



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:32 AM UTC

PDB ID : 8XUT / pdb_00008xut
EMDB ID : EMD-38683
Title : XBB.1.5 Spike Trimer in complex with heparan sulfate
Authors : Yue, C.; Liu, P.; Mao, X.
Deposited on : 2024-01-14
Resolution : 3.20 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:

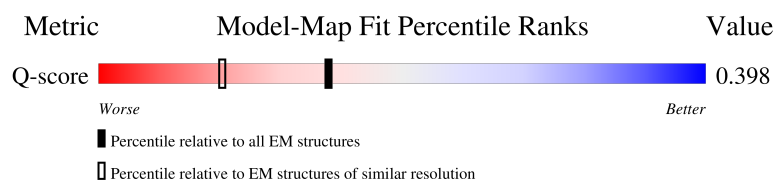
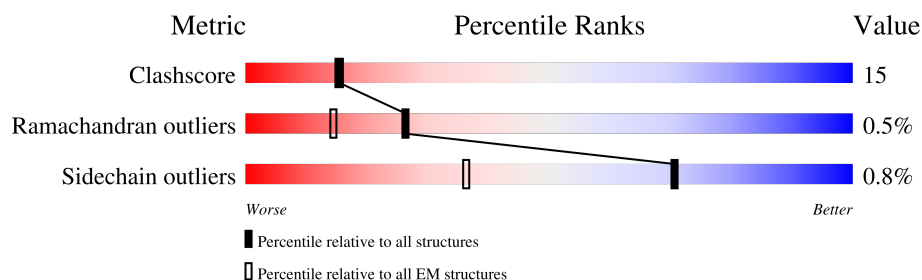
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.20 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	1269	
1	B	1269	
1	C	1269	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 25149 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	1042	Total	C	N	O	S	0	0
			8154	5216	1359	1542	37		
1	A	1042	Total	C	N	O	S	0	0
			8154	5216	1359	1542	37		
1	C	1042	Total	C	N	O	S	0	0
			8154	5216	1359	1542	37		

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	22	ILE	THR	variant	UNP P0DTC2
B	?	-	LEU	deletion	UNP P0DTC2
B	?	-	PRO	deletion	UNP P0DTC2
B	?	-	PRO	deletion	UNP P0DTC2
B	27	SER	ALA	variant	UNP P0DTC2
B	83	ALA	VAL	variant	UNP P0DTC2
B	142	ASP	GLY	variant	UNP P0DTC2
B	?	-	TYR	deletion	UNP P0DTC2
B	146	GLN	HIS	variant	UNP P0DTC2
B	183	GLU	GLN	variant	UNP P0DTC2
B	213	GLU	VAL	variant	UNP P0DTC2
B	252	VAL	GLY	variant	UNP P0DTC2
B	339	HIS	GLY	variant	UNP P0DTC2
B	346	THR	ARG	variant	UNP P0DTC2
B	368	ILE	LEU	variant	UNP P0DTC2
B	371	PHE	SER	variant	UNP P0DTC2
B	373	PRO	SER	variant	UNP P0DTC2
B	375	PHE	SER	variant	UNP P0DTC2
B	376	ALA	THR	variant	UNP P0DTC2
B	405	ASN	ASP	variant	UNP P0DTC2
B	408	SER	ARG	variant	UNP P0DTC2
B	417	ASN	LYS	variant	UNP P0DTC2
B	440	LYS	ASN	variant	UNP P0DTC2
B	445	PRO	VAL	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	446	SER	GLY	variant	UNP P0DTC2
B	460	LYS	ASN	variant	UNP P0DTC2
B	477	ASN	SER	variant	UNP P0DTC2
B	478	LYS	THR	variant	UNP P0DTC2
B	484	ALA	GLU	variant	UNP P0DTC2
B	486	PRO	PHE	variant	UNP P0DTC2
B	490	SER	PHE	variant	UNP P0DTC2
B	498	ARG	GLN	variant	UNP P0DTC2
B	501	TYR	ASN	variant	UNP P0DTC2
B	505	HIS	TYR	variant	UNP P0DTC2
B	614	GLY	ASP	variant	UNP P0DTC2
B	655	TYR	HIS	variant	UNP P0DTC2
B	679	LYS	ASN	variant	UNP P0DTC2
B	681	HIS	PRO	variant	UNP P0DTC2
B	764	LYS	ASN	variant	UNP P0DTC2
B	796	TYR	ASP	variant	UNP P0DTC2
B	954	HIS	GLN	variant	UNP P0DTC2
B	969	LYS	ASN	variant	UNP P0DTC2
A	22	ILE	THR	variant	UNP P0DTC2
A	?	-	LEU	deletion	UNP P0DTC2
A	?	-	PRO	deletion	UNP P0DTC2
A	?	-	PRO	deletion	UNP P0DTC2
A	27	SER	ALA	variant	UNP P0DTC2
A	83	ALA	VAL	variant	UNP P0DTC2
A	142	ASP	GLY	variant	UNP P0DTC2
A	?	-	TYR	deletion	UNP P0DTC2
A	146	GLN	HIS	variant	UNP P0DTC2
A	183	GLU	GLN	variant	UNP P0DTC2
A	213	GLU	VAL	variant	UNP P0DTC2
A	252	VAL	GLY	variant	UNP P0DTC2
A	339	HIS	GLY	variant	UNP P0DTC2
A	346	THR	ARG	variant	UNP P0DTC2
A	368	ILE	LEU	variant	UNP P0DTC2
A	371	PHE	SER	variant	UNP P0DTC2
A	373	PRO	SER	variant	UNP P0DTC2
A	375	PHE	SER	variant	UNP P0DTC2
A	376	ALA	THR	variant	UNP P0DTC2
A	405	ASN	ASP	variant	UNP P0DTC2
A	408	SER	ARG	variant	UNP P0DTC2
A	417	ASN	LYS	variant	UNP P0DTC2
A	440	LYS	ASN	variant	UNP P0DTC2
A	445	PRO	VAL	variant	UNP P0DTC2

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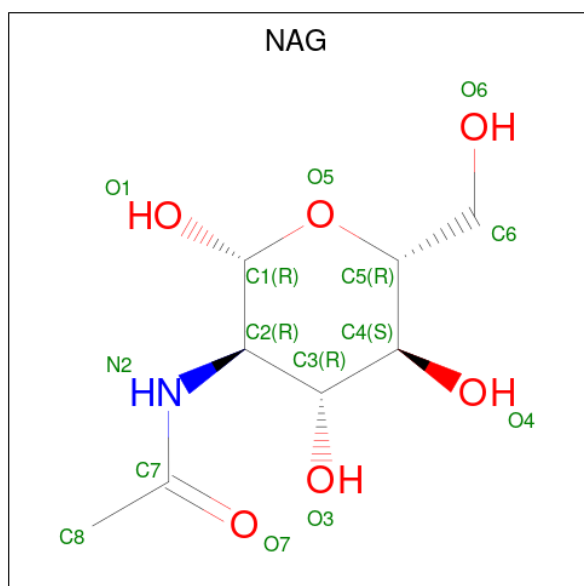
Chain	Residue	Modelled	Actual	Comment	Reference
A	446	SER	GLY	variant	UNP P0DTC2
A	460	LYS	ASN	variant	UNP P0DTC2
A	477	ASN	SER	variant	UNP P0DTC2
A	478	LYS	THR	variant	UNP P0DTC2
A	484	ALA	GLU	variant	UNP P0DTC2
A	486	PRO	PHE	variant	UNP P0DTC2
A	490	SER	PHE	variant	UNP P0DTC2
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A	505	HIS	TYR	variant	UNP P0DTC2
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A	681	HIS	PRO	variant	UNP P0DTC2
A	764	LYS	ASN	variant	UNP P0DTC2
A	796	TYR	ASP	variant	UNP P0DTC2
A	954	HIS	GLN	variant	UNP P0DTC2
A	969	LYS	ASN	variant	UNP P0DTC2
C	22	ILE	THR	variant	UNP P0DTC2
C	?	-	LEU	deletion	UNP P0DTC2
C	?	-	PRO	deletion	UNP P0DTC2
C	?	-	PRO	deletion	UNP P0DTC2
C	27	SER	ALA	variant	UNP P0DTC2
C	83	ALA	VAL	variant	UNP P0DTC2
C	142	ASP	GLY	variant	UNP P0DTC2
C	?	-	TYR	deletion	UNP P0DTC2
C	146	GLN	HIS	variant	UNP P0DTC2
C	183	GLU	GLN	variant	UNP P0DTC2
C	213	GLU	VAL	variant	UNP P0DTC2
C	252	VAL	GLY	variant	UNP P0DTC2
C	339	HIS	GLY	variant	UNP P0DTC2
C	346	THR	ARG	variant	UNP P0DTC2
C	368	ILE	LEU	variant	UNP P0DTC2
C	371	PHE	SER	variant	UNP P0DTC2
C	373	PRO	SER	variant	UNP P0DTC2
C	375	PHE	SER	variant	UNP P0DTC2
C	376	ALA	THR	variant	UNP P0DTC2
C	405	ASN	ASP	variant	UNP P0DTC2
C	408	SER	ARG	variant	UNP P0DTC2
C	417	ASN	LYS	variant	UNP P0DTC2
C	440	LYS	ASN	variant	UNP P0DTC2
C	445	PRO	VAL	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	446	SER	GLY	variant	UNP P0DTC2
C	460	LYS	ASN	variant	UNP P0DTC2
C	477	ASN	SER	variant	UNP P0DTC2
C	478	LYS	THR	variant	UNP P0DTC2
C	484	ALA	GLU	variant	UNP P0DTC2
C	486	PRO	PHE	variant	UNP P0DTC2
C	490	SER	PHE	variant	UNP P0DTC2
C	498	ARG	GLN	variant	UNP P0DTC2
C	501	TYR	ASN	variant	UNP P0DTC2
C	505	HIS	TYR	variant	UNP P0DTC2
C	614	GLY	ASP	variant	UNP P0DTC2
C	655	TYR	HIS	variant	UNP P0DTC2
C	679	LYS	ASN	variant	UNP P0DTC2
C	681	HIS	PRO	variant	UNP P0DTC2
C	764	LYS	ASN	variant	UNP P0DTC2
C	796	TYR	ASP	variant	UNP P0DTC2
C	954	HIS	GLN	variant	UNP P0DTC2
C	969	LYS	ASN	variant	UNP P0DTC2

