



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 05:26 AM UTC

PDB ID : 8R0T / pdb_00008r0t
EMDB ID : EMD-18803
Title : STRUCTURE OF THE MOUSE FCGBP DIMER PROTEIN IN ITS SEMIEXTENDED CONFORMATION
Authors : Gallego, P.; Hansson, G.C.; Johansson, M.E.V.
Deposited on : 2023-10-31
Resolution : 3.90 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
Mogul : 2022.3.0, CSD as543be (2022)
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

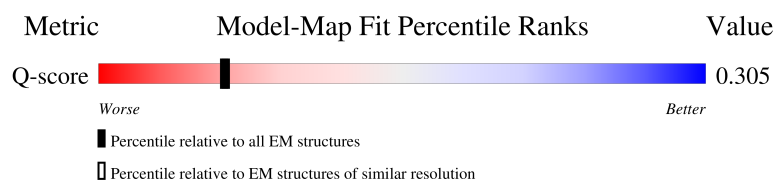
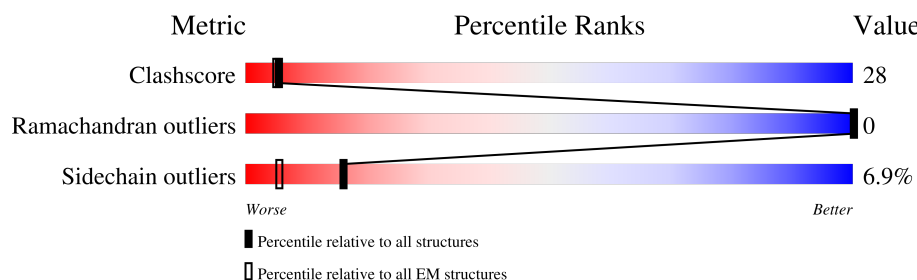
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	8855 (3.40 - 4.40)

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	1232	99%
2	B	399	54% 43%
3	C	930	57% 38%
3	F	930	12% 8% 79%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 11461 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 Fc fragment of IgG binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	13	Total	C	N	O	S	0	0
			110	71	17	21	1		

- Molecule 2 is a protein called Fc fragment of IgG binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	399	Total	C	N	O	S	0	0
			2946	1835	498	576	37		

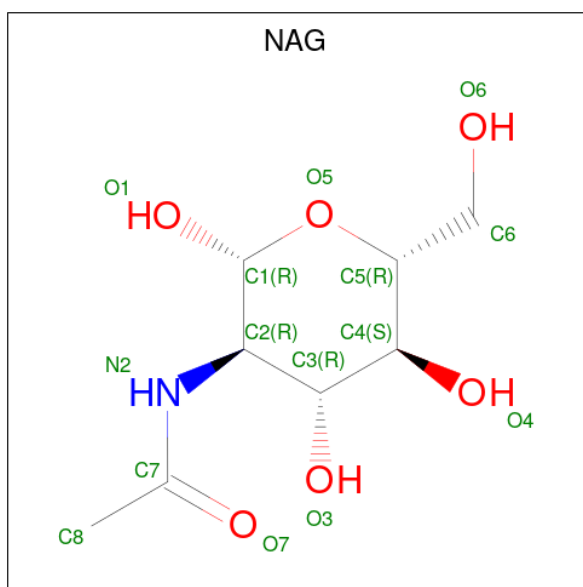
- Molecule 3 is a protein called Fc fragment of IgG binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	927	Total	C	N	O	S	1	0
			6854	4252	1197	1322	83		
3	F	195	Total	C	N	O	S	0	0
			1449	901	259	276	13		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	2584	THR	-	expression tag	UNP E9Q9C6
C	2585	ARG	-	expression tag	UNP E9Q9C6
C	2586	THR	-	expression tag	UNP E9Q9C6
C	2587	ARG	-	expression tag	UNP E9Q9C6
F	2584	THR	-	expression tag	UNP E9Q9C6
F	2585	ARG	-	expression tag	UNP E9Q9C6
F	2586	THR	-	expression tag	UNP E9Q9C6
F	2587	ARG	-	expression tag	UNP E9Q9C6

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	F	1	Total	C	N	O	0
			14	8	1	5	

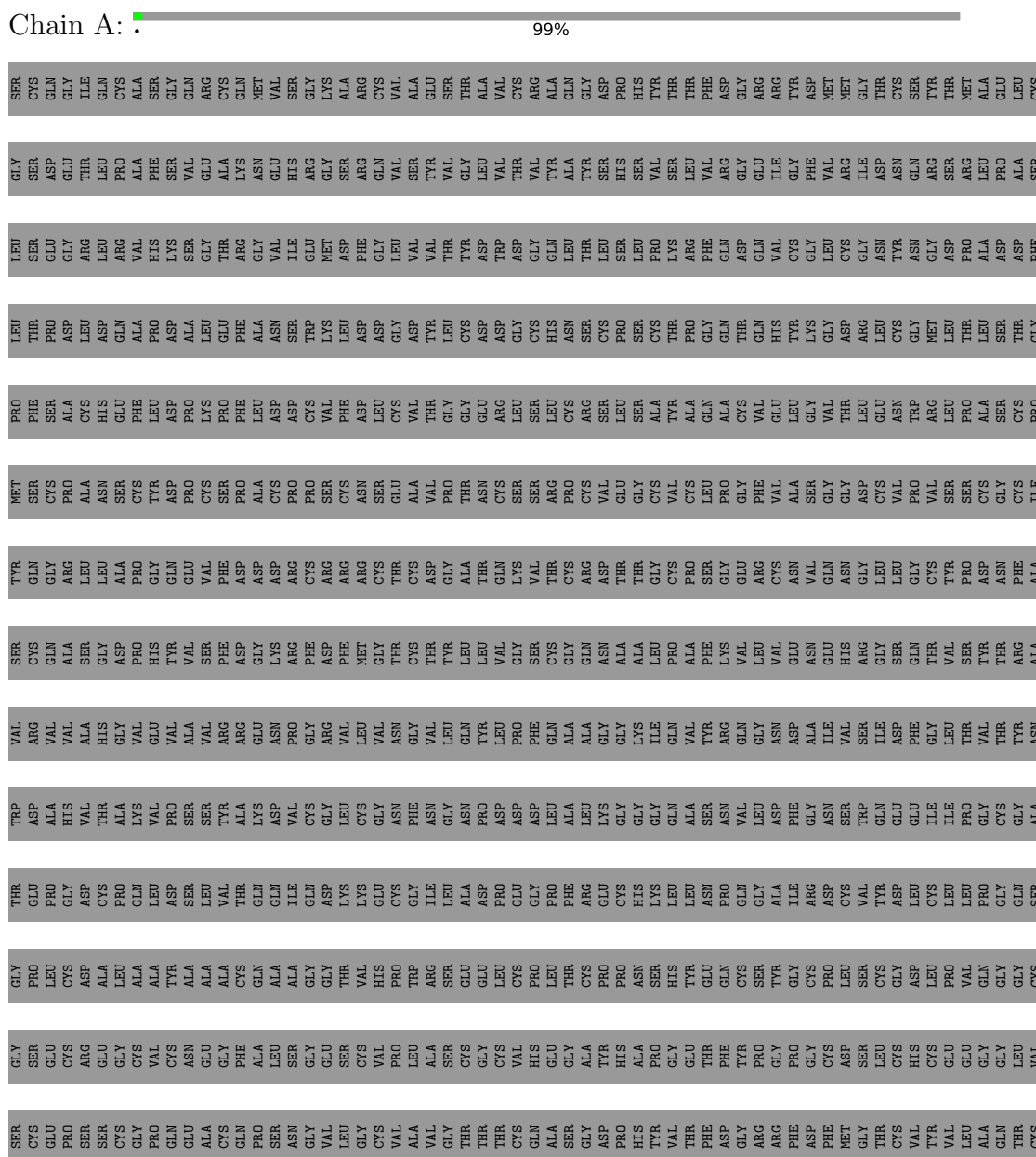
- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
5	B	1	Total	Ca	0
			1	1	
5	C	2	Total	Ca	0
			2	2	
5	F	1	Total	Ca	0
			1	1	

