



wwPDB EM Validation Summary Report ⓘ

Mar 13, 2026 – 06:46 AM UTC

PDB ID : 7KQB / pdb_00007kqb
EMDB ID : EMD-22993
Title : SARS-CoV-2 spike glycoprotein:Fab 5A6 complex I
Authors : Asarnow, D.; Charles, C.; Cheng, Y.
Deposited on : 2020-11-14
Resolution : 2.42 Å(reported)
Based on initial model : 7A94

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:

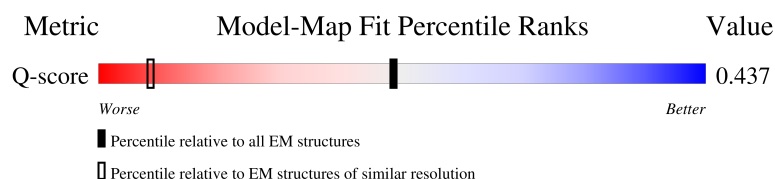
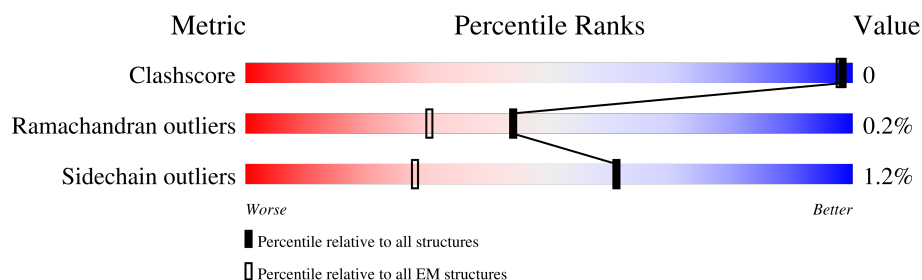
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 2.42 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.



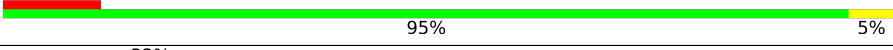
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	5729 (1.92 - 2.92)

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	1208	
1	B	1208	
1	C	1208	
2	H	449	

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Mol	Chain	Length	Quality of chain
2	K	449	
3	J	214	
3	L	214	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 63631 atoms, of which 31416 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	1080	Total	C	H	N	O	S	0	0
			16699	5397	8243	1412	1609	38		
1	B	1079	Total	C	H	N	O	S	0	0
			16677	5390	8232	1409	1608	38		
1	C	1078	Total	C	H	N	O	S	0	0
			16661	5386	8223	1408	1606	38		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	682	GLY	ARG	conflict	UNP P0DTC2
A	683	SER	ARG	conflict	UNP P0DTC2
A	685	SER	ARG	conflict	UNP P0DTC2
A	986	PRO	LYS	conflict	UNP P0DTC2
A	987	PRO	VAL	conflict	UNP P0DTC2
B	682	GLY	ARG	conflict	UNP P0DTC2
B	683	SER	ARG	conflict	UNP P0DTC2
B	685	SER	ARG	conflict	UNP P0DTC2
B	986	PRO	LYS	conflict	UNP P0DTC2
B	987	PRO	VAL	conflict	UNP P0DTC2
C	682	GLY	ARG	conflict	UNP P0DTC2
C	683	SER	ARG	conflict	UNP P0DTC2
C	685	SER	ARG	conflict	UNP P0DTC2
C	986	PRO	LYS	conflict	UNP P0DTC2
C	987	PRO	VAL	conflict	UNP P0DTC2

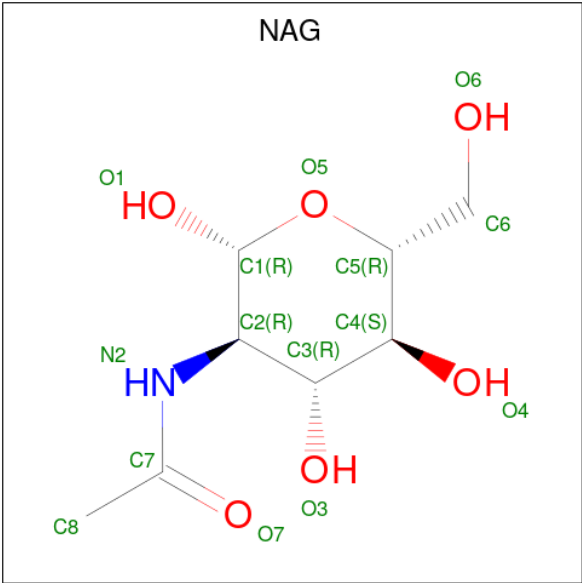
- Molecule 2 is a protein called Fab 5A6 heavy chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	H	220	Total	C	H	N	O	S	0	0
			3257	1034	1612	278	325	8		
2	K	220	Total	C	H	N	O	S	0	0
			3257	1034	1612	278	325	8		

- Molecule 3 is a protein called Fab 5A6 light chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	L	214	Total	C	H	N	O	S	0	0
			3218	1020	1586	274	333	5		
3	J	214	Total	C	H	N	O	S	0	0
			3218	1020	1586	274	333	5		

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



Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	N	O	
4	A	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	A	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	A	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	A	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	A	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	A	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	A	1	Total	C	H	N	O	0
			28	8	14	1	5	

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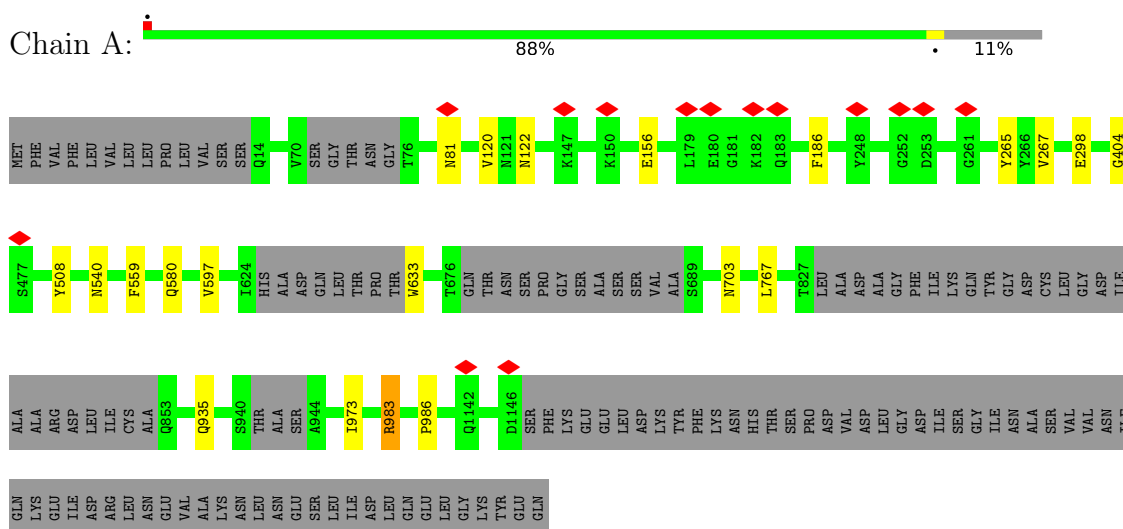
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Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	B	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	B	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	B	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	B	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	B	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	B	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	C	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	C	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	C	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	C	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	C	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	C	1	Total	C	H	N	O	0
			28	8	14	1	5	
4	C	1	Total	C	H	N	O	0
			28	8	14	1	5	

