



## wwPDB EM Validation Summary Report ⓘ

Nov 6, 2022 – 06:22 AM EST

PDB ID : 6B5B  
EMDB ID : EMD-7055  
Title : Cryo-EM structure of the NAIP5-NLRC4-flagellin inflammasome  
Authors : Tenthorey, J.L.; Haloupek, N.; Lopez-Blanco, J.R.; Grob, P.; Adamson, E.; Hartenian, E.; Lind, N.A.; Bourgeois, N.M.; Chacon, P.; Nogales, E.; Vance, R.E.  
Deposited on : 2017-09-29  
Resolution : 5.20 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](mailto:validation@mail.wwpdb.org)

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<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>.

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

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

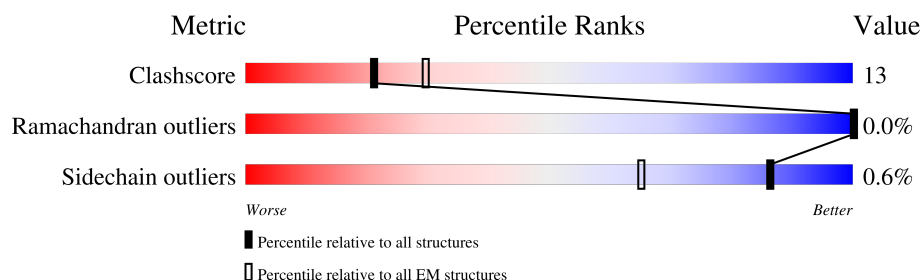
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 5.20 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	1403	<div> <div>18%</div> <div>55%</div> <div>30%</div> <div>•</div> <div>15%</div> </div>
2	B	1024	<div> <div>7%</div> <div>66%</div> <div>22%</div> <div>12%</div> </div>
2	C	1024	<div> <div>7%</div> <div>66%</div> <div>22%</div> <div>12%</div> </div>
3	F	566	<div> <div>8%</div> <div>•</div> <div>88%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 24555 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 Baculoviral IAP repeat-containing protein 1e.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1199	Total	C	N	O	S	0	0
			9583	6128	1608	1790	57		

- Molecule 2 is a protein called NLR family CARD domain-containing protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	903	Total	C	N	O	S	0	0
			7237	4622	1224	1351	40		
2	C	903	Total	C	N	O	S	0	0
			7237	4622	1224	1351	40		

- Molecule 3 is a protein called Flagellin.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	68	Total	C	N	O	S	0	0
			498	302	93	98	5		

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-90	MET	-	initiating methionine	UNP G8U UW9
F	-89	GLU	-	expression tag	UNP G8U UW9
F	-88	GLN	-	expression tag	UNP G8U UW9
F	-87	LYS	-	expression tag	UNP G8U UW9
F	-86	LEU	-	expression tag	UNP G8U UW9
F	-85	ILE	-	expression tag	UNP G8U UW9
F	-84	SER	-	expression tag	UNP G8U UW9
F	-83	GLU	-	expression tag	UNP G8U UW9
F	-82	GLU	-	expression tag	UNP G8U UW9
F	-81	ASP	-	expression tag	UNP G8U UW9
F	-80	LEU	-	expression tag	UNP G8U UW9
F	-79	ASN	-	expression tag	UNP G8U UW9
F	-78	GLU	-	expression tag	UNP G8U UW9

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-77	MET	-	expression tag	UNP G8U UW9
F	-76	GLU	-	expression tag	UNP G8U UW9
F	-75	GLN	-	expression tag	UNP G8U UW9
F	-74	LYS	-	expression tag	UNP G8U UW9
F	-73	LEU	-	expression tag	UNP G8U UW9
F	-72	ILE	-	expression tag	UNP G8U UW9
F	-71	SER	-	expression tag	UNP G8U UW9
F	-70	GLU	-	expression tag	UNP G8U UW9
F	-69	GLU	-	expression tag	UNP G8U UW9
F	-68	ASP	-	expression tag	UNP G8U UW9
F	-67	LEU	-	expression tag	UNP G8U UW9
F	-66	ASN	-	expression tag	UNP G8U UW9
F	-65	GLU	-	expression tag	UNP G8U UW9
F	-64	MET	-	expression tag	UNP G8U UW9
F	-63	GLU	-	expression tag	UNP G8U UW9
F	-62	GLN	-	expression tag	UNP G8U UW9
F	-61	LYS	-	expression tag	UNP G8U UW9
F	-60	LEU	-	expression tag	UNP G8U UW9
F	-59	ILE	-	expression tag	UNP G8U UW9
F	-58	SER	-	expression tag	UNP G8U UW9
F	-57	GLU	-	expression tag	UNP G8U UW9
F	-56	GLU	-	expression tag	UNP G8U UW9
F	-55	ASP	-	expression tag	UNP G8U UW9
F	-54	LEU	-	expression tag	UNP G8U UW9
F	-53	ASN	-	expression tag	UNP G8U UW9
F	-52	GLU	-	expression tag	UNP G8U UW9
F	-51	MET	-	expression tag	UNP G8U UW9
F	-50	GLU	-	expression tag	UNP G8U UW9
F	-49	GLN	-	expression tag	UNP G8U UW9
F	-48	LYS	-	expression tag	UNP G8U UW9
F	-47	LEU	-	expression tag	UNP G8U UW9
F	-46	ILE	-	expression tag	UNP G8U UW9
F	-45	SER	-	expression tag	UNP G8U UW9
F	-44	GLU	-	expression tag	UNP G8U UW9
F	-43	GLU	-	expression tag	UNP G8U UW9
F	-42	ASP	-	expression tag	UNP G8U UW9
F	-41	LEU	-	expression tag	UNP G8U UW9
F	-40	ASN	-	expression tag	UNP G8U UW9
F	-39	GLU	-	expression tag	UNP G8U UW9
F	-38	MET	-	expression tag	UNP G8U UW9
F	-37	GLU	-	expression tag	UNP G8U UW9
F	-36	GLN	-	expression tag	UNP G8U UW9