3 Residue-property plots

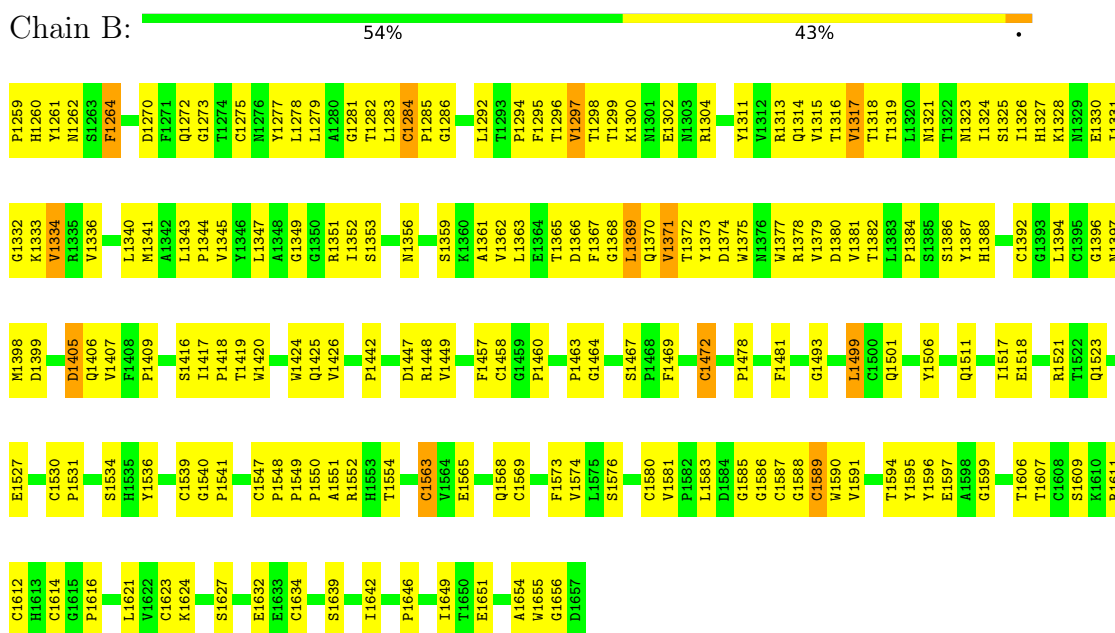
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Fc fragment of IgG binding protein



GLY	THR	CYS	PHE	PRO	LYS	ASP	GLY
ILE	THR	TYR	CYS	THR	PRO	GLY	GLY
THR	HIS	ASN	THR	PRO	ASP	GLY	ASN
CYS	ARG	GLY	MET	LEU	GLY	ILE	PRO
PRO	VAL	VAL	CYS	ALA	GLN	ARG	LEU
GLN	TYR	TYR	PRO	ALA	THR	VAL	HIS
GLU	TYR	THR	PRO	CYS	THR	SER	GLN
THR	GLU	HIS	HIS	HIS	ASP	GLN	PHE
CYS	PRO	PRO	SER	LYS	PRO	HIS	THR
LYS	GLU	GLU	HIS	LEU	SER	GLY	VAL
VAL	GLU	GLU	TYR	LEU	ASP	SER	LEU
GLN	SER	SER	GLU	ASP	PHE	ASP	GLN
GLY	VAL	VAL	VAL	PRO	GLY	VAL	GLU
GLY	LEU	LEU	GLN	GLY	SER	ILE	ASN
GLU	ILE	ILE	ALA	GLY	SER	GLU	ALA
GLY	GLU	GLU	ASP	PRO	TRP	GLU	TRP
VAL	ASN	ASN	THR	LEU	GLU	THR	GLY
CYS	CYS	CYS	CYS	GLN	GLU	ASP	GLY
W1246							
C1263							
W1254							
L1255							
W1266							
G1267							
D1268							

- Molecule 2: Fc fragment of IgG binding protein



- Molecule 3: Fc fragment of IgG binding protein



L2546	L2468	CYS	ALA	MET
F2553	V2469	SER	LEU	CYS
	S2470	PRO	SER	ALA
D2556	K2471	ASN	HIS	ALA
Q2557	V2472	ASN	LEU	LYS
T2558	H2473	GLY	THR	GLY
N2559	I2474	LEU	GLY	ASP
D2560		THR	CYS	GLY
	D2478		THR	ASP
Q2565	G2479	CYS	THR	GLY
G2566	L2480	GLU	THR	ALA
K2567	V2481	ALA	CYS	GLN
T2568	T2482	PHE	LEU	ILE
P2569	V2483	GLU	ARG	MET
	I2484	GLY	THR	SER
	P2485	CYS	GLU	ILE
	S2486	LEU	VAL	PRO
K2572	K2487	CYS	ALA	SER
W2573	G2488	THR	TYR	GLY
	A2489	ASP	ALA	PHE
Q2576	W2490	HIS	GLU	ARG
D2577	V2491	PHE	GLY	GLY
F2578	N2492	GLN	THR	ARG
S2579	G2493	LEU	GLN	ARG
P2580	I2494	ALA	ALA	CYS
C2581	R2495	SER	TYR	GLY
	V2496	HIS	ALA	CYS
T2584	D2497	GLY	GLY	LEU
ARG		ALA	ASN	GLY
ARG	V2502	CYS	VAL	ASN
	L2503	ILE	PRO	ALA
		PRO	ALA	GLY
	R2509	ASN	TRP	ASN
	R2510	ASP	ARG	GLY
	N2511	THR	ILE	TRP
	P2512	CYS	ASP	SER
		GLY	ASP	ASP
		CYS	PRO	ASP
		VAL	VAL	PHE
S2515	S2515	VAL	CYS	GLY
N2516	N2516	PRO	PRO	VAL
L2517	L2517	HIS	ASN	LEU
V2518	V2518	ASN	GLN	PRO
		GLY	ALA	SER
		GLN	CYS	GLY
	V2524	TYR	PRO	ALA
	T2525	K2448	MET	ALA
	V2526	H2449	PRO	HIS
	W2527	V2450	VAL	LYS
	L2528	P2451	SER	ALA
		W2452	ASN	PRO
		Y2453	TYR	VAL
Q2532	Q2532	SER	SER	ASN
L2533	L2533	LEU	LEU	VAL
L2534	L2534	MET	ILE	GLU
D2535	D2535	SER	CYS	ALA
V2536	V2536	SER	THR	ALA
N2537	N2537	SER	GLY	PHE
V2538	V2538	ASP	THR	THR
		CYS	ALA	ALA
	L2542	Q2460	ARG	TRP
	A2543	P2461	CYS	ARG
	A2544	C2462	GLN	ALA
	N2545	N2465	GLY	TRP
			SER	ARG
			CYS	ALA
			VAL	ALA
			TYR	ALA
			ASP	GLY

