



Full wwPDB EM Validation Report ⓘ

Mar 25, 2025 – 12:13 pm GMT

PDB ID : 8R1Z
EMDB ID : EMD-18829
Title : MUC5AC D3 assembly. SNPs rs36189285, rs878913005: Arg996Gln, Arg1201Trp.
Authors : Trillo-Muyo, S.; Hansson, G.C.
Deposited on : 2023-11-02
Resolution : 3.20 Å(reported)
Based on initial model : 8QTV

This is a Full wwPDB EM Validation 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.dev117
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) : 2.41.5

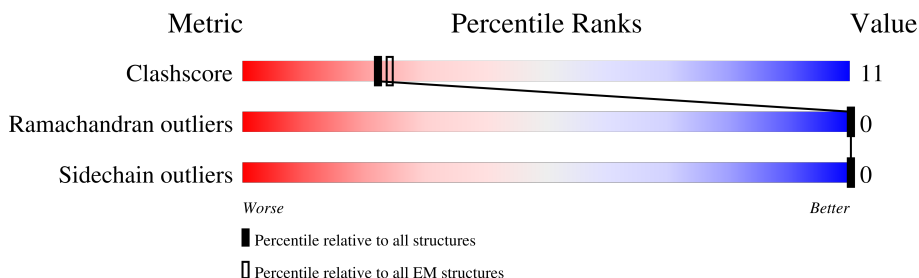
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	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	511	
1	B	511	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5028 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 Mucin-5AC.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	329	Total	C	N	O	S	0	0
			2513	1576	421	484	32		
1	B	329	Total	C	N	O	S	0	0
			2513	1576	421	484	32		

There are 94 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	879	ASP	-	expression tag	UNP P98088
A	880	ALA	-	expression tag	UNP P98088
A	881	ALA	-	expression tag	UNP P98088
A	882	GLN	-	expression tag	UNP P98088
A	883	PRO	-	expression tag	UNP P98088
A	884	ALA	-	expression tag	UNP P98088
A	885	ARG	-	expression tag	UNP P98088
A	886	ARG	-	expression tag	UNP P98088
A	887	ALA	-	expression tag	UNP P98088
A	888	VAL	-	expression tag	UNP P98088
A	889	ARG	-	expression tag	UNP P98088
A	890	SER	-	expression tag	UNP P98088
A	891	SER	-	expression tag	UNP P98088
A	892	ARG	-	expression tag	UNP P98088
A	893	HIS	-	expression tag	UNP P98088
A	894	HIS	-	expression tag	UNP P98088
A	895	HIS	-	expression tag	UNP P98088
A	896	HIS	-	expression tag	UNP P98088
A	897	HIS	-	expression tag	UNP P98088
A	898	HIS	-	expression tag	UNP P98088
A	899	GLY	-	expression tag	UNP P98088
A	900	SER	-	expression tag	UNP P98088
A	996	GLN	ARG	engineered mutation	UNP P98088
A	1201	TRP	ARG	engineered mutation	UNP P98088
A	1367	ASP	SER	conflict	UNP P98088
A	1368	ASP	-	expression tag	UNP P98088

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1369	ASP	-	expression tag	UNP P98088
A	1370	ASP	-	expression tag	UNP P98088
A	1371	LYS	-	expression tag	UNP P98088
A	1372	THR	-	expression tag	UNP P98088
A	1373	SER	-	expression tag	UNP P98088
A	1374	GLU	-	expression tag	UNP P98088
A	1375	GLN	-	expression tag	UNP P98088
A	1376	LYS	-	expression tag	UNP P98088
A	1377	LEU	-	expression tag	UNP P98088
A	1378	ILE	-	expression tag	UNP P98088
A	1379	SER	-	expression tag	UNP P98088
A	1380	GLU	-	expression tag	UNP P98088
A	1381	GLU	-	expression tag	UNP P98088
A	1382	ASP	-	expression tag	UNP P98088
A	1383	LEU	-	expression tag	UNP P98088
A	1384	SER	-	expression tag	UNP P98088
A	1385	ARG	-	expression tag	UNP P98088
A	1386	LYS	-	expression tag	UNP P98088
A	1387	LEU	-	expression tag	UNP P98088
A	1388	THR	-	expression tag	UNP P98088
A	1389	ARG	-	expression tag	UNP P98088
B	879	ASP	-	expression tag	UNP P98088
B	880	ALA	-	expression tag	UNP P98088
B	881	ALA	-	expression tag	UNP P98088
B	882	GLN	-	expression tag	UNP P98088
B	883	PRO	-	expression tag	UNP P98088
B	884	ALA	-	expression tag	UNP P98088
B	885	ARG	-	expression tag	UNP P98088
B	886	ARG	-	expression tag	UNP P98088
B	887	ALA	-	expression tag	UNP P98088
B	888	VAL	-	expression tag	UNP P98088
B	889	ARG	-	expression tag	UNP P98088
B	890	SER	-	expression tag	UNP P98088
B	891	SER	-	expression tag	UNP P98088
B	892	ARG	-	expression tag	UNP P98088
B	893	HIS	-	expression tag	UNP P98088
B	894	HIS	-	expression tag	UNP P98088
B	895	HIS	-	expression tag	UNP P98088
B	896	HIS	-	expression tag	UNP P98088
B	897	HIS	-	expression tag	UNP P98088
B	898	HIS	-	expression tag	UNP P98088
B	899	GLY	-	expression tag	UNP P98088

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Chain	Residue	Modelled	Actual	Comment	Reference
B	900	SER	-	expression tag	UNP P98088
B	996	GLN	ARG	engineered mutation	UNP P98088
B	1201	TRP	ARG	engineered mutation	UNP P98088
B	1367	ASP	SER	conflict	UNP P98088
B	1368	ASP	-	expression tag	UNP P98088
B	1369	ASP	-	expression tag	UNP P98088
B	1370	ASP	-	expression tag	UNP P98088
B	1371	LYS	-	expression tag	UNP P98088
B	1372	THR	-	expression tag	UNP P98088
B	1373	SER	-	expression tag	UNP P98088
B	1374	GLU	-	expression tag	UNP P98088
B	1375	GLN	-	expression tag	UNP P98088
B	1376	LYS	-	expression tag	UNP P98088
B	1377	LEU	-	expression tag	UNP P98088
B	1378	ILE	-	expression tag	UNP P98088
B	1379	SER	-	expression tag	UNP P98088
B	1380	GLU	-	expression tag	UNP P98088
B	1381	GLU	-	expression tag	UNP P98088
B	1382	ASP	-	expression tag	UNP P98088
B	1383	LEU	-	expression tag	UNP P98088
B	1384	SER	-	expression tag	UNP P98088
B	1385	ARG	-	expression tag	UNP P98088
B	1386	LYS	-	expression tag	UNP P98088
B	1387	LEU	-	expression tag	UNP P98088
B	1388	THR	-	expression tag	UNP P98088
B	1389	ARG	-	expression tag	UNP P98088

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
2	A	1	Total Ca 1 1	0
2	B	1	Total Ca 1 1	0

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

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	330230	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.26	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.458	Depositor
Minimum map value	-0.201	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	216.6784, 216.6784, 216.6784	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8464, 0.8464, 0.8464	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.26	0/2581	0.46	0/3516
1	B	0.26	0/2581	0.46	0/3516
All	All	0.26	0/5162	0.46	0/7032

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2513	0	2337	57	0
1	B	2513	0	2337	56	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
All	All	5028	0	4674	109	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 11.