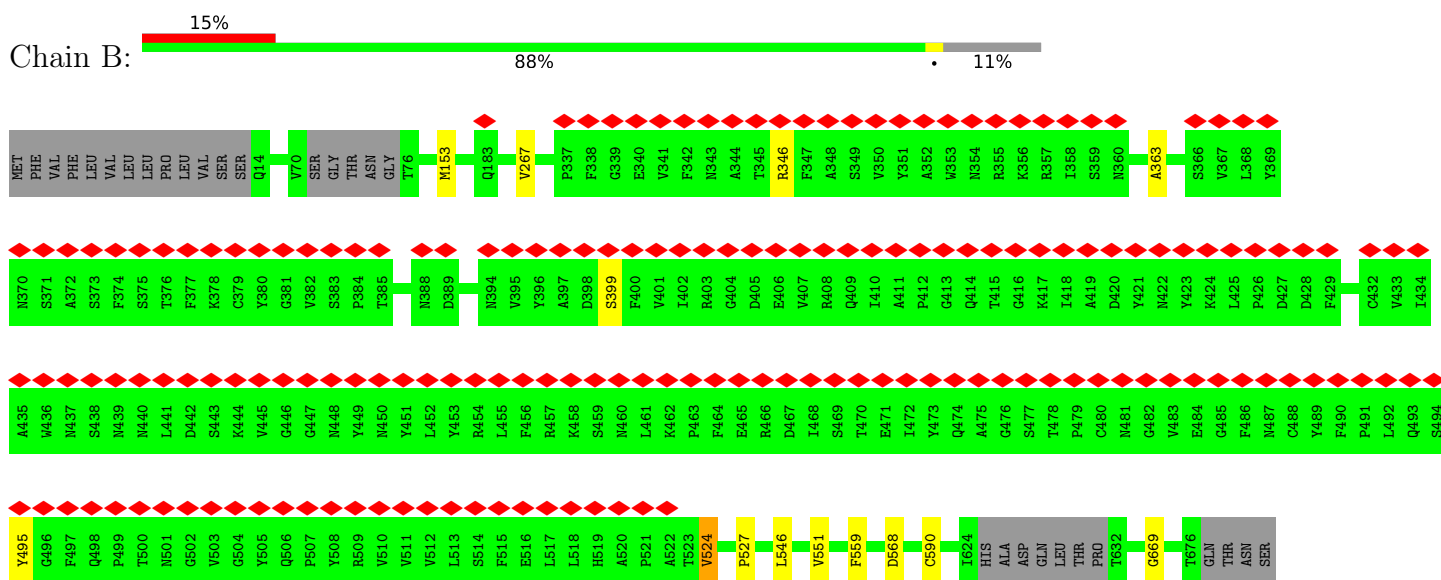
3 Residue-property plots

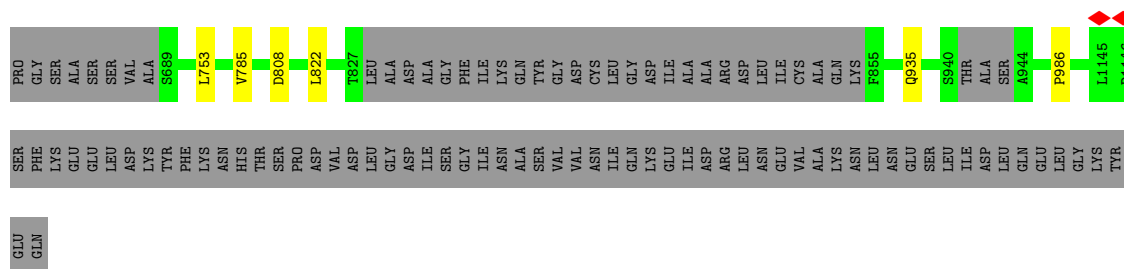
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

