



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:06 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 wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

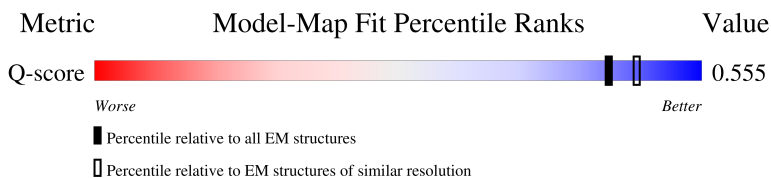
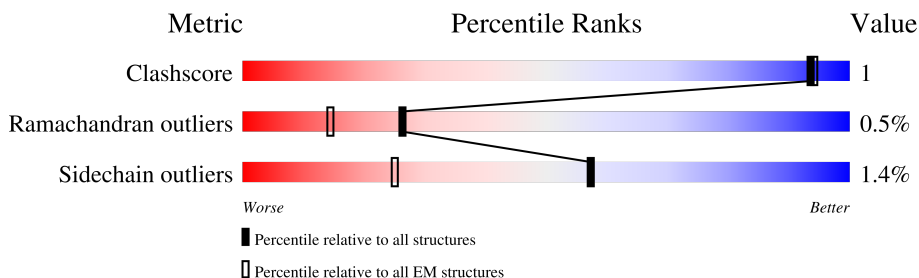
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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


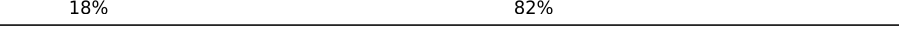

The reported resolution of this entry is 3.21 Å.

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.



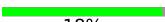





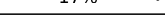
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14613 (2.71 - 3.71)

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	 18%	82%
1	F	320	 18%	82%
1	G	320	 18%	82%
1	H	320	 17%	82%
1	I	320	 17%	82%
1	J	320	 17%	82%
1	K	320	 17%	82%
1	L	320	 17%	82%
1	M	320	 17%	82%
1	N	320	 17%	82%
1	O	320	 18%	82%
1	P	320	 17%	82%
1	Q	320	 17%	82%
1	R	320	 18%	82%
1	S	320	 17%	82%
1	T	320	 17%	82%

2 Entry composition

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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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



553	F75	A109	LYS	LEU	LEU	THR	MET
			PRO	SER	ARG	THR	TYR
			ASN	GLN	ASP	ALA	ALA
			GLY	GLU	PHE	VAL	GLU
			GLY	MET	GLN	GLU	SER
			GLY	ALA	GLN	VAL	PRO
			GLY	SER	TYR	VAL	LYS
			GLN	GLY	ASP	VAL	GLU
			SER	ILE	LYS	ALA	GLN
			SER	GLU	VAL	MET	ASN
TYR	GLN	VAL	ASN	LEU			
GLY	ARG	ILE	ALA	ARG			
GLY	GLY	GLU	ARG	LYS			
SER	ARG	ILE	PRO	LEU			
SER	SER	MET	HIS	PHE			
SER	GLY	THR	LYS	ILE			
SER	SER	ASP	VAL	GLY			
SER	GLY	ARG	ASP	GLY			
SER	ASN	GLY	ARG	LEU			
TYR	PHE	GLY	VAL	PHE			
GLY	GLY	LYS	VAL	GLU			
SER	GLY	LYS	VAL	THR			
SER	GLY	ARG	GLU	GLY			
ARG	ARG	PHE	ALA	SER			
ARG	GLY	VAL	VAL	LEU			
PHE	GLY	THR	ARG	SER			
	ASN	PHE	GLU	HIS			
	ASN	ASP	SER	GLN			
	PHE	HIS	GLN	GLN			
	GLY	ASP	ARG	TRP			
	ARG	SER	GLY	THR			
	GLY	VAL	GLY	THR			
	ASN	LYS	ALA	LEU			
	ASN	LYS	HIS	THR			
	PHE	ILE	LEU	ASP			
	SER	VAL	THR	CYS			
	GLY	ILE	VAL	VAL			
	ARG	GLN	LYS	VAL			
	GLY	GLY	LYS	MET			
	PHE	GLY	TYR	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			
	GLY	CYS	ASP	ARG			
	TYR	VAL	GLY	PHE			
	GLY	ARG	GLU	GLY			
	SER	GLY	HIS	VAL			

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

Chain D:  18% 82%

[illegible]

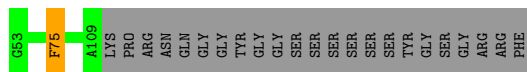
- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

Chain E: 18% 82%

G53	A109	LYS	LEU	LEU	LEU	THR	MET
		GLN	SER	ARG	ASP	TYR	SER
		GLY	LYS	LYS	ALA	ALA	LYS
		GLY	GLN	TYR	PHE	THR	SER
		ARG	GLU	GLU	VAL	GLU	GLU
		ASN	MET	GLN	GLU	GLU	SER
		ASN	ALA	TYR	GLN	VAL	PRO
		GLN	SER	TYR	LYS	LYS	LYS
		GLY	ALA	ASP	GLU	ASP	GLU
		GLY	GLY	LYS	ALA	ALA	PRO
TYR	SER	ILE	ILE	GLU	GLU		
GLY	SER	GLU	GLU	MET	GLN		
GLY	SER	VAL	VAL	ASN	LEU		
GLY	SER	ILE	ILE	ALA	ARG		
SER	SER	GLY	GLY	ARG	LYS		
SER	SER	ARG	ILE	PRO	LEU		
SER	SER	GLY	THR	HIS	PHE		
TYR	SER	GLY	ASP	VAL	GLY		
GLY	SER	ASN	GLY	GLY	GLY		
SER	SER	PHE	GLY	ARG	SER		
GLY	GLY	GLY	GLY	VAL	PHE		
ARG	GLY	GLY	LYS	VAL	GLU		
PHE	GLY	ARG	LYS	GLU	THR		
		PHE	PHE	ALA	ALA		
		GLY	VAL	VAL	LEU		
		GLY	VAL	SER	ARG		
		GLY	THR	GLU	SER		
		ASN	PHE	GLU	HIS		
		ASN	ASP	ASP	PHE		
		PHE	HIS	GLN	GLN		
		GLY	ASP	ARG	TRP		
		GLY	VAL	GLY	THR		
		GLY	ASP	ALA	LEU		
		ASN	LYS	HIS	THR		
		PHE	ILE	LEU	ASP		
		SER	VAL	THR	CYS		
		GLY	ILE	VAL	VAL		
		ARG	GLN	LYS	VAL		
		GLY	LYS	LYS	MET		
		GLY	TYR	ILE	ARG		
		PHE	HIS	PHE	ASP		
		GLY	THR	VAL	PRO		
		GLY	VAL	GLY	ASN		
		SER	GLY	GLY	THR		
		ARG	GLY	ILE	LYS		
		GLY	HIS	LYS	ARG		
		GLY	ASN	GLU	SER		
		GLY	CYS	ASP	ARG		
		GLY	GLY	THR	GLY		
		TYR	VAL	GLU	PHE		
		GLY	ARG	GLU	GLY		
		GLY	LYS	HIS	PHE		
		SER	ALA	THR	VAL		