All (109) 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:1047:PHE:HB2	1:B:1054:VAL:HG13	1.67	0.76
1:A:1047:PHE:HB2	1:A:1054:VAL:HG13	1.67	0.76
1:B:1187:ARG:HD2	1:B:1215:PRO:HB2	1.72	0.71
1:A:1187:ARG:HD2	1:A:1215:PRO:HB2	1.72	0.70
1:A:1188:THR:HG23	1:A:1191:ASN:H	1.58	0.68
1:A:1028:PHE:HA	1:A:1031:ARG:HH22	1.60	0.67
1:B:1028:PHE:HA	1:B:1031:ARG:HH22	1.60	0.66
1:B:1188:THR:HG23	1:B:1191:ASN:H	1.58	0.65
1:B:1191:ASN:ND2	1:B:1195:ASP:O	2.30	0.65
1:A:1191:ASN:ND2	1:A:1195:ASP:O	2.30	0.64
1:A:1179:GLN:HG3	1:A:1182:GLY:H	1.63	0.63
1:B:1179:GLN:HG3	1:B:1182:GLY:H	1.64	0.63
1:A:1220:ASP:OD2	1:A:1221:LYS:NZ	2.31	0.63
1:A:1055:VAL:HG12	1:A:1057:ASP:H	1.64	0.63
1:B:1055:VAL:HG12	1:B:1057:ASP:H	1.64	0.62
1:B:1038:ASN:ND2	1:B:1040:ASP:OD2	2.32	0.62
1:A:1038:ASN:ND2	1:A:1040:ASP:OD2	2.32	0.62
1:B:1057:ASP:HB3	1:B:1060:GLU:HB2	1.83	0.60
1:A:1057:ASP:HB3	1:A:1060:GLU:HB2	1.83	0.60
1:A:929:LEU:HD13	1:A:1035:LEU:HB2	1.84	0.60
1:A:956:THR:HG21	1:A:1125:ALA:HB1	1.82	0.60
1:B:956:THR:HG21	1:B:1125:ALA:HB1	1.82	0.60
1:A:964:ILE:HB	1:A:975:LEU:HD12	1.84	0.59
1:A:1068:SER:HB3	1:A:1071:CYS:HB2	1.85	0.58
1:B:964:ILE:HB	1:B:975:LEU:HD12	1.84	0.58
1:B:929:LEU:HD13	1:B:1035:LEU:HB2	1.84	0.58
1:B:1220:ASP:OD2	1:B:1221:LYS:NZ	2.31	0.58
1:B:1157:THR:HB	1:B:1160:ILE:HG12	1.86	0.58
1:A:904:ALA:HB3	1:A:912:LEU:HB3	1.86	0.57
1:A:931:GLN:OE1	1:A:1050:ARG:NH2	2.38	0.57
1:A:1157:THR:HB	1:A:1160:ILE:HG12	1.86	0.57
1:B:1068:SER:HB3	1:B:1071:CYS:HB2	1.85	0.57
1:B:931:GLN:OE1	1:B:1050:ARG:NH2	2.38	0.57
1:B:904:ALA:HB3	1:B:912:LEU:HB3	1.86	0.56
1:A:1040:ASP:OD2	1:A:1045:ASN:ND2	2.39	0.56
1:B:1040:ASP:OD2	1:B:1045:ASN:ND2	2.39	0.55
1:A:932:ASN:HB3	1:A:943:SER:HA	1.92	0.52
1:B:932:ASN:HB3	1:B:943:SER:HA	1.92	0.52
1:B:905:VAL:HG22	1:B:911:TYR:HD2	1.75	0.52
1:B:1188:THR:HA	1:B:1216:ILE:HG23	1.91	0.52
1:A:1188:THR:HA	1:A:1216:ILE:HG23	1.91	0.52
1:A:905:VAL:HG22	1:A:911:TYR:HD2	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1167:TYR:CG	1:B:1158:PRO:HD3	2.45	0.51
1:A:1128:SER:HA	1:B:1086:PHE:HE2	1.75	0.51
1:B:1147:HIS:NE2	1:B:1181:CYS:O	2.33	0.50
1:B:1079:ASP:OD2	1:B:1082:THR:OG1	2.30	0.50
1:A:1013:LEU:HD13	1:A:1021:PHE:HB2	1.93	0.49
1:B:1013:LEU:HD13	1:B:1021:PHE:HB2	1.93	0.49
1:B:1218:ASP:OD1	1:B:1219:GLU:N	2.46	0.49
1:A:1002:LEU:HB3	1:A:1014:TRP:HB3	1.95	0.49
1:B:1002:LEU:HB3	1:B:1014:TRP:HB3	1.95	0.49
1:A:1147:HIS:NE2	1:A:1181:CYS:O	2.33	0.48
1:A:1218:ASP:OD1	1:A:1219:GLU:N	2.46	0.48
1:B:914:PHE:HE1	1:B:1023:ASN:HA	1.80	0.47
1:A:1049:THR:HG22	1:A:1061:PHE:HD1	1.79	0.47
1:B:1049:THR:HG22	1:B:1061:PHE:HD1	1.79	0.47
1:A:914:PHE:HE1	1:A:1023:ASN:HA	1.80	0.46
1:B:1131:ASP:N	1:B:1131:ASP:OD1	2.49	0.46
1:A:1080:PRO:HB3	1:A:1125:ALA:HB2	1.98	0.46
1:B:997:GLN:NE2	1:B:1001:TYR:O	2.43	0.46
1:A:1131:ASP:N	1:A:1131:ASP:OD1	2.49	0.45
1:B:1025:SER:HB3	1:B:1028:PHE:HE2	1.82	0.45
1:A:1079:ASP:OD2	1:A:1082:THR:OG1	2.30	0.45
1:A:997:GLN:NE2	1:A:1001:TYR:O	2.43	0.45
1:A:1025:SER:HB3	1:A:1028:PHE:CE2	2.52	0.45
1:A:1210:CYS:HB3	1:A:1215:PRO:HA	2.00	0.44
1:B:1025:SER:HB3	1:B:1028:PHE:CE2	2.52	0.44
1:B:1080:PRO:HB3	1:B:1125:ALA:HB2	1.98	0.44
1:B:905:VAL:HB	1:B:1020:ILE:HG23	2.00	0.44
1:B:1051:SER:OG	1:B:1053:SER:OG	2.34	0.44
1:A:1025:SER:HB3	1:A:1028:PHE:HE2	1.82	0.44
1:A:905:VAL:HB	1:A:1020:ILE:HG23	2.00	0.44
1:B:1210:CYS:HB3	1:B:1215:PRO:HA	1.99	0.43
1:A:1045:ASN:HA	1:A:1054:VAL:HG21	2.01	0.43
1:B:1187:ARG:NH2	1:B:1193:ARG:HD3	2.34	0.43
1:A:1164:PHE:HB2	1:B:1162:PRO:HB2	2.02	0.42
1:B:1028:PHE:HA	1:B:1031:ARG:NH2	2.31	0.42
1:A:1051:SER:OG	1:A:1053:SER:OG	2.34	0.42
1:B:1045:ASN:HA	1:B:1054:VAL:HG21	2.01	0.42
1:A:1192:PRO:HD2	1:A:1195:ASP:HB3	2.02	0.42
1:A:1199:ASP:OD1	1:A:1199:ASP:N	2.52	0.42
1:A:938:ASP:HB3	1:A:941:GLN:HA	2.01	0.42
1:A:951:VAL:HG11	1:A:962:LYS:HD3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1192:PRO:HD2	1:B:1195:ASP:HB3	2.02	0.42
1:A:1015:ASP:OD1	1:A:1019:SER:N	2.53	0.42
1:B:938:ASP:HB3	1:B:941:GLN:HA	2.01	0.42
1:B:1050:ARG:HG2	1:B:1065:TRP:CZ2	2.55	0.42
1:B:1015:ASP:OD1	1:B:1019:SER:N	2.53	0.41
1:A:1187:ARG:NH2	1:A:1193:ARG:HD3	2.34	0.41
1:A:933:HIS:ND1	1:A:938:ASP:HA	2.35	0.41
1:B:933:HIS:ND1	1:B:938:ASP:HA	2.35	0.41
1:A:1024:LEU:HD23	1:A:1039:PHE:CD2	2.56	0.41
1:B:965:LYS:HA	1:B:973:LEU:O	2.21	0.41
1:B:1084:ASN:HB3	1:B:1087:ARG:HD3	2.02	0.41
1:A:965:LYS:HA	1:A:973:LEU:O	2.21	0.41
1:A:1050:ARG:HG2	1:A:1065:TRP:CZ2	2.55	0.41
1:B:1024:LEU:HD23	1:B:1039:PHE:CD2	2.56	0.41
1:A:932:ASN:ND2	1:A:943:SER:H	2.19	0.41
1:A:946:VAL:HG12	1:A:966:ILE:HG23	2.02	0.41
1:A:1084:ASN:HB3	1:A:1087:ARG:HD3	2.02	0.41
1:A:1167:TYR:CD1	1:B:1158:PRO:HD3	2.56	0.41
1:B:951:VAL:HG11	1:B:962:LYS:HD3	2.02	0.41
1:B:932:ASN:HD22	1:B:943:SER:H	1.68	0.40
1:A:1182:GLY:HA3	1:A:1202:GLY:CA	2.51	0.40
1:B:946:VAL:HG12	1:B:966:ILE:HG23	2.02	0.40
1:A:1076:ALA:HA	1:A:1077:PRO:HD3	1.97	0.40
1:A:1024:LEU:HD21	1:A:1028:PHE:HB2	2.03	0.40
1:B:932:ASN:ND2	1:B:943:SER:H	2.19	0.40
1:B:1114:ARG:O	1:B:1117:GLU:HG3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	327/511 (64%)	310 (95%)	17 (5%)	0	100	100
1	B	327/511 (64%)	310 (95%)	17 (5%)	0	100	100
All	All	654/1022 (64%)	620 (95%)	34 (5%)	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	278/434 (64%)	278 (100%)	0	100	100
1	B	278/434 (64%)	278 (100%)	0	100	100
All	All	556/868 (64%)	556 (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 ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 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.