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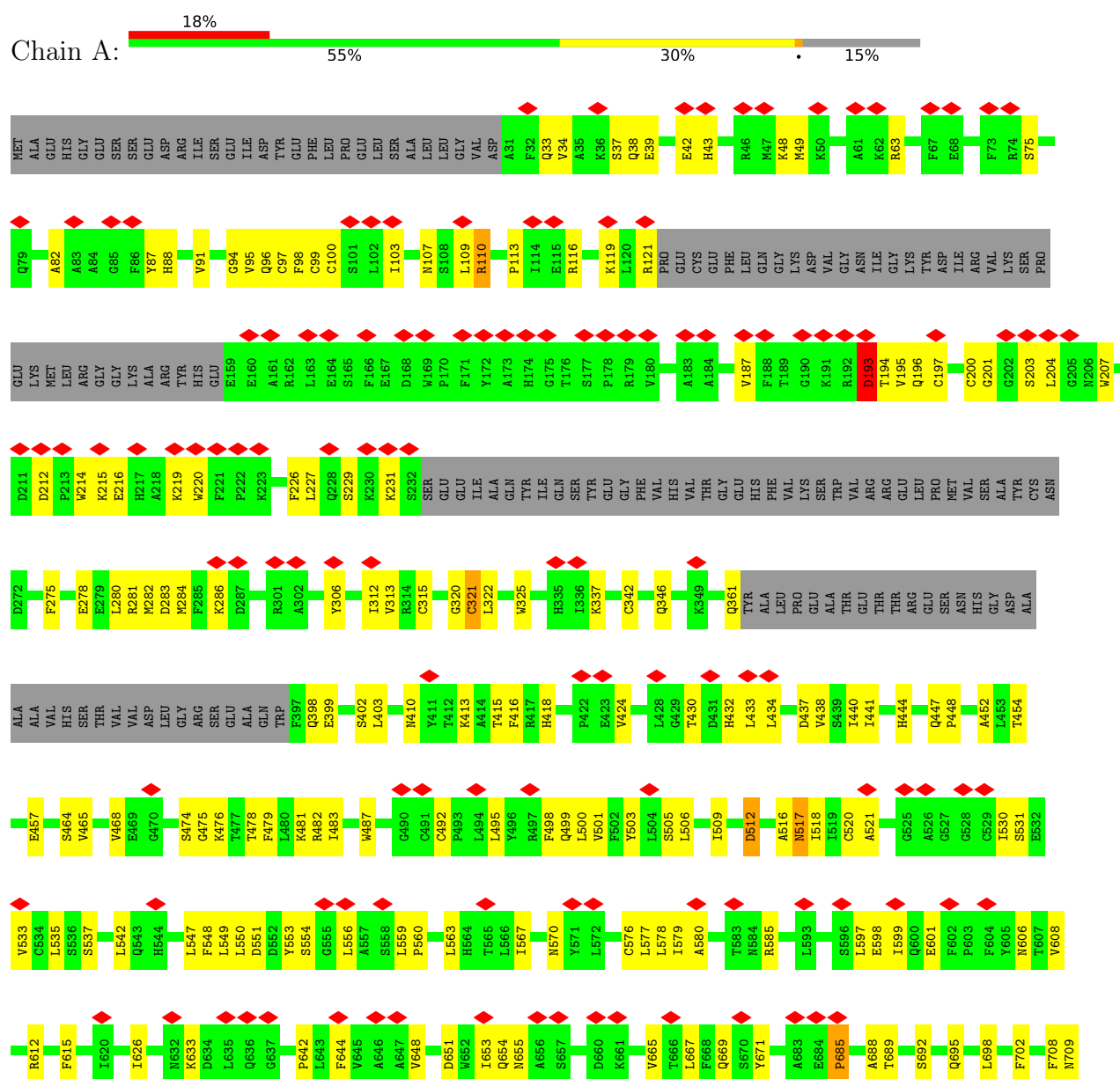
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Chain	Residue	Modelled	Actual	Comment	Reference
F	-35	LYS	-	expression tag	UNP G8U UW9
F	-34	LEU	-	expression tag	UNP G8U UW9
F	-33	ILE	-	expression tag	UNP G8U UW9
F	-32	SER	-	expression tag	UNP G8U UW9
F	-31	GLU	-	expression tag	UNP G8U UW9
F	-30	GLU	-	expression tag	UNP G8U UW9
F	-29	ASP	-	expression tag	UNP G8U UW9
F	-28	LEU	-	expression tag	UNP G8U UW9
F	-27	ASN	-	expression tag	UNP G8U UW9
F	-26	GLU	-	expression tag	UNP G8U UW9
F	-25	MET	-	expression tag	UNP G8U UW9
F	-24	GLU	-	expression tag	UNP G8U UW9
F	-23	SER	-	expression tag	UNP G8U UW9
F	-22	LEU	-	expression tag	UNP G8U UW9
F	-21	GLY	-	expression tag	UNP G8U UW9
F	-20	ASP	-	expression tag	UNP G8U UW9
F	-19	LEU	-	expression tag	UNP G8U UW9
F	-18	THR	-	expression tag	UNP G8U UW9
F	-17	MET	-	expression tag	UNP G8U UW9
F	-16	GLU	-	expression tag	UNP G8U UW9
F	-15	GLN	-	expression tag	UNP G8U UW9
F	-14	LYS	-	expression tag	UNP G8U UW9
F	-13	LEU	-	expression tag	UNP G8U UW9
F	-12	ILE	-	expression tag	UNP G8U UW9
F	-11	SER	-	expression tag	UNP G8U UW9
F	-10	GLU	-	expression tag	UNP G8U UW9
F	-9	GLU	-	expression tag	UNP G8U UW9
F	-8	ASP	-	expression tag	UNP G8U UW9
F	-7	LEU	-	expression tag	UNP G8U UW9
F	-6	ASN	-	expression tag	UNP G8U UW9
F	-5	SER	-	expression tag	UNP G8U UW9
F	-4	GLY	-	expression tag	UNP G8U UW9
F	-3	ARG	-	expression tag	UNP G8U UW9
F	-2	PRO	-	expression tag	UNP G8U UW9
F	-1	ALA	-	expression tag	UNP G8U UW9
F	0	ALA	-	expression tag	UNP G8U UW9
F	1	MET	-	expression tag	UNP G8U UW9

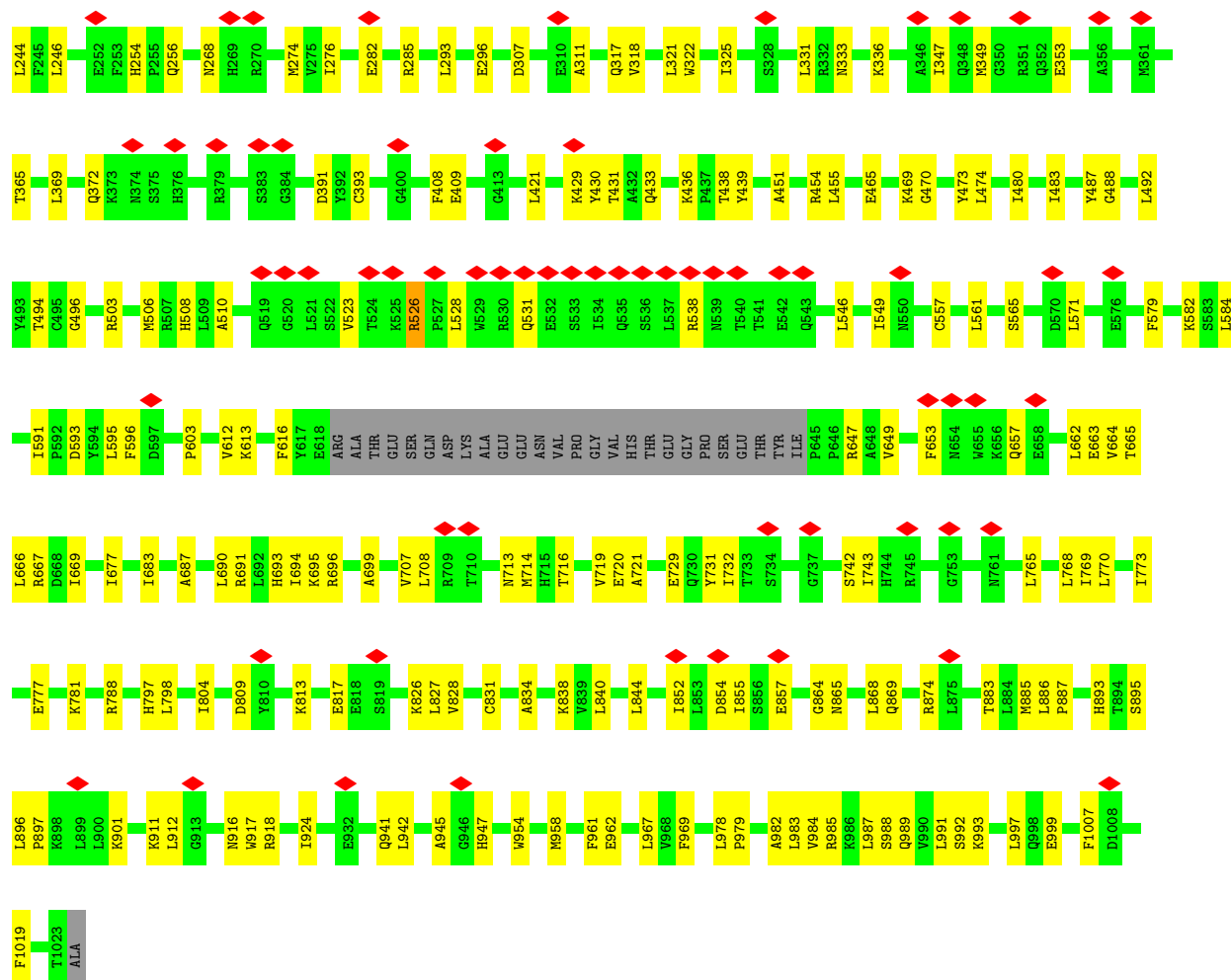
### 3 Residue-property plots

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.

