



wwPDB EM Validation Summary Report ⓘ

Mar 22, 2026 – 05:49 PM UTC

PDB ID : 9BT9 / pdb_00009bt9
EMDB ID : EMD-44884
Title : Cryo-EM Structure of HKU1 spike D1 Domain (Active state, locally refined)
Authors : Jin, M.; Rini, J.M.
Deposited on : 2024-05-14
Resolution : 2.11 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

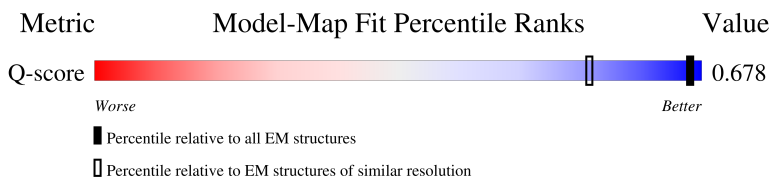
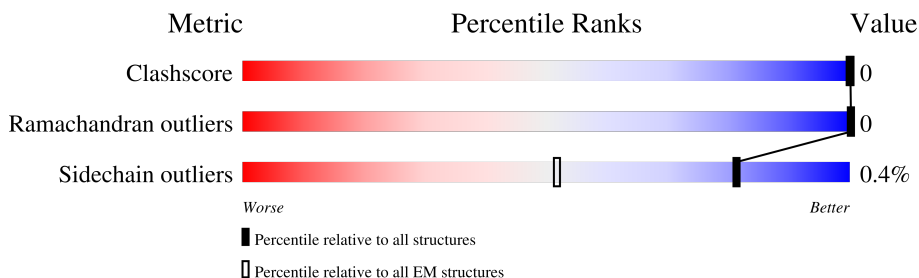
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.11 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	2361 (1.64 - 2.61)

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	1348	20% 80%
2	B	2	100%
2	D	2	100%
3	C	5	20% 80%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2365 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	A	268	Total	C	N	O	S	0	0
			2192	1428	346	410	8		

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1026	PRO	THR	conflict	UNP Q5MQD0
A	1071	PRO	ALA	conflict	UNP Q5MQD0
A	1072	PRO	LEU	conflict	UNP Q5MQD0
A	1299	SER	-	expression tag	UNP Q5MQD0
A	1300	GLY	-	expression tag	UNP Q5MQD0
A	1301	GLY	-	expression tag	UNP Q5MQD0
A	1302	TYR	-	expression tag	UNP Q5MQD0
A	1303	ILE	-	expression tag	UNP Q5MQD0
A	1304	PRO	-	expression tag	UNP Q5MQD0
A	1305	GLU	-	expression tag	UNP Q5MQD0
A	1306	ALA	-	expression tag	UNP Q5MQD0
A	1307	PRO	-	expression tag	UNP Q5MQD0
A	1308	ARG	-	expression tag	UNP Q5MQD0
A	1309	ASP	-	expression tag	UNP Q5MQD0
A	1310	GLY	-	expression tag	UNP Q5MQD0
A	1311	GLN	-	expression tag	UNP Q5MQD0
A	1312	ALA	-	expression tag	UNP Q5MQD0
A	1313	TYR	-	expression tag	UNP Q5MQD0
A	1314	VAL	-	expression tag	UNP Q5MQD0
A	1315	ARG	-	expression tag	UNP Q5MQD0
A	1316	LYS	-	expression tag	UNP Q5MQD0
A	1317	ASP	-	expression tag	UNP Q5MQD0
A	1318	GLY	-	expression tag	UNP Q5MQD0
A	1319	GLU	-	expression tag	UNP Q5MQD0
A	1320	TRP	-	expression tag	UNP Q5MQD0
A	1321	VAL	-	expression tag	UNP Q5MQD0
A	1322	LEU	-	expression tag	UNP Q5MQD0
A	1323	LEU	-	expression tag	UNP Q5MQD0

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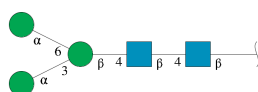
Chain	Residue	Modelled	Actual	Comment	Reference
A	1324	SER	-	expression tag	UNP Q5MQD0
A	1325	THR	-	expression tag	UNP Q5MQD0
A	1326	PHE	-	expression tag	UNP Q5MQD0
A	1327	LEU	-	expression tag	UNP Q5MQD0
A	1328	ASN	-	expression tag	UNP Q5MQD0
A	1329	SER	-	expression tag	UNP Q5MQD0
A	1330	GLY	-	expression tag	UNP Q5MQD0
A	1331	ARG	-	expression tag	UNP Q5MQD0
A	1332	ALA	-	expression tag	UNP Q5MQD0
A	1333	HIS	-	expression tag	UNP Q5MQD0
A	1334	HIS	-	expression tag	UNP Q5MQD0
A	1335	HIS	-	expression tag	UNP Q5MQD0
A	1336	HIS	-	expression tag	UNP Q5MQD0
A	1337	HIS	-	expression tag	UNP Q5MQD0
A	1338	HIS	-	expression tag	UNP Q5MQD0
A	1339	GLY	-	expression tag	UNP Q5MQD0
A	1340	ALA	-	expression tag	UNP Q5MQD0
A	1341	GLY	-	expression tag	UNP Q5MQD0
A	1342	GLY	-	expression tag	UNP Q5MQD0
A	1343	LEU	-	expression tag	UNP Q5MQD0
A	1344	ASN	-	expression tag	UNP Q5MQD0
A	1345	ASP	-	expression tag	UNP Q5MQD0
A	1346	ILE	-	expression tag	UNP Q5MQD0
A	1347	PHE	-	expression tag	UNP Q5MQD0
A	1348	GLU	-	expression tag	UNP Q5MQD0
A	1349	ALA	-	expression tag	UNP Q5MQD0
A	1350	GLN	-	expression tag	UNP Q5MQD0
A	1351	LYS	-	expression tag	UNP Q5MQD0
A	1352	ILE	-	expression tag	UNP Q5MQD0
A	1353	GLU	-	expression tag	UNP Q5MQD0
A	1354	TRP	-	expression tag	UNP Q5MQD0
A	1355	HIS	-	expression tag	UNP Q5MQD0
A	1356	GLU	-	expression tag	UNP Q5MQD0
A	1357	ASP	-	expression tag	UNP Q5MQD0
A	1358	THR	-	expression tag	UNP Q5MQD0
A	1359	ALA	-	expression tag	UNP Q5MQD0
A	1360	ALA	-	expression tag	UNP Q5MQD0
A	1361	ALA	-	expression tag	UNP Q5MQD0

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



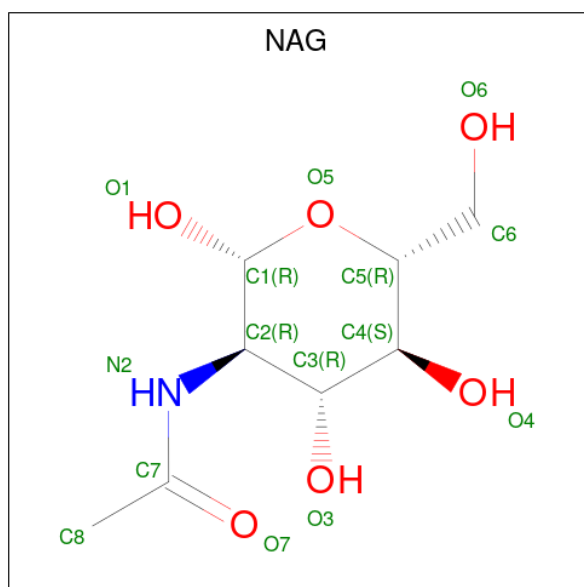
Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	2	Total	C	N	O	0	0
			28	16	2	10		
2	D	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	5	Total	C	N	O	0	0
			61	34	2	25		