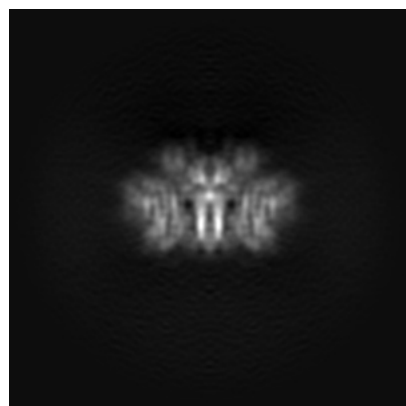
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18829. These allow visual inspection of the internal detail of the map and identification of artifacts.

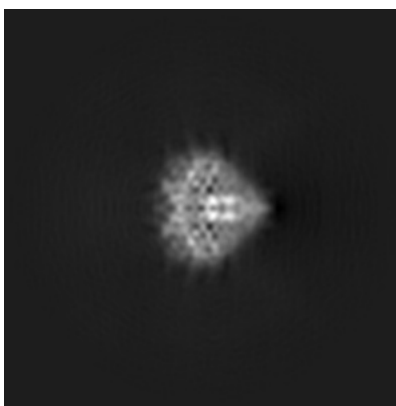
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

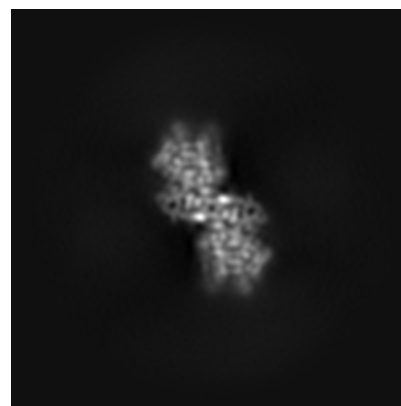
6.1.1 Primary map



X

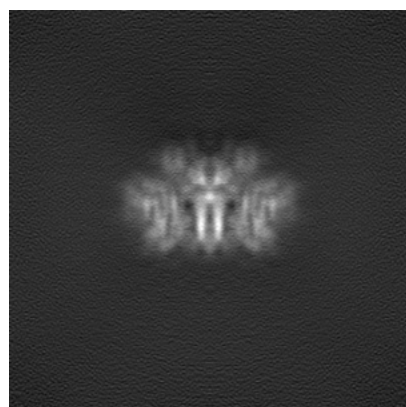


Y

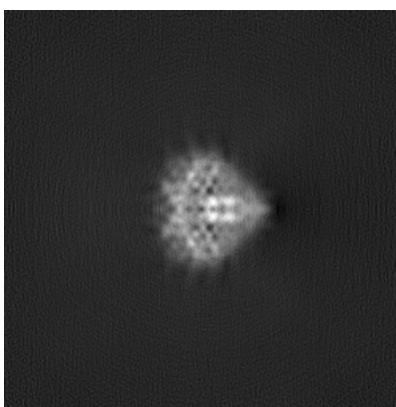


Z

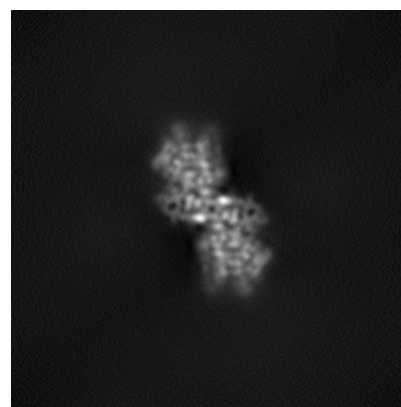
6.1.2 Raw map



X



Y

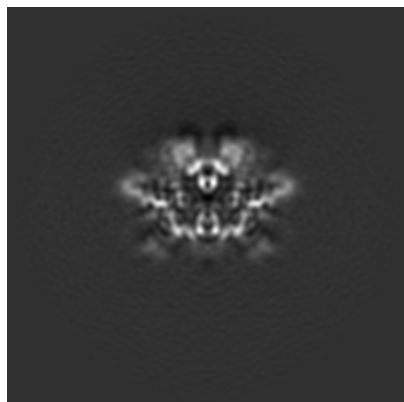


Z

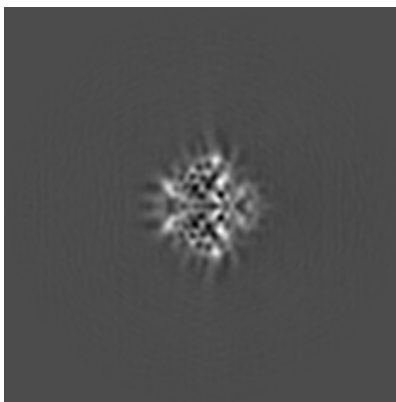
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