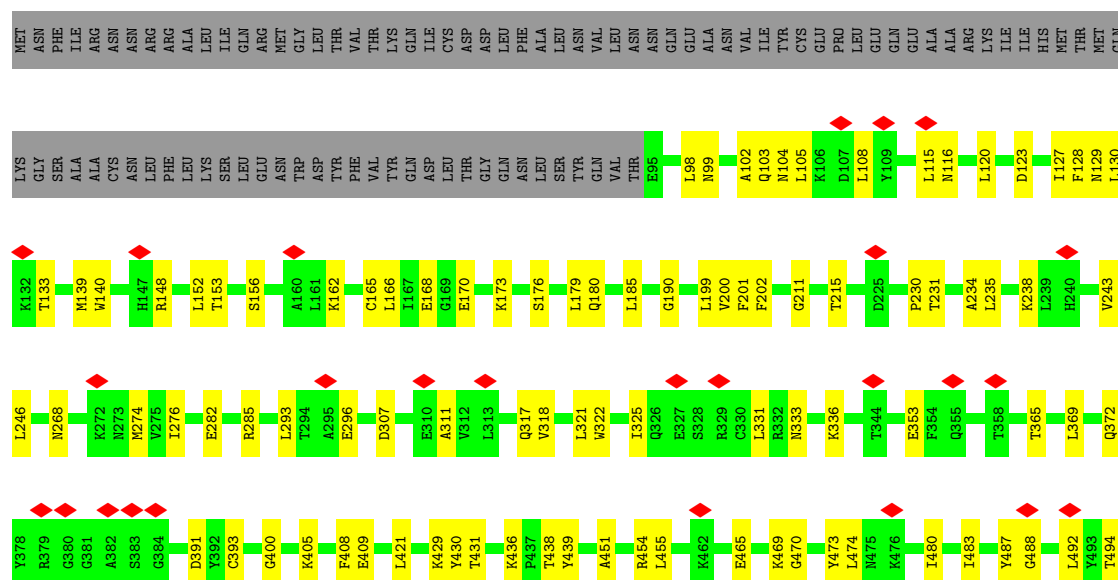
- Molecule 1: Baculoviral IAP repeat-containing protein 1e







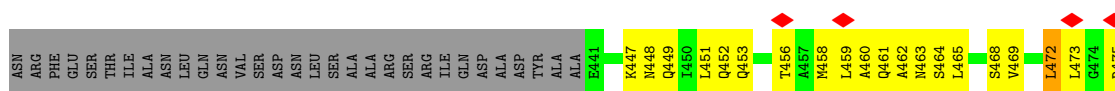
• Molecule 2: NLR family CARD domain-containing protein 4







THR	ILE	THR	GLN	ILE	GLY	SER	ILE	GLU	SER	ILE	GLU	ASP	GLU	MET
ILE	ALA	THR	GLY	GLY	GLY	SER	SER	ASP	SER	GLN	GLN	GLN	GLN	GLN
ILE	VAL	VAL	VAL	ALA	ALA	GLN	GLN	ASN	ARG	ARG	GLU	ASN	ASN	LYS
GLY	GLY	ALA	ALA	VAL	ALA	GLU	GLU	MET	THR	THR	MET	MET	ILE	ILE
THR	THR	SER	THR	THR	THR	ILE	ILE	GLU	ALA	ALA	GLU	GLU	SER	SER
VAL	ALA	ALA	ALA	THR	GLY	SER	SER	ALA	GLN	GLN	THR	THR	GLU	GLU
ALA	ALA	GLN	GLN	GLN	GLY	GLY	GLY	ASP	ASN	ASN	LEU	LEU	ASN	ASN
ASN	ASN	THR	THR	THR	THR	THR	THR	THR	GLU	GLU	GLU	GLU	GLU	GLU
ILE	GLY	GLY	GLY	SER	VAL	LYS	LYS	GLY	ARG	ARG	GLY	ASP	ASP	ASP
GLY	GLY	ASN	GLY	ALA	ALA	SER	SER	ALA	MET	MET	LEU	LEU	ASN	ASN
LEU	LEU	MET	THR	THR	GLY	GLU	GLU	ASP	ASN	ASN	THR	THR	GLU	GLU
ALA	ALA	LEU	ALA	ALA	ALA	GLU	GLU	ALA	GLN	GLN	MET	MET	MET	MET
ASN	ASN	THR	THR	VAL	ALA	ARG	ARG	VAL	VAL	VAL	GLN	GLN	GLN	GLN
ILE	ILE	ALA	GLY	ALA	ALA	ILE	ILE	ARG	ARG	ARG	LYS	LYS	LYS	LYS
SER	SER	ALA	ALA	ASP	ASP	GLN	GLN	ALA	ALA	ALA	LEU	LEU	LEU	LEU
LYS	LYS	ASP	ILE	ILE	ILE	ILE	ILE	ASP	GLY	GLY	ILE	ILE	ILE	ILE
ASP	ASP	THR	GLY	THR	THR	THR	THR	THR	ASN	ASN	SER	SER	SER	SER
THR	THR	THR	THR	THR	THR	THR	THR	THR	GLN	GLN	GLY	GLY	GLY	GLY
LEU	LEU	GLU	GLU	GLY	GLY	GLY	GLY	ALA	ALA	ALA	GLY	GLY	GLY	GLY
ASP	ASP	SER	SER	ALA	ALA	ILE	ILE	ILE	ILE	ILE	PRO	PRO	GLN	GLN
VAL	VAL	GLY	GLY	LEU	THR	ASP	ASP	ALA	GLU	GLU	ALA	ALA	LYS	LYS
SER	SER	THR	THR	THR	ILE	GLY	GLY	ALA	GLY	GLY	ALA	ALA	LEU	LEU
THR	THR	GLY	GLY	ILE	ILE	ASN	ASN	ALA	ALA	ALA	M1	M1	ILE	ILE
GLY	GLY	ALA	ALA	VAL	VAL	SER	SER	VAL	GLN	GLN	N6	N6	GLU	GLU
ALA	ALA	GLY	GLY	ALA	ALA	GLY	GLY	ALA	THR	THR	L12	L12	GLU	GLU
GLN	GLN	THR	THR	ASN	PHE	ALA	ALA	ASN	THR	THR	L12	L12	ASP	ASP
THR	THR	ASP	ASP	TYR	THR	PHE	PHE	THR	ASN	ASN	N20	N20	LEU	LEU
ILE	ILE	GLY	GLY	THR	THR	THR	THR	GLY	ILE	ILE	N20	N20	GLU	GLU
LYS	LYS	THR	THR	VAL	VAL	LYS	LYS	ALA	LEU	LEU	N23	N23	MET	MET
ARG	ARG	VAL	VAL	ASN	ASN	GLY	GLY	VAL	GLN	GLN	N23	N23	GLU	GLU
ILE	ILE	THR	THR	VAL	VAL	ALA	ALA	ARG	ARG	ARG	S28	S28	GLN	GLN
ASP	ASP	GLY	GLY	GLY	GLY	ASN	ASN	ASN	MET	MET	S28	S28	LYS	LYS
ALA	ALA	ALA	THR	THR	THR	SER	SER	THR	ARG	ARG	S33	S33	LEU	LEU
ALA	ALA	PHE	PHE	ALA	ALA	GLN	GLN	LEU	GLU	GLU	S33	S33	ILE	ILE
ASN	ASN	THR	THR	THR	THR	THR	THR	SER	SER	SER	SER	SER	SER	SER
SER	SER	ASP	ASP	ASP	ASP	THR	THR	GLY	GLY	GLY	GLY	GLY	GLU	GLU
VAL	VAL	ALA	ALA	ALA	ALA	ILE	ILE	VAL	VAL	VAL	LEU	LEU	ASP	ASP
ASN	ASN	LEU	LEU	TYR	TYR	PHE	PHE	ALA	ALA	ALA	ILE	ILE	GLU	GLU
SER	SER	LEU	LEU	ALA	ALA	SER	SER	ALA	ALA	ALA	ASN	ASN	ASN	ASN
ASN	ASN	GLY	GLY	LYS	LYS	ILE	ILE	ARG	ARG	ARG	SER	SER	GLU	GLU
ARG	ARG	THR	THR	ASP	ASP									



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	252214	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	45.8	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.188	Depositor
Minimum map value	-0.102	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	586.88, 586.88, 586.88	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3100001, 1.3100001, 1.3100001	Depositor

## 5 Model quality

### 5.1 Standard geometry

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	0.31	0/9782	0.63	11/13218 (0.1%)
2	B	0.27	0/7376	0.50	0/9957
2	C	0.27	0/7376	0.50	0/9957
3	F	0.26	0/497	0.63	1/668 (0.1%)
All	All	0.29	0/25031	0.55	12/33800 (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
1	A	0	9

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	822	LEU	CA-CB-CG	6.98	131.36	115.30
1	A	1241	LEU	CA-CB-CG	6.70	130.70	115.30
3	F	472	LEU	CA-CB-CG	6.65	130.59	115.30
1	A	719	ASP	CB-CG-OD1	6.64	124.28	118.30
1	A	1356	LEU	CA-CB-CG	6.52	130.29	115.30

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1107	LEU	Peptide
1	A	321	CYS	Peptide
1	A	447	GLN	Peptide
1	A	685	PRO	Peptide

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Mol	Chain	Res	Type	Group
1	A	831	TYR	Peptide

## 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	9583	0	9567	310	0
2	B	7237	0	7285	165	0
2	C	7237	0	7285	164	0
3	F	498	0	525	18	0
All	All	24555	0	24662	648	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 13.