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

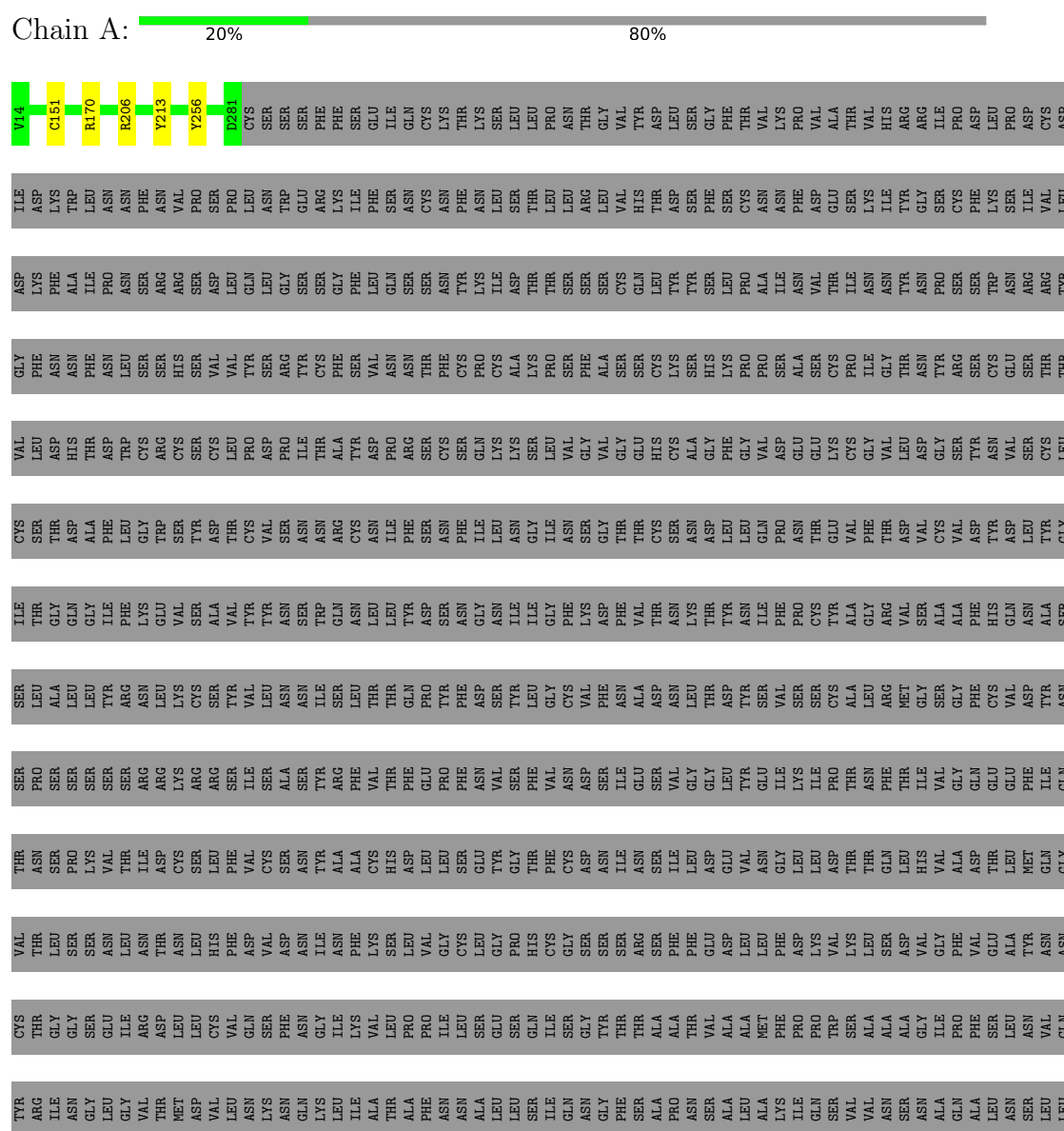


Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total 14	C 8	N 1	O 5	0
4	A	1	Total 14	C 8	N 1	O 5	0
4	A	1	Total 14	C 8	N 1	O 5	0
4	A	1	Total 14	C 8	N 1	O 5	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Spike glycoprotein



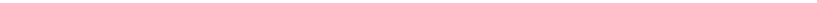
ALA	GLN	LYS	ILE	GLU	ASP	PRO	SER	LEU	GLN
GLN	LYS	ILE	THR	THR	ILE	LYS	GLY	ALA	GLN
ILE	GLU	ILE	GLY	ASP	THR	SER	VAL	GLY	PHE
TRP	TRP	TRP	GLU	PHE	PHE	PHE	ILE	VAL	LYS
HIS	HIS	MET	MET	GLU	GLU	THR	ALA	ASN	PHE
GLU	GLU	TYR	TYR	SER	SER	TYR	PRO	GLY	GLY
ASP	ASP	VAL	VAL	GLU	GLU	LYS	LYS	CYS	ALA
THR	THR	THR	THR	LEU	LEU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

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B: 100%

NAG1
NAG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  100%

NAG1
NAG2

- Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C: 20% 80%

NAG1
NAG2
BMA3
MAN4
MAN5

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	981154	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 ($e^-/\text{\AA}^2$)	36	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	7.456	Depositor
Minimum map value	-3.324	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.065	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	395.52, 395.52, 395.52	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8989091, 0.8989091, 0.8989091	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: BMA, NAG, MAN

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	0.69	0/2256	1.14	2/3076 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	170	ARG	NE-CZ-NH2	6.42	124.97	119.20
1	A	151	CYS	N-CA-C	5.21	118.69	111.71

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	206	ARG	Sidechain
1	A	256	TYR	Sidechain

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	2192	0	2103	0	0
2	B	28	0	25	0	0
2	D	28	0	25	0	0
3	C	61	0	52	0	0
4	A	56	0	52	0	0
All	All	2365	0	2257	0	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 0.

There are no clashes within the asymmetric unit.

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	266/1348 (20%)	243 (91%)	23 (9%)	0	100	100

There are no Ramachandran outliers to report.

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	247/1207 (20%)	246 (100%)	1 (0%)	84	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	213	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	GLN
1	A	152	GLN

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 ⓘ

9 monosaccharides 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	1	2,1	14,14,15	1.22	2 (14%)	17,19,21	0.68	0
2	NAG	B	2	2	14,14,15	1.24	1 (7%)	17,19,21	0.81	1 (5%)
3	NAG	C	1	3,1	14,14,15	1.00	0	17,19,21	0.85	0
3	NAG	C	2	3	14,14,15	1.12	1 (7%)	17,19,21	0.73	1 (5%)
3	BMA	C	3	3	11,11,12	1.39	3 (27%)	15,15,17	0.82	0
3	MAN	C	4	3	11,11,12	1.31	1 (9%)	15,15,17	0.80	1 (6%)
3	MAN	C	5	3	11,11,12	1.38	2 (18%)	15,15,17	0.87	1 (6%)
2	NAG	D	1	2,1	14,14,15	1.12	1 (7%)	17,19,21	1.24	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	D	2	2	14,14,15	1.08	1 (7%)	17,19,21	1.20	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
3	NAG	C	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	BMA	C	3	3	-	0/2/19/22	0/1/1/1
3	MAN	C	4	3	-	0/2/19/22	0/1/1/1
3	MAN	C	5	3	-	1/2/19/22	0/1/1/1
2	NAG	D	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	4	MAN	O5-C5	2.92	1.49	1.43
2	B	2	NAG	O5-C5	2.87	1.49	1.43
2	D	2	NAG	O5-C5	2.66	1.48	1.43
3	C	5	MAN	O5-C5	2.58	1.48	1.43
3	C	3	BMA	O5-C5	2.35	1.48	1.43

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	NAG	C1-O5-C5	4.46	118.16	112.19
3	C	5	MAN	C1-O5-C5	2.47	115.50	112.19
2	D	1	NAG	C2-N2-C7	2.45	126.18	122.90
2	D	1	NAG	C4-C3-C2	-2.42	107.47	111.02
2	D	1	NAG	C1-C2-N2	2.39	114.19	110.43

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C1-C2-N2-C7

Continued on next page...

