



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 02:33 PM EST

PDB ID : 7SN3
EMDB ID : EMD-25210
Title : Structure of human SARS-CoV-2 spike glycoprotein trimer bound by neutralizing antibody C1C-A3 Fab (variable region)
Authors : Pan, J.; Abraham, J.; Shankar, S.
Deposited on : 2021-10-27
Resolution : 3.10 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:

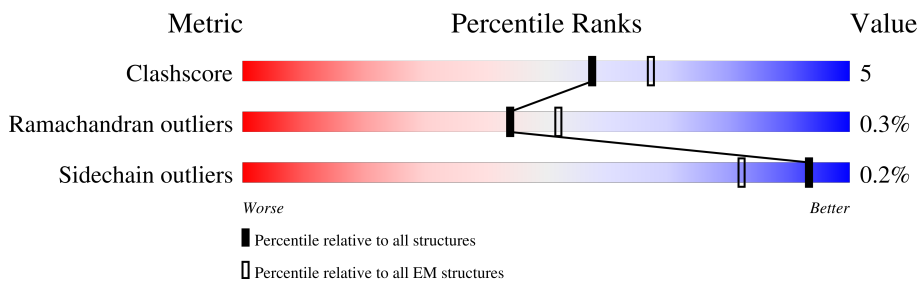
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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 3.10 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.



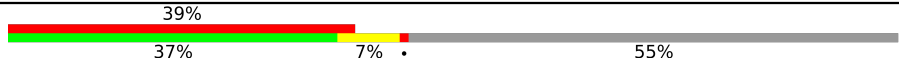
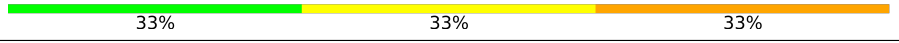
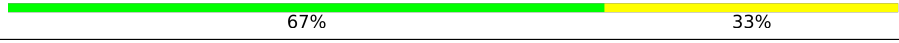
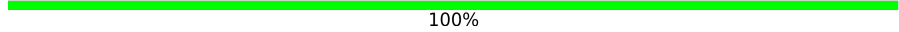
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	1273	
1	B	1273	
1	C	1273	
2	D	250	
2	F	250	
2	H	250	
3	E	238	
3	G	238	

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Mol	Chain	Length	Quality of chain
3	L	238	 <p>39% 37% 7% 55%</p>
4	I	3	 <p>33% 33% 33%</p>
4	J	3	 <p>67% 33%</p>
4	K	3	 <p>100%</p>

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 27447 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
			Total	C	N	O	S		
1	A	925	7136	4563	1186	1354	33	0	0
1	B	924	7133	4560	1185	1355	33	0	0
1	C	915	7055	4511	1173	1338	33	0	0

There are 222 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	682	GLY	ARG	engineered mutation	UNP P0DTC2
A	683	SER	ARG	engineered mutation	UNP P0DTC2
A	685	SER	ARG	engineered mutation	UNP P0DTC2
A	817	PRO	PHE	engineered mutation	UNP P0DTC2
A	892	PRO	ALA	engineered mutation	UNP P0DTC2
A	899	PRO	ALA	engineered mutation	UNP P0DTC2
A	942	PRO	ALA	engineered mutation	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2
A	1209	SER	-	expression tag	UNP P0DTC2
A	1210	GLY	-	expression tag	UNP P0DTC2
A	1211	TYR	-	expression tag	UNP P0DTC2
A	1212	ILE	-	expression tag	UNP P0DTC2
A	1213	PRO	-	expression tag	UNP P0DTC2
A	1214	GLU	-	expression tag	UNP P0DTC2
A	1215	ALA	-	expression tag	UNP P0DTC2
A	1216	PRO	-	expression tag	UNP P0DTC2
A	1217	ARG	-	expression tag	UNP P0DTC2
A	1218	ASP	-	expression tag	UNP P0DTC2
A	1219	GLY	-	expression tag	UNP P0DTC2
A	1220	GLN	-	expression tag	UNP P0DTC2
A	1221	ALA	-	expression tag	UNP P0DTC2
A	1222	TYR	-	expression tag	UNP P0DTC2
A	1223	VAL	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1224	ARG	-	expression tag	UNP P0DTC2
A	1225	LYS	-	expression tag	UNP P0DTC2
A	1226	ASP	-	expression tag	UNP P0DTC2
A	1227	GLY	-	expression tag	UNP P0DTC2
A	1228	GLU	-	expression tag	UNP P0DTC2
A	1229	TRP	-	expression tag	UNP P0DTC2
A	1230	VAL	-	expression tag	UNP P0DTC2
A	1231	LEU	-	expression tag	UNP P0DTC2
A	1232	LEU	-	expression tag	UNP P0DTC2
A	1233	SER	-	expression tag	UNP P0DTC2
A	1234	THR	-	expression tag	UNP P0DTC2
A	1235	PHE	-	expression tag	UNP P0DTC2
A	1236	LEU	-	expression tag	UNP P0DTC2
A	1237	SER	-	expression tag	UNP P0DTC2
A	1238	ALA	-	expression tag	UNP P0DTC2
A	1239	GLY	-	expression tag	UNP P0DTC2
A	1240	GLY	-	expression tag	UNP P0DTC2
A	1241	LEU	-	expression tag	UNP P0DTC2
A	1242	ASN	-	expression tag	UNP P0DTC2
A	1243	ASP	-	expression tag	UNP P0DTC2
A	1244	ILE	-	expression tag	UNP P0DTC2
A	1245	PHE	-	expression tag	UNP P0DTC2
A	1246	GLU	-	expression tag	UNP P0DTC2
A	1247	ALA	-	expression tag	UNP P0DTC2
A	1248	GLN	-	expression tag	UNP P0DTC2
A	1249	LYS	-	expression tag	UNP P0DTC2
A	1250	ILE	-	expression tag	UNP P0DTC2
A	1251	GLU	-	expression tag	UNP P0DTC2
A	1252	TRP	-	expression tag	UNP P0DTC2
A	1253	HIS	-	expression tag	UNP P0DTC2
A	1254	GLU	-	expression tag	UNP P0DTC2
A	1255	GLY	-	expression tag	UNP P0DTC2
A	1256	ALA	-	expression tag	UNP P0DTC2
A	1257	SER	-	expression tag	UNP P0DTC2
A	1258	GLY	-	expression tag	UNP P0DTC2
A	1259	GLU	-	expression tag	UNP P0DTC2
A	1260	ASN	-	expression tag	UNP P0DTC2
A	1261	LEU	-	expression tag	UNP P0DTC2
A	1262	TYR	-	expression tag	UNP P0DTC2
A	1263	PHE	-	expression tag	UNP P0DTC2
A	1264	GLN	-	expression tag	UNP P0DTC2
A	1265	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1266	HIS	-	expression tag	UNP P0DTC2
A	1267	HIS	-	expression tag	UNP P0DTC2
A	1268	HIS	-	expression tag	UNP P0DTC2
A	1269	HIS	-	expression tag	UNP P0DTC2
A	1270	HIS	-	expression tag	UNP P0DTC2
A	1271	HIS	-	expression tag	UNP P0DTC2
A	1272	HIS	-	expression tag	UNP P0DTC2
A	1273	HIS	-	expression tag	UNP P0DTC2
B	682	GLY	ARG	engineered mutation	UNP P0DTC2
B	683	SER	ARG	engineered mutation	UNP P0DTC2
B	685	SER	ARG	engineered mutation	UNP P0DTC2
B	817	PRO	PHE	engineered mutation	UNP P0DTC2
B	892	PRO	ALA	engineered mutation	UNP P0DTC2
B	899	PRO	ALA	engineered mutation	UNP P0DTC2
B	942	PRO	ALA	engineered mutation	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	1209	SER	-	expression tag	UNP P0DTC2
B	1210	GLY	-	expression tag	UNP P0DTC2
B	1211	TYR	-	expression tag	UNP P0DTC2
B	1212	ILE	-	expression tag	UNP P0DTC2
B	1213	PRO	-	expression tag	UNP P0DTC2
B	1214	GLU	-	expression tag	UNP P0DTC2
B	1215	ALA	-	expression tag	UNP P0DTC2
B	1216	PRO	-	expression tag	UNP P0DTC2
B	1217	ARG	-	expression tag	UNP P0DTC2
B	1218	ASP	-	expression tag	UNP P0DTC2
B	1219	GLY	-	expression tag	UNP P0DTC2
B	1220	GLN	-	expression tag	UNP P0DTC2
B	1221	ALA	-	expression tag	UNP P0DTC2
B	1222	TYR	-	expression tag	UNP P0DTC2
B	1223	VAL	-	expression tag	UNP P0DTC2
B	1224	ARG	-	expression tag	UNP P0DTC2
B	1225	LYS	-	expression tag	UNP P0DTC2
B	1226	ASP	-	expression tag	UNP P0DTC2
B	1227	GLY	-	expression tag	UNP P0DTC2
B	1228	GLU	-	expression tag	UNP P0DTC2
B	1229	TRP	-	expression tag	UNP P0DTC2
B	1230	VAL	-	expression tag	UNP P0DTC2
B	1231	LEU	-	expression tag	UNP P0DTC2
B	1232	LEU	-	expression tag	UNP P0DTC2
B	1233	SER	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1234	THR	-	expression tag	UNP P0DTC2
B	1235	PHE	-	expression tag	UNP P0DTC2
B	1236	LEU	-	expression tag	UNP P0DTC2
B	1237	SER	-	expression tag	UNP P0DTC2
B	1238	ALA	-	expression tag	UNP P0DTC2
B	1239	GLY	-	expression tag	UNP P0DTC2
B	1240	GLY	-	expression tag	UNP P0DTC2
B	1241	LEU	-	expression tag	UNP P0DTC2
B	1242	ASN	-	expression tag	UNP P0DTC2
B	1243	ASP	-	expression tag	UNP P0DTC2
B	1244	ILE	-	expression tag	UNP P0DTC2
B	1245	PHE	-	expression tag	UNP P0DTC2
B	1246	GLU	-	expression tag	UNP P0DTC2
B	1247	ALA	-	expression tag	UNP P0DTC2
B	1248	GLN	-	expression tag	UNP P0DTC2
B	1249	LYS	-	expression tag	UNP P0DTC2
B	1250	ILE	-	expression tag	UNP P0DTC2
B	1251	GLU	-	expression tag	UNP P0DTC2
B	1252	TRP	-	expression tag	UNP P0DTC2
B	1253	HIS	-	expression tag	UNP P0DTC2
B	1254	GLU	-	expression tag	UNP P0DTC2
B	1255	GLY	-	expression tag	UNP P0DTC2
B	1256	ALA	-	expression tag	UNP P0DTC2
B	1257	SER	-	expression tag	UNP P0DTC2
B	1258	GLY	-	expression tag	UNP P0DTC2
B	1259	GLU	-	expression tag	UNP P0DTC2
B	1260	ASN	-	expression tag	UNP P0DTC2
B	1261	LEU	-	expression tag	UNP P0DTC2
B	1262	TYR	-	expression tag	UNP P0DTC2
B	1263	PHE	-	expression tag	UNP P0DTC2
B	1264	GLN	-	expression tag	UNP P0DTC2
B	1265	GLY	-	expression tag	UNP P0DTC2
B	1266	HIS	-	expression tag	UNP P0DTC2
B	1267	HIS	-	expression tag	UNP P0DTC2
B	1268	HIS	-	expression tag	UNP P0DTC2
B	1269	HIS	-	expression tag	UNP P0DTC2
B	1270	HIS	-	expression tag	UNP P0DTC2
B	1271	HIS	-	expression tag	UNP P0DTC2
B	1272	HIS	-	expression tag	UNP P0DTC2
B	1273	HIS	-	expression tag	UNP P0DTC2
C	682	GLY	ARG	engineered mutation	UNP P0DTC2
C	683	SER	ARG	engineered mutation	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	685	SER	ARG	engineered mutation	UNP P0DTC2
C	817	PRO	PHE	engineered mutation	UNP P0DTC2
C	892	PRO	ALA	engineered mutation	UNP P0DTC2
C	899	PRO	ALA	engineered mutation	UNP P0DTC2
C	942	PRO	ALA	engineered mutation	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	1209	SER	-	expression tag	UNP P0DTC2
C	1210	GLY	-	expression tag	UNP P0DTC2
C	1211	TYR	-	expression tag	UNP P0DTC2
C	1212	ILE	-	expression tag	UNP P0DTC2
C	1213	PRO	-	expression tag	UNP P0DTC2
C	1214	GLU	-	expression tag	UNP P0DTC2
C	1215	ALA	-	expression tag	UNP P0DTC2
C	1216	PRO	-	expression tag	UNP P0DTC2
C	1217	ARG	-	expression tag	UNP P0DTC2
C	1218	ASP	-	expression tag	UNP P0DTC2
C	1219	GLY	-	expression tag	UNP P0DTC2
C	1220	GLN	-	expression tag	UNP P0DTC2
C	1221	ALA	-	expression tag	UNP P0DTC2
C	1222	TYR	-	expression tag	UNP P0DTC2
C	1223	VAL	-	expression tag	UNP P0DTC2
C	1224	ARG	-	expression tag	UNP P0DTC2
C	1225	LYS	-	expression tag	UNP P0DTC2
C	1226	ASP	-	expression tag	UNP P0DTC2
C	1227	GLY	-	expression tag	UNP P0DTC2
C	1228	GLU	-	expression tag	UNP P0DTC2
C	1229	TRP	-	expression tag	UNP P0DTC2
C	1230	VAL	-	expression tag	UNP P0DTC2
C	1231	LEU	-	expression tag	UNP P0DTC2
C	1232	LEU	-	expression tag	UNP P0DTC2
C	1233	SER	-	expression tag	UNP P0DTC2
C	1234	THR	-	expression tag	UNP P0DTC2
C	1235	PHE	-	expression tag	UNP P0DTC2
C	1236	LEU	-	expression tag	UNP P0DTC2
C	1237	SER	-	expression tag	UNP P0DTC2
C	1238	ALA	-	expression tag	UNP P0DTC2
C	1239	GLY	-	expression tag	UNP P0DTC2
C	1240	GLY	-	expression tag	UNP P0DTC2
C	1241	LEU	-	expression tag	UNP P0DTC2
C	1242	ASN	-	expression tag	UNP P0DTC2
C	1243	ASP	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1244	ILE	-	expression tag	UNP P0DTC2
C	1245	PHE	-	expression tag	UNP P0DTC2
C	1246	GLU	-	expression tag	UNP P0DTC2
C	1247	ALA	-	expression tag	UNP P0DTC2
C	1248	GLN	-	expression tag	UNP P0DTC2
C	1249	LYS	-	expression tag	UNP P0DTC2
C	1250	ILE	-	expression tag	UNP P0DTC2
C	1251	GLU	-	expression tag	UNP P0DTC2
C	1252	TRP	-	expression tag	UNP P0DTC2
C	1253	HIS	-	expression tag	UNP P0DTC2
C	1254	GLU	-	expression tag	UNP P0DTC2
C	1255	GLY	-	expression tag	UNP P0DTC2
C	1256	ALA	-	expression tag	UNP P0DTC2
C	1257	SER	-	expression tag	UNP P0DTC2
C	1258	GLY	-	expression tag	UNP P0DTC2
C	1259	GLU	-	expression tag	UNP P0DTC2
C	1260	ASN	-	expression tag	UNP P0DTC2
C	1261	LEU	-	expression tag	UNP P0DTC2
C	1262	TYR	-	expression tag	UNP P0DTC2
C	1263	PHE	-	expression tag	UNP P0DTC2
C	1264	GLN	-	expression tag	UNP P0DTC2
C	1265	GLY	-	expression tag	UNP P0DTC2
C	1266	HIS	-	expression tag	UNP P0DTC2
C	1267	HIS	-	expression tag	UNP P0DTC2
C	1268	HIS	-	expression tag	UNP P0DTC2
C	1269	HIS	-	expression tag	UNP P0DTC2
C	1270	HIS	-	expression tag	UNP P0DTC2
C	1271	HIS	-	expression tag	UNP P0DTC2
C	1272	HIS	-	expression tag	UNP P0DTC2
C	1273	HIS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called neutralizing antibody C1C-A3 heavy chain variable region.