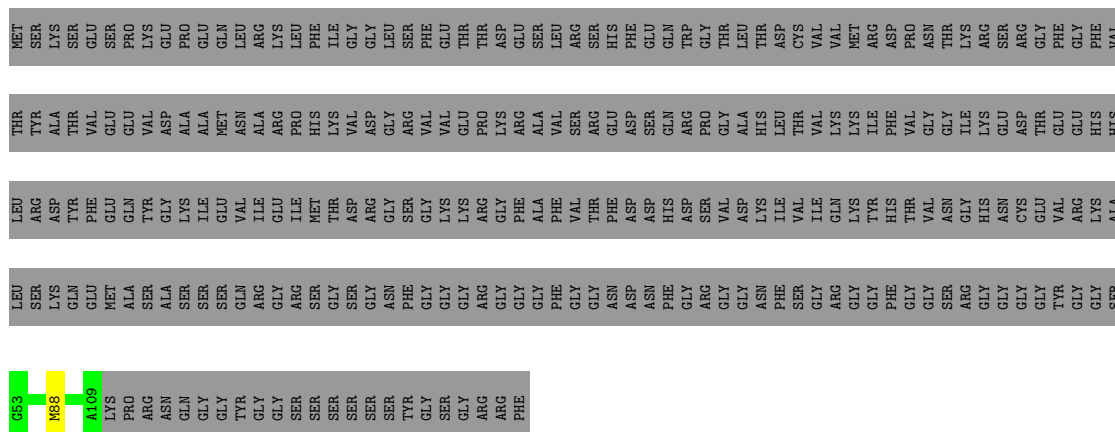
- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

Chain F:  18% 82%



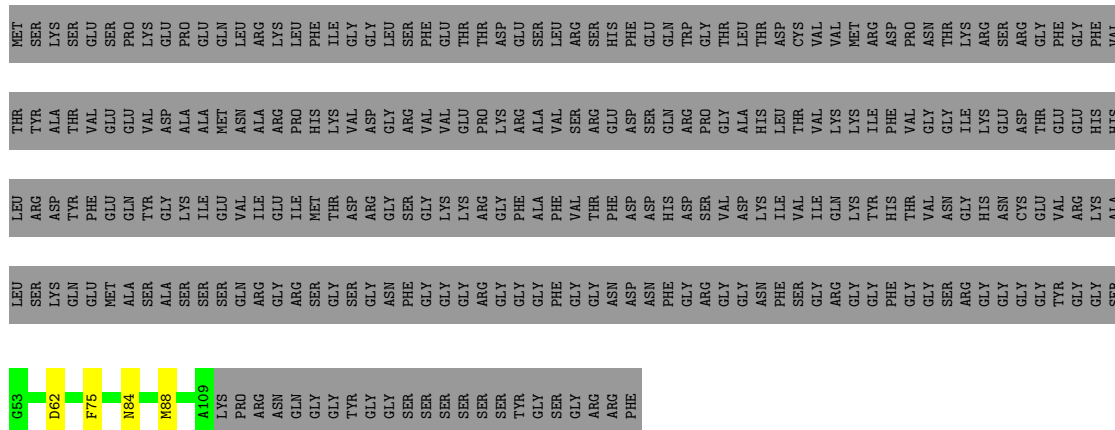
- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

Chain G:  18% 82%



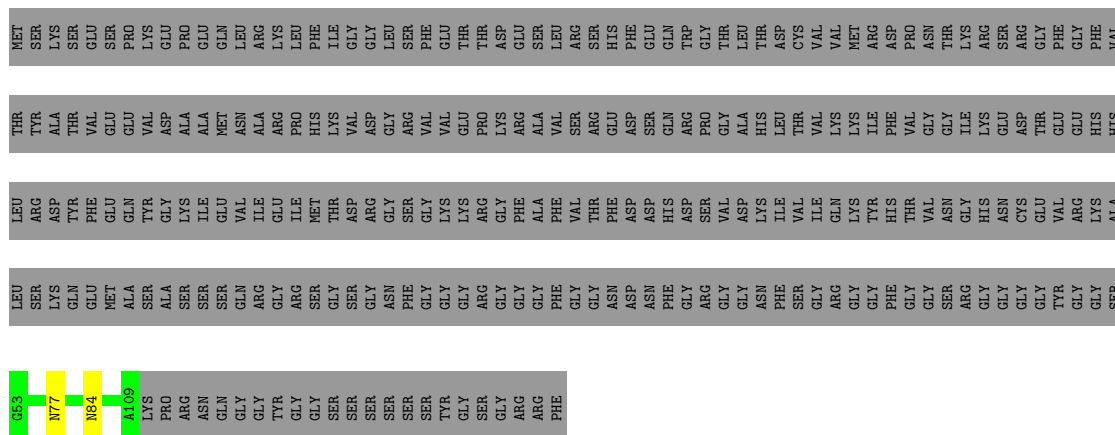
- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

Chain H: 17% 82%



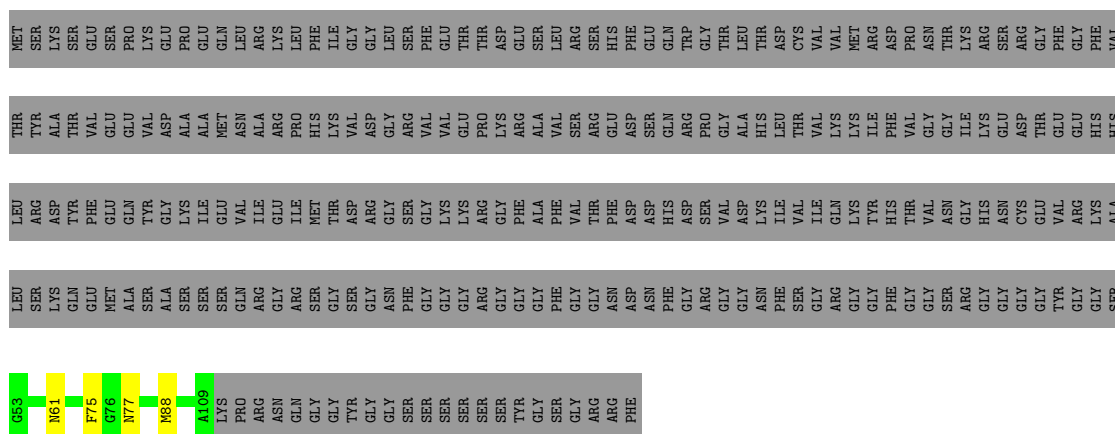
- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

Chain I: 17% : 82%



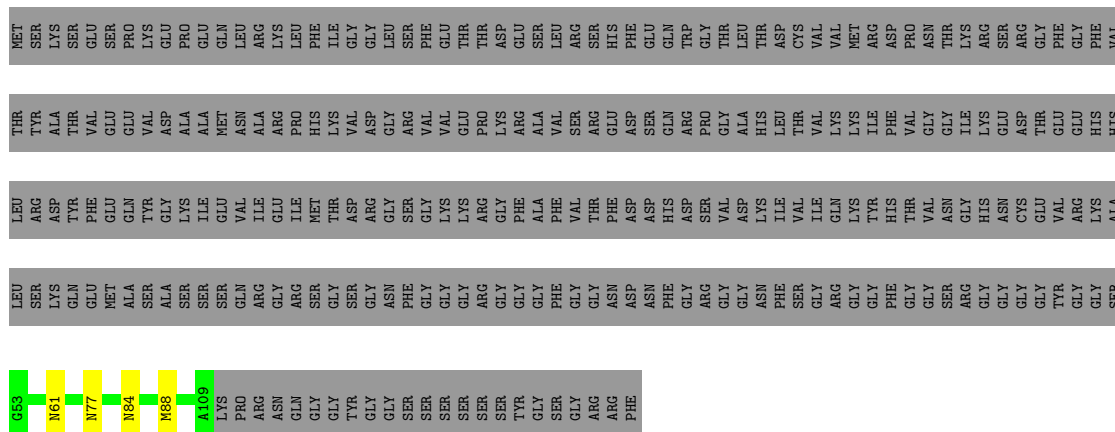
- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

