



wwPDB EM Validation Summary Report ⓘ

Oct 28, 2024 – 01:40 AM EDT

PDB ID : 8FH3
EMDB ID : EMD-29078
Title : Human IFT-A complex structures provide molecular insights into ciliary transport
Authors : Jiang, M.; Palicharla, V.R.; Miller, D.; Hwang, S.H.; Zhu, H.; Hixson, P.; Mukhopadhyay, S.; Sun, J.
Deposited on : 2022-12-13
Resolution : 4.30 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

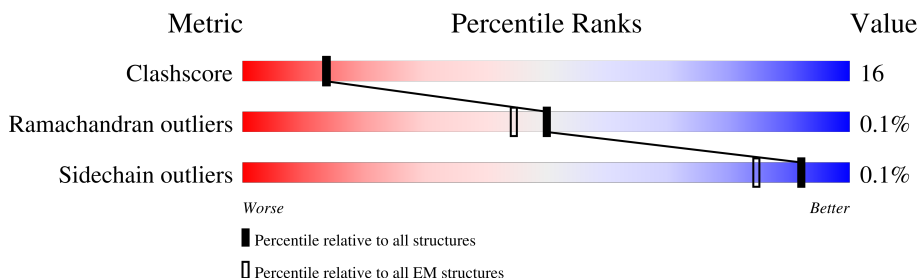
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	1181	
2	B	1241	
3	C	1342	
4	E	1462	
5	I	442	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 26773 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 WD repeat-containing protein 35.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	868	Total	C	N	O	S	0	0
			6761	4313	1142	1263	43		

- Molecule 2 is a protein called Intraflagellar transport protein 122 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1152	Total	C	N	O	S	0	0
			8709	5567	1501	1586	55		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	227S	ASP	GLU	conflict	UNP Q9HBG6

- Molecule 3 is a protein called WD repeat-containing protein 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	996	Total	C	N	O	S	0	0
			6697	4244	1173	1236	44		

- Molecule 4 is a protein called Intraflagellar transport protein 140 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	590	Total	C	N	O	S	0	0
			4298	2710	782	781	25		

- Molecule 5 is a protein called Tubby-related protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	36	Total	C	N	O	S	0	0
			304	192	59	49	4		

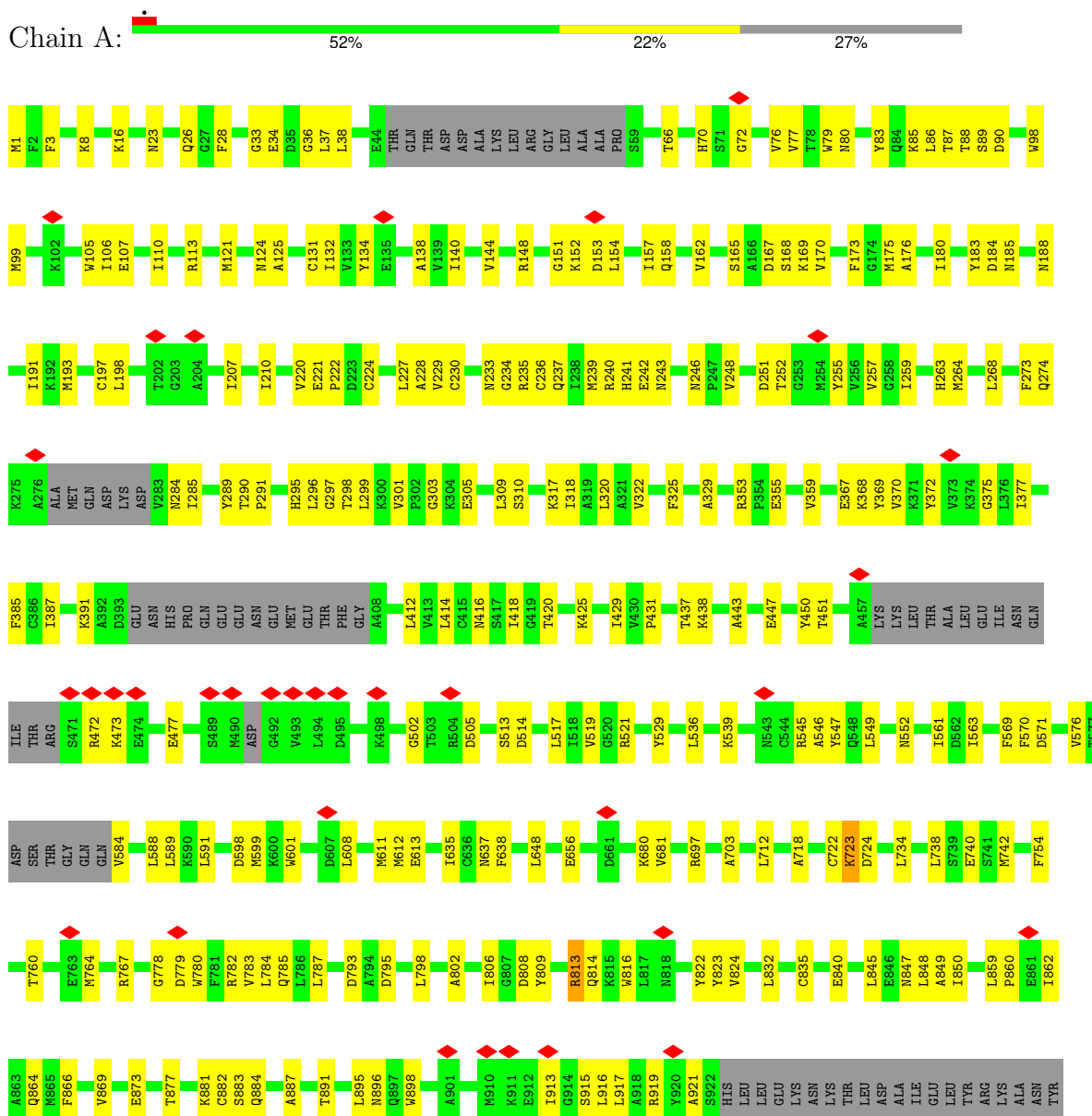
- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
6	B	2	Total 2	Zn 2	0
6	C	2	Total 2	Zn 2	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: WD repeat-containing protein 35