Mol	Chain	Residues	Atoms				AltConf	Trace	
2	D	121	Total	C	N	O	S	0	0
			968	618	169	177	4		
2	F	121	Total	C	N	O	S	0	0
			968	618	169	177	4		
2	H	121	Total	C	N	O	S	0	0
			968	618	169	177	4		

- Molecule 3 is a protein called neutralizing antibody C1C-A3 light chain variable region.

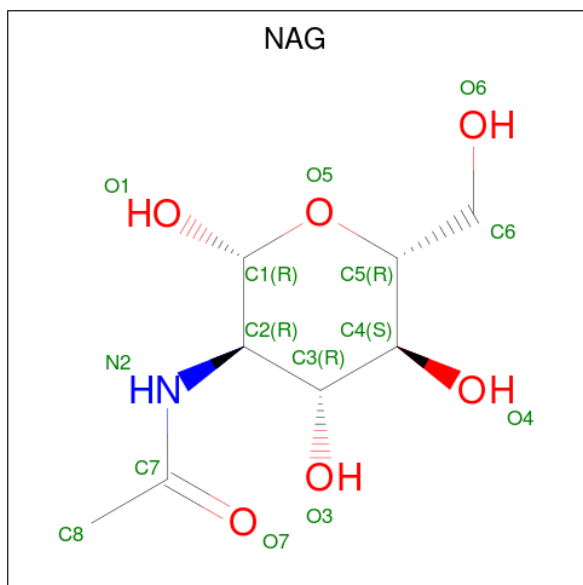
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	E	108	Total 824	C 520	N 141	O 160	S 3	0	0
3	G	108	Total 824	C 520	N 141	O 160	S 3	0	0
3	L	108	Total 824	C 520	N 141	O 160	S 3	0	0

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



Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	I	3	Total 39	C 22	N 2	O 15	0	0
4	J	3	Total 39	C 22	N 2	O 15	0	0
4	K	3	Total 39	C 22	N 2	O 15	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	A	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0

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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
5	B	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0
5	B	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0
5	C	1	Total 210	C 120	N 15	O 75	0

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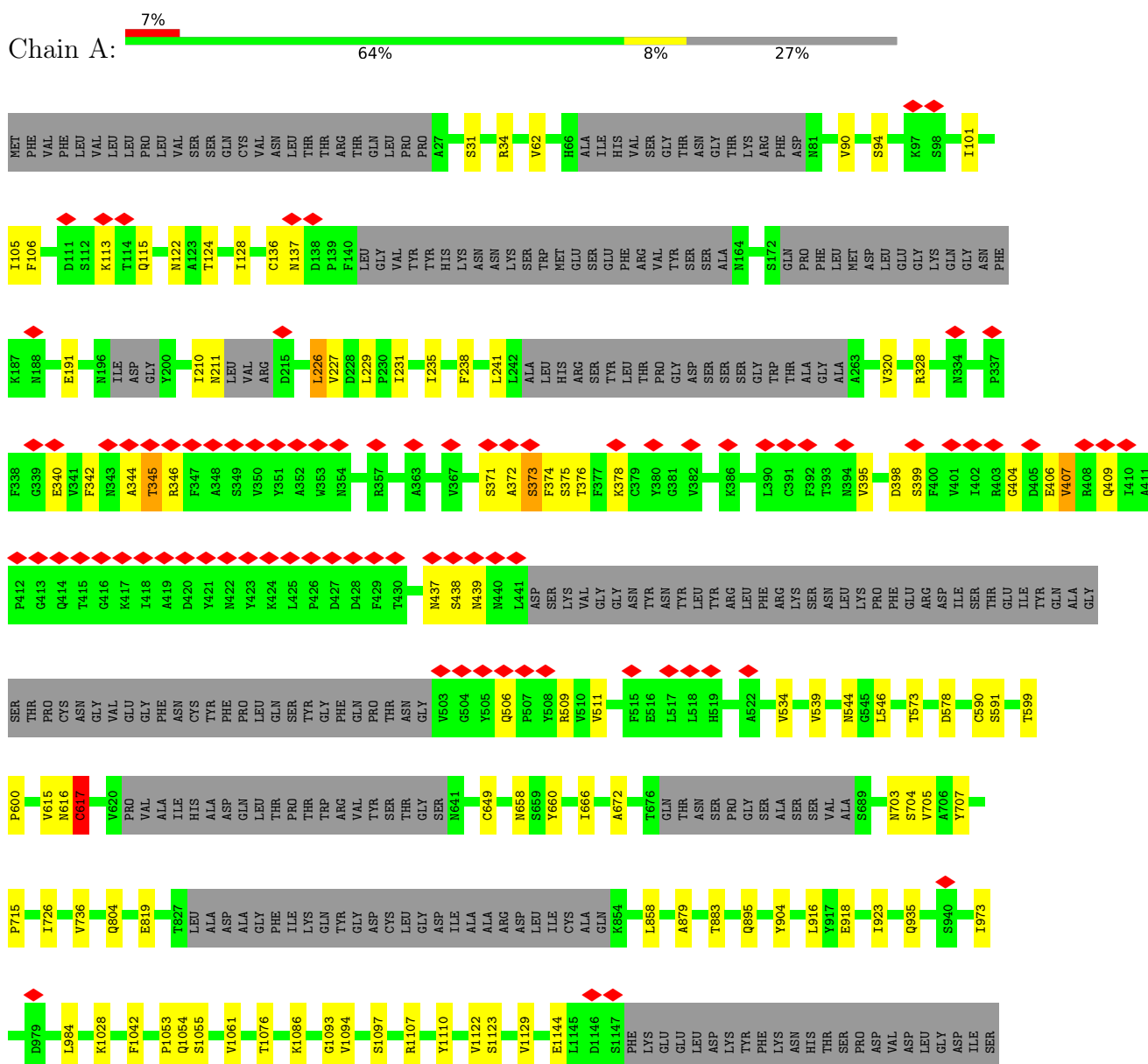
Continued from previous page...

