



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 11:05 AM UTC

PDB ID : 7QTJ / pdb_00007qtj
EMDB ID : EMD-14142
Title : SARS-CoV-2 S Omicron Spike B.1.1.529 - RBD up - 1-P2G3 and 1-P5C3 Fabs (Local)
Authors : Ni, D.; Lau, K.; Turelli, P.; Fenwick, C.; Perez, L.; Pojer, F.; Stahlberg, H.; Pantaleo, G.; Trono, D.
Deposited on : 2022-01-14
Resolution : 4.01 Å (reported)
Based on initial model : 7QO7

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:

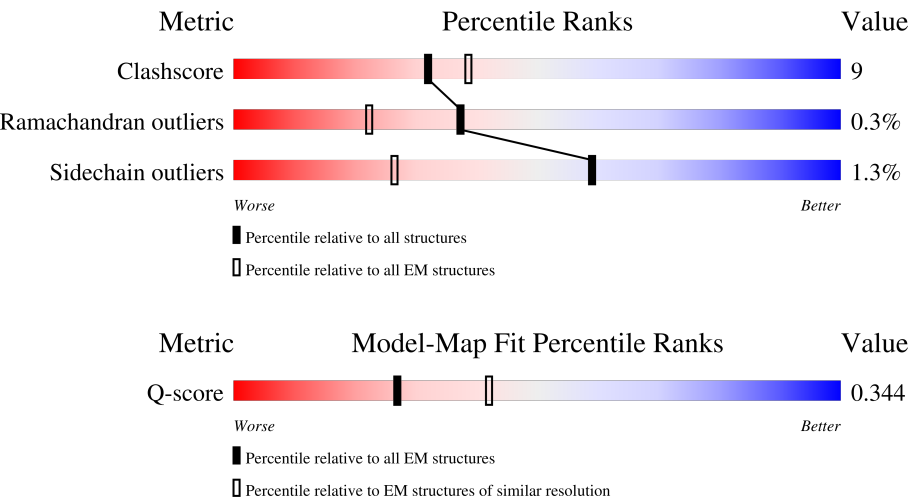
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.01 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	6765 (3.51 - 4.51)

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	228	
2	C	214	
3	A	1285	
3	D	1285	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	E	215	
5	F	221	
6	G	3	
7	H	2	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 9942 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 P2G3 Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	228	Total	C	N	O	S	0	0
			1729	1090	296	337	6		

- Molecule 2 is a protein called P2G3 Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	214	Total	C	N	O	S	0	0
			1640	1026	274	335	5		

- Molecule 3 is a protein called Surface glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	201	Total	C	N	O	S	0	0
			1612	1039	273	292	8		
3	D	201	Total	C	N	O	S	0	0
			1612	1039	273	292	8		