Chain J:  17% : 82%



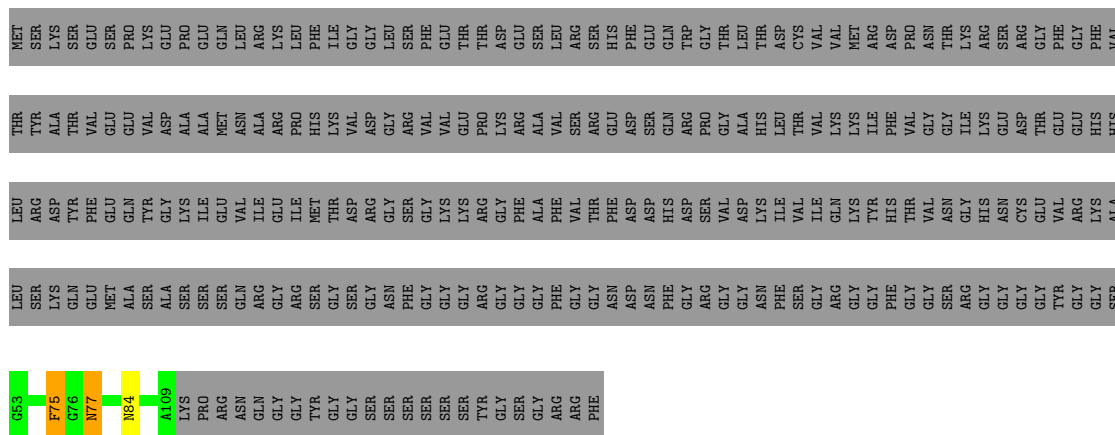
- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

Chain K: 17% 82%

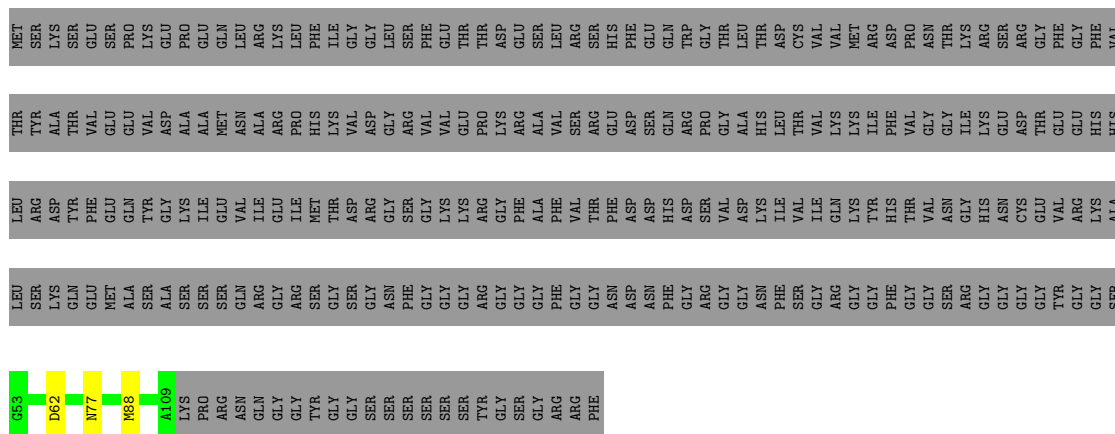


- Molecule 1: Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1

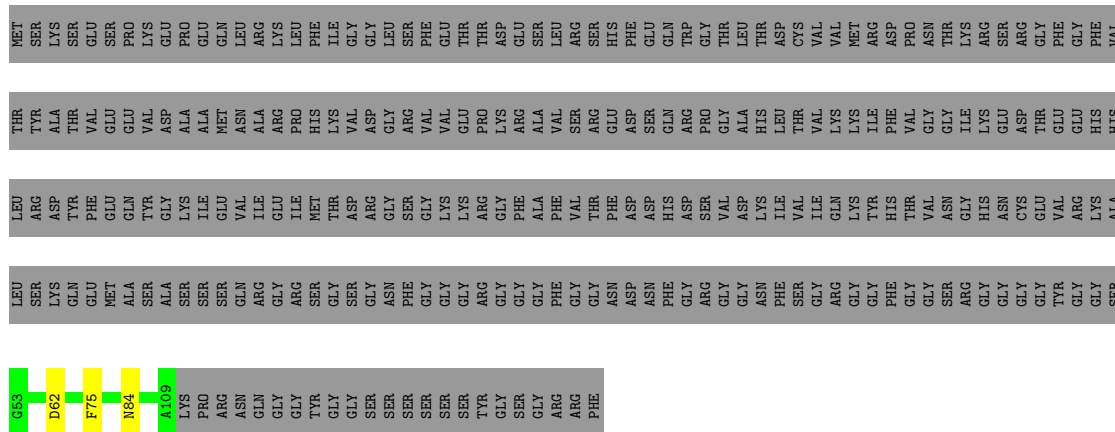
Chain L: 17% 82%



- 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



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 ($e^-/\text{\AA}^2$)	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.

The worst 5 of 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

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	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
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

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	N	62	ASP

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

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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	720/4880 (15%)	710 (99%)	10 (1%)	57 75

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	77	ASN
1	O	75	PHE
1	R	75	PHE
1	J	75	PHE
1	J	77	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	61	ASN
1	N	57	ASN
1	S	61	ASN
1	K	57	ASN
1	L	61	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

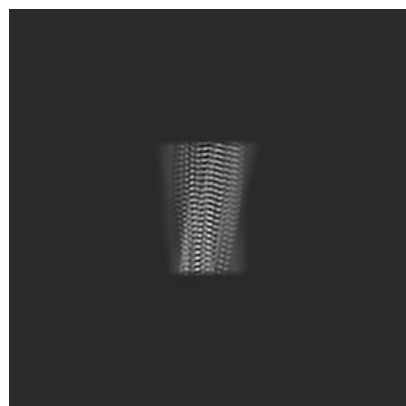
6 Map visualisation [i](#)

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.

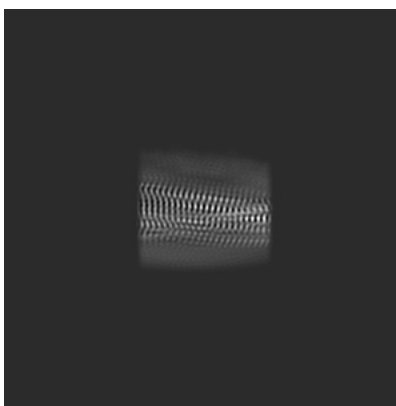
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