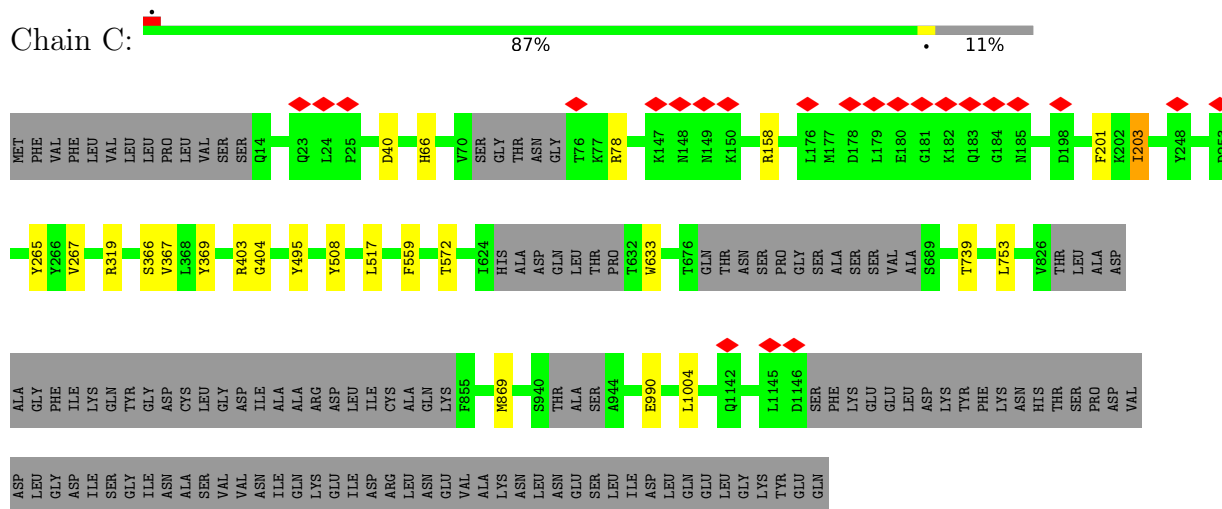


• Molecule 1: Spike glycoprotein

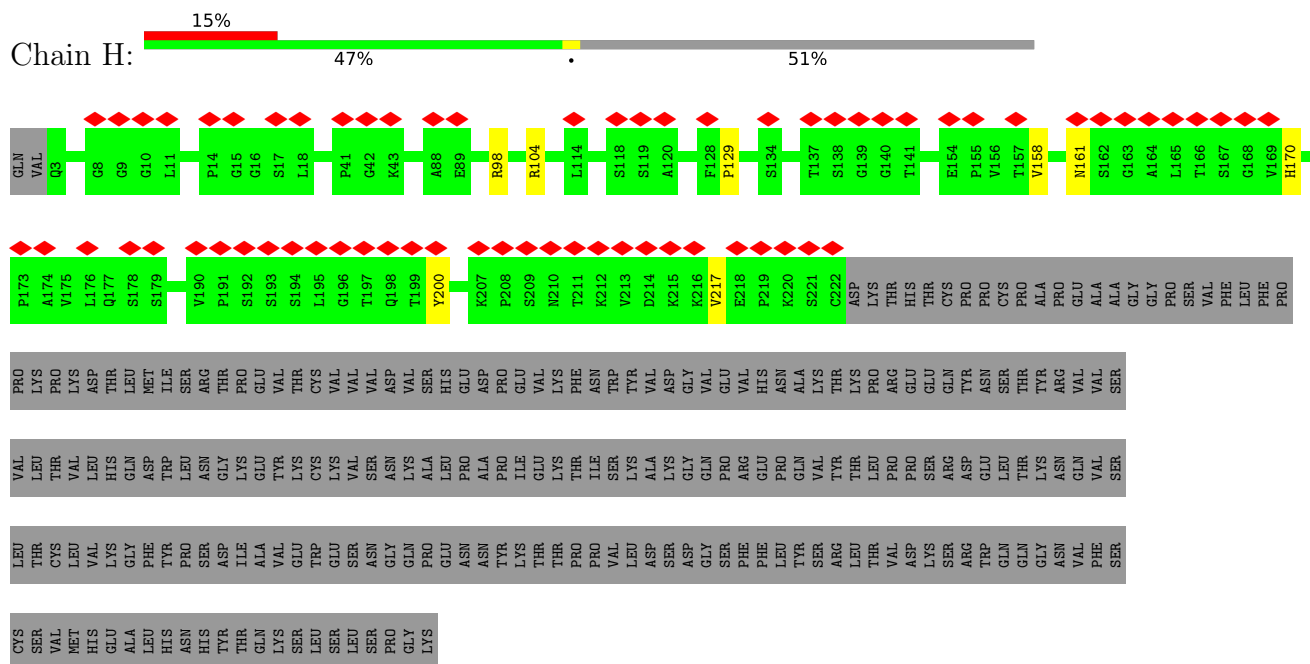




- Molecule 1: Spike glycoprotein

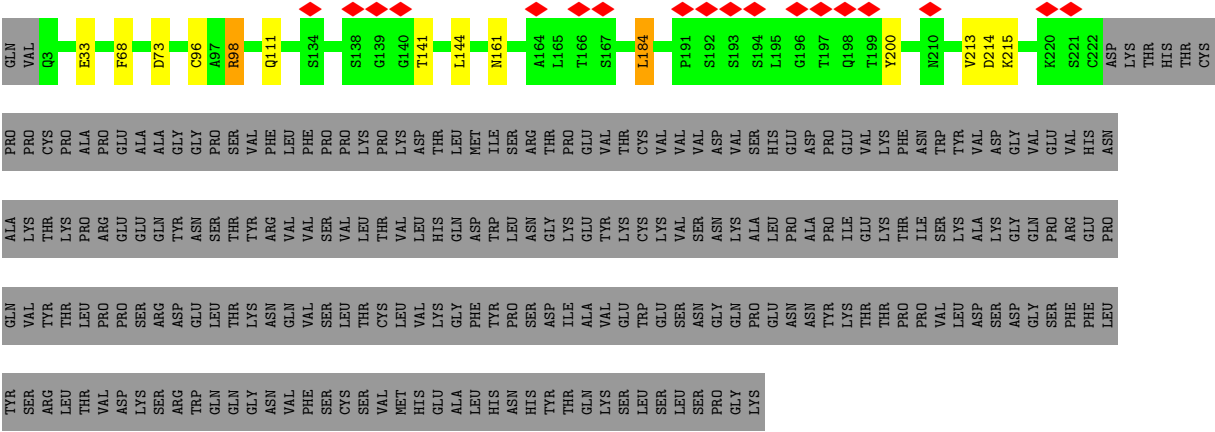


- Molecule 2: Fab 5A6 heavy chain

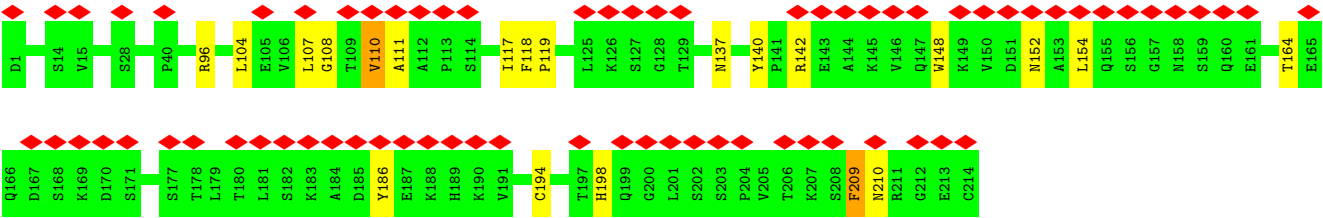
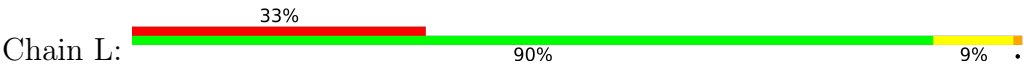


- Molecule 2: Fab 5A6 heavy chain

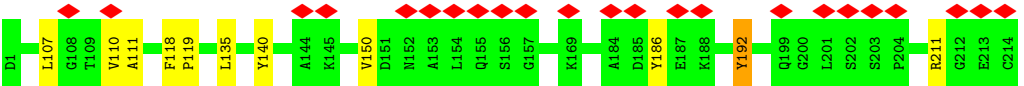
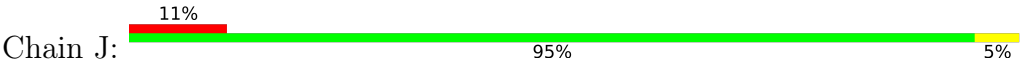




● Molecule 3: Fab 5A6 light chain



● Molecule 3: Fab 5A6 light chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	380163	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 ($e^-/\text{\AA}^2$)	67.7	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.869	Depositor
Minimum map value	-0.563	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.075	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	427.52158, 427.52158, 427.52158	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.18756, 1.18756, 1.18756	Depositor

5 Model quality

5.1 Standard geometry

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	0.71	0/8654	1.20	6/11779 (0.1%)
1	B	0.71	0/8643	1.23	6/11766 (0.1%)
1	C	0.73	0/8636	1.21	3/11756 (0.0%)
2	H	0.72	0/1682	1.30	1/2287 (0.0%)
2	K	0.71	0/1682	1.28	5/2287 (0.2%)
3	J	0.73	0/1667	1.31	2/2263 (0.1%)
3	L	0.74	0/1667	1.32	4/2263 (0.2%)
All	All	0.72	0/32631	1.23	27/44401 (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	3
1	B	0	1
1	C	0	4
2	H	0	1
2	K	0	1
3	J	0	2
3	L	0	2
All	All	0	14

There are no bond length outliers.

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	122	ASN	CA-CB-CG	7.53	120.13	112.60
1	B	559	PHE	CA-CB-CG	6.28	120.08	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	215	LYS	CA-C-N	6.18	129.53	120.82
2	K	215	LYS	C-N-CA	6.18	129.53	120.82
1	B	808	ASP	CA-CB-CG	6.17	118.77	112.60

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	265	TYR	Sidechain
1	A	454	ARG	Sidechain
1	A	983	ARG	Sidechain
1	B	495	TYR	Sidechain
1	C	265	TYR	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	8456	8243	8237	3	0
1	B	8445	8232	8226	4	0
1	C	8438	8223	8217	6	0
2	H	1645	1612	1611	2	0
2	K	1645	1612	1611	2	0
3	J	1632	1586	1586	4	0
3	L	1632	1586	1586	4	0
4	A	126	126	117	0	0
4	B	84	84	78	0	0
4	C	112	112	104	0	0
All	All	32215	31416	31373	21	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.

The worst 5 of 21 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)
3:J:110:VAL:HG22	3:J:111:ALA:H	1.71	0.55
1:C:201:PHE:CD2	1:C:203:ILE:HD11	2.42	0.55
1:A:983:ARG:HD3	1:C:517:LEU:HD13	1.90	0.52
3:L:110:VAL:HG22	3:L:111:ALA:H	1.74	0.51
3:L:148:TRP:CZ3	3:L:194:CYS:SG	3.07	0.47

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	1068/1208 (88%)	1027 (96%)	41 (4%)	0	100	100
1	B	1067/1208 (88%)	1004 (94%)	61 (6%)	2 (0%)	43	57
1	C	1066/1208 (88%)	1016 (95%)	49 (5%)	1 (0%)	48	63
2	H	218/449 (49%)	202 (93%)	15 (7%)	1 (0%)	24	35
2	K	218/449 (49%)	206 (94%)	12 (6%)	0	100	100
3	J	212/214 (99%)	192 (91%)	20 (9%)	0	100	100
3	L	212/214 (99%)	188 (89%)	19 (9%)	5 (2%)	4	4
All	All	4061/4950 (82%)	3835 (94%)	217 (5%)	9 (0%)	44	57

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	633	TRP
3	L	108	GLY
3	L	110	VAL
3	L	107	LEU
1	B	527	PRO

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	945/1053 (90%)	933 (99%)	12 (1%)	61	78
1	B	944/1053 (90%)	938 (99%)	6 (1%)	78	88
1	C	943/1053 (90%)	933 (99%)	10 (1%)	65	81
2	H	184/394 (47%)	182 (99%)	2 (1%)	65	81
2	K	184/394 (47%)	176 (96%)	8 (4%)	26	42
3	J	187/187 (100%)	186 (100%)	1 (0%)	81	90
3	L	187/187 (100%)	182 (97%)	5 (3%)	39	60
All	All	3574/4321 (83%)	3530 (99%)	44 (1%)	61	79

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	158	VAL
2	K	33	GLU
2	H	161	ASN
3	L	154	LEU
2	K	111	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	949	GLN
1	C	969	ASN
3	L	38	GLN
1	B	613	GLN
1	B	606	ASN

5.3.3 RNA ⓘ

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](#)