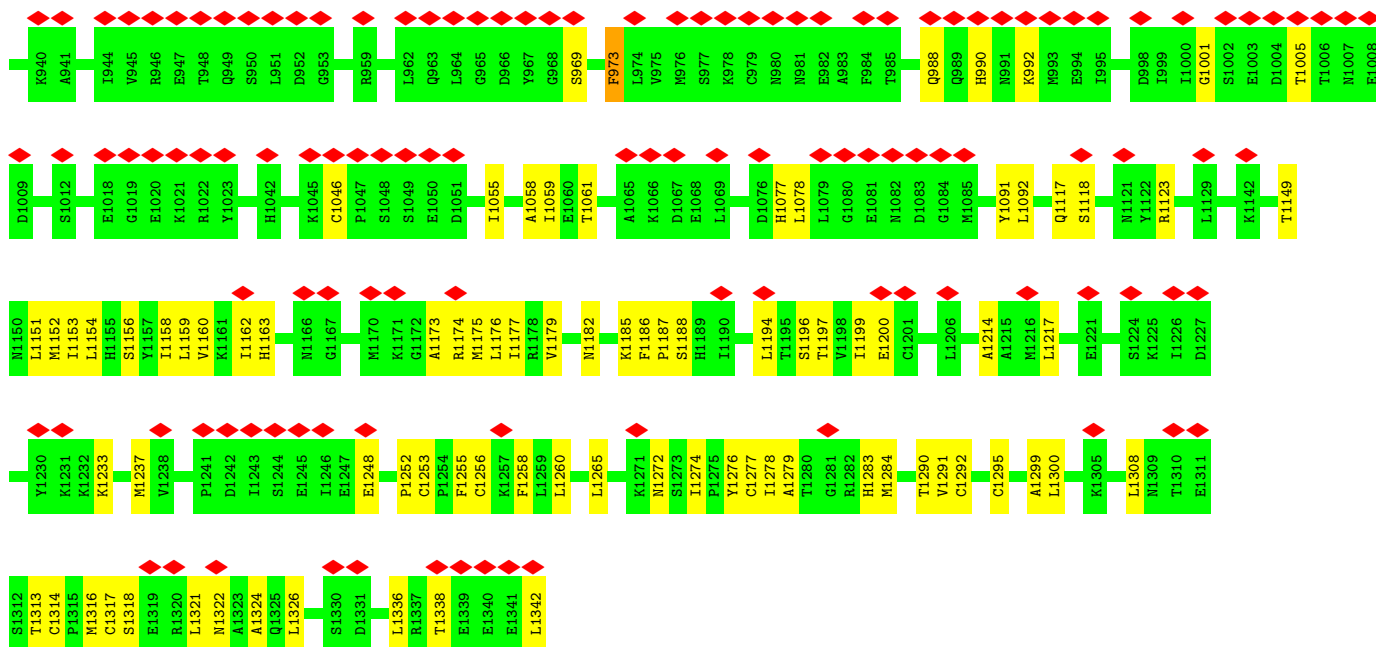


Q1079	PRO
I1082	PHE
S1087	THR
Y1088	ALA
L1091	LYS
H1092	ASP
F1096	LEU
Y1097	SER
L1098	LEU
I1102	PHE
V1103	GLU
D1104	GLN
V1166	GLY
A1107	GLY
I1108	GLY
S1109	GLY
L1110	GLY
I1111	GLY
D1112	GLY
L1113	GLY
E1114	VAL
LEU	LEU
ARG	ARG
PRO	PRO
LYS	LYS
ARG	ARG
ASP	ASP
ASP	ASP
GLN	GLN
LEU	LEU
GLU	GLU
ILE	ILE
ALA	ALA
ASN	ASN
SER	SER
SER	SER
GLN	GLN
ILE	ILE
LEU	LEU
ARG	ARG
VAL	VAL
GLU	GLU
THR	THR
LYS	LYS
ASP	ASP
SER	SER
ILE	ILE
GLY	GLY
ASP	ASP
GLU	GLU
ASP	ASP

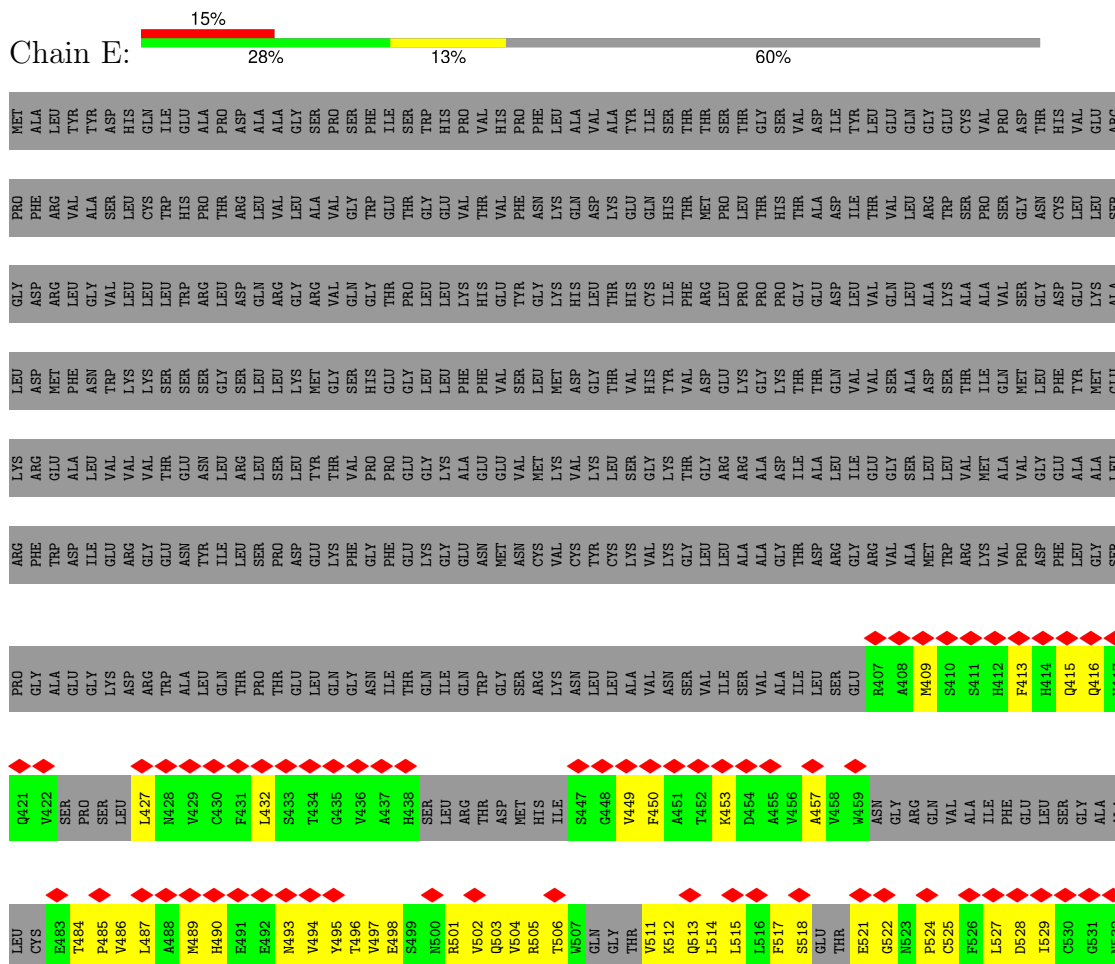
• Molecule 3: WD repeat-containing protein 19