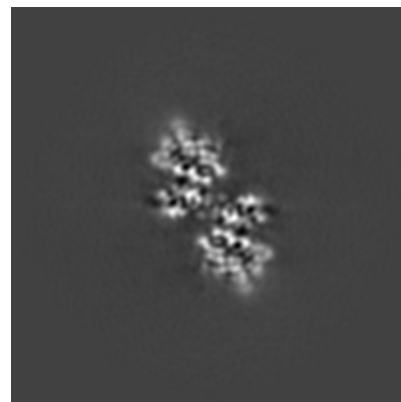
6.2.1 Primary map



X Index: 128

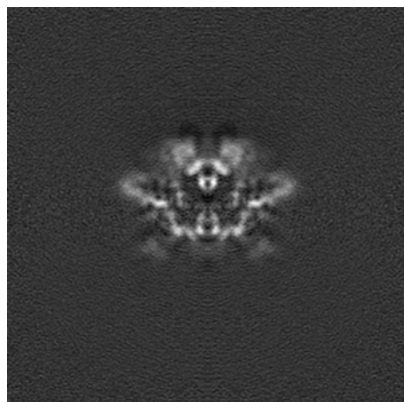


Y Index: 128

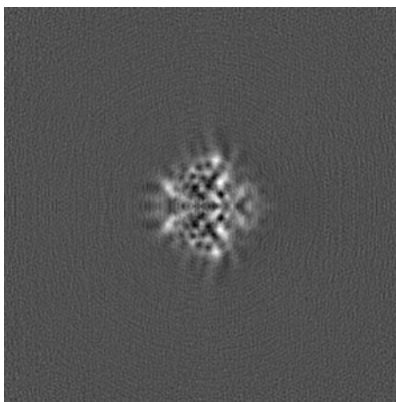


Z Index: 128

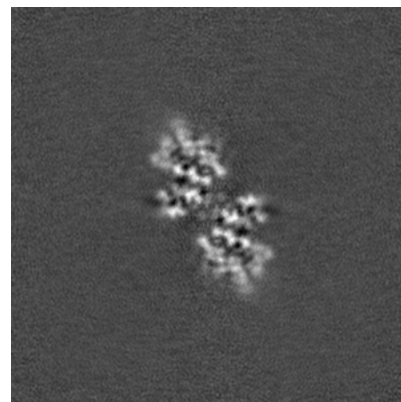
6.2.2 Raw map



X Index: 128



Y Index: 128

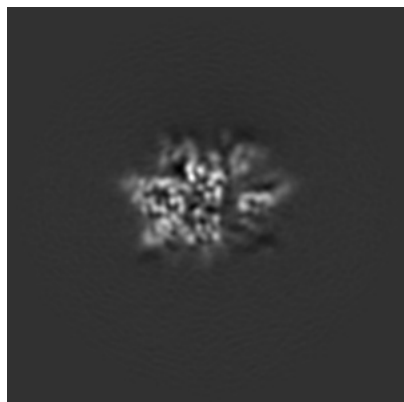


Z Index: 128

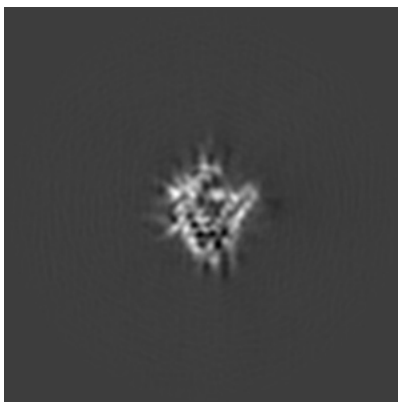
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

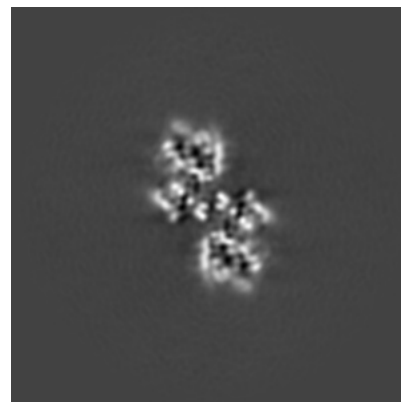
6.3.1 Primary map



X Index: 133

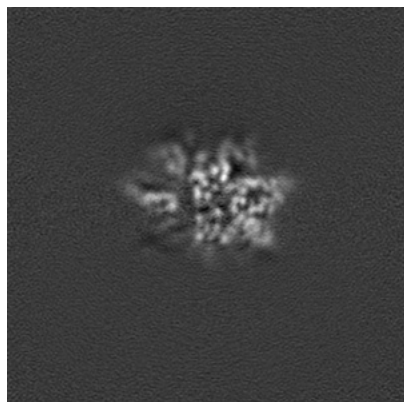


Y Index: 133

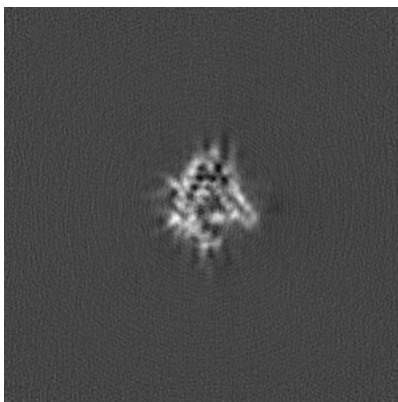


Z Index: 134

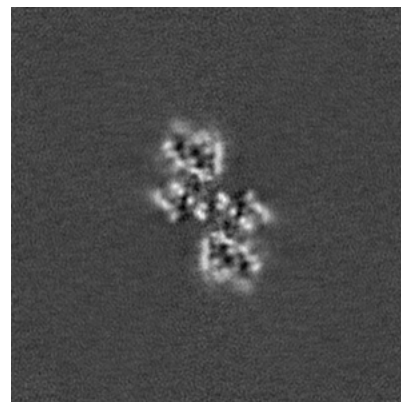
6.3.2 Raw map



X Index: 123



Y Index: 123

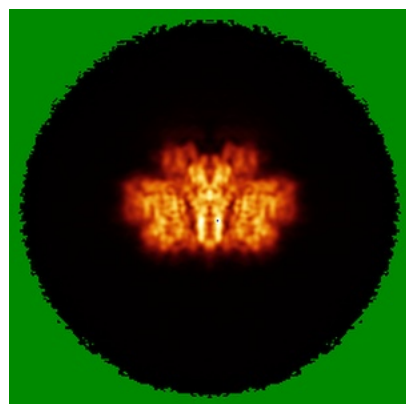


Z Index: 134

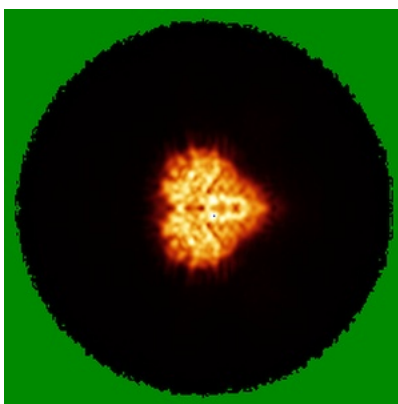
The images above show the largest variance slices of the map in three orthogonal directions.