23 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	C	1307	1	14,14,15	1.08	1 (7%)	17,19,21	0.98	1 (5%)
4	NAG	A	1306	1	14,14,15	1.15	1 (7%)	17,19,21	0.66	0
4	NAG	C	1301	1	14,14,15	1.30	2 (14%)	17,19,21	0.91	0
4	NAG	A	1303	1	14,14,15	1.26	2 (14%)	17,19,21	1.16	2 (11%)
4	NAG	C	1304	1	14,14,15	1.21	1 (7%)	17,19,21	0.98	1 (5%)
4	NAG	A	1308	1	14,14,15	1.12	1 (7%)	17,19,21	1.04	2 (11%)
4	NAG	A	1301	1	14,14,15	1.24	2 (14%)	17,19,21	0.90	1 (5%)
4	NAG	C	1303	1	14,14,15	1.05	1 (7%)	17,19,21	1.11	2 (11%)
4	NAG	A	1302	1	14,14,15	1.21	1 (7%)	17,19,21	0.61	0
4	NAG	B	1303	1	14,14,15	1.27	2 (14%)	17,19,21	0.89	1 (5%)
4	NAG	B	1302	1	14,14,15	1.21	1 (7%)	17,19,21	0.97	1 (5%)
4	NAG	A	1305	1	14,14,15	0.92	0	17,19,21	1.18	1 (5%)
4	NAG	A	1304	1	14,14,15	0.92	1 (7%)	17,19,21	0.88	1 (5%)
4	NAG	C	1302	1	14,14,15	1.26	1 (7%)	17,19,21	0.87	1 (5%)
4	NAG	B	1304	1	14,14,15	1.12	1 (7%)	17,19,21	0.51	0
4	NAG	B	1301	1	14,14,15	1.31	2 (14%)	17,19,21	0.77	0
4	NAG	B	1306	1	14,14,15	1.22	1 (7%)	17,19,21	0.89	1 (5%)
4	NAG	C	1305	1	14,14,15	1.03	1 (7%)	17,19,21	0.94	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	B	1305	1	14,14,15	1.07	1 (7%)	17,19,21	1.10	1 (5%)
4	NAG	C	1306	1	14,14,15	1.22	1 (7%)	17,19,21	0.93	1 (5%)
4	NAG	A	1307	1	14,14,15	1.04	1 (7%)	17,19,21	0.96	1 (5%)
4	NAG	C	1308	1	14,14,15	1.20	1 (7%)	17,19,21	0.96	1 (5%)
4	NAG	A	1309	1	14,14,15	1.22	1 (7%)	17,19,21	0.96	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	C	1307	1	-	1/6/23/26	0/1/1/1
4	NAG	A	1306	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1301	1	-	3/6/23/26	0/1/1/1
4	NAG	A	1303	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1304	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1308	1	-	1/6/23/26	0/1/1/1
4	NAG	A	1301	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1303	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1302	1	-	1/6/23/26	0/1/1/1
4	NAG	B	1303	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1302	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1305	1	-	1/6/23/26	0/1/1/1
4	NAG	A	1304	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1302	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1304	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1306	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1305	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1305	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1306	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1307	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1308	1	-	0/6/23/26	0/1/1/1
4	NAG	A	1309	1	-	0/6/23/26	0/1/1/1

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1302	NAG	O5-C5	2.89	1.49	1.43

Continued on next page...

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1306	NAG	O5-C5	2.87	1.49	1.43
4	C	1304	NAG	O5-C5	2.79	1.48	1.43
4	C	1308	NAG	O5-C5	2.78	1.48	1.43
4	B	1303	NAG	O5-C5	2.77	1.48	1.43

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1305	NAG	C1-O5-C5	3.76	117.22	112.19
4	C	1307	NAG	C1-O5-C5	3.25	116.54	112.19
4	C	1308	NAG	C1-O5-C5	3.19	116.46	112.19
4	C	1306	NAG	C1-O5-C5	3.18	116.45	112.19
4	B	1302	NAG	C1-O5-C5	3.16	116.42	112.19

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1301	NAG	C1-C2-N2-C7
4	C	1301	NAG	C1-C2-N2-C7
4	A	1308	NAG	O5-C5-C6-O6
4	C	1307	NAG	O5-C5-C6-O6
4	C	1301	NAG	O5-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.

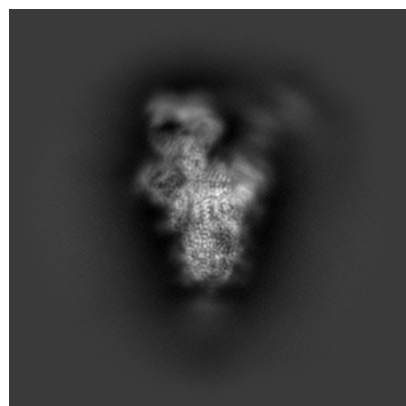
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22993. These allow visual inspection of the internal detail of the map and identification of artifacts.

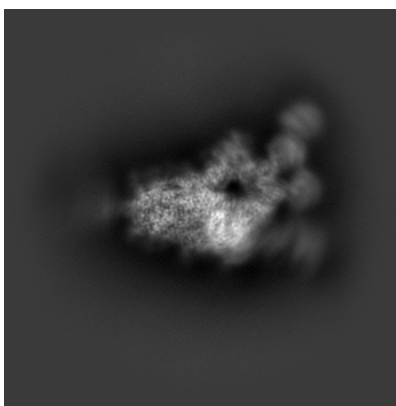
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

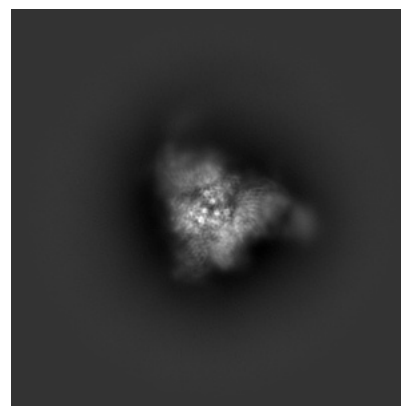
6.1.1 Primary map



X

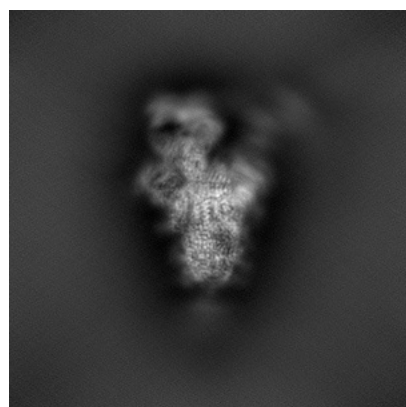


Y

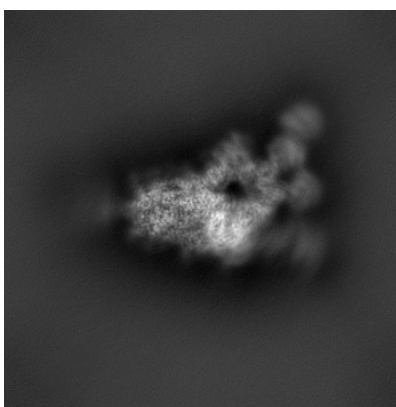


Z

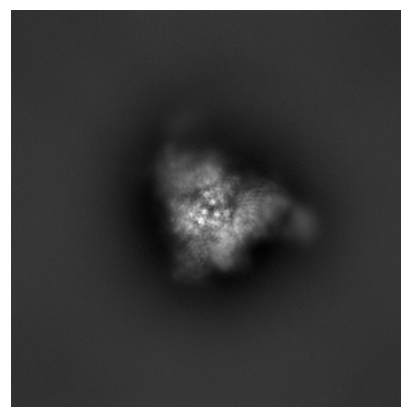
6.1.2 Raw map



X



Y

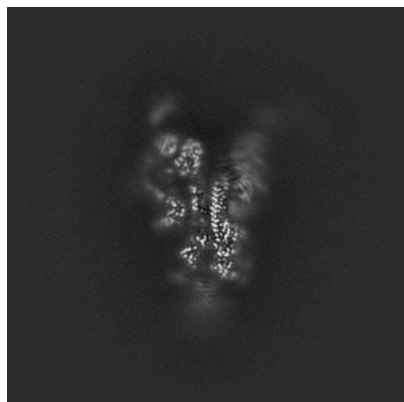


Z

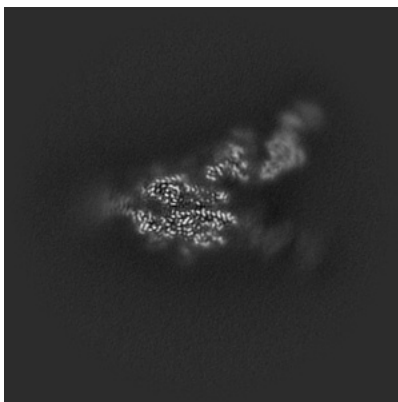
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