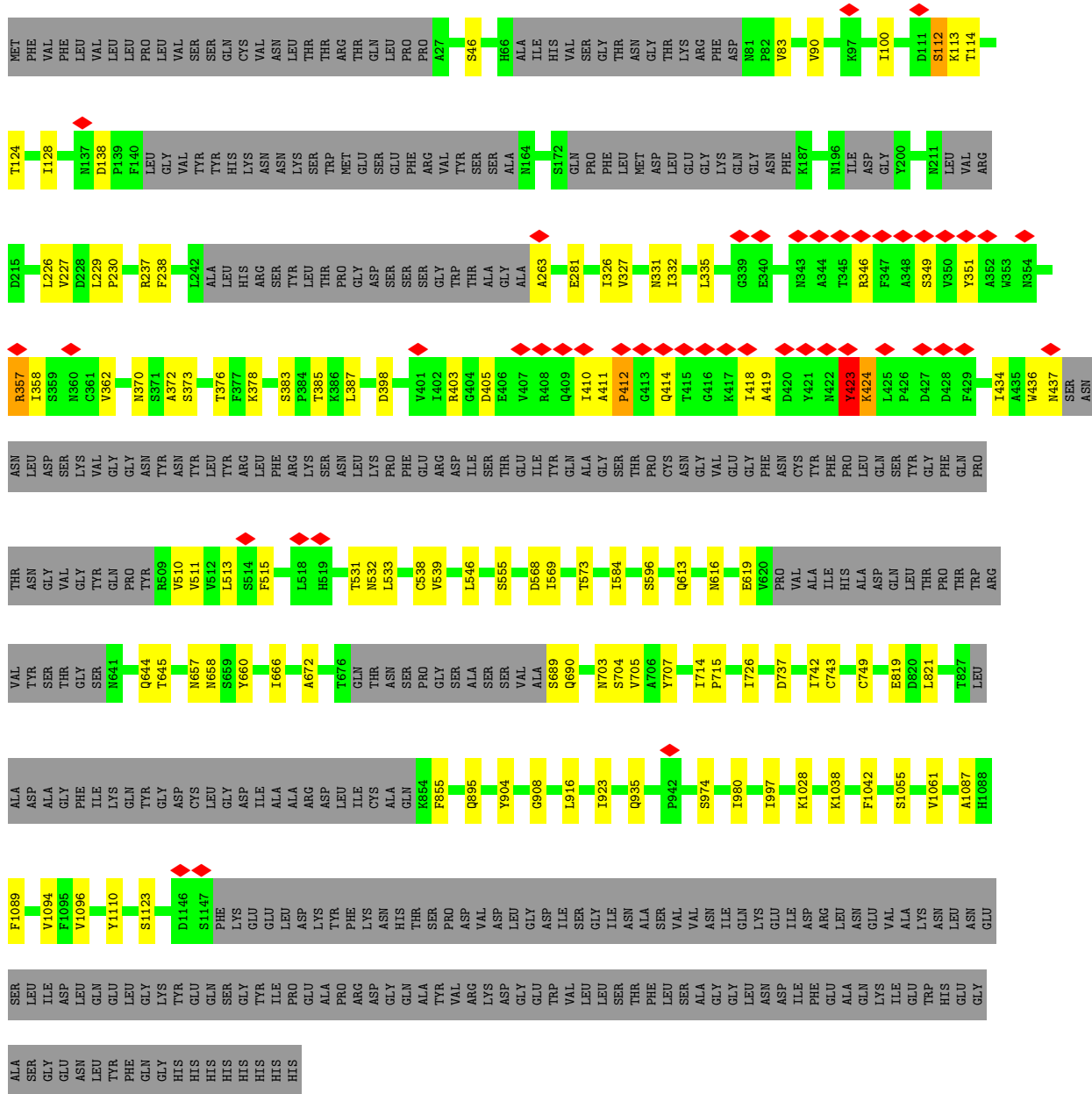
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
5	C	1	210	120	15	75	0
5	C	1	210	120	15	75	0

3 Residue-property plots

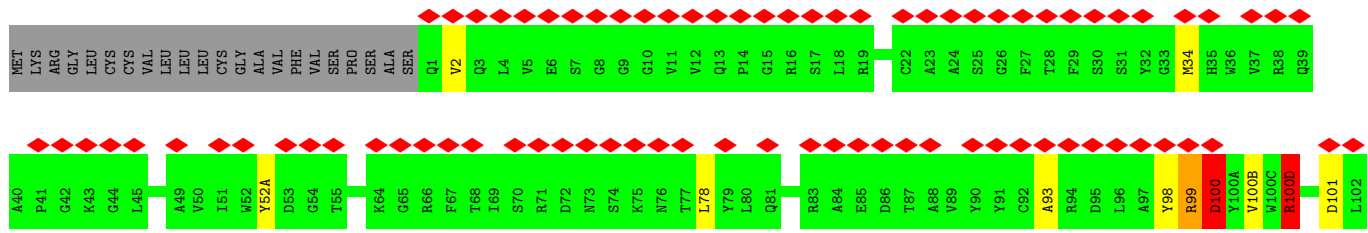
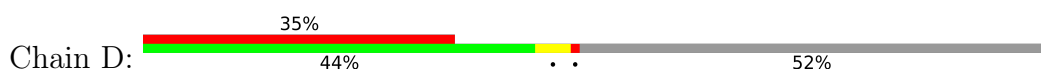
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

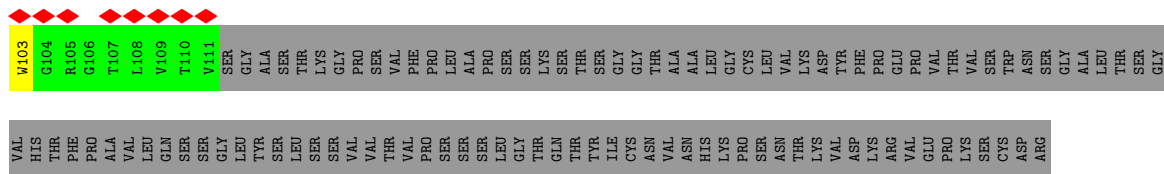
- Molecule 1: Spike glycoprotein



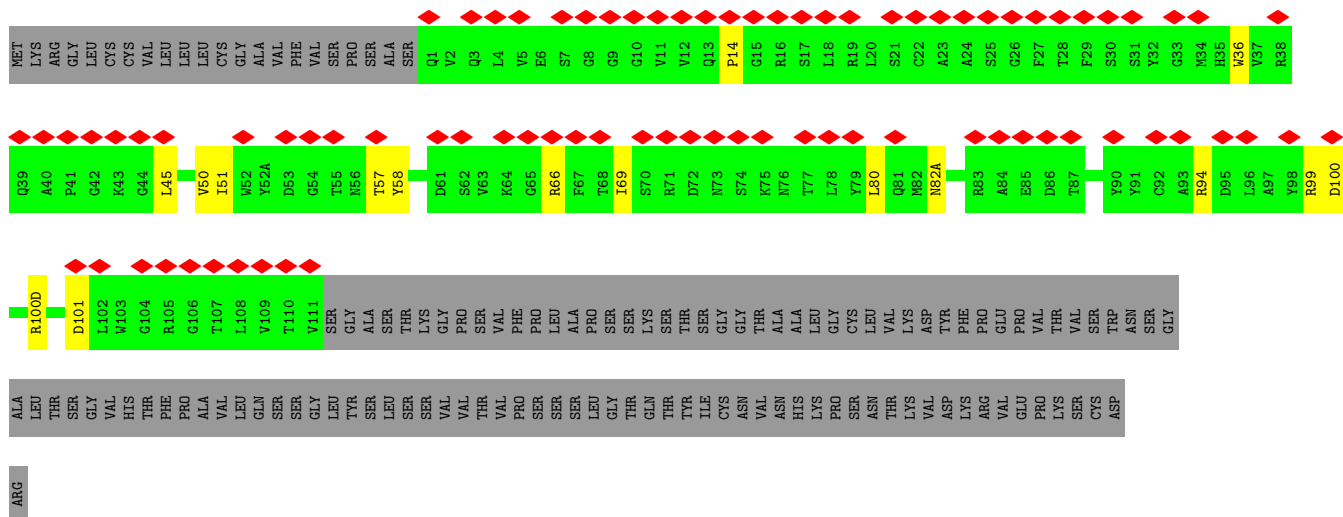
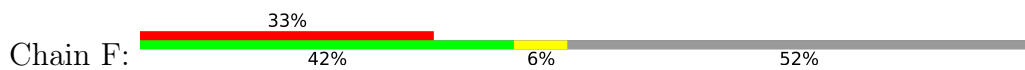


● Molecule 2: neutralizing antibody C1C-A3 heavy chain variable region

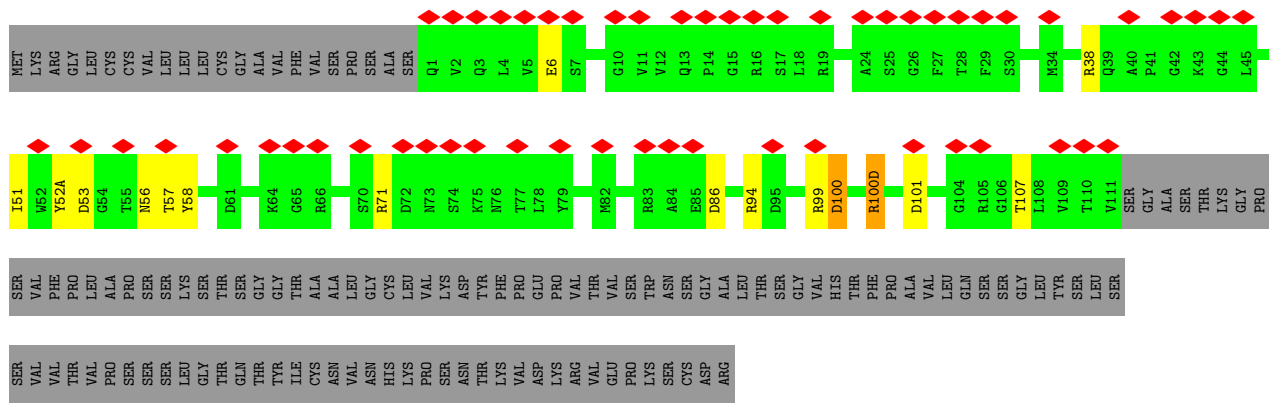
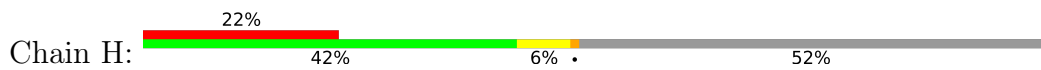




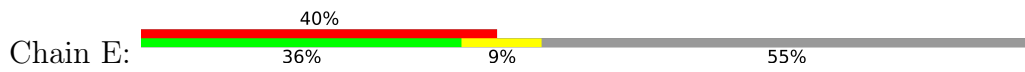
• Molecule 2: neutralizing antibody C1C-A3 heavy chain variable region