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	167045	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.357	Depositor
Minimum map value	-0.141	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0267	Depositor
Map size (Å)	302.72, 302.72, 302.72	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0/115	0.37	0/158
2	B	0.25	0/3033	0.55	5/4150 (0.1%)
3	C	0.39	5/7026 (0.1%)	0.77	27/9580 (0.3%)
3	F	0.41	0/1479	0.77	8/2011 (0.4%)
All	All	0.36	5/11653 (0.0%)	0.72	40/15899 (0.3%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2569	PRO	N-CD	8.09	1.59	1.47
3	C	1741	PRO	N-CD	7.11	1.57	1.47
3	C	2451	PRO	N-CD	-6.06	1.39	1.47
3	C	2252	ARG	CA-C	5.34	1.60	1.52
3	C	2557	GLN	CA-C	5.11	1.59	1.52

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2558	THR	N-CA-C	12.18	126.06	111.33
3	C	1935	PRO	N-CA-C	-11.78	92.00	110.50
3	C	2571	GLU	N-CA-C	-9.18	101.27	111.28
3	C	1741	PRO	N-CA-CB	9.17	108.67	102.25
2	B	1442	PRO	CA-N-CD	-8.87	99.58	112.00

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	110	0	90	13	0
2	B	2946	0	2711	163	0
3	C	6854	0	6448	400	0
3	F	1449	0	1409	73	0
4	A	14	0	13	1	0
4	B	14	0	13	0	0
4	C	56	0	52	4	0
4	F	14	0	13	3	0
5	B	1	0	0	0	0
5	C	2	0	0	0	0
5	F	1	0	0	0	0
All	All	11461	0	10749	618	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 28.

The worst 5 of 618 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)
3:C:2474:ILE:HD12	3:C:2476:PHE:CE2	1.39	1.56
2:B:1282:THR:OG1	2:B:1387:TYR:CE2	1.67	1.43
3:C:1979:TYR:HB3	3:C:1985:PHE:CE1	1.51	1.42
3:C:1700:HIS:CD2	3:C:2313:GLN:HG3	1.56	1.40
2:B:1282:THR:OG1	2:B:1387:TYR:HE2	0.96	1.30

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	11/1232 (1%)	10 (91%)	1 (9%)	0	100	100
2	B	397/399 (100%)	366 (92%)	31 (8%)	0	100	100
3	C	926/930 (100%)	858 (93%)	68 (7%)	0	100	100
3	F	193/930 (21%)	177 (92%)	16 (8%)	0	100	100
All	All	1527/3491 (44%)	1411 (92%)	116 (8%)	0	100	100

There are no Ramachandran outliers to report.

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	12/1023 (1%)	12 (100%)	0	100	100
2	B	322/322 (100%)	301 (94%)	21 (6%)	15	42
3	C	748/750 (100%)	696 (93%)	52 (7%)	14	40
3	F	159/750 (21%)	147 (92%)	12 (8%)	12	38
All	All	1241/2845 (44%)	1156 (93%)	85 (7%)	16	41

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	2279	CYS
3	C	2546	LEU
3	C	2312	CYS
3	C	2436	VAL
3	F	2415	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	2520	GLN
3	F	2400	GLN
3	F	2576	GLN
3	F	2463	HIS
3	C	2225	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 11 ligands modelled in this entry, 4 are monoatomic - leaving 7 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	NAG	F	2601	3	14,14,15	0.52	0	17,19,21	0.83	0
4	NAG	C	2604	3	14,14,15	0.28	0	17,19,21	0.52	0
4	NAG	B	1701	2	14,14,15	0.27	0	17,19,21	1.06	1 (5%)
4	NAG	C	2602	3	14,14,15	0.23	0	17,19,21	0.38	0
4	NAG	C	2601	3	14,14,15	0.94	1 (7%)	17,19,21	1.22	1 (5%)
4	NAG	C	2603	3	14,14,15	0.27	0	17,19,21	0.47	0
4	NAG	A	1301	1	14,14,15	0.89	1 (7%)	17,19,21	1.03	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	F	2601	3	-	4/6/23/26	0/1/1/1
4	NAG	C	2604	3	-	4/6/23/26	0/1/1/1
4	NAG	B	1701	2	-	2/6/23/26	0/1/1/1
4	NAG	C	2602	3	-	3/6/23/26	0/1/1/1
4	NAG	C	2601	3	-	2/6/23/26	0/1/1/1
4	NAG	C	2603	3	-	2/6/23/26	0/1/1/1
4	NAG	A	1301	1	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	2601	NAG	O5-C1	3.25	1.49	1.43
4	A	1301	NAG	O5-C1	2.81	1.48	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	2601	NAG	C1-O5-C5	4.80	118.62	112.19
4	A	1301	NAG	C1-O5-C5	4.00	117.55	112.19
4	B	1701	NAG	C1-O5-C5	3.17	116.43	112.19

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1301	NAG	C4-C5-C6-O6
4	C	2604	NAG	C4-C5-C6-O6
4	C	2603	NAG	C4-C5-C6-O6
4	F	2601	NAG	C4-C5-C6-O6
4	B	1701	NAG	C4-C5-C6-O6

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	2601	NAG	3	0
4	C	2604	NAG	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	2601	NAG	2	0
4	C	2603	NAG	1	0
4	A	1301	NAG	1	0

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.

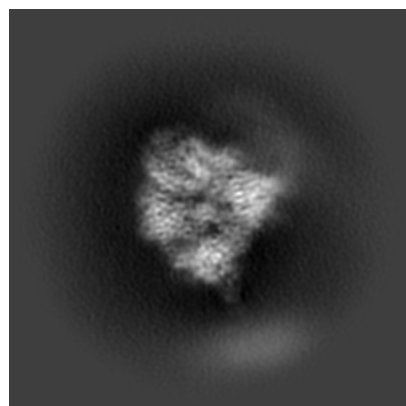
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18803. These allow visual inspection of the internal detail of the map and identification of artifacts.

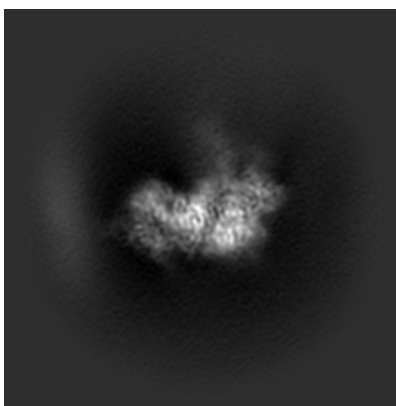
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

