



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 11:01 AM UTC

PDB ID : 7K8Y / pdb_00007k8y
EMDB ID : EMD-22735
Title : Structure of the SARS-CoV-2 S 2P trimer in complex with the human neutralizing antibody Fab fragment, C121 (State 2)
Authors : Abernathy, M.E.; Barnes, C.O.; Bjorkman, P.J.
Deposited on : 2020-09-27
Resolution : 4.40 Å (reported)
Based on initial models : 6VXX, 6W41

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

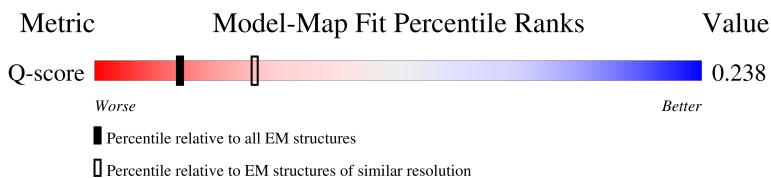
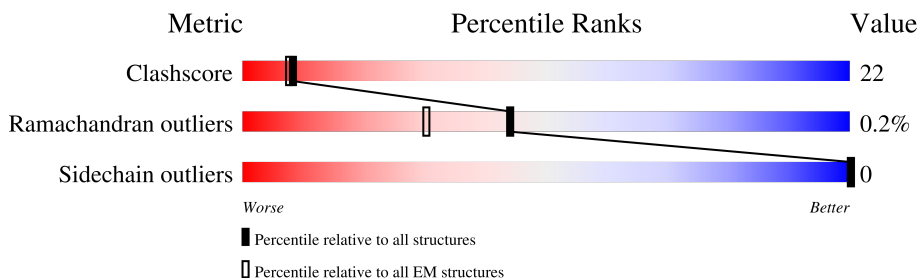
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 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	3132 (3.91 - 4.90)

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	B	1259	
1	D	1259	
1	E	1259	
2	G	241	

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Mol	Chain	Length	Quality of chain
3	I	216	14% 29% 20% 37%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 25560 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	1002	Total	C	N	O	S	0	0
			7823	4996	1300	1492	35		
1	D	1002	Total	C	N	O	S	0	0
			7823	4996	1300	1492	35		
1	E	1002	Total	C	N	O	S	0	0
			7823	4996	1300	1492	35		

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	986	PRO	LYS	conflict	UNP P0DTC2
B	987	PRO	VAL	conflict	UNP P0DTC2
B	1214	SER	-	expression tag	UNP P0DTC2
B	1215	GLY	-	expression tag	UNP P0DTC2
B	1216	ARG	-	expression tag	UNP P0DTC2
B	1217	LEU	-	expression tag	UNP P0DTC2
B	1218	VAL	-	expression tag	UNP P0DTC2
B	1219	PRO	-	expression tag	UNP P0DTC2
B	1220	ARG	-	expression tag	UNP P0DTC2
B	1221	GLY	-	expression tag	UNP P0DTC2
B	1222	SER	-	expression tag	UNP P0DTC2
B	1223	PRO	-	expression tag	UNP P0DTC2
B	1224	GLY	-	expression tag	UNP P0DTC2
B	1225	SER	-	expression tag	UNP P0DTC2
B	1226	GLY	-	expression tag	UNP P0DTC2
B	1227	TYR	-	expression tag	UNP P0DTC2
B	1228	ILE	-	expression tag	UNP P0DTC2
B	1229	PRO	-	expression tag	UNP P0DTC2
B	1230	GLU	-	expression tag	UNP P0DTC2
B	1231	ALA	-	expression tag	UNP P0DTC2
B	1232	PRO	-	expression tag	UNP P0DTC2
B	1233	ARG	-	expression tag	UNP P0DTC2
B	1234	ASP	-	expression tag	UNP P0DTC2
B	1235	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1236	GLN	-	expression tag	UNP P0DTC2
B	1237	ALA	-	expression tag	UNP P0DTC2
B	1238	TYR	-	expression tag	UNP P0DTC2
B	1239	VAL	-	expression tag	UNP P0DTC2
B	1240	ARG	-	expression tag	UNP P0DTC2
B	1241	LYS	-	expression tag	UNP P0DTC2
B	1242	ASP	-	expression tag	UNP P0DTC2
B	1243	GLY	-	expression tag	UNP P0DTC2
B	1244	GLU	-	expression tag	UNP P0DTC2
B	1245	TRP	-	expression tag	UNP P0DTC2
B	1246	VAL	-	expression tag	UNP P0DTC2
B	1247	LEU	-	expression tag	UNP P0DTC2
B	1248	LEU	-	expression tag	UNP P0DTC2
B	1249	SER	-	expression tag	UNP P0DTC2
B	1250	THR	-	expression tag	UNP P0DTC2
B	1251	PHE	-	expression tag	UNP P0DTC2
B	1252	LEU	-	expression tag	UNP P0DTC2
B	1253	GLY	-	expression tag	UNP P0DTC2
B	1254	HIS	-	expression tag	UNP P0DTC2
B	1255	HIS	-	expression tag	UNP P0DTC2
B	1256	HIS	-	expression tag	UNP P0DTC2
B	1257	HIS	-	expression tag	UNP P0DTC2
B	1258	HIS	-	expression tag	UNP P0DTC2
B	1259	HIS	-	expression tag	UNP P0DTC2
D	986	PRO	LYS	conflict	UNP P0DTC2
D	987	PRO	VAL	conflict	UNP P0DTC2
D	1214	SER	-	expression tag	UNP P0DTC2
D	1215	GLY	-	expression tag	UNP P0DTC2
D	1216	ARG	-	expression tag	UNP P0DTC2
D	1217	LEU	-	expression tag	UNP P0DTC2
D	1218	VAL	-	expression tag	UNP P0DTC2
D	1219	PRO	-	expression tag	UNP P0DTC2
D	1220	ARG	-	expression tag	UNP P0DTC2
D	1221	GLY	-	expression tag	UNP P0DTC2
D	1222	SER	-	expression tag	UNP P0DTC2
D	1223	PRO	-	expression tag	UNP P0DTC2
D	1224	GLY	-	expression tag	UNP P0DTC2
D	1225	SER	-	expression tag	UNP P0DTC2
D	1226	GLY	-	expression tag	UNP P0DTC2
D	1227	TYR	-	expression tag	UNP P0DTC2
D	1228	ILE	-	expression tag	UNP P0DTC2
D	1229	PRO	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1230	GLU	-	expression tag	UNP P0DTC2
D	1231	ALA	-	expression tag	UNP P0DTC2
D	1232	PRO	-	expression tag	UNP P0DTC2
D	1233	ARG	-	expression tag	UNP P0DTC2
D	1234	ASP	-	expression tag	UNP P0DTC2
D	1235	GLY	-	expression tag	UNP P0DTC2
D	1236	GLN	-	expression tag	UNP P0DTC2
D	1237	ALA	-	expression tag	UNP P0DTC2
D	1238	TYR	-	expression tag	UNP P0DTC2
D	1239	VAL	-	expression tag	UNP P0DTC2
D	1240	ARG	-	expression tag	UNP P0DTC2
D	1241	LYS	-	expression tag	UNP P0DTC2
D	1242	ASP	-	expression tag	UNP P0DTC2
D	1243	GLY	-	expression tag	UNP P0DTC2
D	1244	GLU	-	expression tag	UNP P0DTC2
D	1245	TRP	-	expression tag	UNP P0DTC2
D	1246	VAL	-	expression tag	UNP P0DTC2
D	1247	LEU	-	expression tag	UNP P0DTC2
D	1248	LEU	-	expression tag	UNP P0DTC2
D	1249	SER	-	expression tag	UNP P0DTC2
D	1250	THR	-	expression tag	UNP P0DTC2
D	1251	PHE	-	expression tag	UNP P0DTC2
D	1252	LEU	-	expression tag	UNP P0DTC2
D	1253	GLY	-	expression tag	UNP P0DTC2
D	1254	HIS	-	expression tag	UNP P0DTC2
D	1255	HIS	-	expression tag	UNP P0DTC2
D	1256	HIS	-	expression tag	UNP P0DTC2
D	1257	HIS	-	expression tag	UNP P0DTC2
D	1258	HIS	-	expression tag	UNP P0DTC2
D	1259	HIS	-	expression tag	UNP P0DTC2
E	986	PRO	LYS	conflict	UNP P0DTC2
E	987	PRO	VAL	conflict	UNP P0DTC2
E	1214	SER	-	expression tag	UNP P0DTC2
E	1215	GLY	-	expression tag	UNP P0DTC2
E	1216	ARG	-	expression tag	UNP P0DTC2
E	1217	LEU	-	expression tag	UNP P0DTC2
E	1218	VAL	-	expression tag	UNP P0DTC2
E	1219	PRO	-	expression tag	UNP P0DTC2
E	1220	ARG	-	expression tag	UNP P0DTC2
E	1221	GLY	-	expression tag	UNP P0DTC2
E	1222	SER	-	expression tag	UNP P0DTC2
E	1223	PRO	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1224	GLY	-	expression tag	UNP P0DTC2
E	1225	SER	-	expression tag	UNP P0DTC2
E	1226	GLY	-	expression tag	UNP P0DTC2
E	1227	TYR	-	expression tag	UNP P0DTC2
E	1228	ILE	-	expression tag	UNP P0DTC2
E	1229	PRO	-	expression tag	UNP P0DTC2
E	1230	GLU	-	expression tag	UNP P0DTC2
E	1231	ALA	-	expression tag	UNP P0DTC2
E	1232	PRO	-	expression tag	UNP P0DTC2
E	1233	ARG	-	expression tag	UNP P0DTC2
E	1234	ASP	-	expression tag	UNP P0DTC2
E	1235	GLY	-	expression tag	UNP P0DTC2
E	1236	GLN	-	expression tag	UNP P0DTC2
E	1237	ALA	-	expression tag	UNP P0DTC2
E	1238	TYR	-	expression tag	UNP P0DTC2
E	1239	VAL	-	expression tag	UNP P0DTC2
E	1240	ARG	-	expression tag	UNP P0DTC2
E	1241	LYS	-	expression tag	UNP P0DTC2
E	1242	ASP	-	expression tag	UNP P0DTC2
E	1243	GLY	-	expression tag	UNP P0DTC2
E	1244	GLU	-	expression tag	UNP P0DTC2
E	1245	TRP	-	expression tag	UNP P0DTC2
E	1246	VAL	-	expression tag	UNP P0DTC2
E	1247	LEU	-	expression tag	UNP P0DTC2
E	1248	LEU	-	expression tag	UNP P0DTC2
E	1249	SER	-	expression tag	UNP P0DTC2
E	1250	THR	-	expression tag	UNP P0DTC2
E	1251	PHE	-	expression tag	UNP P0DTC2
E	1252	LEU	-	expression tag	UNP P0DTC2
E	1253	GLY	-	expression tag	UNP P0DTC2
E	1254	HIS	-	expression tag	UNP P0DTC2
E	1255	HIS	-	expression tag	UNP P0DTC2
E	1256	HIS	-	expression tag	UNP P0DTC2
E	1257	HIS	-	expression tag	UNP P0DTC2
E	1258	HIS	-	expression tag	UNP P0DTC2
E	1259	HIS	-	expression tag	UNP P0DTC2

