



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 08:21 AM UTC

PDB ID : 8H16 / pdb_00008h16
EMDB ID : EMD-34426
Title : Structure of SARS-CoV-1 Spike Protein (S/native) at pH 5.5, Open Conformation
Authors : Zhang, X.; Li, Z.; Liu, Y.; Wang, J.; Fu, L.; Wang, P.; He, J.; Xiong, X.
Deposited on : 2022-09-30
Resolution : 3.36 Å(reported)
Based on initial model : 7XTZ

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.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

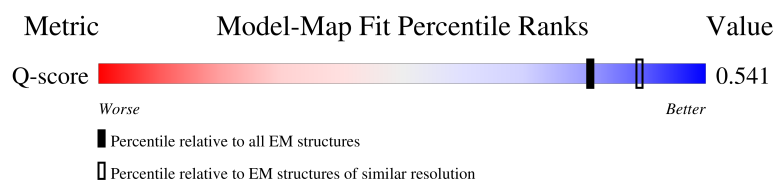
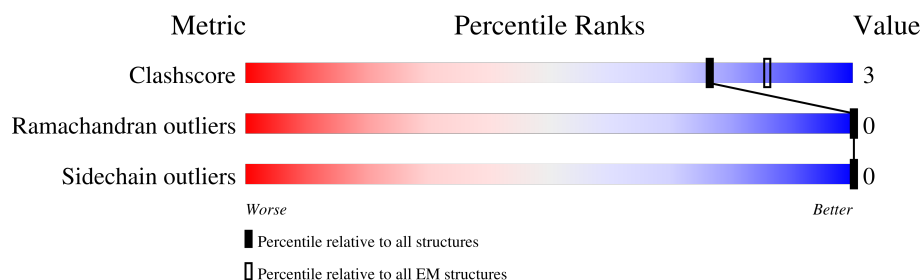
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.36 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	14301 (2.86 - 3.85)

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	 7% 60% 6% 35%
1	B	1232	 5% 72% 7% 22%
1	C	1232	 5% 73% 7% 20%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 21934 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	966	Total	C	N	O	S	0	0
			7549	4827	1255	1428	39		
1	A	805	Total	C	N	O	S	0	0
			6252	3984	1040	1197	31		
1	C	983	Total	C	N	O	S	0	0
			7685	4910	1276	1458	41		

There are 159 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	11	GLU	-	expression tag	UNP P59594
B	12	THR	-	expression tag	UNP P59594
B	13	GLY	-	expression tag	UNP P59594
B	14	THR	-	expression tag	UNP P59594
B	1194	GLY	-	expression tag	UNP P59594
B	1195	SER	-	expression tag	UNP P59594
B	1196	GLY	-	expression tag	UNP P59594
B	1197	ARG	-	expression tag	UNP P59594
B	1198	GLU	-	expression tag	UNP P59594
B	1199	ASN	-	expression tag	UNP P59594
B	1200	LEU	-	expression tag	UNP P59594
B	1201	TYR	-	expression tag	UNP P59594
B	1202	PHE	-	expression tag	UNP P59594
B	1203	GLN	-	expression tag	UNP P59594
B	1204	GLY	-	expression tag	UNP P59594
B	1205	GLY	-	expression tag	UNP P59594
B	1206	GLY	-	expression tag	UNP P59594
B	1207	GLY	-	expression tag	UNP P59594
B	1208	SER	-	expression tag	UNP P59594
B	1209	GLY	-	expression tag	UNP P59594
B	1210	TYR	-	expression tag	UNP P59594
B	1211	ILE	-	expression tag	UNP P59594
B	1212	PRO	-	expression tag	UNP P59594
B	1213	GLU	-	expression tag	UNP P59594

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1214	ALA	-	expression tag	UNP P59594
B	1215	PRO	-	expression tag	UNP P59594
B	1216	ARG	-	expression tag	UNP P59594
B	1217	ASP	-	expression tag	UNP P59594
B	1218	GLY	-	expression tag	UNP P59594
B	1219	GLN	-	expression tag	UNP P59594
B	1220	ALA	-	expression tag	UNP P59594
B	1221	TYR	-	expression tag	UNP P59594
B	1222	VAL	-	expression tag	UNP P59594
B	1223	ARG	-	expression tag	UNP P59594
B	1224	LYS	-	expression tag	UNP P59594
B	1225	ASP	-	expression tag	UNP P59594
B	1226	GLY	-	expression tag	UNP P59594
B	1227	GLU	-	expression tag	UNP P59594
B	1228	TRP	-	expression tag	UNP P59594
B	1229	VAL	-	expression tag	UNP P59594
B	1230	LEU	-	expression tag	UNP P59594
B	1231	LEU	-	expression tag	UNP P59594
B	1232	SER	-	expression tag	UNP P59594
B	1233	THR	-	expression tag	UNP P59594
B	1234	PHE	-	expression tag	UNP P59594
B	1235	LEU	-	expression tag	UNP P59594
B	1236	GLY	-	expression tag	UNP P59594
B	1237	HIS	-	expression tag	UNP P59594
B	1238	HIS	-	expression tag	UNP P59594
B	1239	HIS	-	expression tag	UNP P59594
B	1240	HIS	-	expression tag	UNP P59594
B	1241	HIS	-	expression tag	UNP P59594
B	1242	HIS	-	expression tag	UNP P59594
A	11	GLU	-	expression tag	UNP P59594
A	12	THR	-	expression tag	UNP P59594
A	13	GLY	-	expression tag	UNP P59594
A	14	THR	-	expression tag	UNP P59594
A	1194	GLY	-	expression tag	UNP P59594
A	1195	SER	-	expression tag	UNP P59594
A	1196	GLY	-	expression tag	UNP P59594
A	1197	ARG	-	expression tag	UNP P59594
A	1198	GLU	-	expression tag	UNP P59594
A	1199	ASN	-	expression tag	UNP P59594
A	1200	LEU	-	expression tag	UNP P59594
A	1201	TYR	-	expression tag	UNP P59594
A	1202	PHE	-	expression tag	UNP P59594

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1203	GLN	-	expression tag	UNP P59594
A	1204	GLY	-	expression tag	UNP P59594
A	1205	GLY	-	expression tag	UNP P59594
A	1206	GLY	-	expression tag	UNP P59594
A	1207	GLY	-	expression tag	UNP P59594
A	1208	SER	-	expression tag	UNP P59594
A	1209	GLY	-	expression tag	UNP P59594
A	1210	TYR	-	expression tag	UNP P59594
A	1211	ILE	-	expression tag	UNP P59594
A	1212	PRO	-	expression tag	UNP P59594
A	1213	GLU	-	expression tag	UNP P59594
A	1214	ALA	-	expression tag	UNP P59594
A	1215	PRO	-	expression tag	UNP P59594
A	1216	ARG	-	expression tag	UNP P59594
A	1217	ASP	-	expression tag	UNP P59594
A	1218	GLY	-	expression tag	UNP P59594
A	1219	GLN	-	expression tag	UNP P59594
A	1220	ALA	-	expression tag	UNP P59594
A	1221	TYR	-	expression tag	UNP P59594
A	1222	VAL	-	expression tag	UNP P59594
A	1223	ARG	-	expression tag	UNP P59594
A	1224	LYS	-	expression tag	UNP P59594
A	1225	ASP	-	expression tag	UNP P59594
A	1226	GLY	-	expression tag	UNP P59594
A	1227	GLU	-	expression tag	UNP P59594
A	1228	TRP	-	expression tag	UNP P59594
A	1229	VAL	-	expression tag	UNP P59594
A	1230	LEU	-	expression tag	UNP P59594
A	1231	LEU	-	expression tag	UNP P59594
A	1232	SER	-	expression tag	UNP P59594
A	1233	THR	-	expression tag	UNP P59594
A	1234	PHE	-	expression tag	UNP P59594
A	1235	LEU	-	expression tag	UNP P59594
A	1236	GLY	-	expression tag	UNP P59594
A	1237	HIS	-	expression tag	UNP P59594
A	1238	HIS	-	expression tag	UNP P59594
A	1239	HIS	-	expression tag	UNP P59594
A	1240	HIS	-	expression tag	UNP P59594
A	1241	HIS	-	expression tag	UNP P59594
A	1242	HIS	-	expression tag	UNP P59594
C	11	GLU	-	expression tag	UNP P59594
C	12	THR	-	expression tag	UNP P59594