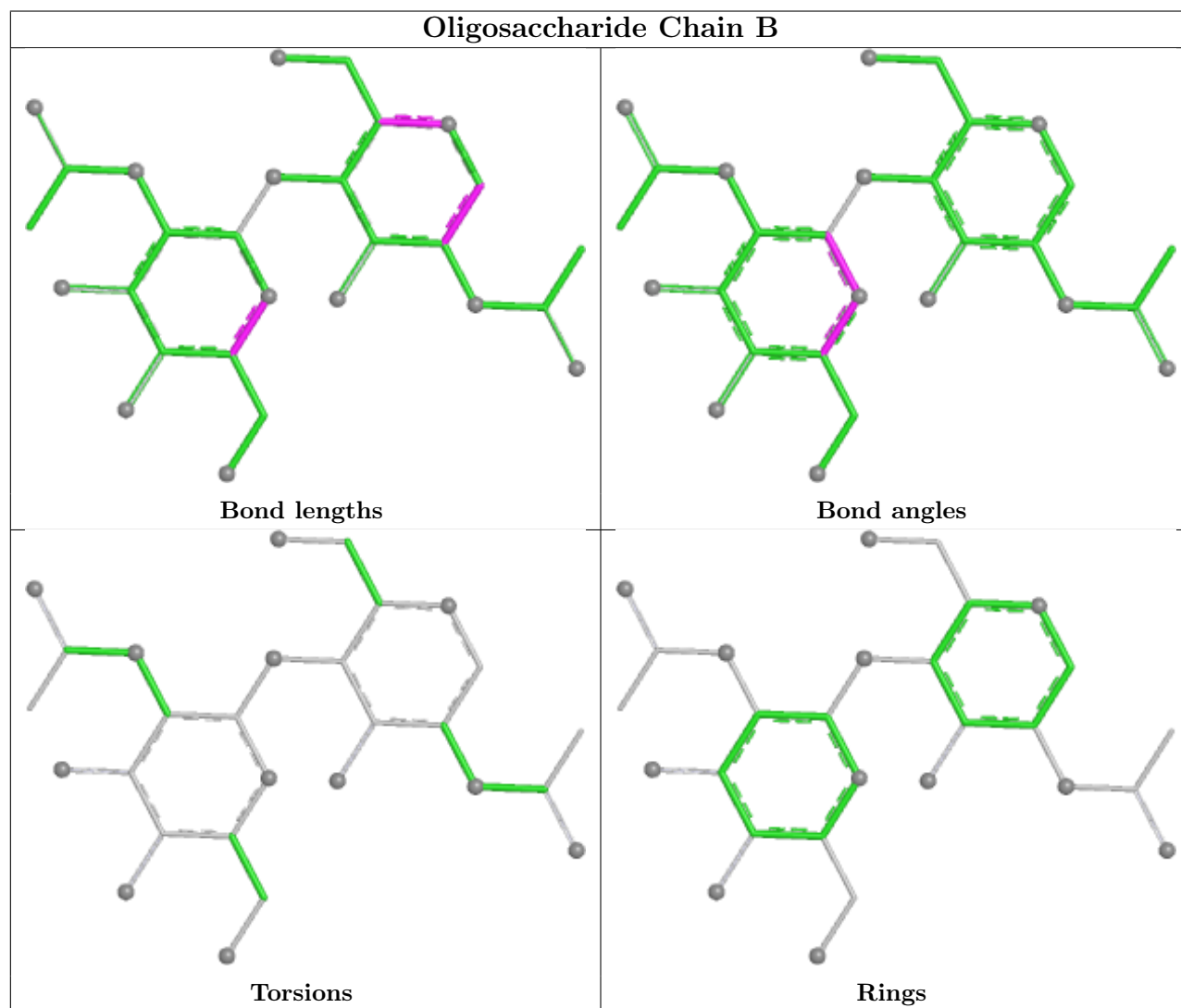
Continued from previous page...

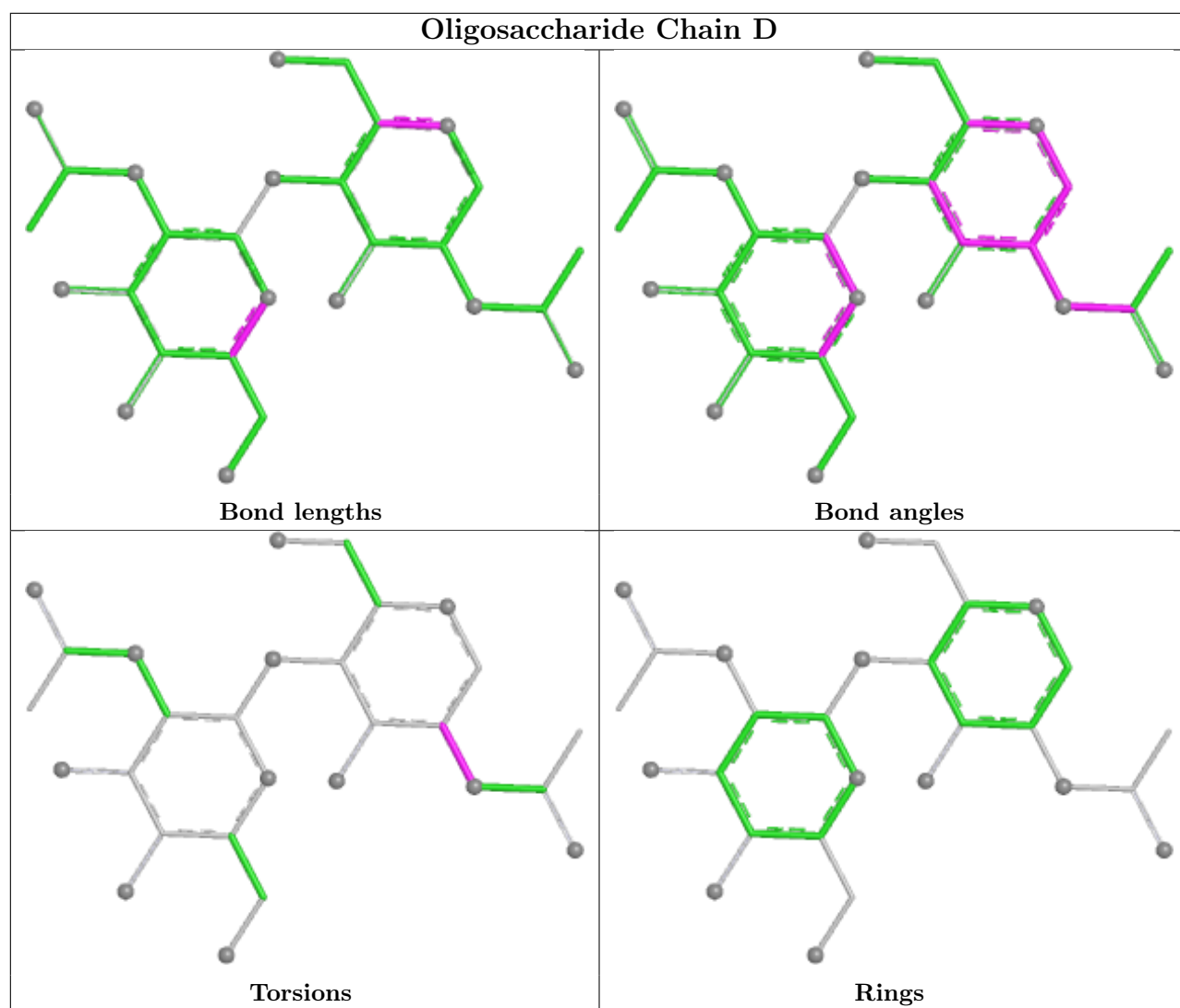
Mol	Chain	Res	Type	Atoms
3	C	5	MAN	O5-C5-C6-O6

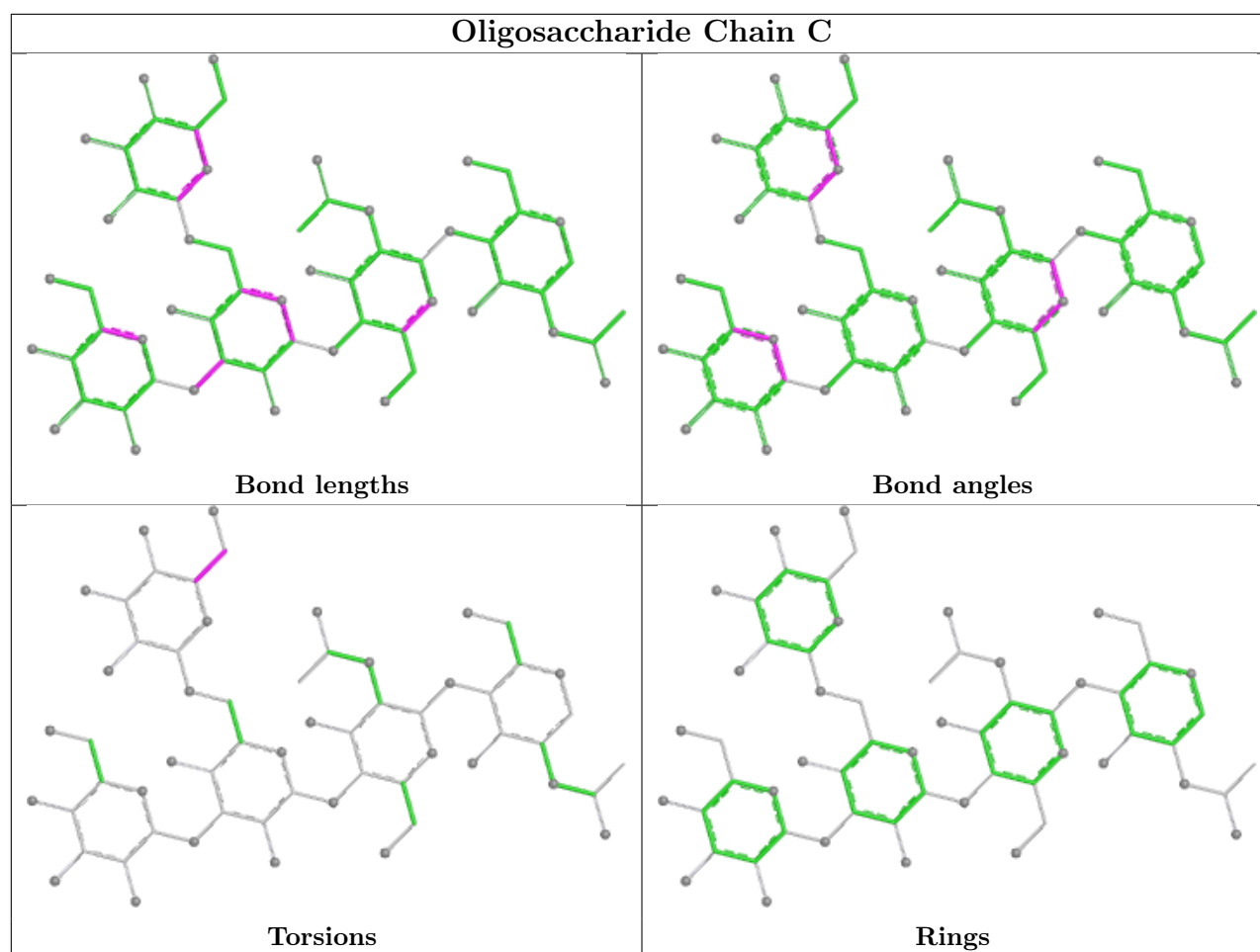
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.