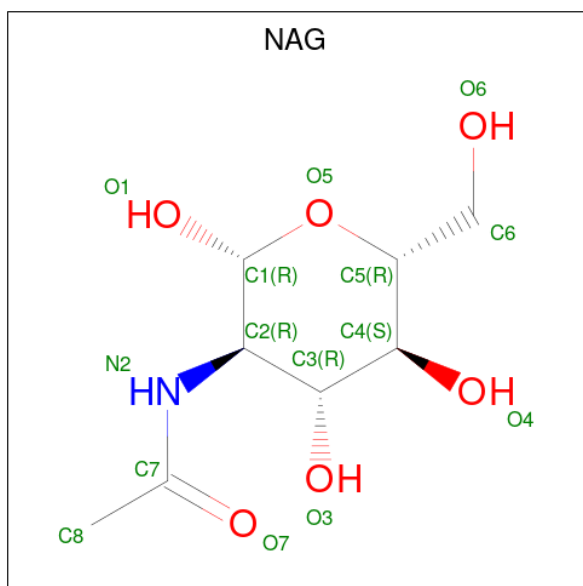
- Molecule 2 is a protein called C121 Fab Heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	128	Total	C	N	O	S	0	0
			991	631	166	187	7		

- Molecule 3 is a protein called C121 Fab Light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	I	108	778	481	130	163	4	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

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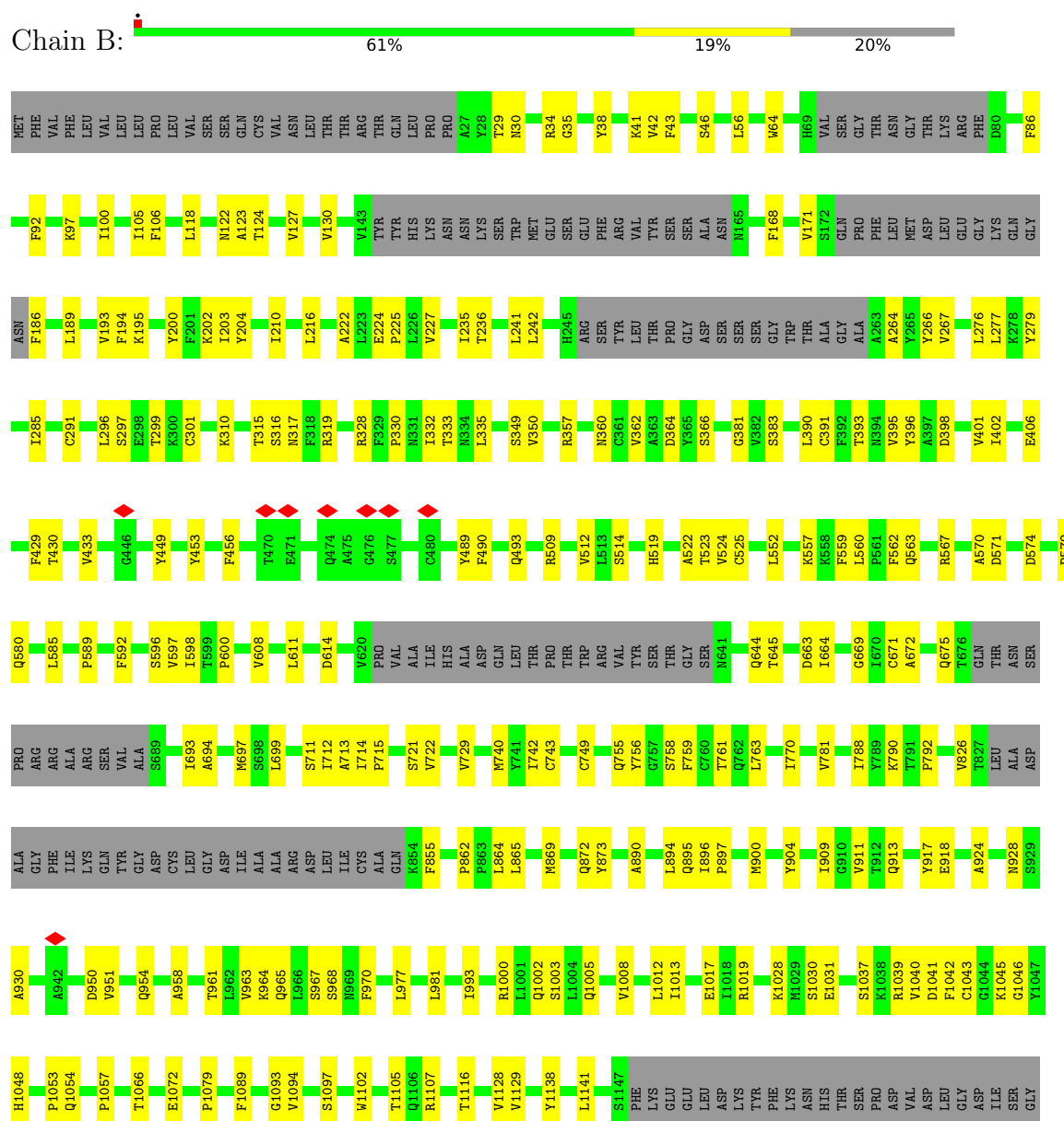
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Mol	Chain	Residues	Atoms				AltConf
4	D	1	Total 14	C 8	N 1	O 5	0
4	D	1	Total 14	C 8	N 1	O 5	0
4	D	1	Total 14	C 8	N 1	O 5	0
4	D	1	Total 14	C 8	N 1	O 5	0
4	D	1	Total 14	C 8	N 1	O 5	0
4	D	1	Total 14	C 8	N 1	O 5	0
4	E	1	Total 14	C 8	N 1	O 5	0
4	E	1	Total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