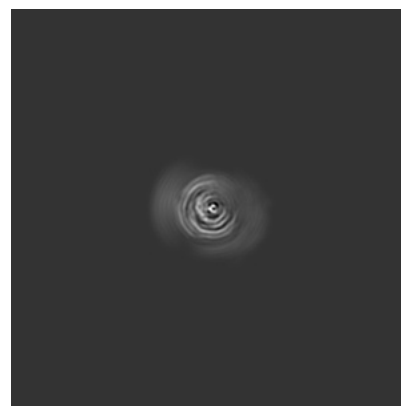
6.1.1 Primary map



X

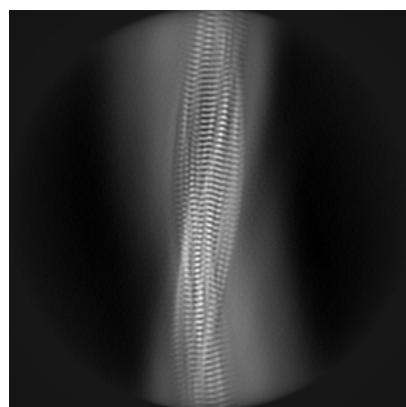


Y

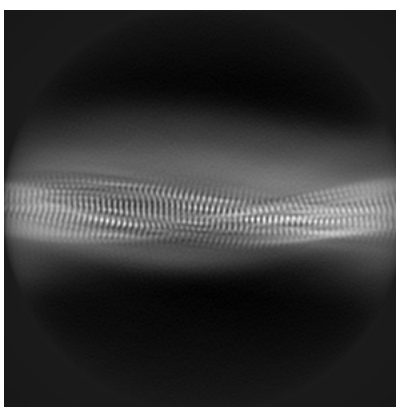


Z

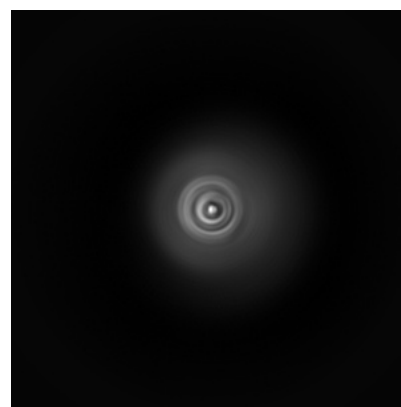
6.1.2 Raw map



X



Y

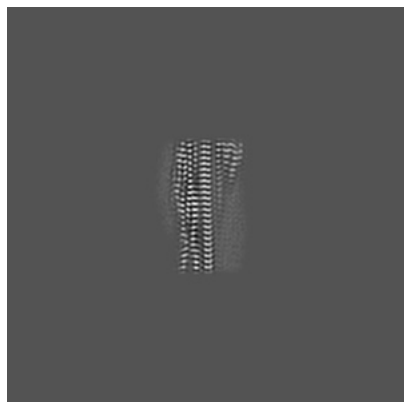


Z

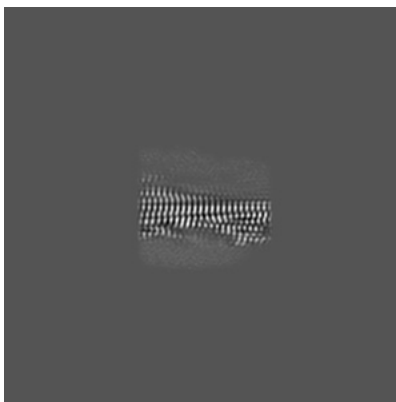
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

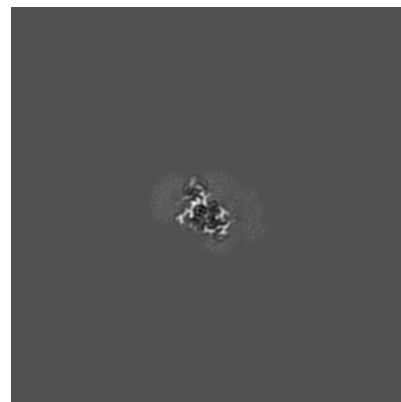
6.2.1 Primary map



X Index: 128

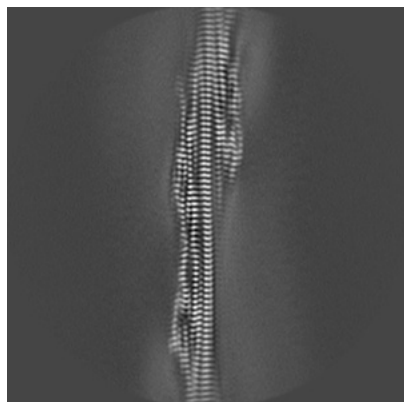


Y Index: 128

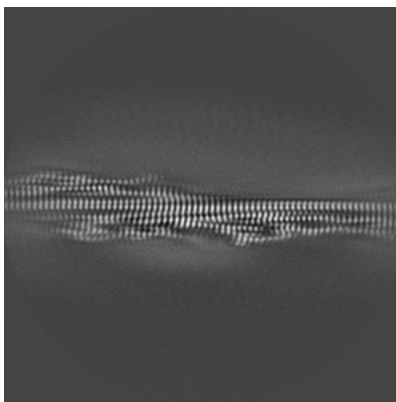


Z Index: 128

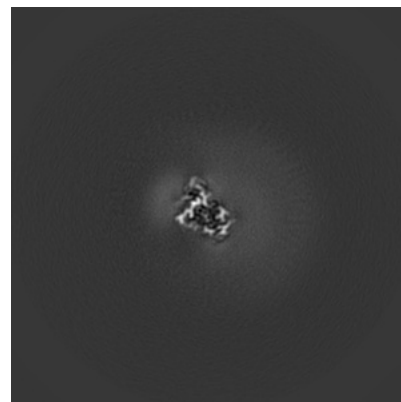
6.2.2 Raw map



X Index: 128



Y Index: 128

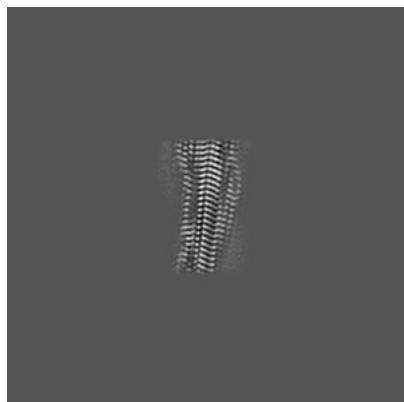


Z Index: 128

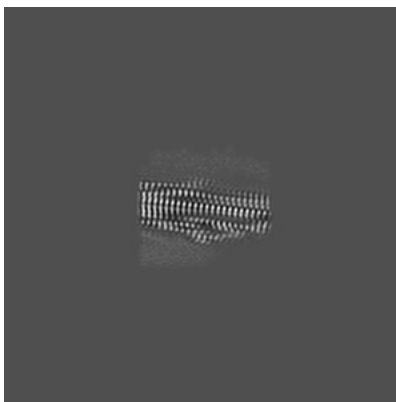
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