The worst 5 of 648 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:313:VAL:O	1:A:321:CYS:HA	1.10	1.25
1:A:313:VAL:O	1:A:321:CYS:CA	2.01	1.07
1:A:785:ALA:O	1:A:789:PHE:HB2	1.58	1.03
1:A:1252:ALA:O	1:A:1256:VAL:HB	1.62	0.98
3:F:459:LEU:O	3:F:463:ASN:HB2	1.64	0.97

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	1187/1403 (85%)	1011 (85%)	175 (15%)	1 (0%)	51	85
2	B	899/1024 (88%)	839 (93%)	60 (7%)	0	100	100
2	C	899/1024 (88%)	839 (93%)	60 (7%)	0	100	100
3	F	64/566 (11%)	60 (94%)	4 (6%)	0	100	100
All	All	3049/4017 (76%)	2749 (90%)	299 (10%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	193	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	1080/1258 (86%)	1069 (99%)	11 (1%)	76	86
2	B	807/913 (88%)	805 (100%)	2 (0%)	93	96
2	C	807/913 (88%)	805 (100%)	2 (0%)	93	96
3	F	56/437 (13%)	54 (96%)	2 (4%)	35	59
All	All	2750/3521 (78%)	2733 (99%)	17 (1%)	86	91

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	526	ARG
3	F	475	ARG
1	A	1234	LEU
1	A	1235	ARG
1	A	1322	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	144	HIS
3	F	449	GLN
2	B	797	HIS
2	C	869	GLN
2	B	317	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

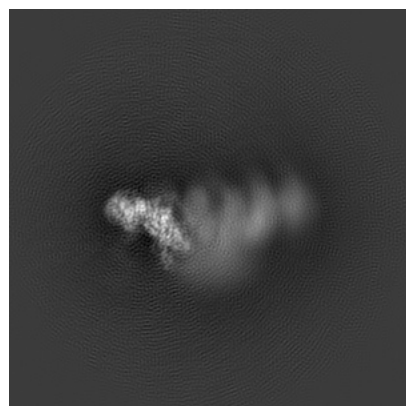
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7055. These allow visual inspection of the internal detail of the map and identification of artifacts.

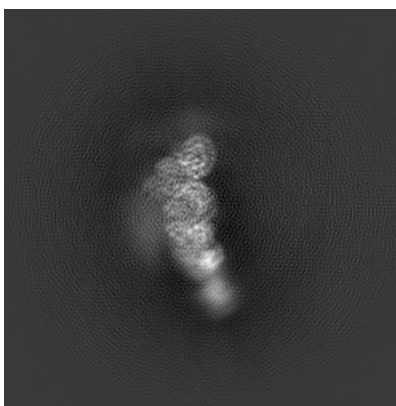
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

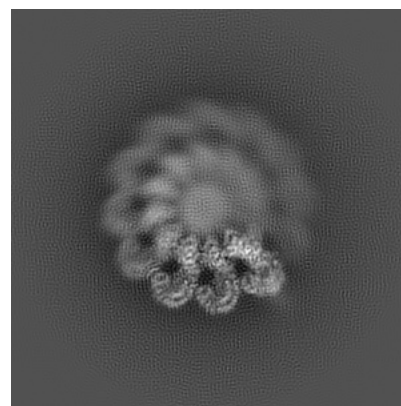
#### 6.1.1 Primary map



X

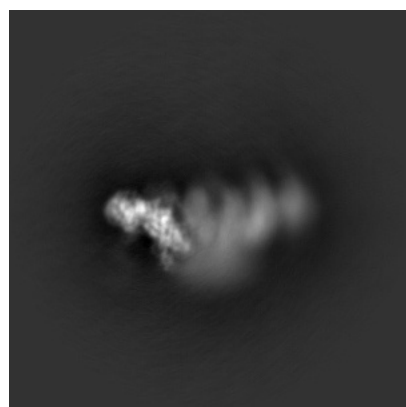


Y

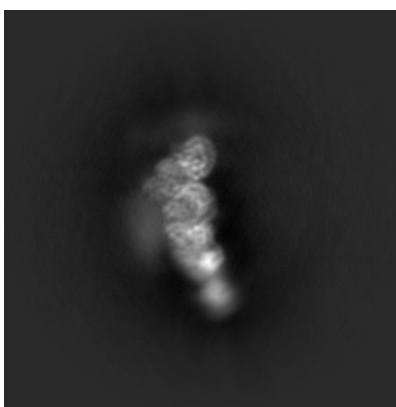


Z

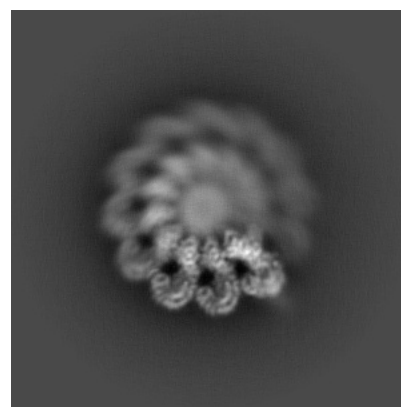
#### 6.1.2 Raw map



X



Y

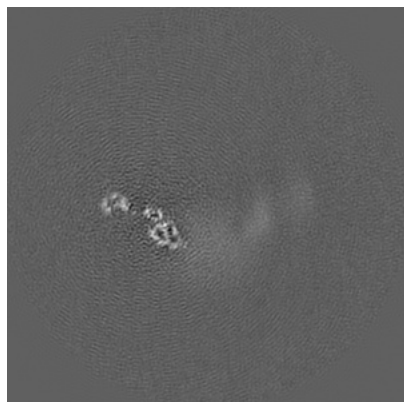


Z

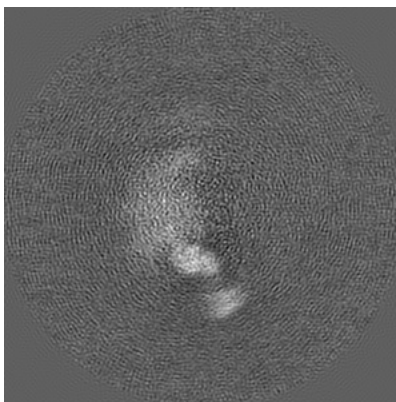
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