3 Residue-property plots

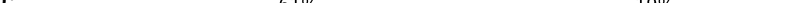
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

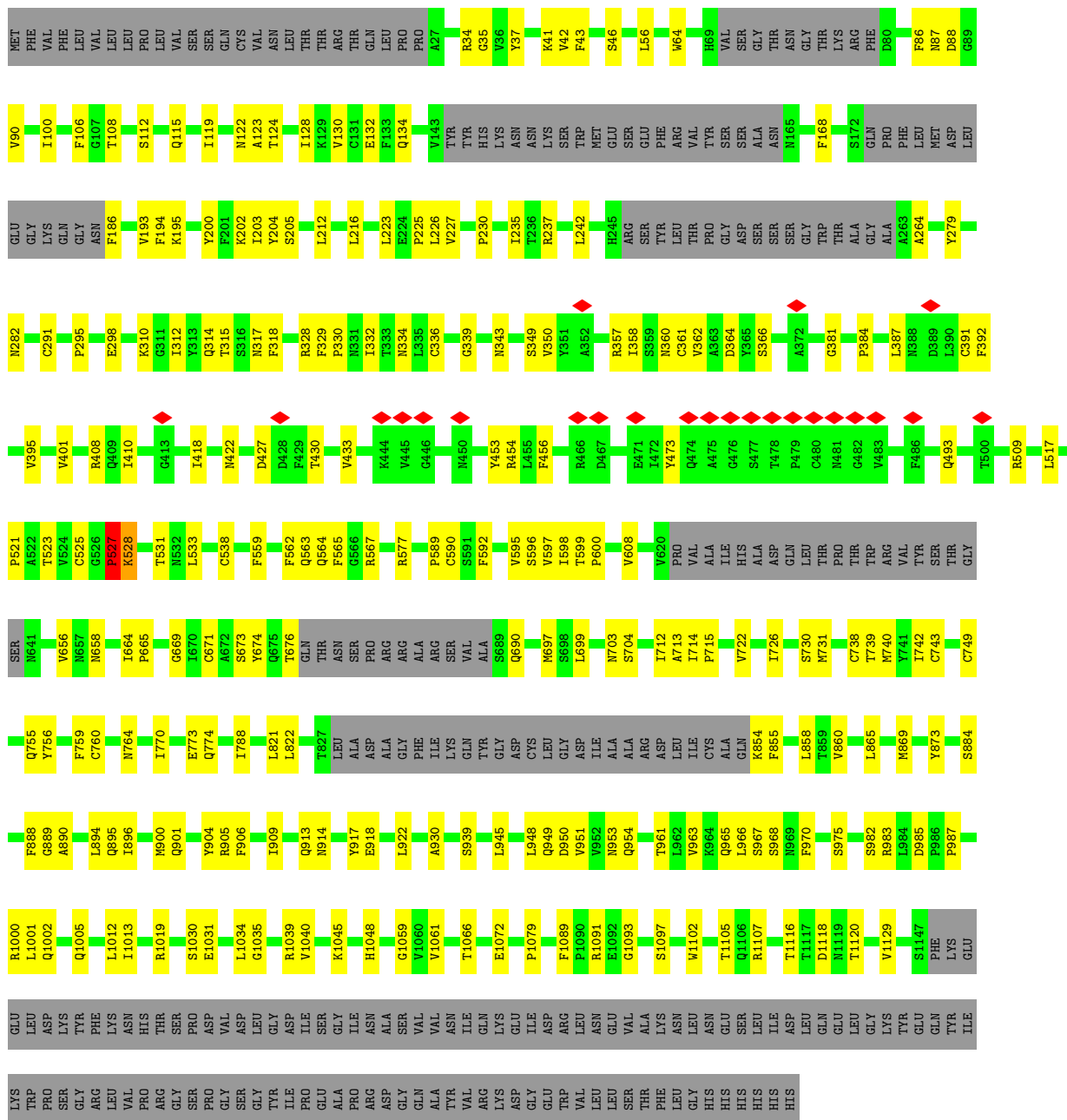
• Molecule 1: Spike glycoprotein



PRO	ARG	ASP	GLY	GLN	ALA	THR	VAL	ARG	ASP	GLY	GLU	TRP	VAL	LEU	SER	THR	PHE	HIS	HIS	HIS	HIS	HIS
TLE	ASN	ALA	SER	VAL	VAL	ASN	TLE	GLN	LYS	LYS	GIJ	TLE	ASP	ARG	ASN	ASN	GLU	LEU	GLN	GLU	LEU	ALA