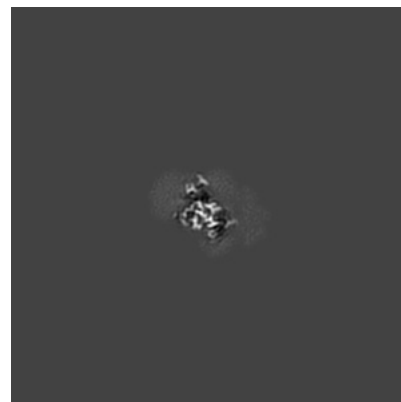
6.3.1 Primary map



X Index: 121

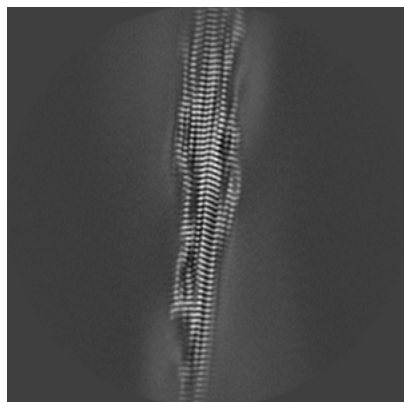


Y Index: 120

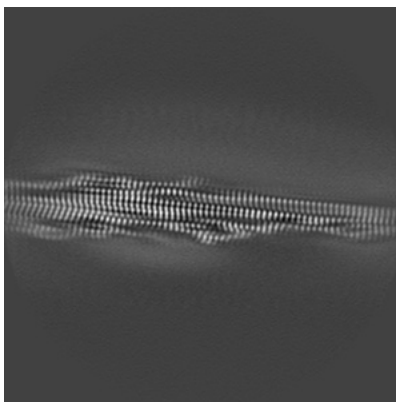


Z Index: 133

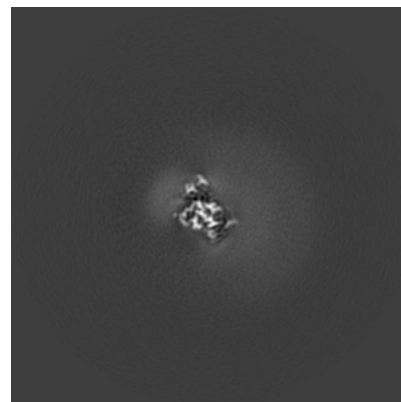
6.3.2 Raw map



X Index: 121



Y Index: 121

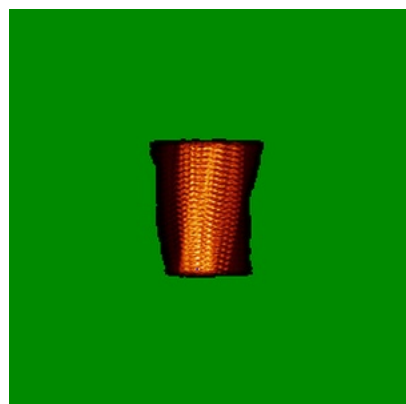


Z Index: 133

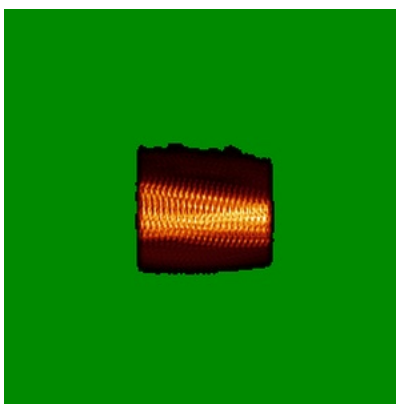
The images above show the largest variance slices of the map in three orthogonal directions.

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

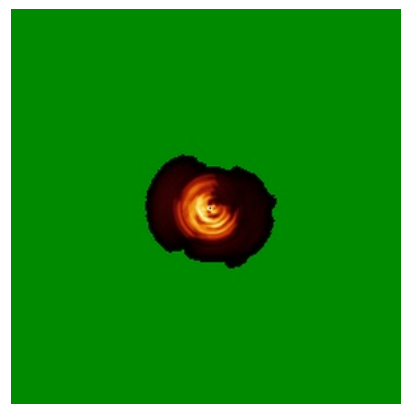
6.4.1 Primary map



X

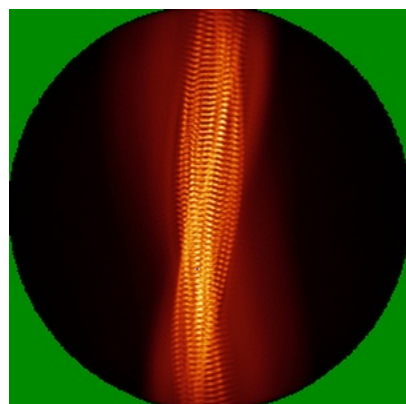


Y

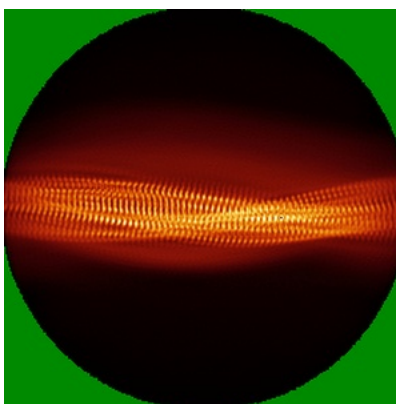


Z

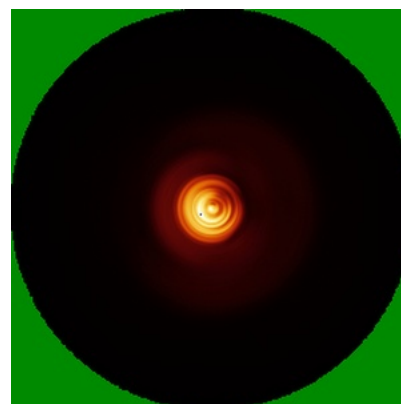
6.4.2 Raw map



X



Y

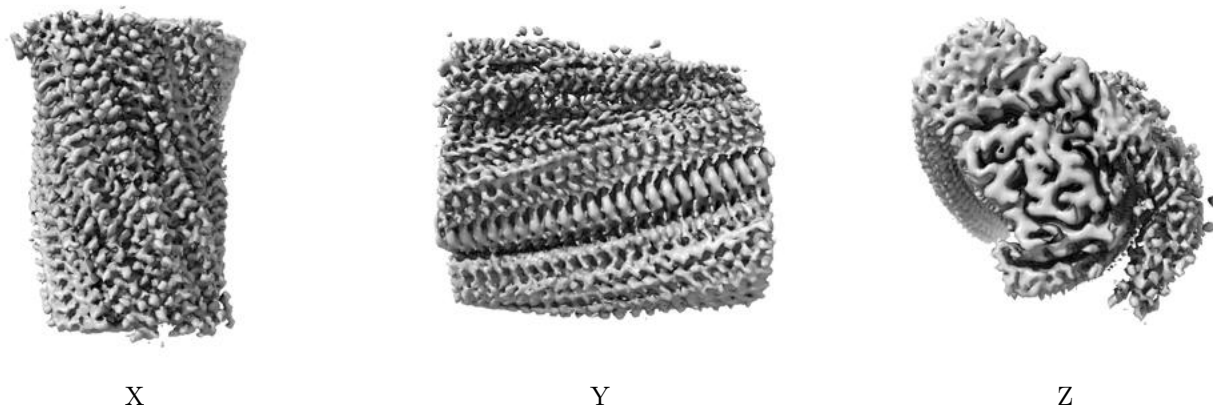


Z

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.

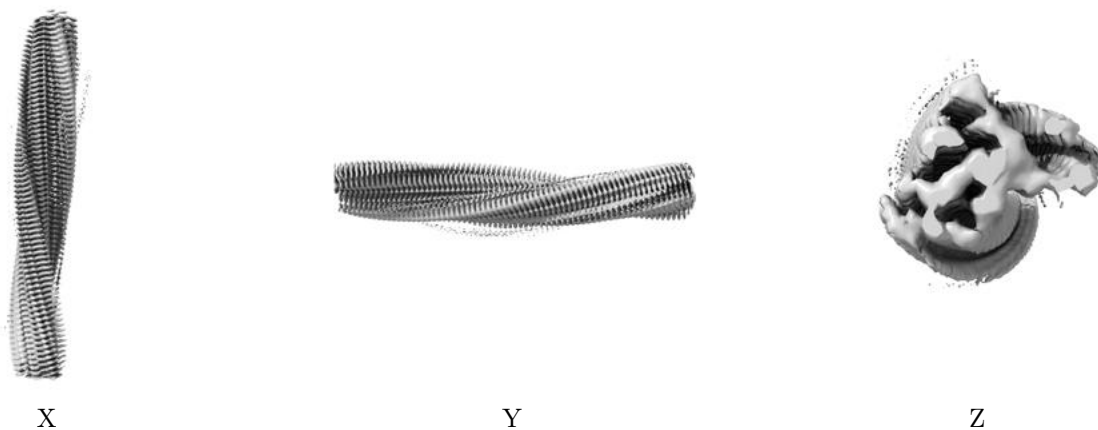
6.5 Orthogonal surface views [i](#)

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.