There are 238 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	70	VAL	ALA	conflict	UNP A0A8A4XEV3
A	?	-	HIS	deletion	UNP A0A8A4XEV3
A	?	-	VAL	deletion	UNP A0A8A4XEV3
A	96	ILE	THR	conflict	UNP A0A8A4XEV3
A	?	-	ASN	deletion	UNP A0A8A4XEV3
A	209	ILE	LEU	conflict	UNP A0A8A4XEV3
A	212	GLU	-	insertion	UNP A0A8A4XEV3
A	213	PRO	-	insertion	UNP A0A8A4XEV3
A	214	GLU	-	insertion	UNP A0A8A4XEV3
A	339	ASP	GLY	conflict	UNP A0A8A4XEV3
A	371	LEU	SER	conflict	UNP A0A8A4XEV3
A	373	PRO	SER	conflict	UNP A0A8A4XEV3
A	375	PHE	SER	conflict	UNP A0A8A4XEV3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	417	ASN	LYS	conflict	UNP A0A8A4XEV3
A	440	LYS	ASN	conflict	UNP A0A8A4XEV3
A	446	SER	GLY	conflict	UNP A0A8A4XEV3
A	477	ASN	SER	conflict	UNP A0A8A4XEV3
A	478	LYS	THR	conflict	UNP A0A8A4XEV3
A	484	ALA	ARG	conflict	UNP A0A8A4XEV3
A	493	ARG	GLN	conflict	UNP A0A8A4XEV3
A	496	SER	GLY	conflict	UNP A0A8A4XEV3
A	498	ARG	GLN	conflict	UNP A0A8A4XEV3
A	501	TYR	ASN	conflict	UNP A0A8A4XEV3
A	505	HIS	TYR	conflict	UNP A0A8A4XEV3
A	547	LYS	THR	conflict	UNP A0A8A4XEV3
A	655	TYR	HIS	conflict	UNP A0A8A4XEV3
A	679	LYS	ASN	conflict	UNP A0A8A4XEV3
A	681	HIS	PRO	conflict	UNP A0A8A4XEV3
A	682	GLY	ARG	conflict	UNP A0A8A4XEV3
A	683	SER	ARG	conflict	UNP A0A8A4XEV3
A	685	SER	ARG	conflict	UNP A0A8A4XEV3
A	764	LYS	ASN	conflict	UNP A0A8A4XEV3
A	796	TYR	ASP	conflict	UNP A0A8A4XEV3
A	856	LYS	ASN	conflict	UNP A0A8A4XEV3
A	954	HIS	GLN	conflict	UNP A0A8A4XEV3
A	969	LYS	ASN	conflict	UNP A0A8A4XEV3
A	981	PHE	LEU	conflict	UNP A0A8A4XEV3
A	986	PRO	LYS	conflict	UNP A0A8A4XEV3
A	987	PRO	VAL	conflict	UNP A0A8A4XEV3
A	1209	GLY	-	expression tag	UNP A0A8A4XEV3
A	1210	SER	-	expression tag	UNP A0A8A4XEV3
A	1211	GLY	-	expression tag	UNP A0A8A4XEV3
A	1212	TYR	-	expression tag	UNP A0A8A4XEV3
A	1213	ILE	-	expression tag	UNP A0A8A4XEV3
A	1214	PRO	-	expression tag	UNP A0A8A4XEV3
A	1215	GLU	-	expression tag	UNP A0A8A4XEV3
A	1216	ALA	-	expression tag	UNP A0A8A4XEV3
A	1217	PRO	-	expression tag	UNP A0A8A4XEV3
A	1218	ARG	-	expression tag	UNP A0A8A4XEV3
A	1219	ASP	-	expression tag	UNP A0A8A4XEV3
A	1220	GLY	-	expression tag	UNP A0A8A4XEV3
A	1221	GLN	-	expression tag	UNP A0A8A4XEV3
A	1222	ALA	-	expression tag	UNP A0A8A4XEV3
A	1223	TYR	-	expression tag	UNP A0A8A4XEV3
A	1224	VAL	-	expression tag	UNP A0A8A4XEV3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	1225	ARG	-	expression tag	UNP A0A8A4XEV3
A	1226	LYS	-	expression tag	UNP A0A8A4XEV3
A	1227	ASP	-	expression tag	UNP A0A8A4XEV3
A	1228	GLY	-	expression tag	UNP A0A8A4XEV3
A	1229	GLU	-	expression tag	UNP A0A8A4XEV3
A	1230	TRP	-	expression tag	UNP A0A8A4XEV3
A	1231	VAL	-	expression tag	UNP A0A8A4XEV3
A	1232	LEU	-	expression tag	UNP A0A8A4XEV3
A	1233	LEU	-	expression tag	UNP A0A8A4XEV3
A	1234	SER	-	expression tag	UNP A0A8A4XEV3
A	1235	THR	-	expression tag	UNP A0A8A4XEV3
A	1236	PHE	-	expression tag	UNP A0A8A4XEV3
A	1237	LEU	-	expression tag	UNP A0A8A4XEV3
A	1238	GLY	-	expression tag	UNP A0A8A4XEV3
A	1239	ARG	-	expression tag	UNP A0A8A4XEV3
A	1240	SER	-	expression tag	UNP A0A8A4XEV3
A	1241	LEU	-	expression tag	UNP A0A8A4XEV3
A	1242	GLU	-	expression tag	UNP A0A8A4XEV3
A	1243	VAL	-	expression tag	UNP A0A8A4XEV3
A	1244	LEU	-	expression tag	UNP A0A8A4XEV3
A	1245	PHE	-	expression tag	UNP A0A8A4XEV3
A	1246	GLN	-	expression tag	UNP A0A8A4XEV3
A	1247	GLY	-	expression tag	UNP A0A8A4XEV3
A	1248	PRO	-	expression tag	UNP A0A8A4XEV3
A	1249	GLY	-	expression tag	UNP A0A8A4XEV3
A	1250	HIS	-	expression tag	UNP A0A8A4XEV3
A	1251	HIS	-	expression tag	UNP A0A8A4XEV3
A	1252	HIS	-	expression tag	UNP A0A8A4XEV3
A	1253	HIS	-	expression tag	UNP A0A8A4XEV3
A	1254	HIS	-	expression tag	UNP A0A8A4XEV3
A	1255	HIS	-	expression tag	UNP A0A8A4XEV3
A	1256	HIS	-	expression tag	UNP A0A8A4XEV3
A	1257	HIS	-	expression tag	UNP A0A8A4XEV3
A	1258	SER	-	expression tag	UNP A0A8A4XEV3
A	1259	ALA	-	expression tag	UNP A0A8A4XEV3
A	1260	TRP	-	expression tag	UNP A0A8A4XEV3
A	1261	SER	-	expression tag	UNP A0A8A4XEV3
A	1262	HIS	-	expression tag	UNP A0A8A4XEV3
A	1263	PRO	-	expression tag	UNP A0A8A4XEV3
A	1264	GLN	-	expression tag	UNP A0A8A4XEV3
A	1265	PHE	-	expression tag	UNP A0A8A4XEV3
A	1266	GLU	-	expression tag	UNP A0A8A4XEV3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	1267	LYS	-	expression tag	UNP A0A8A4XEV3
A	1268	GLY	-	expression tag	UNP A0A8A4XEV3
A	1269	GLY	-	expression tag	UNP A0A8A4XEV3
A	1270	GLY	-	expression tag	UNP A0A8A4XEV3
A	1271	SER	-	expression tag	UNP A0A8A4XEV3
A	1272	GLY	-	expression tag	UNP A0A8A4XEV3
A	1273	GLY	-	expression tag	UNP A0A8A4XEV3
A	1274	GLY	-	expression tag	UNP A0A8A4XEV3
A	1275	GLY	-	expression tag	UNP A0A8A4XEV3
A	1276	SER	-	expression tag	UNP A0A8A4XEV3
A	1277	GLY	-	expression tag	UNP A0A8A4XEV3
A	1278	GLY	-	expression tag	UNP A0A8A4XEV3
A	1279	SER	-	expression tag	UNP A0A8A4XEV3
A	1280	ALA	-	expression tag	UNP A0A8A4XEV3
A	1281	TRP	-	expression tag	UNP A0A8A4XEV3
A	1282	SER	-	expression tag	UNP A0A8A4XEV3
A	1283	HIS	-	expression tag	UNP A0A8A4XEV3
A	1284	PRO	-	expression tag	UNP A0A8A4XEV3
A	1285	GLN	-	expression tag	UNP A0A8A4XEV3
A	1286	PHE	-	expression tag	UNP A0A8A4XEV3
A	1287	GLU	-	expression tag	UNP A0A8A4XEV3
A	1288	LYS	-	expression tag	UNP A0A8A4XEV3
D	70	VAL	ALA	conflict	UNP A0A8A4XEV3
D	?	-	HIS	deletion	UNP A0A8A4XEV3
D	?	-	VAL	deletion	UNP A0A8A4XEV3
D	96	ILE	THR	conflict	UNP A0A8A4XEV3
D	?	-	ASN	deletion	UNP A0A8A4XEV3
D	209	ILE	LEU	conflict	UNP A0A8A4XEV3
D	212	GLU	-	insertion	UNP A0A8A4XEV3
D	213	PRO	-	insertion	UNP A0A8A4XEV3
D	214	GLU	-	insertion	UNP A0A8A4XEV3
D	339	ASP	GLY	conflict	UNP A0A8A4XEV3
D	371	LEU	SER	conflict	UNP A0A8A4XEV3
D	373	PRO	SER	conflict	UNP A0A8A4XEV3
D	375	PHE	SER	conflict	UNP A0A8A4XEV3
D	417	ASN	LYS	conflict	UNP A0A8A4XEV3
D	440	LYS	ASN	conflict	UNP A0A8A4XEV3
D	446	SER	GLY	conflict	UNP A0A8A4XEV3
D	477	ASN	SER	conflict	UNP A0A8A4XEV3
D	478	LYS	THR	conflict	UNP A0A8A4XEV3
D	484	ALA	ARG	conflict	UNP A0A8A4XEV3
D	493	ARG	GLN	conflict	UNP A0A8A4XEV3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	496	SER	GLY	conflict	UNP A0A8A4XEV3
D	498	ARG	GLN	conflict	UNP A0A8A4XEV3
D	501	TYR	ASN	conflict	UNP A0A8A4XEV3
D	505	HIS	TYR	conflict	UNP A0A8A4XEV3
D	547	LYS	THR	conflict	UNP A0A8A4XEV3
D	655	TYR	HIS	conflict	UNP A0A8A4XEV3
D	679	LYS	ASN	conflict	UNP A0A8A4XEV3
D	681	HIS	PRO	conflict	UNP A0A8A4XEV3
D	682	GLY	ARG	conflict	UNP A0A8A4XEV3
D	683	SER	ARG	conflict	UNP A0A8A4XEV3
D	685	SER	ARG	conflict	UNP A0A8A4XEV3
D	764	LYS	ASN	conflict	UNP A0A8A4XEV3
D	796	TYR	ASP	conflict	UNP A0A8A4XEV3
D	856	LYS	ASN	conflict	UNP A0A8A4XEV3
D	954	HIS	GLN	conflict	UNP A0A8A4XEV3
D	969	LYS	ASN	conflict	UNP A0A8A4XEV3
D	981	PHE	LEU	conflict	UNP A0A8A4XEV3
D	986	PRO	LYS	conflict	UNP A0A8A4XEV3
D	987	PRO	VAL	conflict	UNP A0A8A4XEV3
D	1209	GLY	-	expression tag	UNP A0A8A4XEV3
D	1210	SER	-	expression tag	UNP A0A8A4XEV3
D	1211	GLY	-	expression tag	UNP A0A8A4XEV3
D	1212	TYR	-	expression tag	UNP A0A8A4XEV3
D	1213	ILE	-	expression tag	UNP A0A8A4XEV3
D	1214	PRO	-	expression tag	UNP A0A8A4XEV3
D	1215	GLU	-	expression tag	UNP A0A8A4XEV3
D	1216	ALA	-	expression tag	UNP A0A8A4XEV3
D	1217	PRO	-	expression tag	UNP A0A8A4XEV3
D	1218	ARG	-	expression tag	UNP A0A8A4XEV3
D	1219	ASP	-	expression tag	UNP A0A8A4XEV3
D	1220	GLY	-	expression tag	UNP A0A8A4XEV3
D	1221	GLN	-	expression tag	UNP A0A8A4XEV3
D	1222	ALA	-	expression tag	UNP A0A8A4XEV3
D	1223	TYR	-	expression tag	UNP A0A8A4XEV3
D	1224	VAL	-	expression tag	UNP A0A8A4XEV3
D	1225	ARG	-	expression tag	UNP A0A8A4XEV3
D	1226	LYS	-	expression tag	UNP A0A8A4XEV3
D	1227	ASP	-	expression tag	UNP A0A8A4XEV3
D	1228	GLY	-	expression tag	UNP A0A8A4XEV3
D	1229	GLU	-	expression tag	UNP A0A8A4XEV3
D	1230	TRP	-	expression tag	UNP A0A8A4XEV3
D	1231	VAL	-	expression tag	UNP A0A8A4XEV3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	1232	LEU	-	expression tag	UNP A0A8A4XEV3
D	1233	LEU	-	expression tag	UNP A0A8A4XEV3
D	1234	SER	-	expression tag	UNP A0A8A4XEV3
D	1235	THR	-	expression tag	UNP A0A8A4XEV3
D	1236	PHE	-	expression tag	UNP A0A8A4XEV3
D	1237	LEU	-	expression tag	UNP A0A8A4XEV3
D	1238	GLY	-	expression tag	UNP A0A8A4XEV3
D	1239	ARG	-	expression tag	UNP A0A8A4XEV3
D	1240	SER	-	expression tag	UNP A0A8A4XEV3
D	1241	LEU	-	expression tag	UNP A0A8A4XEV3
D	1242	GLU	-	expression tag	UNP A0A8A4XEV3
D	1243	VAL	-	expression tag	UNP A0A8A4XEV3
D	1244	LEU	-	expression tag	UNP A0A8A4XEV3
D	1245	PHE	-	expression tag	UNP A0A8A4XEV3
D	1246	GLN	-	expression tag	UNP A0A8A4XEV3
D	1247	GLY	-	expression tag	UNP A0A8A4XEV3
D	1248	PRO	-	expression tag	UNP A0A8A4XEV3
D	1249	GLY	-	expression tag	UNP A0A8A4XEV3
D	1250	HIS	-	expression tag	UNP A0A8A4XEV3
D	1251	HIS	-	expression tag	UNP A0A8A4XEV3
D	1252	HIS	-	expression tag	UNP A0A8A4XEV3
D	1253	HIS	-	expression tag	UNP A0A8A4XEV3
D	1254	HIS	-	expression tag	UNP A0A8A4XEV3
D	1255	HIS	-	expression tag	UNP A0A8A4XEV3
D	1256	HIS	-	expression tag	UNP A0A8A4XEV3
D	1257	HIS	-	expression tag	UNP A0A8A4XEV3
D	1258	SER	-	expression tag	UNP A0A8A4XEV3
D	1259	ALA	-	expression tag	UNP A0A8A4XEV3
D	1260	TRP	-	expression tag	UNP A0A8A4XEV3
D	1261	SER	-	expression tag	UNP A0A8A4XEV3
D	1262	HIS	-	expression tag	UNP A0A8A4XEV3
D	1263	PRO	-	expression tag	UNP A0A8A4XEV3
D	1264	GLN	-	expression tag	UNP A0A8A4XEV3
D	1265	PHE	-	expression tag	UNP A0A8A4XEV3
D	1266	GLU	-	expression tag	UNP A0A8A4XEV3
D	1267	LYS	-	expression tag	UNP A0A8A4XEV3
D	1268	GLY	-	expression tag	UNP A0A8A4XEV3
D	1269	GLY	-	expression tag	UNP A0A8A4XEV3
D	1270	GLY	-	expression tag	UNP A0A8A4XEV3
D	1271	SER	-	expression tag	UNP A0A8A4XEV3
D	1272	GLY	-	expression tag	UNP A0A8A4XEV3
D	1273	GLY	-	expression tag	UNP A0A8A4XEV3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	1274	GLY	-	expression tag	UNP A0A8A4XEV3
D	1275	GLY	-	expression tag	UNP A0A8A4XEV3
D	1276	SER	-	expression tag	UNP A0A8A4XEV3
D	1277	GLY	-	expression tag	UNP A0A8A4XEV3
D	1278	GLY	-	expression tag	UNP A0A8A4XEV3
D	1279	SER	-	expression tag	UNP A0A8A4XEV3
D	1280	ALA	-	expression tag	UNP A0A8A4XEV3
D	1281	TRP	-	expression tag	UNP A0A8A4XEV3
D	1282	SER	-	expression tag	UNP A0A8A4XEV3
D	1283	HIS	-	expression tag	UNP A0A8A4XEV3
D	1284	PRO	-	expression tag	UNP A0A8A4XEV3
D	1285	GLN	-	expression tag	UNP A0A8A4XEV3
D	1286	PHE	-	expression tag	UNP A0A8A4XEV3
D	1287	GLU	-	expression tag	UNP A0A8A4XEV3
D	1288	LYS	-	expression tag	UNP A0A8A4XEV3

