



wwPDB EM Validation Summary Report ⓘ

Jul 1, 2026 – 05:14 pm BST

PDB ID : 9HAA / pdb_00009haa
EMDB ID : EMD-51980
Title : a5b3 GABAA Receptor resting state
Authors : Cowgill, J.; Fan, C.; Howard, R.J.; Lindahl, E.
Deposited on : 2024-11-02
Resolution : 3.14 Å(reported)
Based on initial model : .

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.dev133
Mogul : 1.8.4, CSD as541be (2020)
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) : 2.50

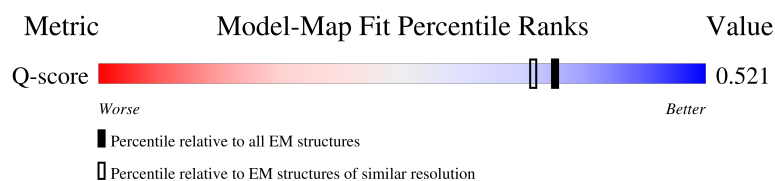
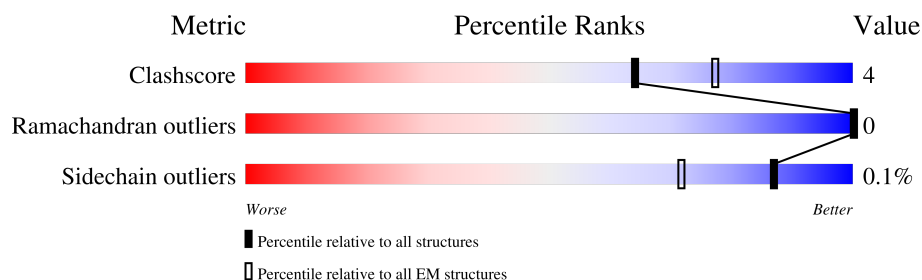
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.14 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.



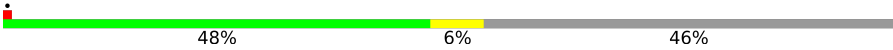
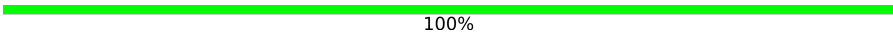
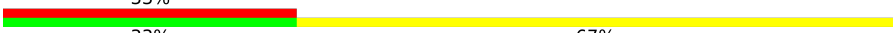
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14483 (2.64 - 3.64)

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	679	
1	D	679	
2	B	623	
2	C	623	

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Mol	Chain	Length	Quality of chain
2	E	623	
3	F	2	
4	G	3	
4	I	3	
4	N	3	
5	H	6	
5	M	6	
6	J	3	
7	K	6	
8	L	2	

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 14256 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 Green fluorescent protein, Gamma-aminobutyric acid receptor subunit alpha-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	343	Total	C	N	O	S	0	0
			2750	1772	455	507	16		
1	D	339	Total	C	N	O	S	0	0
			2719	1754	451	498	16		