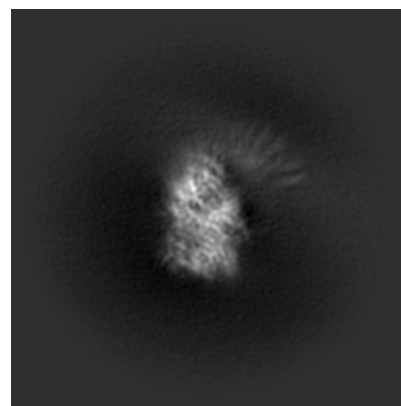
6.1.1 Primary map



X

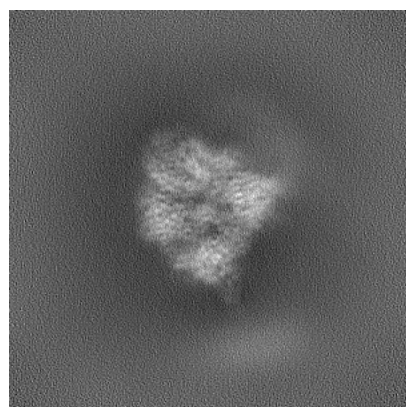


Y

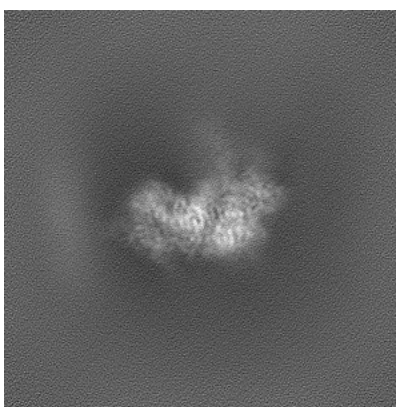


Z

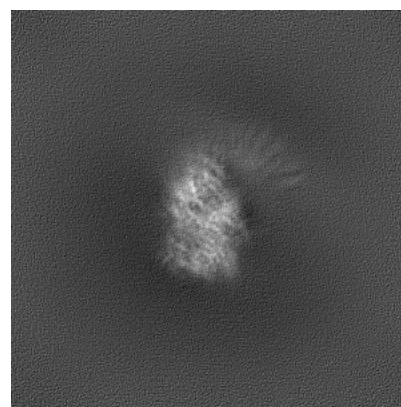
6.1.2 Raw map



X



Y

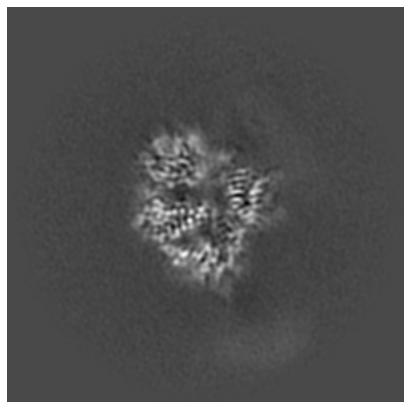


Z

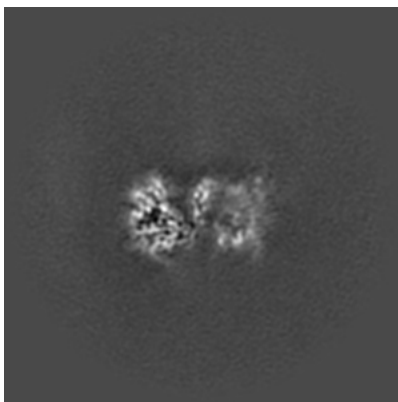
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

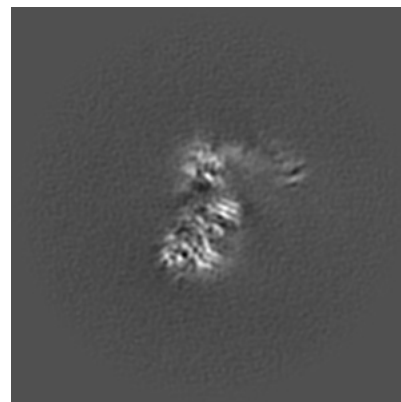
6.2.1 Primary map



X Index: 176

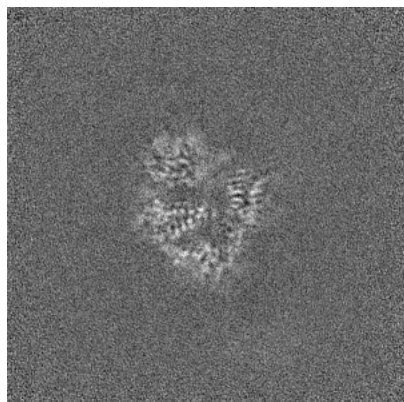


Y Index: 176

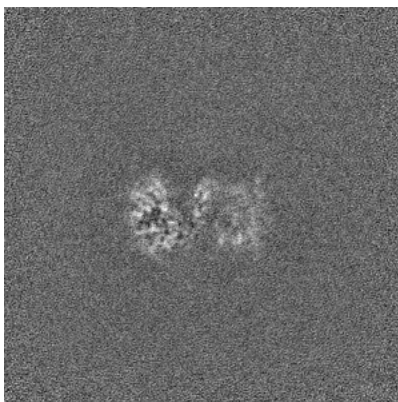


Z Index: 176

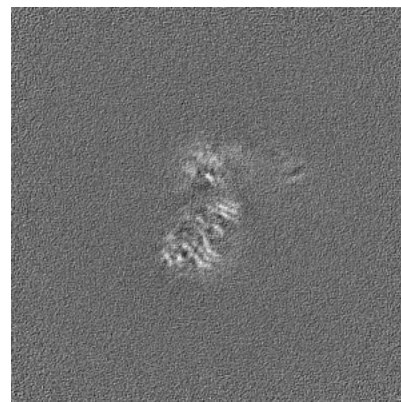
6.2.2 Raw map



X Index: 176



Y Index: 176

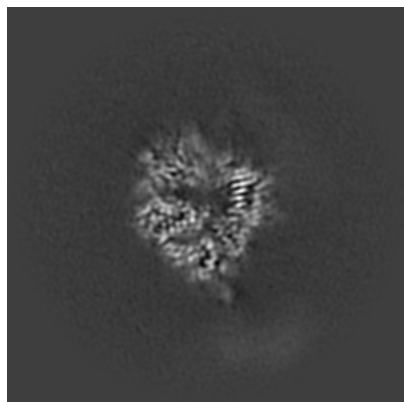


Z Index: 176

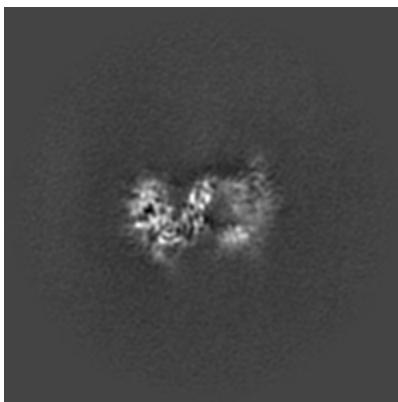
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