5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
4	NAG	A	1403	1	14,14,15	1.18	1 (7%)	17,19,21	0.85	1 (5%)
4	NAG	A	1404	1	14,14,15	1.28	2 (14%)	17,19,21	0.86	1 (5%)
4	NAG	A	1401	1	14,14,15	1.30	2 (14%)	17,19,21	0.84	1 (5%)
4	NAG	A	1402	1	14,14,15	1.14	1 (7%)	17,19,21	0.88	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	1403	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1404	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1401	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1402	1	-	0/6/23/26	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1401	NAG	O5-C5	2.83	1.49	1.43
4	A	1403	NAG	O5-C5	2.74	1.48	1.43
4	A	1404	NAG	O5-C5	2.65	1.48	1.43
4	A	1402	NAG	O5-C5	2.40	1.48	1.43
4	A	1401	NAG	C1-C2	2.29	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1403	NAG	C1-O5-C5	2.88	116.05	112.19
4	A	1401	NAG	C1-O5-C5	2.83	115.98	112.19
4	A	1402	NAG	C1-O5-C5	2.74	115.86	112.19
4	A	1404	NAG	C1-O5-C5	2.61	115.69	112.19

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

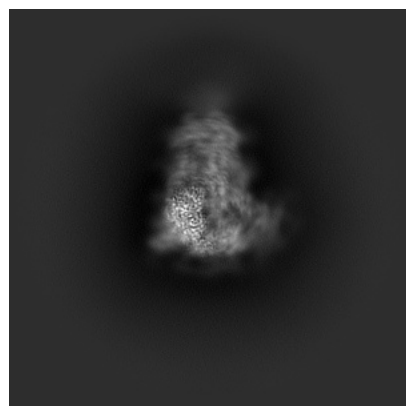
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44884. These allow visual inspection of the internal detail of the map and identification of artifacts.

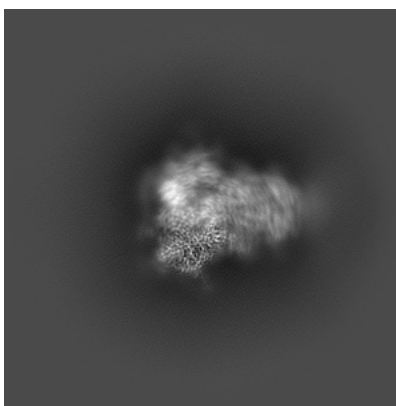
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

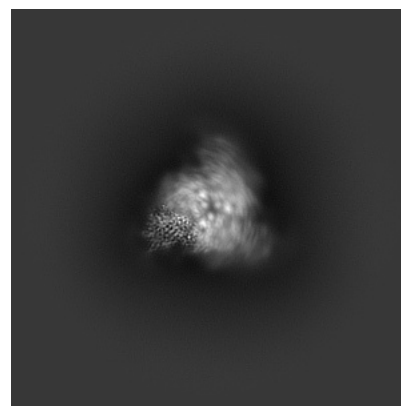
6.1.1 Primary map



X

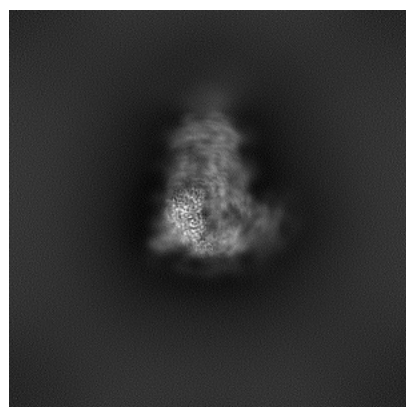


Y

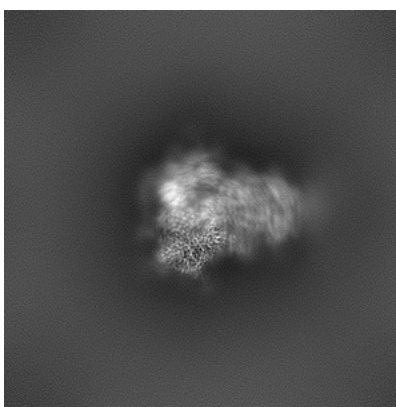


Z

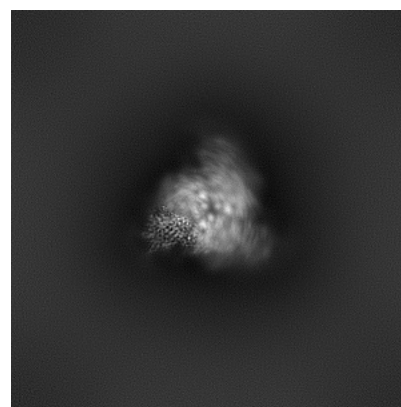
6.1.2 Raw map



X



Y

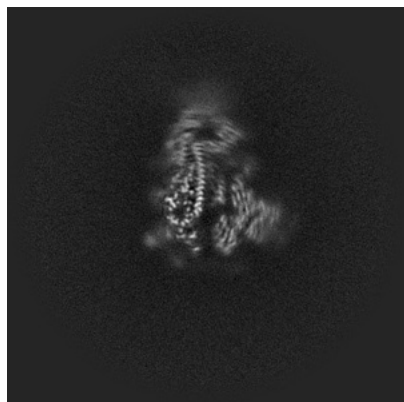


Z

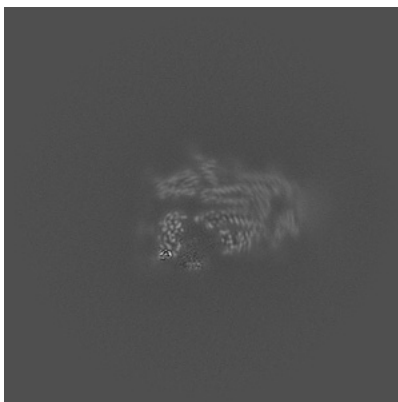
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

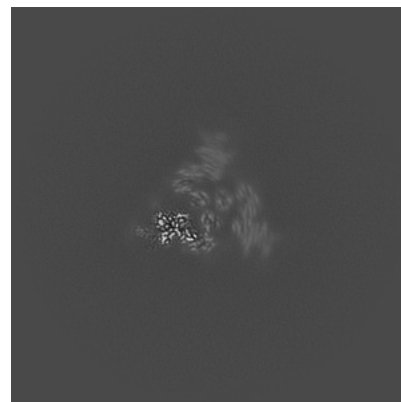
6.2.1 Primary map



X Index: 220



Y Index: 220

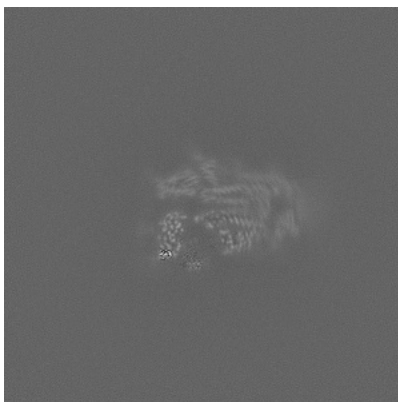


Z Index: 220

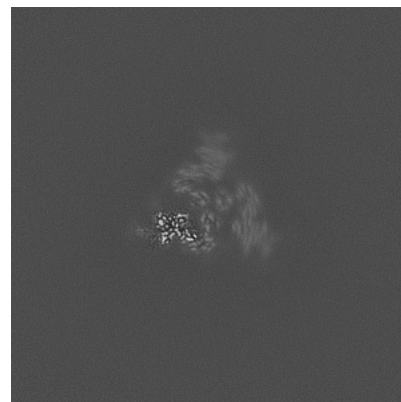
6.2.2 Raw map



X Index: 220



Y Index: 220

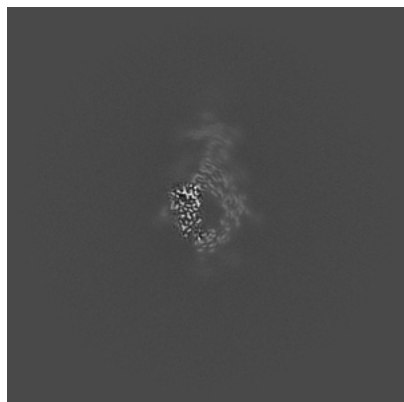


Z Index: 220

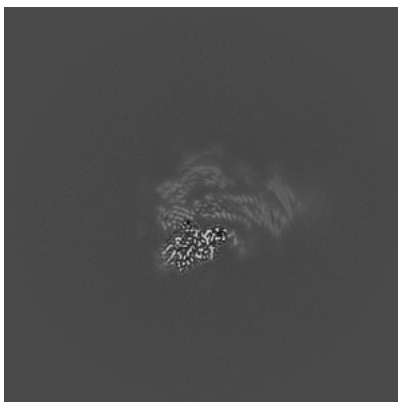
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