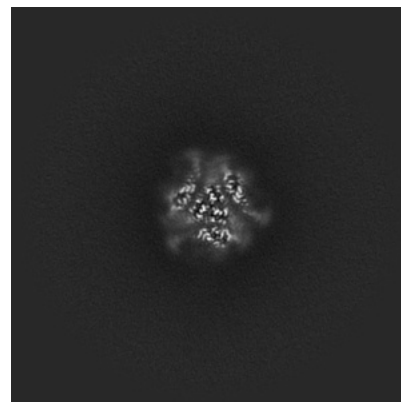
6.2.1 Primary map



X Index: 180

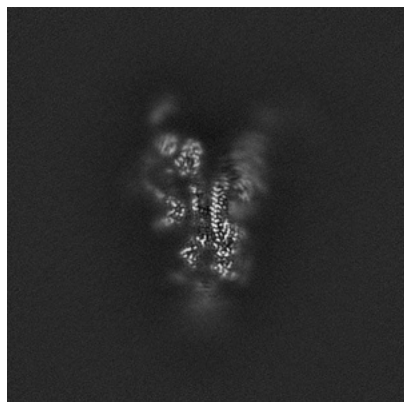


Y Index: 180

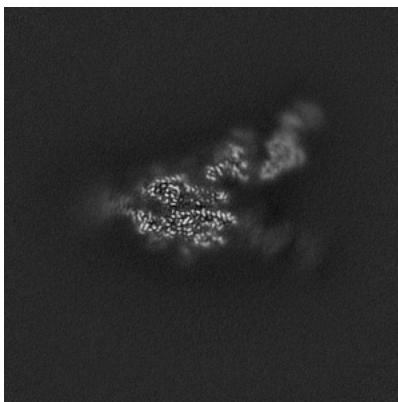


Z Index: 180

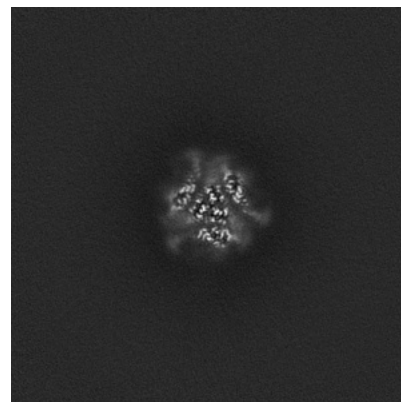
6.2.2 Raw map



X Index: 180



Y Index: 180

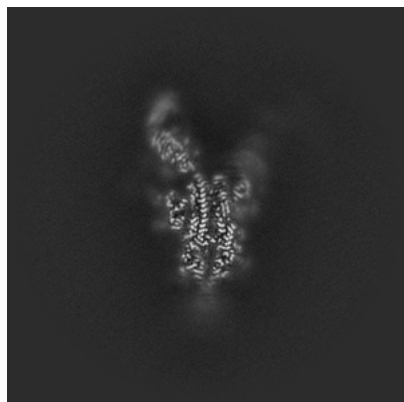


Z Index: 180

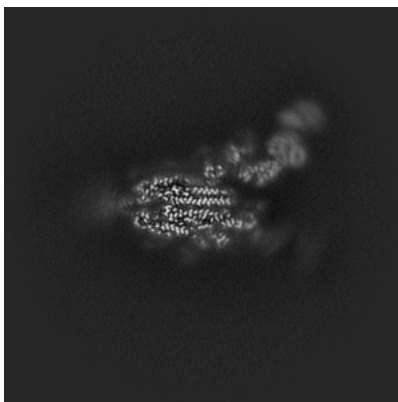
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

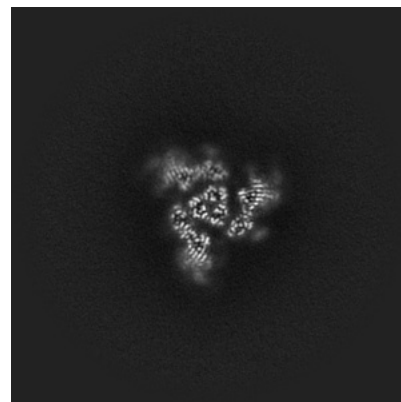
6.3.1 Primary map



X Index: 186

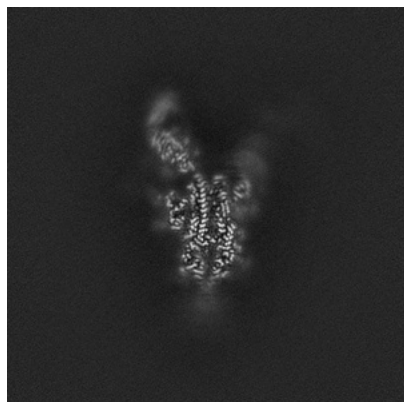


Y Index: 176

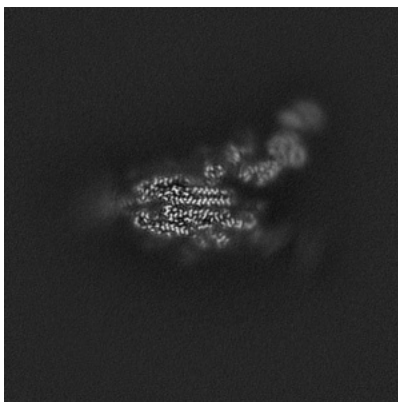


Z Index: 196

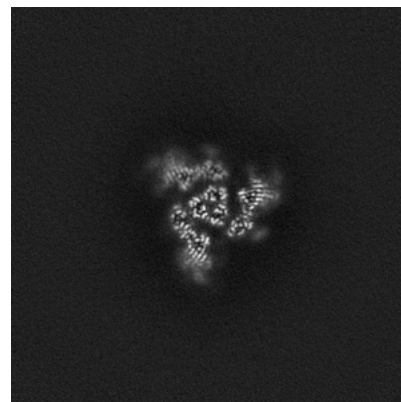
6.3.2 Raw map



X Index: 186



Y Index: 176

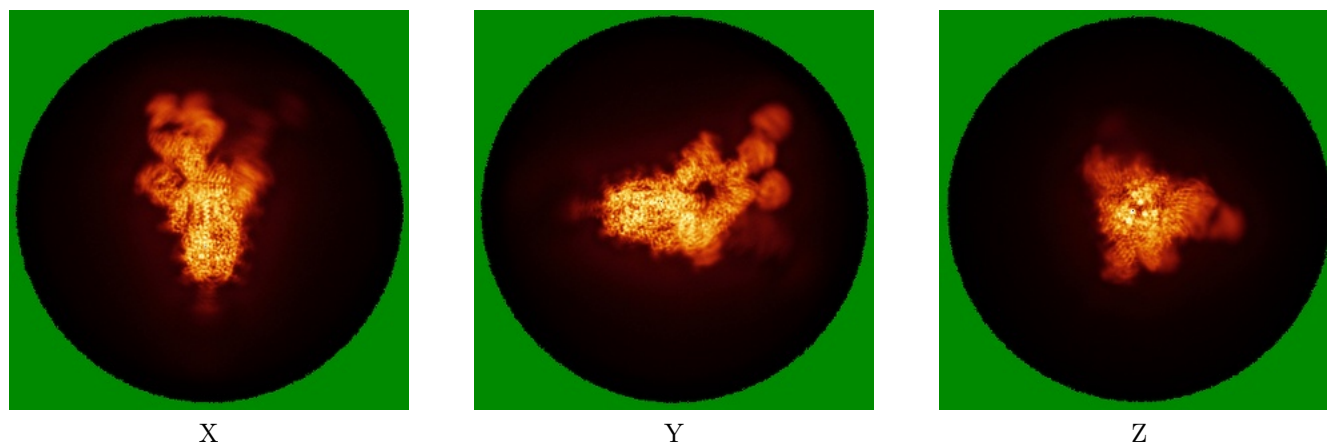


Z Index: 196

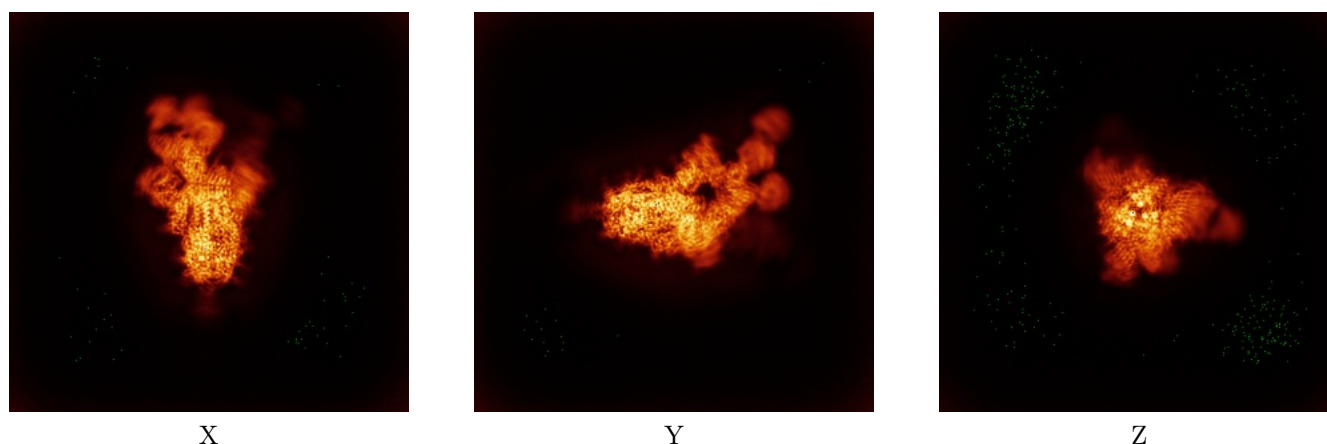
The images above show the largest variance slices of the map in three orthogonal directions.