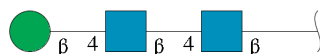
- Molecule 4 is a protein called P5C3 Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	215	Total	C	N	O	S	0	0
			1645	1028	279	333	5		

- Molecule 5 is a protein called P5C3 Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	221	Total	C	N	O	S	0	0
			1637	1025	274	328	10		

- Molecule 6 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
6	G	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 7 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

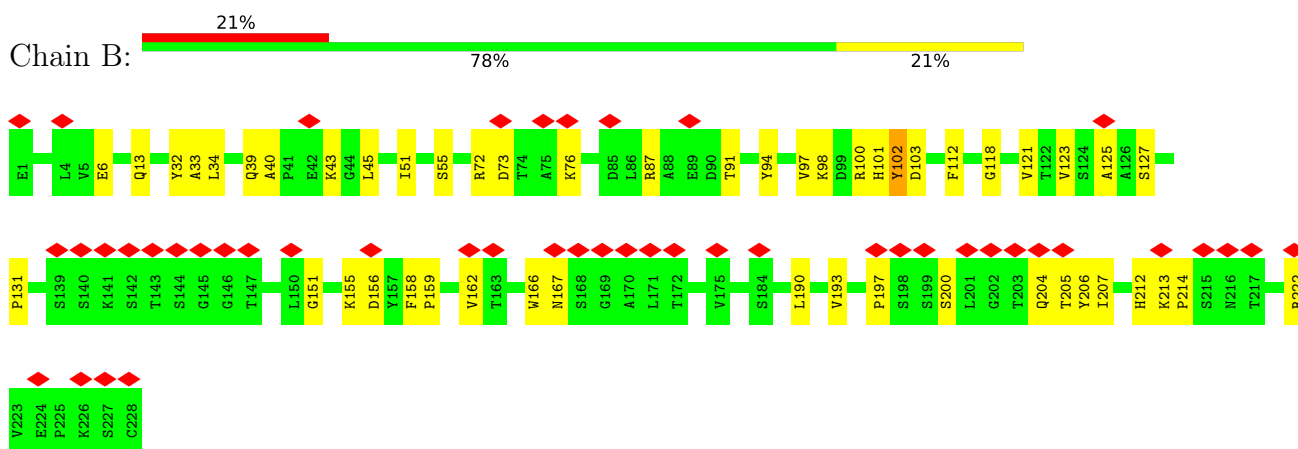


Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	H	2	28	16	2	10	0	0

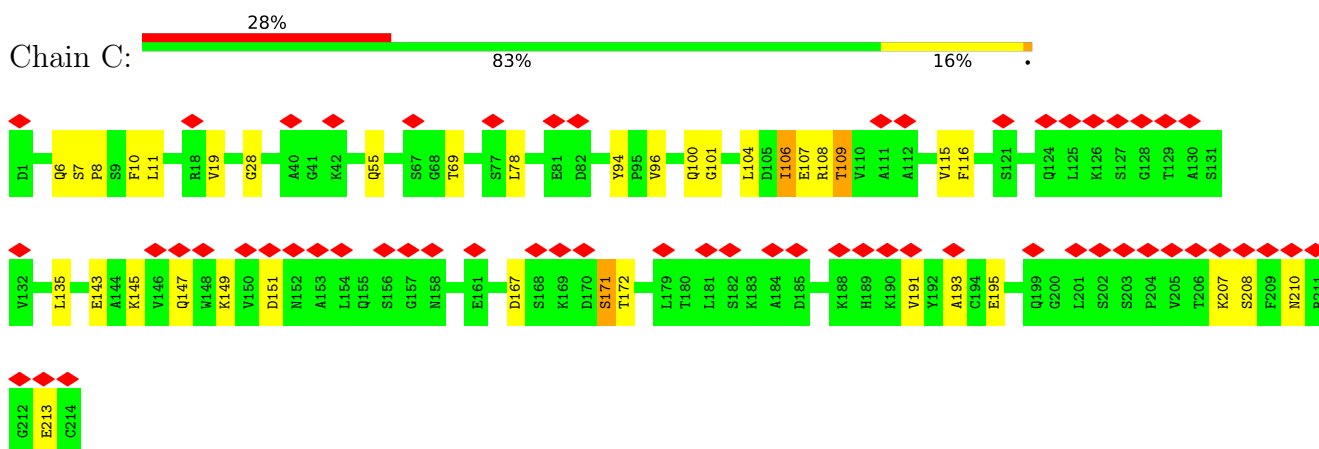
3 Residue-property plots

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.