- 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	

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

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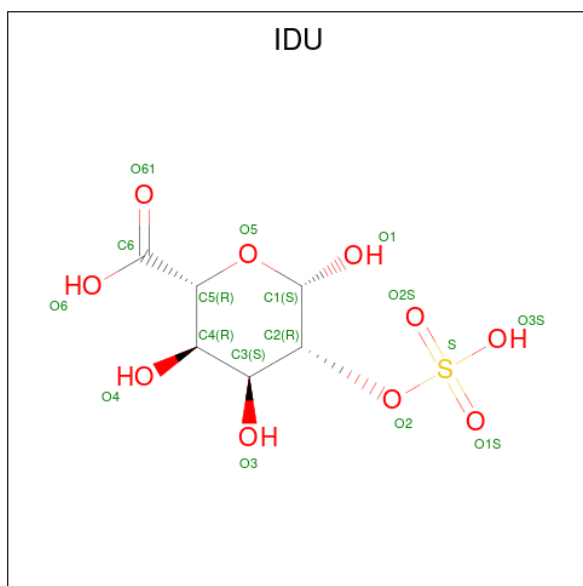
Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	A	1	Total 14	C 8	N 1	O 5	0
2	C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

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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	

- Molecule 3 is 2-O-sulfo-beta-L-altropyranuronic acid (CCD ID: IDU) (formula: C₆H₁₀O₁₀S) (labeled as "Ligand of Interest" by depositor).

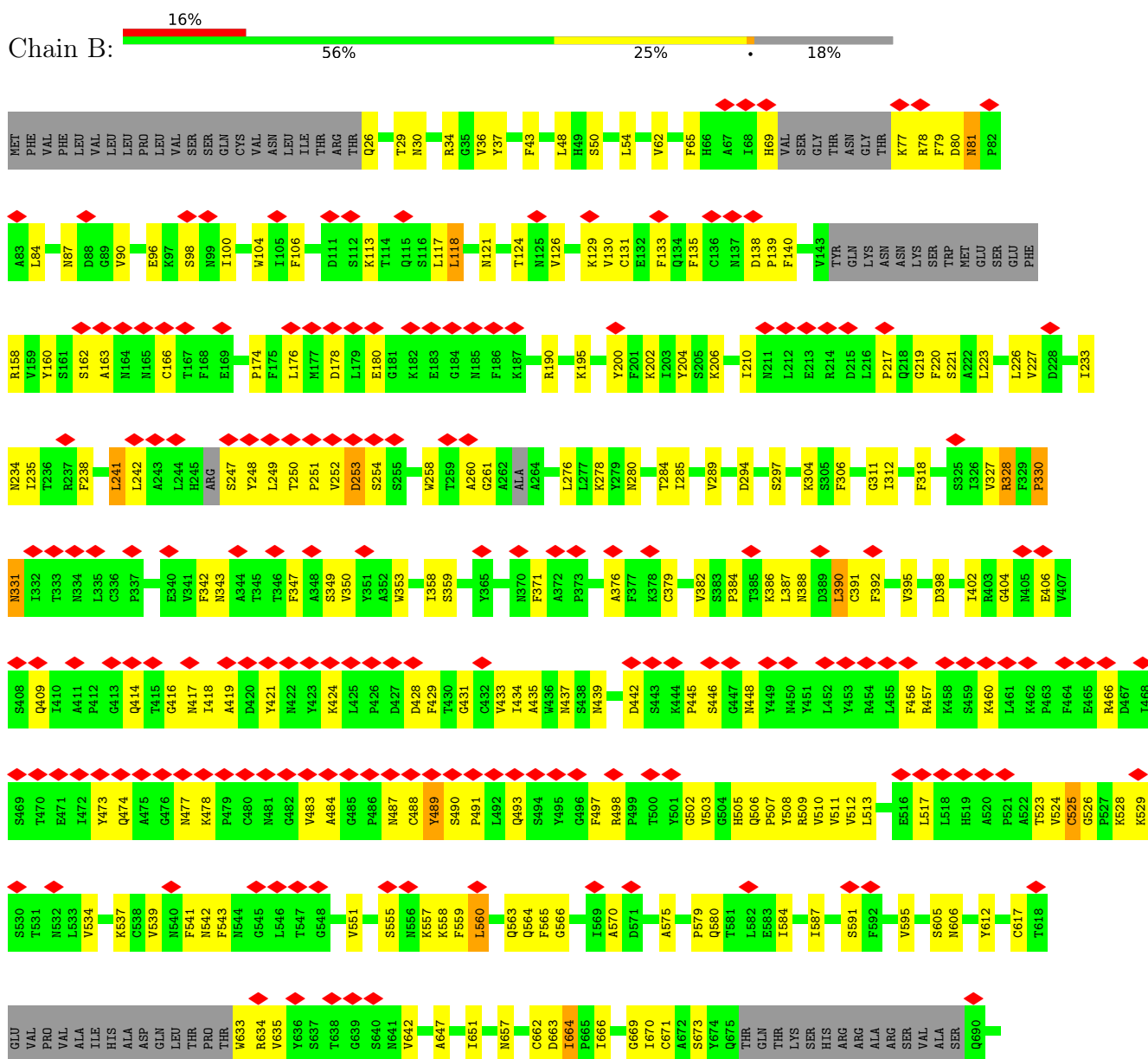


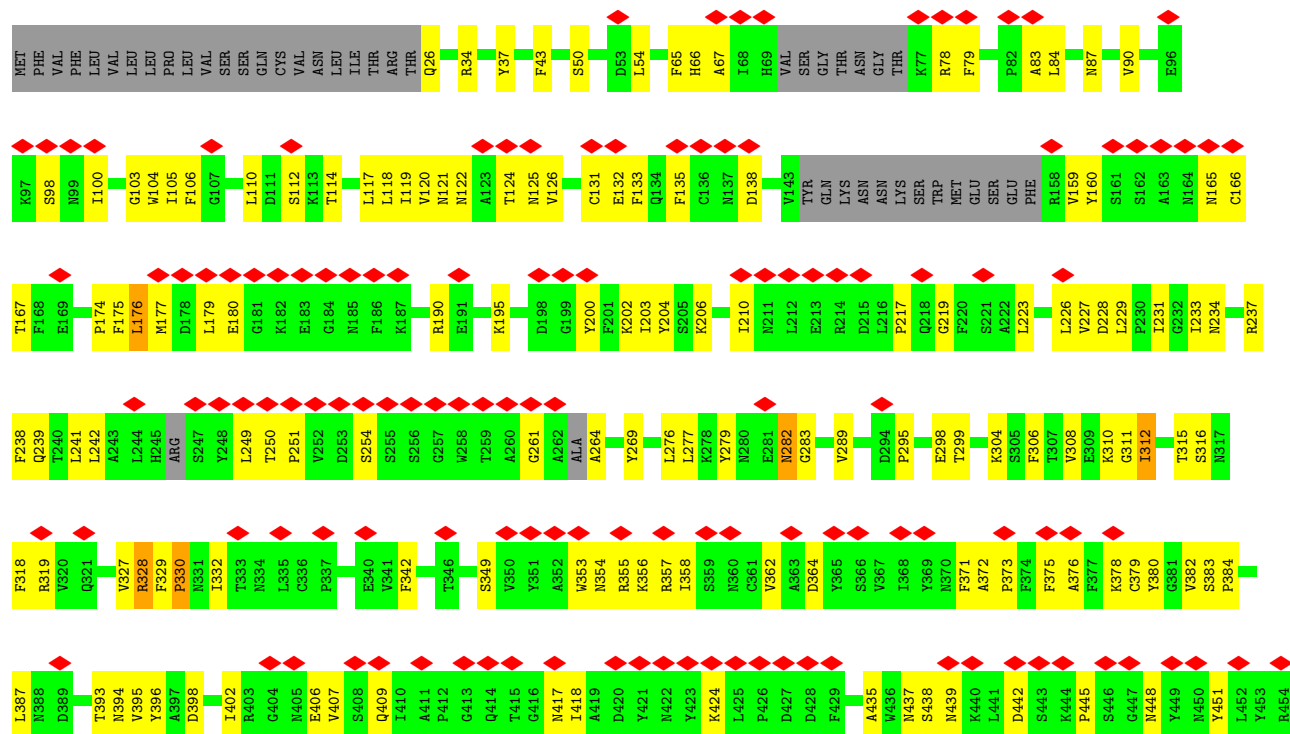
Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	O	S	0
			15	6	8	1	