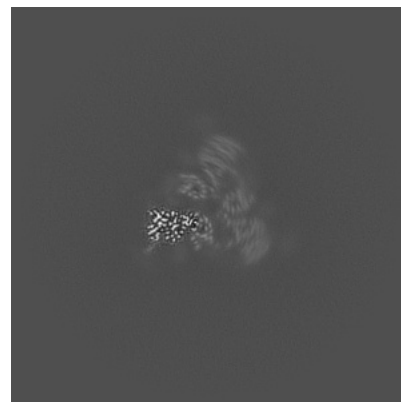
6.3.1 Primary map



X Index: 189

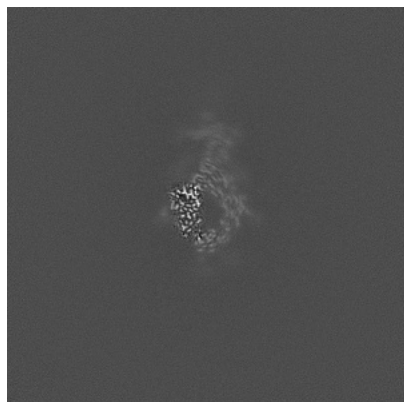


Y Index: 205

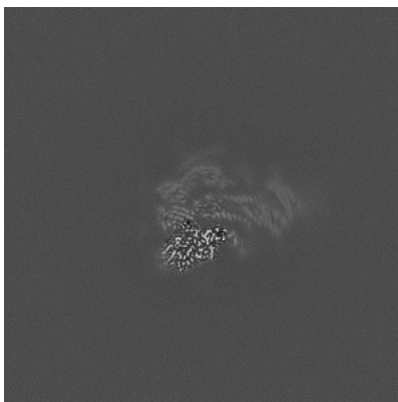


Z Index: 202

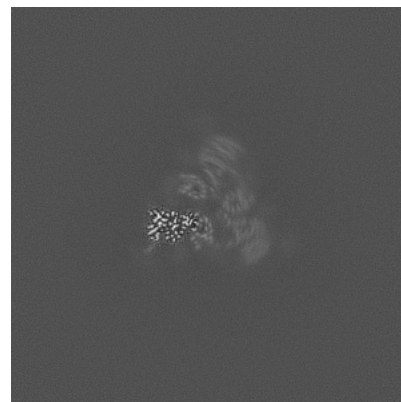
6.3.2 Raw map



X Index: 189



Y Index: 205

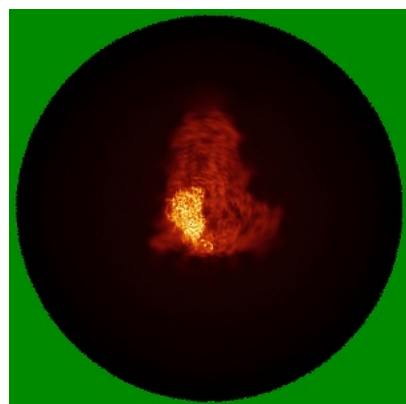


Z Index: 202

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

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

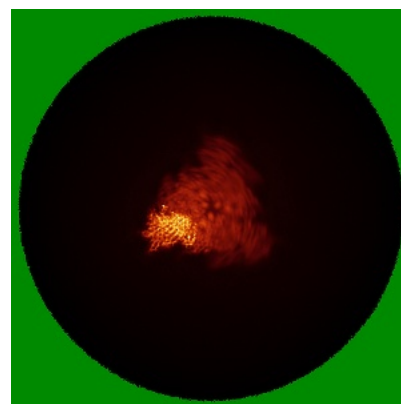
6.4.1 Primary map



X

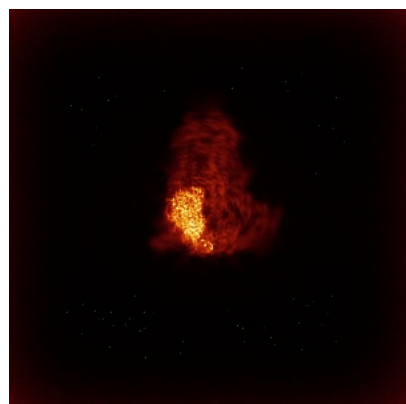


Y

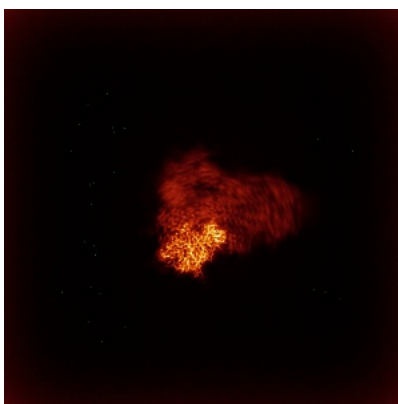


Z

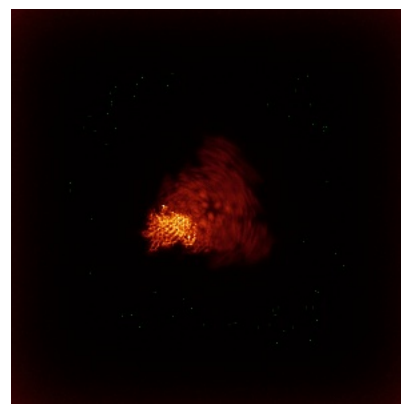
6.4.2 Raw map



X



Y

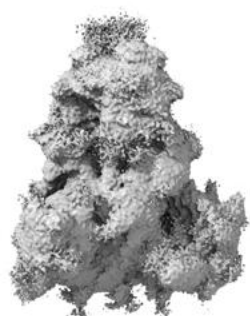


Z

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



X



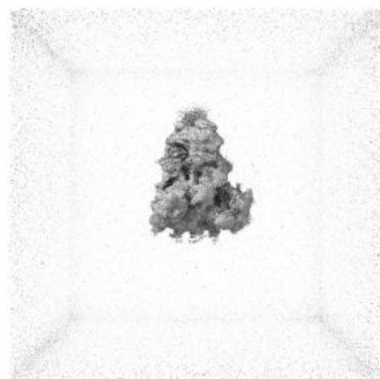
Y



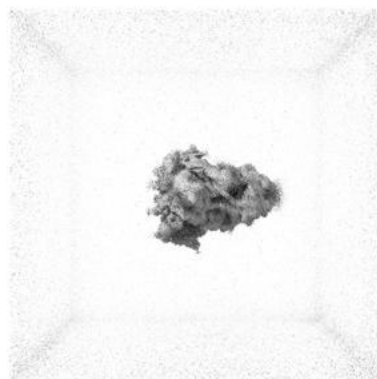
Z

The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

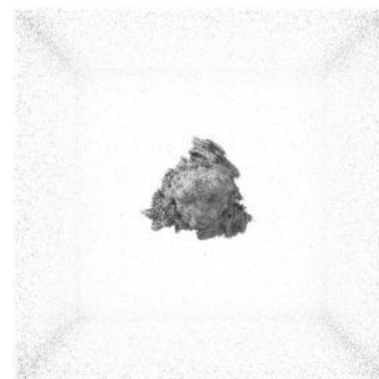
6.5.2 Raw map



X



Y



Z

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.