There are 194 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-315	MET	-	initiating methionine	UNP P42212
A	-314	ARG	-	expression tag	UNP P42212
A	-313	LYS	-	expression tag	UNP P42212
A	-312	SER	-	expression tag	UNP P42212
A	-311	PRO	-	expression tag	UNP P42212
A	-310	GLY	-	expression tag	UNP P42212
A	-309	LEU	-	expression tag	UNP P42212
A	-308	SER	-	expression tag	UNP P42212
A	-307	ASP	-	expression tag	UNP P42212
A	-306	CYS	-	expression tag	UNP P42212
A	-305	LEU	-	expression tag	UNP P42212
A	-304	TRP	-	expression tag	UNP P42212
A	-303	ALA	-	expression tag	UNP P42212
A	-302	TRP	-	expression tag	UNP P42212
A	-301	ILE	-	expression tag	UNP P42212
A	-300	LEU	-	expression tag	UNP P42212
A	-299	LEU	-	expression tag	UNP P42212
A	-298	LEU	-	expression tag	UNP P42212
A	-297	SER	-	expression tag	UNP P42212
A	-296	THR	-	expression tag	UNP P42212
A	-295	LEU	-	expression tag	UNP P42212
A	-294	THR	-	expression tag	UNP P42212
A	-293	GLY	-	expression tag	UNP P42212
A	-292	ARG	-	expression tag	UNP P42212
A	-291	SER	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-290	TYR	-	expression tag	UNP P42212
A	-289	GLY	-	expression tag	UNP P42212
A	-288	GLN	-	expression tag	UNP P42212
A	-258	ARG	SER	engineered mutation	UNP P42212
A	-249	ASN	TYR	engineered mutation	UNP P42212
A	-224	LEU	PHE	engineered mutation	UNP P42212
A	-223	THR	SER	engineered mutation	UNP P42212
A	-208	ARG	GLN	engineered mutation	UNP P42212
A	-189	SER	PHE	engineered mutation	UNP P42212
A	-183	THR	ASN	engineered mutation	UNP P42212
A	-143	PHE	TYR	engineered mutation	UNP P42212
A	-135	THR	MET	engineered mutation	UNP P42212
A	-125	ALA	VAL	engineered mutation	UNP P42212
A	-117	VAL	ILE	engineered mutation	UNP P42212
A	-82	VAL	ALA	engineered mutation	UNP P42212
A	-49	ALA	-	linker	UNP P42212
A	-48	ALA	-	linker	UNP P42212
A	-47	ASN	-	linker	UNP P42212
A	-46	ALA	-	linker	UNP P42212
A	-45	LEU	-	linker	UNP P42212
A	-44	ALA	-	linker	UNP P42212
A	-43	ALA	-	linker	UNP P42212
A	-42	TRP	-	linker	UNP P42212
A	-41	SER	-	linker	UNP P42212
A	-40	HIS	-	linker	UNP P42212
A	-39	PRO	-	linker	UNP P42212
A	-38	GLN	-	linker	UNP P42212
A	-37	PHE	-	linker	UNP P42212
A	-36	GLU	-	linker	UNP P42212
A	-35	LYS	-	linker	UNP P42212
A	-34	GLY	-	linker	UNP P42212
A	-33	GLY	-	linker	UNP P42212
A	-32	GLY	-	linker	UNP P42212
A	-31	SER	-	linker	UNP P42212
A	-30	GLY	-	linker	UNP P42212
A	-29	GLY	-	linker	UNP P42212
A	-28	GLY	-	linker	UNP P42212
A	-27	SER	-	linker	UNP P42212
A	-26	GLY	-	linker	UNP P42212
A	-25	GLY	-	linker	UNP P42212
A	-24	GLY	-	linker	UNP P42212
A	-23	SER	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	TRP	-	linker	UNP P42212
A	-21	SER	-	linker	UNP P42212
A	-20	HIS	-	linker	UNP P42212
A	-19	PRO	-	linker	UNP P42212
A	-18	GLN	-	linker	UNP P42212
A	-17	PHE	-	linker	UNP P42212
A	-16	GLU	-	linker	UNP P42212
A	-15	LYS	-	linker	UNP P42212
A	-14	SER	-	linker	UNP P42212
A	-13	SER	-	linker	UNP P42212
A	-12	SER	-	linker	UNP P42212
A	-11	ASN	-	linker	UNP P42212
A	-10	ASN	-	linker	UNP P42212
A	-9	ASN	-	linker	UNP P42212
A	-8	ASN	-	linker	UNP P42212
A	-7	ASN	-	linker	UNP P42212
A	-6	GLU	-	linker	UNP P42212
A	-5	ASN	-	linker	UNP P42212
A	-4	LEU	-	linker	UNP P42212
A	-3	TYR	-	linker	UNP P42212
A	-2	PHE	-	linker	UNP P42212
A	-1	GLN	-	linker	UNP P42212
A	0	ALA	-	linker	UNP P42212
A	315	SER	-	linker	UNP P31644
A	316	GLN	-	linker	UNP P31644
A	317	PRO	-	linker	UNP P31644
A	318	ALA	-	linker	UNP P31644
A	319	ARG	-	linker	UNP P31644
A	320	ALA	-	linker	UNP P31644