3 Residue-property plots

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

• Molecule 1: Spike glycoprotein





PHE	THR	G1046	F906	F812	N709	ILE	N544	S469	F392	F318	F220
ILE	SER	Y1047	I909	K814	N710	HIS	G545	T470	T393	R319	S221
ALA	PRO	H1048	I909	K814	N711	ALA	L546	E471	N394		A222
GLY	ASP	L1049	A924	R815	I712	GLN	T547	I472	N405		L223
LEU	VAL	S816	F927	F817	I714	LEU	G548	Y473			L226
ILE	ASP	F1052	N928	I818	T724	THR	V551	Q474	S408		V227
ALA	GLY	S1055	I931	E819	E725	PRO	L552	A475	Q409		D228
VAL	ASP	V1061	I931	I821	I726	THR	T553	G476	I410		I231
MET	ILE	T1076	I934	L822	K733	THR	E554	N477	A411		I232
THR	GLY	Q935	Q935	T827	T734	THR	S555	K478	P412		I233
ILE	ILE	K1086	S939	LEU	S735	THR	N556	P479	Q413		H234
MET	ASN		S940	ALA	V736	THR	K557	C480	Q414		
LEU	ALA	R1091	T941	ASP	D737	THR	K558	N481	T415		R237
CYS	SER	S940	T941	ASP	C738	THR	F559	G482	G416		F238
VAL	VAL	V1094	A942	ALA	T739	THR	L560	V483	N417		Q239
MET	THR	F1095	A942	GLY	W740	THR	Q663	A484	I418		T240
THR	ASN	V1096	A944	PHE	Y741	THR	Q664	G485	A419		L241
SER	ILE	V1097	L945	ILE	I742	THR	F643	P486	D420		L242
CYS	GLN	N1098	L945	LYS	C743	THR	Q665	S490	Y421		A243
LYS	LYS		K947	GLN	G744	THR	D567	P491	T345		L244
CYS	GLY		L966	TYR	D745	THR	R567	L492	T346		H245
ILE	ASP	W1102	S975	ASP	E746	THR	D568	Q493	F347		ARG
ASP	ARG	V1103	K969	CYS		THR	I569	S494	N360		S247
LYS	LEU	V1104	A972	LEU	L752	THR	A570	P497	C361		Y248
ASN	ASN	T1105	S975	GLY	L753	THR	D571	R498	V362		Y252
CYS	GLY	P1112	A972	GLY	Y756	THR	A575	P499	A363		D253
CYS	GLY	I1115	S975	ILE	C671	THR	R577	T500	D364		S254
GLY	ASN	D1118	D979	ALA	A672	THR	D578	Y501	Y365		S255
CYS	ASN	D1127	I980	ARG	Q675	THR	F579	G502	Y369		S256
LYS	GLY	V1128	R983	ASP		THR	Q880	V503	N370		G257
ASP	SER	V1129	L984	LEU		THR	T581	H504	F371		W258
GLY	ILE	V1137	D985	C851	L763	THR	L582	H505	A372		T259
ASP	ASP	F1140	K986	A852	K764	THR	E883	G447	P373		A260
ASP	ASP		K987	K854	L767	THR	I584	N448	G261		G261
GLY	GLY		E988	F855	I770	THR	L585	R509	F374		A262
PRO	GLY		A989	T859	D776	THR	C590	V510	F375		ALA
VAL	LEU		E990	W860	K776	THR	S591	V511	A376		A264
LYS	LEU		D994	L861	N777	THR	F592		F377		
GLY	GLY		T998	L864	V781	THR	G593		F374		
VAL	GLN		L1004	E868	I788	THR	S596		A376		
LYS	TYR		V1008	L878	I794	THR	V597		F377		
THR	THR		A1015	L878	L794	THR	I598		K378		
THR	THR		L894	A890	G798	THR	A609		C379		N280
THR	THR		N1023	L894	G799	THR	Q613		Y380		T284
LEU	THR		T1027	F897	F800	THR	C617		V382		
GLY	ASN		E1031	Y904	N801	THR	T618		S383		D290
				R905	F802	THR	GLU		T385		S297
					I805	THR	VAL		K386		C301
						THR	PRO		L387		K304
						THR	VAL		N388		L390
						THR	ALA		D389		I312
						THR	ALA		C391		N317

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	257757	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.838	Depositor
Minimum map value	-1.122	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.057	Depositor
Recommended contour level	0.3	Depositor
Map size ($\text{\AA}$)	310.80002, 310.80002, 310.80002	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.036, 1.036, 1.036	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IDU, 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	0.36	0/8345	0.51	0/11349
1	B	0.33	0/8345	0.47	1/11349 (0.0%)
1	C	0.28	0/8345	0.43	0/11349
All	All	0.33	0/25035	0.47	1/34047 (0.0%)

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	1
1	B	0	2
All	All	0	3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	862	PRO	O-C-N	-5.04	118.78	121.15

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	328	ARG	Sidechain
1	B	158	ARG	Sidechain
1	B	328	ARG	Sidechain

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	8154	0	7959	278	0
1	B	8154	0	7959	278	0
1	C	8154	0	7959	238	0
2	A	224	0	208	2	0
2	B	224	0	208	5	0
2	C	224	0	208	4	0
3	A	15	0	4	0	0
All	All	25149	0	24505	732	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 15.

The worst 5 of 732 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:277:LEU:HD11	1:A:279:TYR:CE1	1.76	1.20
1:A:126:VAL:HG21	1:A:175:PHE:HE2	0.99	1.12
1:A:126:VAL:HG21	1:A:175:PHE:CE2	1.86	1.10
1:B:121:ASN:HD22	1:B:176:LEU:HD23	1.07	1.07
1:B:697:MET:HE2	1:B:697:MET:HA	1.38	1.04

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	1026/1269 (81%)	911 (89%)	109 (11%)	6 (1%)	21	56
1	B	1026/1269 (81%)	923 (90%)	96 (9%)	7 (1%)	18	52
1	C	1026/1269 (81%)	936 (91%)	87 (8%)	3 (0%)	36	68
All	All	3078/3807 (81%)	2770 (90%)	292 (10%)	16 (0%)	26	59

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	331	ASN
1	B	253	ASP
1	B	788	ILE
1	B	798	GLY
1	A	788	ILE

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	908/1109 (82%)	901 (99%)	7 (1%)	73	82
1	B	908/1109 (82%)	898 (99%)	10 (1%)	65	79
1	C	908/1109 (82%)	904 (100%)	4 (0%)	84	86
All	All	2724/3327 (82%)	2703 (99%)	21 (1%)	70	82

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	525	CYS
1	C	203	ILE
1	C	1104	VAL
1	C	693	ILE
1	A	546	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1011	GLN
1	C	394	ASN
1	C	1011	GLN
1	A	1023	ASN
1	C	30	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

