



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 04:08 AM UTC

PDB ID : 8P83 / pdb_00008p83
EMDB ID : EMD-17540
Title : Cryo-EM structure of full-length human UBR5 (homotetramer)
Authors : Aguirre, J.D.; Kater, L.; Kempf, G.; Cavadini, S.; Thoma, N.H.
Deposited on : 2023-05-31
Resolution : 3.87 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

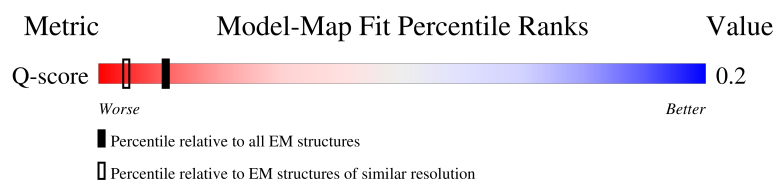
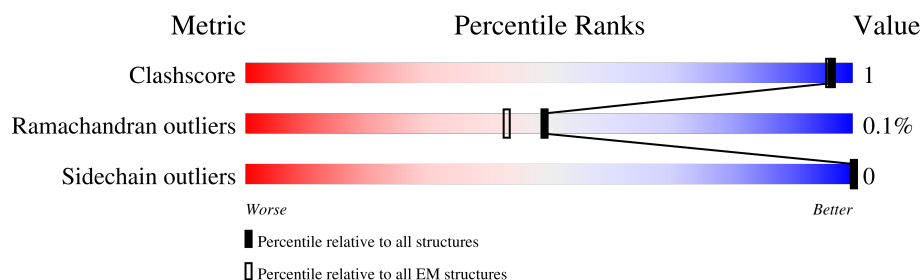
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.87 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	8831 (3.37 - 4.37)

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	2831	10% 62% 38%
1	B	2831	10% 61% 38%
1	C	2831	10% 61% 38%
1	D	2831	10% 61% 38%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 35656 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 E3 ubiquitin-protein ligase UBR5.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	1759	Total	C	N	O	0	0
			8914	5396	1759	1759		
1	B	1759	Total	C	N	O	0	0
			8914	5396	1759	1759		
1	C	1759	Total	C	N	O	0	0
			8914	5396	1759	1759		
1	D	1759	Total	C	N	O	0	0
			8914	5396	1759	1759		

There are 128 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-31	MET	-	initiating methionine	UNP O95071
A	-30	ASP	-	expression tag	UNP O95071
A	-29	TYR	-	expression tag	UNP O95071
A	-28	LYS	-	expression tag	UNP O95071
A	-27	ASP	-	expression tag	UNP O95071
A	-26	ASP	-	expression tag	UNP O95071
A	-25	ASP	-	expression tag	UNP O95071
A	-24	ASP	-	expression tag	UNP O95071
A	-23	LYS	-	expression tag	UNP O95071
A	-22	LEU	-	expression tag	UNP O95071
A	-21	ALA	-	expression tag	UNP O95071
A	-20	ALA	-	expression tag	UNP O95071
A	-19	ALA	-	expression tag	UNP O95071
A	-18	ASN	-	expression tag	UNP O95071
A	-17	SER	-	expression tag	UNP O95071
A	-16	SER	-	expression tag	UNP O95071
A	-15	ILE	-	expression tag	UNP O95071
A	-14	ASP	-	expression tag	UNP O95071
A	-13	LEU	-	expression tag	UNP O95071
A	-12	ILE	-	expression tag	UNP O95071
A	-11	SER	-	expression tag	UNP O95071
A	-10	THR	-	expression tag	UNP O95071

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	SER	-	expression tag	UNP O95071
A	-8	LEU	-	expression tag	UNP O95071
A	-7	TYR	-	expression tag	UNP O95071
A	-6	LYS	-	expression tag	UNP O95071
A	-5	LYS	-	expression tag	UNP O95071
A	-4	ALA	-	expression tag	UNP O95071
A	-3	GLY	-	expression tag	UNP O95071
A	-2	PHE	-	expression tag	UNP O95071
A	-1	ARG	-	expression tag	UNP O95071
A	0	THR	-	expression tag	UNP O95071
B	-31	MET	-	initiating methionine	UNP O95071
B	-30	ASP	-	expression tag	UNP O95071
B	-29	TYR	-	expression tag	UNP O95071
B	-28	LYS	-	expression tag	UNP O95071
B	-27	ASP	-	expression tag	UNP O95071
B	-26	ASP	-	expression tag	UNP O95071
B	-25	ASP	-	expression tag	UNP O95071
B	-24	ASP	-	expression tag	UNP O95071
B	-23	LYS	-	expression tag	UNP O95071
B	-22	LEU	-	expression tag	UNP O95071
B	-21	ALA	-	expression tag	UNP O95071
B	-20	ALA	-	expression tag	UNP O95071
B	-19	ALA	-	expression tag	UNP O95071
B	-18	ASN	-	expression tag	UNP O95071
B	-17	SER	-	expression tag	UNP O95071
B	-16	SER	-	expression tag	UNP O95071
B	-15	ILE	-	expression tag	UNP O95071
B	-14	ASP	-	expression tag	UNP O95071
B	-13	LEU	-	expression tag	UNP O95071
B	-12	ILE	-	expression tag	UNP O95071
B	-11	SER	-	expression tag	UNP O95071
B	-10	THR	-	expression tag	UNP O95071
B	-9	SER	-	expression tag	UNP O95071
B	-8	LEU	-	expression tag	UNP O95071
B	-7	TYR	-	expression tag	UNP O95071
B	-6	LYS	-	expression tag	UNP O95071
B	-5	LYS	-	expression tag	UNP O95071
B	-4	ALA	-	expression tag	UNP O95071
B	-3	GLY	-	expression tag	UNP O95071
B	-2	PHE	-	expression tag	UNP O95071
B	-1	ARG	-	expression tag	UNP O95071
B	0	THR	-	expression tag	UNP O95071

