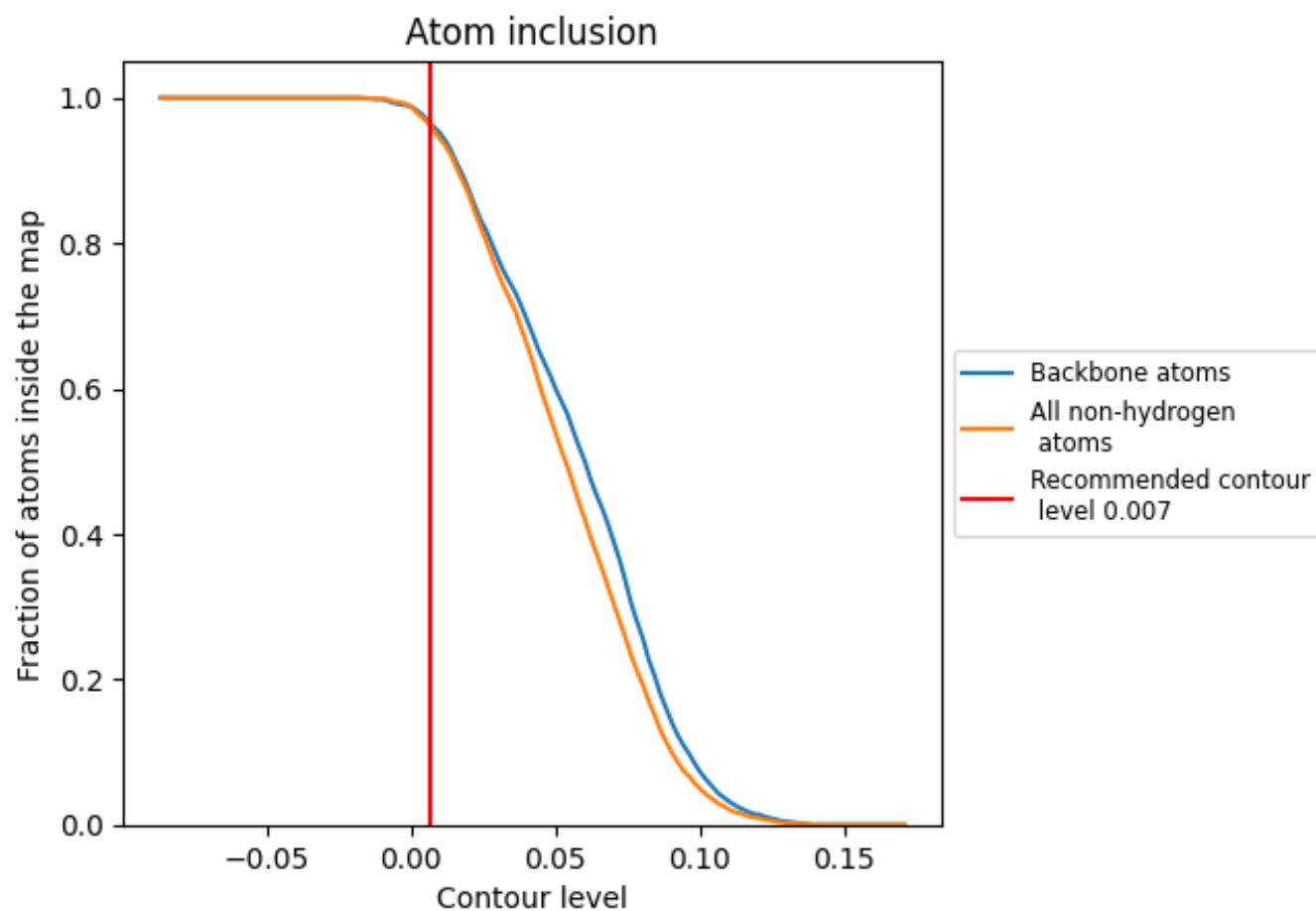


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.











































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9610	 0.5550
A	 0.7680	 0.4770
B	 0.9670	 0.5530
C	 0.9670	 0.5570
D	 0.9700	 0.5560
E	 0.9770	 0.5610
F	 0.9770	 0.5580
G	 0.9750	 0.5560
H	 0.9670	 0.5580
I	 0.9650	 0.5570
J	 0.9750	 0.5630
K	 0.9700	 0.5610
L	 0.9770	 0.5560
M	 0.9750	 0.5620
N	 0.9750	 0.5640
O	 0.9600	 0.5600
P	 0.9670	 0.5600
Q	 0.9720	 0.5570
R	 0.9750	 0.5600
S	 0.9700	 0.5570
T	 0.9670	 0.5610