49 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	C	1311	1	14,14,15	0.41	0	17,19,21	0.53	0
2	NAG	B	1301	1	14,14,15	0.23	0	17,19,21	0.48	0
2	NAG	A	1314	1	14,14,15	0.25	0	17,19,21	0.51	0
2	NAG	B	1305	1	14,14,15	0.33	0	17,19,21	0.44	0
2	NAG	B	1311	1	14,14,15	0.39	0	17,19,21	0.45	0
2	NAG	A	1311	1	14,14,15	0.41	0	17,19,21	0.52	0
2	NAG	A	1312	1	14,14,15	0.22	0	17,19,21	0.51	0
2	NAG	C	1315	1	14,14,15	0.21	0	17,19,21	0.49	0
3	IDU	A	1317	-	15,15,17	0.94	1 (6%)	14,22,26	1.14	1 (7%)
2	NAG	C	1303	1	14,14,15	0.39	0	17,19,21	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	C	1314	1	14,14,15	0.25	0	17,19,21	0.54	0
2	NAG	B	1302	1	14,14,15	0.19	0	17,19,21	0.48	0
2	NAG	B	1315	1	14,14,15	0.22	0	17,19,21	0.49	0
2	NAG	B	1314	1	14,14,15	0.37	0	17,19,21	0.67	0
2	NAG	C	1306	1	14,14,15	0.34	0	17,19,21	0.45	0
2	NAG	C	1307	1	14,14,15	0.27	0	17,19,21	0.50	0
2	NAG	A	1316	1	14,14,15	0.20	0	17,19,21	0.44	0
2	NAG	A	1306	1	14,14,15	0.28	0	17,19,21	0.47	0
2	NAG	A	1308	1	14,14,15	0.22	0	17,19,21	0.44	0
2	NAG	A	1301	1	14,14,15	0.23	0	17,19,21	0.44	0
2	NAG	A	1310	1	14,14,15	0.39	0	17,19,21	0.37	0
2	NAG	B	1308	1	14,14,15	0.18	0	17,19,21	0.45	0
2	NAG	C	1305	1	14,14,15	0.53	0	17,19,21	0.45	0
2	NAG	A	1304	1	14,14,15	0.25	0	17,19,21	0.46	0
2	NAG	C	1301	1	14,14,15	0.32	0	17,19,21	0.48	0
2	NAG	B	1306	1	14,14,15	0.35	0	17,19,21	0.42	0
2	NAG	A	1302	1	14,14,15	0.28	0	17,19,21	0.51	0
2	NAG	A	1309	1	14,14,15	0.22	0	17,19,21	0.42	0
2	NAG	C	1312	1	14,14,15	0.20	0	17,19,21	0.48	0
2	NAG	C	1316	1	14,14,15	0.23	0	17,19,21	0.47	0
2	NAG	B	1313	1	14,14,15	0.23	0	17,19,21	0.48	0
2	NAG	A	1305	1	14,14,15	0.40	0	17,19,21	0.42	0
2	NAG	C	1313	1	14,14,15	0.25	0	17,19,21	0.51	0
2	NAG	B	1309	1	14,14,15	0.21	0	17,19,21	0.42	0
2	NAG	B	1312	1	14,14,15	0.24	0	17,19,21	0.47	0
2	NAG	A	1303	1	14,14,15	0.38	0	17,19,21	0.40	0
2	NAG	A	1313	1	14,14,15	0.24	0	17,19,21	0.50	0
2	NAG	C	1310	1	14,14,15	0.27	0	17,19,21	0.50	0
2	NAG	B	1316	1	14,14,15	0.23	0	17,19,21	0.46	0
2	NAG	C	1304	1	14,14,15	0.25	0	17,19,21	0.45	0
2	NAG	A	1307	1	14,14,15	0.26	0	17,19,21	0.49	0
2	NAG	B	1303	1	14,14,15	0.99	1 (7%)	17,19,21	1.30	1 (5%)
2	NAG	B	1307	1	14,14,15	0.22	0	17,19,21	0.50	0
2	NAG	B	1304	1	14,14,15	0.25	0	17,19,21	0.48	0
2	NAG	B	1310	1	14,14,15	0.36	0	17,19,21	0.52	0
2	NAG	C	1302	1	14,14,15	0.20	0	17,19,21	0.48	0
2	NAG	C	1308	1	14,14,15	0.23	0	17,19,21	0.43	0
2	NAG	C	1309	1	14,14,15	0.23	0	17,19,21	0.42	0
2	NAG	A	1315	1	14,14,15	0.21	0	17,19,21	0.51	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	C	1311	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1301	1	-	1/6/23/26	0/1/1/1
2	NAG	A	1314	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1305	1	-	3/6/23/26	0/1/1/1
2	NAG	B	1311	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1311	1	-	3/6/23/26	0/1/1/1
2	NAG	A	1312	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1315	1	-	2/6/23/26	0/1/1/1
3	IDU	A	1317	-	-	4/9/22/29	1/1/1/1
2	NAG	C	1303	1	-	1/6/23/26	0/1/1/1
2	NAG	C	1314	1	-	4/6/23/26	0/1/1/1
2	NAG	B	1302	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1315	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1314	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1306	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1307	1	-	3/6/23/26	0/1/1/1
2	NAG	A	1316	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1306	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1308	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1301	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1310	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1308	1	-	1/6/23/26	0/1/1/1
2	NAG	C	1305	1	-	3/6/23/26	0/1/1/1
2	NAG	A	1304	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1301	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1306	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1302	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1309	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1312	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1316	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1313	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1305	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1313	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1309	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1312	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1303	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1313	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1310	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1316	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1304	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1307	1	-	2/6/23/26	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	B	1304	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1310	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1302	1	-	2/6/23/26	0/1/1/1
2	NAG	C	1308	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1309	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1315	1	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1303	NAG	O5-C1	3.55	1.49	1.43
3	A	1317	IDU	O6-C6	-2.99	1.21	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1303	NAG	C1-O5-C5	5.13	119.06	112.19
3	A	1317	IDU	O6-C6-C5	2.61	119.49	112.71

There are no chirality outliers.

5 of 69 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1317	IDU	C1-C2-O2-S
3	A	1317	IDU	C3-C2-O2-S
2	C	1307	NAG	C4-C5-C6-O6
2	B	1307	NAG	C4-C5-C6-O6
2	C	1314	NAG	O5-C5-C6-O6

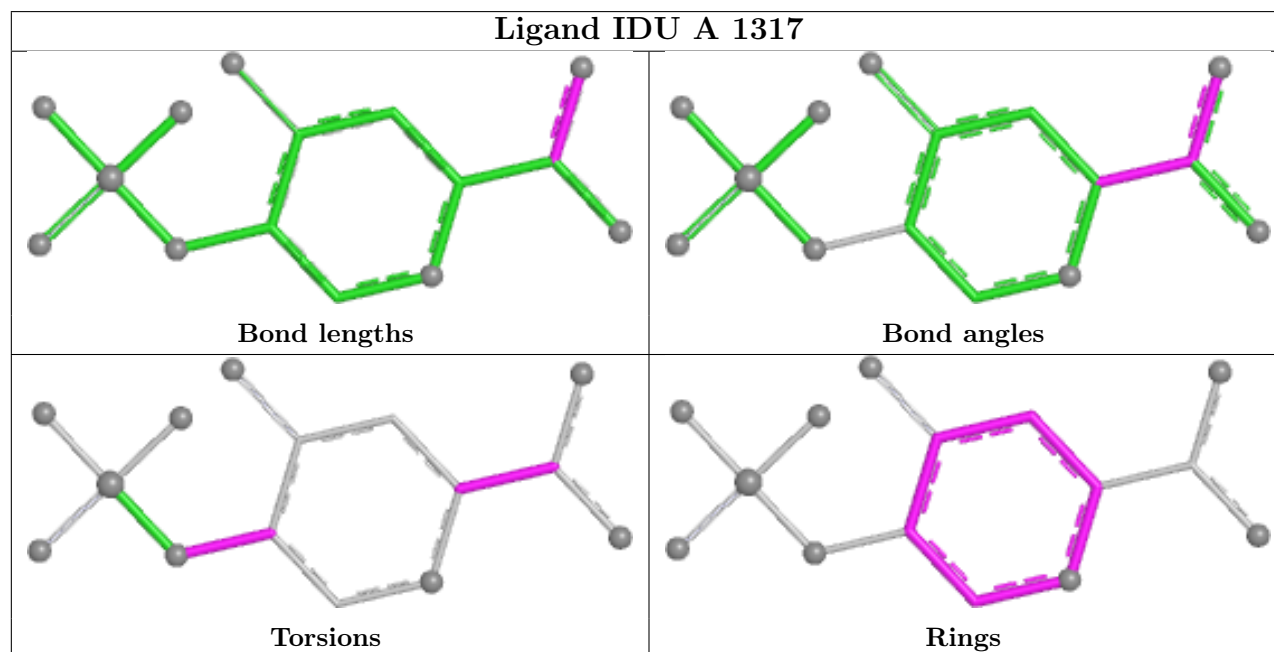
All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1317	IDU	C1-C2-C3-C4-C5-O5

9 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1311	NAG	1	0
2	B	1311	NAG	1	0
2	B	1302	NAG	1	0
2	C	1301	NAG	2	0
2	B	1306	NAG	1	0
2	A	1309	NAG	2	0
2	B	1312	NAG	1	0
2	B	1310	NAG	1	0
2	C	1302	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

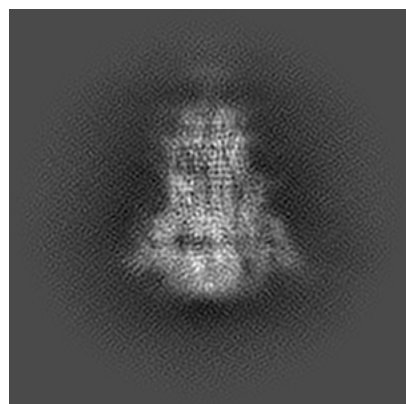
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38683. These allow visual inspection of the internal detail of the map and identification of artifacts.