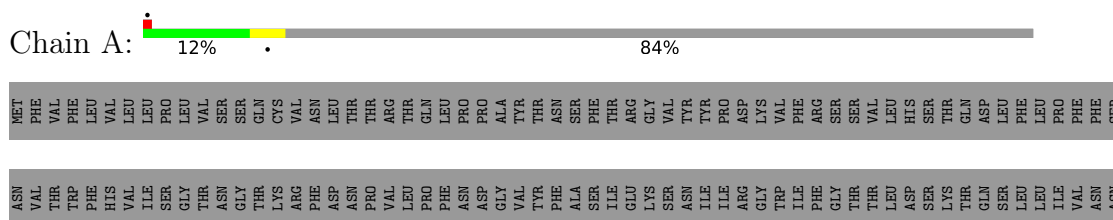
• Molecule 1: P2G3 Heavy Chain



• Molecule 2: P2G3 Light Chain

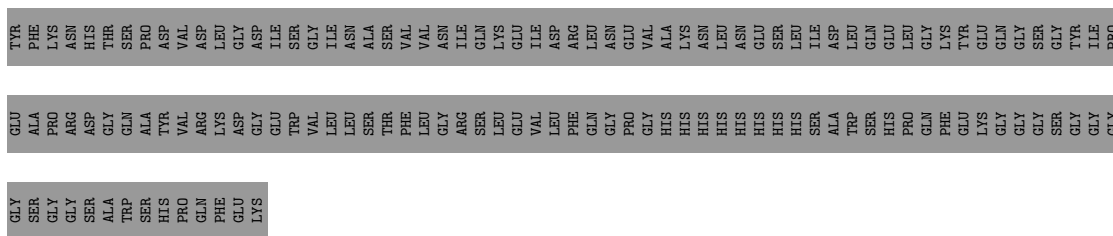


• Molecule 3: Surface glycoprotein

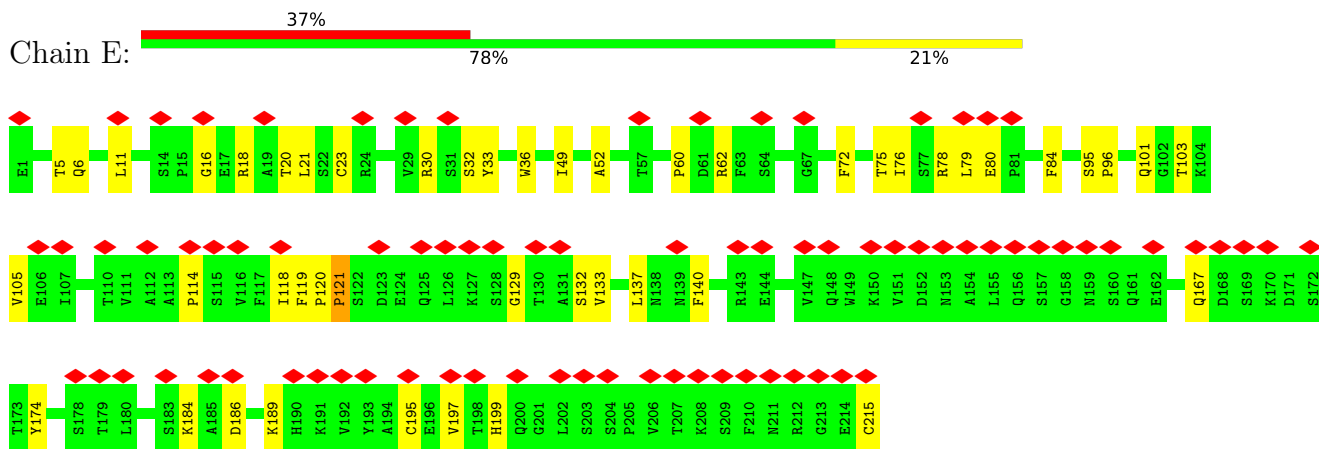




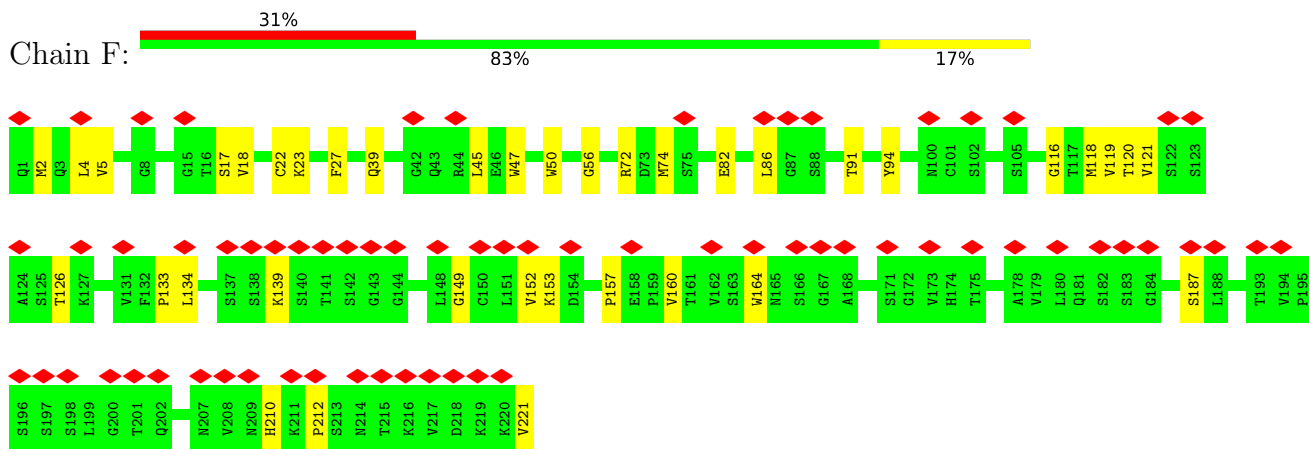




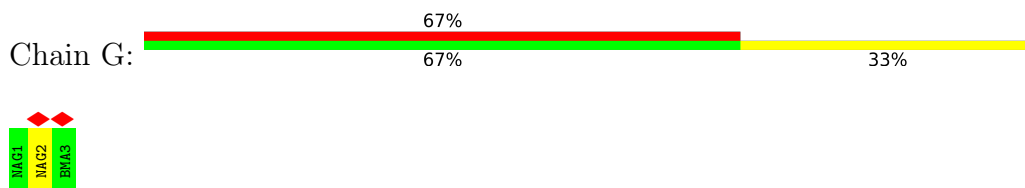
- Molecule 4: P5C3 Light Chain



- Molecule 5: P5C3 Heavy Chain



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18839	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.115	Depositor
Minimum map value	-1.949	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.192	Depositor
Map size ($\text{\AA}$)	414.99, 414.99, 414.99	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3833, 1.3833, 1.3833	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, BMA

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	0.27	0/1771	0.46	0/2409
2	C	0.22	0/1675	0.44	3/2278 (0.1%)
3	A	0.23	0/1660	0.55	3/2258 (0.1%)
3	D	0.13	0/1660	0.33	1/2258 (0.0%)
4	E	0.21	1/1682 (0.1%)	0.42	2/2283 (0.1%)
5	F	0.10	0/1674	0.31	0/2280
All	All	0.20	1/10122 (0.0%)	0.43	9/13766 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	121	PRO	CG-CD	-5.99	1.30	1.50

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	121	PRO	CA-N-CD	-11.02	96.57	112.00
3	A	346	ARG	CG-CD-NE	-8.90	92.41	112.00
4	E	121	PRO	N-CD-CG	-8.31	90.73	103.20
3	A	377	PHE	CB-CA-C	-8.17	99.84	111.85
2	C	172	THR	CB-CA-C	-6.30	106.53	114.40

There are no chirality outliers.

There are no planarity outliers.

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	B	1729	0	1684	34	0
2	C	1640	0	1585	24	0
3	A	1612	0	1548	29	0
3	D	1612	0	1550	29	0
4	E	1645	0	1591	30	0
5	F	1637	0	1595	25	0
6	G	39	0	34	1	0
7	H	28	0	25	1	0
All	All	9942	0	9612	168	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 9.

The worst 5 of 168 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)
2:C:8:PRO:HB2	2:C:11:LEU:HD11	1.64	0.77
1:B:94:TYR:O	1:B:118:GLY:HA2	1.85	0.77
4:E:30:ARG:HB2	4:E:33:TYR:HB2	1.67	0.76
5:F:91:THR:HG22	5:F:121:VAL:H	1.54	0.72
1:B:167:ASN:HD21	1:B:204:GLN:HE22	1.39	0.69

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	226/228 (99%)	215 (95%)	10 (4%)	1 (0%)	30 65
2	C	212/214 (99%)	195 (92%)	17 (8%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	A	199/1285 (16%)	187 (94%)	10 (5%)	2 (1%)	12	45
3	D	199/1285 (16%)	184 (92%)	14 (7%)	1 (0%)	24	60
4	E	213/215 (99%)	205 (96%)	8 (4%)	0	100	100
5	F	219/221 (99%)	212 (97%)	7 (3%)	0	100	100
All	All	1268/3448 (37%)	1198 (94%)	66 (5%)	4 (0%)	37	70

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	372	ALA
3	D	332	ILE
1	B	102	TYR
3	A	332	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	192/192 (100%)	190 (99%)	2 (1%)	68	76
2	C	187/187 (100%)	183 (98%)	4 (2%)	47	65
3	A	176/1113 (16%)	168 (96%)	8 (4%)	24	47
3	D	176/1113 (16%)	176 (100%)	0	100	100
4	E	185/185 (100%)	185 (100%)	0	100	100
5	F	186/186 (100%)	186 (100%)	0	100	100
All	All	1102/2976 (37%)	1088 (99%)	14 (1%)	59	72

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	375	PHE
3	A	377	PHE
3	A	434	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	A	432	CYS
3	A	433	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
3	A	506	GLN
3	D	439	ASN
5	F	174	HIS
4	E	167	GLN
3	A	370	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

5 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	$\# Z > 2$
6	NAG	G	1	6,3	14,14,15	0.16	0	17,19,21	0.46	0
6	NAG	G	2	6	14,14,15	0.32	0	17,19,21	0.60	0
6	BMA	G	3	6	11,11,12	0.57	0	15,15,17	0.83	0
7	NAG	H	1	3,7	14,14,15	0.90	1 (7%)	17,19,21	0.73	0
7	NAG	H	2	7	14,14,15	0.28	0	17,19,21	0.51	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	G	1	6,3	-	2/6/23/26	0/1/1/1
6	NAG	G	2	6	-	2/6/23/26	0/1/1/1
6	BMA	G	3	6	-	1/2/19/22	0/1/1/1
7	NAG	H	1	3,7	-	2/6/23/26	0/1/1/1
7	NAG	H	2	7	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	H	1	NAG	C1-C2	2.95	1.56	1.52

There are no bond angle outliers.

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

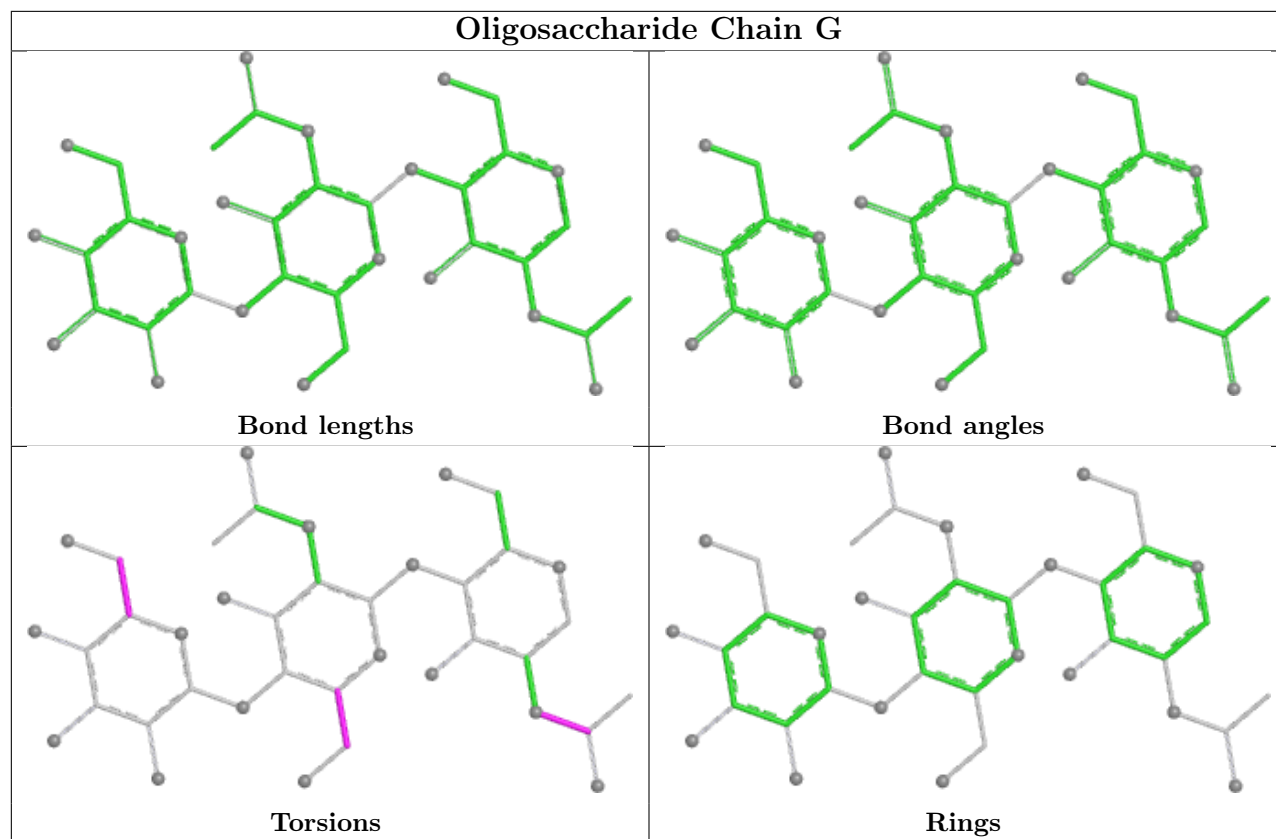
Mol	Chain	Res	Type	Atoms
7	H	2	NAG	C4-C5-C6-O6
6	G	2	NAG	O5-C5-C6-O6
7	H	1	NAG	O5-C5-C6-O6
7	H	2	NAG	O5-C5-C6-O6
6	G	1	NAG	C8-C7-N2-C2