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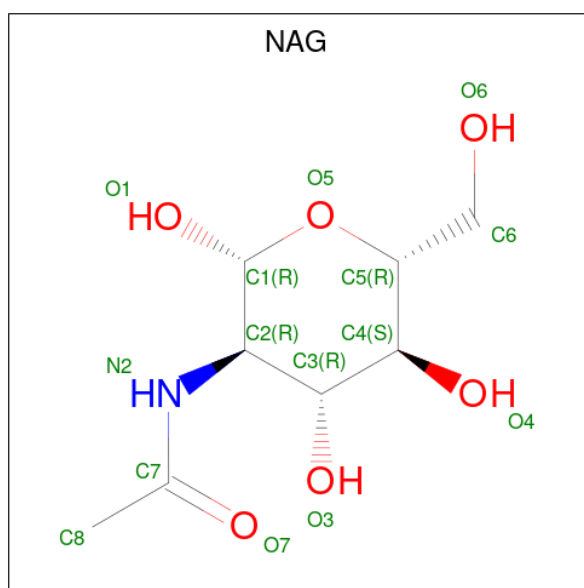
Chain	Residue	Modelled	Actual	Comment	Reference
C	13	GLY	-	expression tag	UNP P59594
C	14	THR	-	expression tag	UNP P59594
C	1194	GLY	-	expression tag	UNP P59594
C	1195	SER	-	expression tag	UNP P59594
C	1196	GLY	-	expression tag	UNP P59594
C	1197	ARG	-	expression tag	UNP P59594
C	1198	GLU	-	expression tag	UNP P59594
C	1199	ASN	-	expression tag	UNP P59594
C	1200	LEU	-	expression tag	UNP P59594
C	1201	TYR	-	expression tag	UNP P59594
C	1202	PHE	-	expression tag	UNP P59594
C	1203	GLN	-	expression tag	UNP P59594
C	1204	GLY	-	expression tag	UNP P59594
C	1205	GLY	-	expression tag	UNP P59594
C	1206	GLY	-	expression tag	UNP P59594
C	1207	GLY	-	expression tag	UNP P59594
C	1208	SER	-	expression tag	UNP P59594
C	1209	GLY	-	expression tag	UNP P59594
C	1210	TYR	-	expression tag	UNP P59594
C	1211	ILE	-	expression tag	UNP P59594
C	1212	PRO	-	expression tag	UNP P59594
C	1213	GLU	-	expression tag	UNP P59594
C	1214	ALA	-	expression tag	UNP P59594
C	1215	PRO	-	expression tag	UNP P59594
C	1216	ARG	-	expression tag	UNP P59594
C	1217	ASP	-	expression tag	UNP P59594
C	1218	GLY	-	expression tag	UNP P59594
C	1219	GLN	-	expression tag	UNP P59594
C	1220	ALA	-	expression tag	UNP P59594
C	1221	TYR	-	expression tag	UNP P59594
C	1222	VAL	-	expression tag	UNP P59594
C	1223	ARG	-	expression tag	UNP P59594
C	1224	LYS	-	expression tag	UNP P59594
C	1225	ASP	-	expression tag	UNP P59594
C	1226	GLY	-	expression tag	UNP P59594
C	1227	GLU	-	expression tag	UNP P59594
C	1228	TRP	-	expression tag	UNP P59594
C	1229	VAL	-	expression tag	UNP P59594
C	1230	LEU	-	expression tag	UNP P59594
C	1231	LEU	-	expression tag	UNP P59594
C	1232	SER	-	expression tag	UNP P59594
C	1233	THR	-	expression tag	UNP P59594

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1234	PHE	-	expression tag	UNP P59594
C	1235	LEU	-	expression tag	UNP P59594
C	1236	GLY	-	expression tag	UNP P59594
C	1237	HIS	-	expression tag	UNP P59594
C	1238	HIS	-	expression tag	UNP P59594
C	1239	HIS	-	expression tag	UNP P59594
C	1240	HIS	-	expression tag	UNP P59594
C	1241	HIS	-	expression tag	UNP P59594
C	1242	HIS	-	expression tag	UNP P59594

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	

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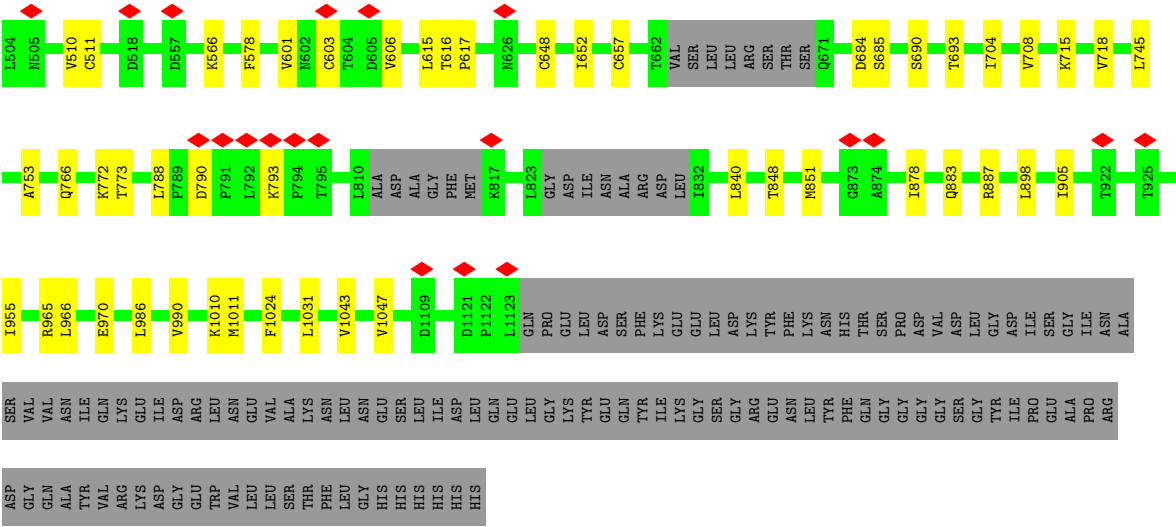
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Mol	Chain	Residues	Atoms				AltConf
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C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

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Mol	Chain	Residues	Atoms				AltConf
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	308387	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	45000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.463	Depositor
Minimum map value	-0.268	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	345.6, 345.6, 345.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.35, 1.35, 1.35	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

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	0/6381	0.51	0/8668
1	B	0.25	0/7712	0.52	1/10472 (0.0%)
1	C	0.26	0/7852	0.52	2/10664 (0.0%)
All	All	0.26	0/21945	0.51	3/29804 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	218	PRO	CA-N-CD	-5.53	104.25	112.00
1	C	652	ILE	CA-C-N	-5.14	115.60	122.54
1	C	652	ILE	C-N-CA	-5.14	115.60	122.54

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	6252	0	6120	44	0
1	B	7549	0	7393	49	0
1	C	7685	0	7502	45	0
2	A	154	0	143	0	0
2	B	126	0	117	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	168	0	156	0	0
All	All	21934	0	21431	131	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 3.