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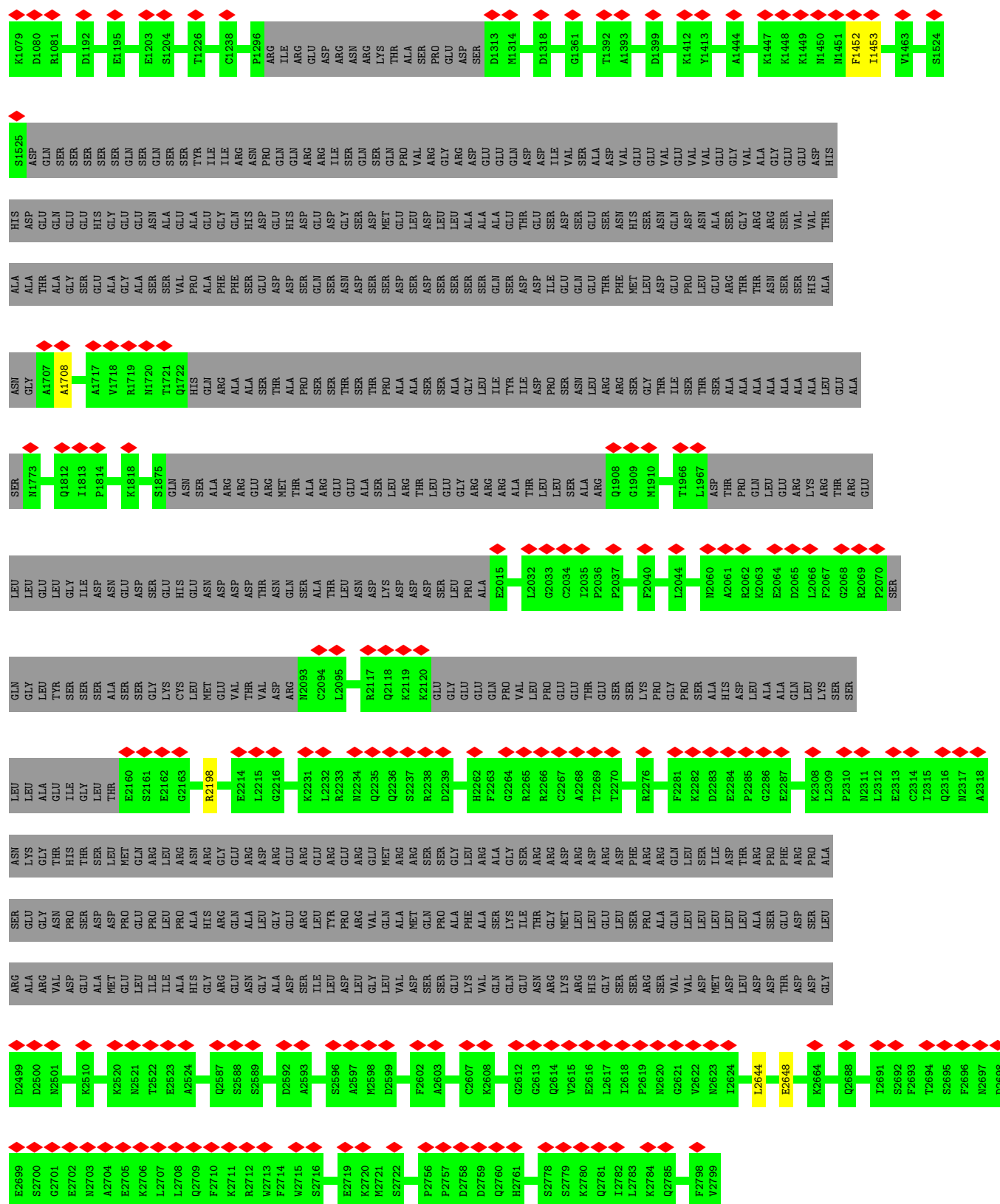
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Chain	Residue	Modelled	Actual	Comment	Reference
C	-31	MET	-	initiating methionine	UNP O95071
C	-30	ASP	-	expression tag	UNP O95071
C	-29	TYR	-	expression tag	UNP O95071
C	-28	LYS	-	expression tag	UNP O95071
C	-27	ASP	-	expression tag	UNP O95071
C	-26	ASP	-	expression tag	UNP O95071
C	-25	ASP	-	expression tag	UNP O95071
C	-24	ASP	-	expression tag	UNP O95071
C	-23	LYS	-	expression tag	UNP O95071
C	-22	LEU	-	expression tag	UNP O95071
C	-21	ALA	-	expression tag	UNP O95071
C	-20	ALA	-	expression tag	UNP O95071
C	-19	ALA	-	expression tag	UNP O95071
C	-18	ASN	-	expression tag	UNP O95071
C	-17	SER	-	expression tag	UNP O95071
C	-16	SER	-	expression tag	UNP O95071
C	-15	ILE	-	expression tag	UNP O95071
C	-14	ASP	-	expression tag	UNP O95071
C	-13	LEU	-	expression tag	UNP O95071
C	-12	ILE	-	expression tag	UNP O95071
C	-11	SER	-	expression tag	UNP O95071
C	-10	THR	-	expression tag	UNP O95071
C	-9	SER	-	expression tag	UNP O95071
C	-8	LEU	-	expression tag	UNP O95071
C	-7	TYR	-	expression tag	UNP O95071
C	-6	LYS	-	expression tag	UNP O95071
C	-5	LYS	-	expression tag	UNP O95071
C	-4	ALA	-	expression tag	UNP O95071
C	-3	GLY	-	expression tag	UNP O95071
C	-2	PHE	-	expression tag	UNP O95071
C	-1	ARG	-	expression tag	UNP O95071
C	0	THR	-	expression tag	UNP O95071
D	-31	MET	-	initiating methionine	UNP O95071
D	-30	ASP	-	expression tag	UNP O95071
D	-29	TYR	-	expression tag	UNP O95071
D	-28	LYS	-	expression tag	UNP O95071
D	-27	ASP	-	expression tag	UNP O95071
D	-26	ASP	-	expression tag	UNP O95071
D	-25	ASP	-	expression tag	UNP O95071
D	-24	ASP	-	expression tag	UNP O95071
D	-23	LYS	-	expression tag	UNP O95071
D	-22	LEU	-	expression tag	UNP O95071

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-21	ALA	-	expression tag	UNP O95071
D	-20	ALA	-	expression tag	UNP O95071
D	-19	ALA	-	expression tag	UNP O95071
D	-18	ASN	-	expression tag	UNP O95071
D	-17	SER	-	expression tag	UNP O95071
D	-16	SER	-	expression tag	UNP O95071
D	-15	ILE	-	expression tag	UNP O95071
D	-14	ASP	-	expression tag	UNP O95071
D	-13	LEU	-	expression tag	UNP O95071
D	-12	ILE	-	expression tag	UNP O95071
D	-11	SER	-	expression tag	UNP O95071
D	-10	THR	-	expression tag	UNP O95071
D	-9	SER	-	expression tag	UNP O95071
D	-8	LEU	-	expression tag	UNP O95071
D	-7	TYR	-	expression tag	UNP O95071
D	-6	LYS	-	expression tag	UNP O95071
D	-5	LYS	-	expression tag	UNP O95071
D	-4	ALA	-	expression tag	UNP O95071
D	-3	GLY	-	expression tag	UNP O95071
D	-2	PHE	-	expression tag	UNP O95071
D	-1	ARG	-	expression tag	UNP O95071
D	0	THR	-	expression tag	UNP O95071



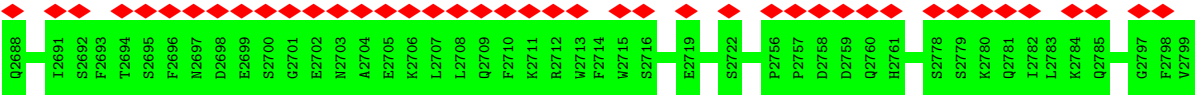
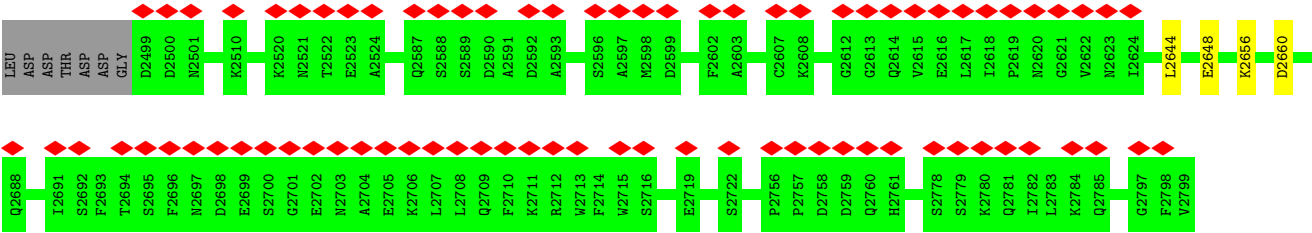
• Molecule 1: E3 ubiquitin-protein ligase UBR5