A	321	ALA	-	linker	UNP P31644
D	-315	MET	-	initiating methionine	UNP P42212
D	-314	ARG	-	expression tag	UNP P42212
D	-313	LYS	-	expression tag	UNP P42212
D	-312	SER	-	expression tag	UNP P42212
D	-311	PRO	-	expression tag	UNP P42212
D	-310	GLY	-	expression tag	UNP P42212
D	-309	LEU	-	expression tag	UNP P42212
D	-308	SER	-	expression tag	UNP P42212
D	-307	ASP	-	expression tag	UNP P42212
D	-306	CYS	-	expression tag	UNP P42212
D	-305	LEU	-	expression tag	UNP P42212
D	-304	TRP	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-303	ALA	-	expression tag	UNP P42212
D	-302	TRP	-	expression tag	UNP P42212
D	-301	ILE	-	expression tag	UNP P42212
D	-300	LEU	-	expression tag	UNP P42212
D	-299	LEU	-	expression tag	UNP P42212
D	-298	LEU	-	expression tag	UNP P42212
D	-297	SER	-	expression tag	UNP P42212
D	-296	THR	-	expression tag	UNP P42212
D	-295	LEU	-	expression tag	UNP P42212
D	-294	THR	-	expression tag	UNP P42212
D	-293	GLY	-	expression tag	UNP P42212
D	-292	ARG	-	expression tag	UNP P42212
D	-291	SER	-	expression tag	UNP P42212
D	-290	TYR	-	expression tag	UNP P42212
D	-289	GLY	-	expression tag	UNP P42212
D	-288	GLN	-	expression tag	UNP P42212
D	-258	ARG	SER	engineered mutation	UNP P42212
D	-249	ASN	TYR	engineered mutation	UNP P42212
D	-224	LEU	PHE	engineered mutation	UNP P42212
D	-223	THR	SER	engineered mutation	UNP P42212
D	-208	ARG	GLN	engineered mutation	UNP P42212
D	-189	SER	PHE	engineered mutation	UNP P42212
D	-183	THR	ASN	engineered mutation	UNP P42212
D	-143	PHE	TYR	engineered mutation	UNP P42212
D	-135	THR	MET	engineered mutation	UNP P42212
D	-125	ALA	VAL	engineered mutation	UNP P42212
D	-117	VAL	ILE	engineered mutation	UNP P42212
D	-82	VAL	ALA	engineered mutation	UNP P42212
D	-49	ALA	-	linker	UNP P42212
D	-48	ALA	-	linker	UNP P42212
D	-47	ASN	-	linker	UNP P42212
D	-46	ALA	-	linker	UNP P42212
D	-45	LEU	-	linker	UNP P42212
D	-44	ALA	-	linker	UNP P42212
D	-43	ALA	-	linker	UNP P42212
D	-42	TRP	-	linker	UNP P42212
D	-41	SER	-	linker	UNP P42212
D	-40	HIS	-	linker	UNP P42212
D	-39	PRO	-	linker	UNP P42212
D	-38	GLN	-	linker	UNP P42212
D	-37	PHE	-	linker	UNP P42212
D	-36	GLU	-	linker	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-35	LYS	-	linker	UNP P42212
D	-34	GLY	-	linker	UNP P42212
D	-33	GLY	-	linker	UNP P42212
D	-32	GLY	-	linker	UNP P42212
D	-31	SER	-	linker	UNP P42212
D	-30	GLY	-	linker	UNP P42212
D	-29	GLY	-	linker	UNP P42212
D	-28	GLY	-	linker	UNP P42212
D	-27	SER	-	linker	UNP P42212
D	-26	GLY	-	linker	UNP P42212
D	-25	GLY	-	linker	UNP P42212
D	-24	GLY	-	linker	UNP P42212
D	-23	SER	-	linker	UNP P42212
D	-22	TRP	-	linker	UNP P42212
D	-21	SER	-	linker	UNP P42212
D	-20	HIS	-	linker	UNP P42212
D	-19	PRO	-	linker	UNP P42212
D	-18	GLN	-	linker	UNP P42212
D	-17	PHE	-	linker	UNP P42212
D	-16	GLU	-	linker	UNP P42212
D	-15	LYS	-	linker	UNP P42212
D	-14	SER	-	linker	UNP P42212
D	-13	SER	-	linker	UNP P42212
D	-12	SER	-	linker	UNP P42212
D	-11	ASN	-	linker	UNP P42212
D	-10	ASN	-	linker	UNP P42212
D	-9	ASN	-	linker	UNP P42212
D	-8	ASN	-	linker	UNP P42212
D	-7	ASN	-	linker	UNP P42212
D	-6	GLU	-	linker	UNP P42212
D	-5	ASN	-	linker	UNP P42212
D	-4	LEU	-	linker	UNP P42212
D	-3	TYR	-	linker	UNP P42212
D	-2	PHE	-	linker	UNP P42212
D	-1	GLN	-	linker	UNP P42212
D	0	ALA	-	linker	UNP P42212
D	315	SER	-	linker	UNP P31644
D	316	GLN	-	linker	UNP P31644
D	317	PRO	-	linker	UNP P31644
D	318	ALA	-	linker	UNP P31644
D	319	ARG	-	linker	UNP P31644
D	320	ALA	-	linker	UNP P31644