MET	ASP	LEU	PRO	GLY	GLN	V384	Q461	Y570	L649	L756	A872
LYS	TRP	LEU	SER	ASP	ASP	S385	E462	G571	L649	Q757	A873
ARG	LYS	ILE	ASN	GLY	VAL	S386	T466	V572	P651	H758	S874
THR	ASP	TYR	MET	ILE	ASP	D387	P470	F573	L657	W759	
LYS	GLY	ASN	GLN	MET	LEU	V393	P470	I574	L658		
PHE	ASP	GLY	THR	ILE	LYS	A394	I478	D577	L659		
SER	VAL	THR	SER	GLY	ASP	V395	L479	T583	F662		
LEU	VAL	LEU	ARG	PHE	MET	G396	G480	Y584	F663		
LEU	ALA	LYS	VAL	GLY	TRP	L397	H481	V585	P770		
GLY	ILE	VAL	GLY	CYS	VAL	L400	A482	F586	A771		
GLY	ALA	PRO	ASP	GLY	ILE	A401	T483	H587	I774		
GLY	ALA	VAL	ASP	THR	ASN	G403	T484	S590	Y781		
GLY	LYS	LEU	THR	PHE	LEU	R407	S485	I591	L785		
ALA	SER	GLY	ILE	GLY	ASP	V412	F486	Q592	A794		
GLN	ILE	GLY	ALA	THR	GLY	G414	L488	G593	L794		
PHE	TYR	THR	GLY	HIS	ASN	E415	T489	A594	A794		
ALA	ALA	ARG	LYS	THR	LYS	A416	Y490	K595	D801		
ASN	THR	VAL	ARG	THR	GLY	A417	L413	L598	D805		
GLY	THR	CYS	GLY	GLY	ILE	V418	G491	A599	L809		
ASN	THR	TRP	GLY	GLY	GLY	L421	T492	G600	E809		
ASN	LYS	ASN	LYS	GLY	THR	K422	D493	S601	D810		
LEU	THR	GLY	ALA	THR	LEU	Y426	T494	T602	E811		
GLY	ALA	VAL	GLY	ALA	LEU	L427	G495	V604	L814		
ASP	GLY	GLN	ASN	ARG	LEU	V430	V497	K603			
ASP	GLY	LEU	LEU	THR	GLY	F444	Y499	P605			
GLY	ASP	LEU	ASN	GLY	GLN	L433	F500	H608			
ASP	ASP	ALA	LEU	HIS	LEU	C434	Y501	K609			
GLN	MET	GLY	GLY	ASP	LEU	L435	E503	P610			
LEU	TYR	GLY	ASN	LEU	ALA	H436	F507	L612			
GLY	ILE	ARG	ASN	LEU	THR	S437	Y511	N615			
ASP	VAL	ASP	GLY	GLY	GLN	H438	H512	G616			
PHE	THR	PHE	ILE	ILE	ASP	S439	P514	E617			
ARG	GLY	LEU	PRO	VAL	ASN	Y440	V515	L618			
LEU	ASP	LEU	ALA	THR	LEU	L443	S516	V627			
LEU	TRP	LEU	VAL	SER	GLN	F444	K519	N628			
GLY	GLY	LYS	GLN	THR	THR	P447	I520	G630			
THR	THR	ASP	ASP	LYS	PHE	V448	P524	L632			
ILE	ILE	THR	PHE	ALA	VAL	Q449	T527	T634			
ALA	ALA	LEU	GLY	THR	THR	L450	I558	H635			
GLY	VAL	VAL	ASN	GLY	GLY	H451	K559	G636			
PRO	GLY	VAL	ILE	CYS	CYS	L452	W563	S639			
GLY	THR	THR	GLN	ASN	ASN	E454	E564	N640			
ASN	THR	THR	VAL	CYS	THR	S455	W565	L641			
CYS	VAL	VAL	TYR	CYS	TYR	E456	P567	K642			
VAL	VAL	VAL	ILE	ILE	ASP	I457	M568	D643			
LYS	LYS	LYS	TRP	TRP	TRP	L458	D569	T644			
ALA	ASN	ASN	ALA	ILE	ILE	A460		P646			



- Molecule 4: Intraflagellar transport protein 140 homolog





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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	113784	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	53.06	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.691	Depositor
Minimum map value	-0.186	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.063	Depositor
Recommended contour level	0.7	Depositor
Map size (\AA)	572.16003, 572.16003, 572.16003	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.4900001, 1.4900001, 1.4900001	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.64	0/6899	0.62	2/9359 (0.0%)
2	B	0.57	0/8902	0.63	5/12098 (0.0%)
3	C	0.46	0/6827	0.58	1/9373 (0.0%)
4	E	0.39	0/4382	0.56	0/5953
5	I	0.35	0/308	0.62	0/408
All	All	0.54	0/27318	0.60	8/37191 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	C	0	5

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	723	LYS	N-CA-C	-7.54	90.66	111.00
2	B	806	GLU	C-N-CD	-7.15	104.88	120.60
2	B	223	PRO	N-CA-CB	7.14	111.86	103.30
1	A	723	LYS	CB-CA-C	6.04	122.49	110.40
2	B	247	LEU	CA-CB-CG	5.78	128.60	115.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	850	LEU	Peptide
3	C	855	GLN	Peptide
3	C	858	GLU	Peptide
3	C	973	PHE	Peptide
3	C	990	HIS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6761	0	6570	192	0
2	B	8709	0	8238	259	0
3	C	6697	0	5686	219	0
4	E	4298	0	3829	143	0
5	I	304	0	318	19	0
6	B	2	0	0	0	0
6	C	2	0	0	0	0
All	All	26773	0	24641	802	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 16.

The worst 5 of 802 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)
2:B:1057:CYS:HB2	2:B:1074:CYS:SG	1.83	1.17
2:B:534:GLU:O	2:B:535:ASN:ND2	2.01	0.94
3:C:449:GLN:HE22	3:C:451:HIS:HB3	1.36	0.91
4:E:502:VAL:HB	4:E:515:LEU:HB2	1.51	0.90
3:C:988:GLN:O	3:C:992:LYS:HA	1.71	0.89

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	854/1181 (72%)	780 (91%)	74 (9%)	0	100	100
2	B	1144/1241 (92%)	1070 (94%)	72 (6%)	2 (0%)	44	78
3	C	994/1342 (74%)	906 (91%)	88 (9%)	0	100	100
4	E	566/1462 (39%)	533 (94%)	32 (6%)	1 (0%)	44	78
5	I	34/442 (8%)	34 (100%)	0	0	100	100
All	All	3592/5668 (63%)	3323 (92%)	266 (7%)	3 (0%)	50	83

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	223	PRO
2	B	807	PRO
4	E	506	THR

5.3.2 Protein sidechains [i](#)

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	714/1018 (70%)	713 (100%)	1 (0%)	92	95
2	B	867/1091 (80%)	867 (100%)	0	100	100
3	C	528/1156 (46%)	528 (100%)	0	100	100
4	E	384/1246 (31%)	384 (100%)	0	100	100
5	I	32/387 (8%)	31 (97%)	1 (3%)	35	56

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2525/4898 (52%)	2523 (100%)	2 (0%)	92 95

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	813	ARG
5	I	37	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	481	HIS
3	C	449	GLN
2	B	1092	HIS
2	B	983	HIS
3	C	406	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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

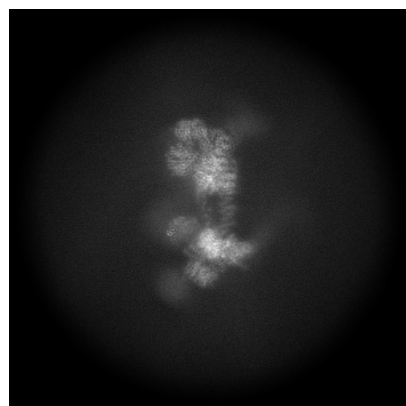
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29078. These allow visual inspection of the internal detail of the map and identification of artifacts.

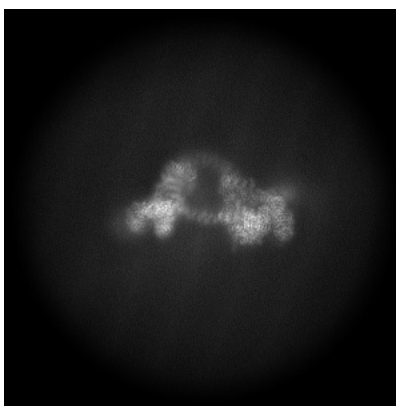
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