S702	S703	L704	L705	C708	K720	T721	G722	G723	D729	C730	F731	A774	I811	S842	G845	M846	G847	N857	A864	K873	C883	V900	L901	E902	P932	T933	T938	K939	E940	E941	E942	GLU	ALA	GLU	ARG	SER	GLU	ARG	ASN	THR	PHE	ALA	GLU	ARG	LEU				
SER	ALA	VAL	GLU	ALA	ILE	ALA	VAL	SER	ASN	ASN	PRO	GLY	ALA	SER	SER	ARG	LEU	ARG	LEU	GLY	MET	MET	ARG	ALA	ALA	GLY	LEU	GLY	ALA	ALA	SER	SER	SER	ASP	HIS	GLU	GLN	ASP	PRO										
VAL	SER	PRO	PRO	ILE	ALA	PRO	PRO	ASN	PRO	ALA	MET	ASP	PRO	ASP	GLY	ILE	ALA	VAL	GLY	LEU	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR		
E1077	S1078	K1079	D1080	R1081	A1140	I1144	S1145	K1149	E1150	D1192	E1203	S1204	C1238	F1296	ARG	ILE	GLU	ASP	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		
S1524	S1525	ASP	GLN	SER	SER	SER	SER	SER	SER	TYR	ILE	ARG	ASN	PRO	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		
HIS	HIS	ASP	GLN	GLU	GLU	HIS	GLY	GLU	GLU	GLU	GLY	GLN	HIS	ASP	GLU	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN		
THR	ALA	ALA	THR	ALA	GLY	GLY	ALA	SER	VAL	PHE	PHE	SER	GLU	ASP	GLU	THR	ASP	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		
ALA	ASN	GLY	A1707	A1708	A1717	V1718	R1719	M1720	T1721	Q1722	HIS	GLN	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	
ALA	SER	N1773	Q1812	I1813	K1818	S1875	GLN	ASN	SER	ALA	ARG	GLU	ARG	ARG	MET	THR	ALA	ALA	ARG	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		
LEU	LEU	LEU	LEU	ILE	ASP	ASN	GLU	GLU	GLU	GLU	ASN	ASP	ASP	THR	ASN	GLN	LYS	ASP	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		
GLY	LEU	TYR	SER	SER	ALA	SER	GLY	LYS	CYS	LEU	MET	N2093	C2094	L2095	N2113	R2117	Q2118	K2119	K2120	GLU	GLY	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		
SER	LEU	ALA	GLU	ILE	GLY	THR	E2160	S2161	E2162	G2163	R2198	E2214	L2215	G2216	G2217	F2218	K2231	L2232	R2233	N2234	S2237	R2238	D2239	D2245	R2246	D2247	L2250	G2264	R2265	R2266	C2267	A2268	T2269	T2270	R2276	T2280	F2281	K2282	D2283	E2284	P2285	G2286	E2287	K2308	L2309	P2310	N2311		
L2312	E2313	C2314	T2315	Q2316	N2317	A2318	ASN	GLY	GLY	THR	HIS	ASP	ASP	GLU	PRO	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	
THR	ARG	PRO	PHE	ARG	PRO	ALA	GLU	ASN	VAL	PRO	THR	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
LEU	ALA	SER	GLU	ASP	SER	GLU	ARG	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU		



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	393327	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.579	Depositor
Minimum map value	-0.294	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.0859	Depositor
Map size (Å)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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	0.19	0/9004	0.42	0/12613
1	B	0.21	0/9004	0.44	1/12613 (0.0%)
1	C	0.19	0/9004	0.42	0/12613
1	D	0.20	0/9004	0.43	0/12613
All	All	0.20	0/36016	0.43	1/50452 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1147	SER	CB-CA-C	-6.26	106.58	114.40

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	8914	0	4487	8	0
1	B	8914	0	4487	18	0
1	C	8914	0	4487	9	0
1	D	8914	0	4487	10	0
All	All	35656	0	17948	45	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 45 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:B:553:ALA:HB1	1:B:850:SER:CB	2.25	0.67
1:D:1140:ALA:HA	1:D:1144:ILE:CB	2.34	0.58
1:B:482:TYR:CB	1:B:495:GLY:HA3	2.34	0.57
1:D:482:TYR:CB	1:D:495:GLY:HA3	2.34	0.57
1:A:482:TYR:CB	1:A:495:GLY:HA3	2.34	0.56

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	1733/2831 (61%)	1698 (98%)	34 (2%)	1 (0%)	48	80
1	B	1733/2831 (61%)	1699 (98%)	33 (2%)	1 (0%)	48	80
1	C	1733/2831 (61%)	1697 (98%)	34 (2%)	2 (0%)	48	80
1	D	1733/2831 (61%)	1694 (98%)	37 (2%)	2 (0%)	48	80
All	All	6932/11324 (61%)	6788 (98%)	138 (2%)	6 (0%)	49	80

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	662	VAL
1	D	454	VAL
1	A	431	SER
1	B	431	SER
1	C	431	SER

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	103/2446 (4%)	103 (100%)	0	100	100
1	B	103/2446 (4%)	103 (100%)	0	100	100
1	C	103/2446 (4%)	103 (100%)	0	100	100
1	D	103/2446 (4%)	103 (100%)	0	100	100
All	All	412/9784 (4%)	412 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

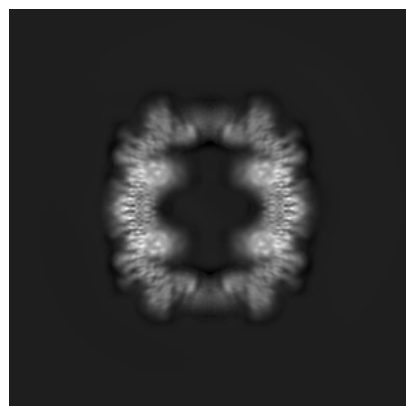
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17540. These allow visual inspection of the internal detail of the map and identification of artifacts.

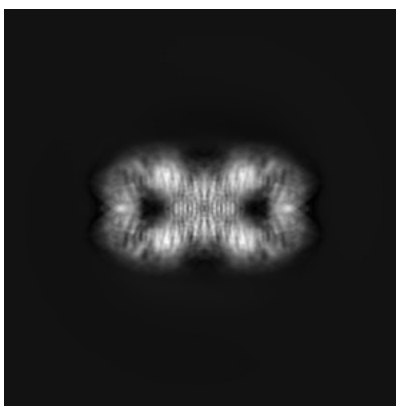
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