All (131) 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:932:ASP:O	1:A:936:GLN:NE2	2.24	0.71
1:B:1108:CYS:HB2	1:B:1114:ILE:HG12	1.78	0.65
1:C:378:CYS:HA	1:C:511:CYS:HB3	1.79	0.63
1:C:1010:LYS:NZ	1:C:1024:PHE:O	2.31	0.63
1:B:390:LYS:NZ	1:B:392:ASP:OD2	2.28	0.62
1:C:848:THR:H	1:C:851:MET:HE3	1.65	0.62
1:B:102:VAL:HG13	1:B:234:ILE:HD11	1.82	0.62
1:A:716:THR:HG22	1:A:842:VAL:HG22	1.83	0.61
1:B:1010:LYS:NZ	1:B:1024:PHE:O	2.35	0.60
1:A:38:ARG:NH1	1:A:184:GLU:OE2	2.33	0.60
1:B:38:ARG:NH1	1:B:184:GLU:OE2	2.35	0.59
1:C:116:ILE:HG12	1:C:125:ILE:HG12	1.84	0.59
1:A:786:GLN:NE2	1:A:917:GLN:OE1	2.35	0.59
1:B:128:CYS:SG	1:B:129:ASN:N	2.76	0.58
1:C:603:CYS:HB2	1:C:606:VAL:HG22	1.86	0.58
1:A:52:LEU:HD22	1:A:263:MET:HE3	1.86	0.57
1:B:93:GLU:OE1	1:B:183:ARG:NH1	2.36	0.57
1:A:932:ASP:OD2	1:A:936:GLN:NE2	2.32	0.57
1:C:316:PHE:O	1:C:566:LYS:NZ	2.35	0.57
1:A:709:MET:HE1	1:A:1006:LEU:HD23	1.87	0.57
1:B:378:CYS:HA	1:B:511:CYS:HB3	1.87	0.56
1:B:615:LEU:HG	1:B:617:PRO:HD2	1.86	0.56
1:A:745:LEU:HD22	1:A:990:VAL:HG21	1.88	0.55
1:A:316:PHE:O	1:A:566:LYS:NZ	2.36	0.55
1:A:129:ASN:HB2	1:A:157:PHE:HB2	1.89	0.55
1:A:772:LYS:NZ	1:C:684:ASP:OD1	2.39	0.55
1:B:62:PHE:O	1:B:620:ARG:NH2	2.37	0.54
1:B:388:VAL:HG22	1:B:495:ARG:HG2	1.89	0.54
1:B:206:VAL:HG11	1:B:210:PRO:HG3	1.90	0.54
1:A:95:SER:OG	1:A:96:ASN:N	2.42	0.53
1:A:97:VAL:HG22	1:A:235:LEU:HD12	1.91	0.53
1:B:315:ARG:HH12	1:B:519:LEU:HD22	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:822:CYS:HB2	1:B:833:CYS:HA	1.91	0.52
1:B:686:SER:HB2	1:C:772:LYS:HZ1	1.73	0.52
1:C:38:ARG:NH2	1:C:210:PRO:O	2.43	0.52
1:B:380:SER:O	1:B:509:THR:OG1	2.22	0.52
1:C:966:LEU:HD13	1:C:970:GLU:HG3	1.92	0.51
1:A:78:ASN:HD22	1:A:78:ASN:N	2.07	0.51
1:A:198:LYS:HB3	1:A:219:ILE:HG13	1.92	0.50
1:A:742:CYS:O	1:A:746:ASN:ND2	2.45	0.50
1:B:47:PHE:HE2	1:A:543:LYS:HD3	1.76	0.50
1:A:203:ILE:HG21	1:A:210:PRO:HG2	1.94	0.50
1:A:196:VAL:HB	1:A:220:PHE:HB2	1.94	0.49
1:C:118:ASN:HB3	1:C:123:VAL:HG22	1.92	0.49
1:C:690:SER:HB2	1:C:693:THR:HG22	1.94	0.49
1:A:695:ALA:HA	1:A:1055:ARG:O	2.12	0.49
1:A:772:LYS:NZ	1:C:685:SER:O	2.42	0.49
1:B:808:VAL:HG23	1:B:927:LEU:HD23	1.94	0.49
1:C:615:LEU:HG	1:C:617:PRO:HD2	1.95	0.48
1:B:316:PHE:O	1:B:566:LYS:NZ	2.46	0.48
1:B:198:LYS:HB3	1:B:219:ILE:HG13	1.95	0.48
1:B:347:ASN:H	1:B:509:THR:HB	1.78	0.48
1:C:324:PRO:HB2	1:C:327:GLU:HG2	1.95	0.48
1:C:704:ILE:HG12	1:C:1047:VAL:HG22	1.95	0.48
1:C:323:CYS:HB3	1:C:348:CYS:HB3	1.72	0.47
1:B:745:LEU:HG	1:B:990:VAL:HG21	1.95	0.47
1:B:548:PHE:HD2	1:C:45:GLU:HG3	1.80	0.47
1:B:392:ASP:O	1:B:395:ARG:NH1	2.48	0.47
1:C:955:ILE:HD12	1:C:965:ARG:HH21	1.79	0.46
1:A:1073:ARG:NH1	1:A:1100:ASP:O	2.49	0.46
1:B:821:GLU:HG2	1:B:842:VAL:HB	1.97	0.46
1:C:878:ILE:HG23	1:C:883:GLN:HE21	1.79	0.46
1:C:444:ARG:NH2	1:C:454:ASP:OD1	2.43	0.46
1:C:766:GLN:HG3	1:C:1011:MET:HG2	1.97	0.46
1:B:409:ASN:HD21	1:B:441:ARG:H	1.64	0.45
1:A:188:LYS:HE3	1:A:195:TYR:HD2	1.80	0.45
1:C:898:LEU:HD12	1:C:905:ILE:HD12	1.98	0.45
1:A:78:ASN:N	1:A:78:ASN:ND2	2.65	0.45
1:C:38:ARG:NH1	1:C:184:GLU:OE2	2.49	0.45
1:A:1080:ASN:HD22	1:A:1085:PHE:HE2	1.64	0.45
1:A:524:CYS:HB2	1:A:576:CYS:HB3	1.84	0.45
1:B:197:TYR:HD2	1:B:218:PRO:HD3	1.82	0.45
1:B:305:PHE:HZ	1:B:601:VAL:HG11	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:704:ILE:HA	1:A:1046:HIS:O	2.17	0.45
1:B:180:LYS:HE2	1:B:205:VAL:HA	1.99	0.44
1:B:51:THR:HG22	1:A:555:VAL:HG12	2.00	0.44
1:B:391:GLY:HA3	1:B:491:TYR:HD2	1.82	0.44
1:C:306:ARG:H	1:C:616:THR:HG22	1.83	0.43
1:B:1075:GLY:HA3	1:B:1087:THR:O	2.19	0.43
1:C:124:VAL:HG23	1:C:164:ILE:HG13	2.00	0.43
1:A:776:LEU:HD23	1:A:778:TYR:H	1.83	0.43
1:B:426:ARG:HB3	1:B:492:GLN:HB3	2.01	0.43
1:B:882:MET:HE1	1:A:1059:THR:HG23	2.01	0.43
1:A:840:LEU:HD13	1:A:941:LEU:HD22	2.01	0.43
1:C:180:LYS:N	1:C:203:ILE:O	2.51	0.43
1:B:914:SER:O	1:B:918:GLU:HG2	2.19	0.43
1:A:790:ASP:HB3	1:A:793:LYS:HE3	2.01	0.43
1:C:887:ARG:NH1	1:C:1031:LEU:O	2.52	0.43
1:A:195:TYR:HE1	1:A:221:LYS:HE3	1.83	0.43
1:C:708:VAL:HG22	1:C:1043:VAL:HG22	1.99	0.43
1:C:417:MET:HE1	1:C:503:LEU:HD11	2.00	0.42
1:B:41:TYR:OH	1:B:58:LEU:O	2.29	0.42
1:B:968:LYS:O	1:B:972:GLU:HG2	2.19	0.42
1:C:227:ASN:N	1:C:227:ASN:OD1	2.50	0.42
1:C:382:VAL:HG23	1:C:510:VAL:HG11	2.01	0.42
1:C:745:LEU:HG	1:C:990:VAL:HG21	2.01	0.42
1:A:1064:CYS:HB2	1:A:1108:CYS:HB3	1.88	0.42
1:C:337:VAL:HG21	1:C:405:ILE:HD11	2.00	0.42
1:B:125:ILE:HD13	1:B:222:LEU:HD21	2.02	0.42
1:A:598:TYR:HE2	1:A:637:ILE:HD12	1.83	0.42
1:C:718:VAL:HG11	1:C:986:LEU:HD11	2.01	0.42
1:B:425:THR:HG21	1:B:495:ARG:HD2	2.01	0.42
1:A:929:LYS:HE3	1:A:929:LYS:HB3	1.82	0.42
1:B:405:ILE:HD13	1:B:405:ILE:HA	1.93	0.41
1:C:773:THR:HG23	1:C:788:LEU:HD22	2.01	0.41
1:C:790:ASP:HB2	1:C:793:LYS:HE2	2.02	0.41
1:B:1035:PRO:O	1:B:1036:GLN:NE2	2.53	0.41
1:A:966:LEU:HD23	1:A:966:LEU:HA	1.90	0.41
1:C:718:VAL:HG22	1:C:840:LEU:HD22	2.02	0.41
1:A:803:LEU:O	1:A:807:LYS:HG2	2.21	0.41
1:C:601:VAL:HG13	1:C:603:CYS:HB3	2.02	0.41
1:B:44:ASP:N	1:B:44:ASP:OD1	2.52	0.41
1:C:198:LYS:HB3	1:C:219:ILE:HG13	2.01	0.41
1:B:709:MET:HE2	1:B:709:MET:HB3	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:ASP:CG	1:A:48:ARG:HH12	2.27	0.41
1:B:185:PHE:HB3	1:B:187:PHE:CE1	2.55	0.41
1:B:94:LYS:NZ	1:B:180:LYS:HG2	2.36	0.40
1:C:195:TYR:CE2	1:C:221:LYS:HE2	2.56	0.40
1:B:103:PHE:HZ	1:B:187:PHE:HD2	1.69	0.40
1:B:310:SER:OG	1:B:523:GLN:OE1	2.38	0.40
1:A:788:LEU:HD23	1:A:788:LEU:HA	1.95	0.40
1:C:107:MET:HE3	1:C:107:MET:HB3	1.97	0.40
1:B:807:LYS:HD3	1:B:807:LYS:HA	1.84	0.40
1:C:305:PHE:O	1:C:578:PHE:HA	2.21	0.40
1:C:648:CYS:HB2	1:C:657:CYS:HB2	1.71	0.40
1:A:42:TYR:HA	1:A:43:PRO:HD3	1.98	0.40
1:A:807:LYS:HE2	1:A:924:SER:HB2	2.03	0.40
1:B:911:LYS:HA	1:B:911:LYS:HD3	1.82	0.40
1:A:44:ASP:OD1	1:A:48:ARG:NH1	2.49	0.40
1:A:766:GLN:HG3	1:A:1011:MET:HG2	2.04	0.40
1:C:715:LYS:HD2	1:C:753:ALA:HB1	2.02	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	787/1232 (64%)	758 (96%)	29 (4%)	0	100	100
1	B	942/1232 (76%)	920 (98%)	22 (2%)	0	100	100
1	C	961/1232 (78%)	931 (97%)	30 (3%)	0	100	100
All	All	2690/3696 (73%)	2609 (97%)	81 (3%)	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	697/1065 (65%)	697 (100%)	0	100	100
1	B	838/1065 (79%)	838 (100%)	0	100	100
1	C	854/1065 (80%)	854 (100%)	0	100	100
All	All	2389/3195 (75%)	2389 (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. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	304	ASN
1	B	381	ASN
1	B	401	GLN
1	B	546	GLN
1	B	550	GLN
1	B	746	ASN
1	B	904	GLN
1	B	907	ASN
1	B	960	ASN
1	B	1036	GLN
1	A	70	HIS
1	A	96	ASN
1	A	122	ASN
1	A	129	ASN
1	A	599	GLN
1	A	746	ASN
1	A	786	GLN
1	A	883	GLN
1	A	915	GLN
1	A	947	GLN
1	A	974	GLN
1	A	1005	ASN
1	C	78	ASN
1	C	109	ASN

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Mol	Chain	Res	Type
1	C	505	ASN
1	C	661	HIS
1	C	746	ASN
1	C	883	GLN
1	C	939	GLN
1	C	1088	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

32 ligands are modelled in this entry.