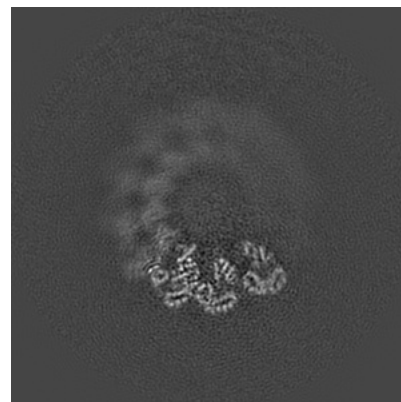
### 6.2.1 Primary map



X Index: 224

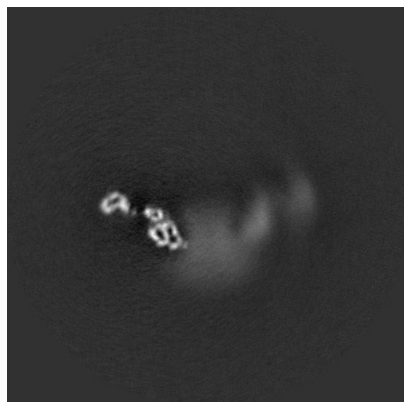


Y Index: 224

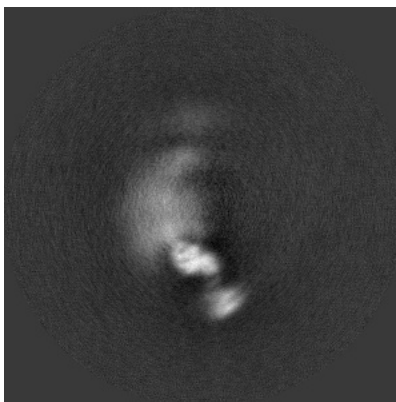


Z Index: 224

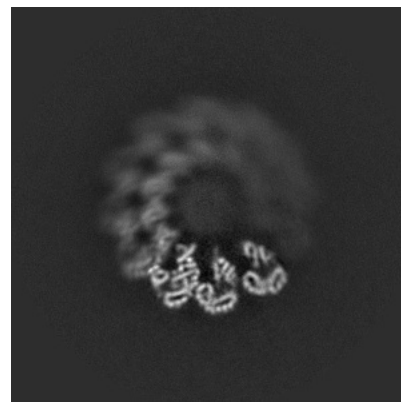
### 6.2.2 Raw map



X Index: 224



Y Index: 224



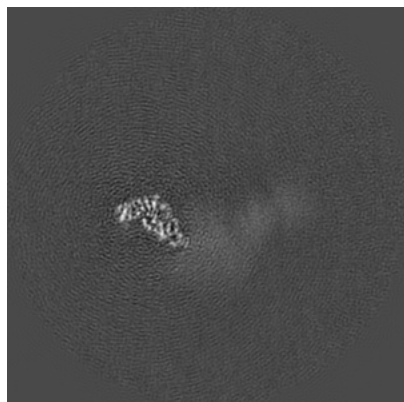
Z Index: 224

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

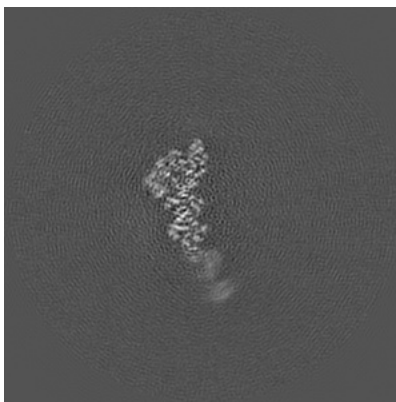


## 6.3 Largest variance slices [i](#)

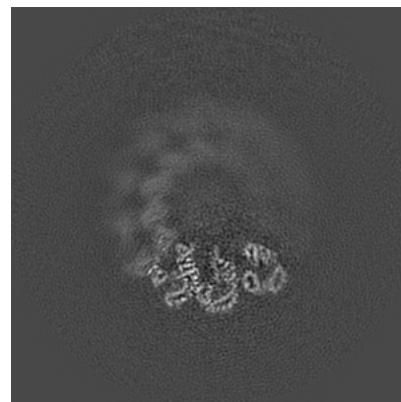
### 6.3.1 Primary map



X Index: 201

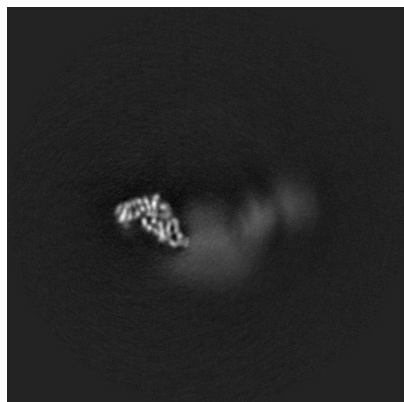


Y Index: 173

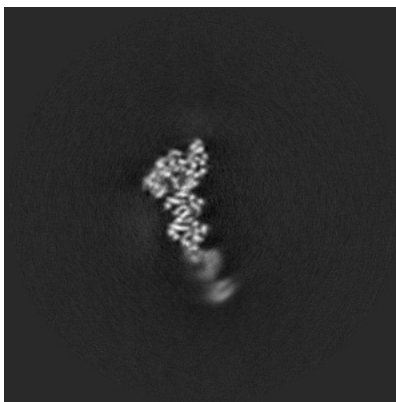


Z Index: 222

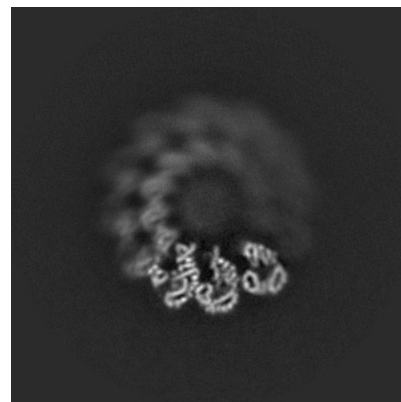
### 6.3.2 Raw map



X Index: 201



Y Index: 173



Z Index: 222

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

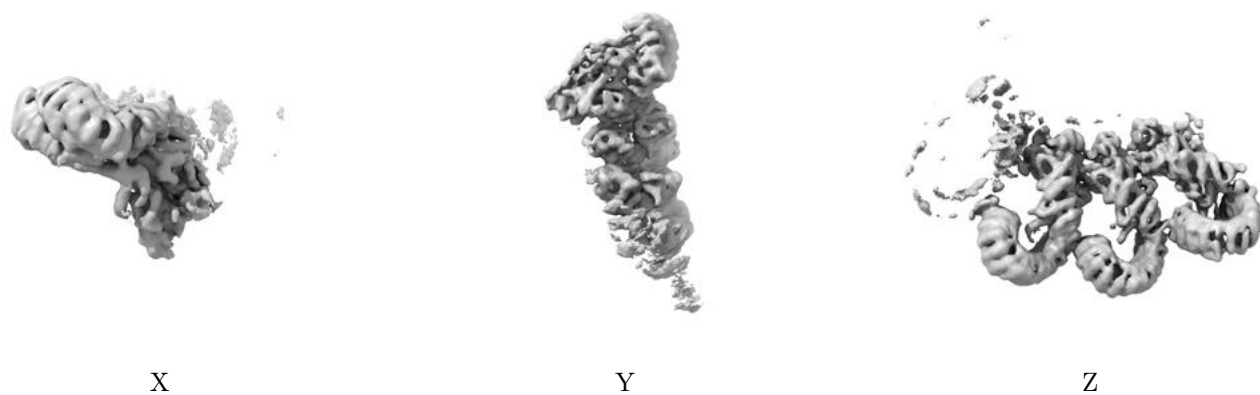
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map



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

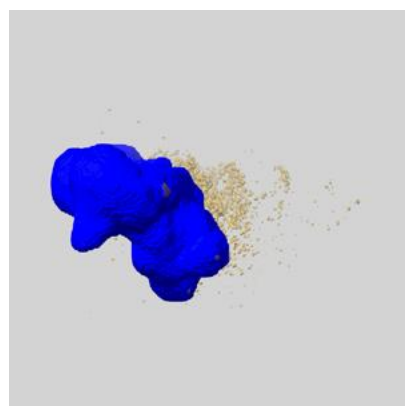
## 6.5 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

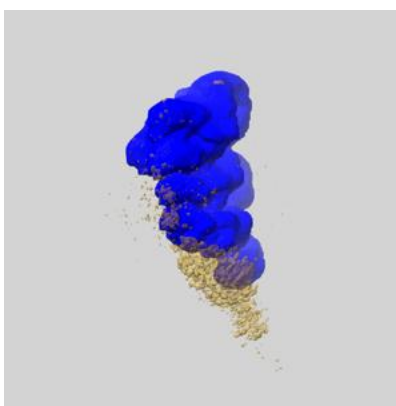
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

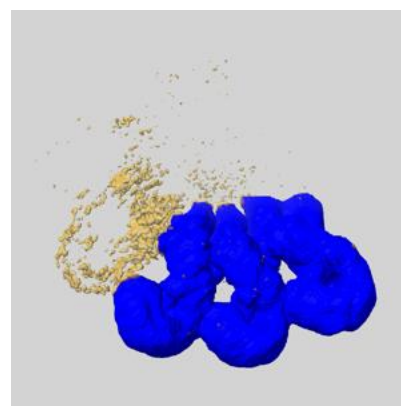
### 6.5.1 emd\_7055\_msk\_1.map [i](#)