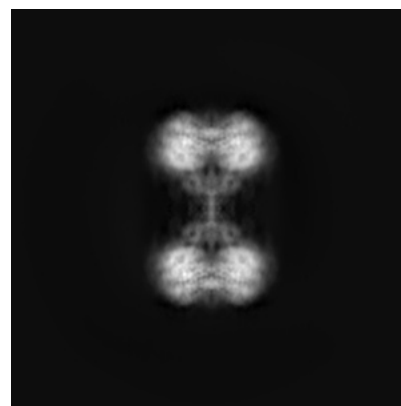
6.1.1 Primary map



X

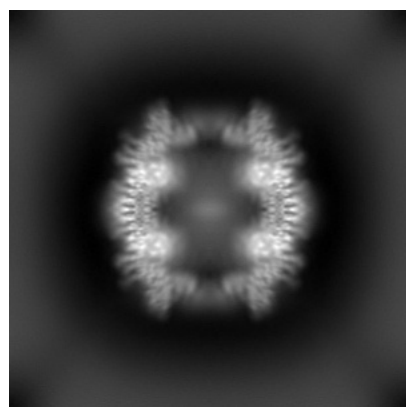


Y

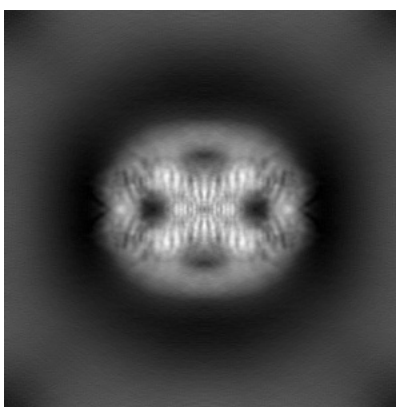


Z

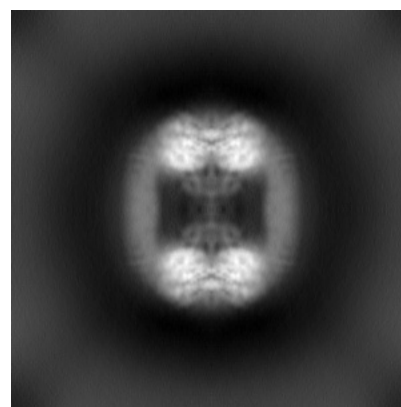
6.1.2 Raw map



X



Y

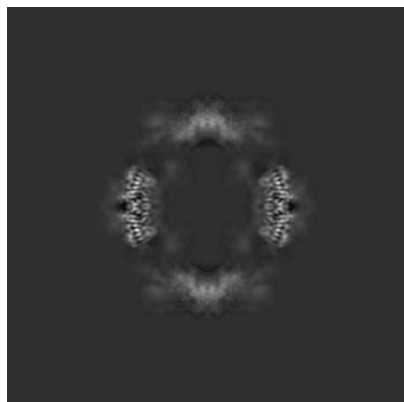


Z

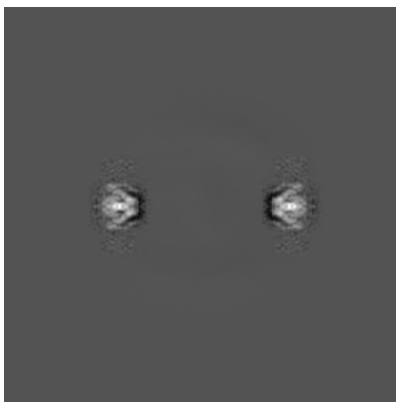
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

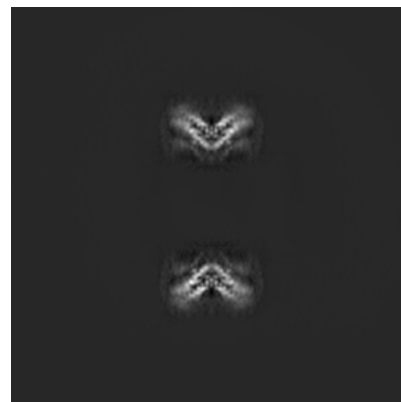
6.2.1 Primary map



X Index: 192

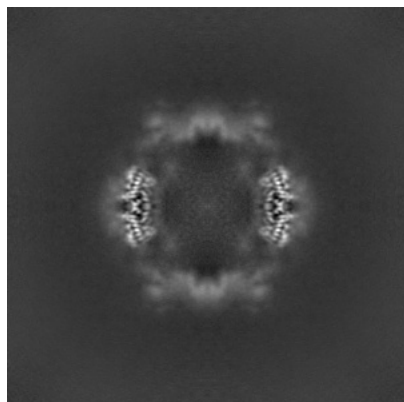


Y Index: 192

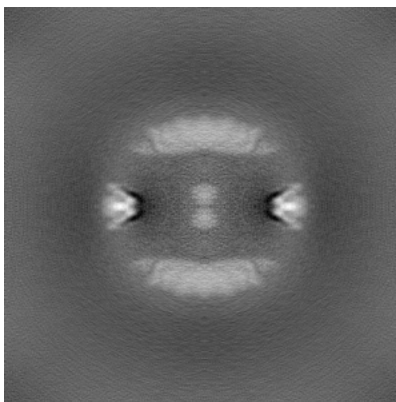


Z Index: 192

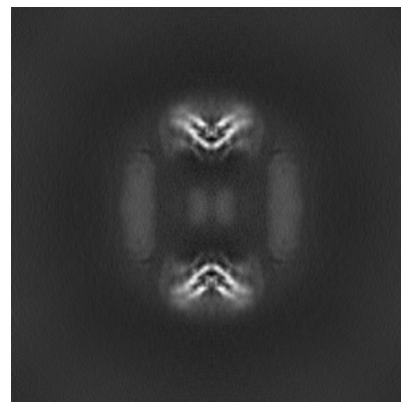
6.2.2 Raw map



X Index: 192



Y Index: 192

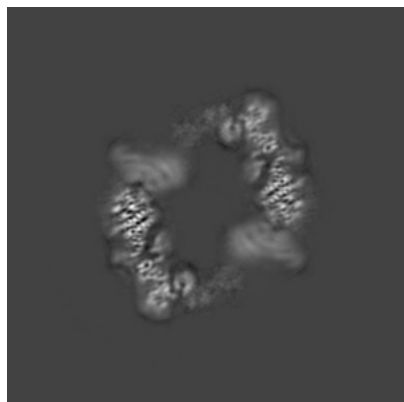


Z Index: 192

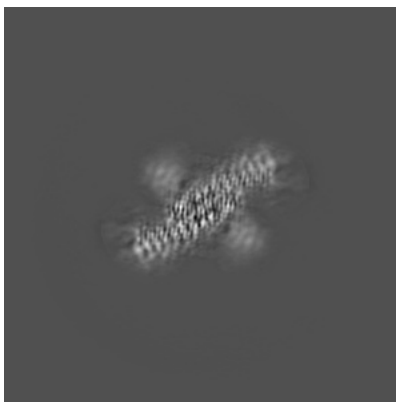
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

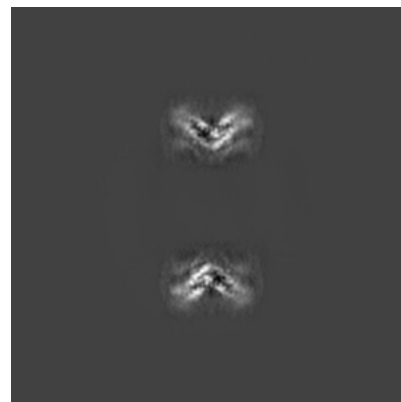
6.3.1 Primary map



X Index: 172

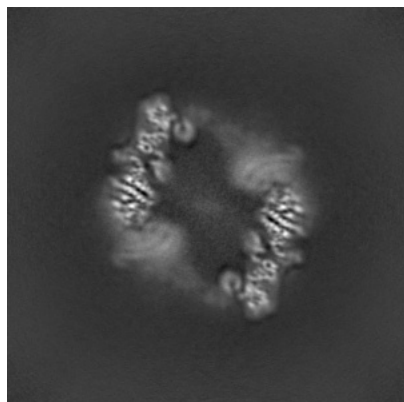


Y Index: 125

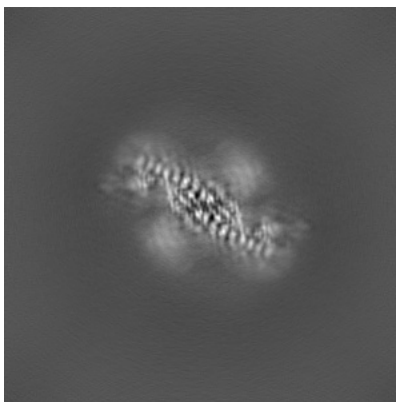


Z Index: 191

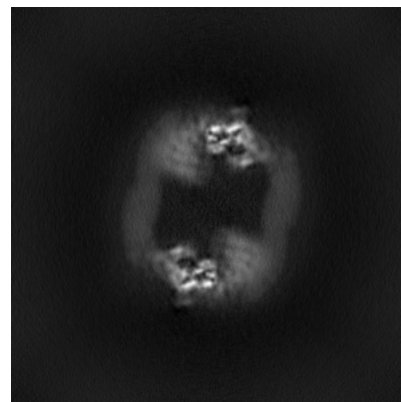
6.3.2 Raw map



X Index: 212



Y Index: 256

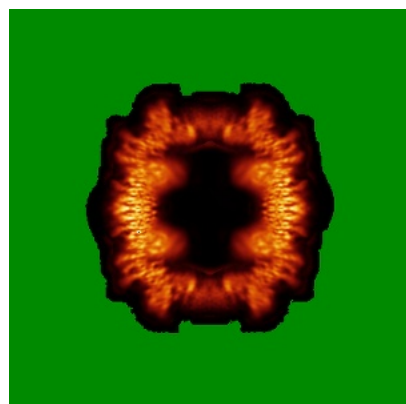


Z Index: 165

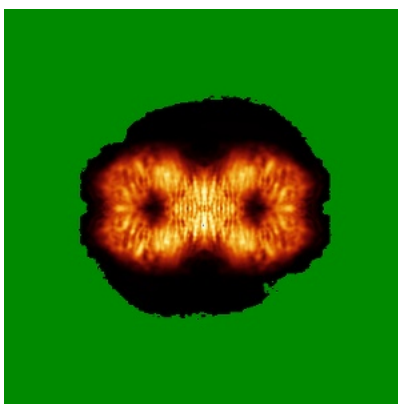
The images above show the largest variance slices of the map in three orthogonal directions.