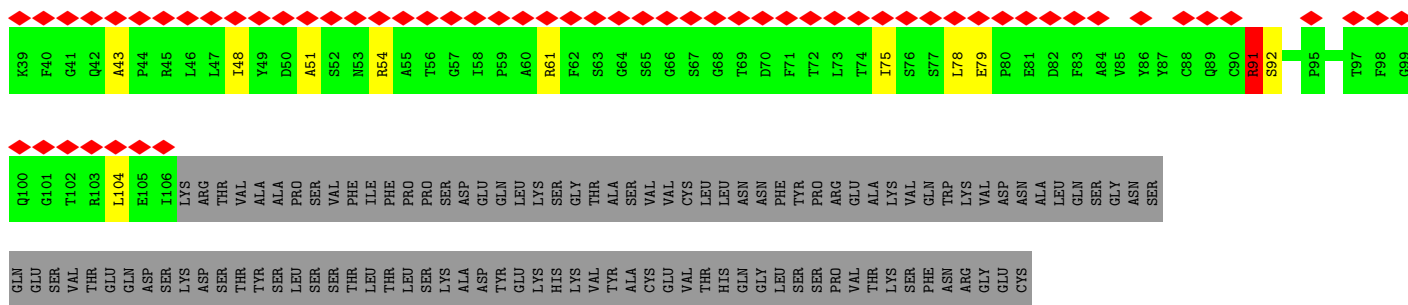


• Molecule 2: neutralizing antibody C1C-A3 heavy chain variable region

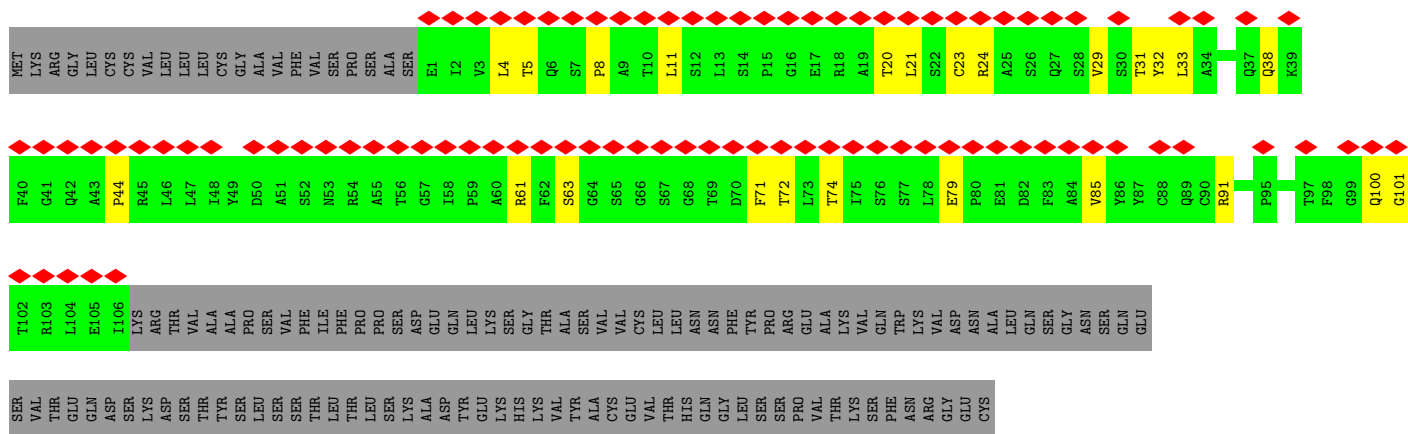
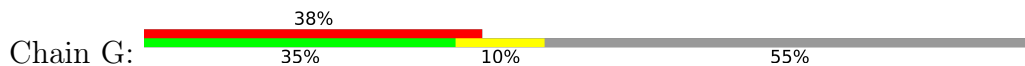


• Molecule 3: neutralizing antibody C1C-A3 light chain variable region

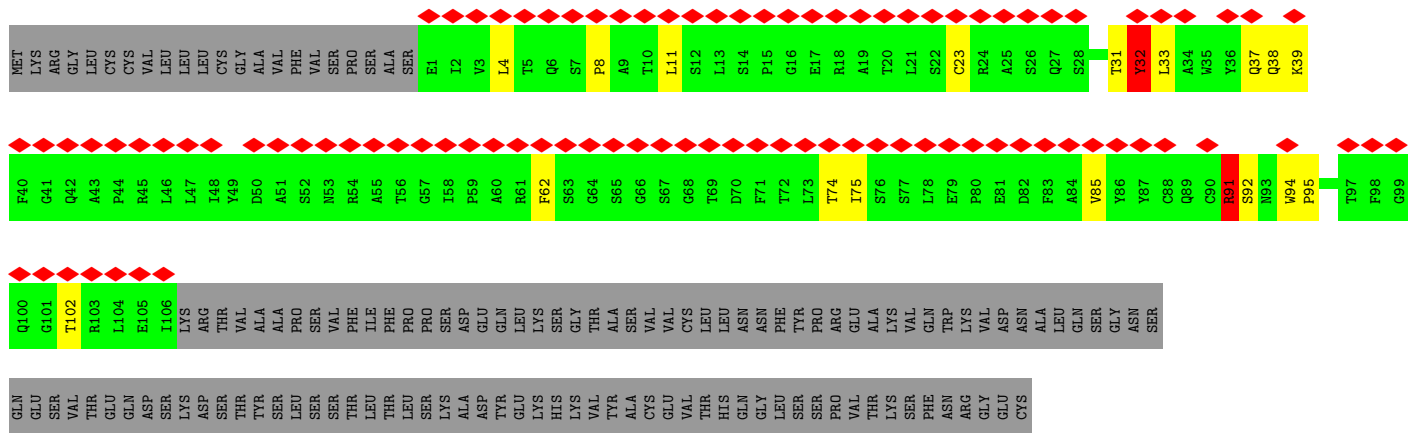
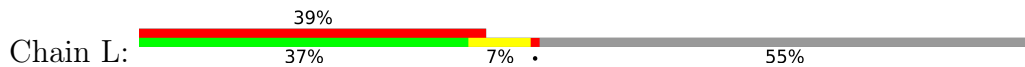




• Molecule 3: neutralizing antibody C1C-A3 light chain variable region



• Molecule 3: neutralizing antibody C1C-A3 light chain variable region



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





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

Chain J:  67% 33%



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

Chain K:  100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	344920	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.6	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	60606	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.073	Depositor
Minimum map value	-1.124	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.056	Depositor
Recommended contour level	0.25	Depositor
Map size (\AA)	297.0, 297.0, 297.0	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.825, 0.825, 0.825	Depositor

5 Model quality i

5.1 Standard geometry i

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

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	0.50	2/7294 (0.0%)	0.67	2/9939 (0.0%)
1	B	0.48	0/7291	0.66	0/9935
1	C	0.49	0/7210	0.69	3/9823 (0.0%)
2	D	0.37	0/994	0.84	2/1351 (0.1%)
2	F	0.38	0/994	0.78	0/1351
2	H	0.36	0/994	0.84	2/1351 (0.1%)
3	E	0.34	0/844	0.80	1/1150 (0.1%)
3	G	0.33	0/844	0.73	0/1150
3	L	0.57	2/844 (0.2%)	1.14	5/1150 (0.4%)
All	All	0.47	4/27309 (0.0%)	0.71	15/37200 (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	4
1	B	0	7
1	C	0	5
2	D	0	3
2	H	0	1
3	E	0	2
3	G	0	1
3	L	0	4
All	All	0	27

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	32	TYR	CD1-CE1	-10.73	1.23	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	617	CYS	CB-SG	-8.93	1.67	1.82
1	A	649	CYS	CB-SG	-8.09	1.68	1.82
3	L	32	TYR	CD2-CE2	5.50	1.47	1.39

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	32	TYR	CB-CG-CD1	-19.56	109.27	121.00
3	L	32	TYR	CB-CG-CD2	15.19	130.12	121.00
2	H	100	ASP	CB-CG-OD2	12.77	129.79	118.30
2	H	100	ASP	CB-CG-OD1	-9.70	109.57	118.30
2	D	100	ASP	N-CA-CB	9.33	127.39	110.60

There are no chirality outliers.

5 of 27 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	346	ARG	Peptide
1	A	371	SER	Peptide
1	A	373	SER	Peptide
1	A	617	CYS	Peptide
1	B	113	LYS	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7136	0	6930	75	0
1	B	7133	0	6922	71	0
1	C	7055	0	6853	75	0
2	D	968	0	925	17	0
2	F	968	0	925	12	0
2	H	968	0	925	14	0
3	E	824	0	799	14	0
3	G	824	0	799	19	0
3	L	824	0	799	14	0
4	I	39	0	34	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	J	39	0	34	1	0
4	K	39	0	34	0	0
5	A	210	0	195	3	0
5	B	210	0	195	2	0
5	C	210	0	194	2	0
All	All	27447	0	26563	269	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 5.

The worst 5 of 269 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:B:372:ALA:O	2:F:100(D):ARG:NH2	1.92	1.03
1:C:372:ALA:O	2:H:100(D):ARG:NH2	1.93	1.01
1:A:372:ALA:O	2:D:100(D):ARG:NH2	1.94	1.00
1:A:128:ILE:HG21	1:A:229:LEU:HD21	1.51	0.93
1:A:376:THR:HA	2:D:100:ASP:OD2	1.77	0.83

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	903/1273 (71%)	895 (99%)	3 (0%)	5 (1%)	25 59
1	B	902/1273 (71%)	899 (100%)	2 (0%)	1 (0%)	51 83
1	C	893/1273 (70%)	885 (99%)	4 (0%)	4 (0%)	34 69
2	D	119/250 (48%)	119 (100%)	0	0	100 100
2	F	119/250 (48%)	119 (100%)	0	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	119/250 (48%)	119 (100%)	0	0	100	100
3	E	106/238 (44%)	105 (99%)	1 (1%)	0	100	100
3	G	106/238 (44%)	105 (99%)	1 (1%)	0	100	100
3	L	106/238 (44%)	105 (99%)	1 (1%)	0	100	100
All	All	3373/5283 (64%)	3351 (99%)	12 (0%)	10 (0%)	44	73

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	113	LYS
1	A	345	THR
1	A	407	VAL
1	B	115	GLN
1	C	112	SER

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	793/1108 (72%)	792 (100%)	1 (0%)	93	98
1	B	793/1108 (72%)	792 (100%)	1 (0%)	93	98
1	C	784/1108 (71%)	780 (100%)	4 (0%)	88	94
2	D	99/210 (47%)	99 (100%)	0	100	100
2	F	99/210 (47%)	98 (99%)	1 (1%)	76	90
2	H	99/210 (47%)	99 (100%)	0	100	100
3	E	89/205 (43%)	89 (100%)	0	100	100
3	G	89/205 (43%)	89 (100%)	0	100	100
3	L	89/205 (43%)	89 (100%)	0	100	100
All	All	2934/4569 (64%)	2927 (100%)	7 (0%)	93	97

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	403	ARG
1	C	616	ASN
2	F	14	PRO
1	C	657	ASN
1	C	357	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	439	ASN
1	B	437	ASN
1	B	804	GLN
1	C	437	ASN
3	G	100	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](#)

9 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	I	1	4,1	14,14,15	0.44	0	17,19,21	0.71	1 (5%)
4	NAG	I	2	4	14,14,15	0.20	0	17,19,21	0.54	0
4	BMA	I	3	4	11,11,12	0.60	0	15,15,17	1.28	2 (13%)
4	NAG	J	1	4,1	14,14,15	0.43	0	17,19,21	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	J	2	4	14,14,15	0.18	0	17,19,21	0.46	0
4	BMA	J	3	4	11,11,12	0.61	0	15,15,17	0.89	0
4	NAG	K	1	4,1	14,14,15	0.25	0	17,19,21	0.42	0
4	NAG	K	2	4	14,14,15	0.35	0	17,19,21	0.47	0
4	BMA	K	3	4	11,11,12	0.50	0	15,15,17	0.95	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	I	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	I	2	4	-	2/6/23/26	0/1/1/1
4	BMA	I	3	4	-	0/2/19/22	0/1/1/1
4	NAG	J	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	J	2	4	-	1/6/23/26	0/1/1/1
4	BMA	J	3	4	-	0/2/19/22	0/1/1/1
4	NAG	K	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	K	2	4	-	1/6/23/26	0/1/1/1
4	BMA	K	3	4	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	3	BMA	C1-O5-C5	2.83	116.02	112.19
4	I	3	BMA	O2-C2-C3	-2.25	105.64	110.14
4	I	1	NAG	C1-O5-C5	2.23	115.21	112.19