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	$\# Z > 2$
2	NAG	B	1305	1	14,14,15	0.31	0	17,19,21	0.39	0
2	NAG	B	1301	1	14,14,15	0.18	0	17,19,21	0.54	0
2	NAG	A	1307	1	14,14,15	0.29	0	17,19,21	0.40	0
2	NAG	C	1303	1	14,14,15	0.26	0	17,19,21	0.53	0
2	NAG	B	1302	1	14,14,15	0.30	0	17,19,21	0.49	0
2	NAG	C	1309	1	14,14,15	0.37	0	17,19,21	0.52	0
2	NAG	C	1306	1	14,14,15	0.26	0	17,19,21	0.50	0
2	NAG	C	1304	1	14,14,15	0.73	1 (7%)	17,19,21	0.85	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	1301	1	14,14,15	0.23	0	17,19,21	0.48	0
2	NAG	A	1306	1	14,14,15	0.28	0	17,19,21	0.51	0
2	NAG	C	1308	1	14,14,15	0.25	0	17,19,21	0.40	0
2	NAG	C	1302	1	14,14,15	0.32	0	17,19,21	0.39	0
2	NAG	B	1306	1	14,14,15	0.16	0	17,19,21	0.52	0
2	NAG	A	1303	1	14,14,15	0.33	0	17,19,21	0.56	0
2	NAG	A	1302	1	14,14,15	0.45	0	17,19,21	0.36	0
2	NAG	A	1301	1	14,14,15	0.49	0	17,19,21	0.38	0
2	NAG	B	1303	1	14,14,15	0.24	0	17,19,21	0.48	0
2	NAG	B	1307	1	14,14,15	0.38	0	17,19,21	0.66	1 (5%)
2	NAG	C	1307	1	14,14,15	0.26	0	17,19,21	0.49	0
2	NAG	B	1304	1	14,14,15	0.28	0	17,19,21	0.55	0
2	NAG	C	1310	1	14,14,15	0.42	0	17,19,21	0.60	0
2	NAG	C	1305	1	14,14,15	0.38	0	17,19,21	0.52	0
2	NAG	C	1312	1	14,14,15	0.23	0	17,19,21	0.48	0
2	NAG	A	1308	1	14,14,15	0.28	0	17,19,21	0.46	0
2	NAG	A	1305	1	14,14,15	0.31	0	17,19,21	0.34	0
2	NAG	C	1311	1	14,14,15	0.37	0	17,19,21	0.51	0
2	NAG	B	1308	1	14,14,15	0.52	0	17,19,21	0.39	0
2	NAG	A	1309	1	14,14,15	0.43	0	17,19,21	0.70	1 (5%)
2	NAG	A	1310	1	14,14,15	0.26	0	17,19,21	0.41	0
2	NAG	A	1304	1	14,14,15	0.32	0	17,19,21	0.52	0
2	NAG	A	1311	1	14,14,15	0.23	0	17,19,21	0.52	0
2	NAG	B	1309	1	14,14,15	0.27	0	17,19,21	0.55	0

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
2	NAG	B	1305	1	-	3/6/23/26	0/1/1/1
2	NAG	B	1301	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1307	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1303	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1302	1	-	1/6/23/26	0/1/1/1
2	NAG	C	1309	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1306	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1304	1	-	4/6/23/26	0/1/1/1
2	NAG	C	1301	1	-	1/6/23/26	0/1/1/1
2	NAG	A	1306	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1308	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1302	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1306	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1303	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1302	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1301	1	-	1/6/23/26	0/1/1/1
2	NAG	B	1303	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1307	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1307	1	-	4/6/23/26	0/1/1/1
2	NAG	B	1304	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1310	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1305	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1312	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1308	1	-	1/6/23/26	0/1/1/1
2	NAG	A	1305	1	-	1/6/23/26	0/1/1/1
2	NAG	C	1311	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1308	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1309	1	-	4/6/23/26	0/1/1/1
2	NAG	A	1310	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1304	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1311	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1309	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1304	NAG	C1-C2	2.39	1.55	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1304	NAG	C1-O5-C5	2.71	115.82	112.19
2	A	1309	NAG	C1-O5-C5	2.17	115.09	112.19
2	B	1307	NAG	C1-O5-C5	2.07	114.96	112.19

There are no chirality outliers.

All (56) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1304	NAG	O5-C5-C6-O6
2	C	1312	NAG	O5-C5-C6-O6
2	C	1302	NAG	O5-C5-C6-O6
2	A	1310	NAG	C4-C5-C6-O6
2	A	1311	NAG	C4-C5-C6-O6
2	C	1312	NAG	C4-C5-C6-O6
2	C	1306	NAG	O5-C5-C6-O6
2	C	1304	NAG	C4-C5-C6-O6
2	A	1302	NAG	O5-C5-C6-O6
2	A	1302	NAG	C4-C5-C6-O6
2	B	1306	NAG	O5-C5-C6-O6
2	A	1306	NAG	O5-C5-C6-O6
2	A	1310	NAG	O5-C5-C6-O6
2	A	1311	NAG	O5-C5-C6-O6
2	A	1306	NAG	C4-C5-C6-O6
2	B	1306	NAG	C4-C5-C6-O6
2	C	1302	NAG	C4-C5-C6-O6
2	A	1303	NAG	O5-C5-C6-O6
2	C	1306	NAG	C4-C5-C6-O6
2	A	1303	NAG	C4-C5-C6-O6
2	B	1307	NAG	C8-C7-N2-C2
2	B	1307	NAG	O7-C7-N2-C2
2	A	1309	NAG	C8-C7-N2-C2
2	A	1309	NAG	O7-C7-N2-C2
2	C	1303	NAG	C8-C7-N2-C2
2	C	1303	NAG	O7-C7-N2-C2
2	C	1304	NAG	C8-C7-N2-C2
2	C	1304	NAG	O7-C7-N2-C2
2	C	1307	NAG	C8-C7-N2-C2
2	C	1307	NAG	O7-C7-N2-C2
2	C	1310	NAG	C8-C7-N2-C2
2	C	1310	NAG	O7-C7-N2-C2
2	A	1304	NAG	O5-C5-C6-O6
2	C	1301	NAG	O5-C5-C6-O6
2	C	1305	NAG	C4-C5-C6-O6
2	B	1303	NAG	C4-C5-C6-O6
2	A	1309	NAG	C4-C5-C6-O6
2	B	1309	NAG	O5-C5-C6-O6
2	C	1307	NAG	C4-C5-C6-O6
2	C	1308	NAG	C4-C5-C6-O6
2	A	1305	NAG	O5-C5-C6-O6
2	B	1303	NAG	O5-C5-C6-O6
2	C	1305	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
2	C	1307	NAG	O5-C5-C6-O6
2	A	1301	NAG	O5-C5-C6-O6
2	A	1308	NAG	O5-C5-C6-O6
2	A	1309	NAG	O5-C5-C6-O6
2	C	1308	NAG	O5-C5-C6-O6
2	B	1305	NAG	C4-C5-C6-O6
2	B	1302	NAG	C4-C5-C6-O6
2	A	1307	NAG	C4-C5-C6-O6
2	A	1304	NAG	C4-C5-C6-O6
2	A	1307	NAG	O5-C5-C6-O6
2	B	1305	NAG	O5-C5-C6-O6
2	B	1305	NAG	C1-C2-N2-C7
2	B	1309	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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-34426. These allow visual inspection of the internal detail of the map and identification of artifacts.

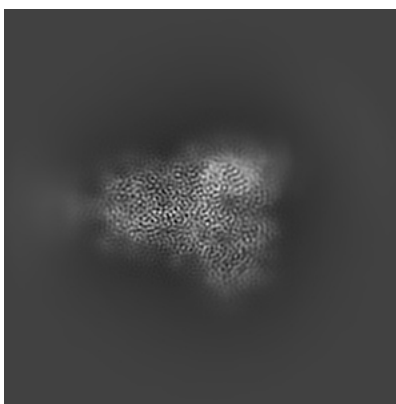
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