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

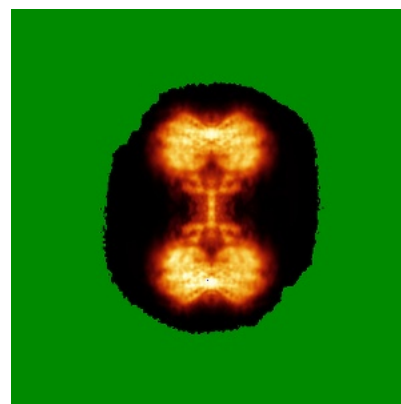
6.4.1 Primary map



X

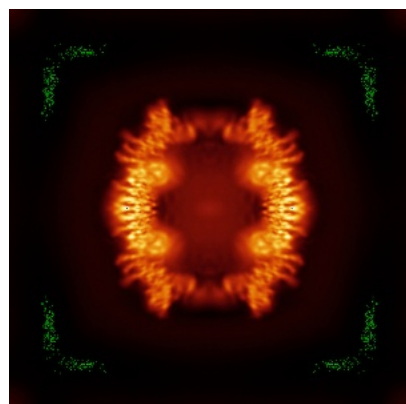


Y

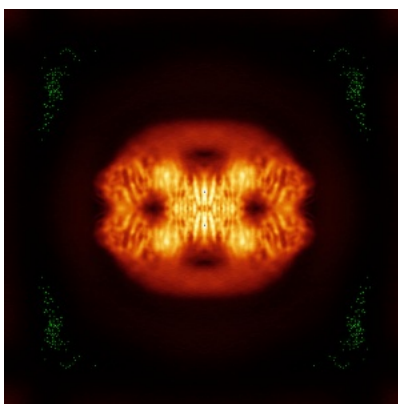


Z

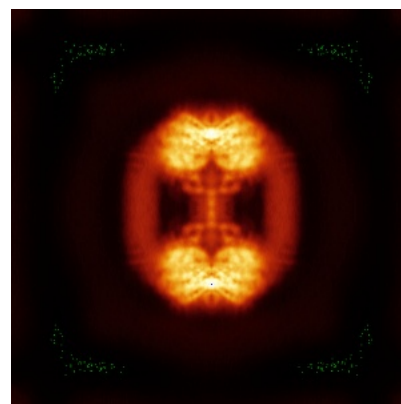
6.4.2 Raw map



X



Y

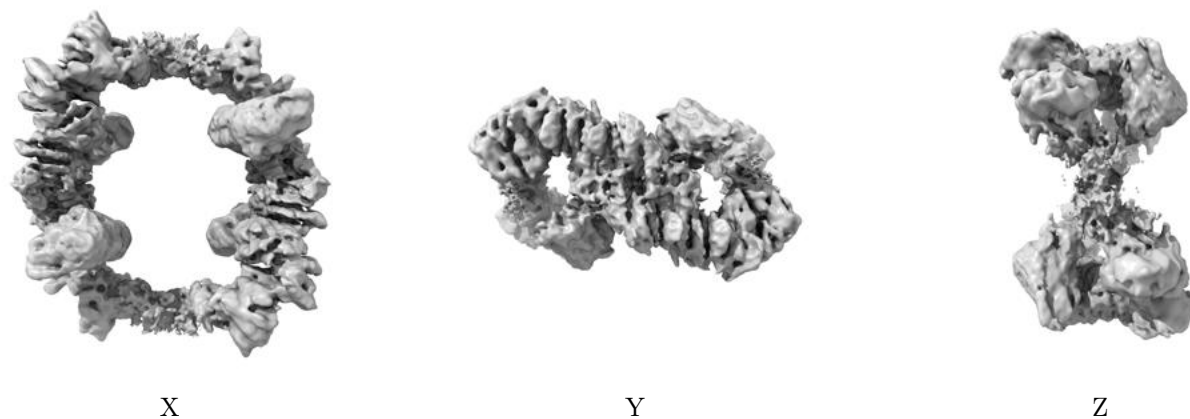


Z

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.

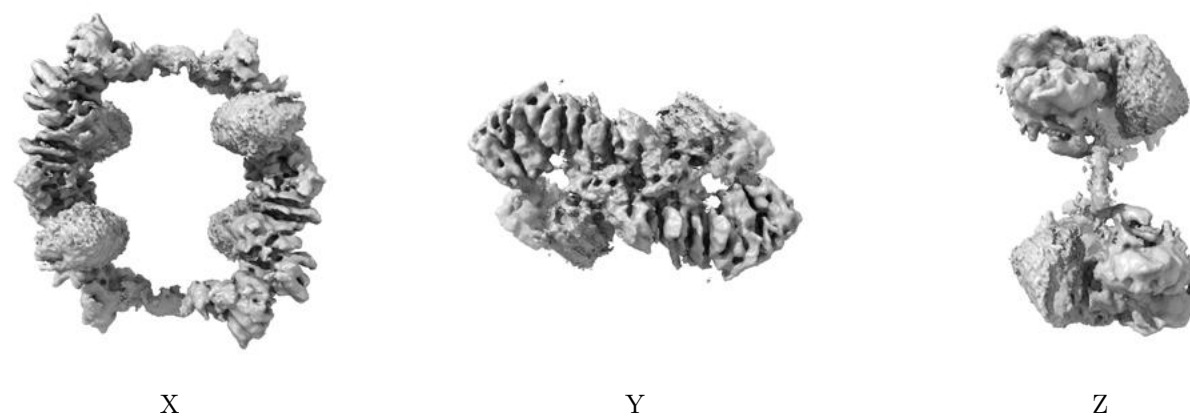
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0859. 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.