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

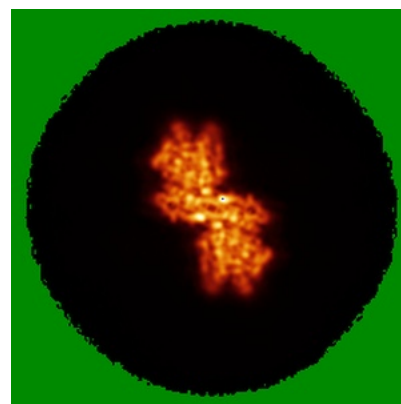
6.4.1 Primary map



X

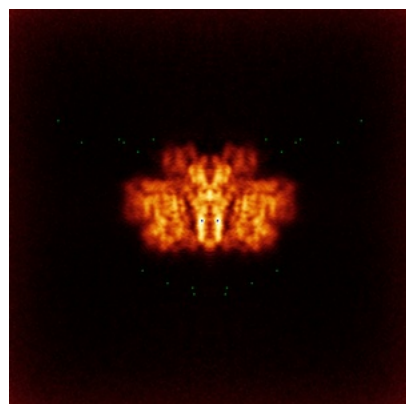


Y

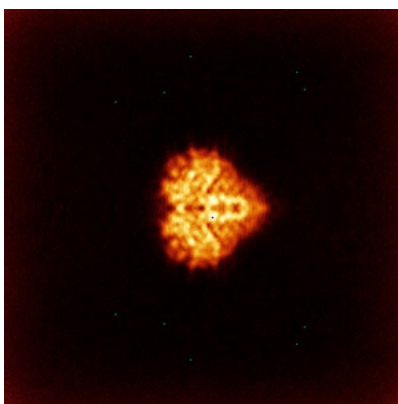


Z

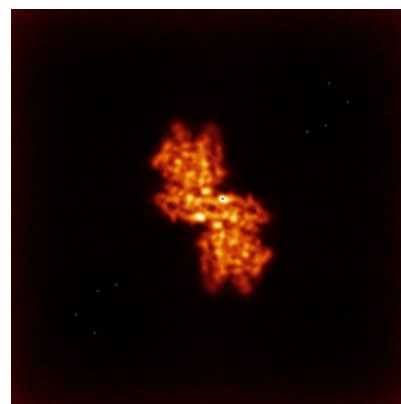
6.4.2 Raw map



X



Y

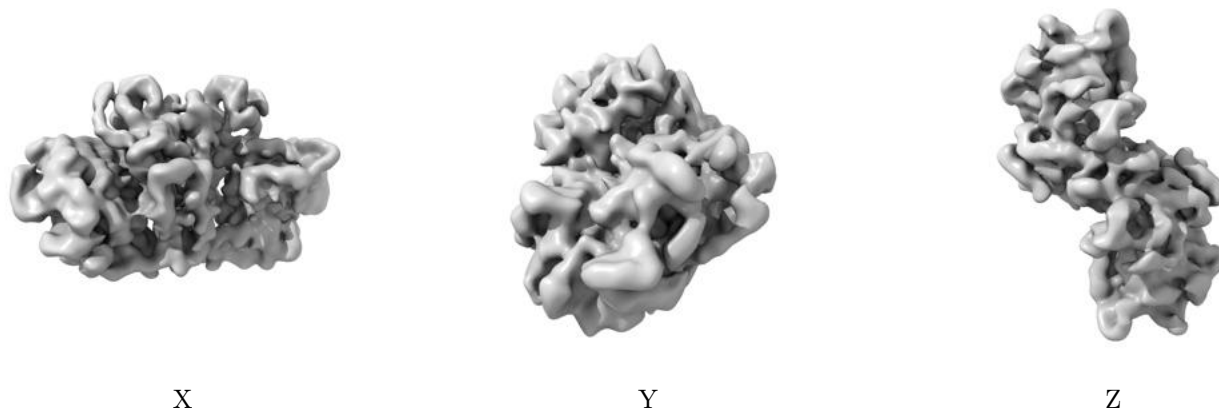


Z

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.

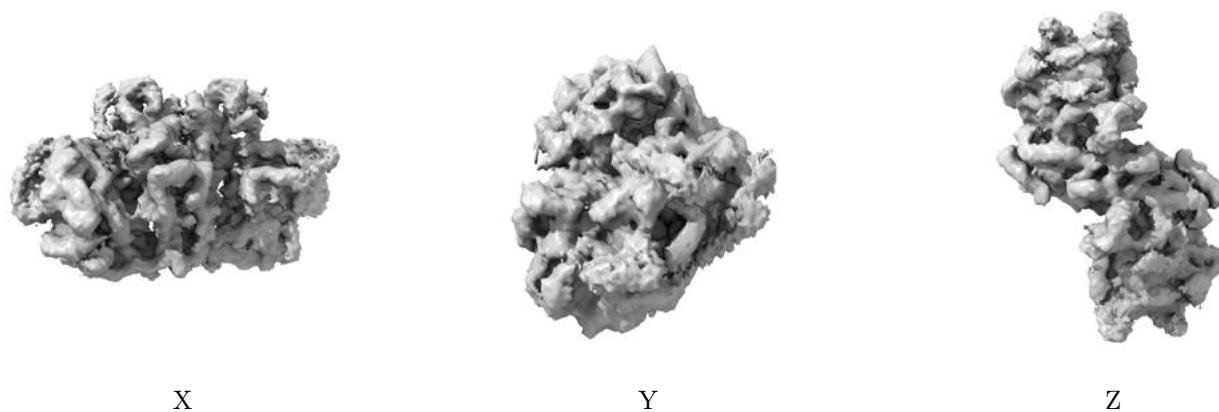
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.11. 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.

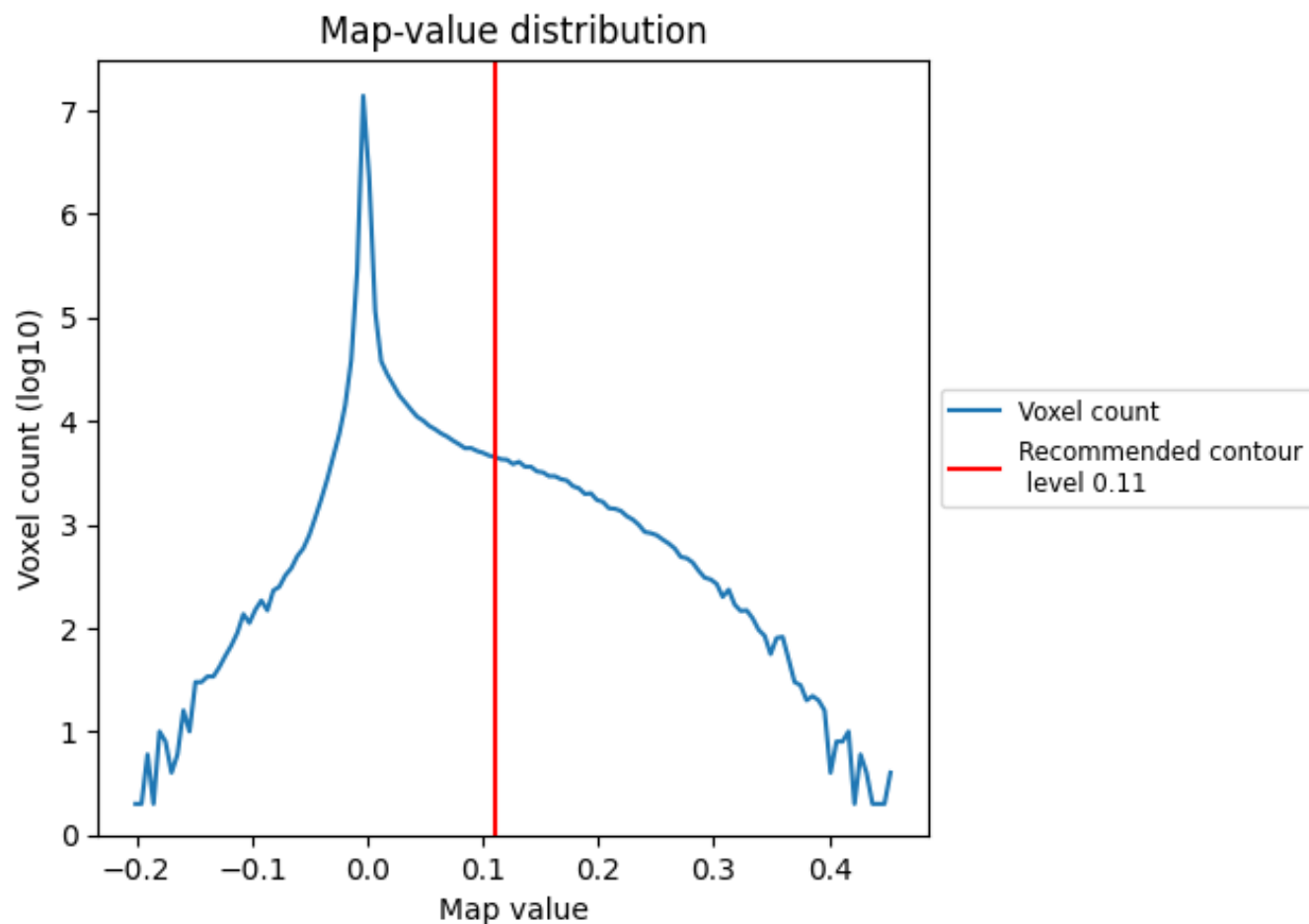
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