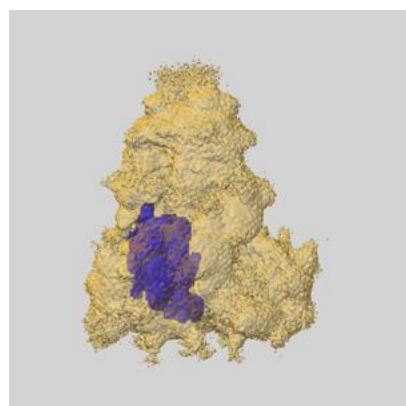
6.6 Mask visualisation [i](#)

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

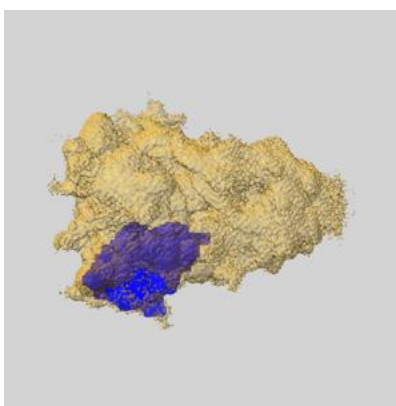
A mask typically either:

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

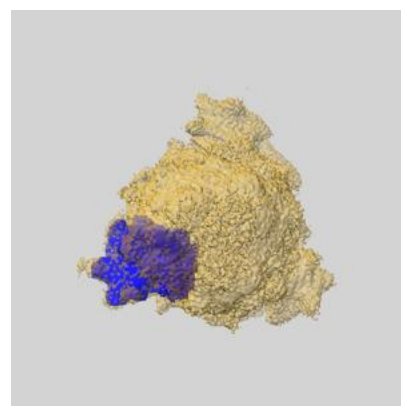
6.6.1 emd_44884_msk_1.map [i](#)



X



Y

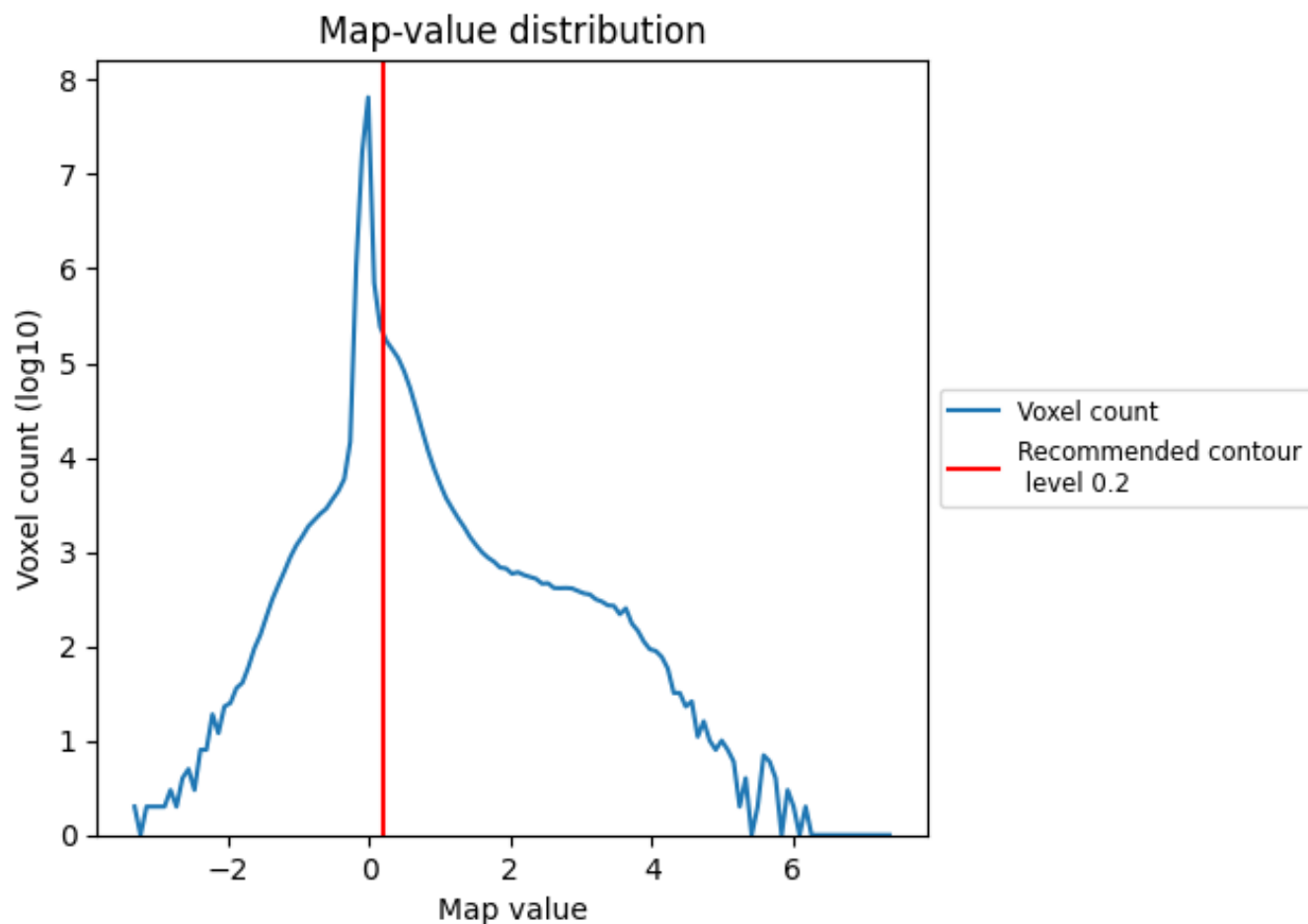


Z

7 Map analysis [i](#)

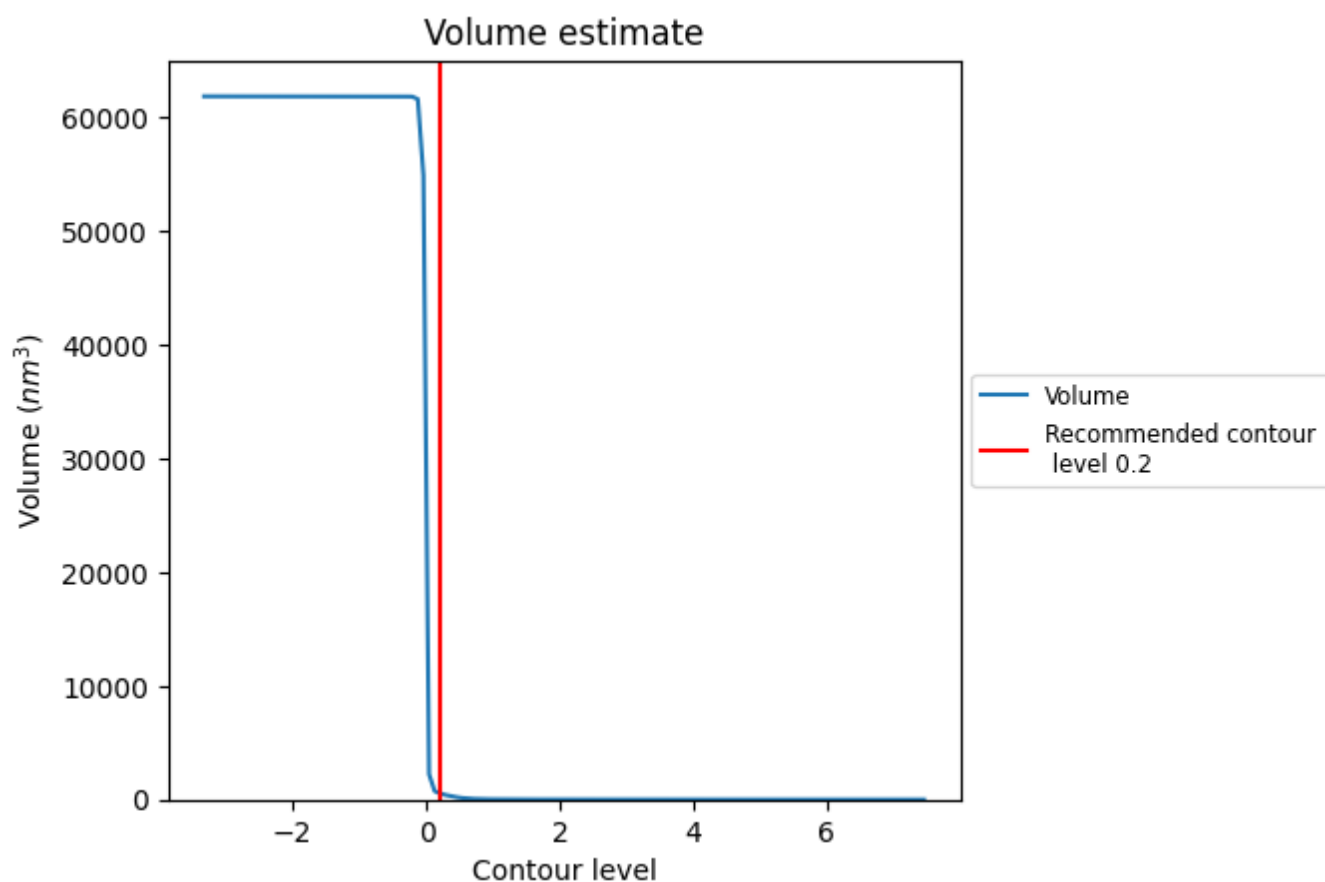
This section contains the results of statistical analysis of the map.