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.

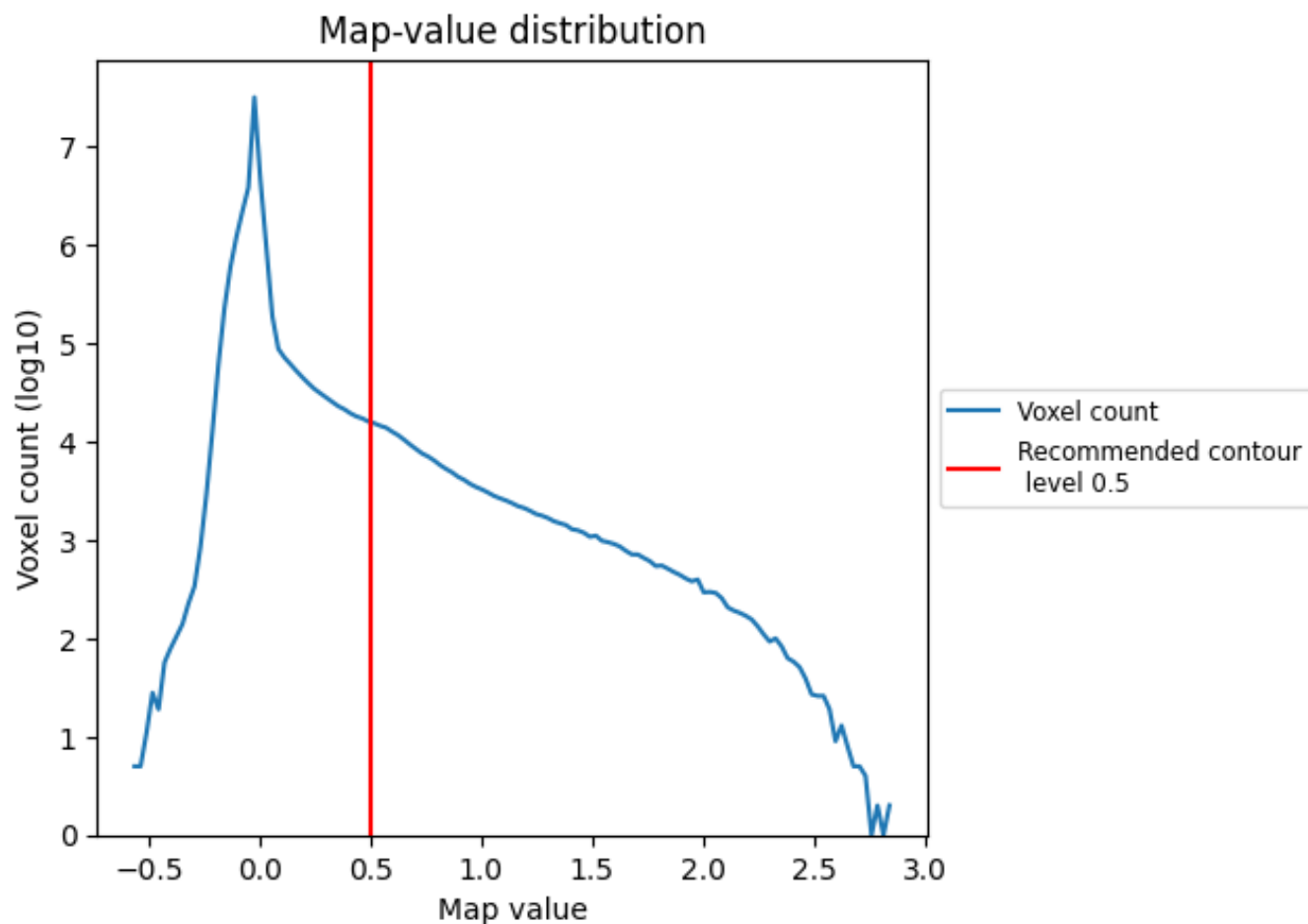
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

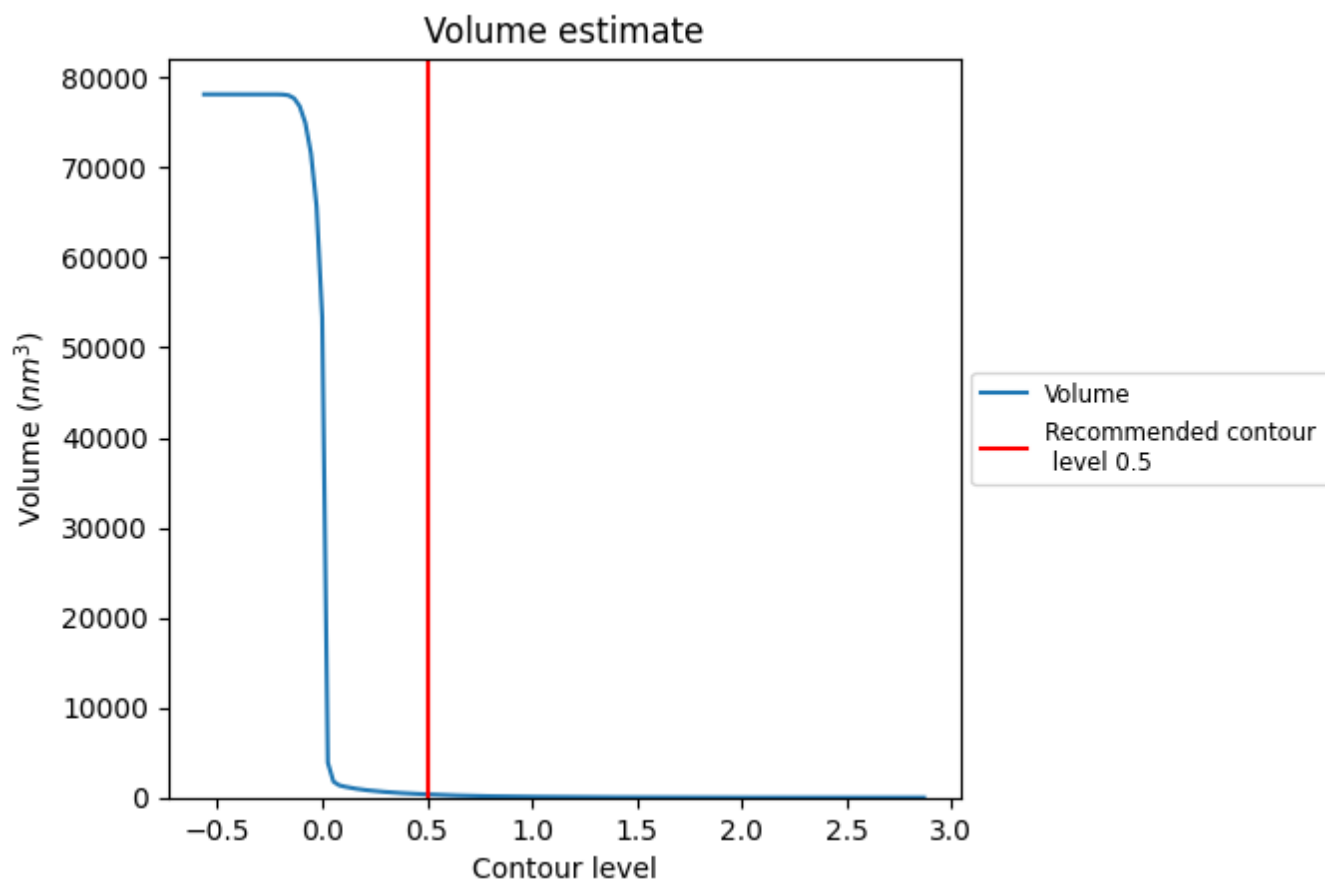
This section contains the results of statistical analysis of the map.

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.