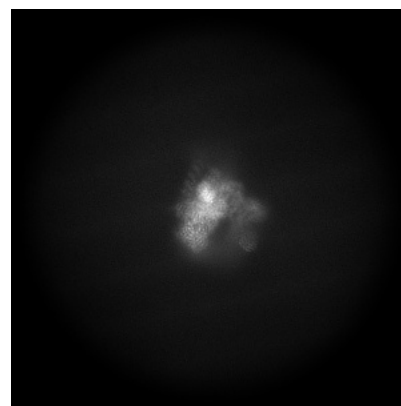
6.1.1 Primary map



X

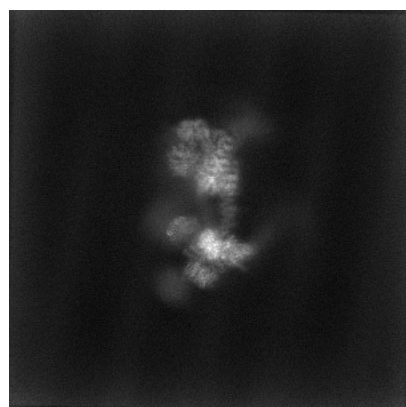


Y

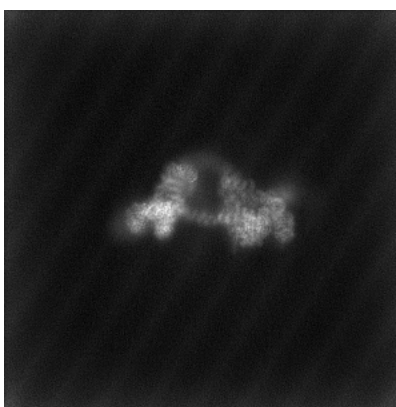


Z

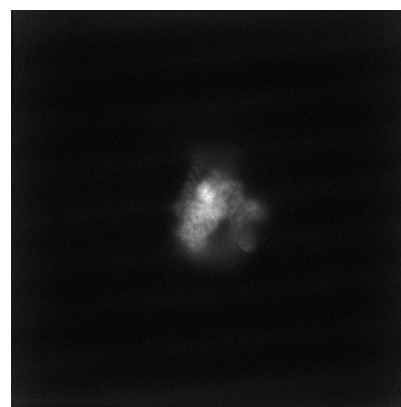
6.1.2 Raw map



X



Y

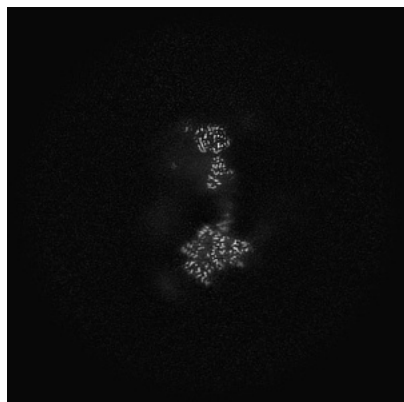


Z

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

6.2 Central slices [i](#)

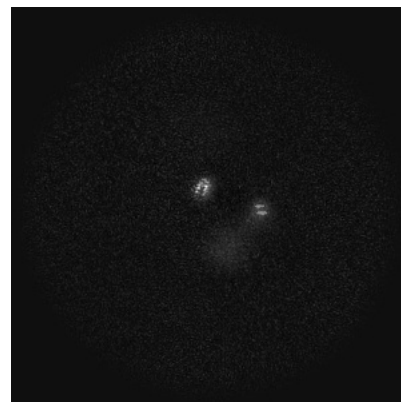
6.2.1 Primary map



X Index: 192

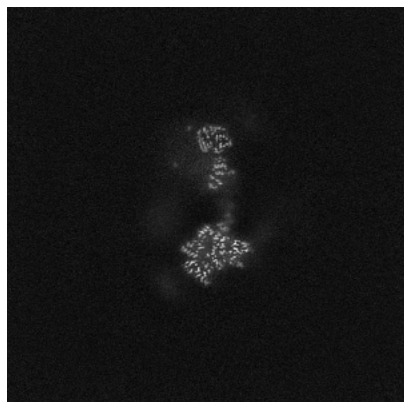


Y Index: 192



Z Index: 192

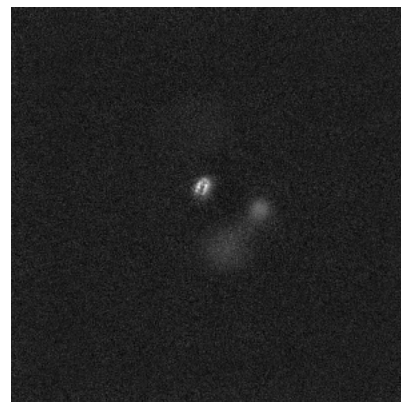
6.2.2 Raw map



X Index: 192



Y Index: 192

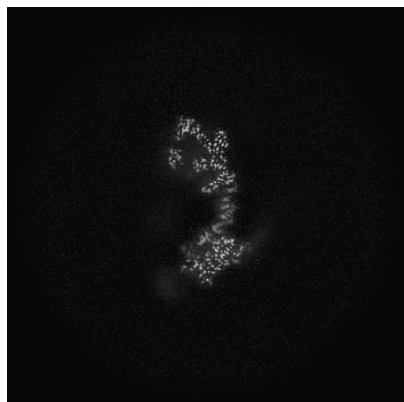


Z Index: 192

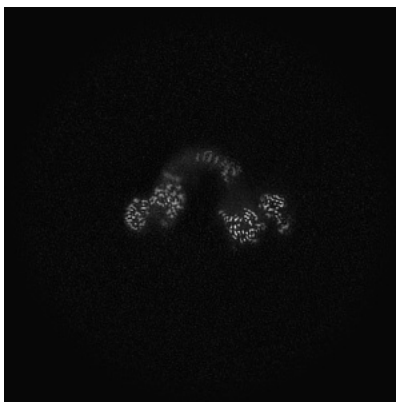
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

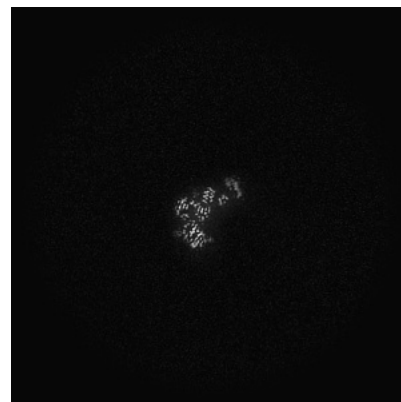
6.3.1 Primary map



X Index: 187

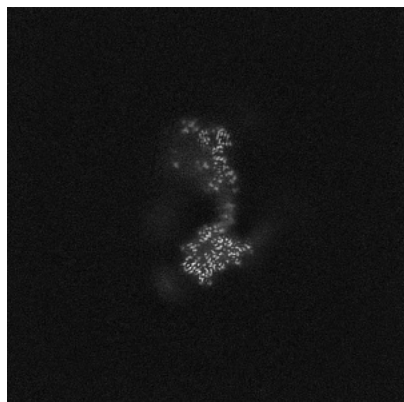


Y Index: 187

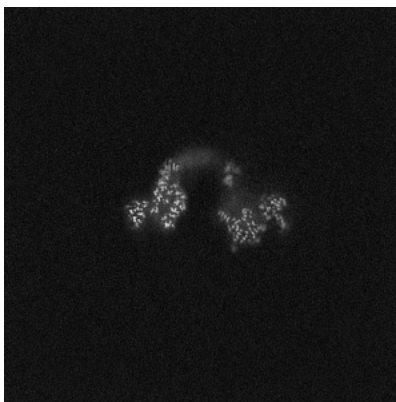


Z Index: 231

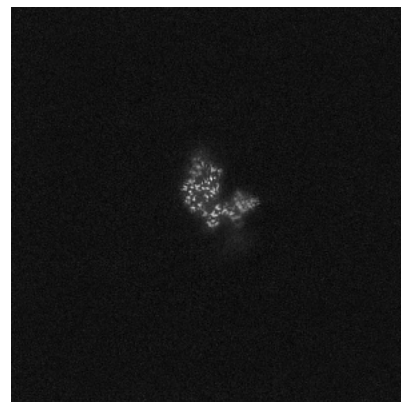
6.3.2 Raw map



X Index: 189



Y Index: 191

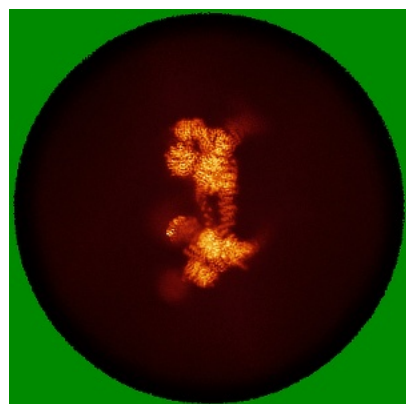


Z Index: 156

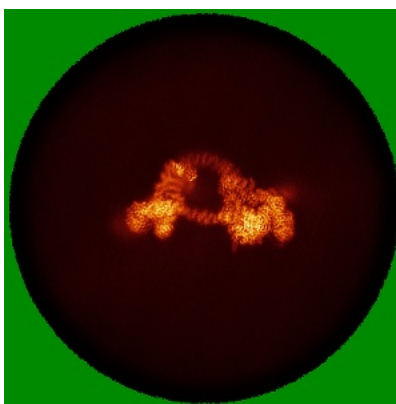
The images above show the largest variance slices of the map in three orthogonal directions.