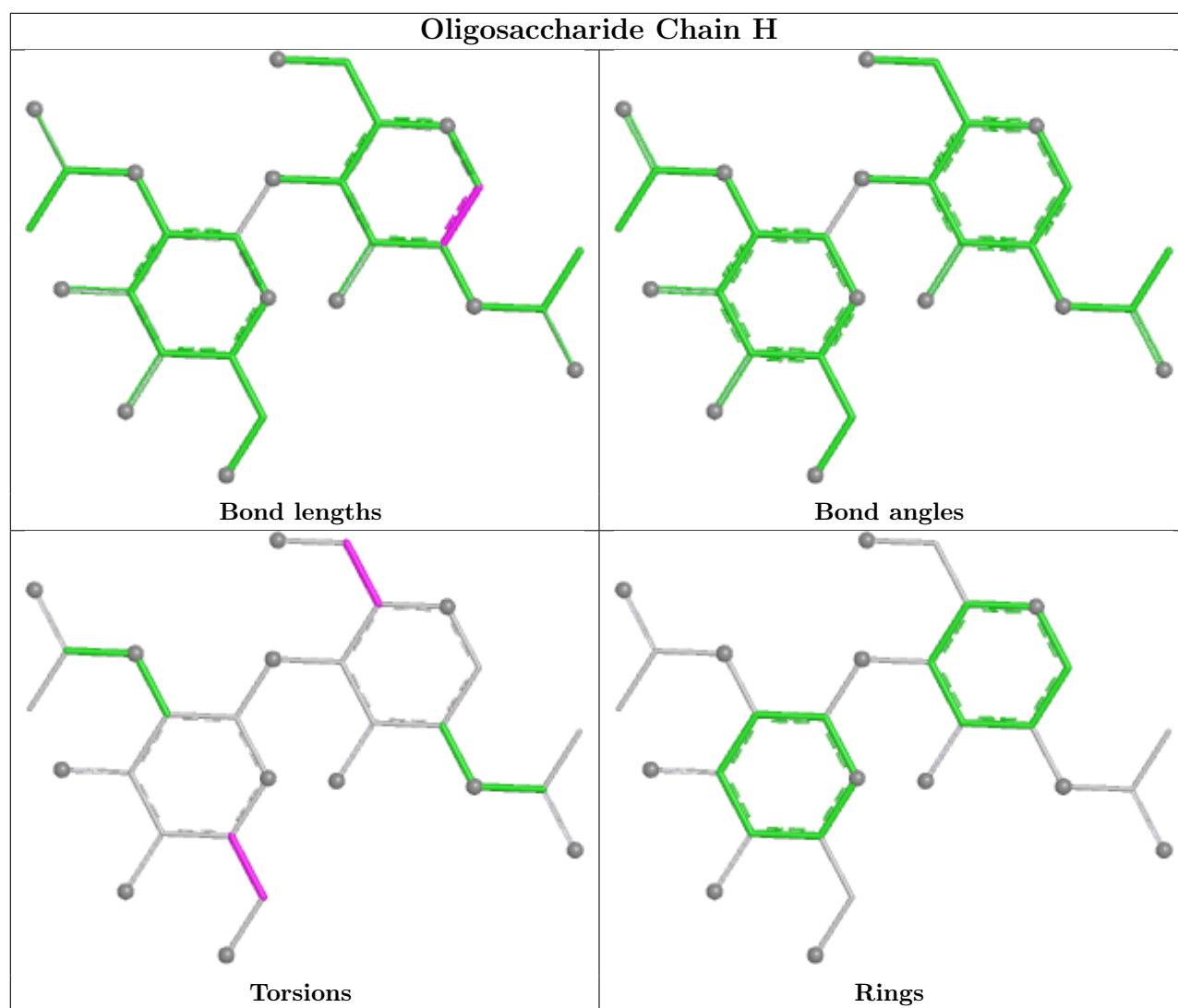
There are no ring outliers.

3 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	H	2	NAG	1	0
6	G	2	NAG	1	0
7	H	1	NAG	1	0

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





5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

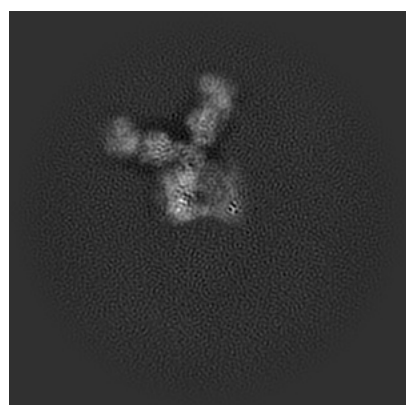
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14142. These allow visual inspection of the internal detail of the map and identification of artifacts.

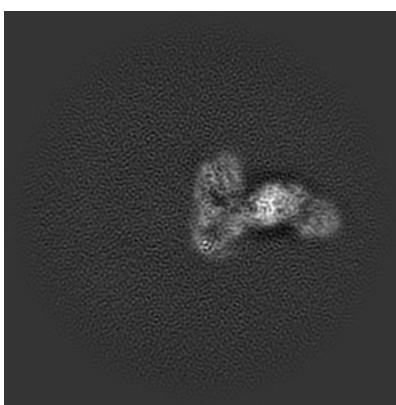
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

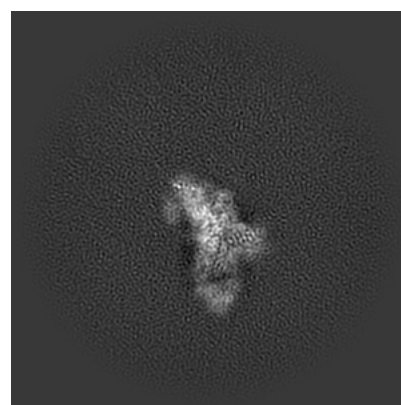
6.1.1 Primary map



X



Y

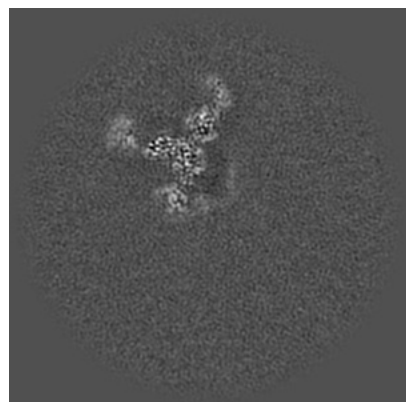


Z

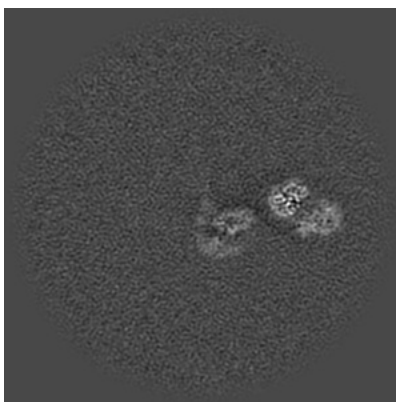
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

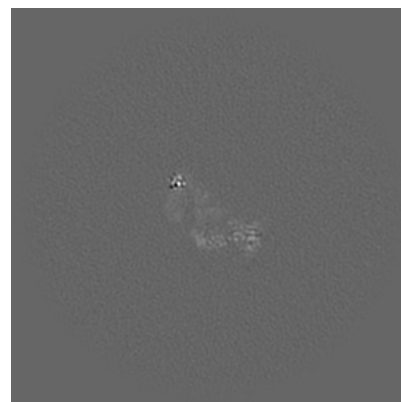
6.2.1 Primary map



X Index: 150



Y Index: 150

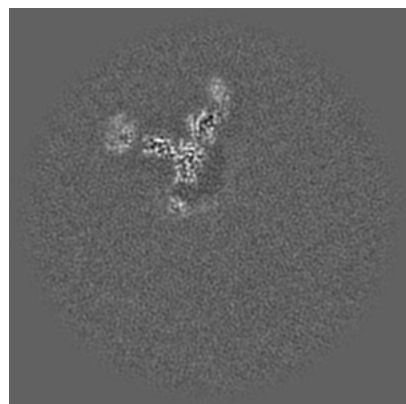


Z Index: 150

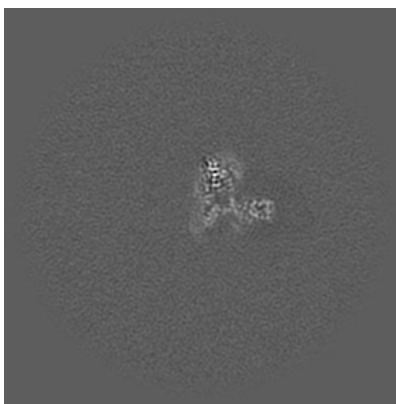
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