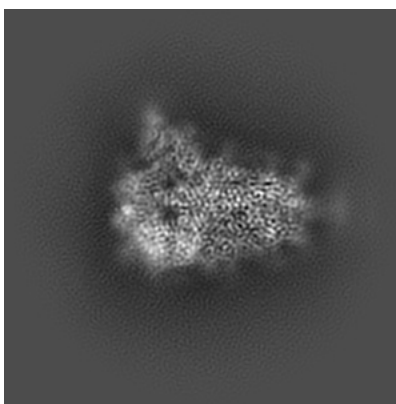
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

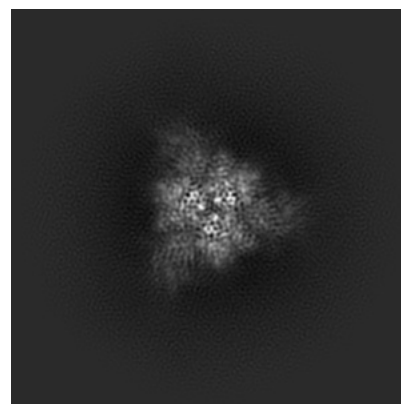
6.1.1 Primary map



X

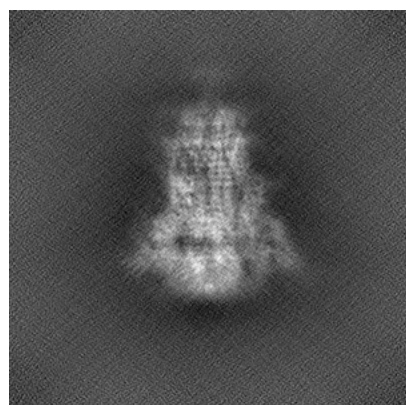


Y

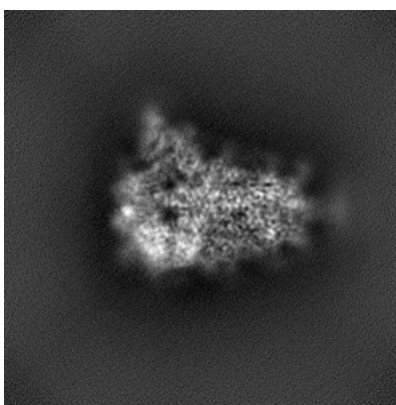


Z

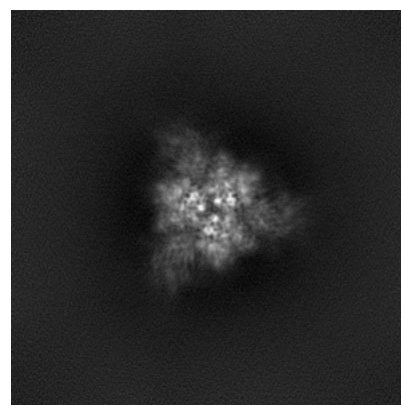
6.1.2 Raw map



X



Y

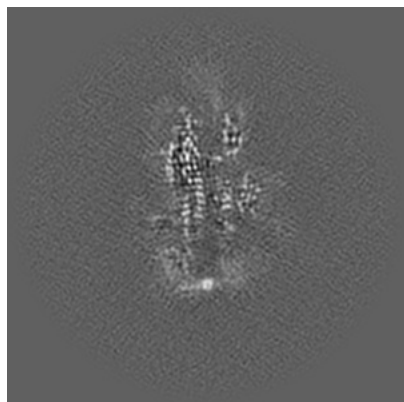


Z

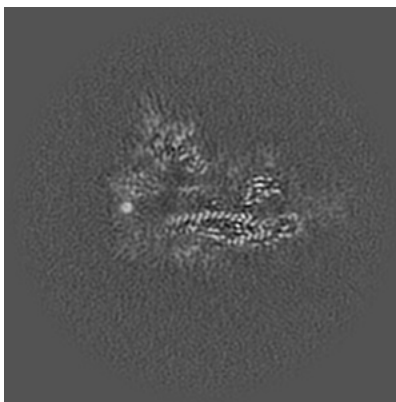
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

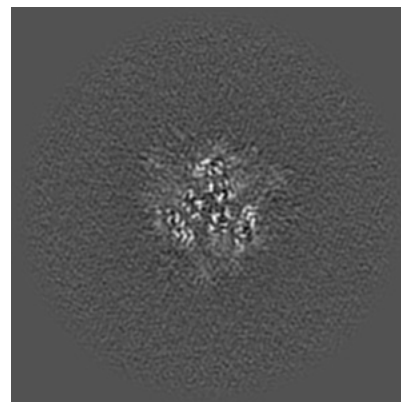
6.2.1 Primary map



X Index: 150

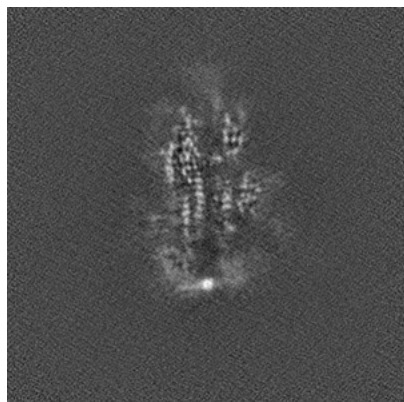


Y Index: 150



Z Index: 150

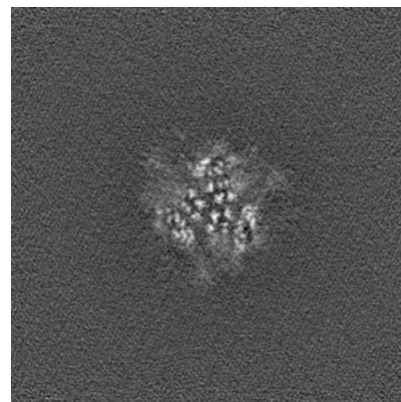
6.2.2 Raw map



X Index: 150



Y Index: 150

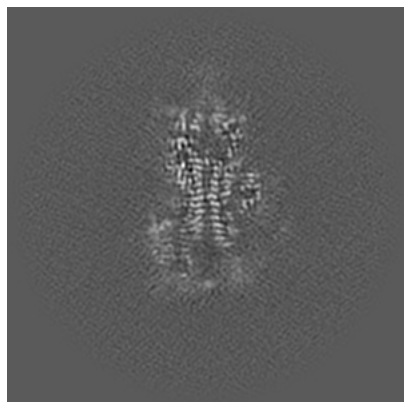


Z Index: 150

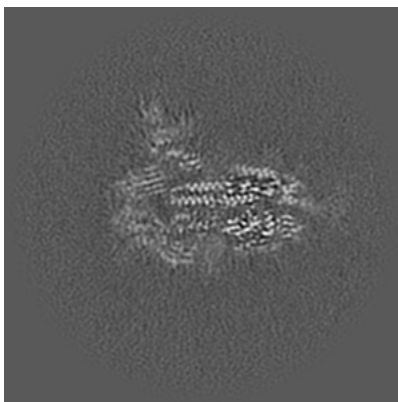
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