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

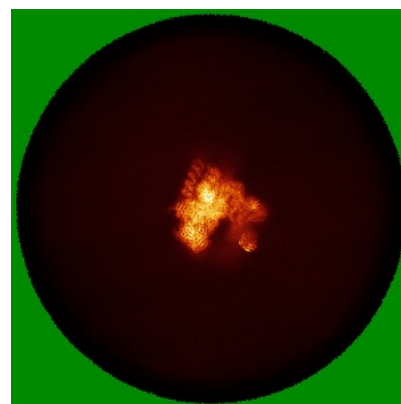
6.4.1 Primary map



X

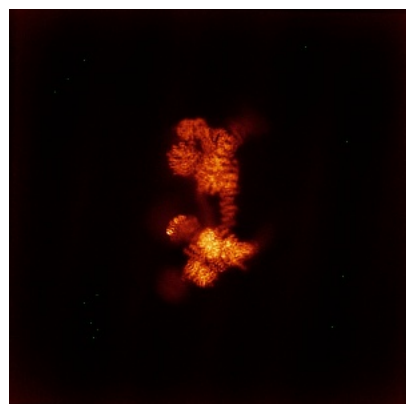


Y

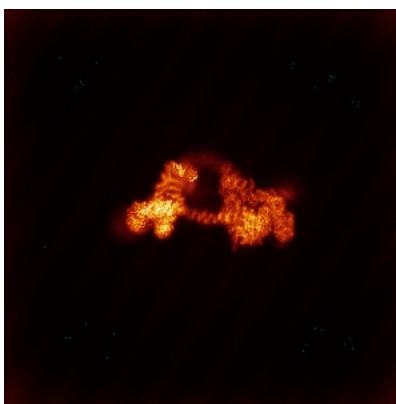


Z

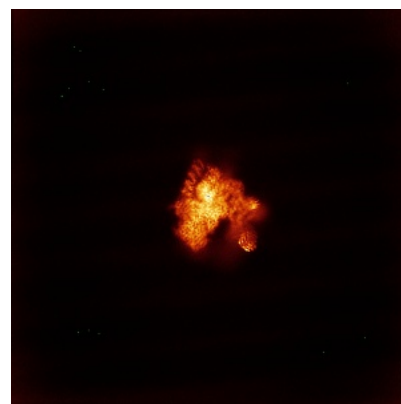
6.4.2 Raw map



X



Y

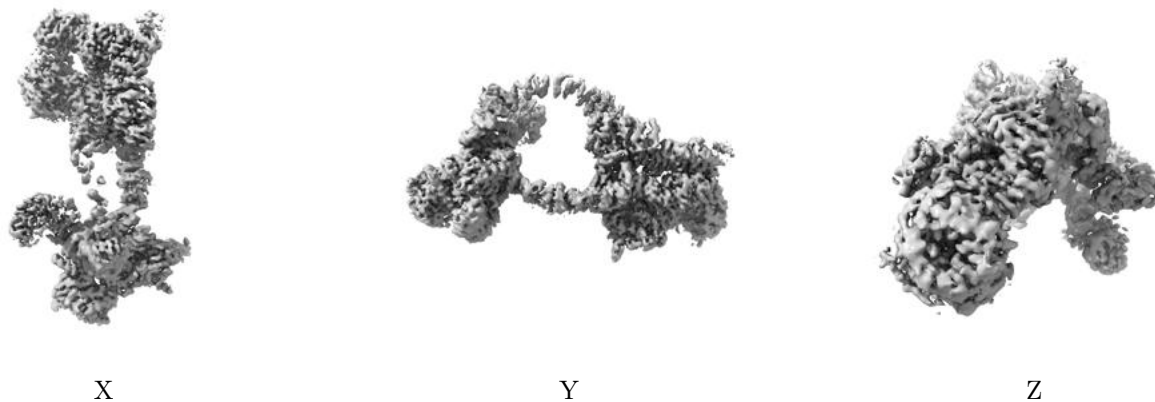


Z

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.

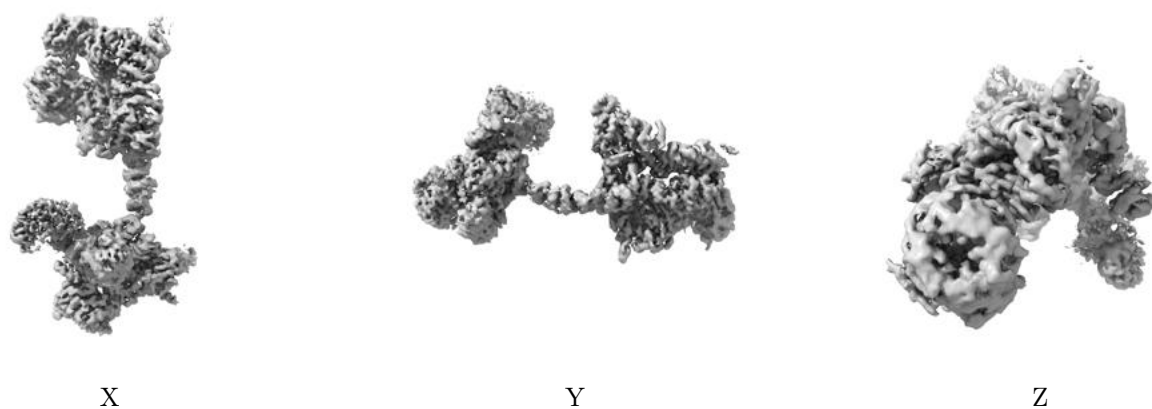
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.7. 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.