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

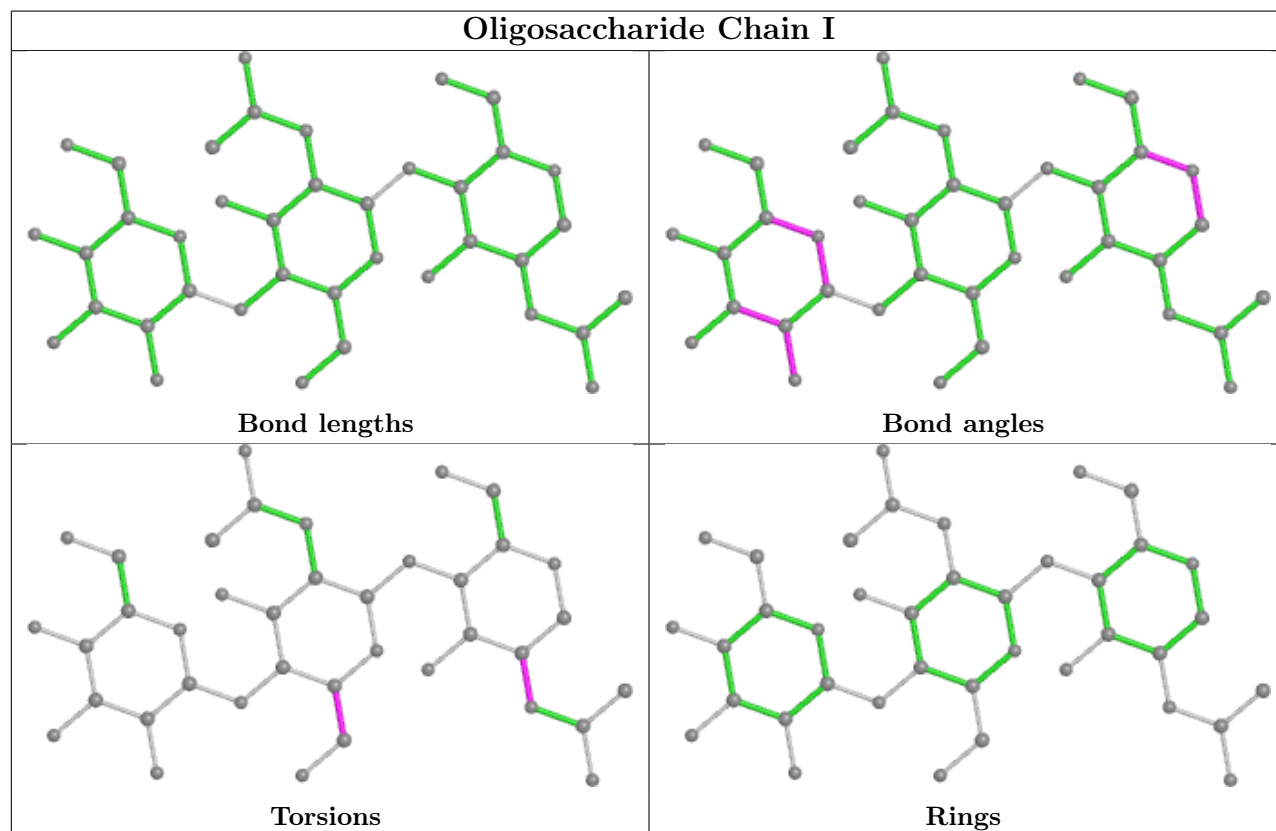
Mol	Chain	Res	Type	Atoms
4	I	1	NAG	C1-C2-N2-C7
4	K	3	BMA	O5-C5-C6-O6
4	K	3	BMA	C4-C5-C6-O6
4	K	1	NAG	O5-C5-C6-O6
4	I	2	NAG	O5-C5-C6-O6

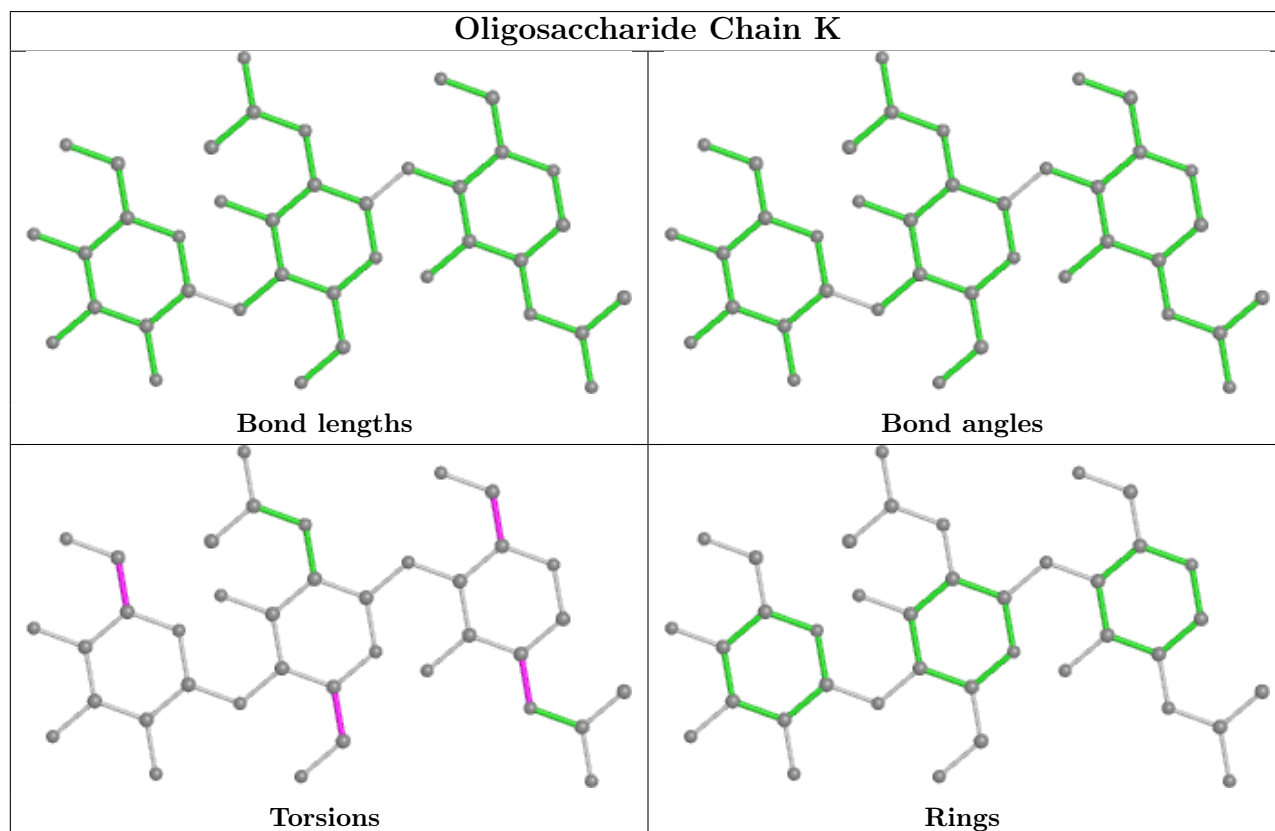
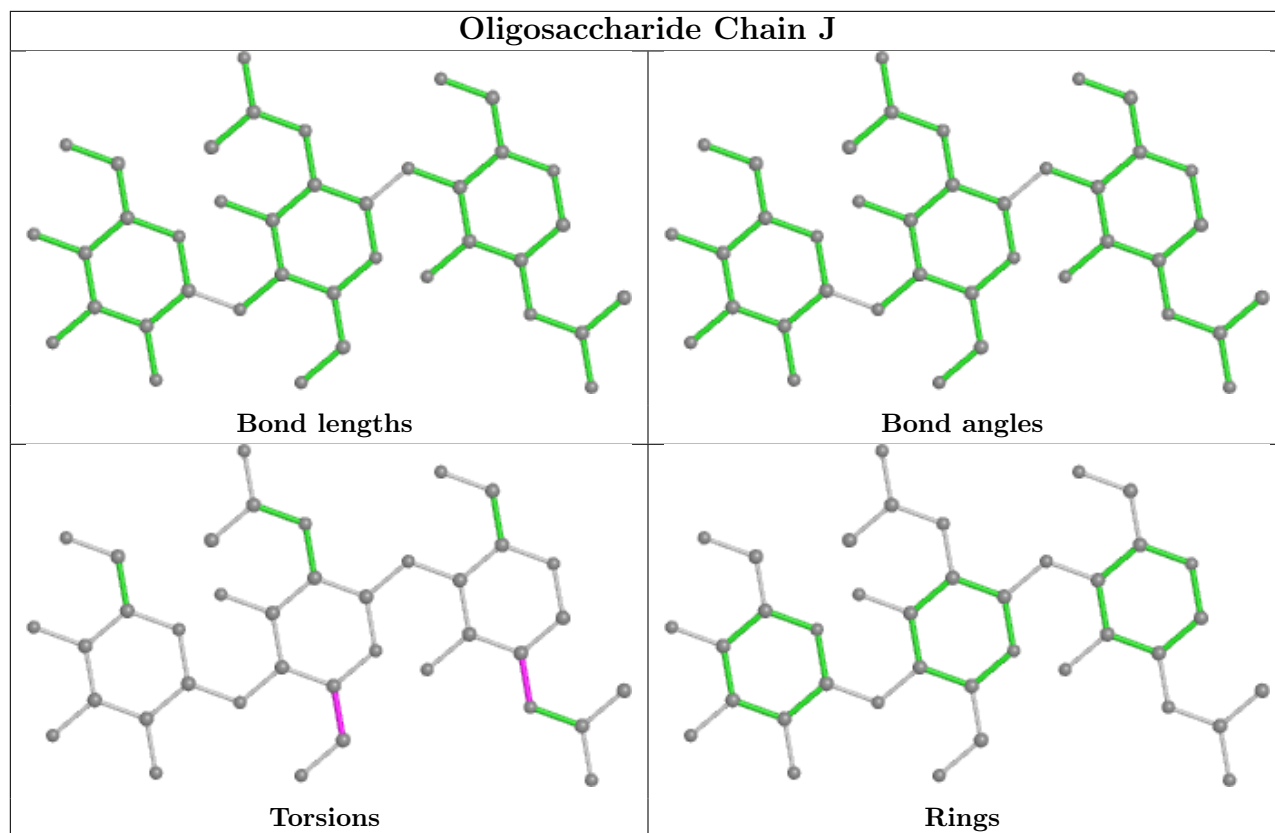
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	J	1	NAG	1	0
4	I	1	NAG	3	0