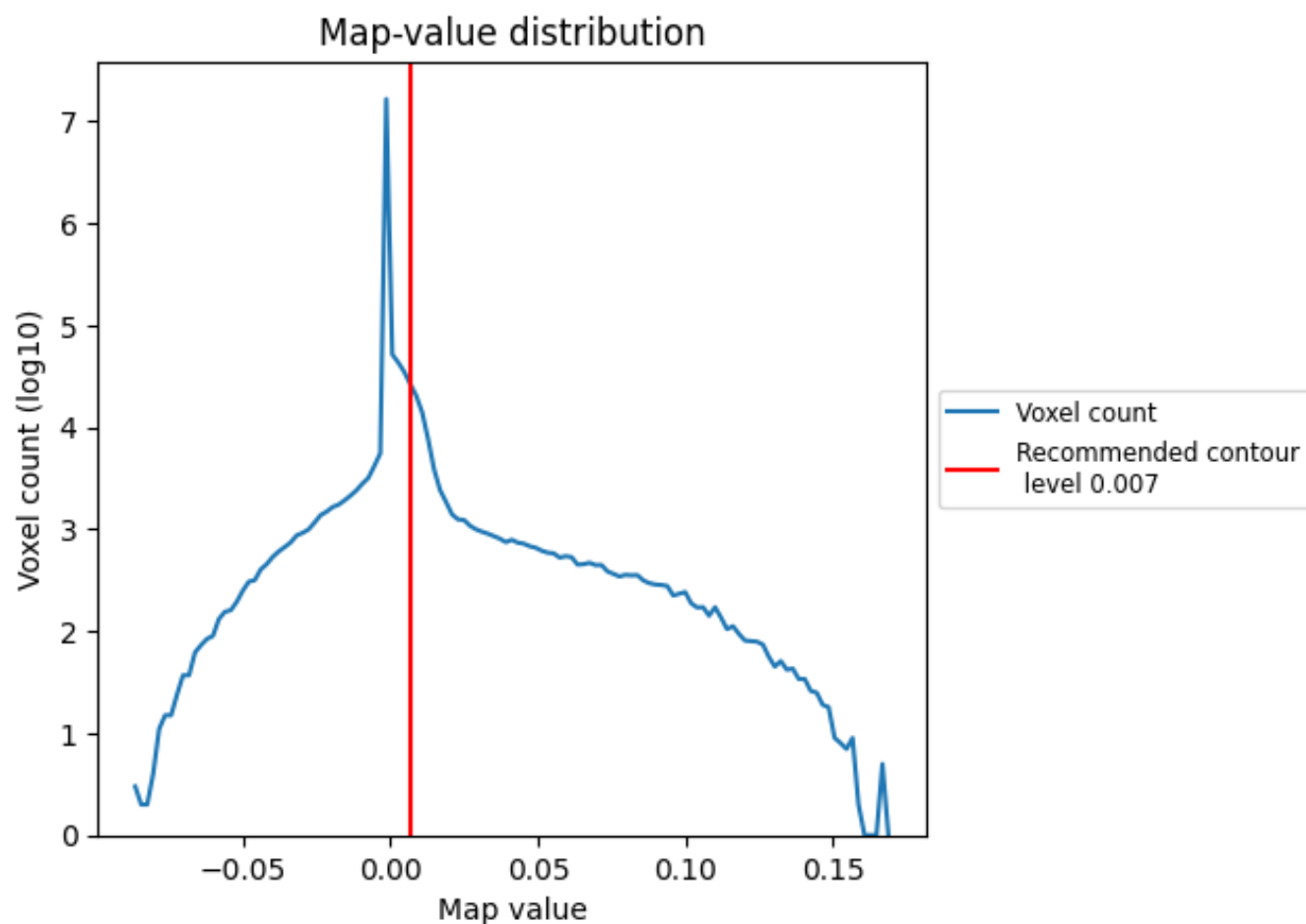
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

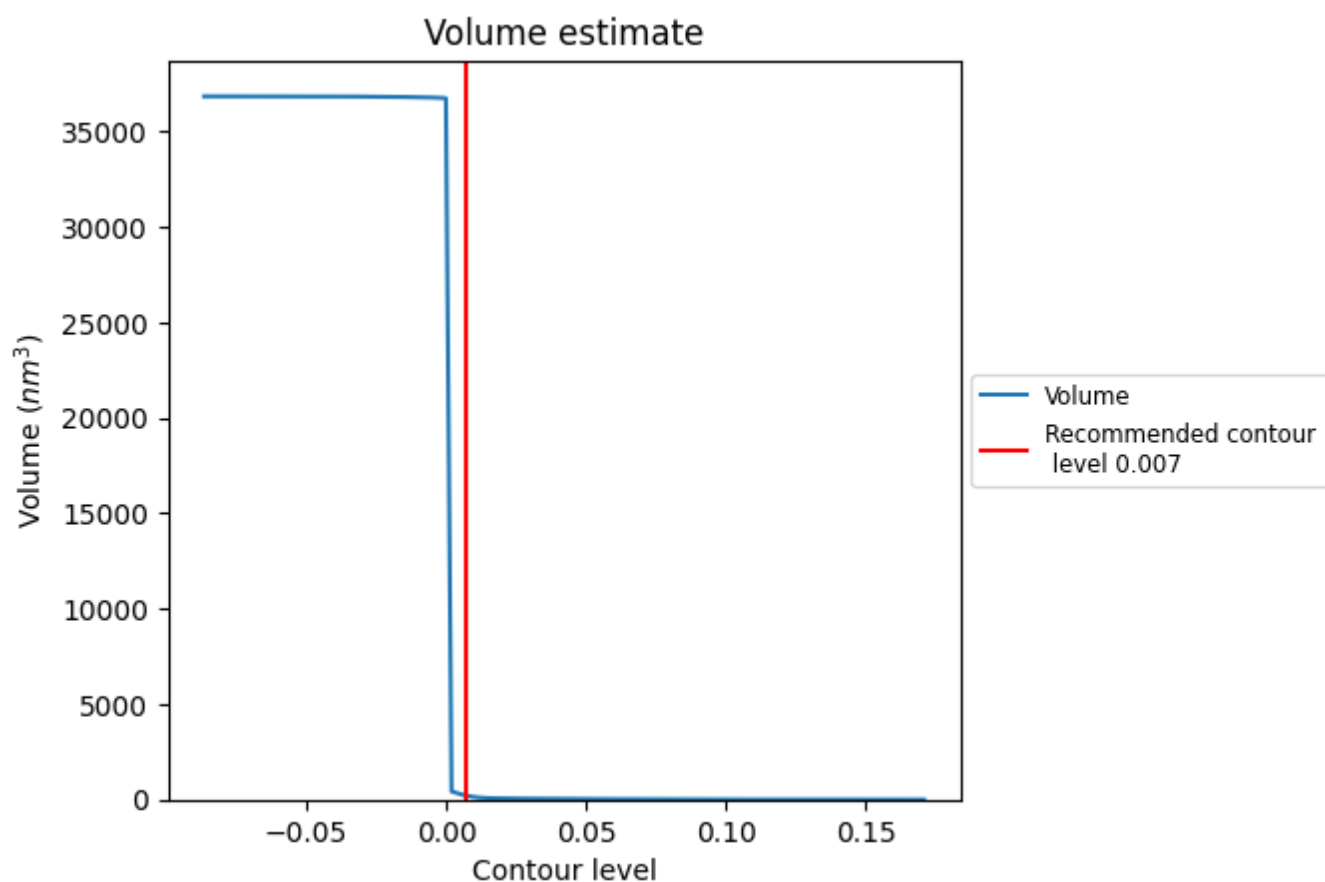
This section contains the results of statistical analysis of the map.

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.