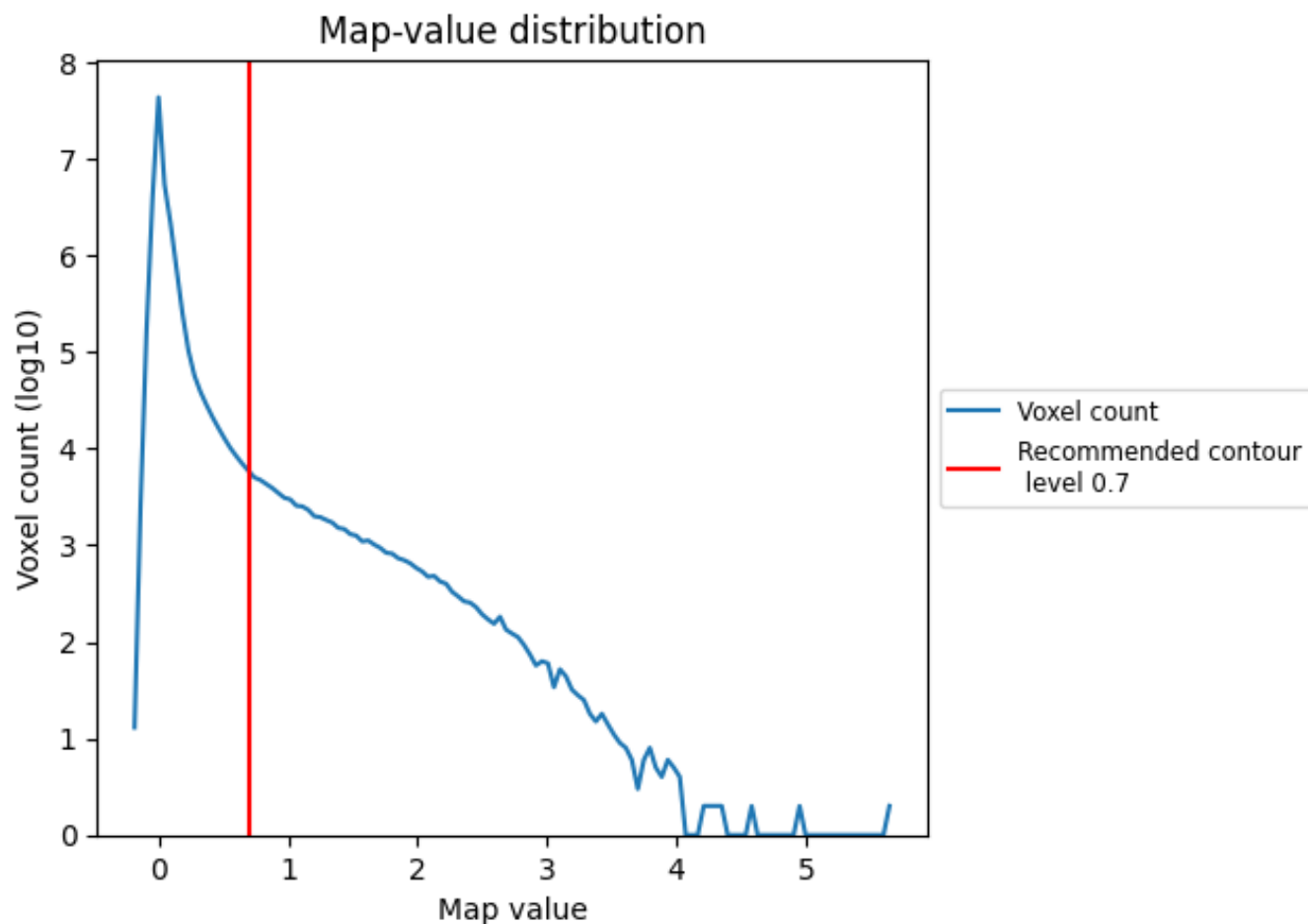
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

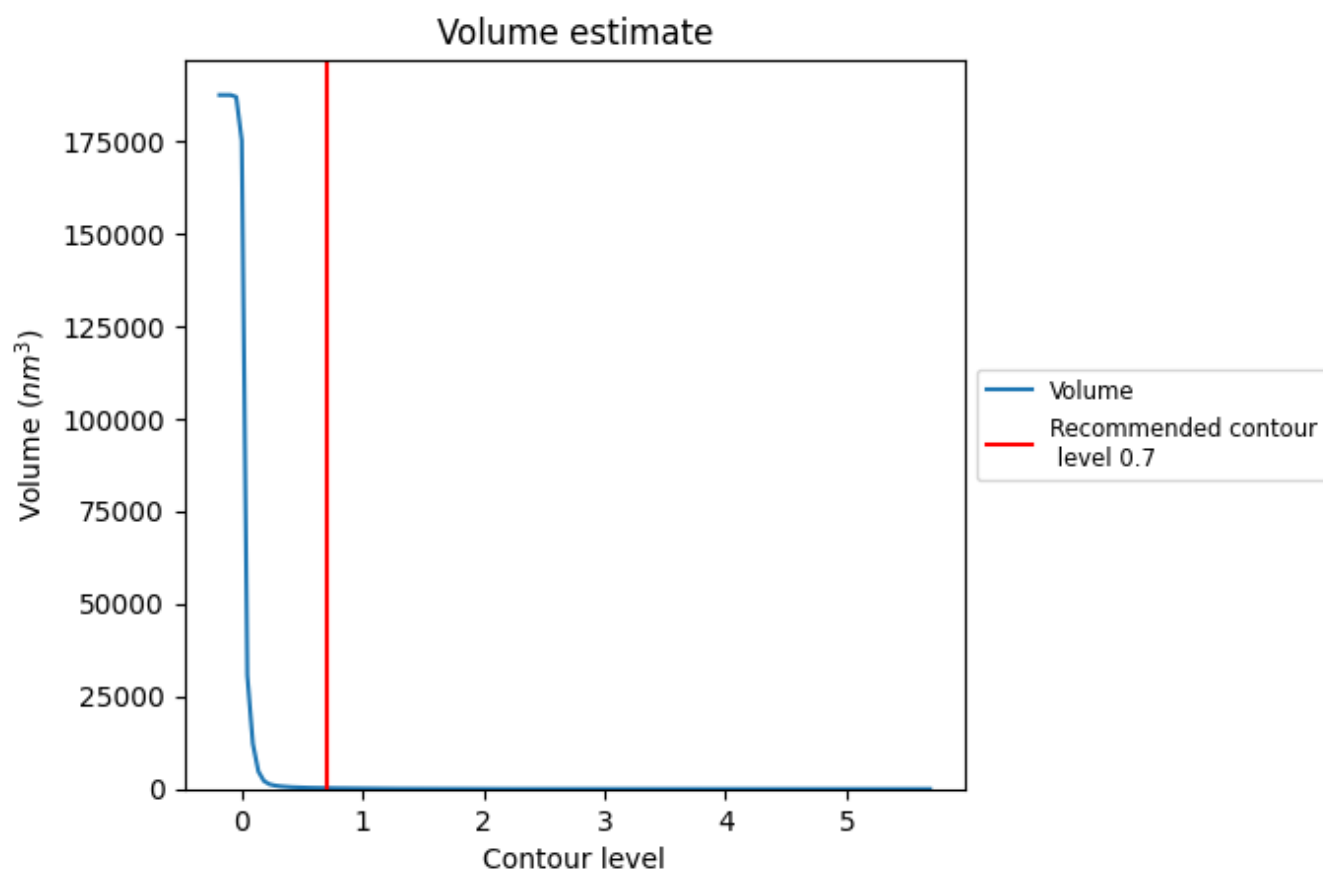
This section contains the results of statistical analysis of the map.

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.