X



Y

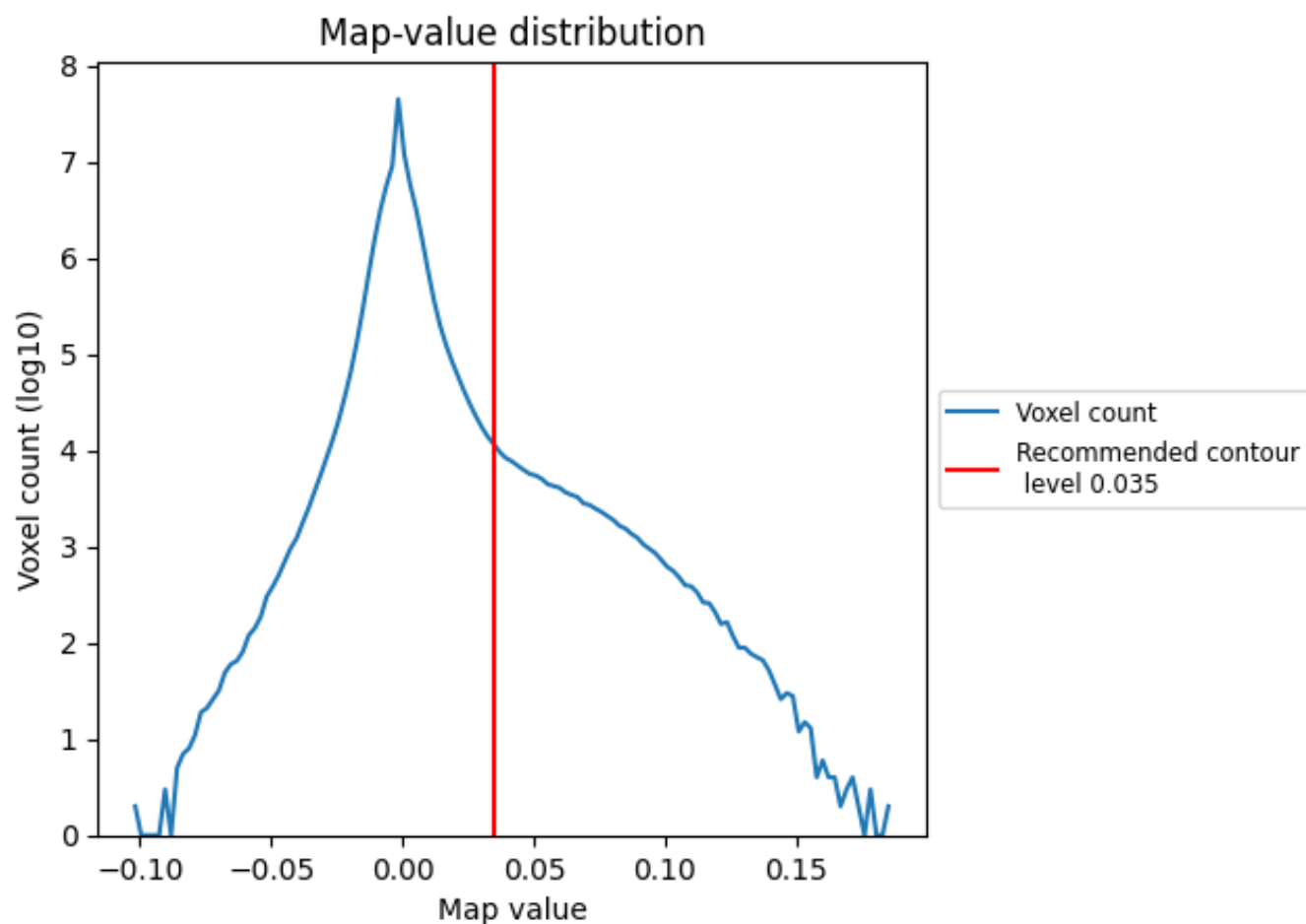


Z

## 7 Map analysis [i](#)

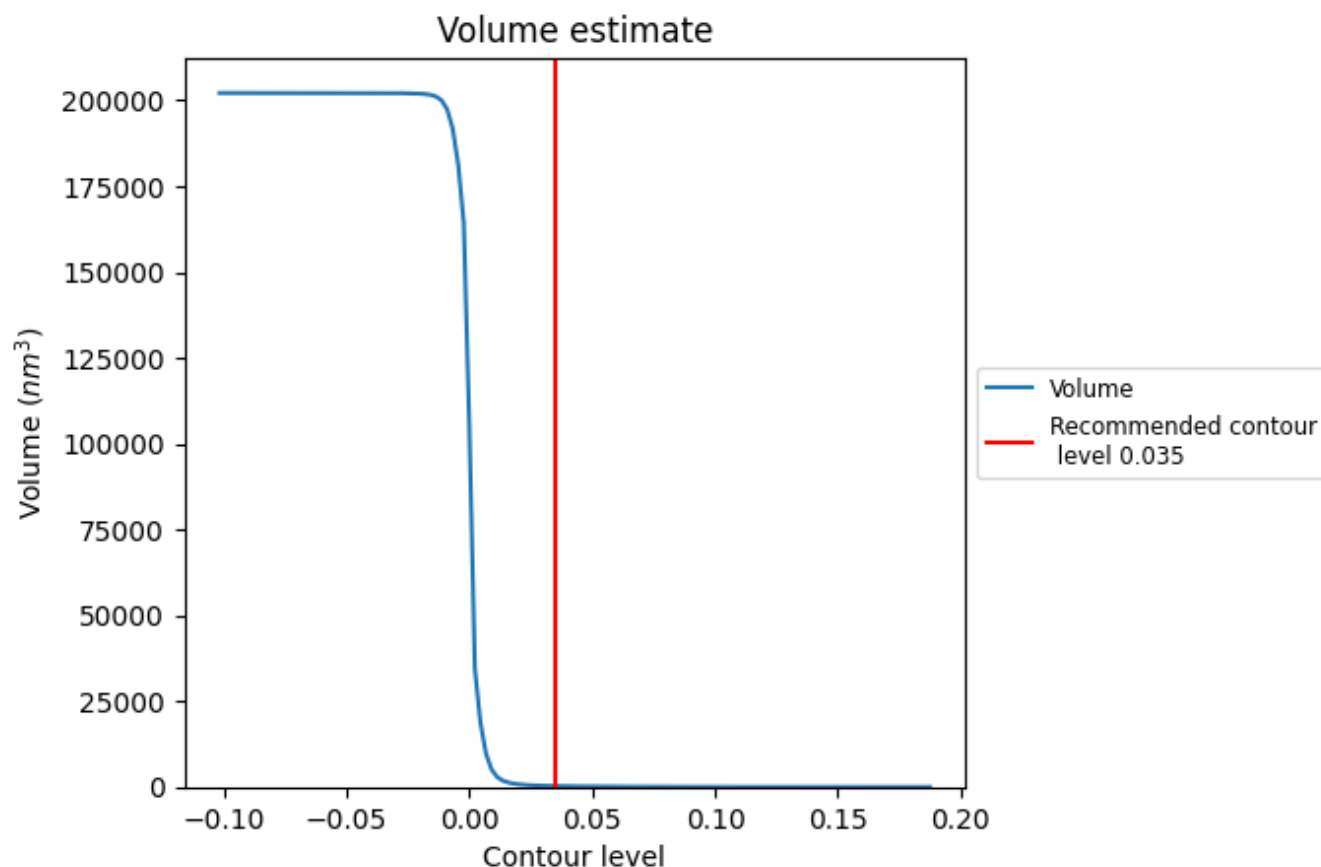
This section contains the results of statistical analysis of the map.