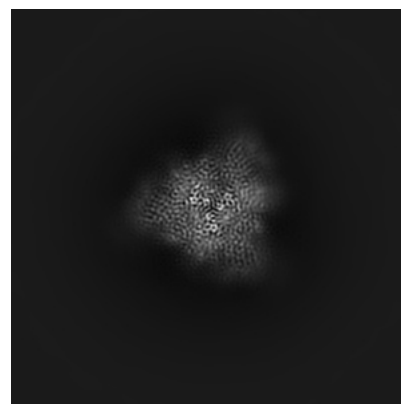
6.1.1 Primary map



X

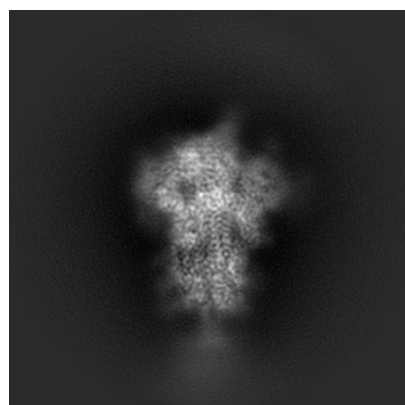


Y

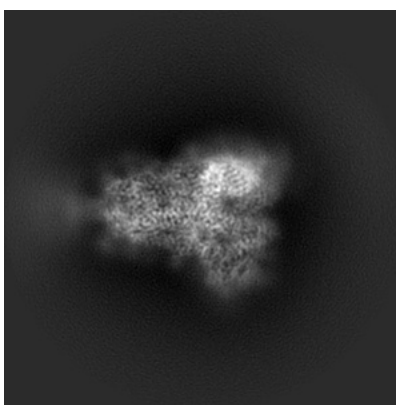


Z

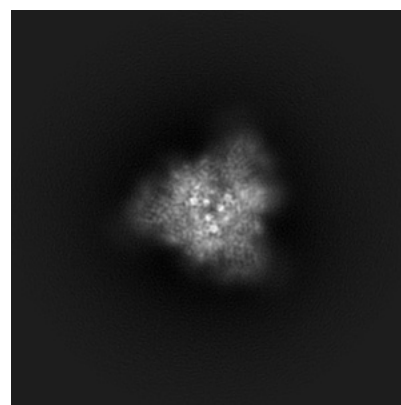
6.1.2 Raw map



X



Y

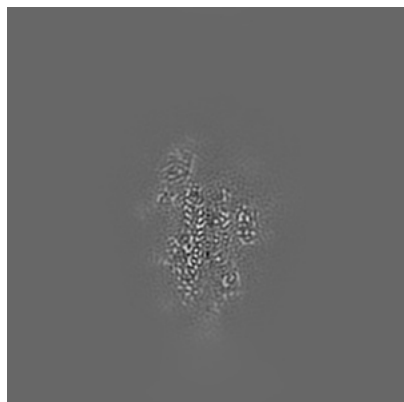


Z

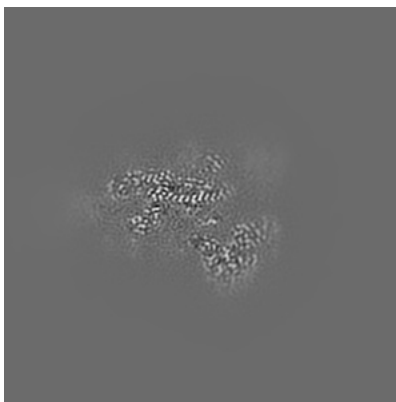
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

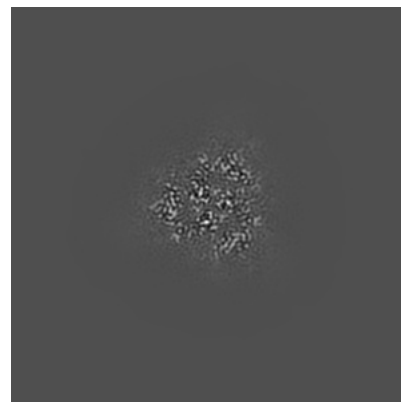
6.2.1 Primary map



X Index: 128

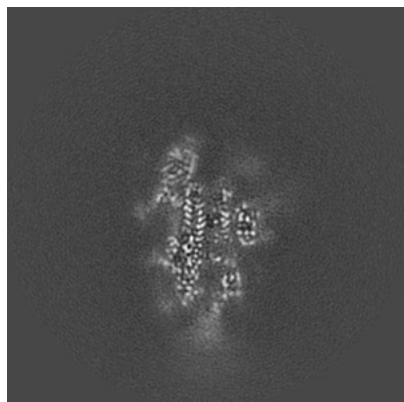


Y Index: 128

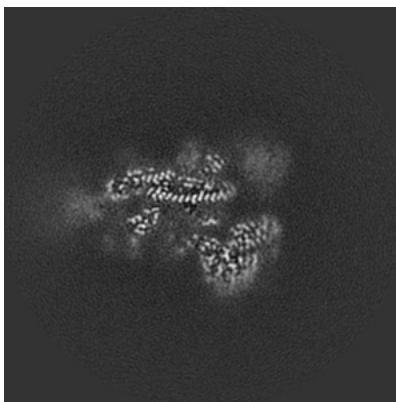


Z Index: 128

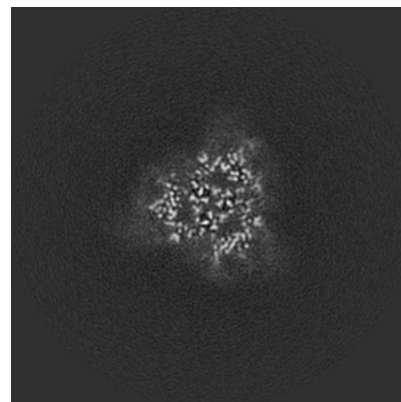
6.2.2 Raw map



X Index: 128



Y Index: 128

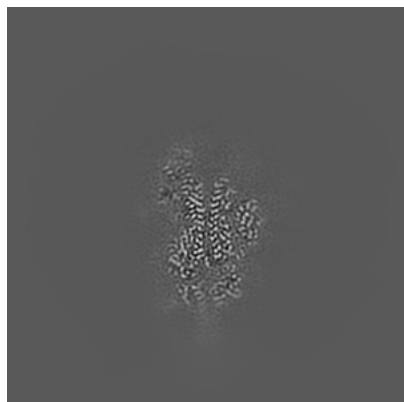


Z Index: 128

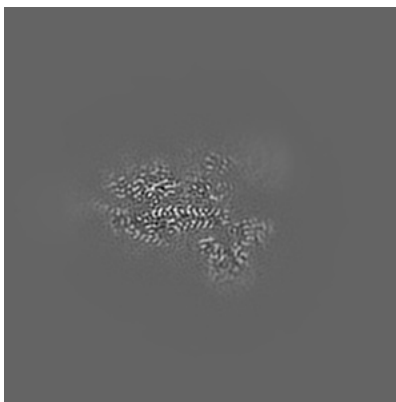
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

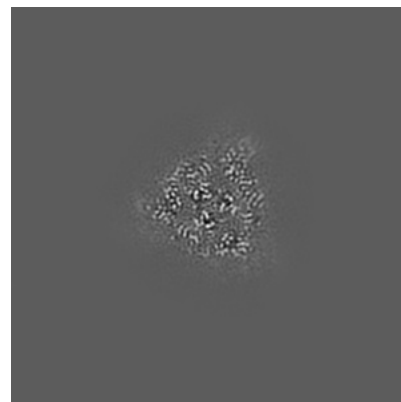
6.3.1 Primary map



X Index: 125

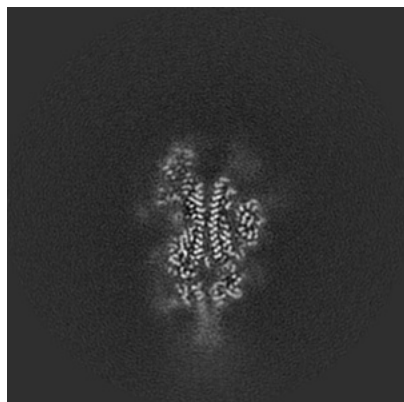


Y Index: 133

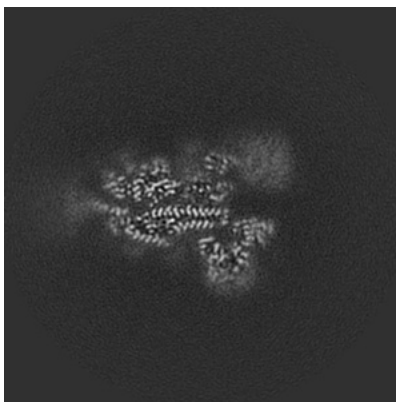


Z Index: 130

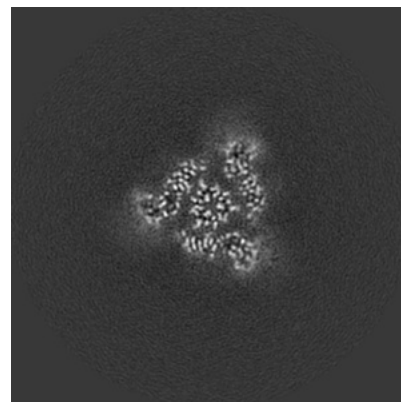
6.3.2 Raw map



X Index: 125



Y Index: 133

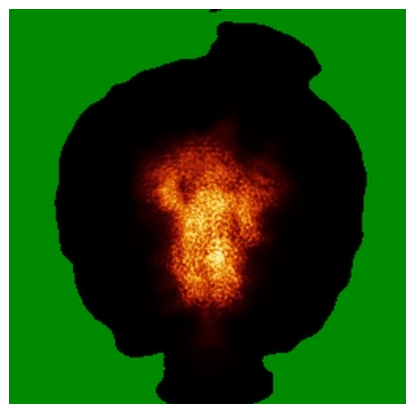


Z Index: 133

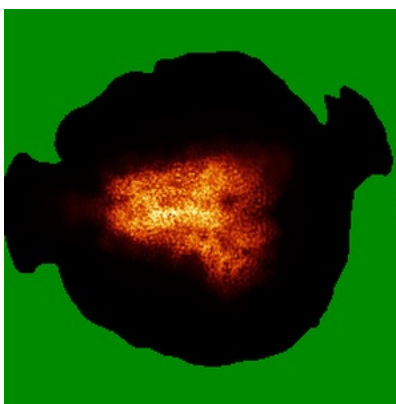
The images above show the largest variance slices of the map in three orthogonal directions.