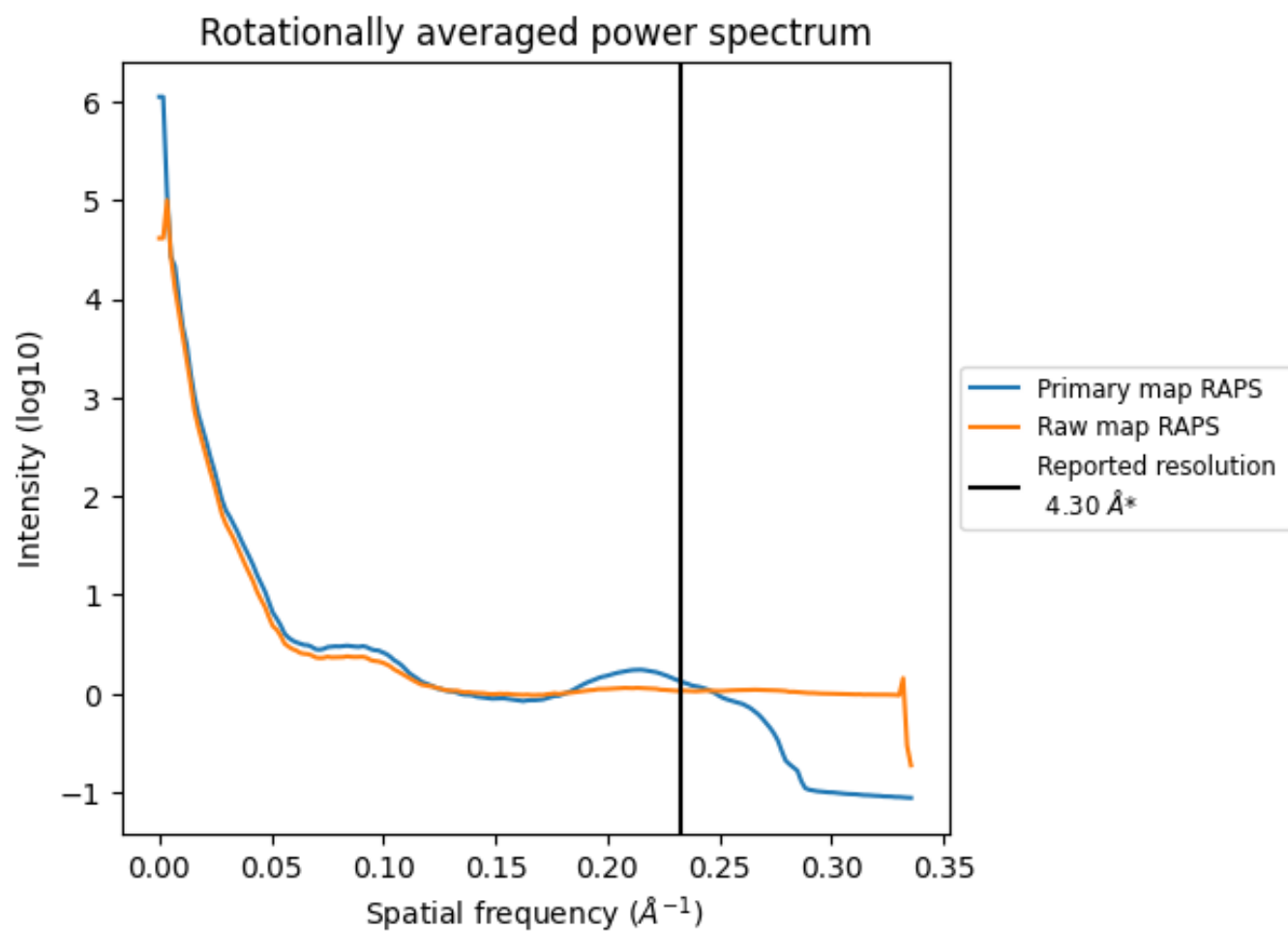
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 222 nm^3 ; this corresponds to an approximate mass of 201 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 ⓘ

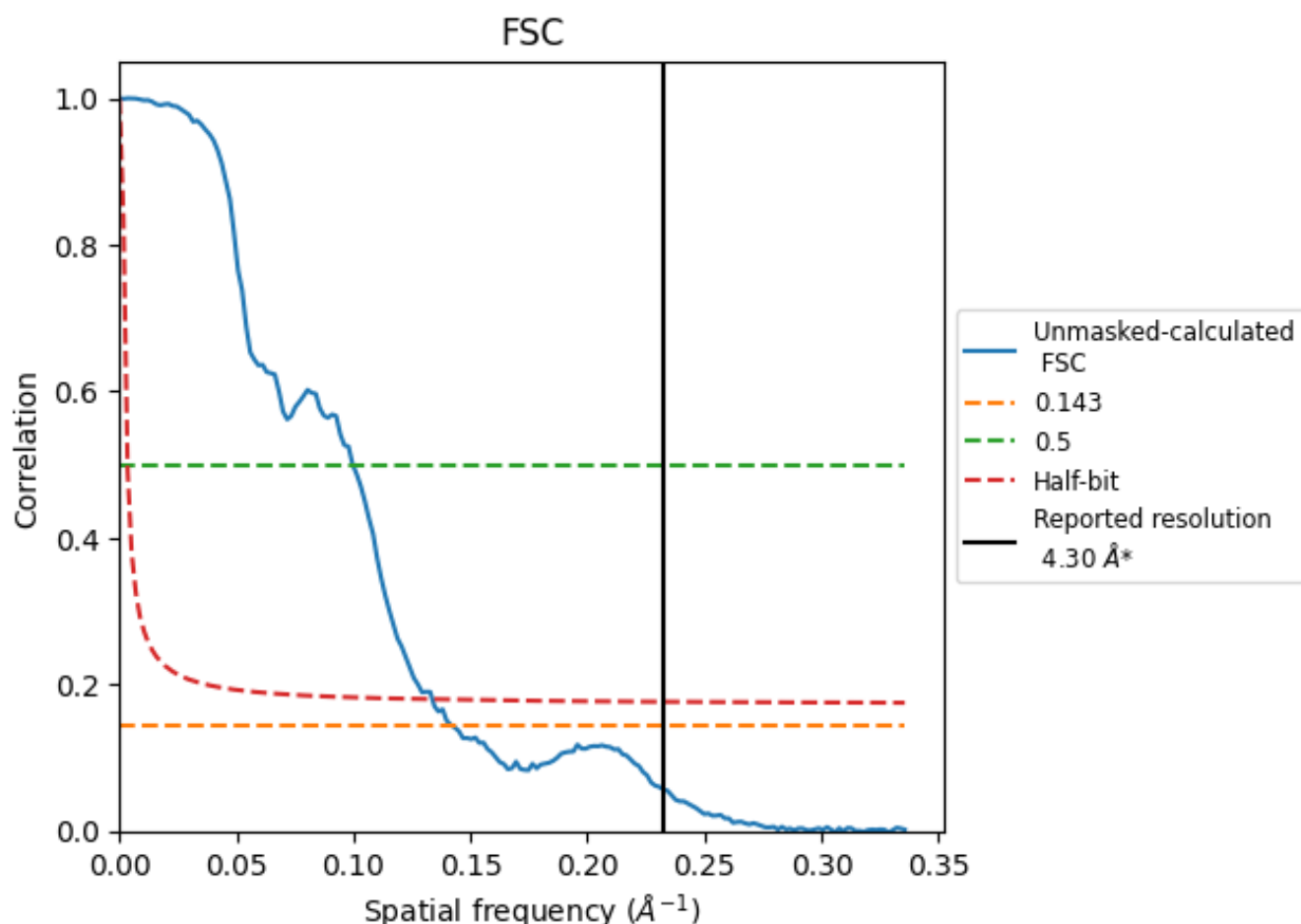


*Reported resolution corresponds to spatial frequency of 0.233 Å⁻¹

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 0.233 Å⁻¹

8.2 Resolution estimates [i](#)

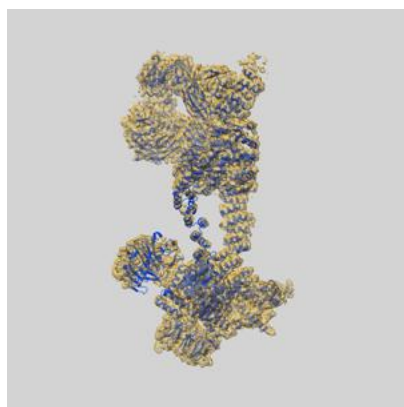
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.03	10.03	7.48

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.03 differs from the reported value 4.3 by more than 10 %

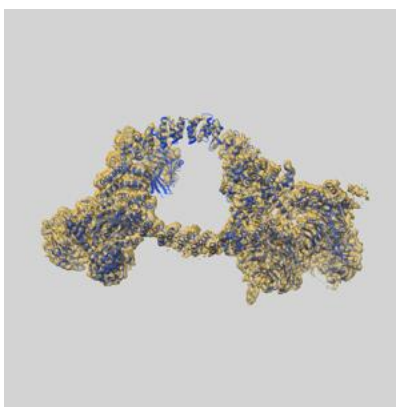
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-29078 and PDB model 8FH3. Per-residue inclusion information can be found in section [3](#) on page [5](#).