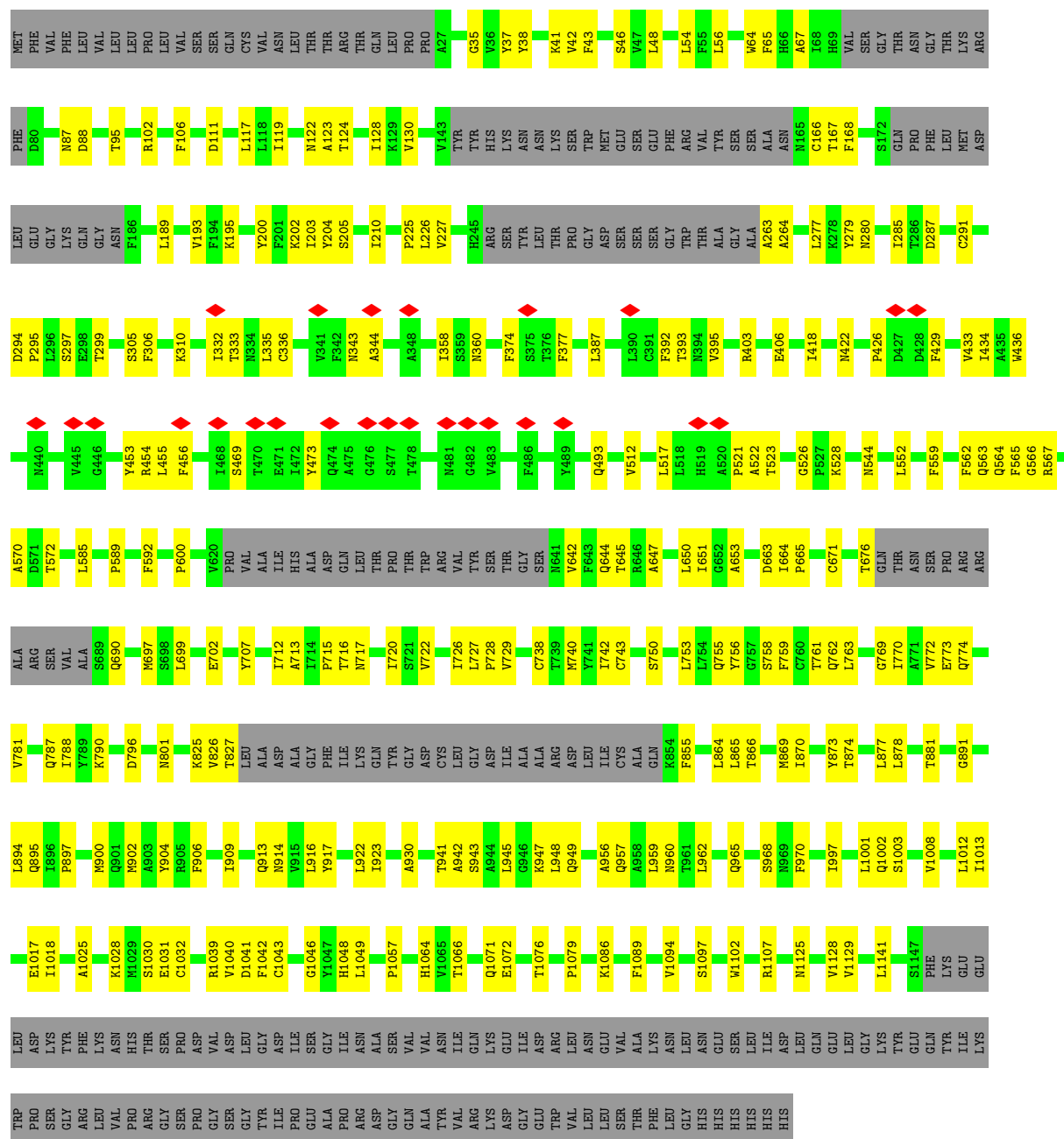
- Molecule 1: Spike glycoprotein

Chain D:  61% 19% 20%

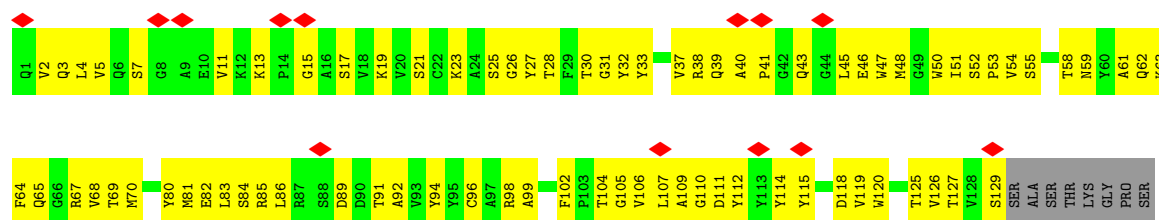
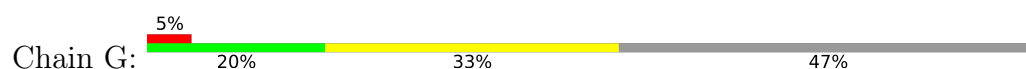


- Molecule 1: Spike glycoprotein

Chain E:



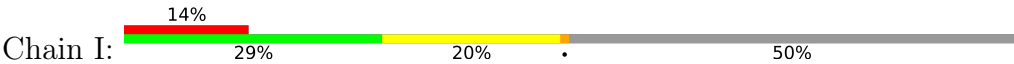
• Molecule 2: C121 Fab Heavy chain



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

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

● Molecule 3: C121 Fab Light chain



Gln Ser A3 I4 T5 Q6 P7 A8 S9 V11 S12 G13 S14 P15 G16 Q17 S18 I19 T20 I21 S22 C23 D27B V27C G28 S29 Y30 N31 L32 Y33 S34 W35 Y36 Q37 Q38 H39 P40 G41 K42 A43 P44 K45 L46 P47 I48 Y49 E50 G51 S52 K53 R54 S55 S56 G57 V58 S59 N60 R61 F62

K66 S67 G68 R69 T70 L73 G77 L78 Q79 A80 E81 D82 E83 A84 D85 Y86 Y87 C88 C89 S90 S95 T95A L96 Y97 F98 G99 G100 T101 T102 K103 L104 T105 V106 L107 GLY Gln Pro Lys Ala Ala Ser Pro Val Thr Phe Pro Pro Ser Ser Glu Leu Ala Asn

Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Pro Lys Gln Ser Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Thr Phe Glu Trp Lys Ser His

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Val Ala Pro Thr Glu Cys Ser

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	14999	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.282	Depositor
Minimum map value	-0.090	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.0555	Depositor
Map size (Å)	377.872, 377.872, 377.872	wwPDB
Map dimensions	452, 452, 452	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.836, 0.836, 0.836	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	B	0.10	0/7999	0.28	0/10885
1	D	0.11	0/7999	0.28	0/10885
1	E	0.11	0/7999	0.31	0/10885
2	G	0.25	0/1018	0.56	1/1384 (0.1%)
3	I	0.42	2/793 (0.3%)	0.68	3/1075 (0.3%)
All	All	0.14	2/25808 (0.0%)	0.32	4/35114 (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	D	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	98	PHE	CA-C	5.60	1.59	1.53
3	I	97	VAL	CA-C	5.41	1.59	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	98	PHE	N-CA-C	13.37	125.89	108.24
3	I	98	PHE	CA-C-N	6.44	130.85	121.96
3	I	98	PHE	C-N-CA	6.44	130.85	121.96
2	G	104	THR	N-CA-C	-5.53	106.20	113.17

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	527	PRO	Peptide

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	B	7823	0	7634	547	0
1	D	7823	0	7630	508	0
1	E	7823	0	7632	506	0
2	G	991	0	953	116	0
3	I	778	0	749	71	0
4	B	98	0	90	0	0
4	D	112	0	104	3	0
4	E	112	0	104	3	0
All	All	25560	0	24896	1095	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 22.

The worst 5 of 1095 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:D:589:PRO:HG2	1:E:855:PHE:CD1	1.30	1.63
3:I:87:TYR:CD1	3:I:98:PHE:CE1	1.80	1.63
1:B:1002:GLN:HE22	1:D:1001:LEU:CD1	1.15	1.53
1:B:559:PHE:CE1	1:D:43:PHE:CG	1.97	1.53
1:B:559:PHE:HE1	1:D:43:PHE:CD2	1.23	1.52

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	B	829/1259 (66%)	810 (98%)	18 (2%)	1 (0%)	48	83
1	D	949/1259 (75%)	920 (97%)	26 (3%)	3 (0%)	36	71
1	E	986/1259 (78%)	969 (98%)	16 (2%)	1 (0%)	48	83
2	G	118/241 (49%)	103 (87%)	15 (13%)	0	100	100
3	I	106/216 (49%)	97 (92%)	7 (7%)	2 (2%)	6	32
All	All	2988/4234 (71%)	2899 (97%)	82 (3%)	7 (0%)	44	77

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	I	95(A)	THR
1	B	123	ALA
1	D	123	ALA
1	D	528	LYS
1	E	123	ALA