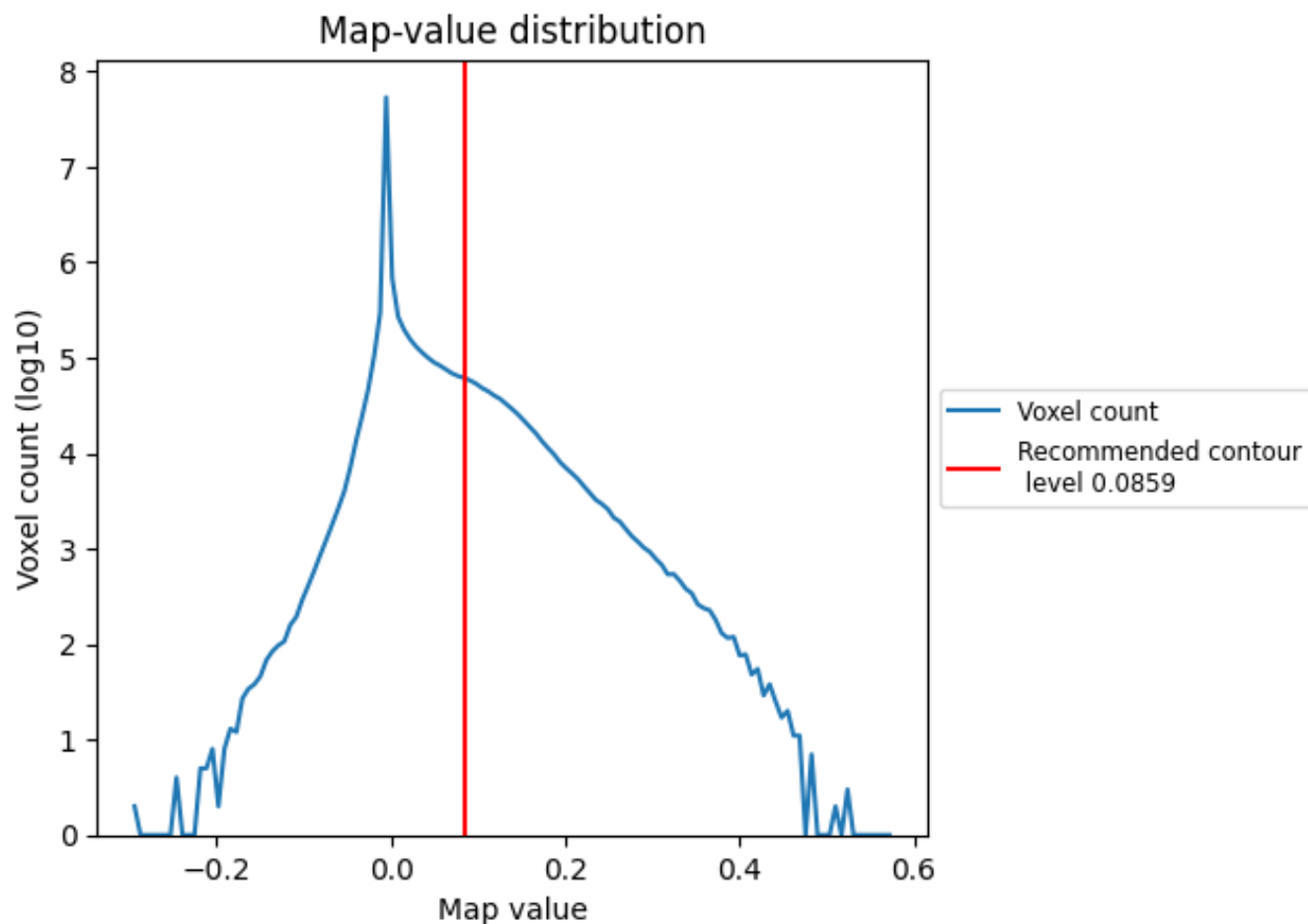
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

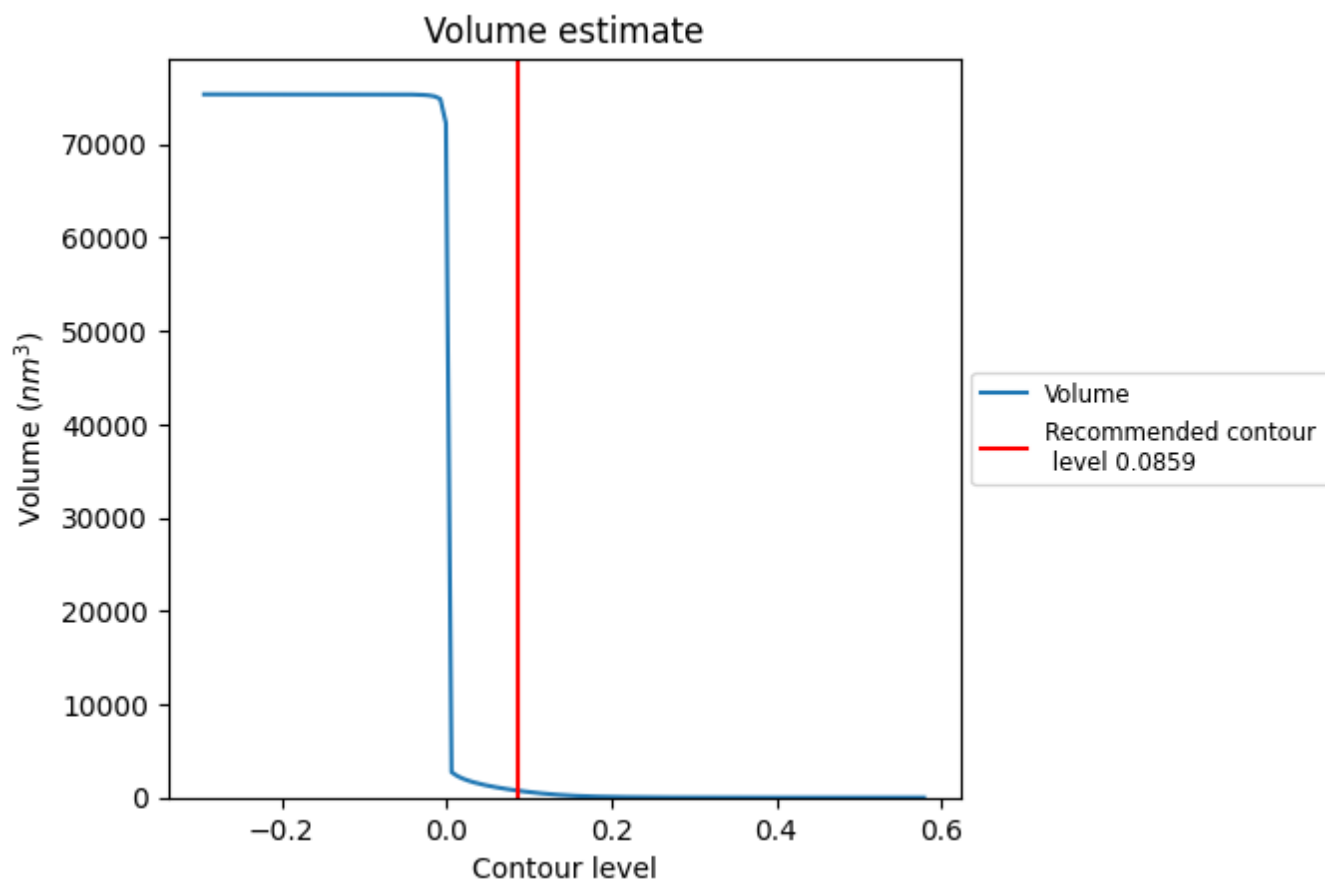
This section contains the results of statistical analysis of the map.

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.