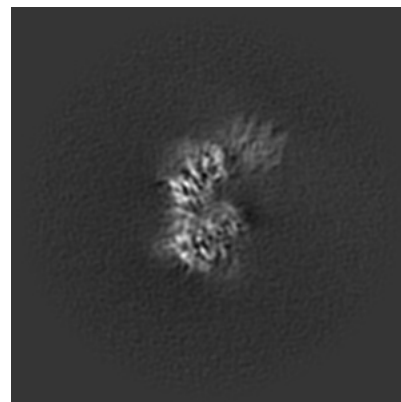
6.3.1 Primary map



X Index: 172

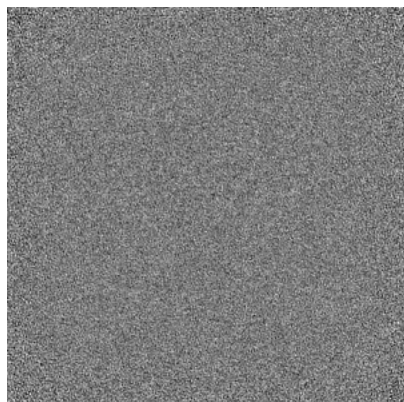


Y Index: 171

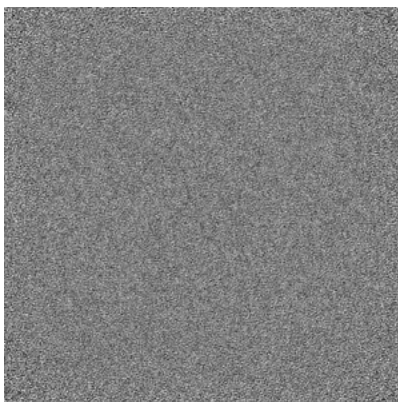


Z Index: 199

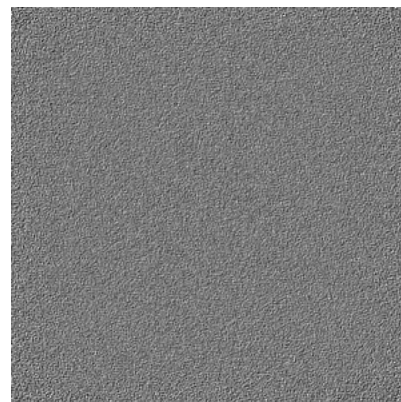
6.3.2 Raw map



X Index: 0



Y Index: 0

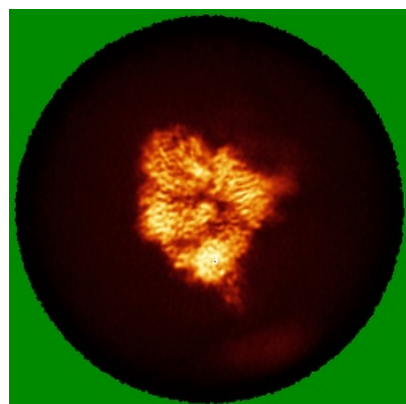


Z Index: 351

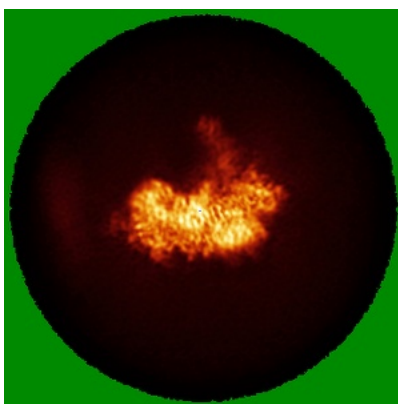
The images above show the largest variance slices of the map in three orthogonal directions.

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

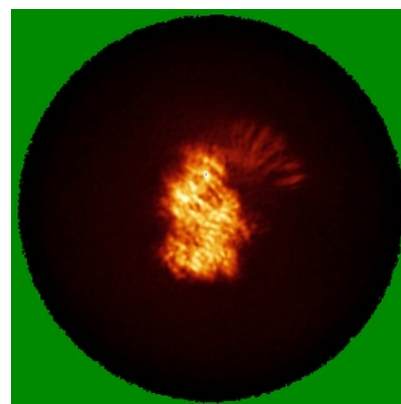
6.4.1 Primary map



X

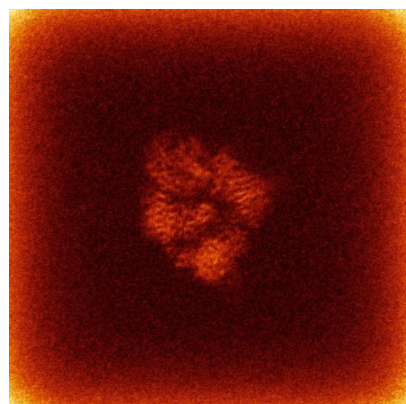


Y

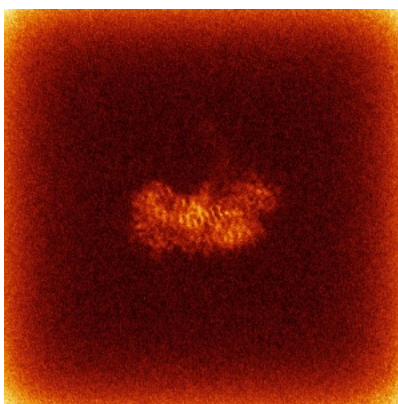


Z

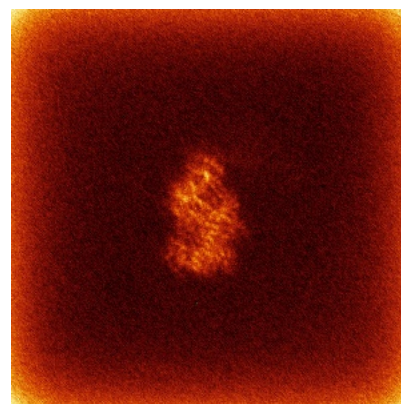
6.4.2 Raw map



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.

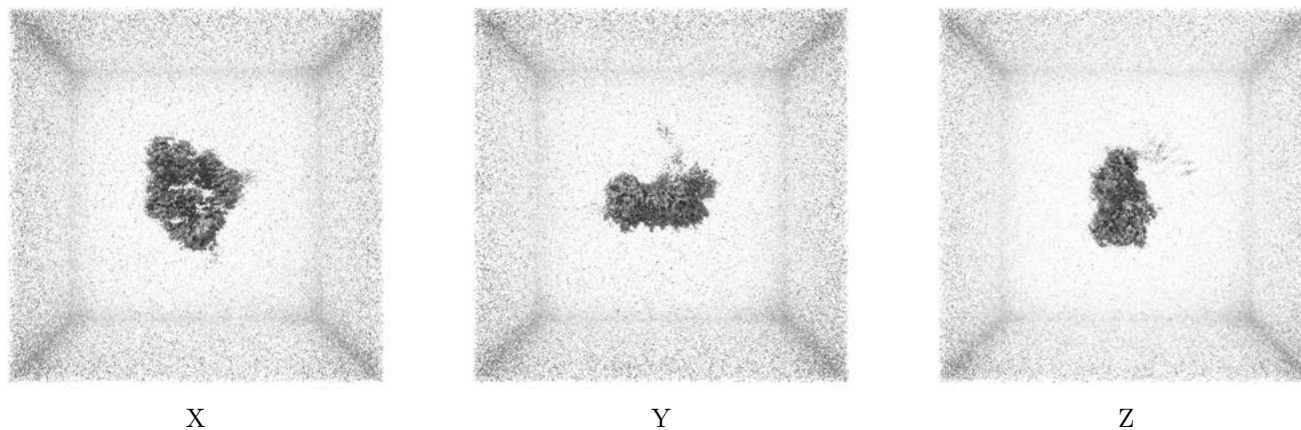
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0267. 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.

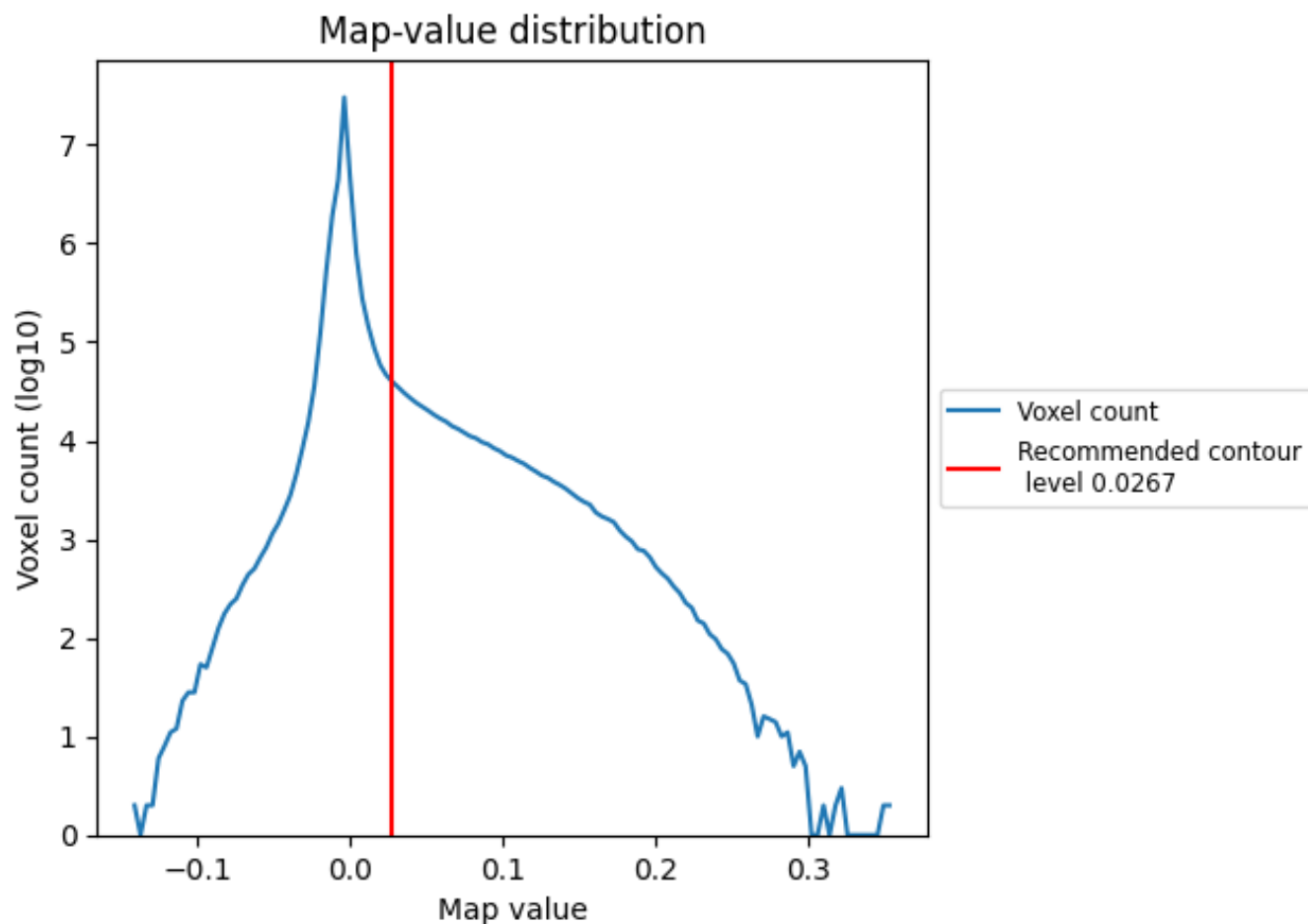
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