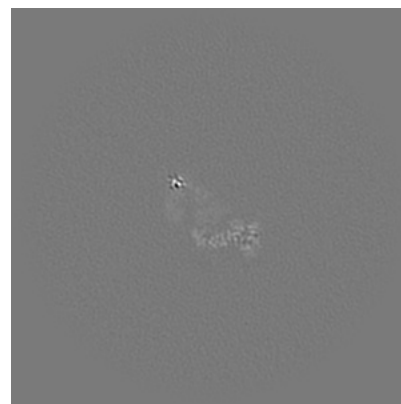
6.3.1 Primary map



X Index: 154



Y Index: 129

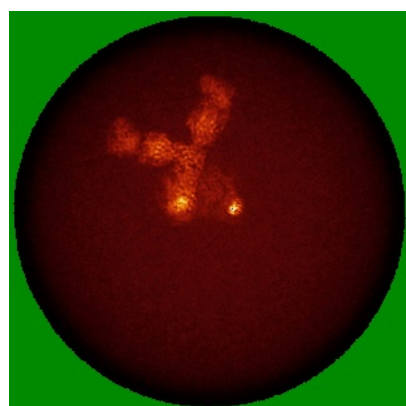


Z Index: 151

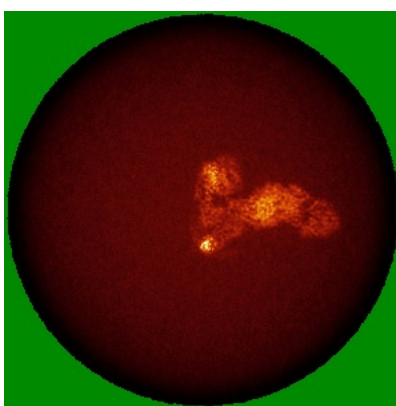
The images above show the largest variance slices of the map in three orthogonal directions.

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

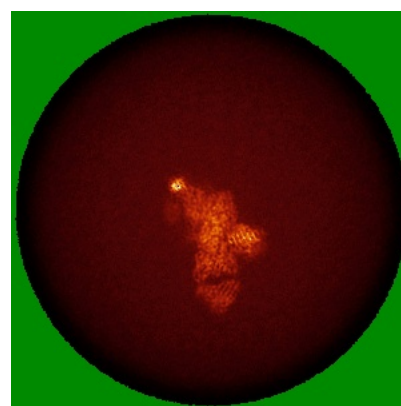
6.4.1 Primary map



X



Y

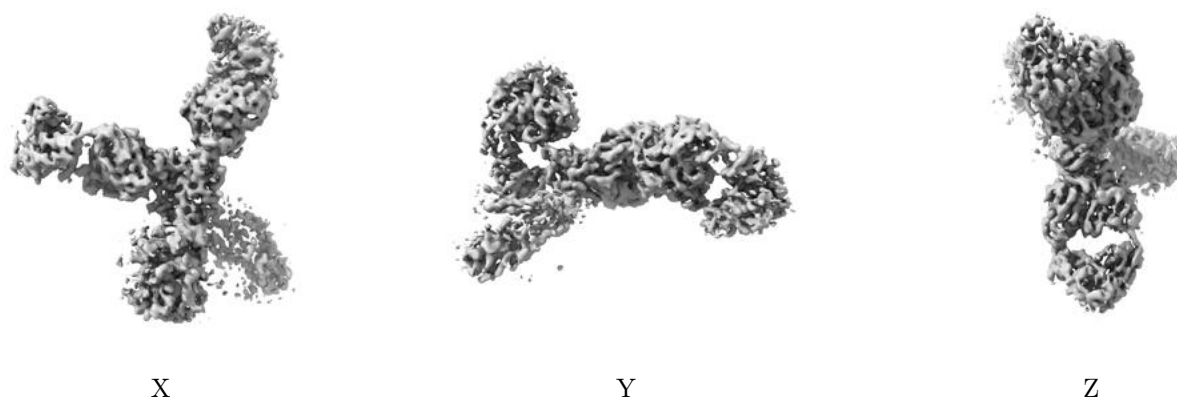


Z

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 0.192. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

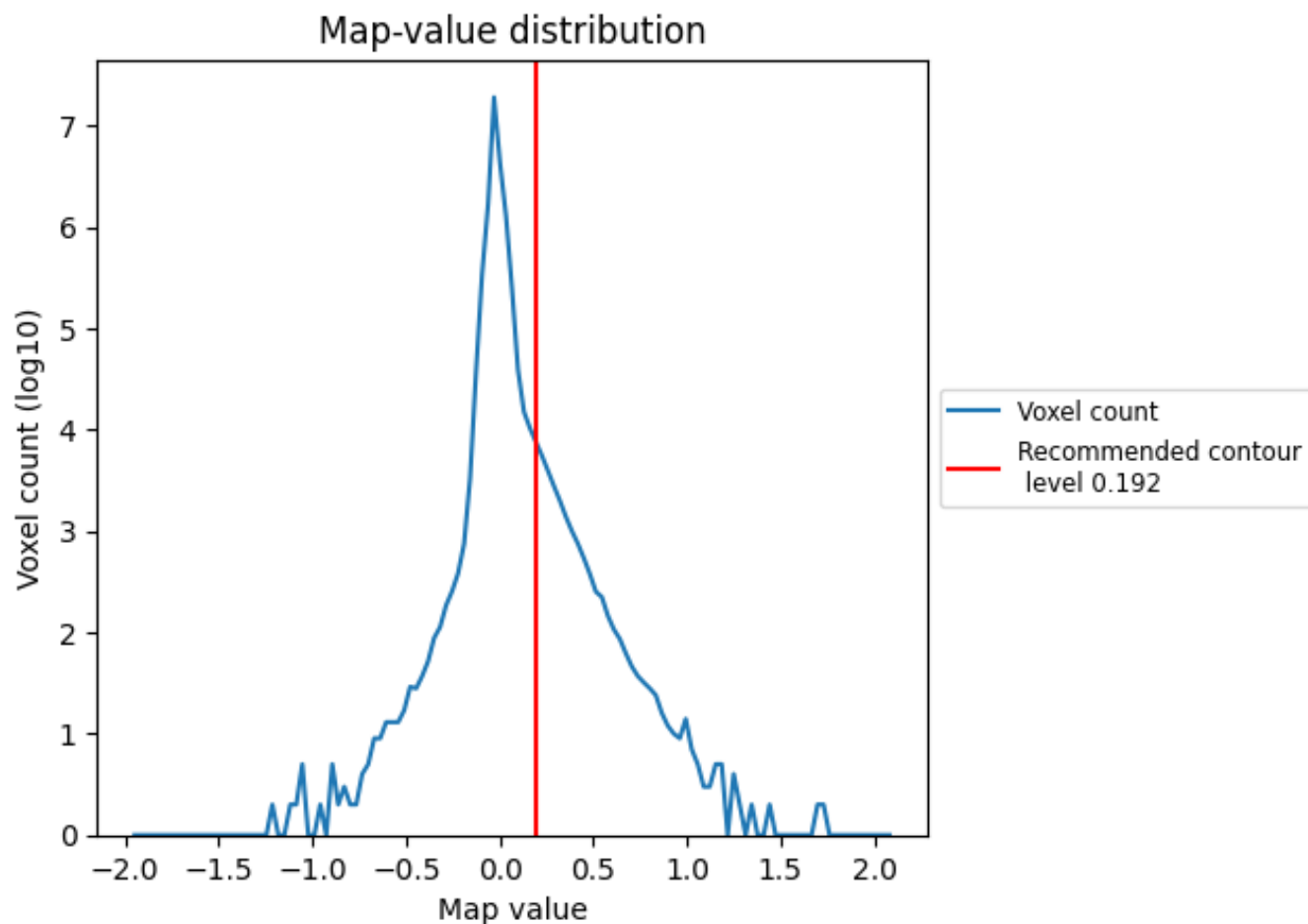
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