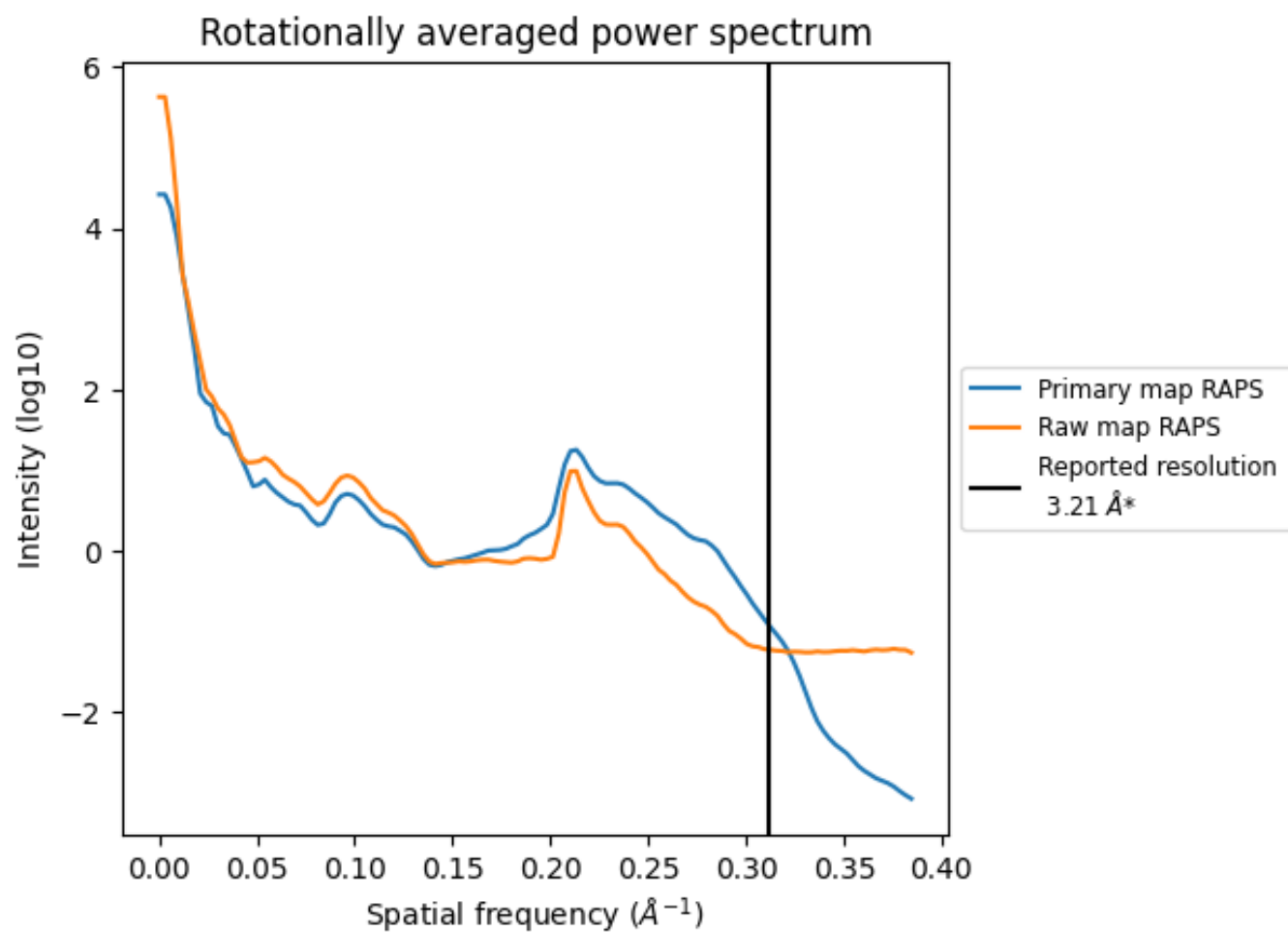
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 217 nm³; 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 ⓘ

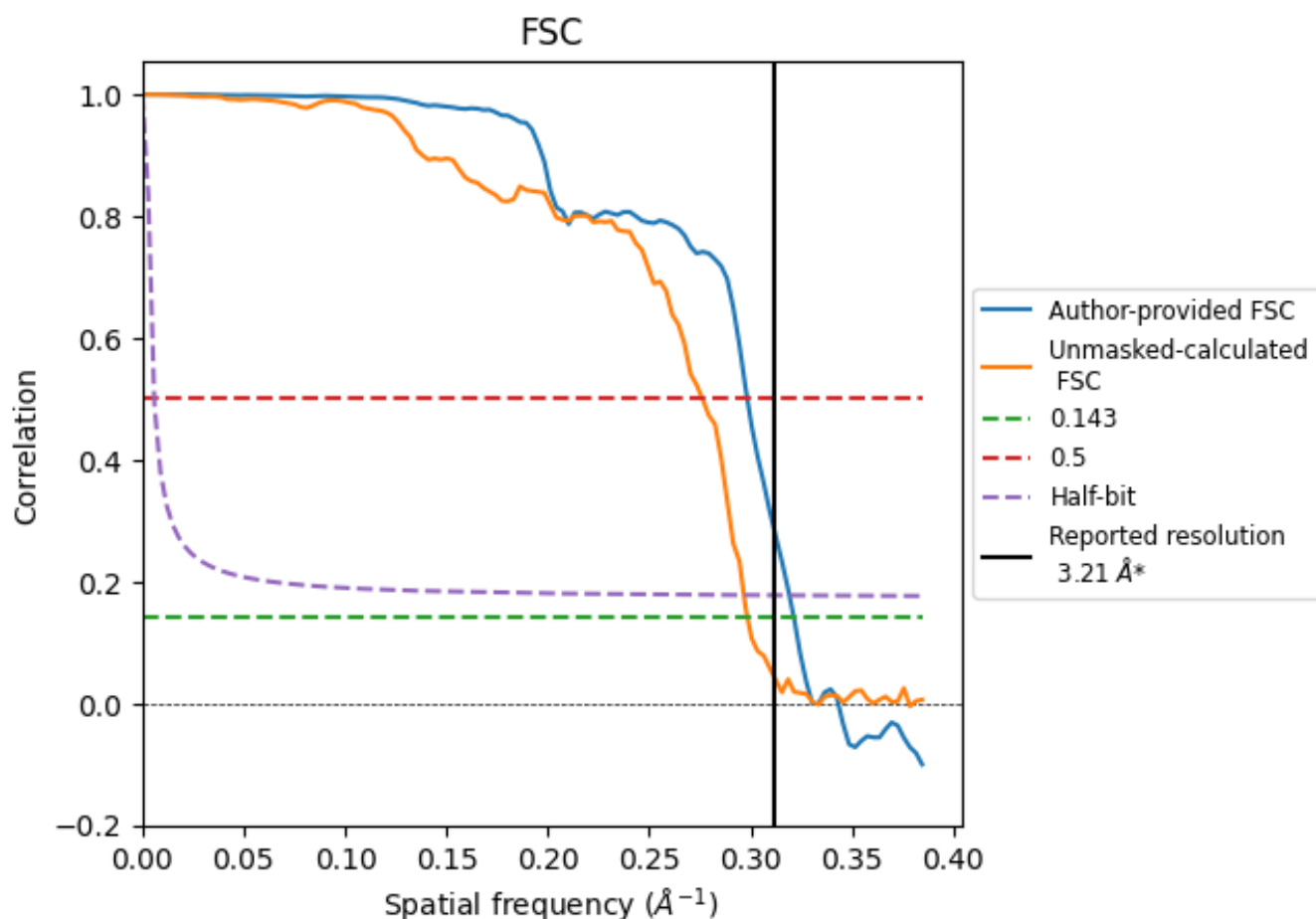


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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](#)