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

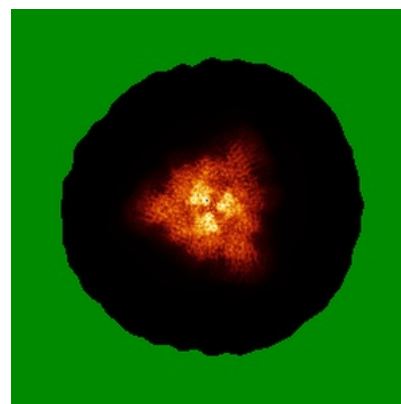
6.4.1 Primary map



X

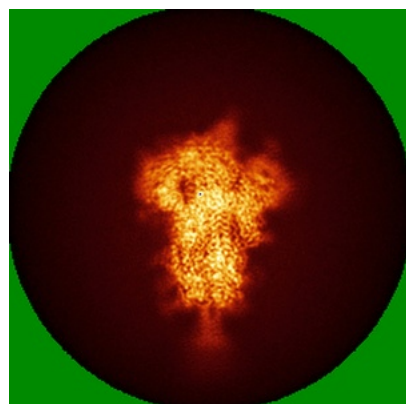


Y

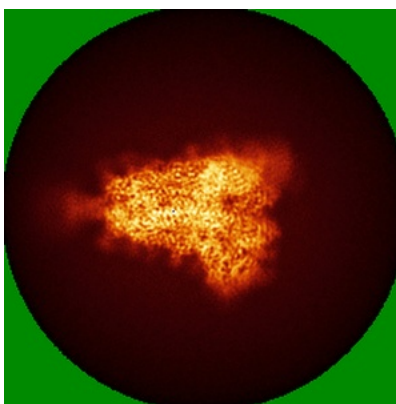


Z

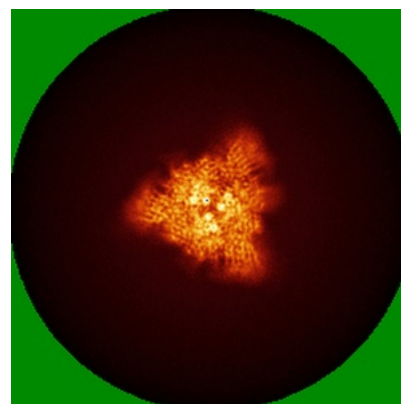
6.4.2 Raw map



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](#)

This section was not generated.

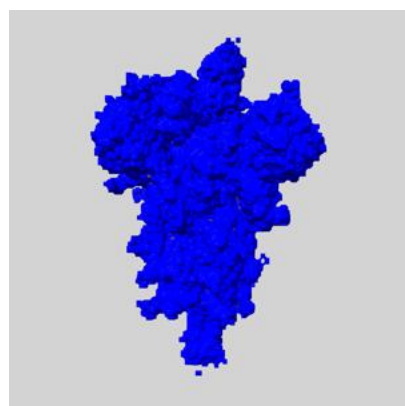
6.6 Mask visualisation [i](#)

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

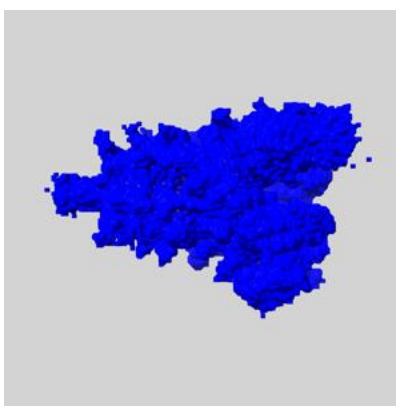
A mask typically either:

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

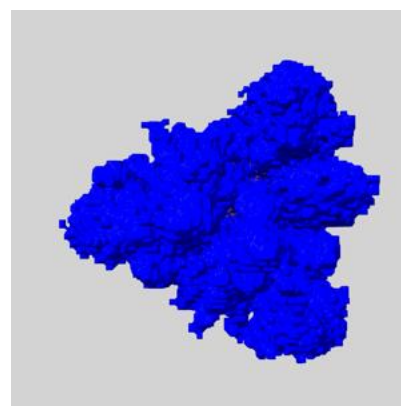
6.6.1 emd_34426_msk_1.map [i](#)