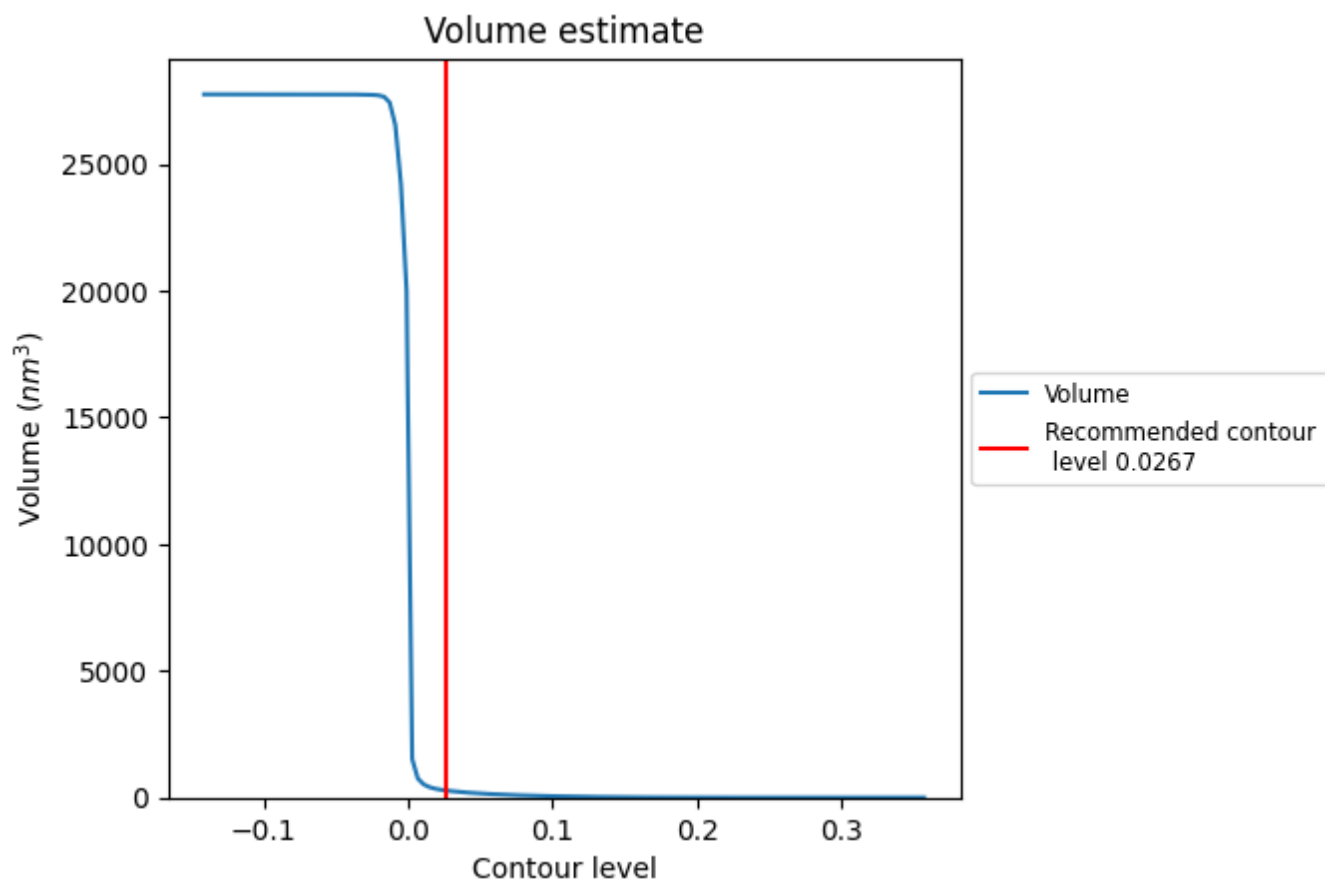
This section contains the results of statistical analysis of the map.

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.

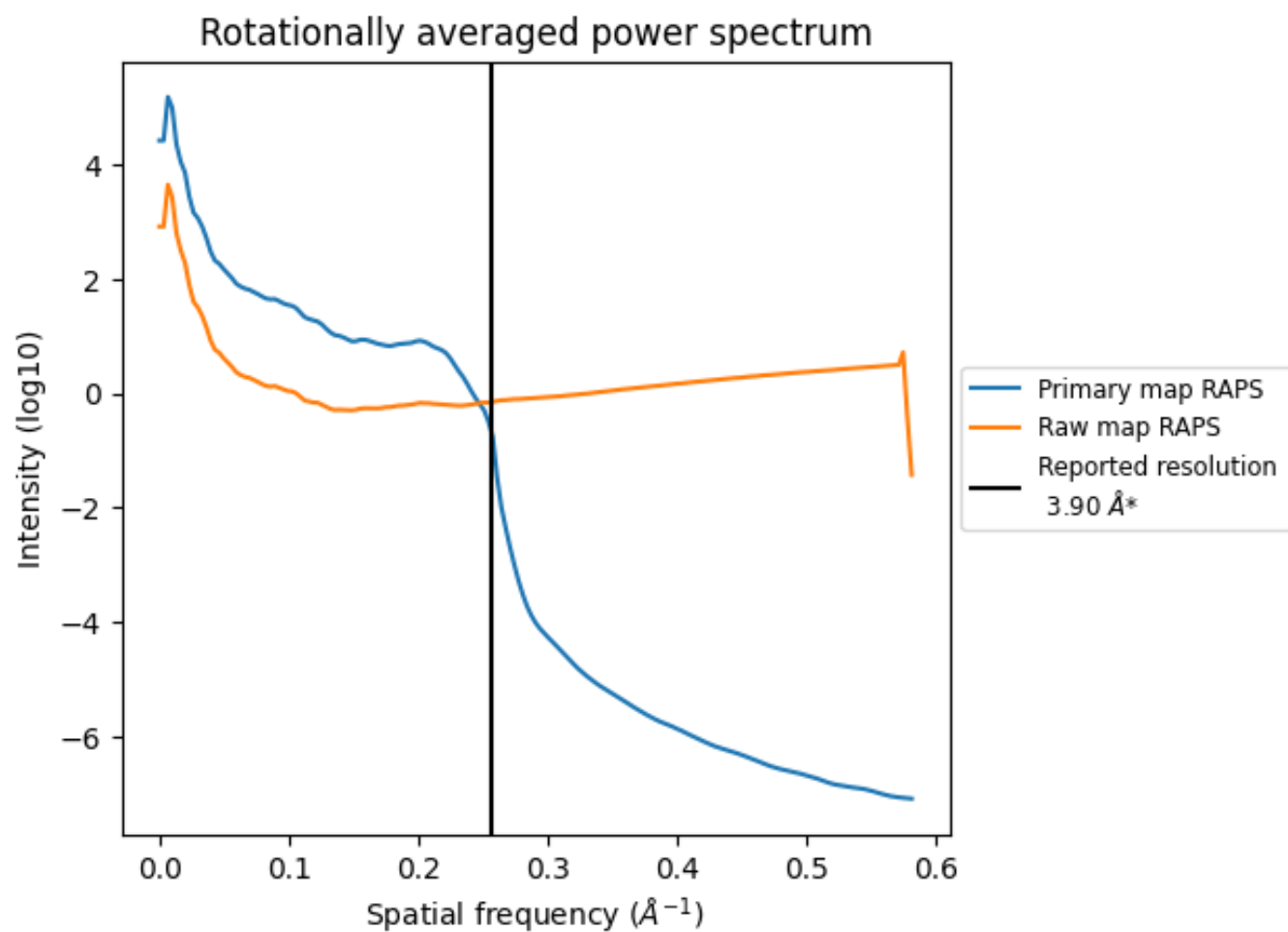
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 278 nm³; this corresponds to an approximate mass of 251 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 ⓘ