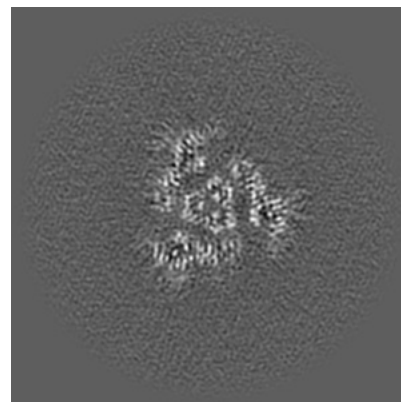
6.3.1 Primary map



X Index: 153

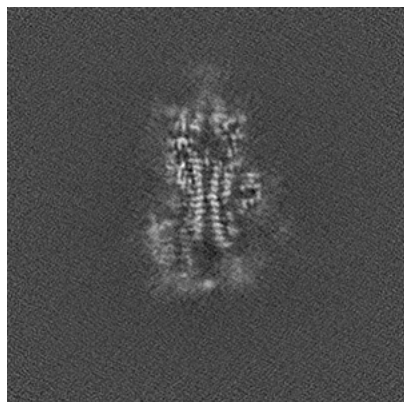


Y Index: 157

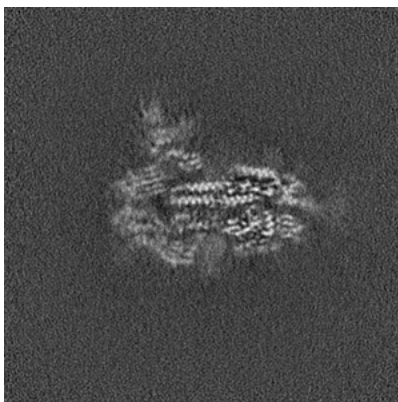


Z Index: 132

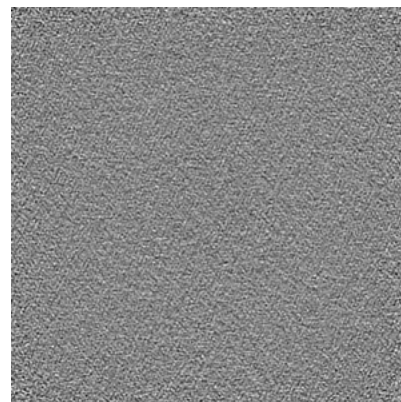
6.3.2 Raw map



X Index: 153



Y Index: 157

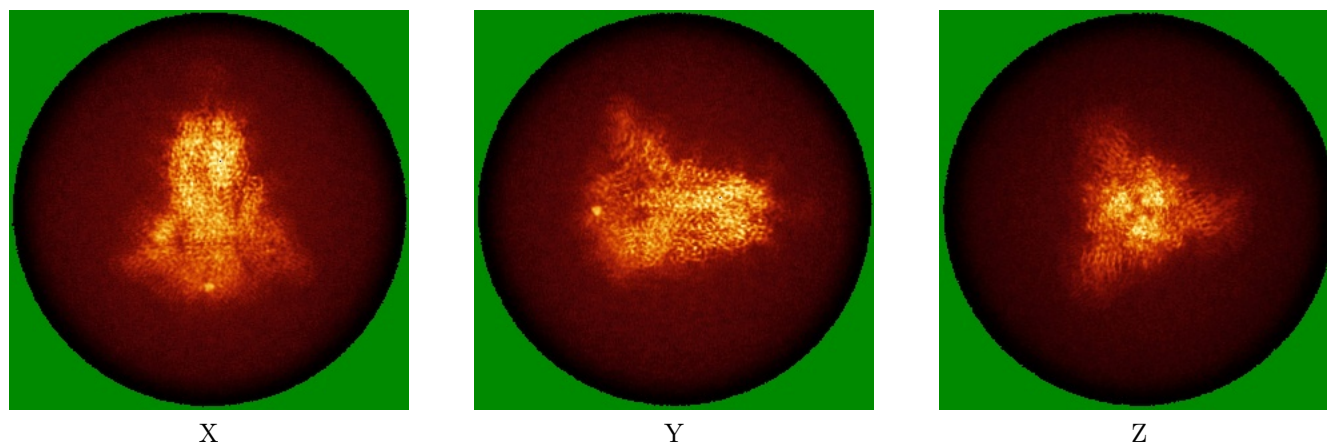


Z Index: 0

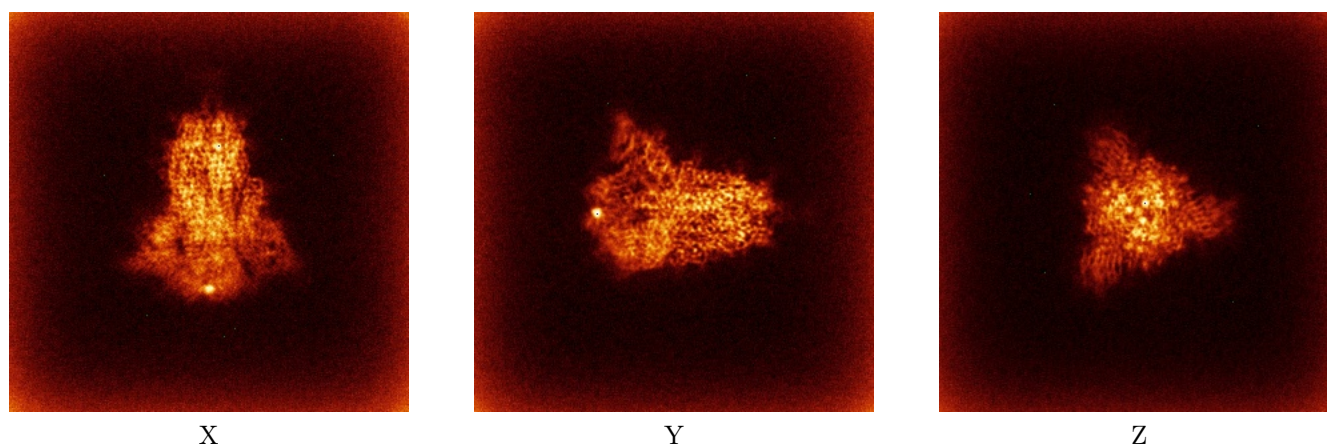
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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.

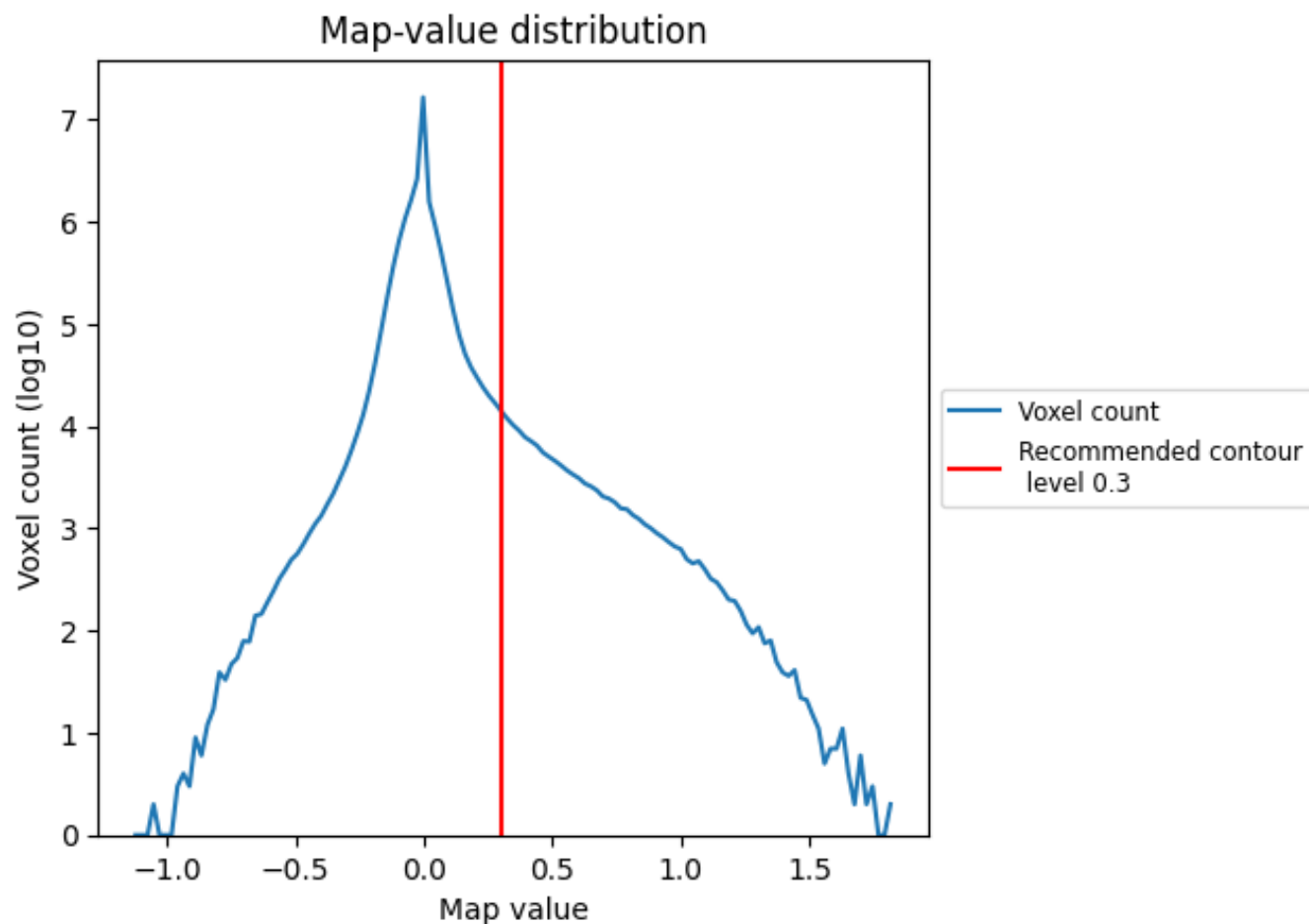
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

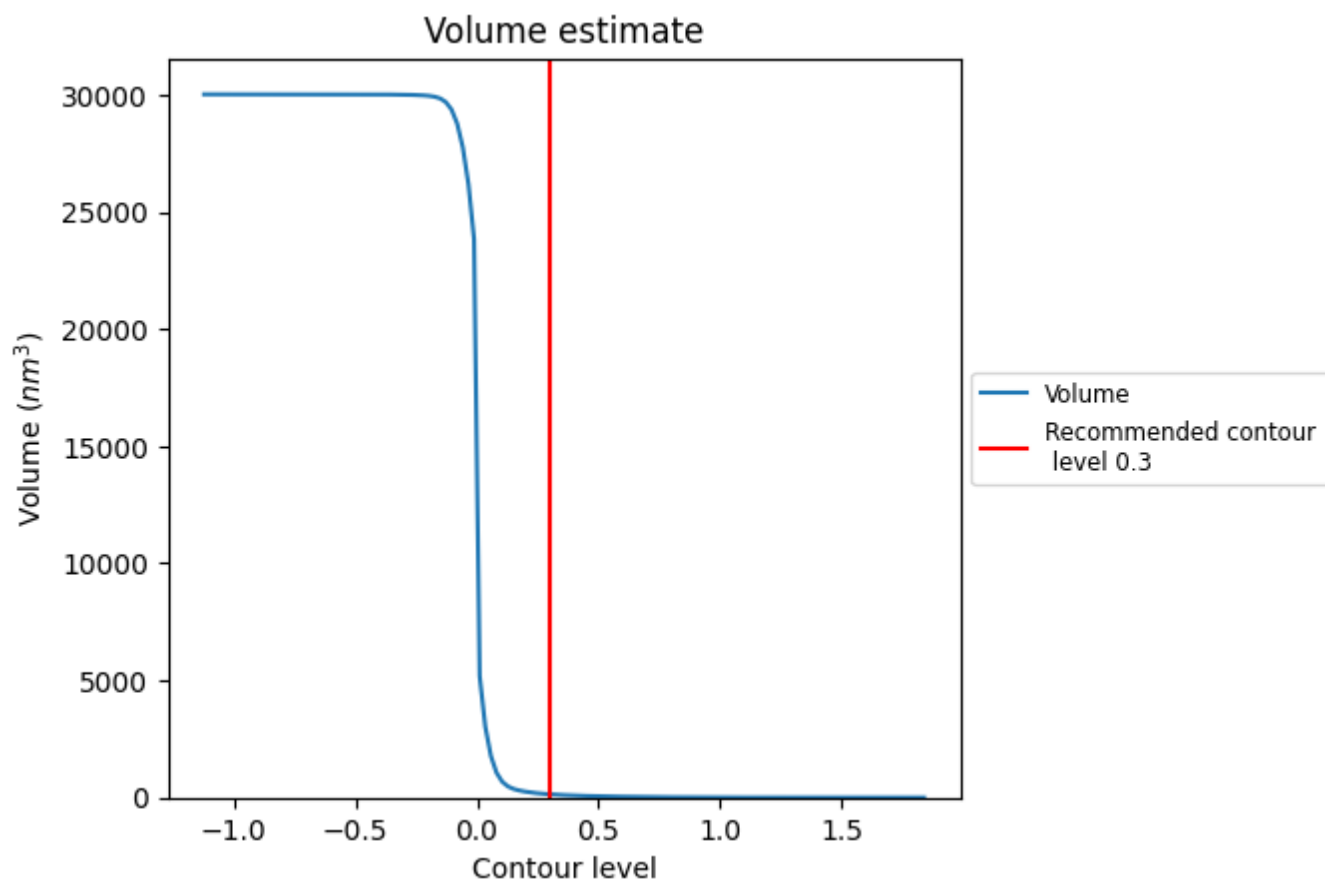
This section contains the results of statistical analysis of the map.