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	B	10/1096 (1%)	10 (100%)	0	100	100
1	D	88/1096 (8%)	88 (100%)	0	100	100
3	I	15/180 (8%)	15 (100%)	0	100	100
All	All	113/2372 (5%)	113 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	D	1002	GLN
3	I	37	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	E	1301	1	14,14,15	0.21	0	17,19,21	0.48	0
4	NAG	D	1305	1	14,14,15	0.51	0	17,19,21	1.34	2 (11%)
4	NAG	B	1302	1	14,14,15	0.21	0	17,19,21	0.43	0
4	NAG	E	1302	1	14,14,15	0.26	0	17,19,21	0.44	0
4	NAG	D	1308	1	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	B	1301	1	14,14,15	0.26	0	17,19,21	0.56	0
4	NAG	D	1306	1	14,14,15	0.26	0	17,19,21	0.55	0
4	NAG	E	1306	1	14,14,15	0.30	0	17,19,21	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	B	1304	1	14,14,15	0.28	0	17,19,21	0.56	0
4	NAG	D	1303	1	14,14,15	0.23	0	17,19,21	0.45	0
4	NAG	E	1303	1	14,14,15	0.26	0	17,19,21	0.45	0
4	NAG	B	1305	1	14,14,15	0.22	0	17,19,21	0.43	0
4	NAG	E	1305	-	14,14,15	0.24	0	17,19,21	0.44	0
4	NAG	D	1302	1	14,14,15	0.26	0	17,19,21	0.39	0
4	NAG	D	1307	1	14,14,15	0.25	0	17,19,21	0.43	0
4	NAG	B	1307	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	B	1306	1	14,14,15	0.25	0	17,19,21	0.45	0
4	NAG	D	1301	1	14,14,15	0.52	0	17,19,21	0.63	0
4	NAG	E	1307	1	14,14,15	0.85	1 (7%)	17,19,21	1.01	1 (5%)
4	NAG	E	1308	1	14,14,15	0.25	0	17,19,21	0.47	0
4	NAG	E	1304	1	14,14,15	0.27	0	17,19,21	0.55	0
4	NAG	B	1303	1	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	D	1304	1	14,14,15	0.24	0	17,19,21	0.42	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
4	NAG	E	1301	1	-	0/6/23/26	0/1/1/1
4	NAG	D	1305	1	-	5/6/23/26	0/1/1/1
4	NAG	B	1302	1	-	0/6/23/26	0/1/1/1
4	NAG	E	1302	1	-	4/6/23/26	0/1/1/1
4	NAG	D	1308	1	-	1/6/23/26	0/1/1/1
4	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
4	NAG	D	1306	1	-	3/6/23/26	0/1/1/1
4	NAG	E	1306	1	-	4/6/23/26	0/1/1/1
4	NAG	B	1304	1	-	3/6/23/26	0/1/1/1
4	NAG	D	1303	1	-	0/6/23/26	0/1/1/1
4	NAG	E	1303	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1305	1	-	2/6/23/26	0/1/1/1
4	NAG	E	1305	-	-	1/6/23/26	0/1/1/1
4	NAG	D	1302	1	-	4/6/23/26	0/1/1/1
4	NAG	D	1307	1	-	0/6/23/26	0/1/1/1
4	NAG	B	1307	1	-	1/6/23/26	0/1/1/1
4	NAG	B	1306	1	-	1/6/23/26	0/1/1/1
4	NAG	D	1301	1	-	4/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	E	1307	1	-	0/6/23/26	0/1/1/1
4	NAG	E	1308	1	-	2/6/23/26	0/1/1/1
4	NAG	E	1304	1	-	4/6/23/26	0/1/1/1
4	NAG	B	1303	1	-	2/6/23/26	0/1/1/1
4	NAG	D	1304	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1307	NAG	O5-C1	2.71	1.48	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1305	NAG	C2-N2-C7	4.58	129.03	122.90
4	E	1307	NAG	C1-O5-C5	3.91	117.43	112.19
4	D	1305	NAG	C1-C2-N2	2.13	113.79	110.43

There are no chirality outliers.

5 of 43 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	1302	NAG	O5-C5-C6-O6
4	D	1302	NAG	C4-C5-C6-O6
4	B	1303	NAG	O5-C5-C6-O6
4	E	1306	NAG	O5-C5-C6-O6
4	E	1306	NAG	C4-C5-C6-O6

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	1305	NAG	1	0
4	D	1306	NAG	1	0
4	E	1306	NAG	1	0
4	D	1301	NAG	1	0
4	E	1307	NAG	2	0

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.

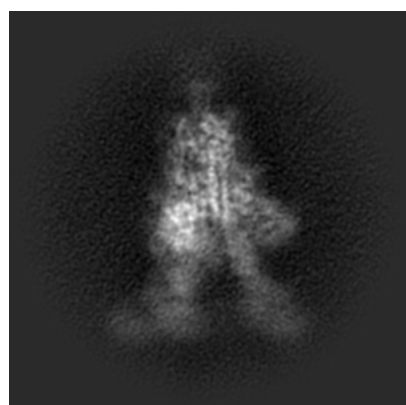
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22735. These allow visual inspection of the internal detail of the map and identification of artifacts.

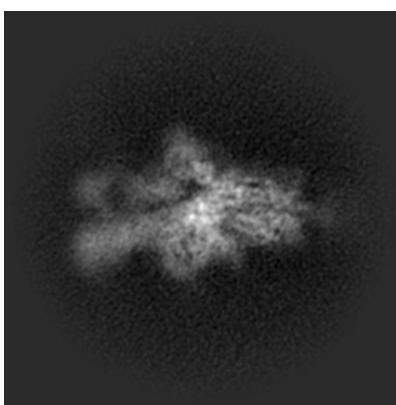
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

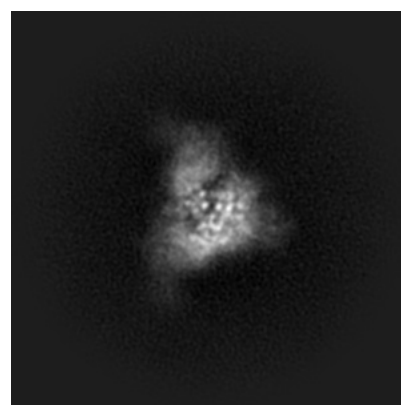
6.1.1 Primary map



X



Y

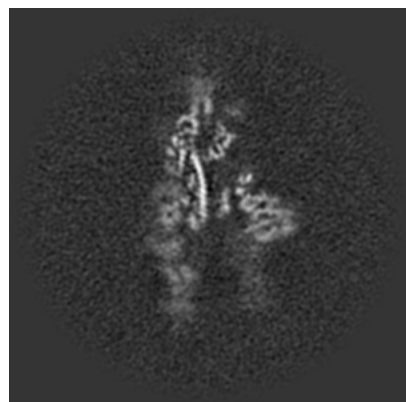


Z

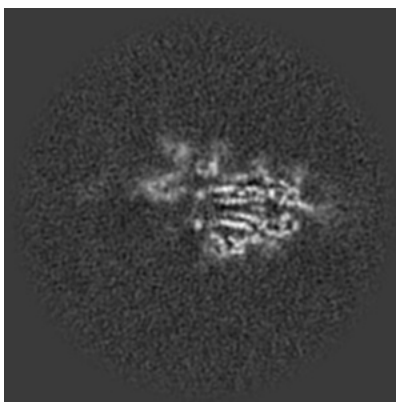
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

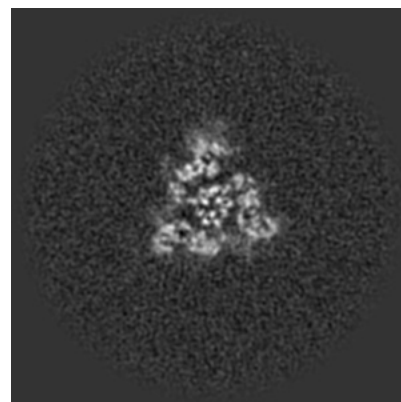
6.2.1 Primary map



X Index: 226



Y Index: 226

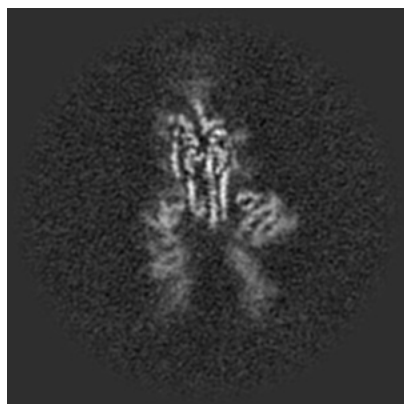


Z Index: 226

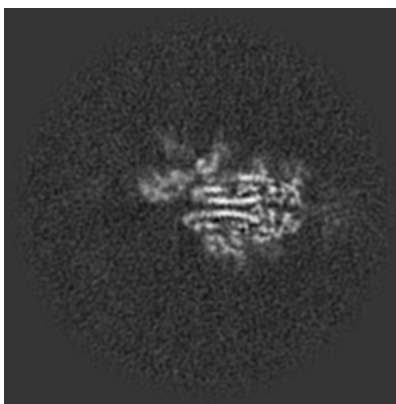
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