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.

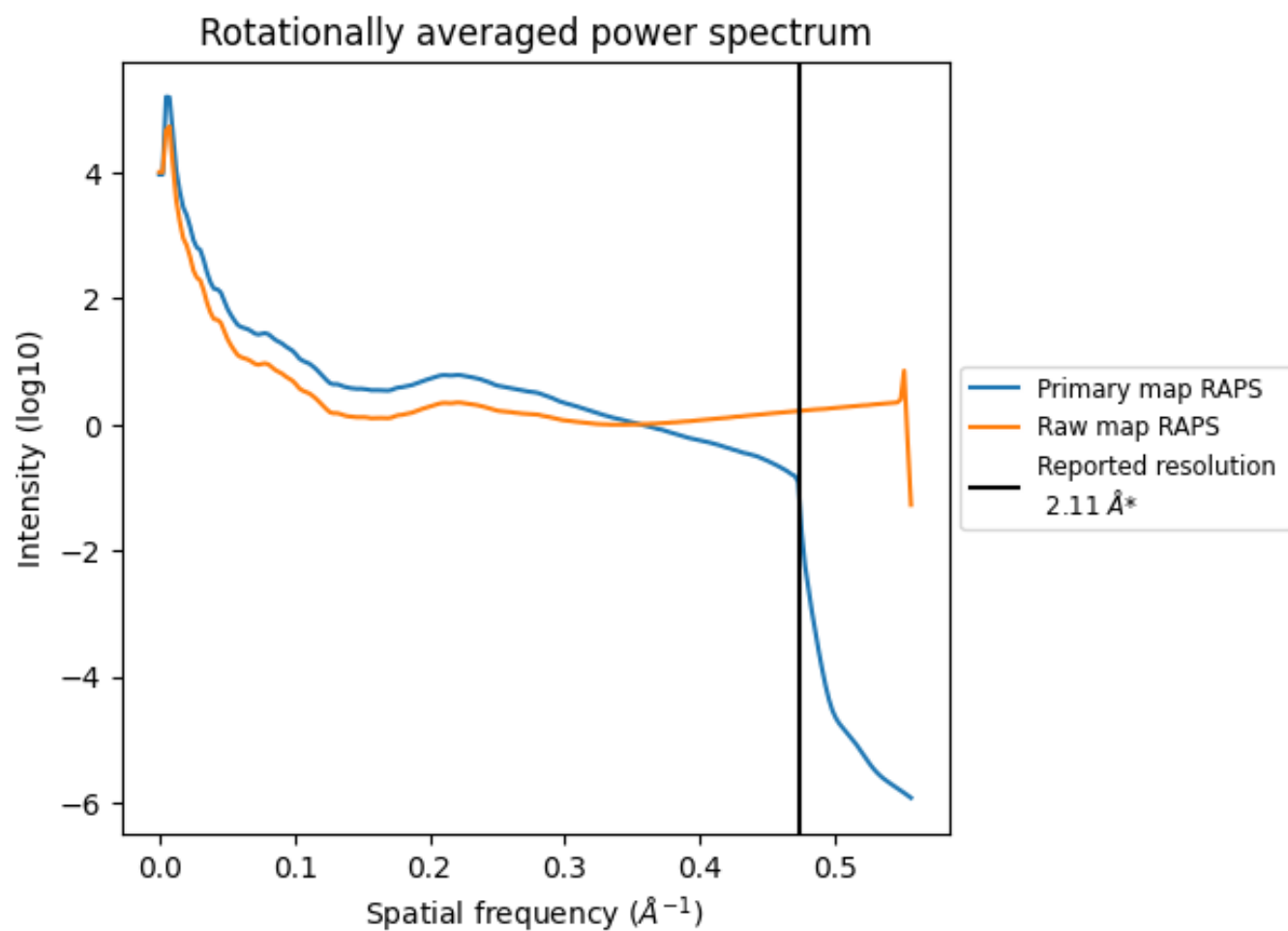
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 565 nm^3 ; this corresponds to an approximate mass of 510 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 ⓘ

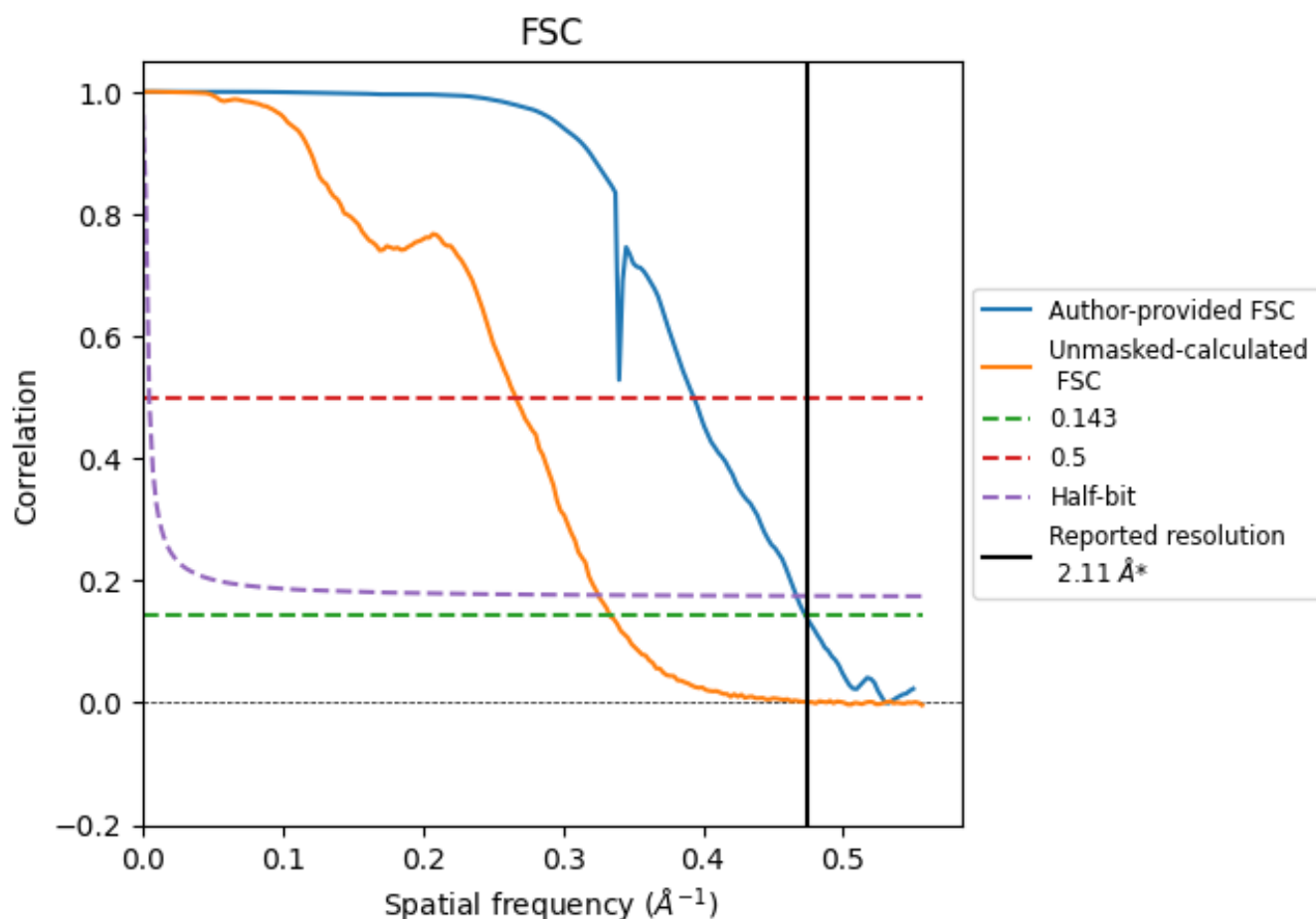


*Reported resolution corresponds to spatial frequency of 0.474 Å⁻¹

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 0.474 \AA^{-1}

8.2 Resolution estimates [i](#)

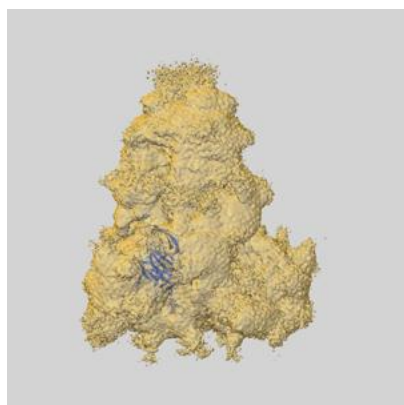
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.11	-	-
Author-provided FSC curve	2.11	2.54	2.14
Unmasked-calculated*	3.00	3.76	3.08

*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 3.00 differs from the reported value 2.11 by more than 10 %

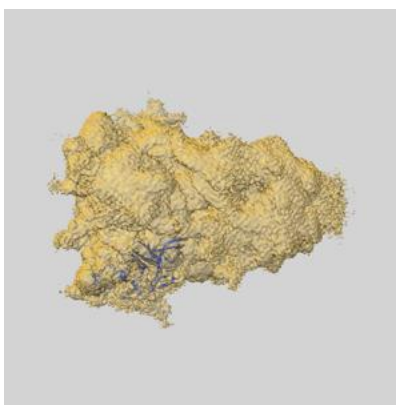
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-44884 and PDB model 9BT9. Per-residue inclusion information can be found in section [3](#) on page [7](#).