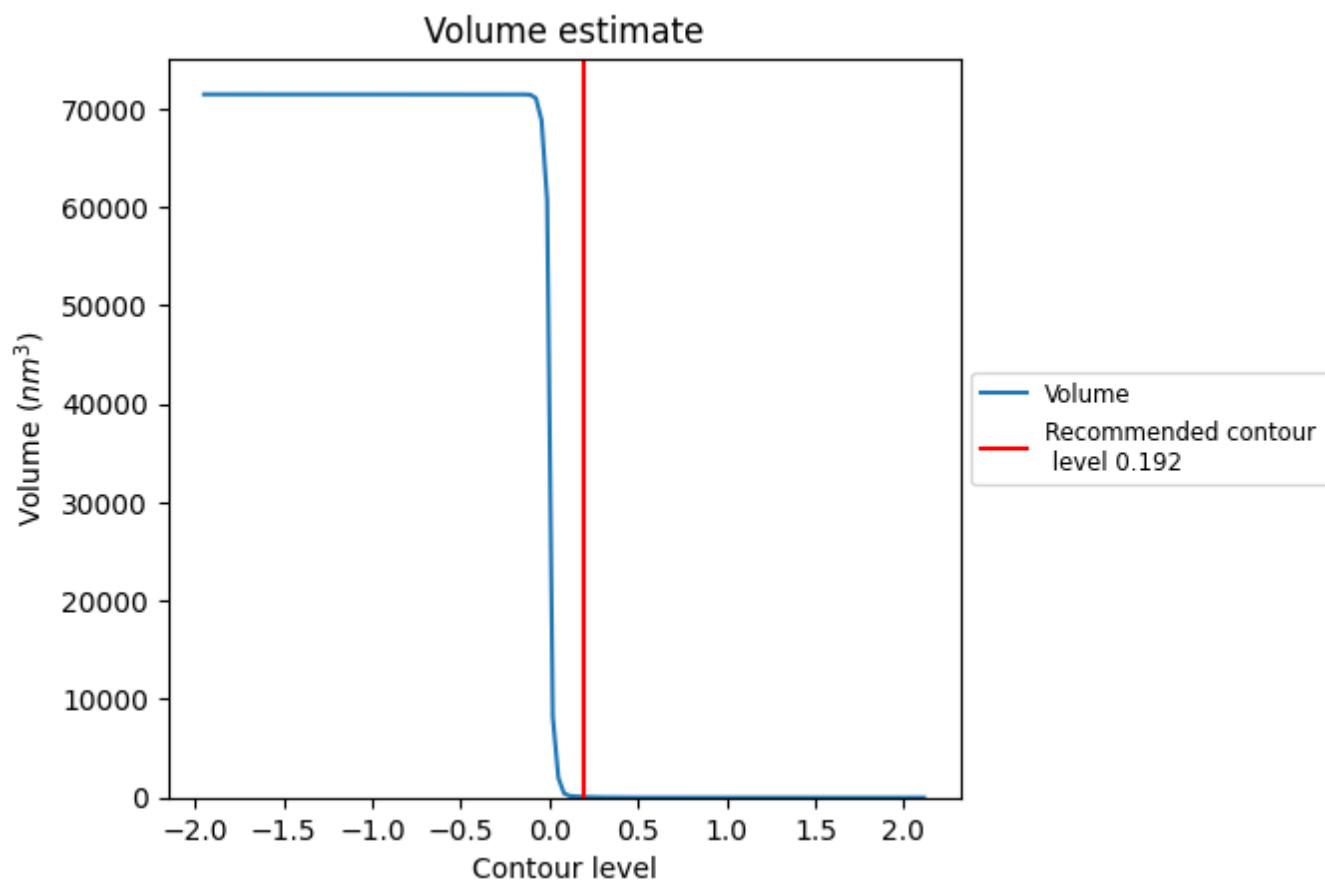
This section contains the results of statistical analysis of the map.

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.

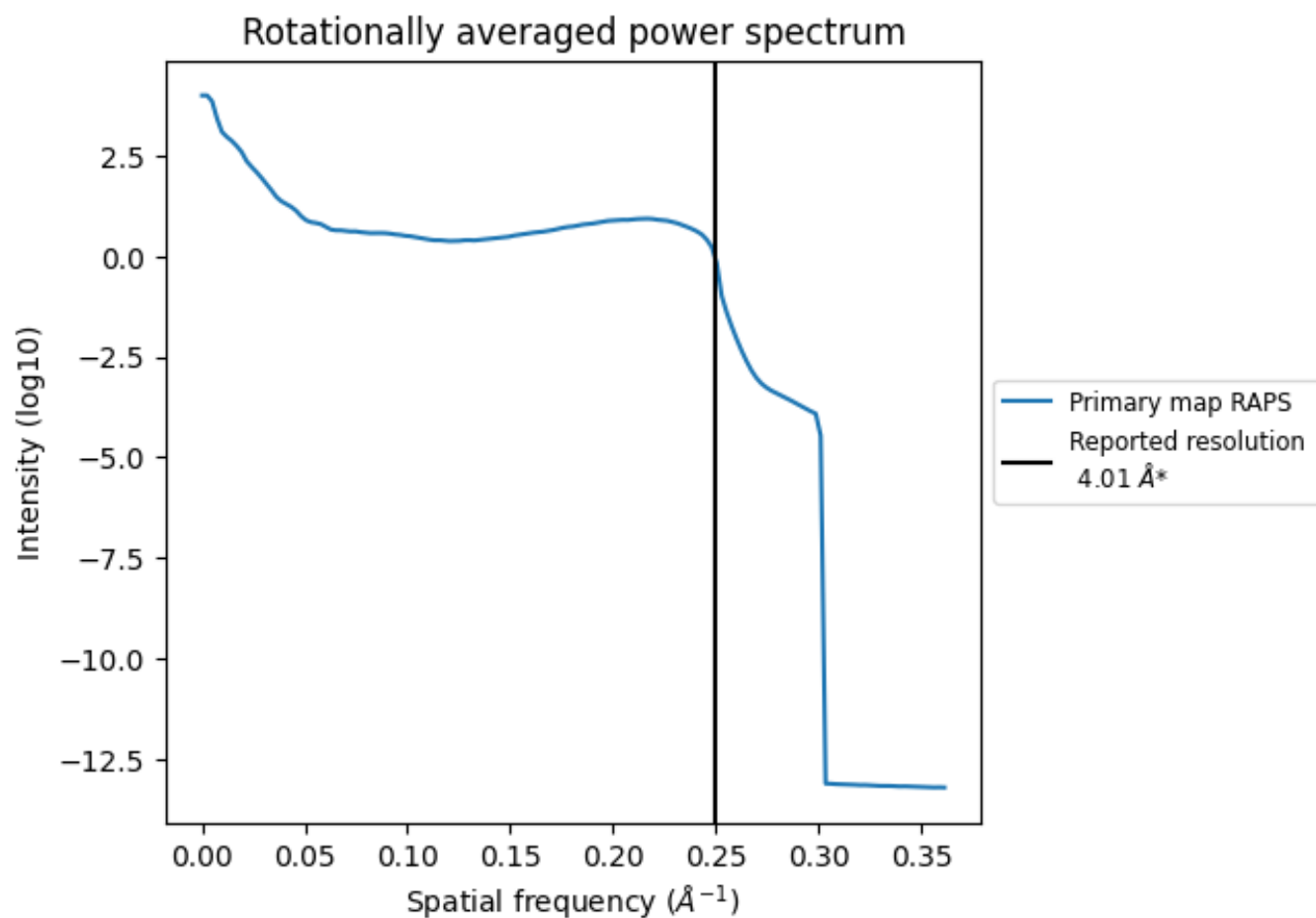
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 74 nm³; this corresponds to an approximate mass of 67 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 ⓘ