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





5.6 Ligand geometry

45 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
5	NAG	C	1314	1	14,14,15	0.40	0	17,19,21	0.33	0
5	NAG	C	1315	1	14,14,15	0.26	0	17,19,21	0.35	0
5	NAG	C	1305	1	14,14,15	0.58	0	17,19,21	0.97	1 (5%)
5	NAG	B	1311	1	14,14,15	0.42	0	17,19,21	0.50	0
5	NAG	B	1314	1	14,14,15	0.29	0	17,19,21	0.40	0
5	NAG	A	1314	1	14,14,15	0.37	0	17,19,21	0.52	0
5	NAG	B	1309	1	14,14,15	0.38	0	17,19,21	0.41	0
5	NAG	B	1302	1	14,14,15	0.43	0	17,19,21	0.40	0
5	NAG	B	1305	1	14,14,15	0.35	0	17,19,21	0.47	0
5	NAG	A	1315	1	14,14,15	0.36	0	17,19,21	0.56	0
5	NAG	A	1305	1	14,14,15	0.25	0	17,19,21	0.84	1 (5%)
5	NAG	B	1306	1	14,14,15	0.26	0	17,19,21	0.35	0
5	NAG	C	1313	1	14,14,15	0.21	0	17,19,21	0.38	0
5	NAG	B	1315	1	14,14,15	0.21	0	17,19,21	0.57	0
5	NAG	B	1304	1	14,14,15	0.36	0	17,19,21	0.56	0
5	NAG	C	1301	1	14,14,15	0.34	0	17,19,21	0.37	0
5	NAG	A	1311	1	14,14,15	0.45	0	17,19,21	0.40	0
5	NAG	A	1307	1	14,14,15	0.38	0	17,19,21	0.59	0
5	NAG	A	1310	1	14,14,15	0.26	0	17,19,21	0.58	0
5	NAG	B	1310	1	14,14,15	0.29	0	17,19,21	0.56	0
5	NAG	A	1303	1	14,14,15	0.34	0	17,19,21	0.37	0
5	NAG	A	1304	1	14,14,15	0.30	0	17,19,21	0.54	0
5	NAG	C	1304	1	14,14,15	0.37	0	17,19,21	0.36	0
5	NAG	A	1313	1	14,14,15	0.25	0	17,19,21	0.35	0
5	NAG	C	1312	1	14,14,15	0.37	0	17,19,21	0.42	0
5	NAG	A	1301	1	14,14,15	0.33	0	17,19,21	0.44	0
5	NAG	C	1303	1	14,14,15	0.31	0	17,19,21	0.34	0
5	NAG	B	1308	1	14,14,15	0.38	0	17,19,21	0.56	0
5	NAG	B	1313	1	14,14,15	0.21	0	17,19,21	0.44	0
5	NAG	C	1307	1	14,14,15	0.36	0	17,19,21	0.40	0
5	NAG	C	1302	1	14,14,15	0.45	0	17,19,21	0.36	0
5	NAG	C	1309	1	14,14,15	0.45	0	17,19,21	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	B	1303	1	14,14,15	0.38	0	17,19,21	0.52	0
5	NAG	C	1306	1	14,14,15	0.30	0	17,19,21	0.43	0
5	NAG	B	1307	1	14,14,15	0.35	0	17,19,21	0.47	0
5	NAG	A	1302	1	14,14,15	0.59	0	17,19,21	0.83	1 (5%)
5	NAG	A	1306	1	14,14,15	0.16	0	17,19,21	0.40	0
5	NAG	C	1310	1	14,14,15	0.33	0	17,19,21	0.51	0
5	NAG	C	1308	1	14,14,15	0.20	0	17,19,21	0.39	0
5	NAG	A	1308	1	14,14,15	0.17	0	17,19,21	0.61	1 (5%)
5	NAG	C	1311	1	14,14,15	0.35	0	17,19,21	0.56	0
5	NAG	A	1309	1	14,14,15	0.53	0	17,19,21	0.38	0
5	NAG	B	1301	1	14,14,15	0.21	0	17,19,21	0.40	0
5	NAG	A	1312	1	14,14,15	0.30	0	17,19,21	0.54	0
5	NAG	B	1312	1	14,14,15	0.17	0	17,19,21	0.59	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
5	NAG	C	1314	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1315	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1305	1	-	4/6/23/26	0/1/1/1
5	NAG	B	1311	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1314	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1314	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1309	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1302	1	-	4/6/23/26	0/1/1/1
5	NAG	B	1305	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1315	1	-	3/6/23/26	0/1/1/1
5	NAG	A	1305	1	-	3/6/23/26	0/1/1/1
5	NAG	B	1306	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1313	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1315	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1304	1	-	1/6/23/26	0/1/1/1
5	NAG	C	1301	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1311	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1307	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1310	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	B	1310	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1303	1	-	1/6/23/26	0/1/1/1
5	NAG	A	1304	1	-	4/6/23/26	0/1/1/1
5	NAG	C	1304	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1313	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1312	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1301	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1303	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1308	1	-	4/6/23/26	0/1/1/1
5	NAG	B	1313	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1307	1	-	0/6/23/26	0/1/1/1
5	NAG	C	1302	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1309	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1303	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1306	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1307	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1302	1	-	4/6/23/26	0/1/1/1
5	NAG	A	1306	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1310	1	-	1/6/23/26	0/1/1/1
5	NAG	C	1308	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1308	1	-	2/6/23/26	0/1/1/1
5	NAG	C	1311	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1309	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1301	1	-	0/6/23/26	0/1/1/1
5	NAG	A	1312	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1312	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	1305	NAG	C1-O5-C5	3.51	116.95	112.19
5	A	1305	NAG	C1-O5-C5	3.16	116.47	112.19
5	A	1302	NAG	C1-O5-C5	2.96	116.20	112.19
5	A	1308	NAG	C1-O5-C5	2.08	115.01	112.19

There are no chirality outliers.

5 of 81 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1304	NAG	O5-C5-C6-O6
5	A	1302	NAG	O5-C5-C6-O6
5	B	1314	NAG	O5-C5-C6-O6
5	A	1314	NAG	O5-C5-C6-O6
5	C	1315	NAG	O5-C5-C6-O6

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1305	NAG	1	0
5	B	1302	NAG	2	0
5	A	1315	NAG	2	0
5	C	1303	NAG	1	0
5	A	1302	NAG	1	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.

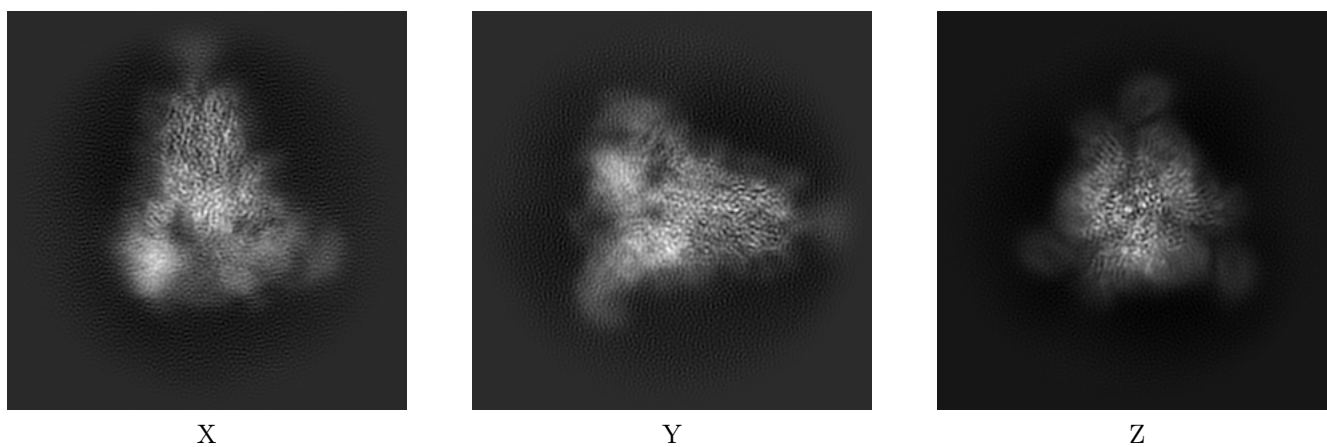
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25210. 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](#)

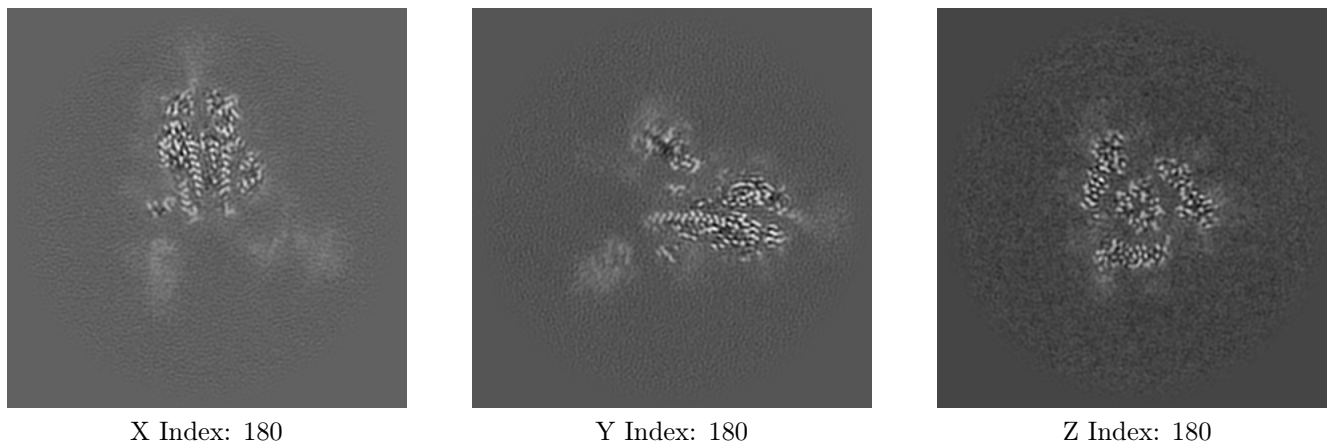
6.1.1 Primary map



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

6.2 Central slices [i](#)

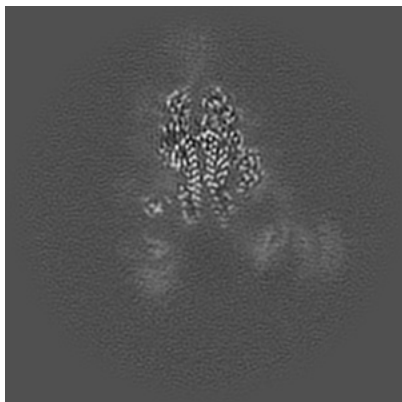
6.2.1 Primary map



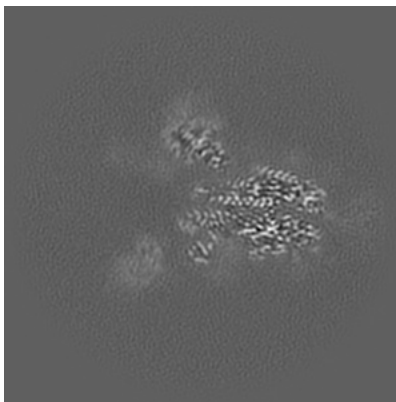
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