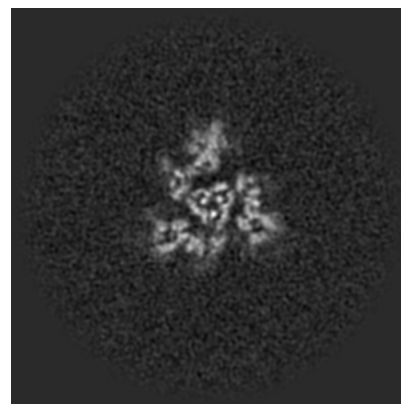
6.3.1 Primary map



X Index: 216



Y Index: 230

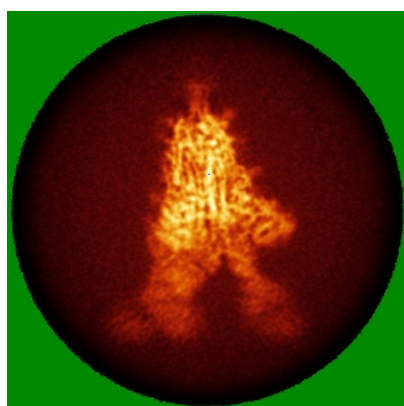


Z Index: 221

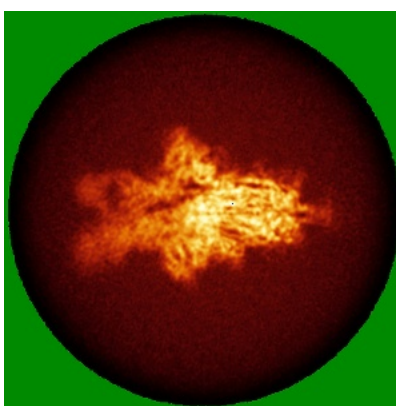
The images above show the largest variance slices of the map in three orthogonal directions.

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

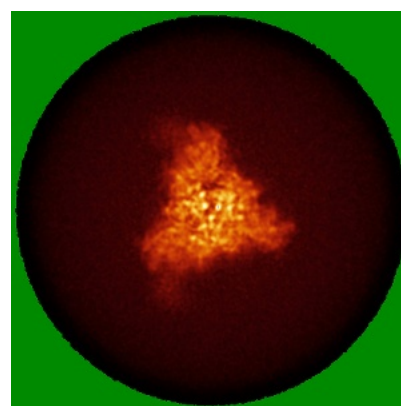
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0555. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

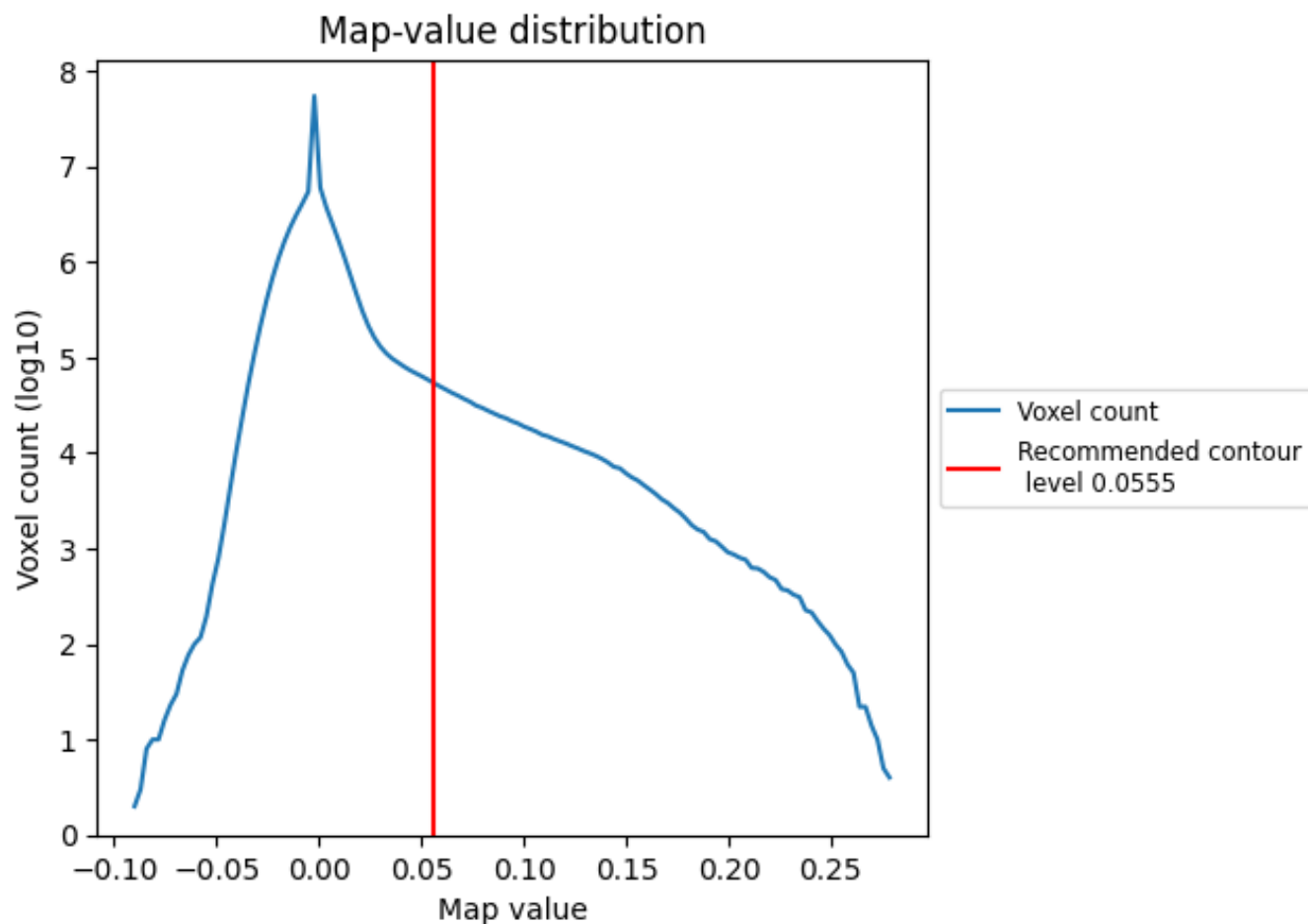
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