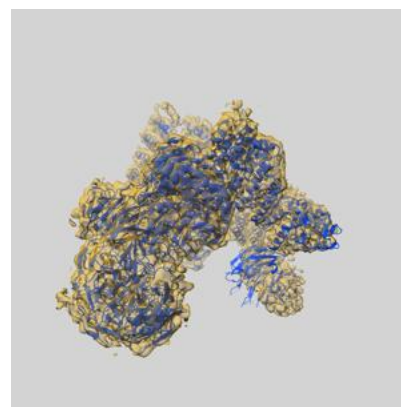
9.1 Map-model overlay [i](#)



X



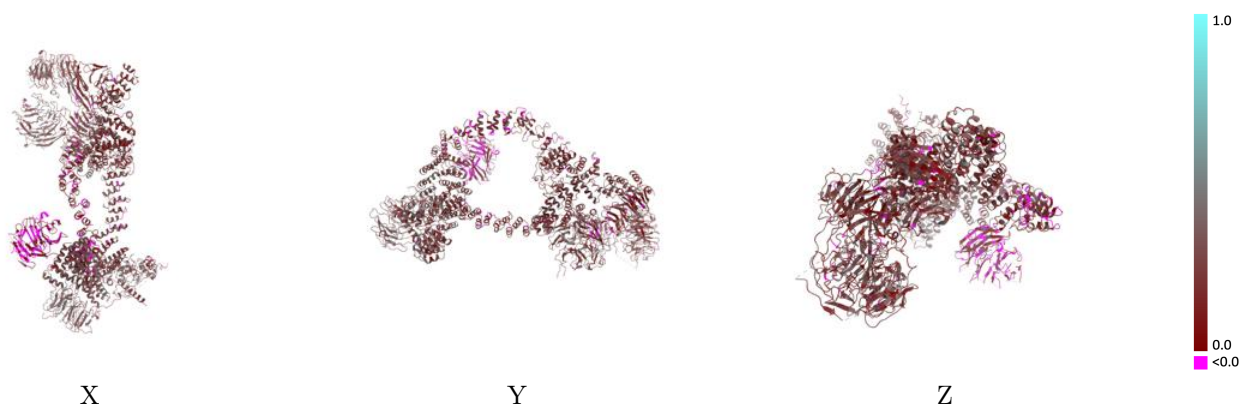
Y



Z

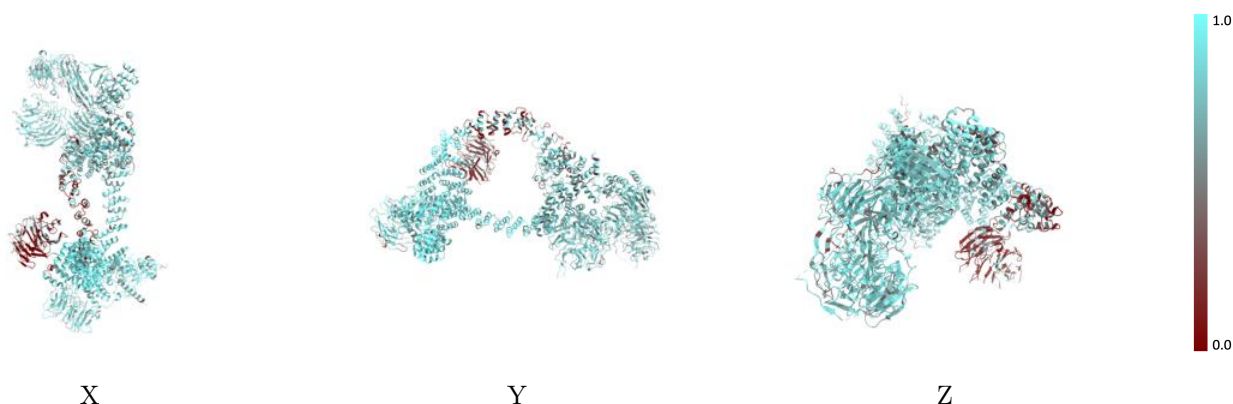
The images above show the 3D surface view of the map at the recommended contour level 0.7 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



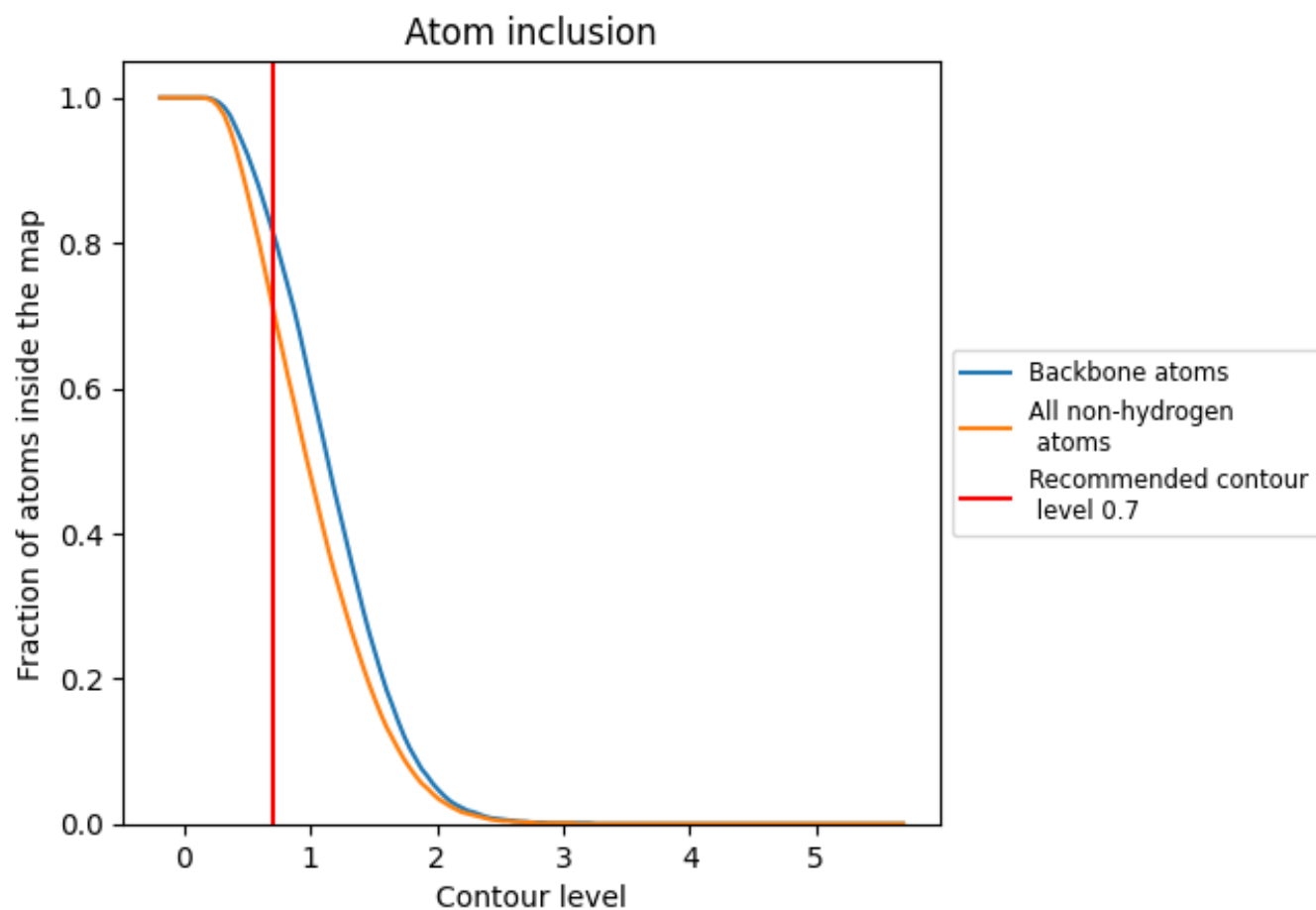
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 72% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7150	<div></div> 0.2480
A	<div></div> 0.7650	<div></div> 0.2720
B	<div></div> 0.7650	<div></div> 0.2510
C	<div></div> 0.7050	<div></div> 0.2650
E	<div></div> 0.5530	<div></div> 0.1740
I	<div></div> 0.6450	<div></div> 0.2830