### 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.

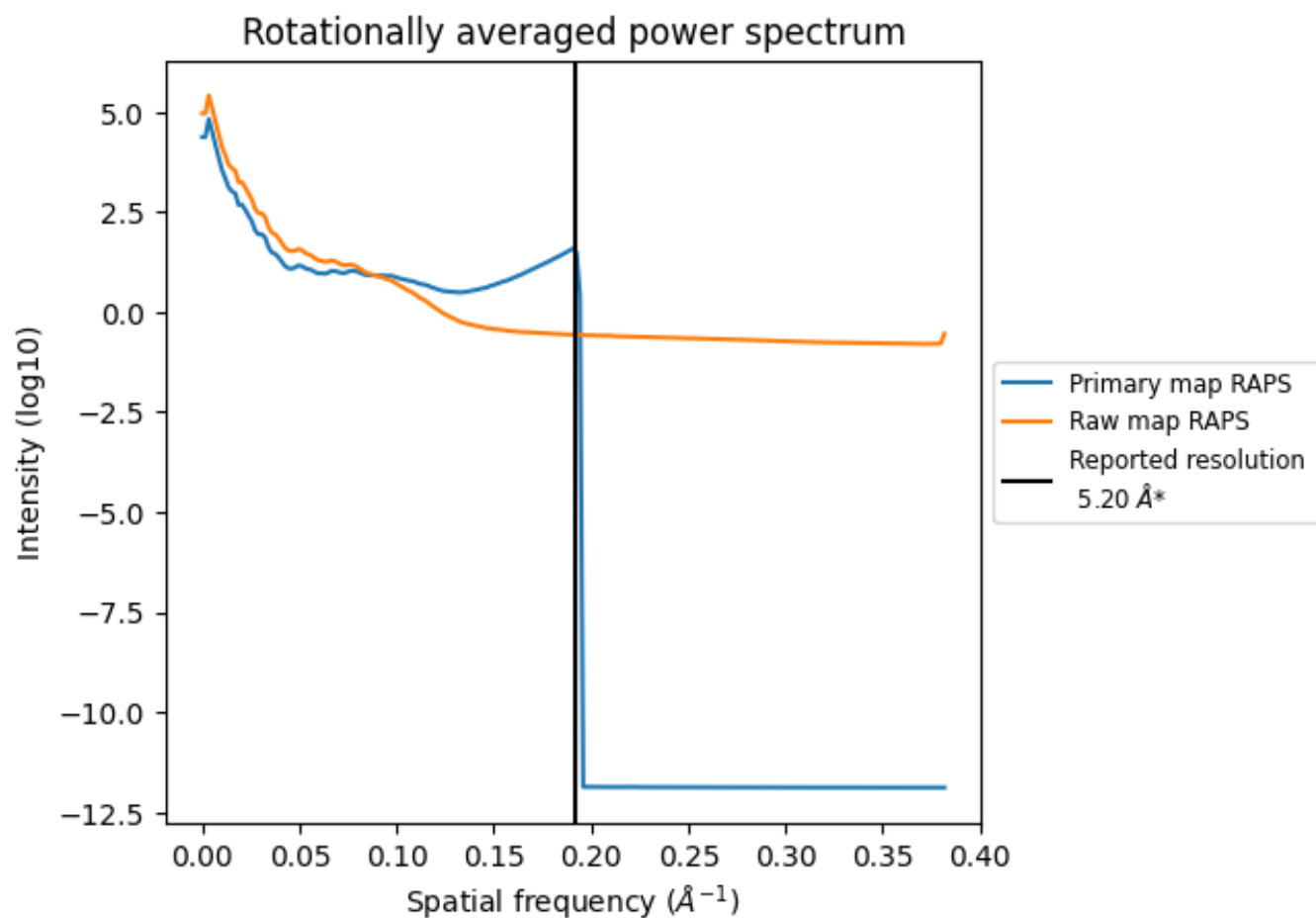
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 265  $\text{nm}^3$ ; this corresponds to an approximate mass of 239 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 ⓘ

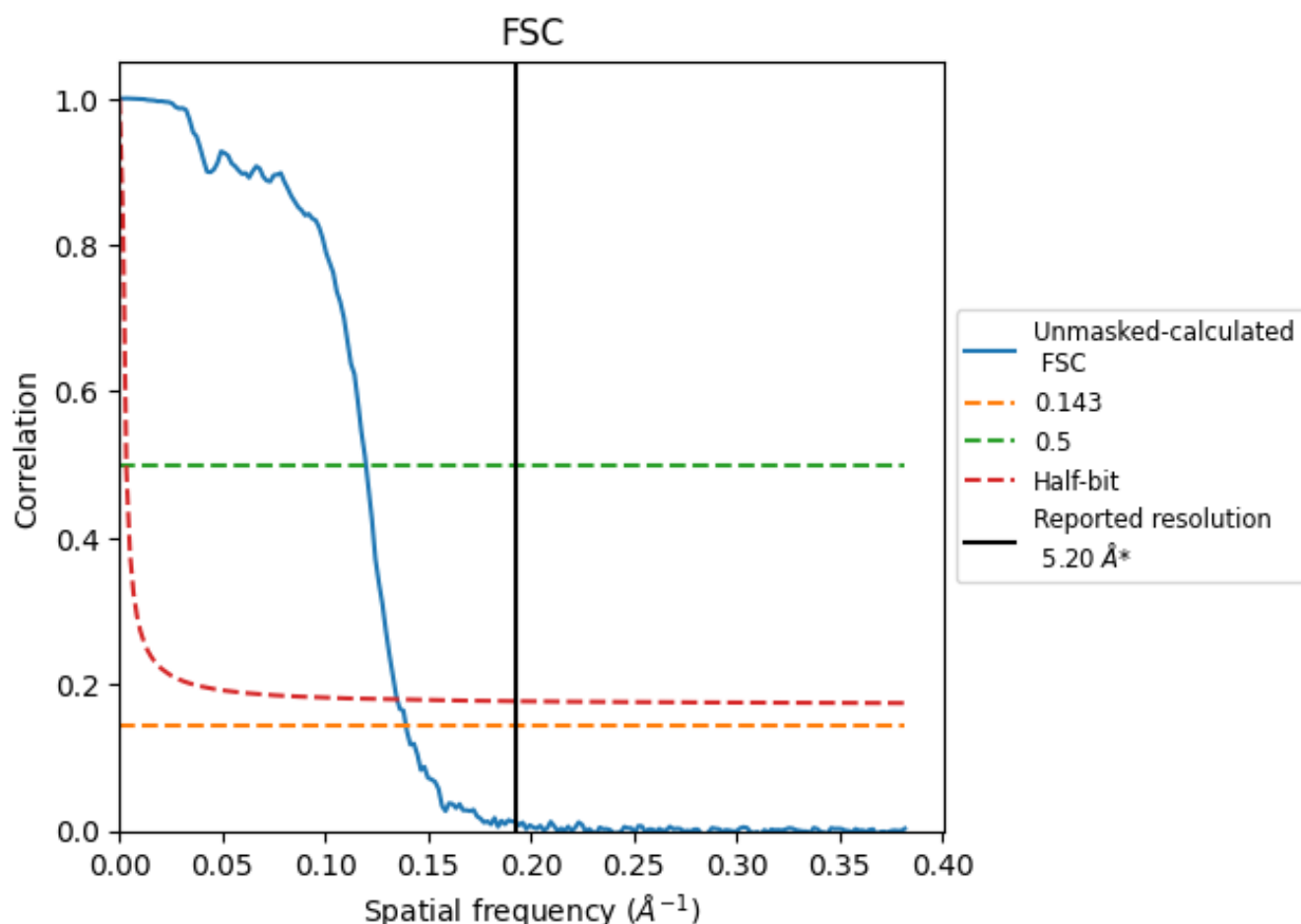


\*Reported resolution corresponds to spatial frequency of 0.192  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.192 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	7.18	8.35	7.41

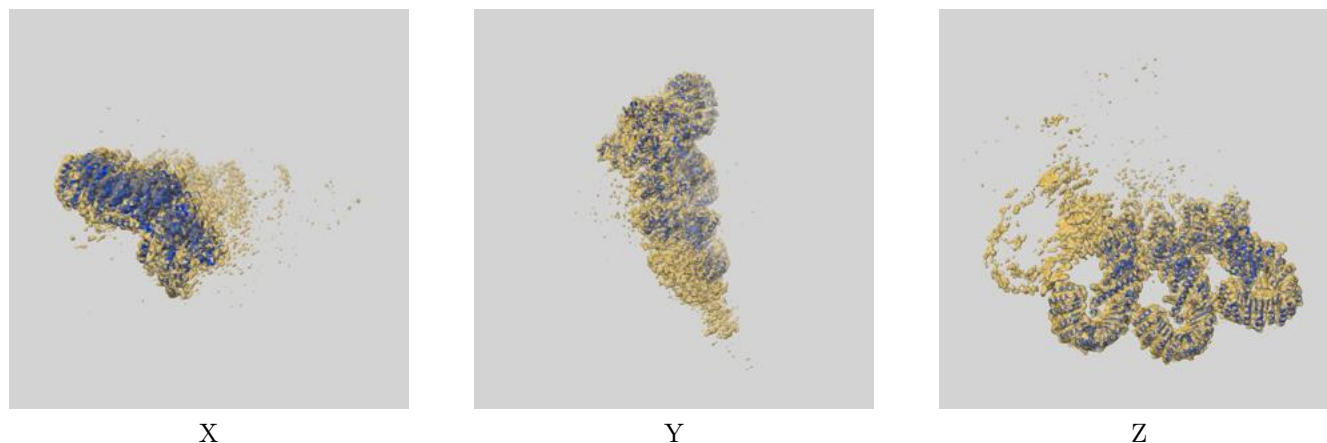
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.18 differs from the reported value 5.2 by more than 10 %