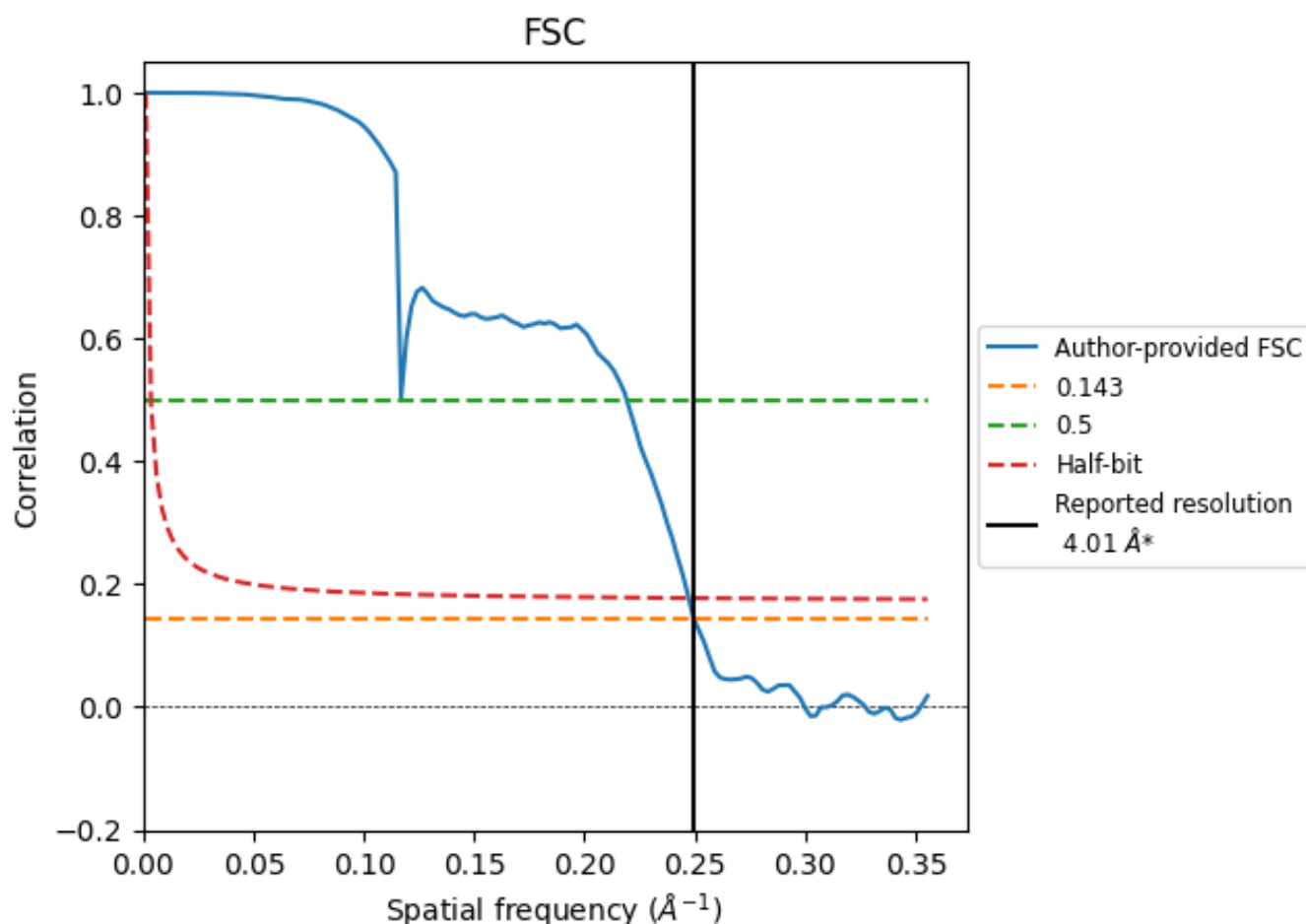


*Reported resolution corresponds to spatial frequency of 0.249 $\text{\AA}^{-1}$

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 0.249 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.01	-	-
Author-provided FSC curve	4.01	4.56	4.05
Unmasked-calculated*	-	-	-

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

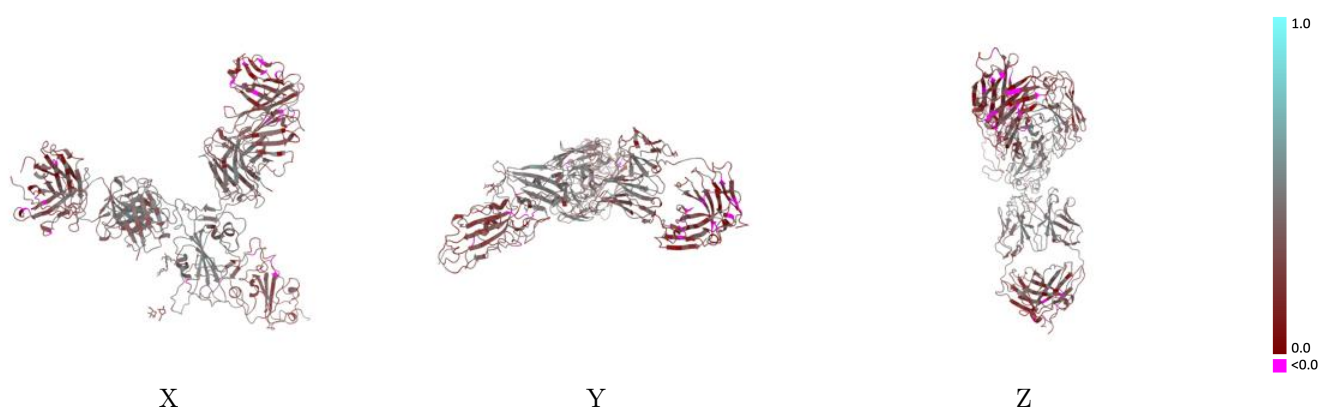
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14142 and PDB model 7QTJ. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)

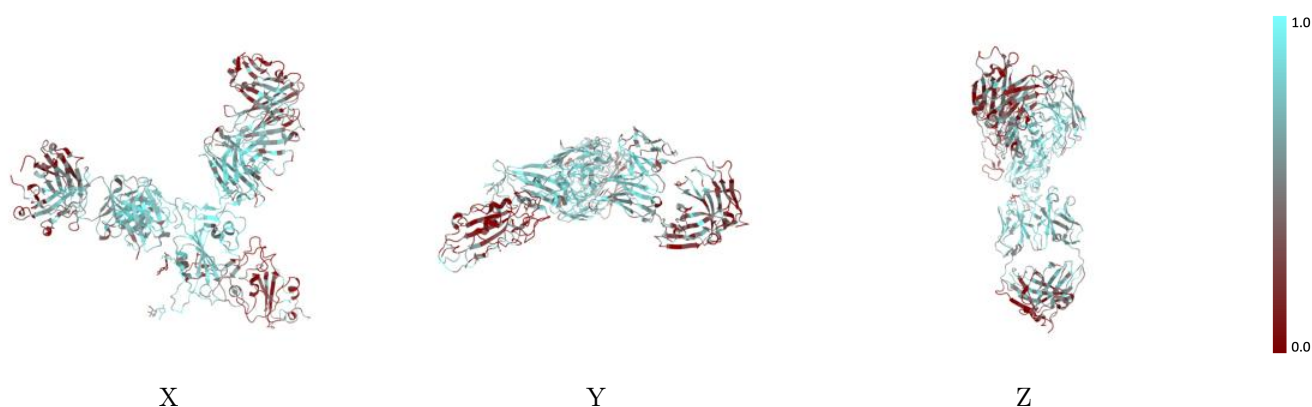
This section was not generated.

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



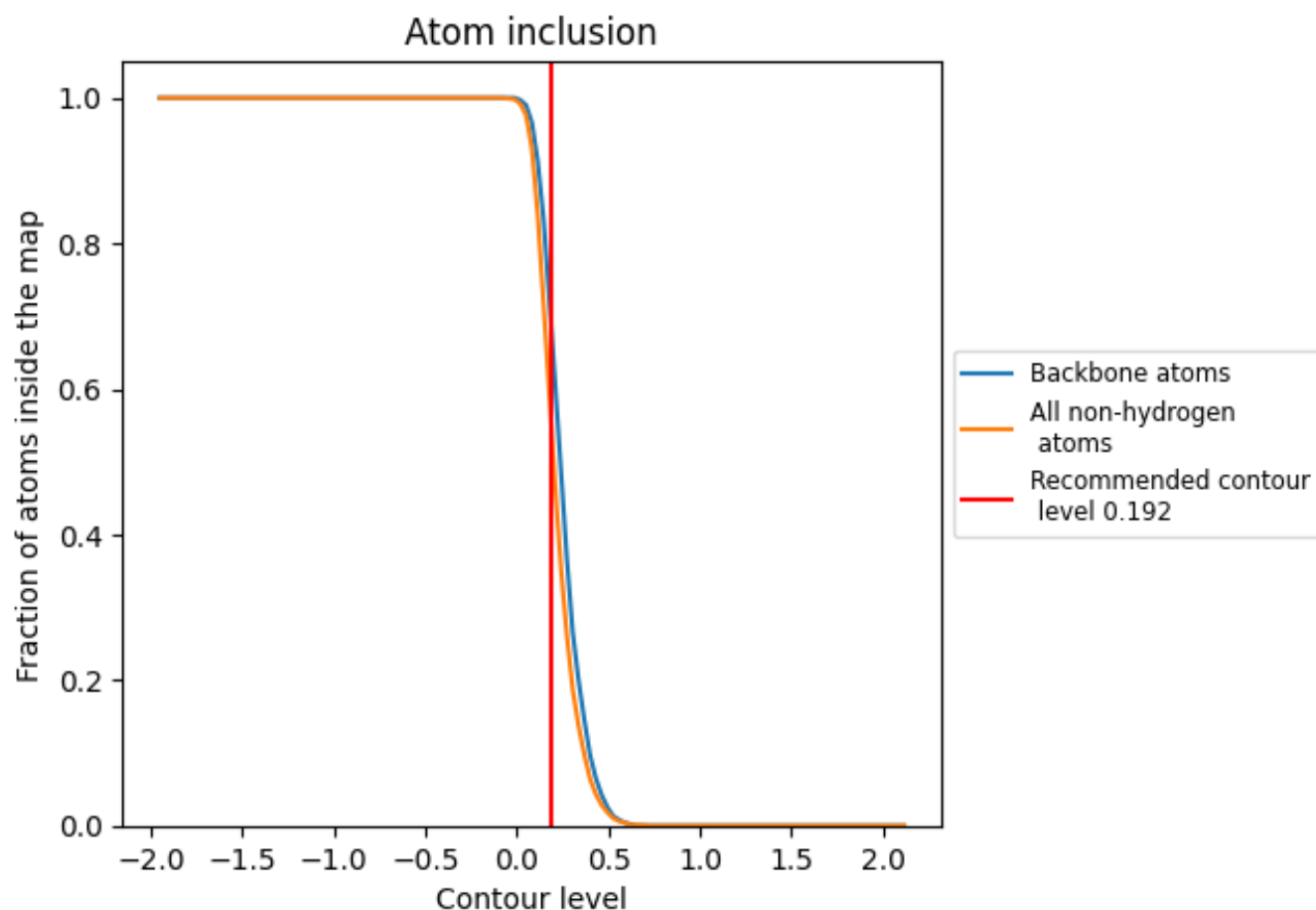
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.192).

9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 53% 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 (0.192) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5330	0.3440
A	0.7300	0.4370
B	0.6070	0.3740
C	0.5600	0.3590
D	0.2430	0.2850
E	0.5090	0.2890
F	0.5460	0.3180
G	0.3080	0.4070
H	0.5710	0.2500

1.0

0.0

<0.0