X



Y

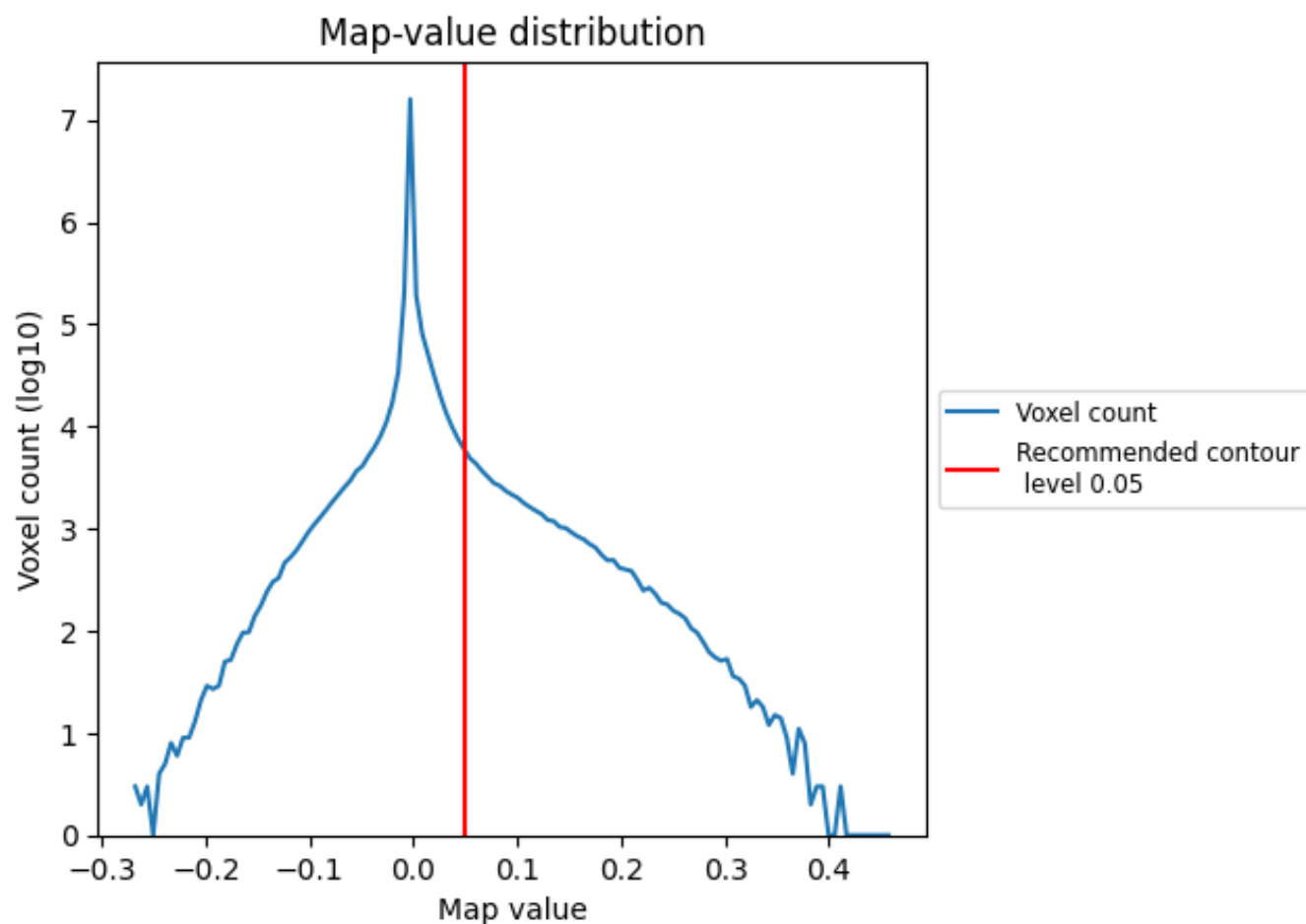


Z

7 Map analysis [i](#)

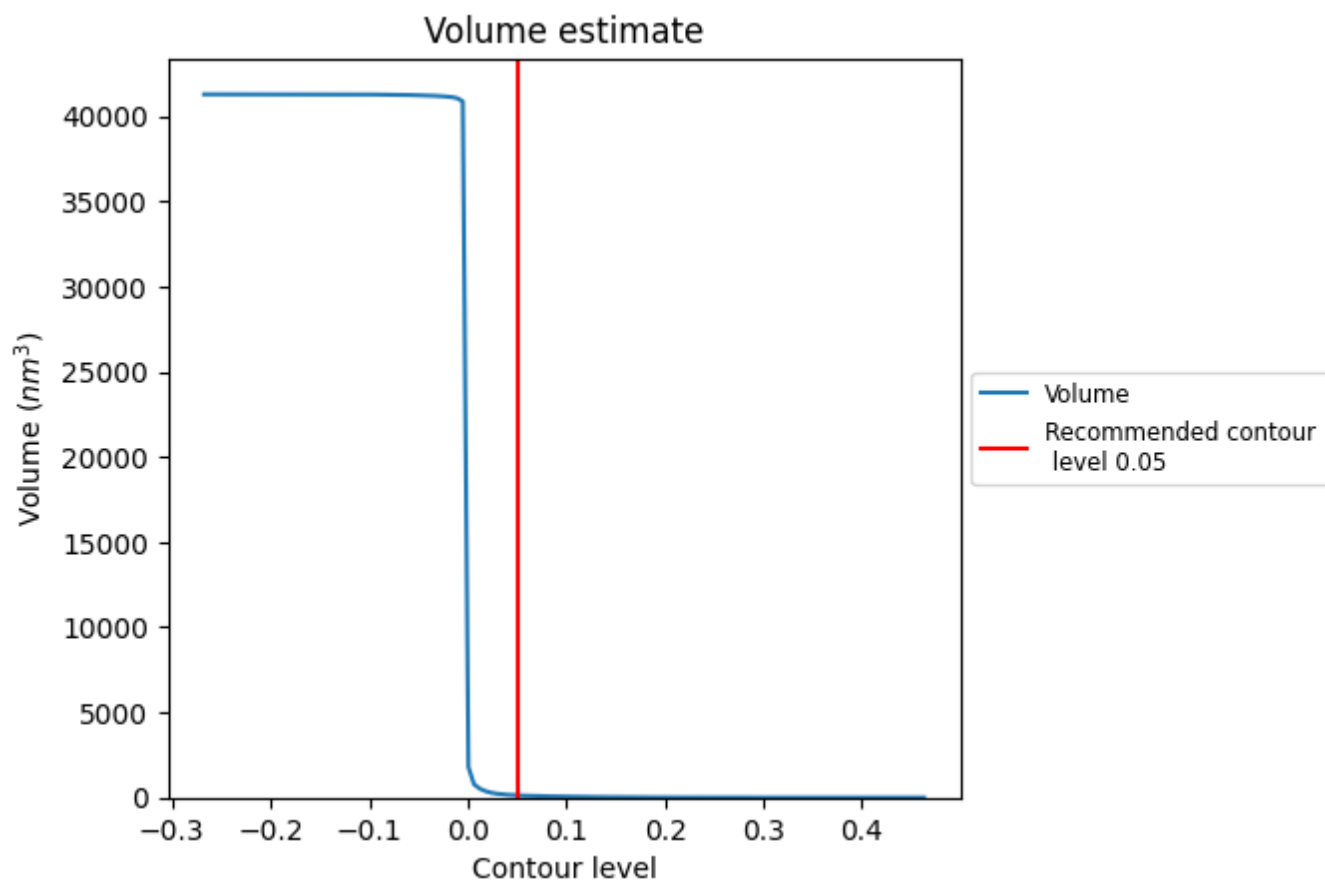
This section contains the results of statistical analysis of the map.

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.

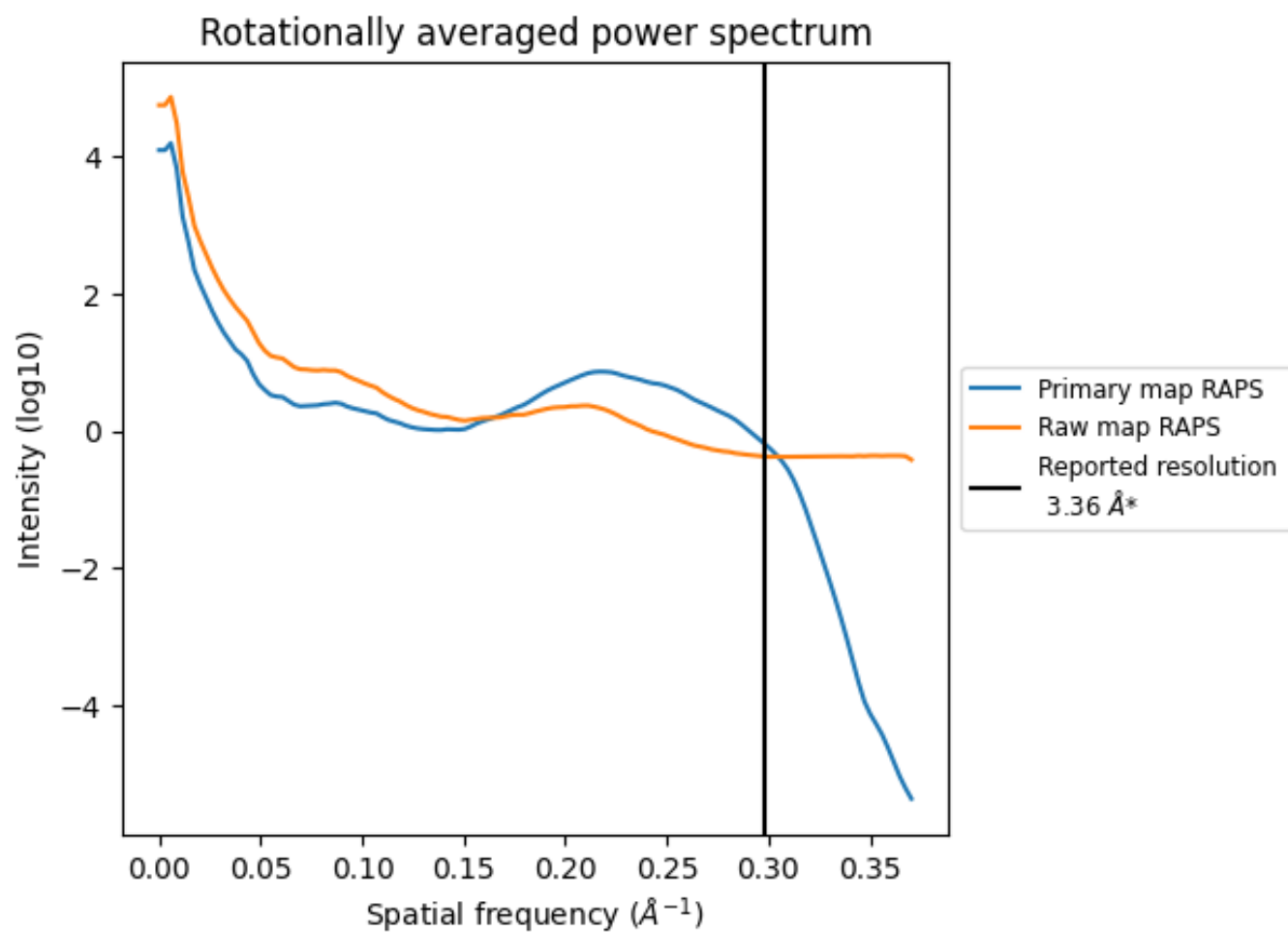
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 130 nm^3 ; this corresponds to an approximate mass of 118 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 ⓘ