## 9 Map-model fit [i](#)

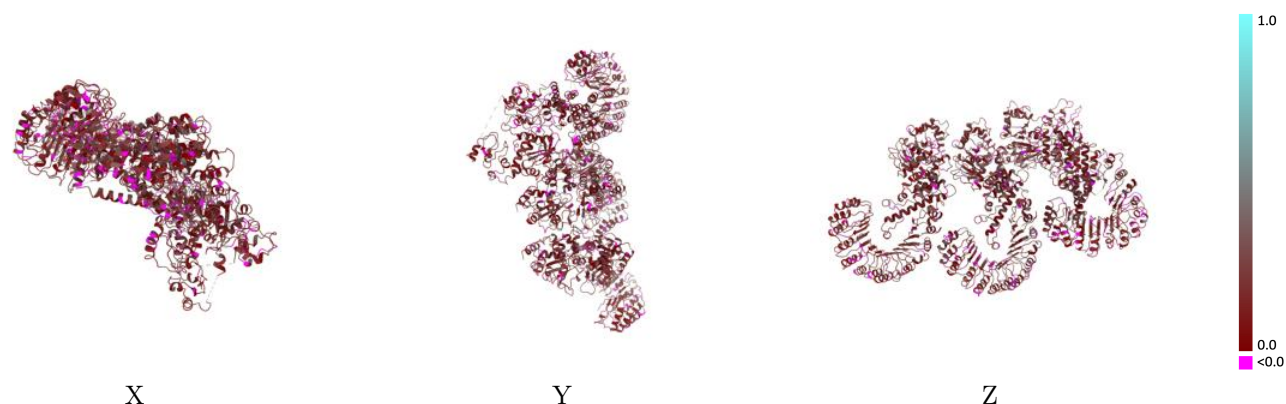
This section contains information regarding the fit between EMDB map EMD-7055 and PDB model 6B5B. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

### 9.1 Map-model overlay [i](#)



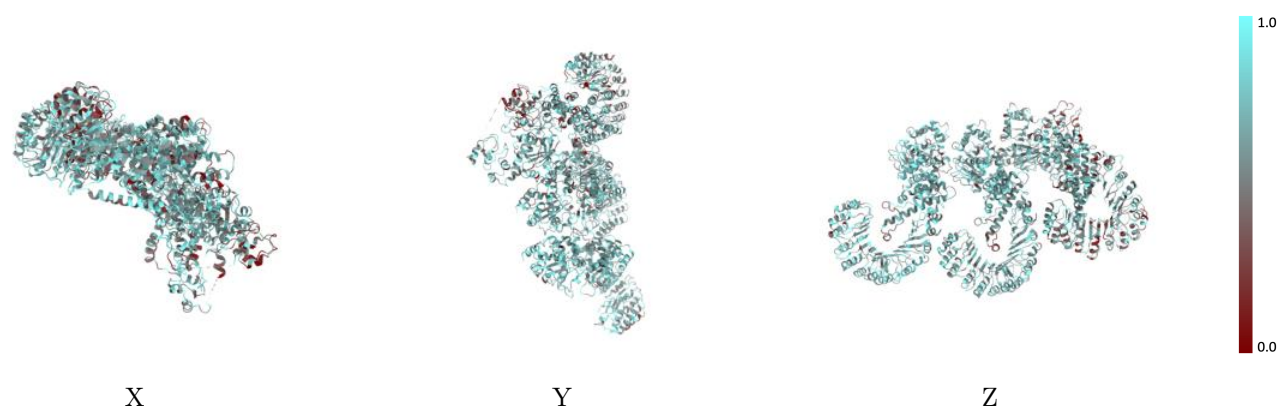
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



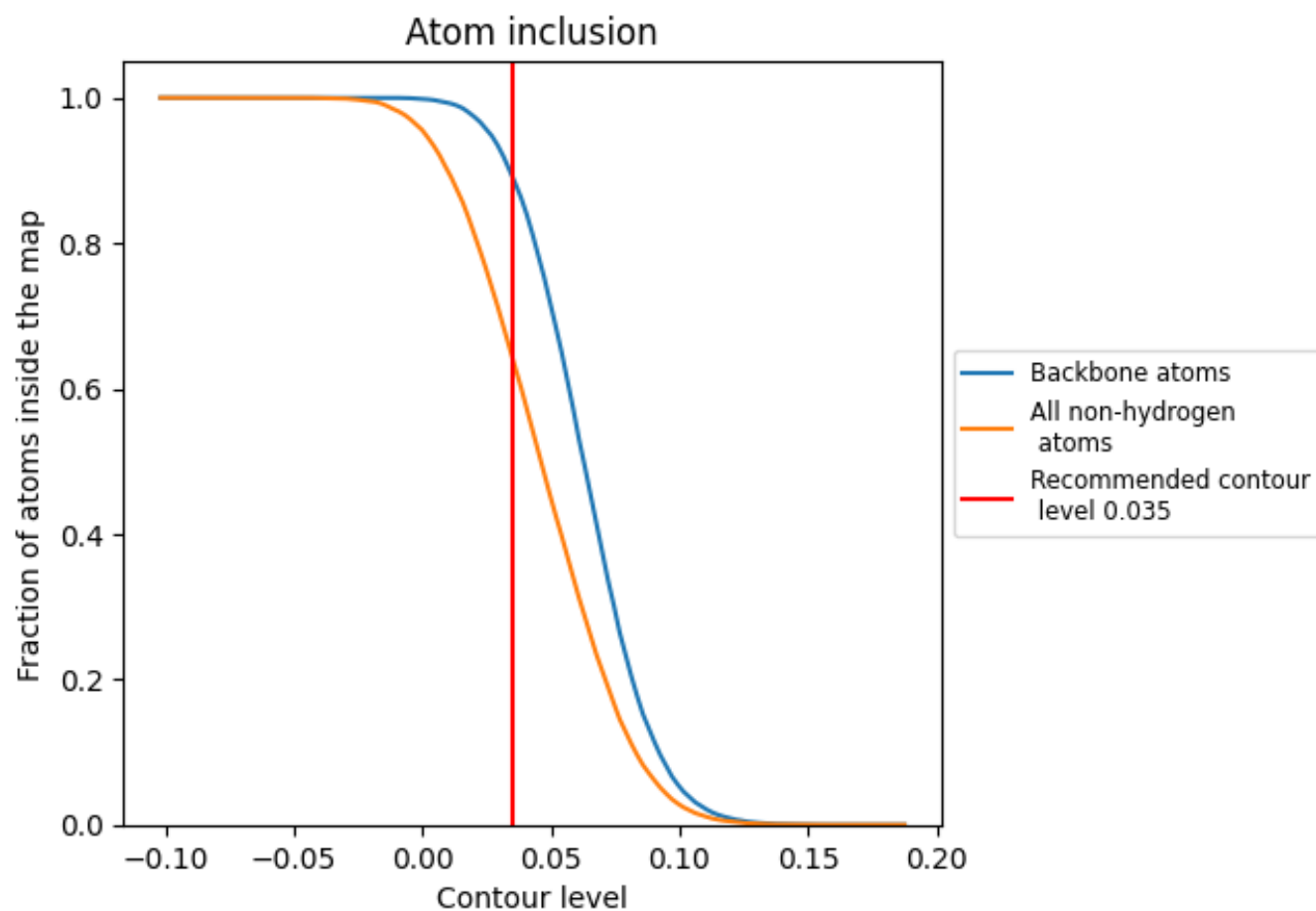
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 64% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6425	<div></div> 0.1880
A	<div></div> 0.5994	<div></div> 0.1790
B	<div></div> 0.6617	<div></div> 0.2030
C	<div></div> 0.6784	<div></div> 0.1850
F	<div></div> 0.6687	<div></div> 0.1740