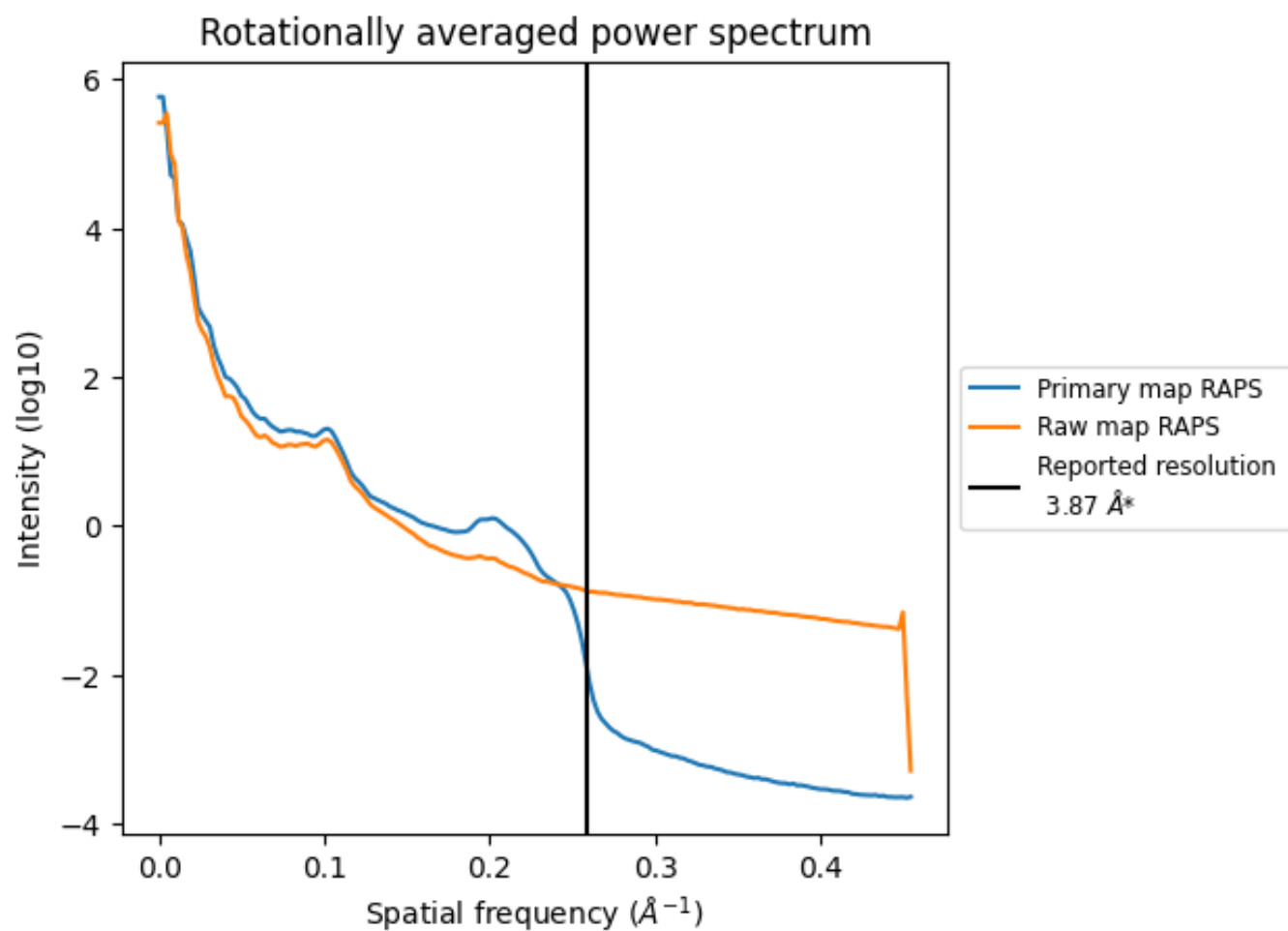
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 753 nm³; this corresponds to an approximate mass of 680 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 ⓘ

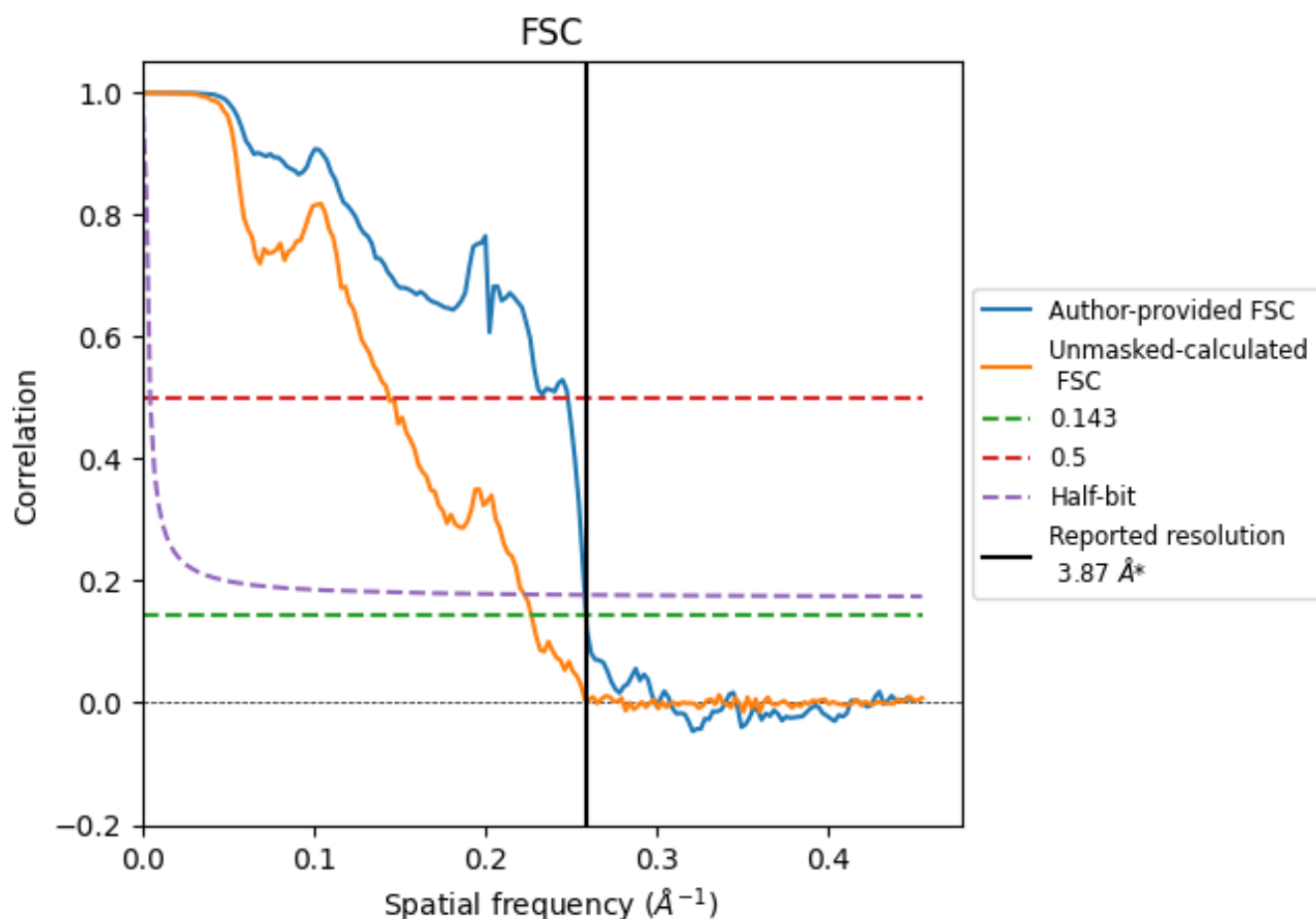


*Reported resolution corresponds to spatial frequency of 0.258 Å⁻¹

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 $0.258 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

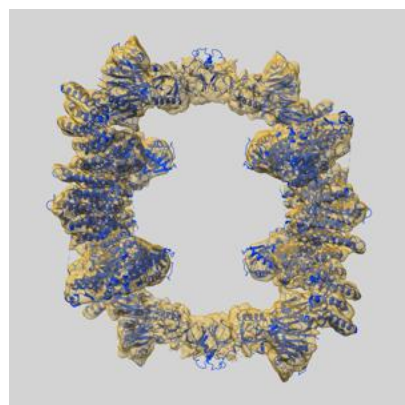
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.87	-	-
Author-provided FSC curve	3.87	4.03	3.88
Unmasked-calculated*	4.41	6.95	4.49

*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 4.41 differs from the reported value 3.87 by more than 10 %

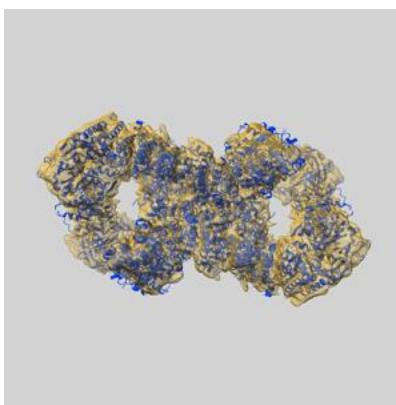
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-17540 and PDB model 8P83. Per-residue inclusion information can be found in section [3](#) on page [7](#).