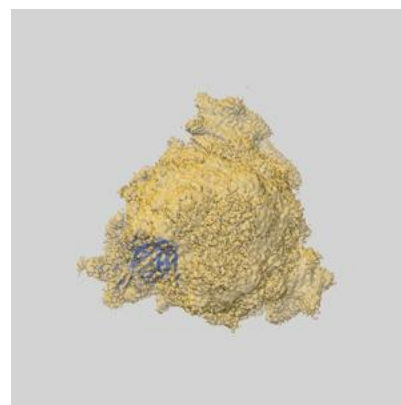
9.1 Map-model overlay [i](#)



X



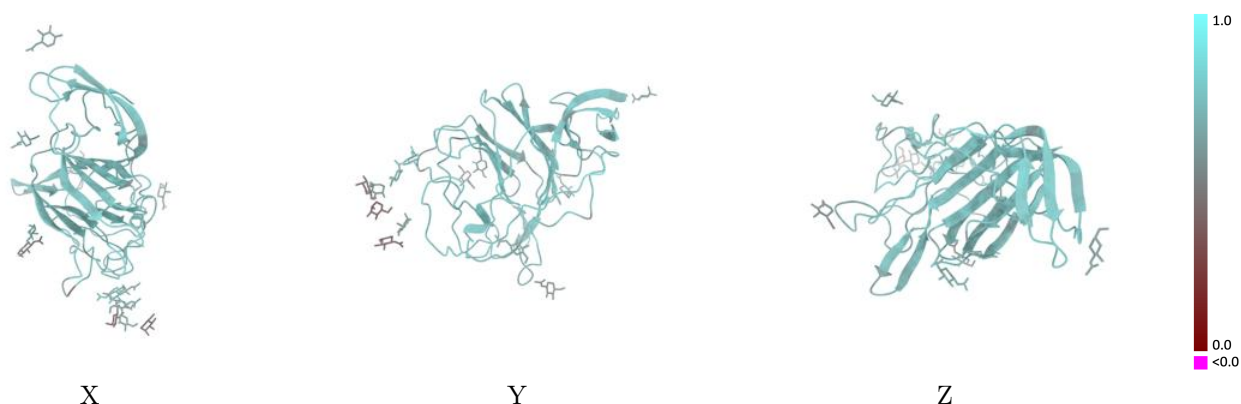
Y



Z

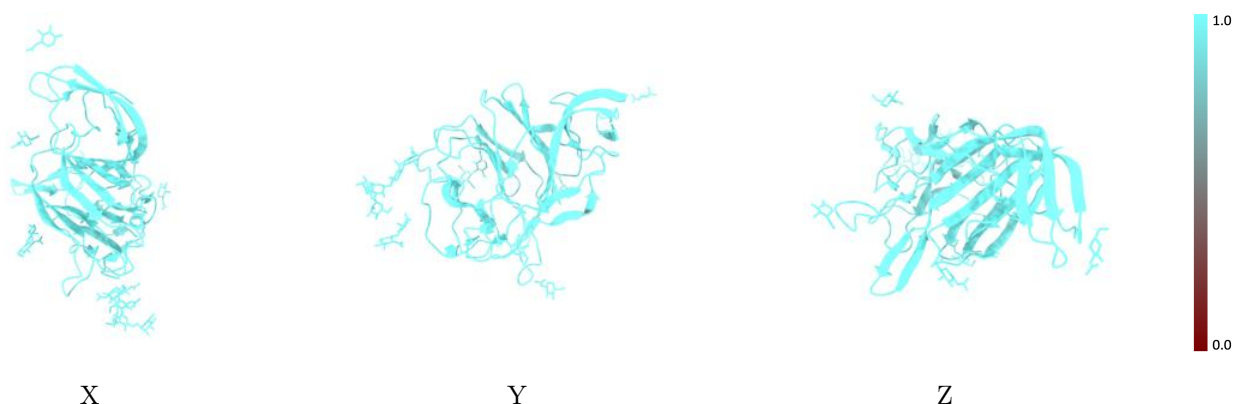
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



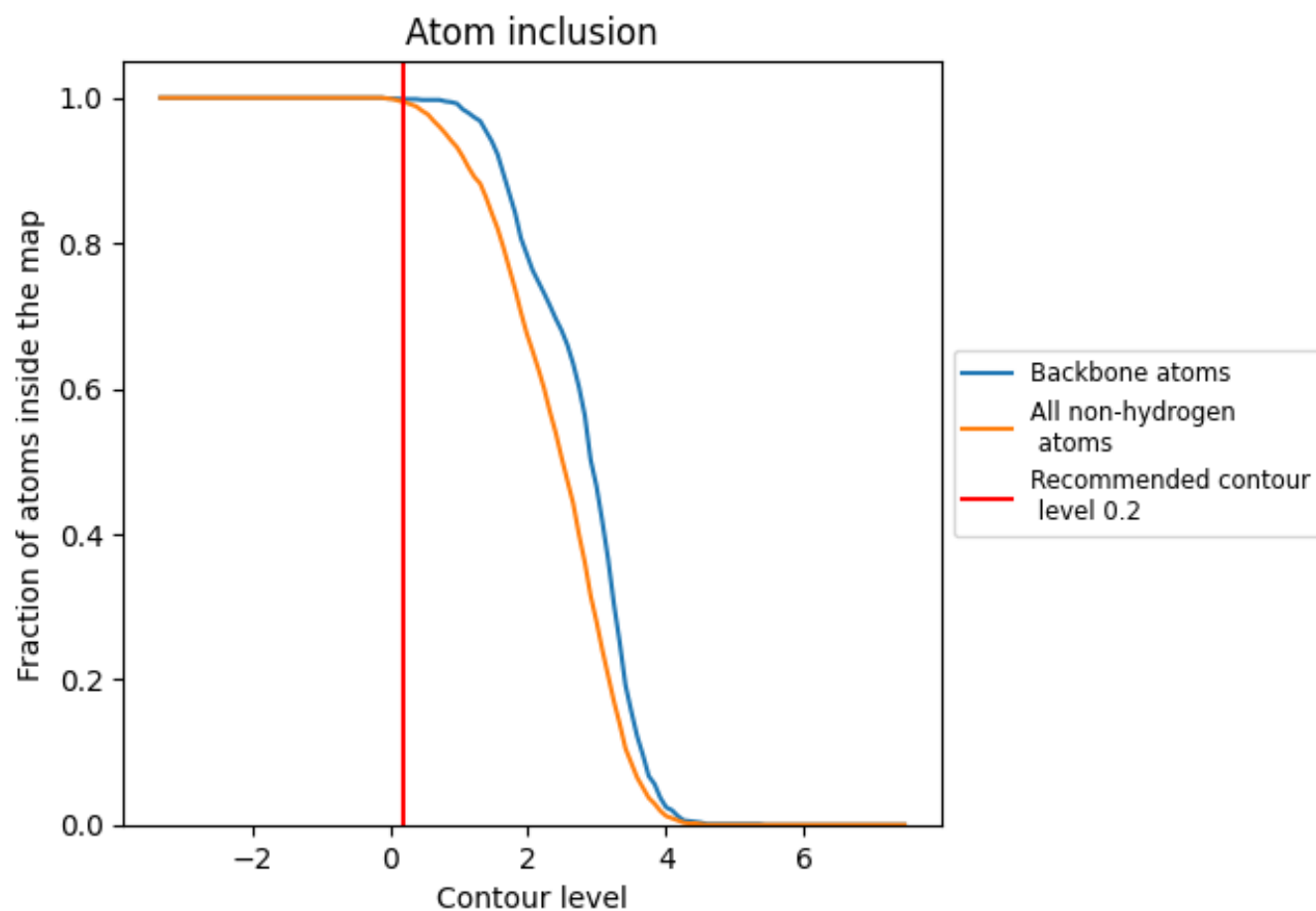
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 99% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9940	<div></div> 0.6780
A	<div></div> 0.9940	<div></div> 0.6850
B	<div></div> 1.0000	<div></div> 0.4840
C	<div></div> 1.0000	<div></div> 0.5580
D	<div></div> 1.0000	<div></div> 0.5680