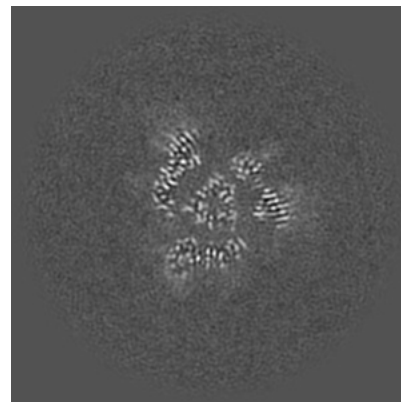
6.3.1 Primary map



X Index: 183



Y Index: 184

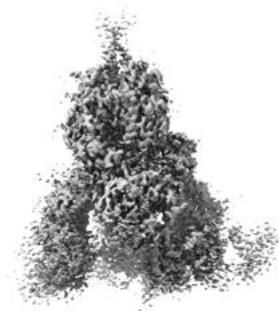


Z Index: 177

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

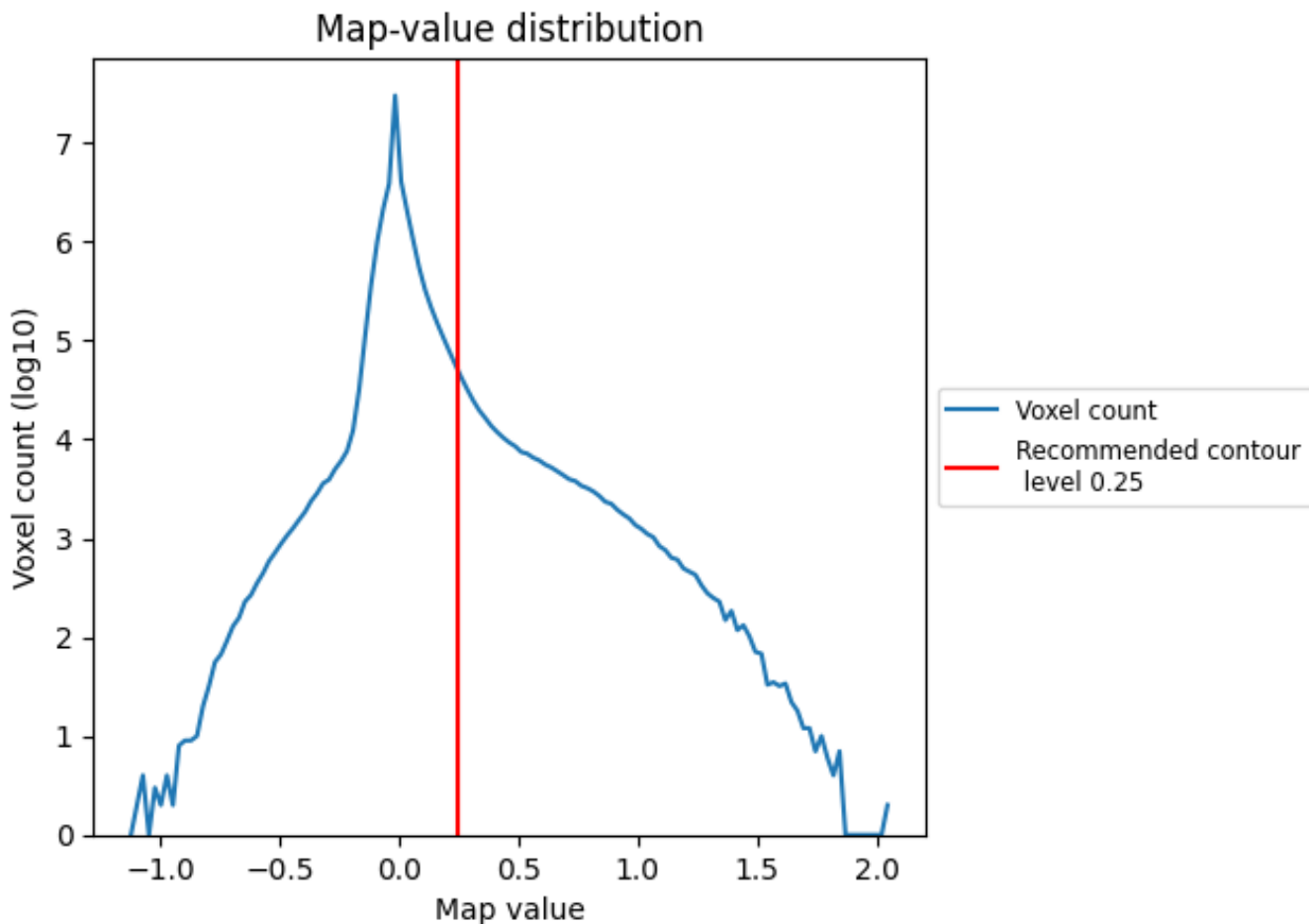
6.5 Mask visualisation

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

7 Map analysis [i](#)

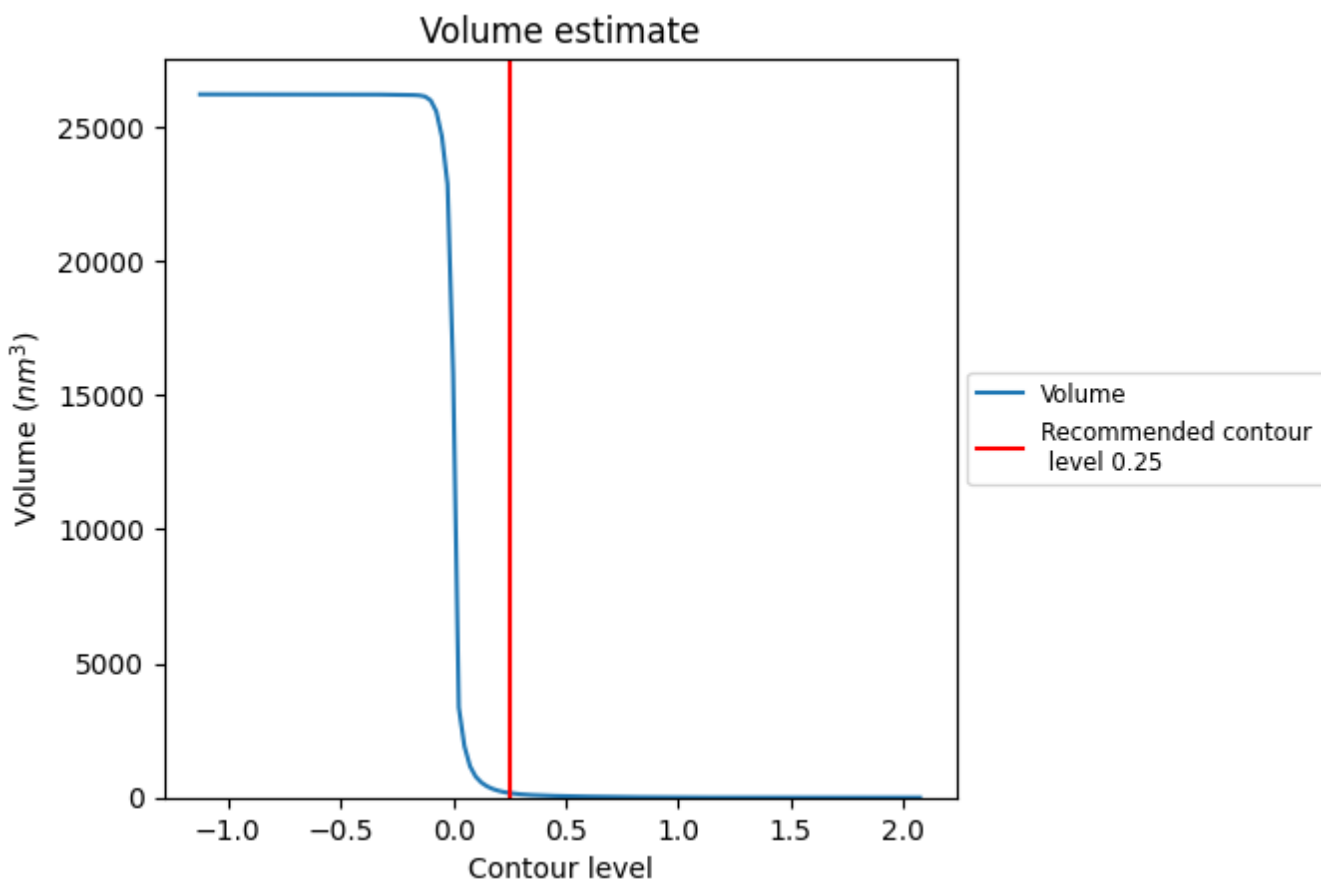
This section contains the results of statistical analysis of the map.

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.

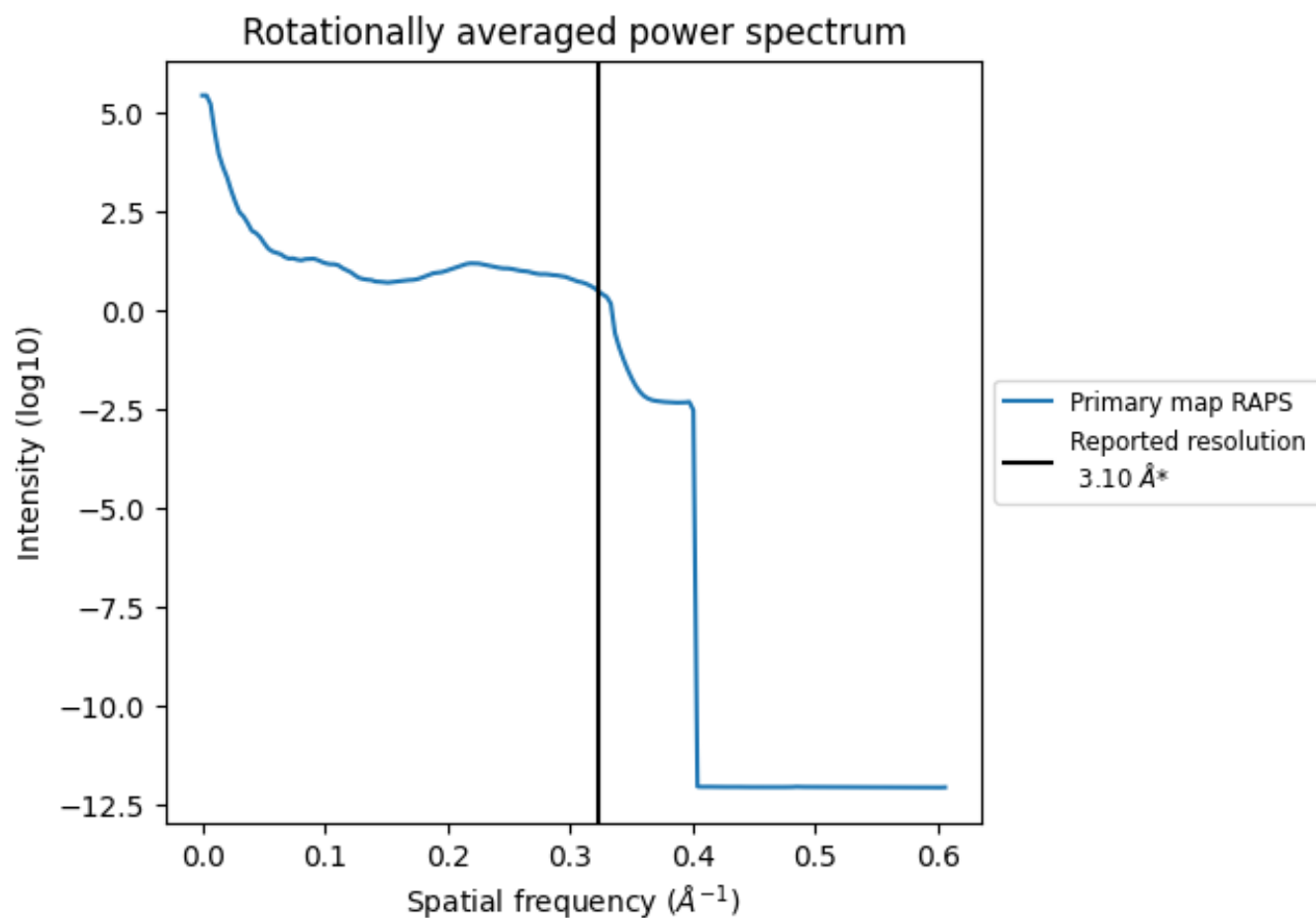
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 168 nm³; this corresponds to an approximate mass of 152 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 [i](#)