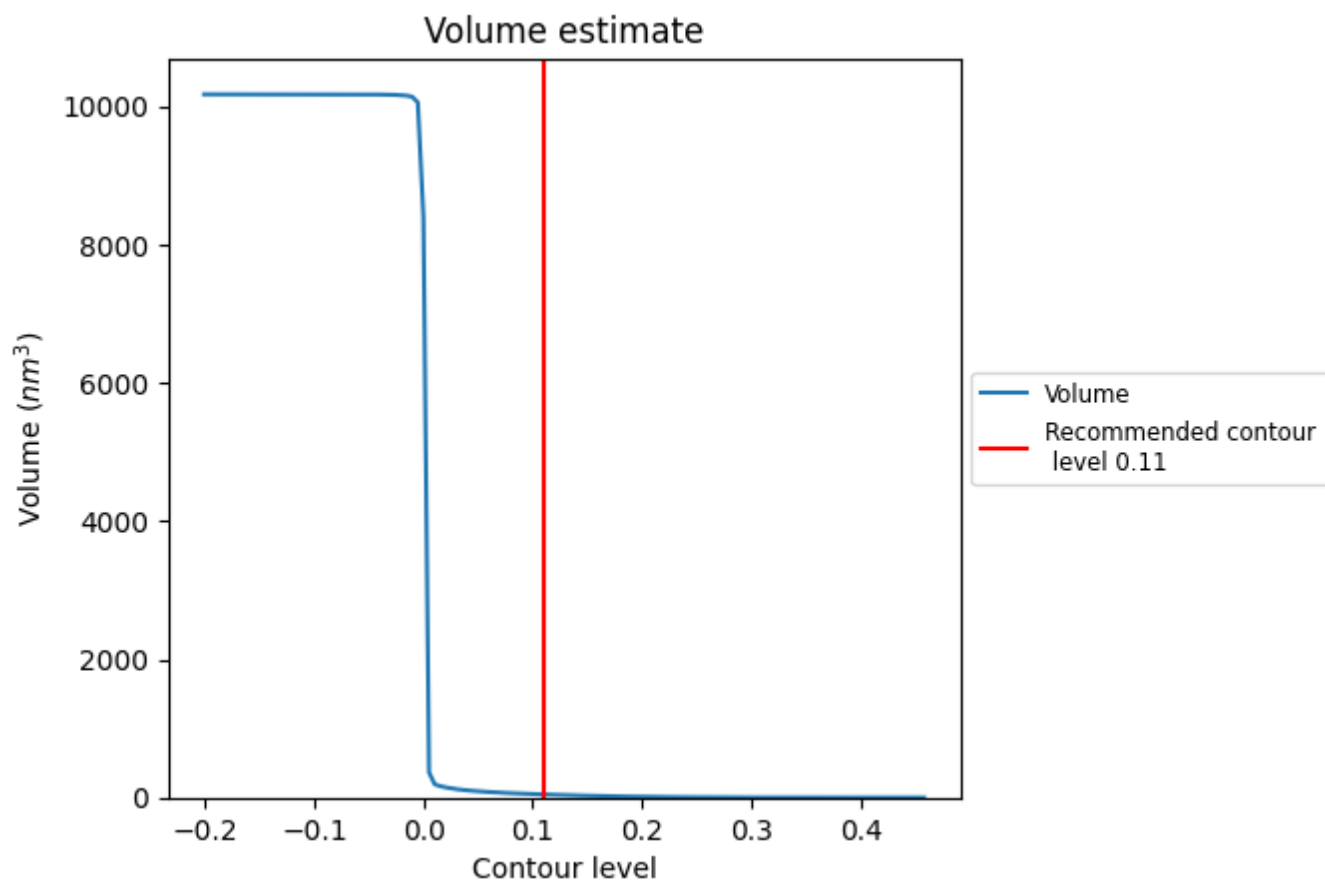
This section contains the results of statistical analysis of the map.

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.

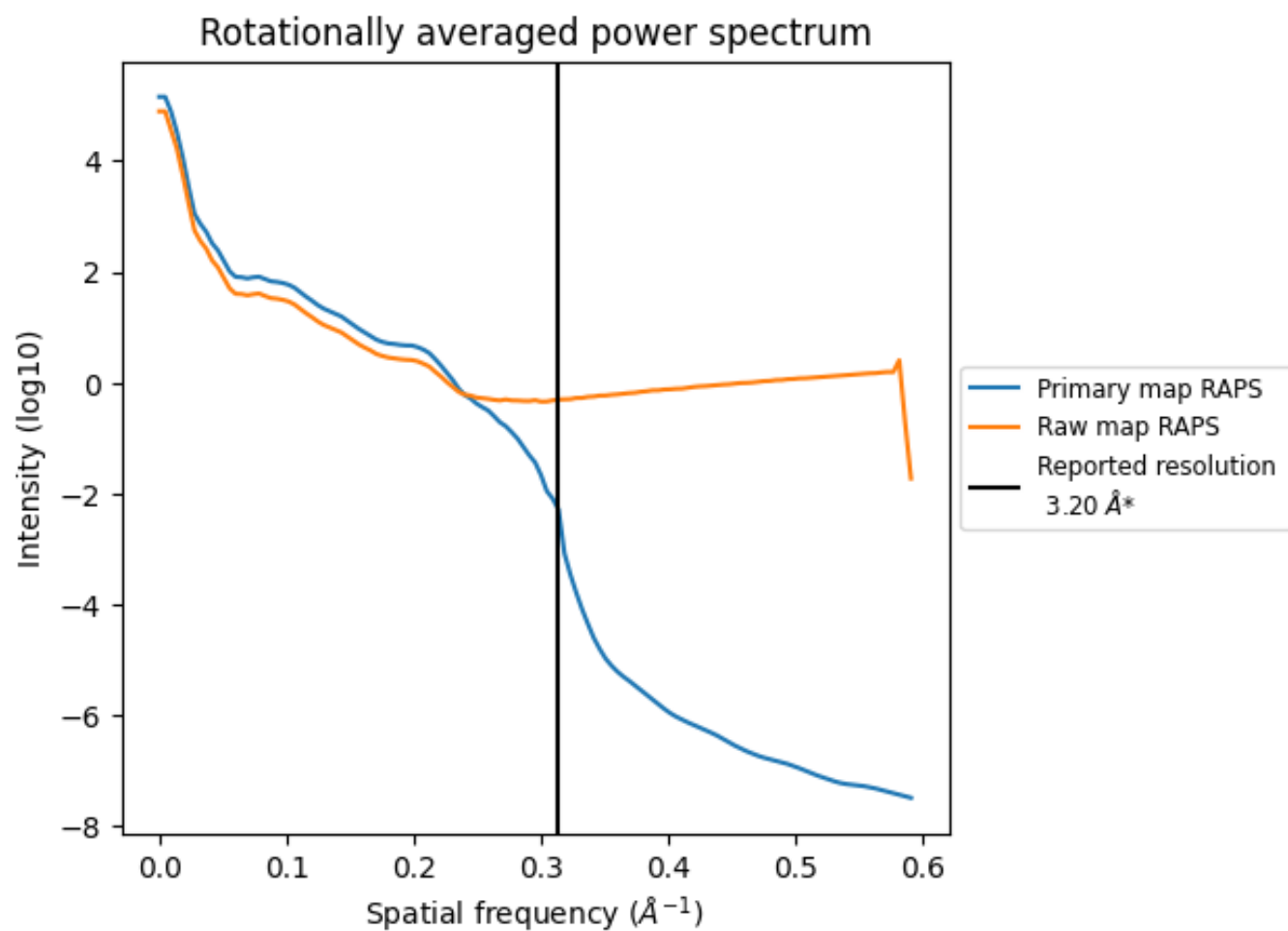
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 45 nm^3 ; this corresponds to an approximate mass of 41 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