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.

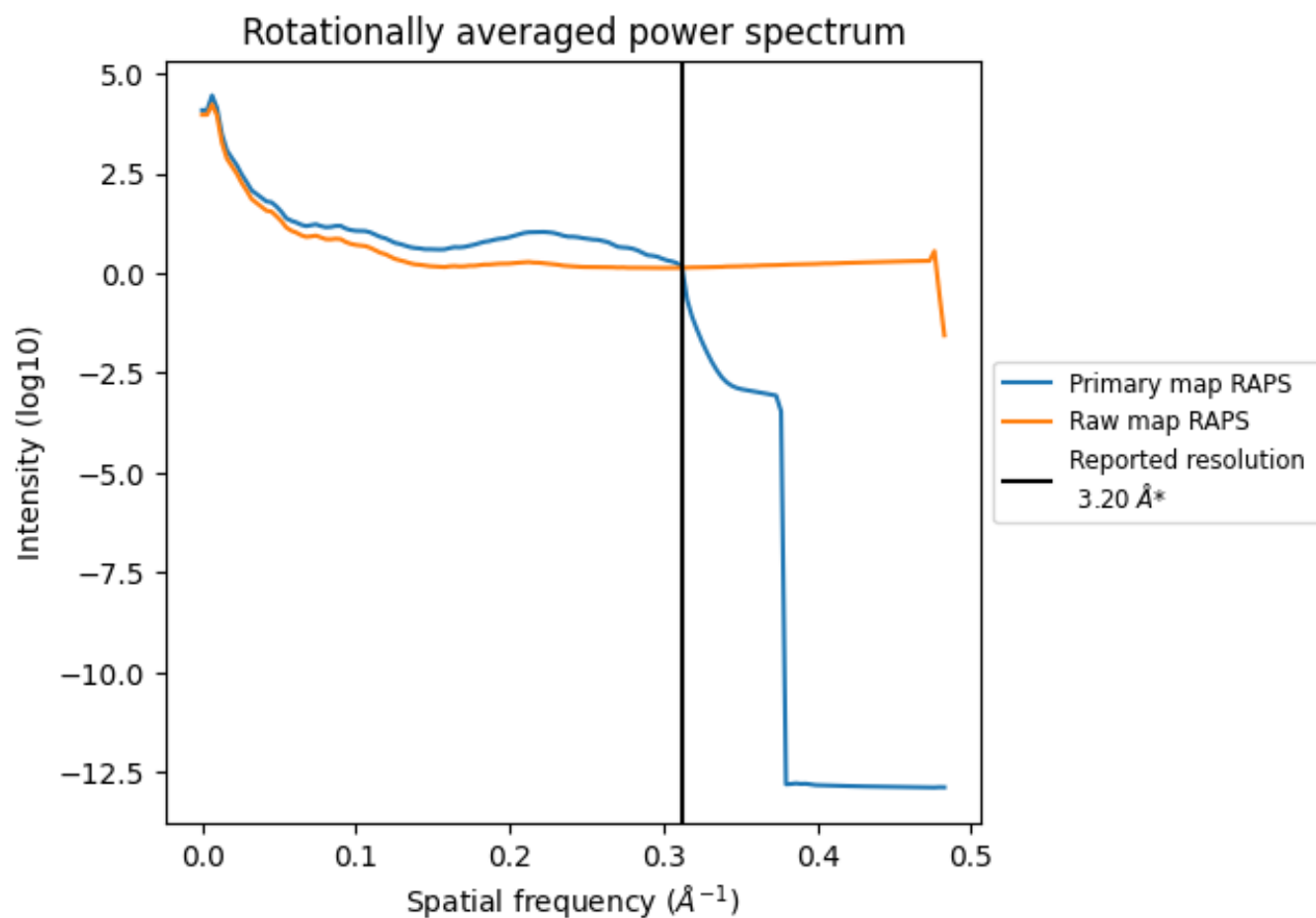
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 139 nm³; this corresponds to an approximate mass of 126 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 ⓘ