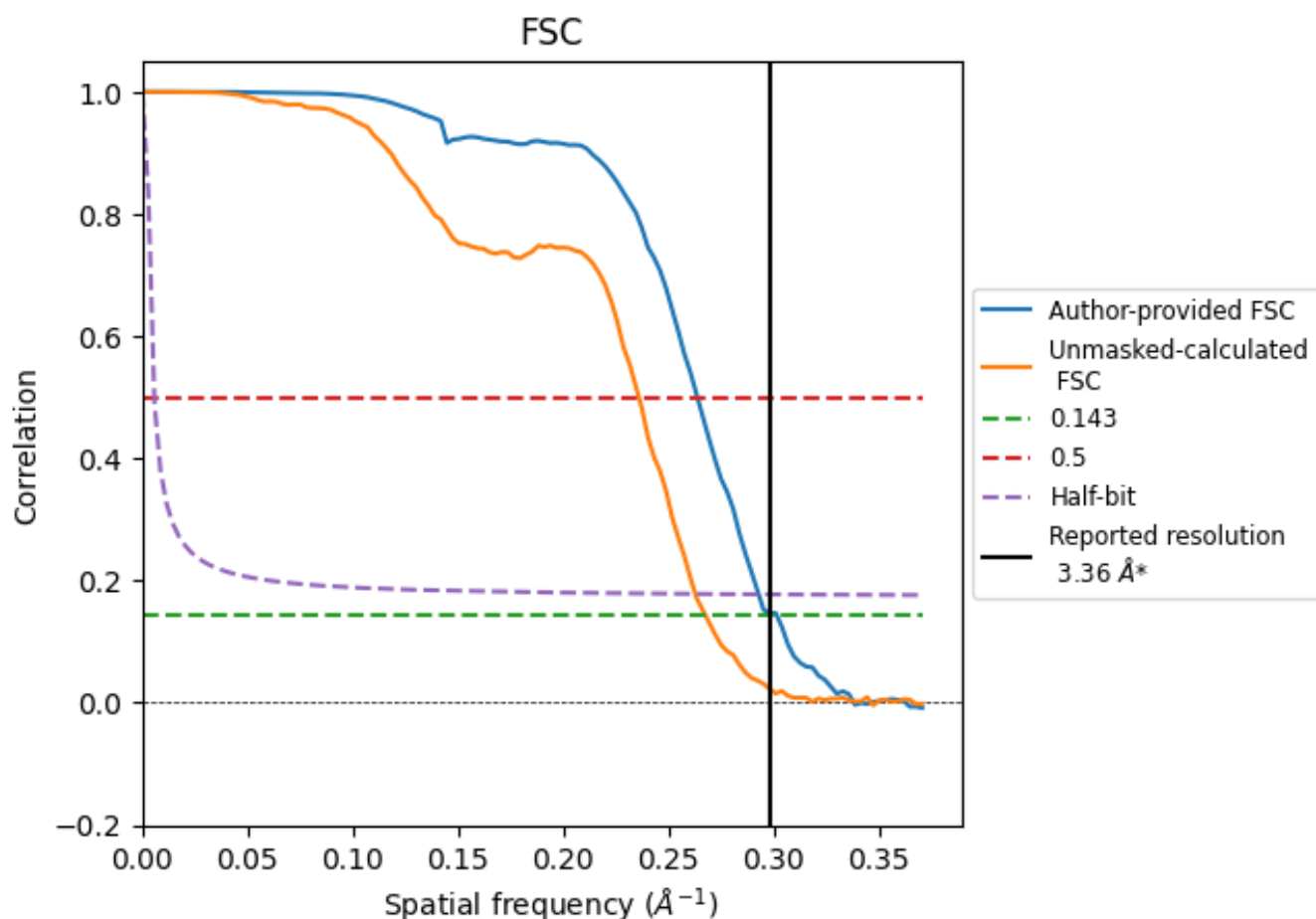


*Reported resolution corresponds to spatial frequency of 0.298 Å⁻¹

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 0.298 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.36	-	-
Author-provided FSC curve	3.32	3.79	3.42
Unmasked-calculated*	3.74	4.24	3.81

*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 3.74 differs from the reported value 3.35534 by more than 10 %

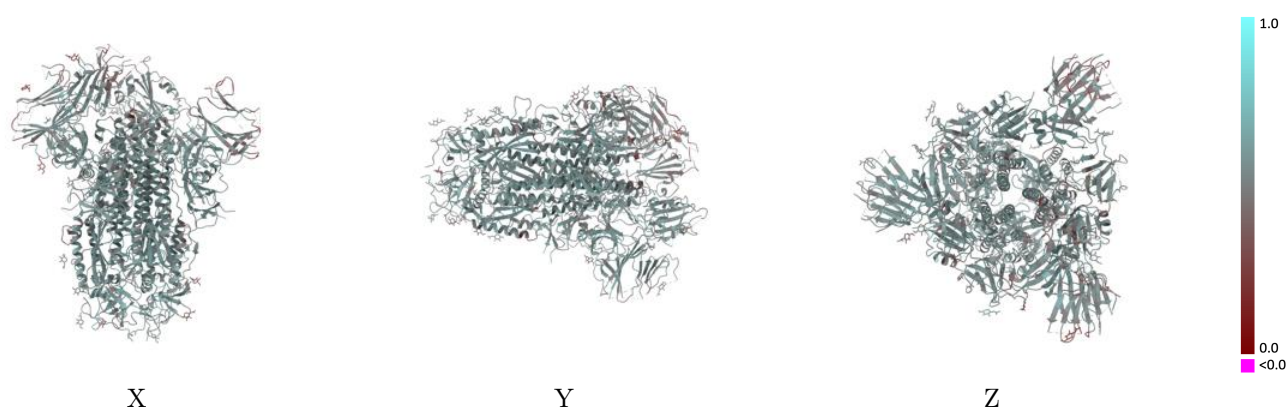
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34426 and PDB model 8H16. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)

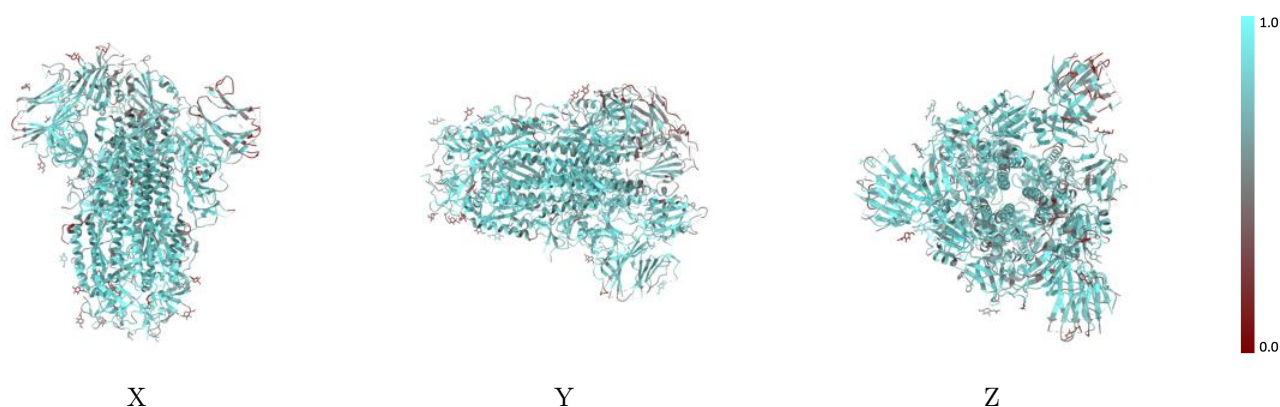
This section was not generated.

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



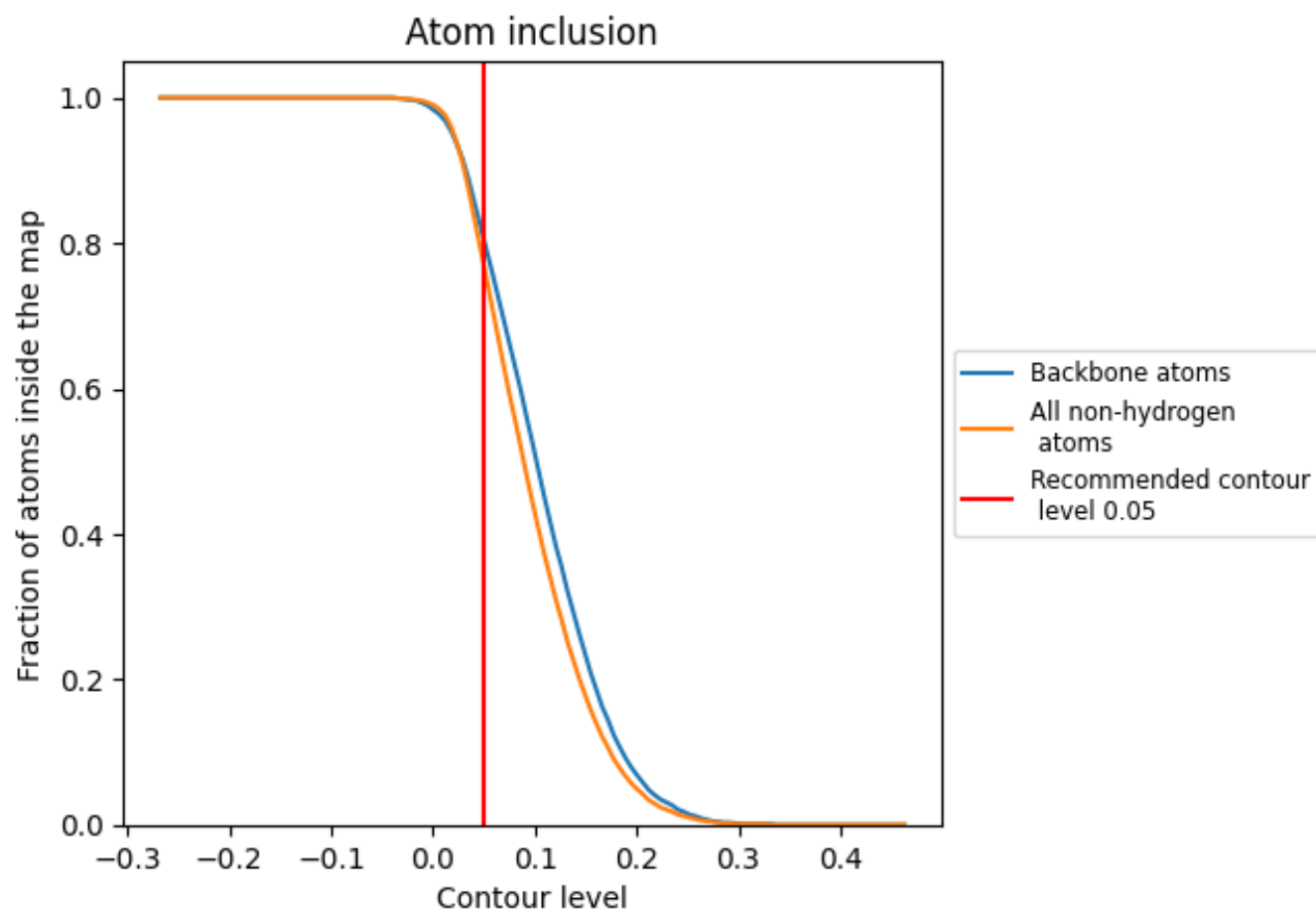
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 77% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7690	0.5410
A	0.7870	0.5450
B	0.7510	0.5340
C	0.7710	0.5460