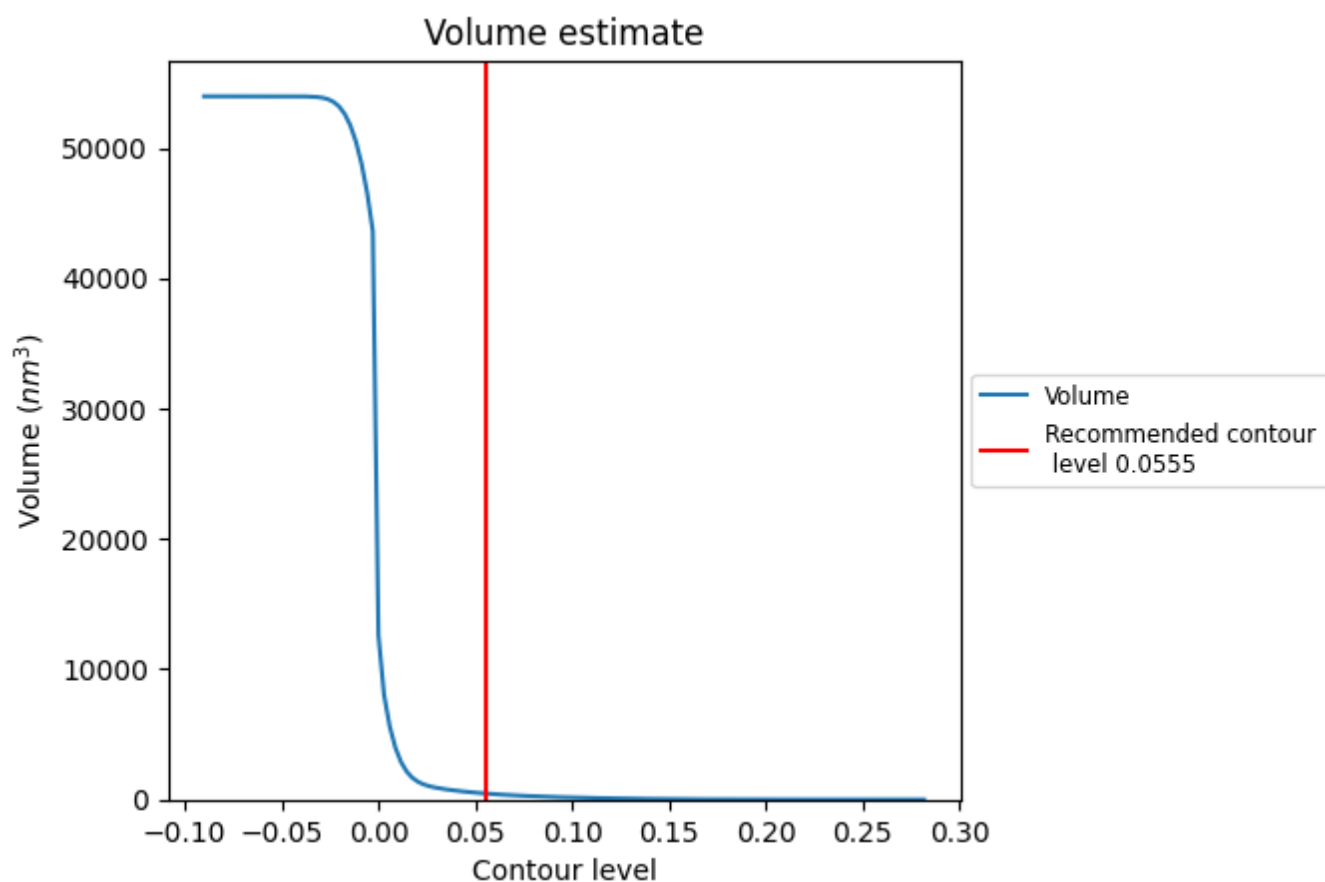
This section contains the results of statistical analysis of the map.

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.

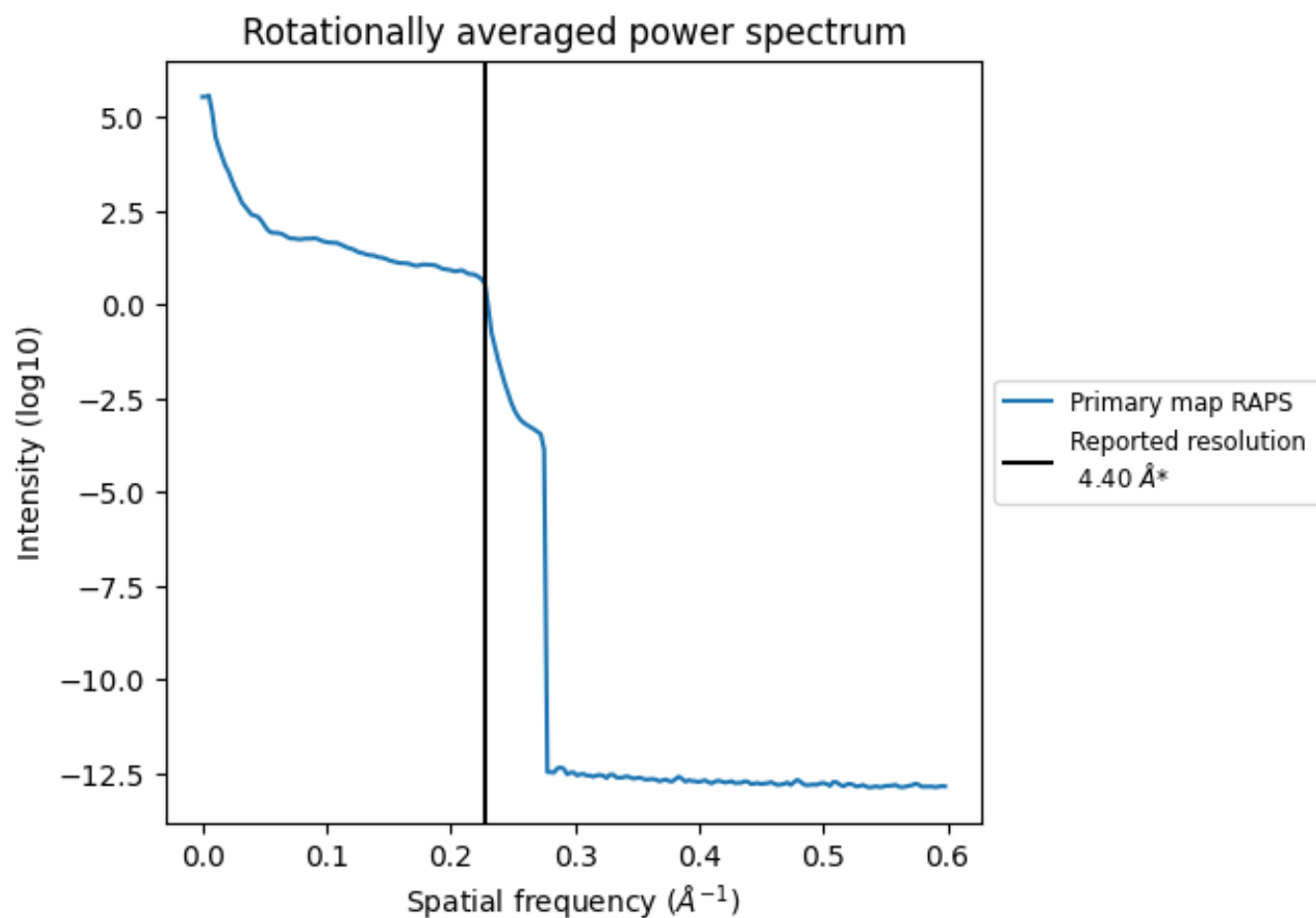
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 461 nm³; this corresponds to an approximate mass of 417 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 ⓘ