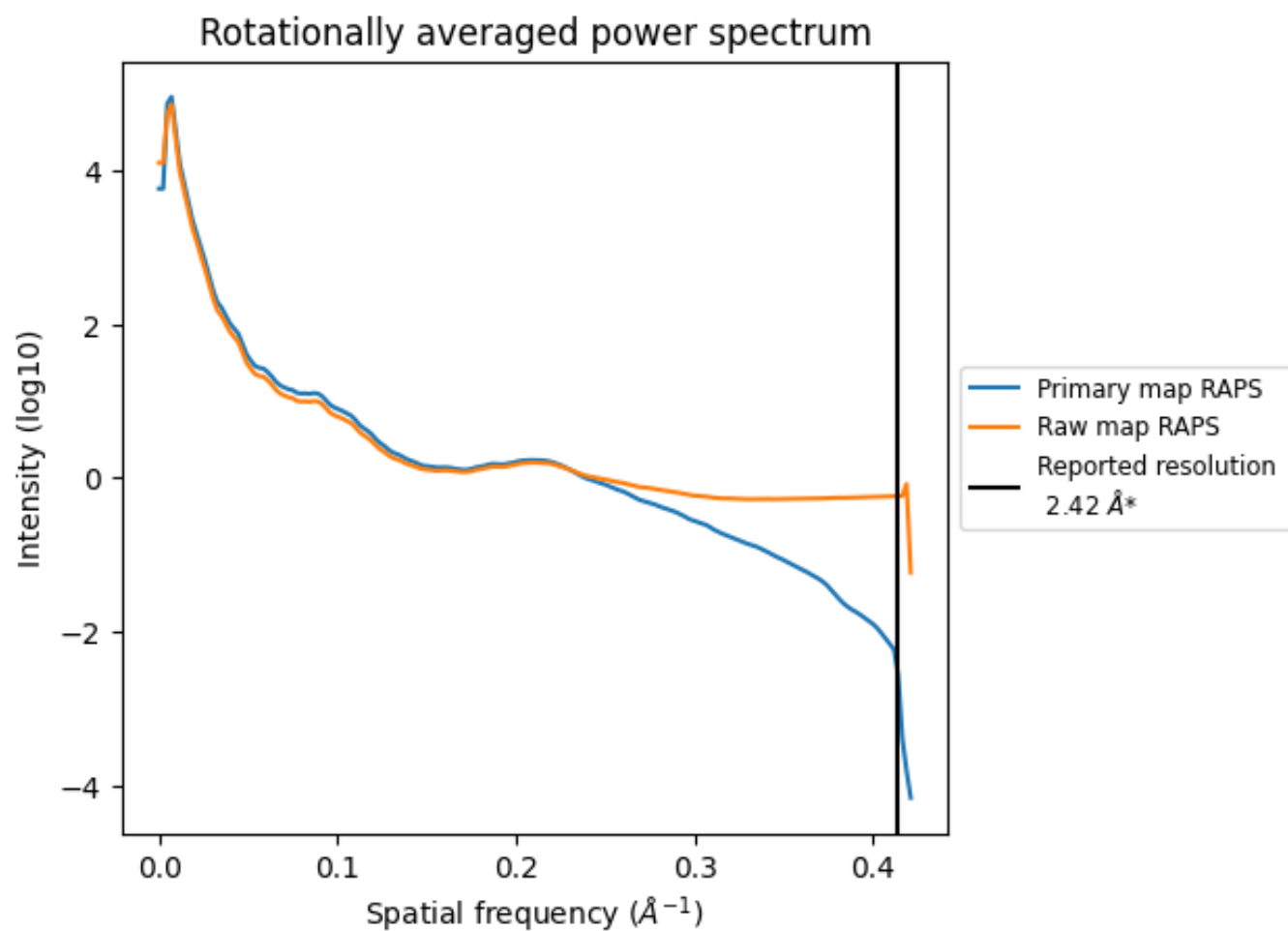
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 356 nm^3 ; this corresponds to an approximate mass of 321 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 ⓘ

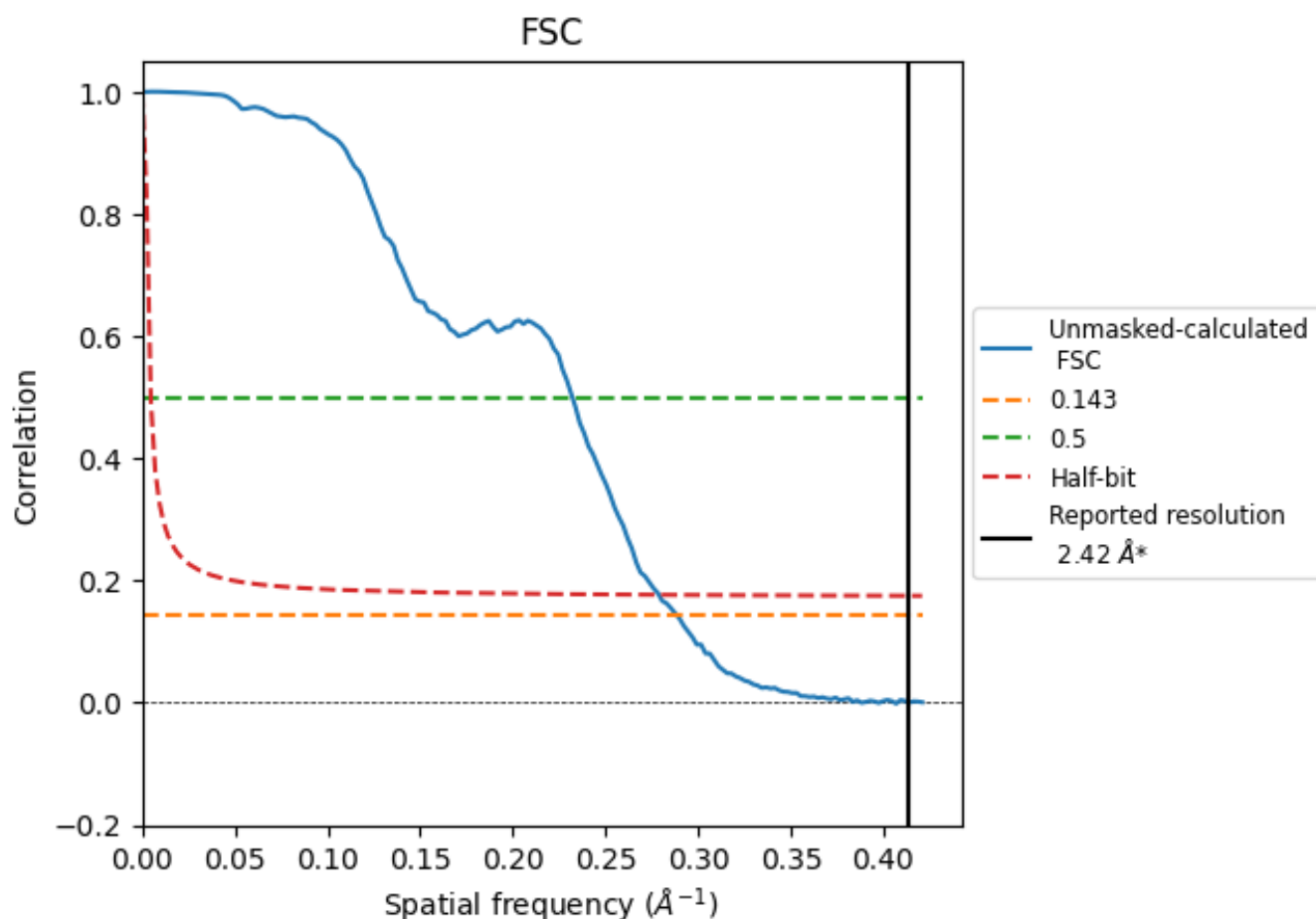


*Reported resolution corresponds to spatial frequency of 0.413 Å⁻¹

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 $0.413 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

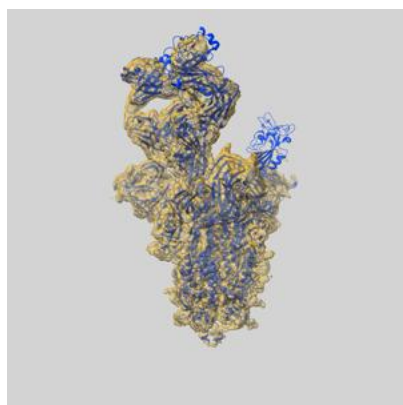
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.42	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.47	4.31	3.59

*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 3.47 differs from the reported value 2.42 by more than 10 %