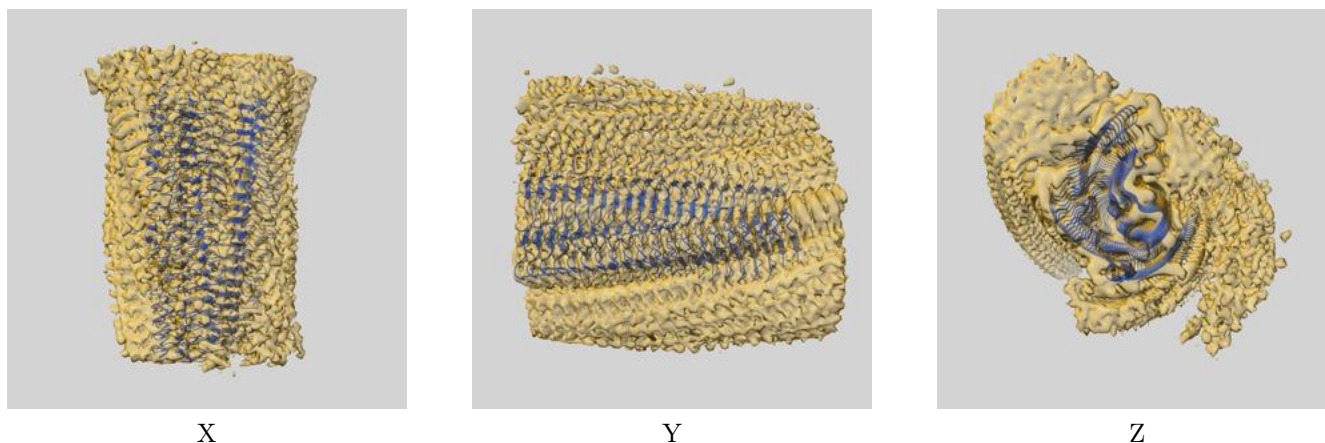
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.21	-	-
Author-provided FSC curve	3.11	3.35	3.13
Unmasked-calculated*	3.35	3.62	3.37

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

9 Map-model fit [i](#)

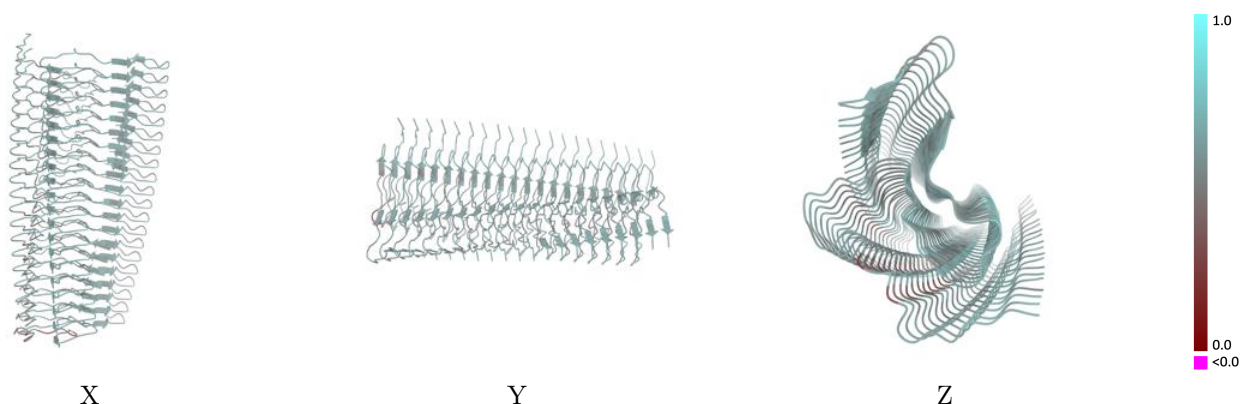
This section contains information regarding the fit between EMDB map EMD-51419 and PDB model 9GKF. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

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](#)

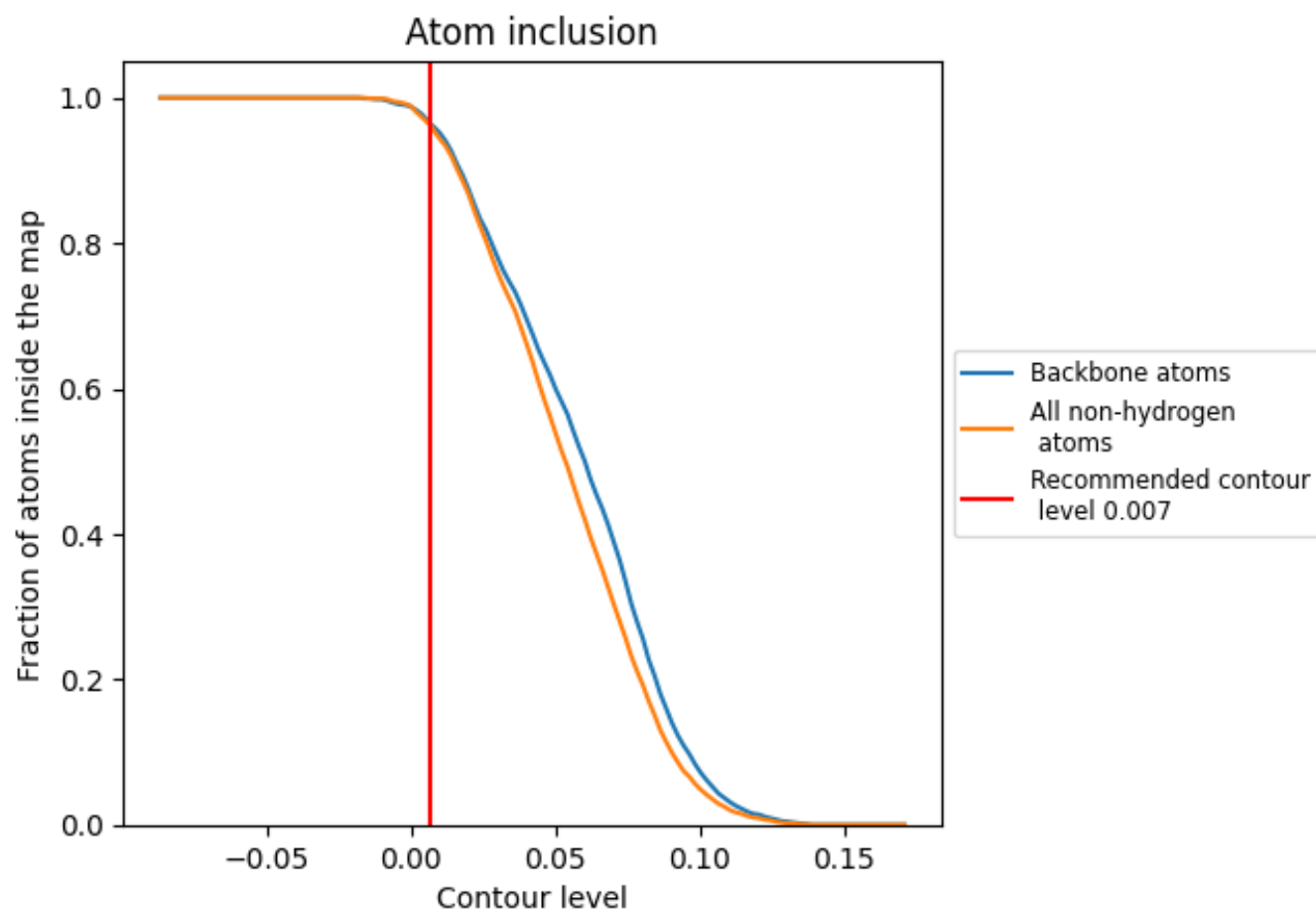


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