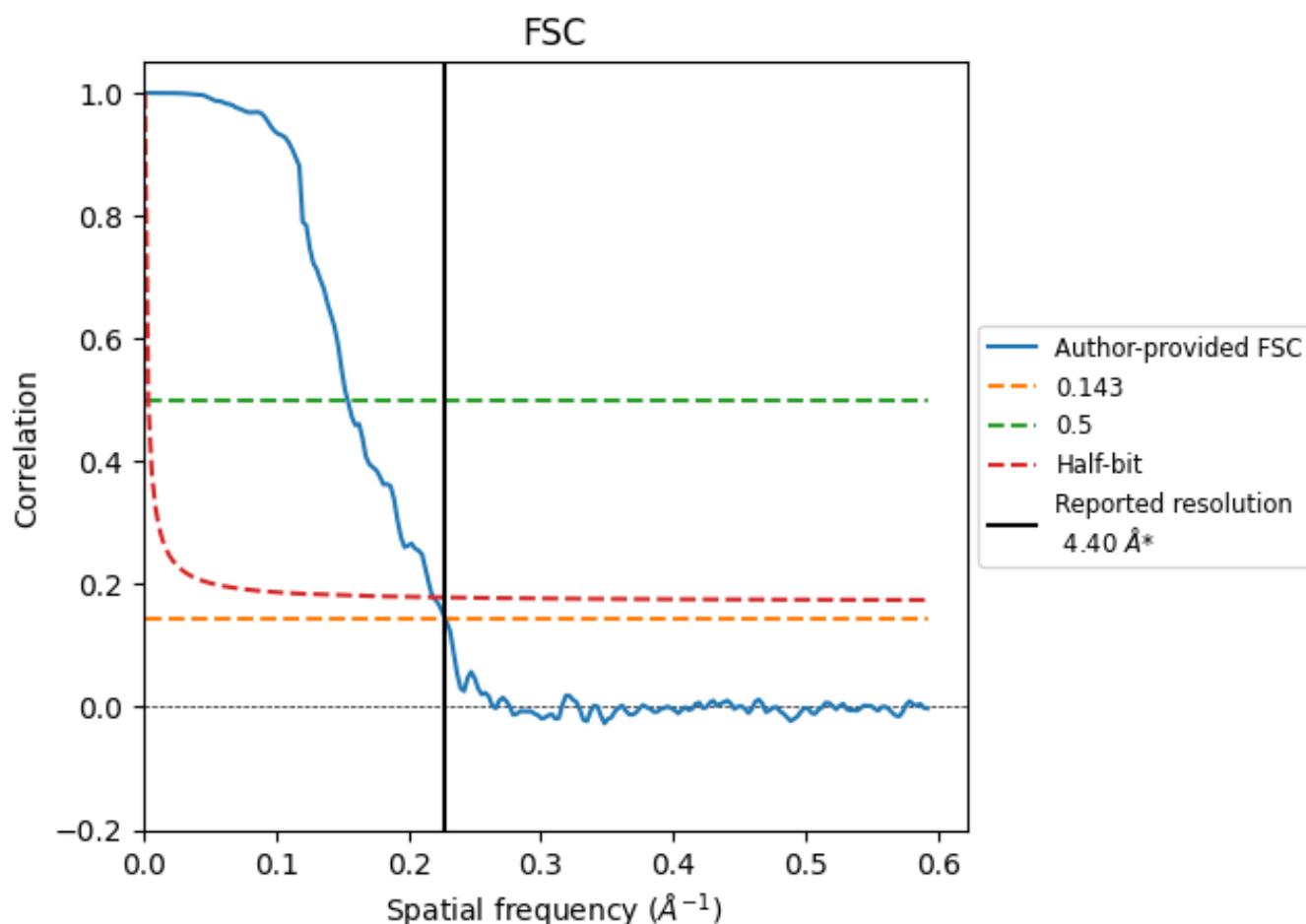


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

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 0.227 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	4.38	6.49	4.58
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22735 and PDB model 7K8Y. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)

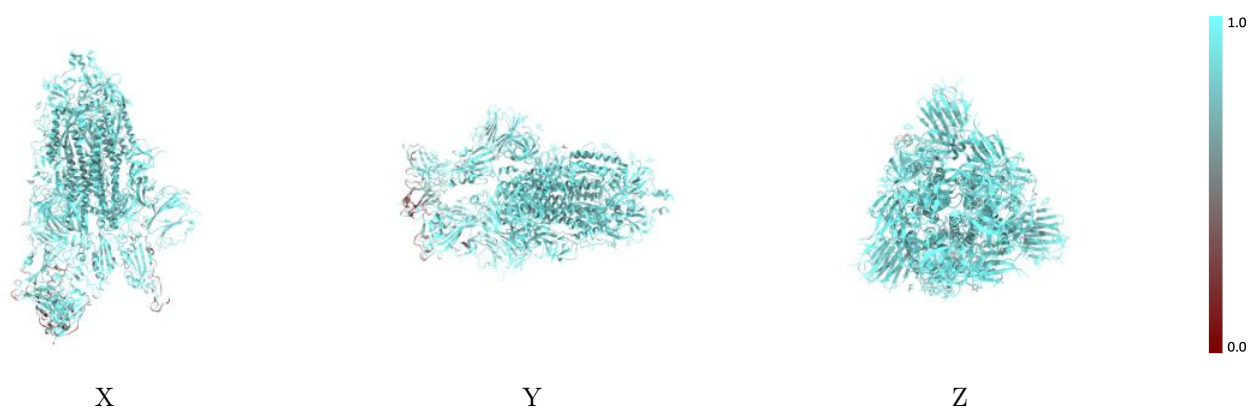
This section was not generated.

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



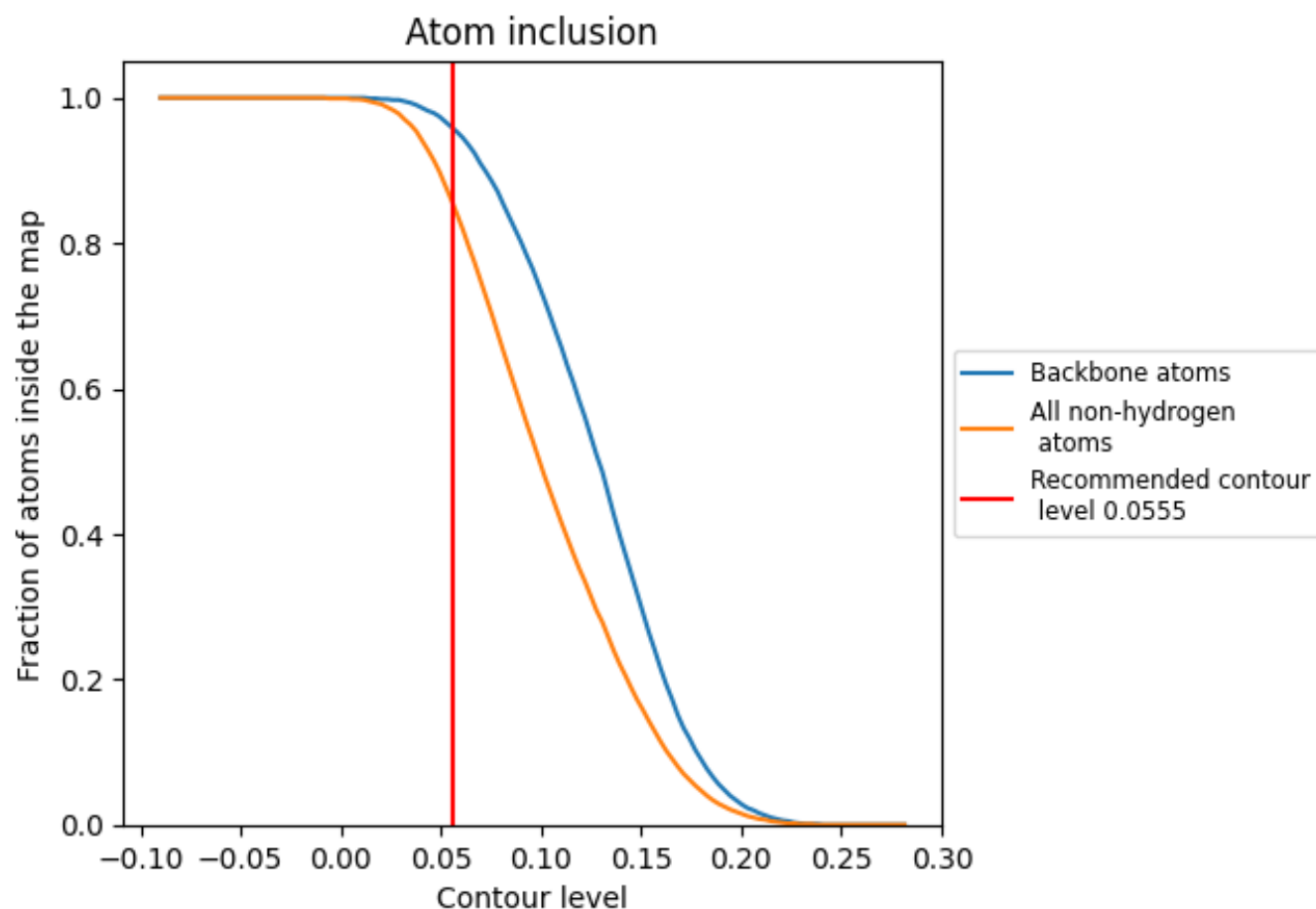
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0555).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 86% 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 (0.0555) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8580	0.2380
B	0.8830	0.2580
D	0.8640	0.2450
E	0.8670	0.2360
G	0.7800	0.1520
I	0.5720	0.1010