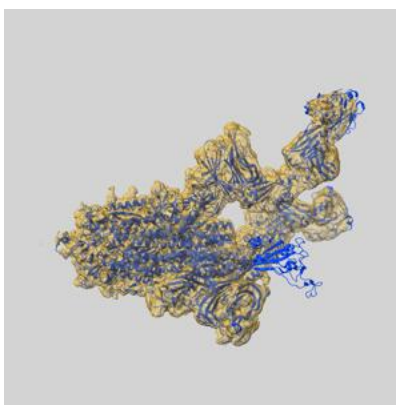
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22993 and PDB model 7KQB. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

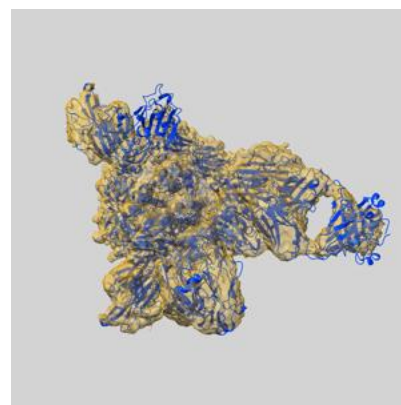
9.1 Map-model overlay [i](#)



X



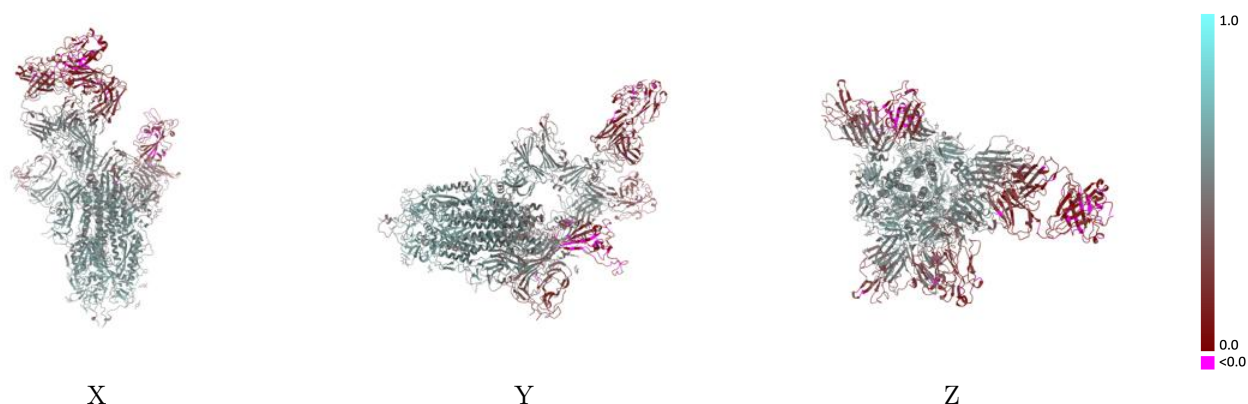
Y



Z

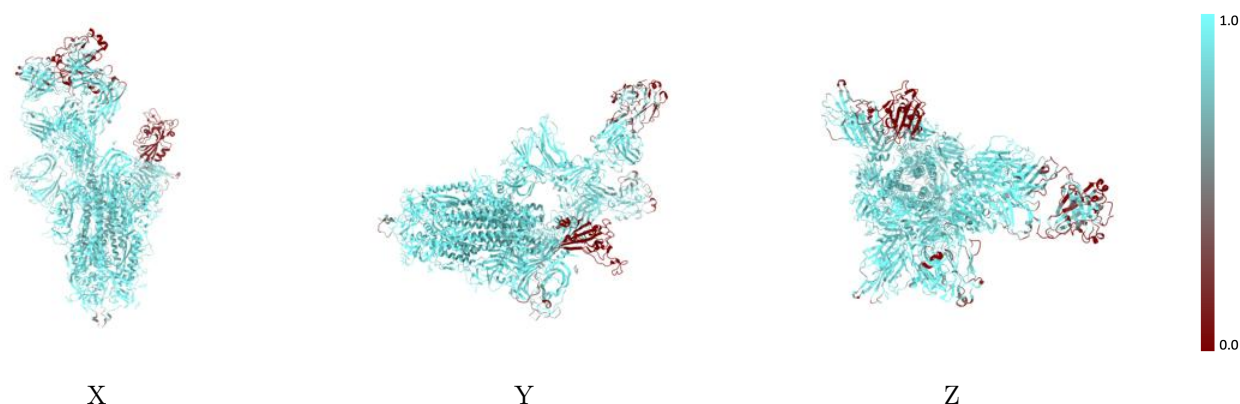
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



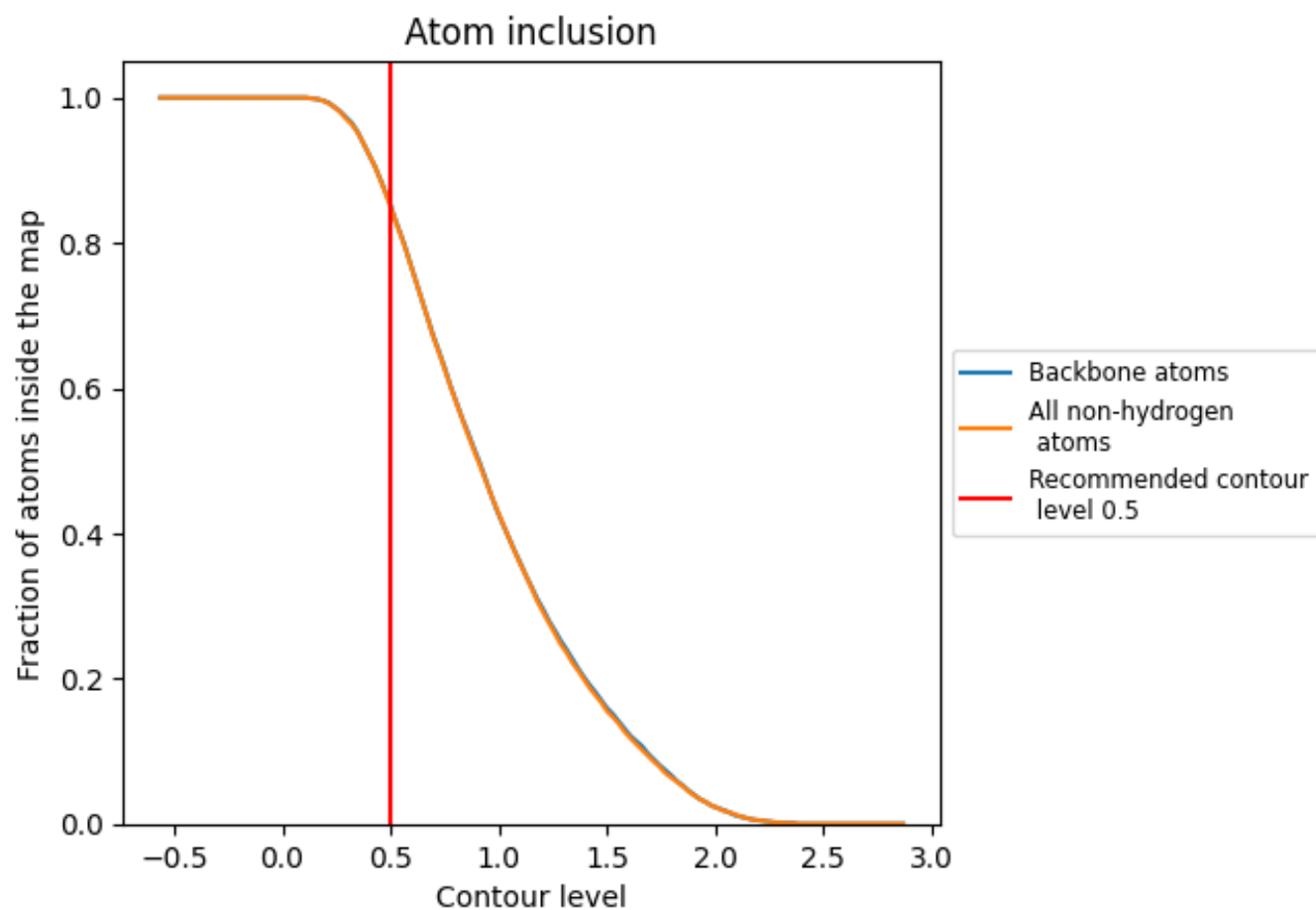
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 85% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8510	0.4370
A	0.9390	0.5100
B	0.7930	0.4460
C	0.9240	0.4950
H	0.6660	0.1730
J	0.8280	0.3340
K	0.8780	0.3600
L	0.6060	0.1500

1.0

0.0

<0.0