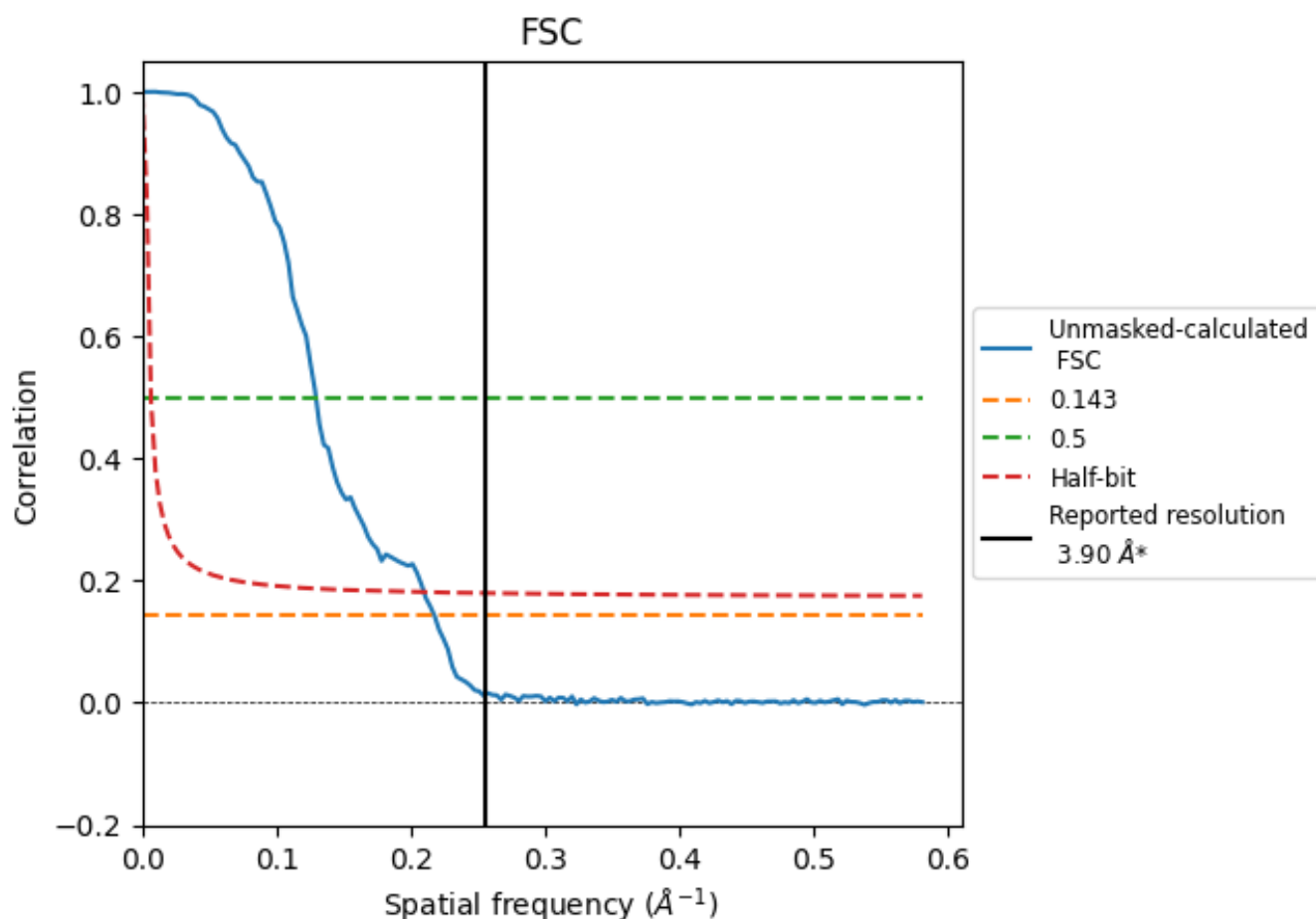


*Reported resolution corresponds to spatial frequency of $0.256 \text{ \AA}^{-1}$

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 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

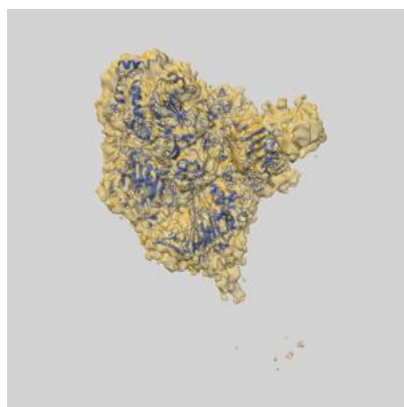
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.59	7.72	4.76

*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 4.59 differs from the reported value 3.9 by more than 10 %

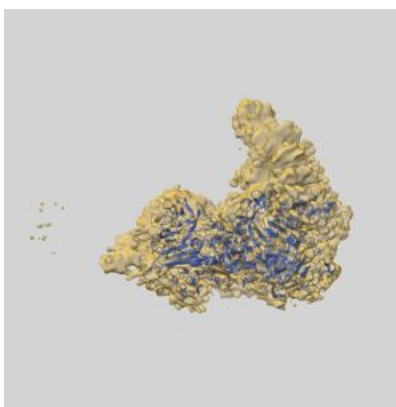
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-18803 and PDB model 8R0T. Per-residue inclusion information can be found in section [3](#) on page [5](#).