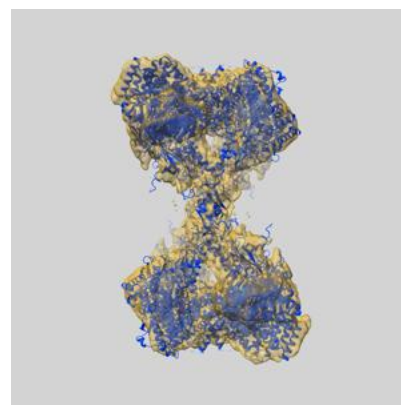
9.1 Map-model overlay [i](#)



X



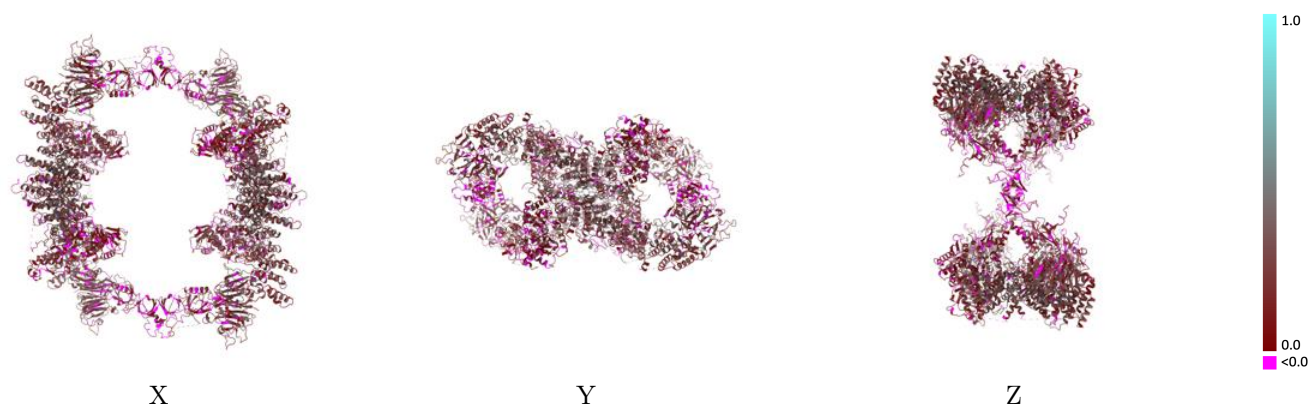
Y



Z

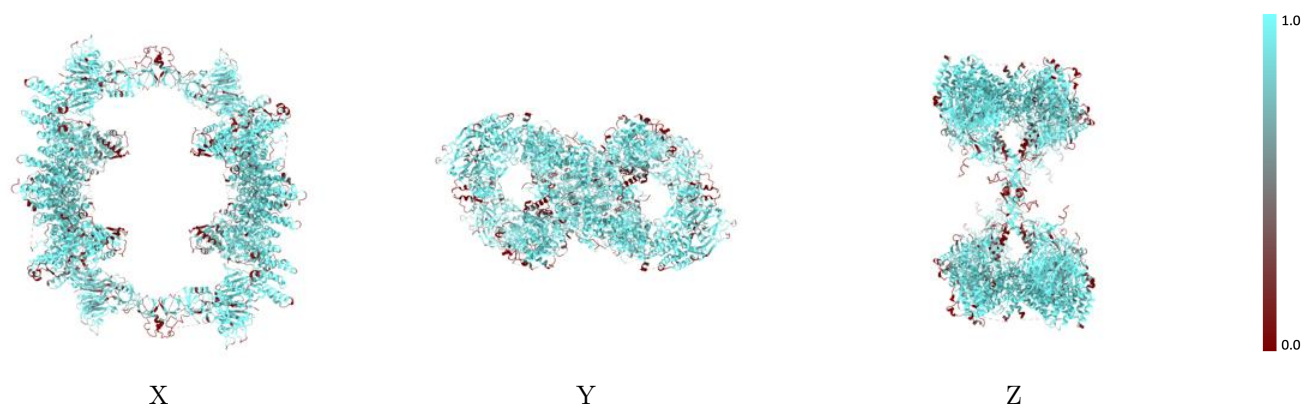
The images above show the 3D surface view of the map at the recommended contour level 0.0859 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



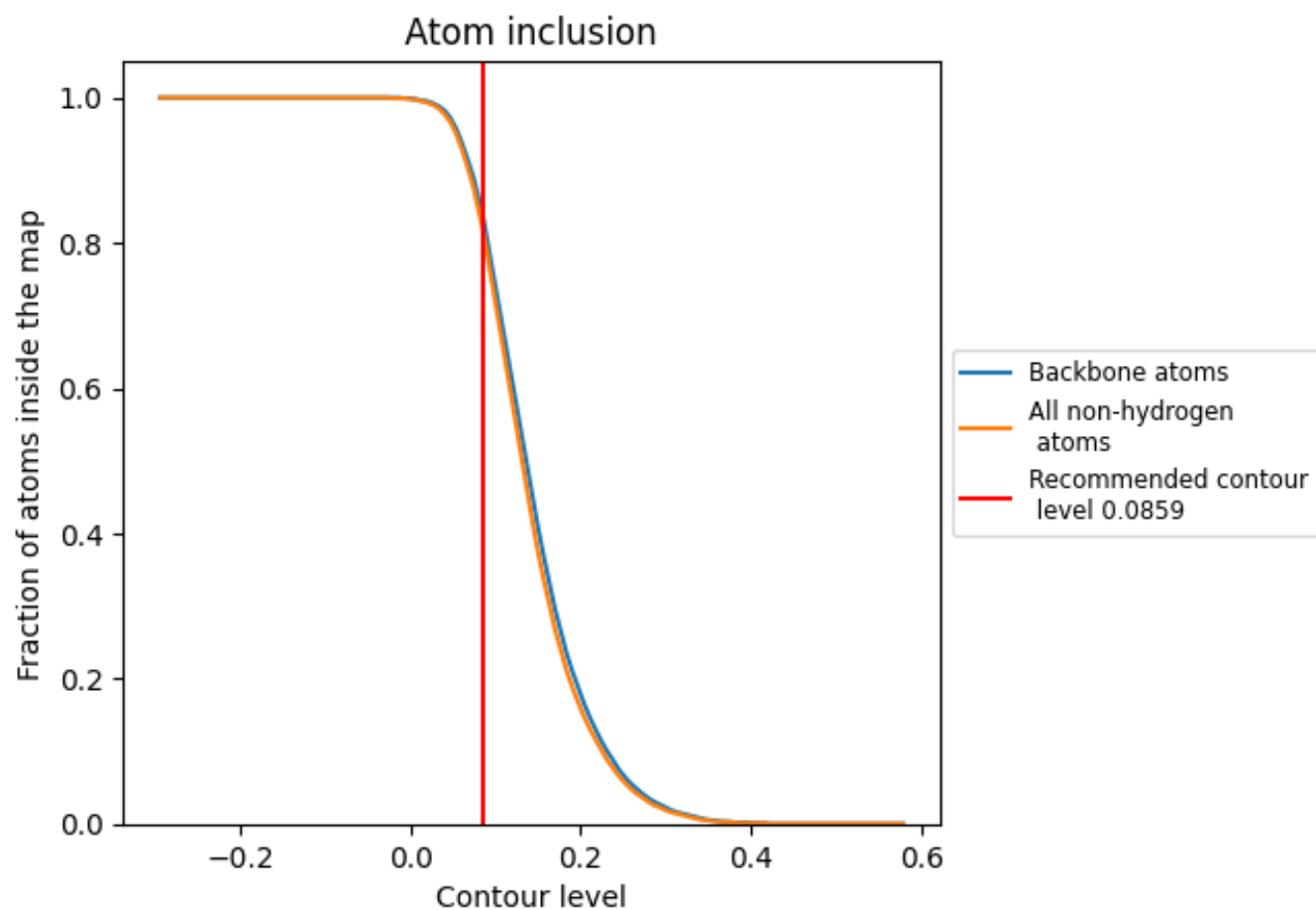
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0859).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 81% 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 (0.0859) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8140	0.2000
A	0.8150	0.2000
B	0.8150	0.2010
C	0.8110	0.1970
D	0.8160	0.2010