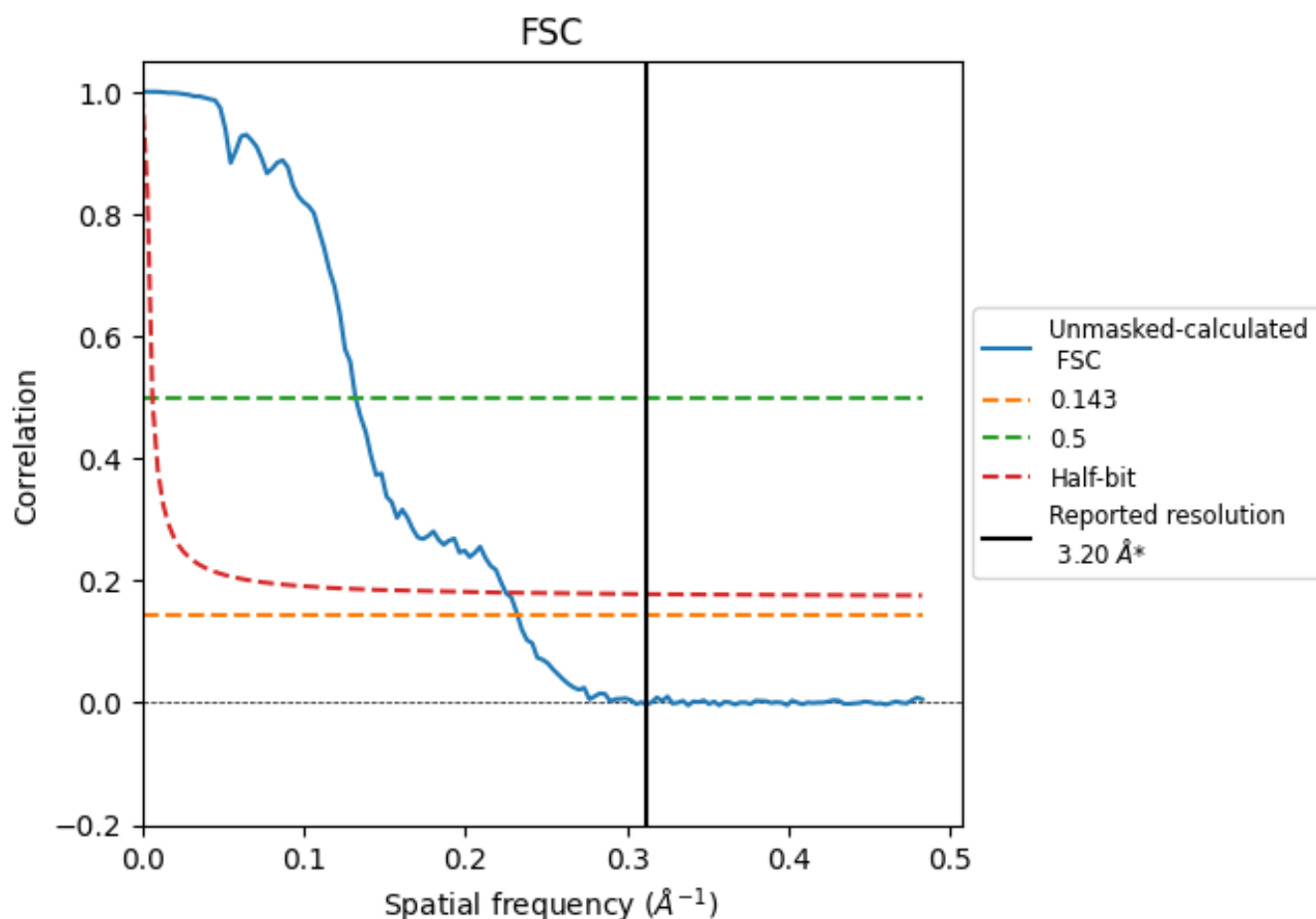


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 Å⁻¹

8.2 Resolution estimates [i](#)

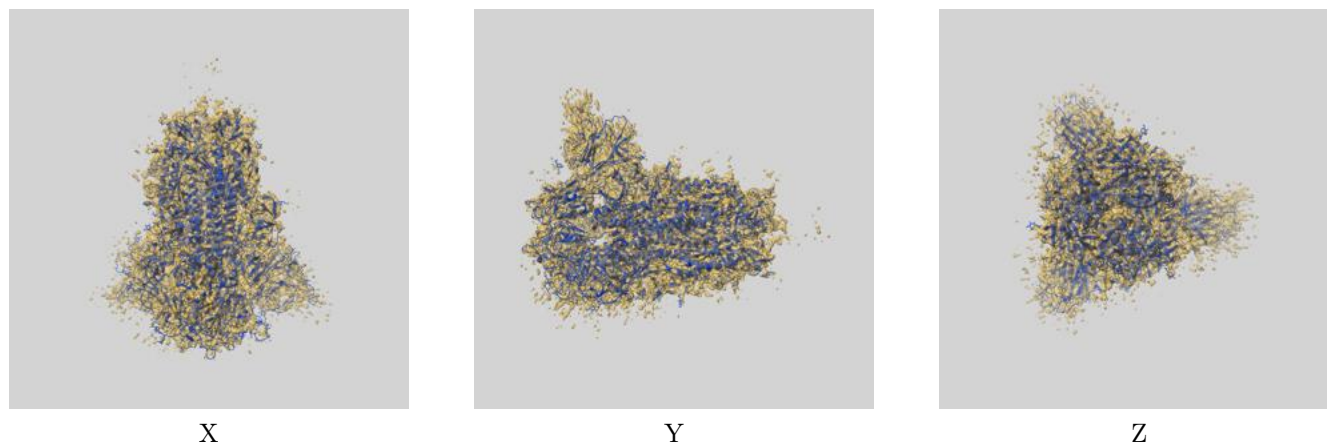
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.31	7.58	4.44

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.31 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

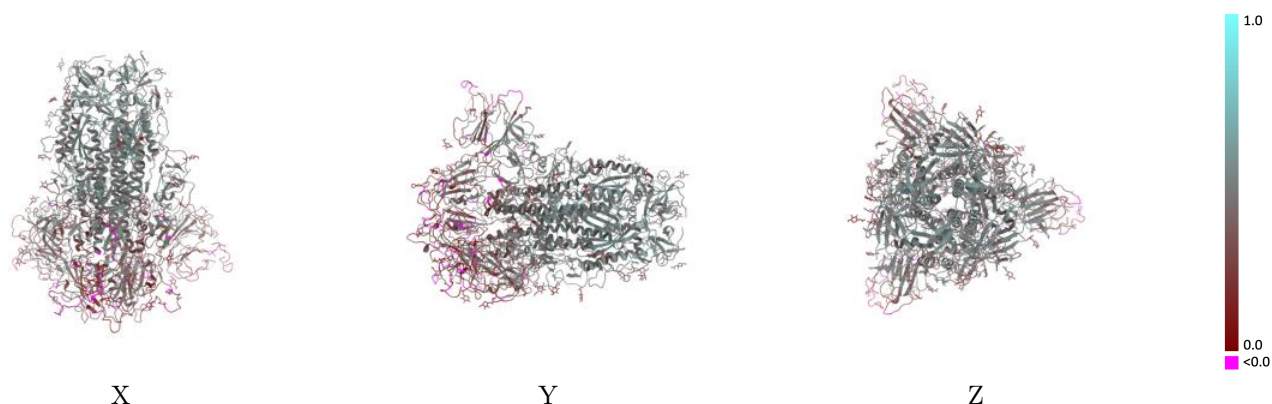
This section contains information regarding the fit between EMDB map EMD-38683 and PDB model 8XUT. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



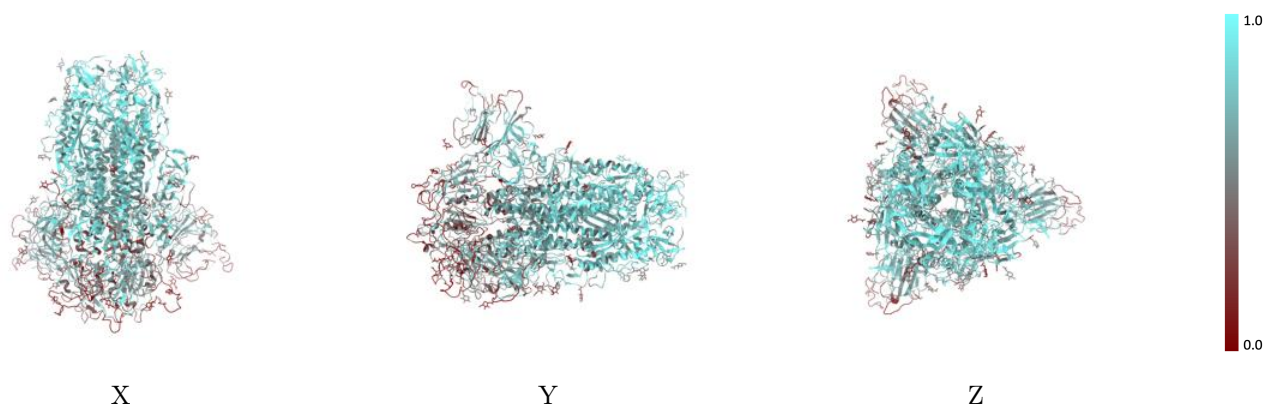
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



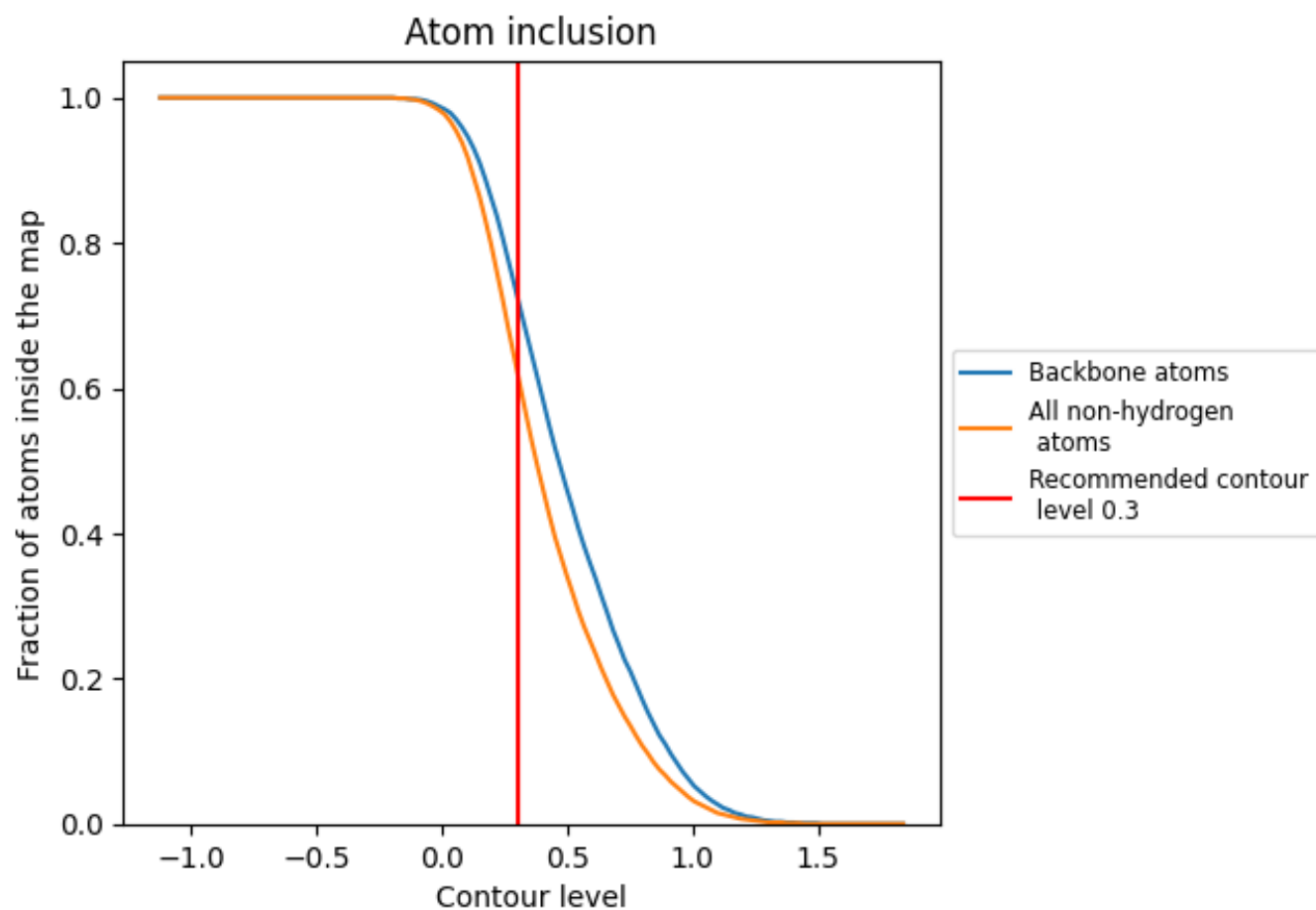
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 73% of all backbone atoms, 62% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6230	0.3980
A	0.6180	0.3930
B	0.6410	0.4040
C	0.6120	0.3960