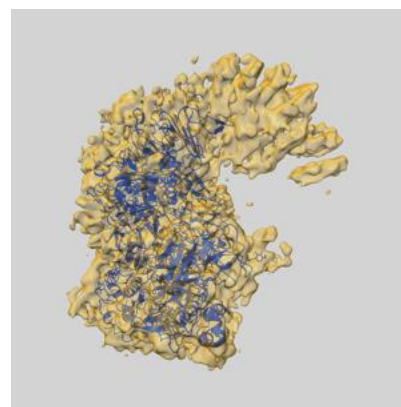
9.1 Map-model overlay [i](#)



X



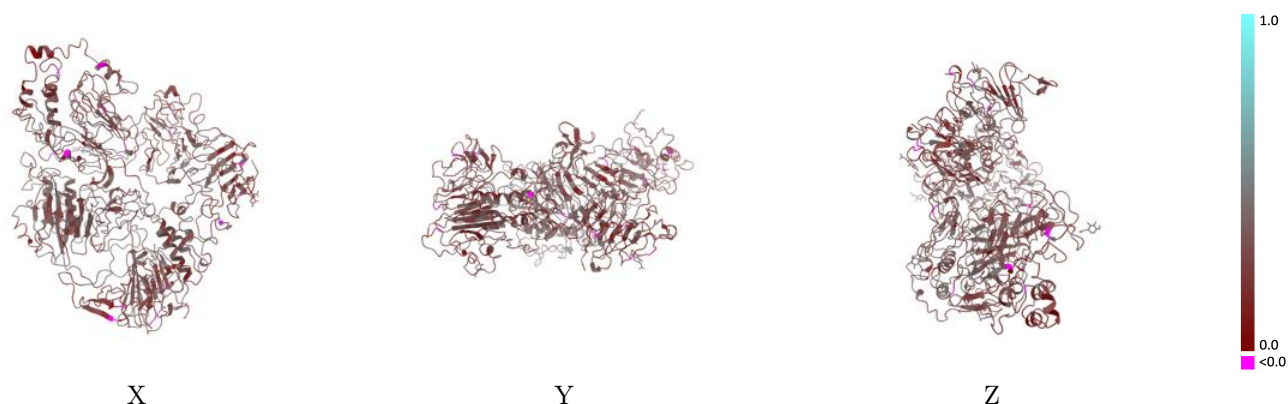
Y



Z

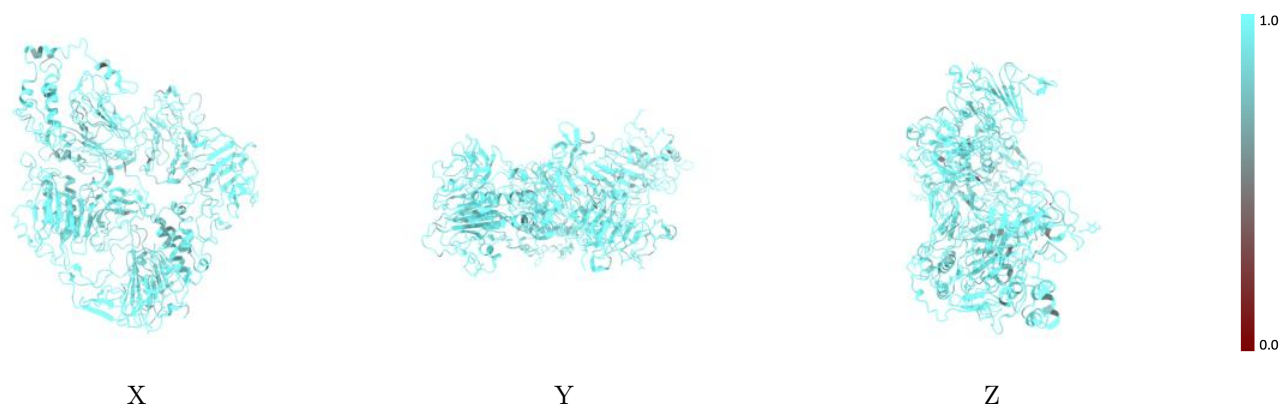
The images above show the 3D surface view of the map at the recommended contour level 0.0267 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



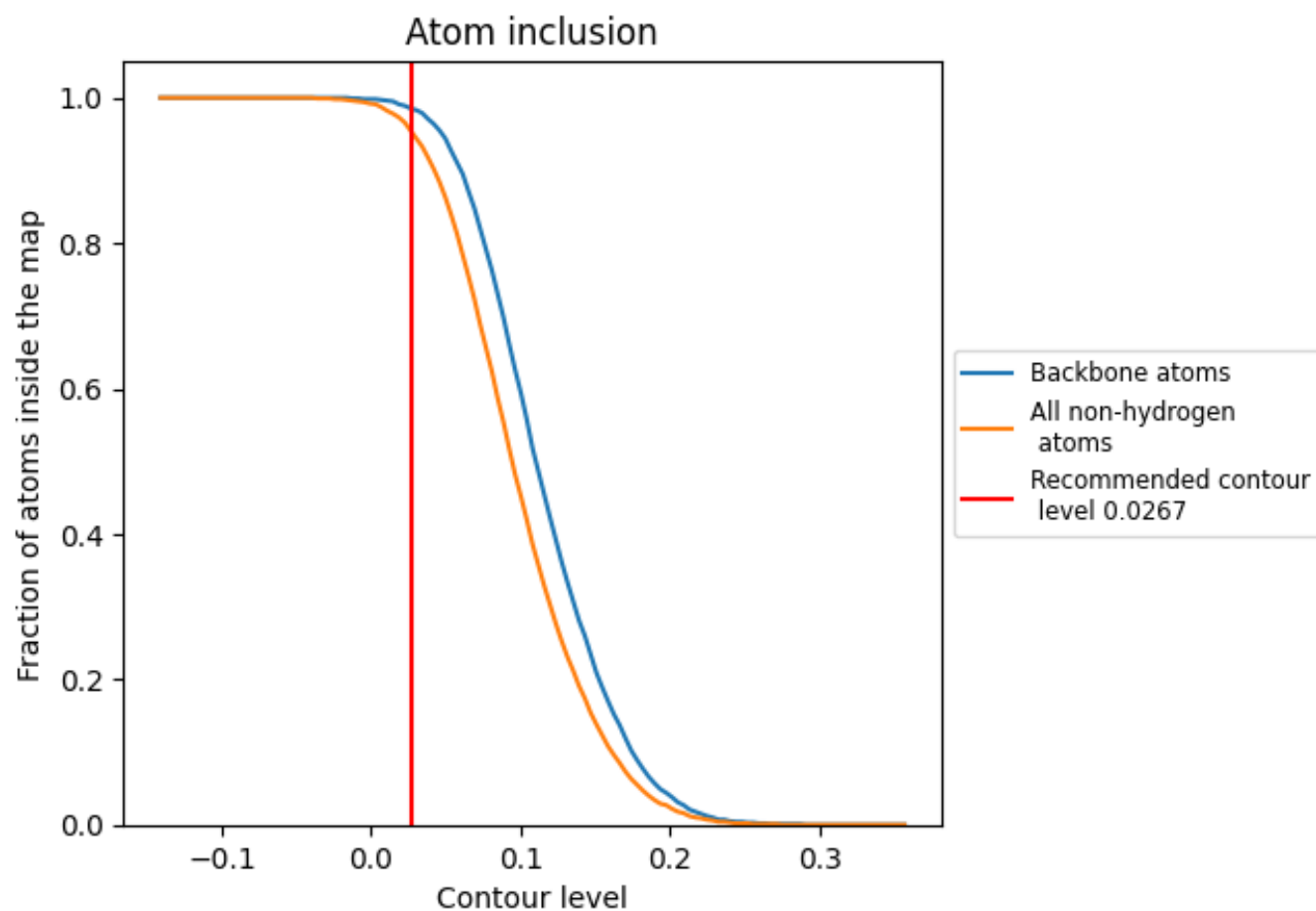
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0267).

9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 95% 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 (0.0267) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9540	0.3050
A	0.9010	0.3230
B	0.9630	0.2920
C	0.9510	0.3110
F	0.9560	0.2980