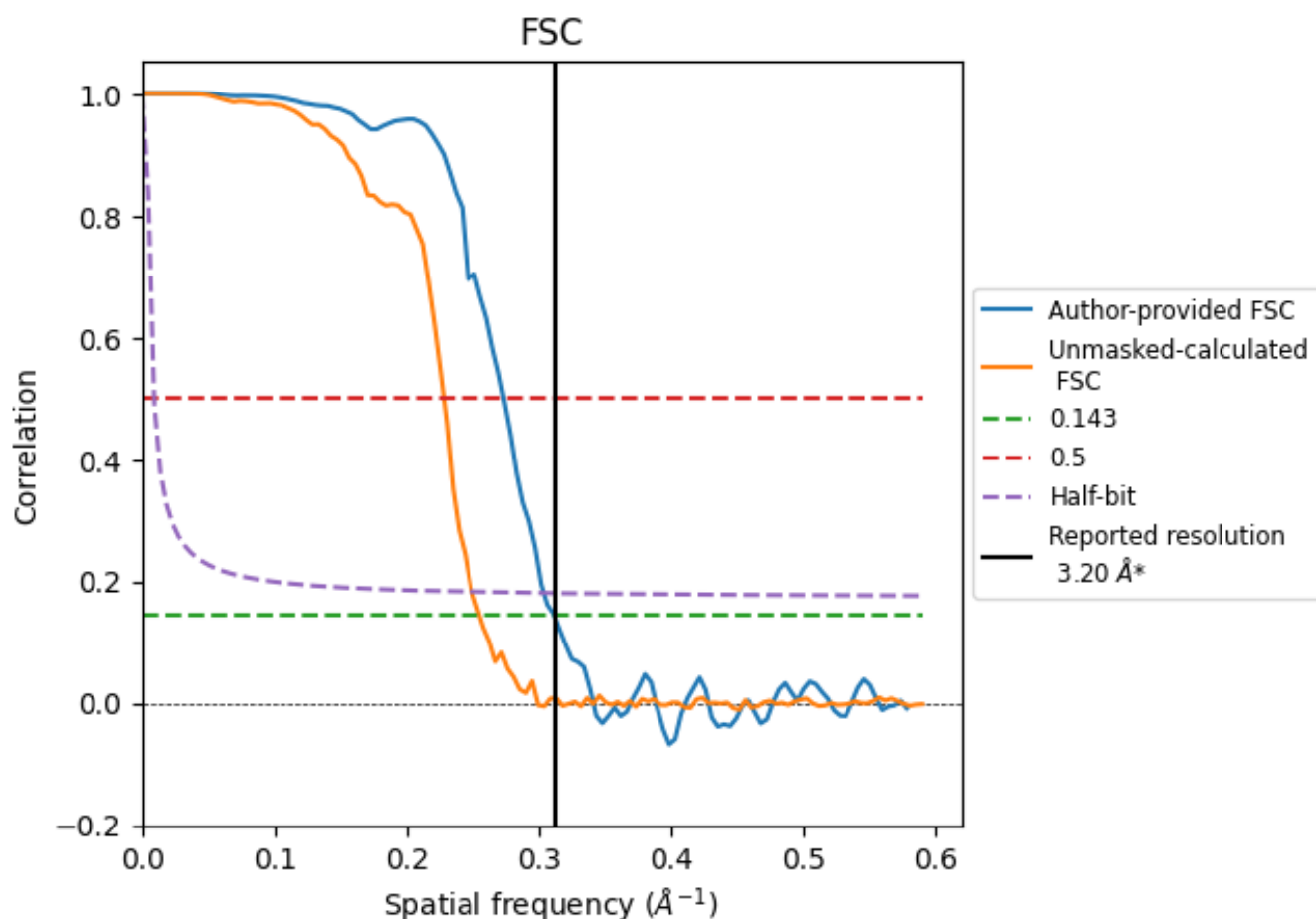


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 \AA^{-1}

8.2 Resolution estimates

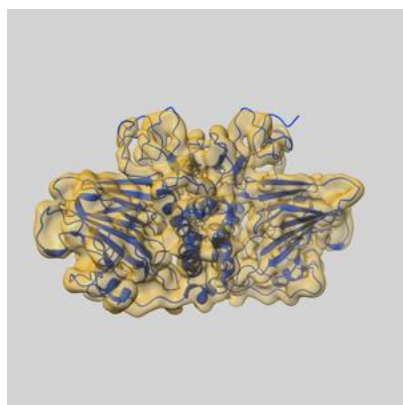
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.20	3.65	3.29
Unmasked-calculated*	3.91	4.38	4.00

*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 3.91 differs from the reported value 3.2 by more than 10 %

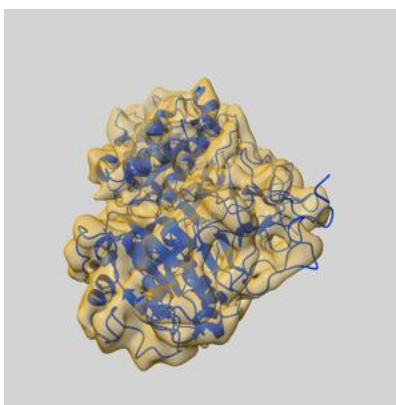
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-18829 and PDB model 8R1Z. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

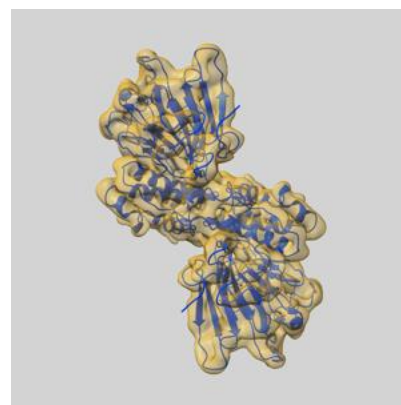
9.1 Map-model overlay [i](#)