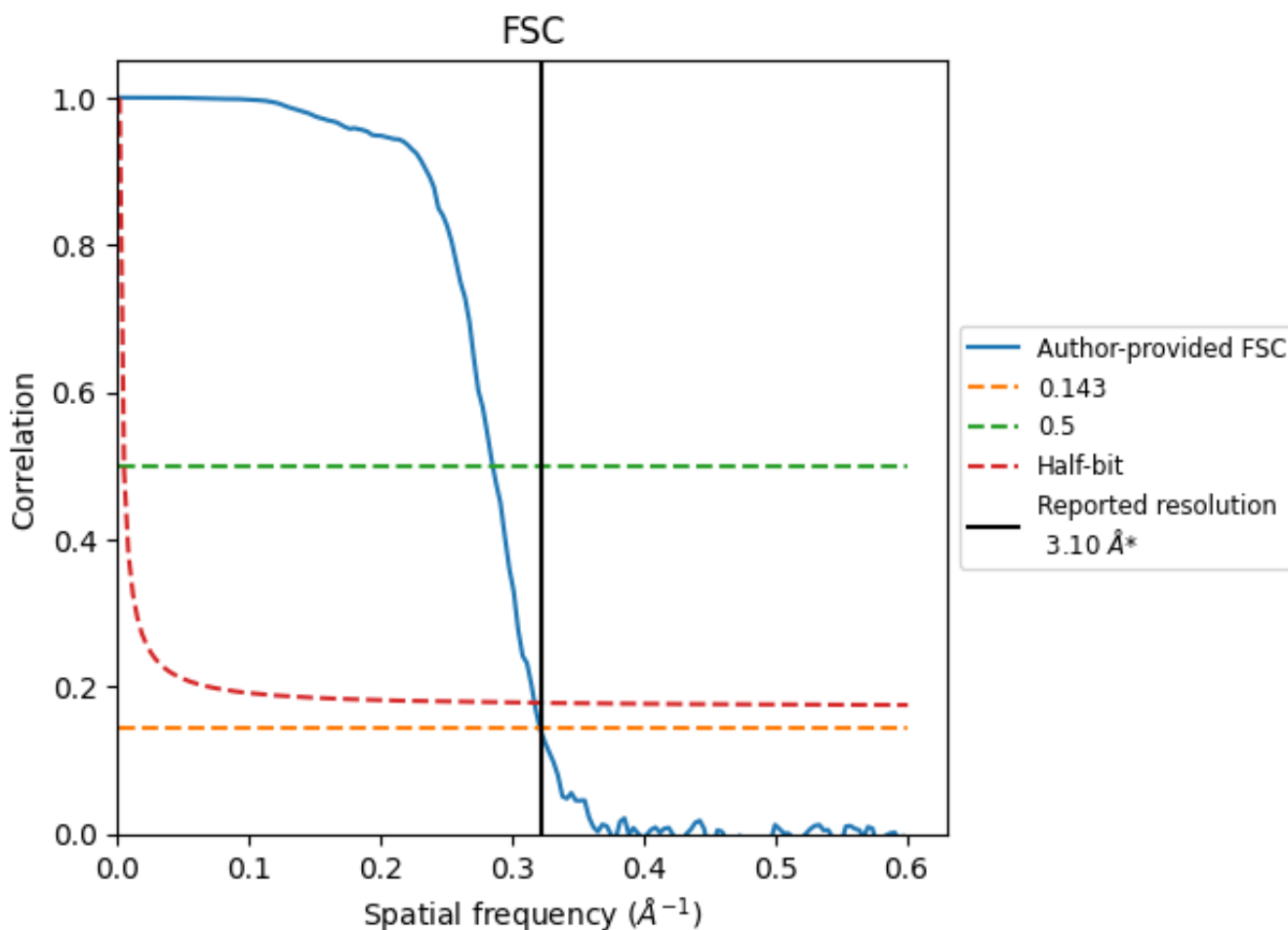


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

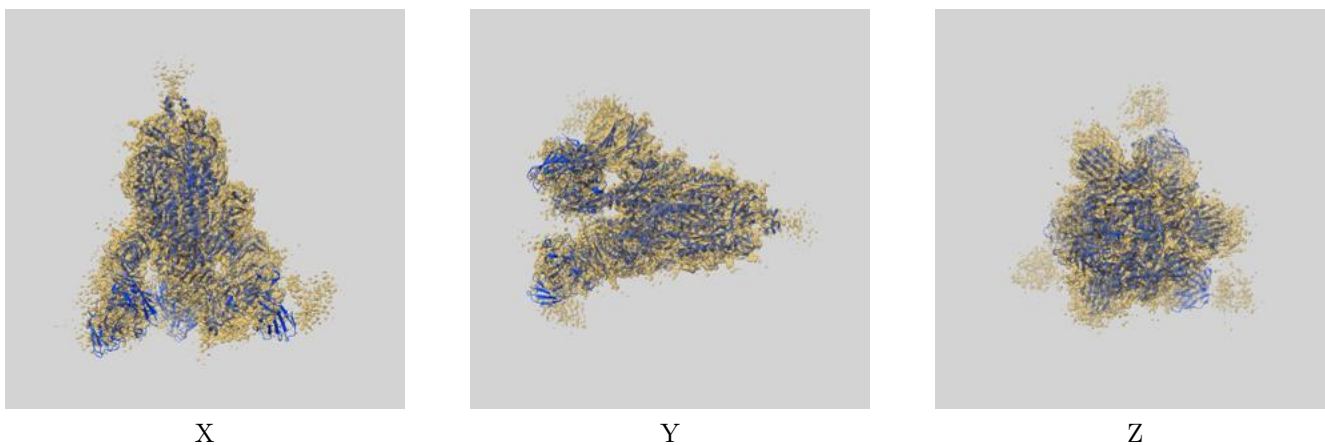
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.11	3.51	3.15
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

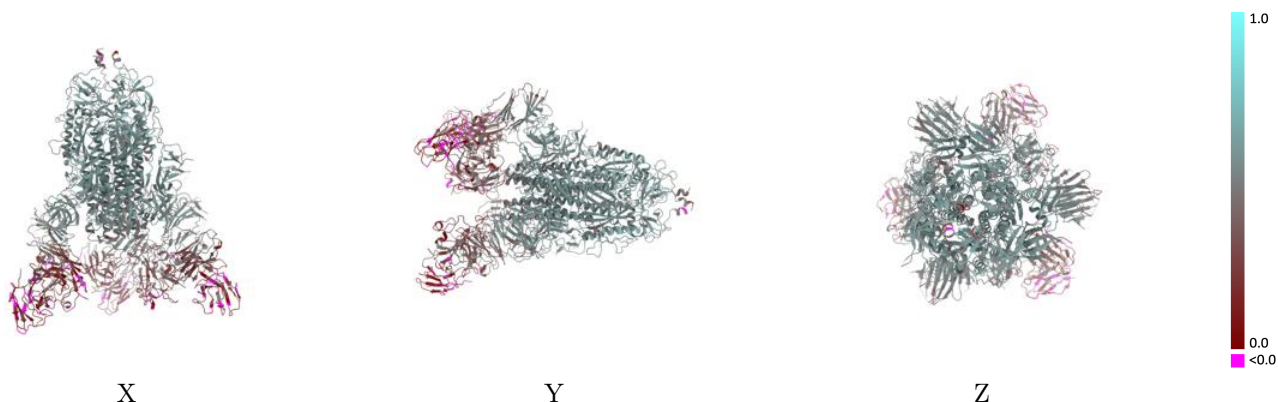
This section contains information regarding the fit between EMDB map EMD-25210 and PDB model 7SN3. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



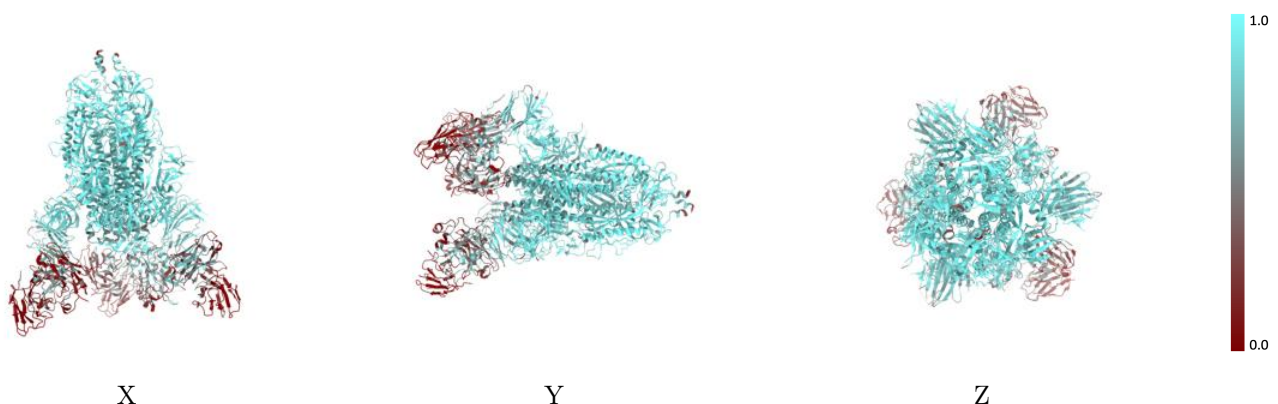
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



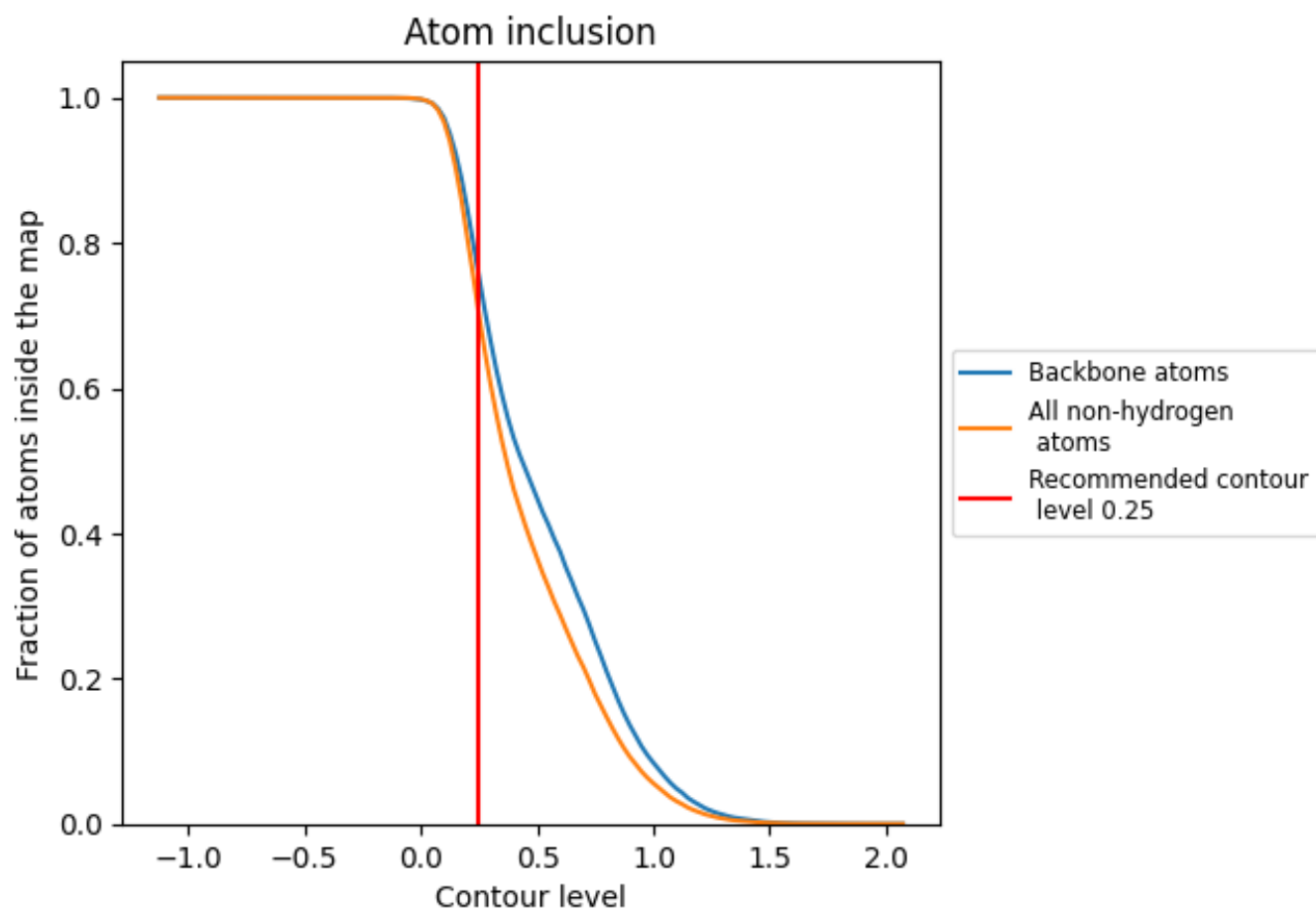
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).



























9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 70% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7011	 0.4510
A	 0.8005	 0.5000
B	 0.8040	 0.5010
C	 0.8206	 0.5110
D	 0.2454	 0.2150
E	 0.1382	 0.1630
F	 0.3301	 0.2970
G	 0.1880	 0.1920
H	 0.4341	 0.3300
I	 0.5128	 0.3690
J	 0.5385	 0.4040
K	 0.6154	 0.4350
L	 0.1743	 0.1920