X



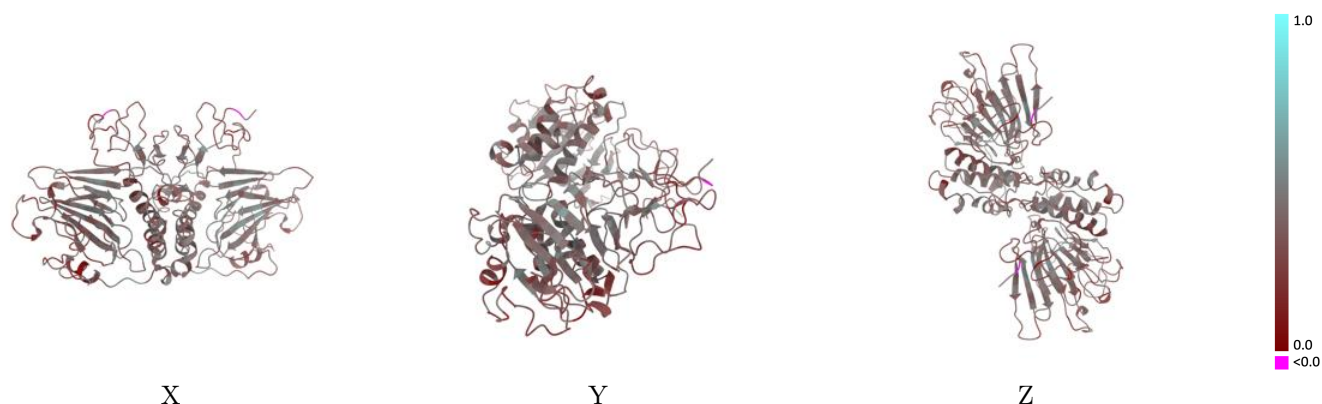
Y



Z

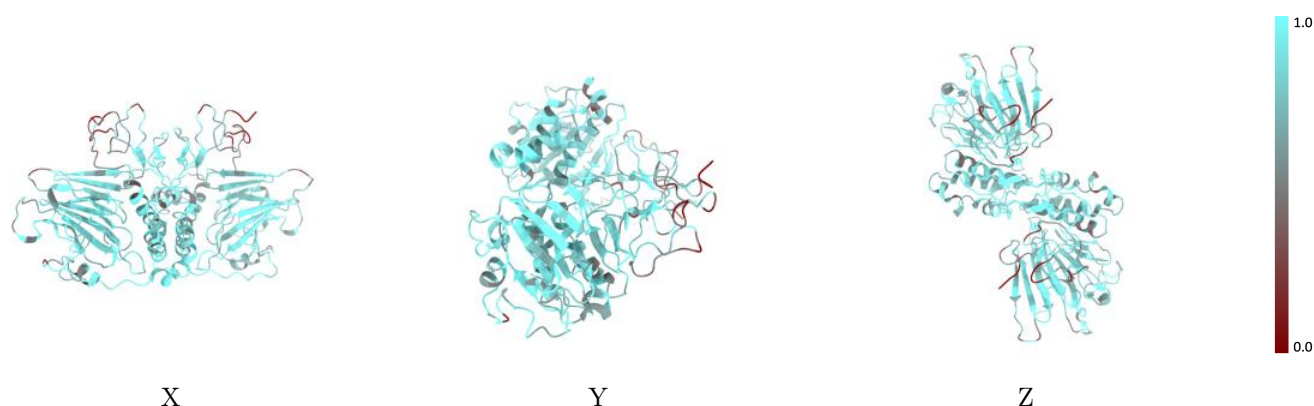
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



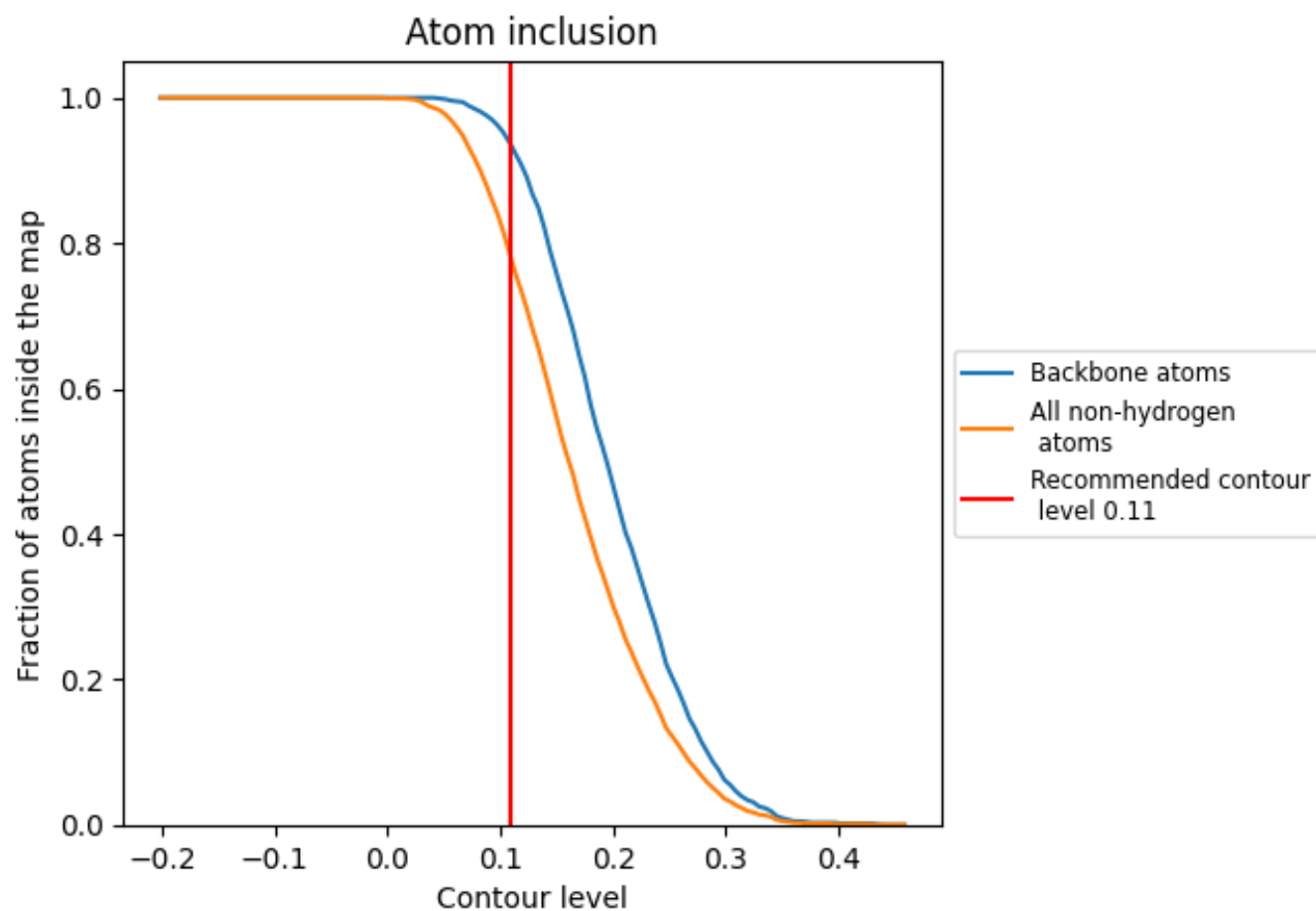
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 78% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7770	<div></div> 0.3600
A	<div></div> 0.7780	<div></div> 0.3590
B	<div></div> 0.7750	<div></div> 0.3610