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Chain	Residue	Modelled	Actual	Comment	Reference
D	321	ALA	-	linker	UNP P31644

- Molecule 2 is a protein called Gamma-aminobutyric acid receptor subunit beta-3, Green fluorescent protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	340	Total	C	N	O	S	0	0
			2785	1822	455	492	16		
2	C	340	Total	C	N	O	S	0	0
			2785	1822	455	492	16		
2	E	336	Total	C	N	O	S	0	0
			2747	1797	450	484	16		

There are 153 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	308	SER	-	linker	UNP P28472
B	309	GLN	-	linker	UNP P28472
B	310	PRO	-	linker	UNP P28472
B	311	GLY	-	linker	UNP P28472
B	312	ARG	-	linker	UNP P28472
B	313	ALA	-	linker	UNP P28472
B	314	MET	-	linker	UNP P28472
B	315	VAL	-	linker	UNP P28472
B	332	MET	LEU	conflict	UNP P42212
B	339	ARG	HIS	conflict	UNP P42212
B	344	ARG	SER	conflict	UNP P42212
B	346	VAL	GLU	conflict	UNP P42212
B	353	HIS	TYR	conflict	UNP P42212
B	364	SER	THR	conflict	UNP P42212
B	378	LEU	PHE	conflict	UNP P42212
B	419	SER	ASN	conflict	UNP P42212
B	438	VAL	GLU	conflict	UNP P42212
B	442	THR	ILE	conflict	UNP P42212
B	459	MET	TYR	conflict	UNP P42212
B	461	VAL	SER	conflict	UNP P42212
B	462	GLY	HIS	conflict	UNP P42212
B	467	THR	MET	conflict	UNP P42212
B	477	ALA	VAL	conflict	UNP P42212
B	480	GLU	LYS	conflict	UNP P42212
B	485	VAL	ILE	conflict	UNP P42212
B	489	GLY	SER	conflict	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
B	506	SER	PRO	conflict	UNP P42212
B	517	VAL	THR	conflict	UNP P42212
B	519	VAL	SER	conflict	UNP P42212
B	520	LYS	ALA	conflict	UNP P42212
B	538	ARG	VAL	conflict	UNP P42212
B	545	PRO	HIS	conflict	UNP P42212
B	553	GLY	-	linker	UNP P42212
B	554	ARG	-	linker	UNP P42212
B	555	ALA	-	linker	UNP P42212
B	556	ALA	-	linker	UNP P42212
B	584	SER	-	expression tag	UNP P28472
B	585	ARG	-	expression tag	UNP P28472
B	586	GLU	-	expression tag	UNP P28472
B	587	ASN	-	expression tag	UNP P28472
B	588	LEU	-	expression tag	UNP P28472
B	589	TYR	-	expression tag	UNP P28472
B	590	PHE	-	expression tag	UNP P28472
B	591	GLN	-	expression tag	UNP P28472
B	592	ALA	-	expression tag	UNP P28472
B	593	HIS	-	expression tag	UNP P28472
B	594	HIS	-	expression tag	UNP P28472
B	595	HIS	-	expression tag	UNP P28472
B	596	HIS	-	expression tag	UNP P28472
B	597	HIS	-	expression tag	UNP P28472
B	598	HIS	-	expression tag	UNP P28472
C	308	SER	-	linker	UNP P28472
C	309	GLN	-	linker	UNP P28472
C	310	PRO	-	linker	UNP P28472
C	311	GLY	-	linker	UNP P28472
C	312	ARG	-	linker	UNP P28472
C	313	ALA	-	linker	UNP P28472
C	314	MET	-	linker	UNP P28472
C	315	VAL	-	linker	UNP P28472
C	332	MET	LEU	conflict	UNP P42212
C	339	ARG	HIS	conflict	UNP P42212
C	344	ARG	SER	conflict	UNP P42212
C	346	VAL	GLU	conflict	UNP P42212
C	353	HIS	TYR	conflict	UNP P42212
C	364	SER	THR	conflict	UNP P42212
C	378	LEU	PHE	conflict	UNP P42212
C	419	SER	ASN	conflict	UNP P42212
C	438	VAL	GLU	conflict	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
C	442	THR	ILE	conflict	UNP P42212
C	459	MET	TYR	conflict	UNP P42212
C	461	VAL	SER	conflict	UNP P42212
C	462	GLY	HIS	conflict	UNP P42212
C	467	THR	MET	conflict	UNP P42212
C	477	ALA	VAL	conflict	UNP P42212
C	480	GLU	LYS	conflict	UNP P42212
C	485	VAL	ILE	conflict	UNP P42212
C	489	GLY	SER	conflict	UNP P42212
C	506	SER	PRO	conflict	UNP P42212
C	517	VAL	THR	conflict	UNP P42212
C	519	VAL	SER	conflict	UNP P42212
C	520	LYS	ALA	conflict	UNP P42212
C	538	ARG	VAL	conflict	UNP P42212
C	545	PRO	HIS	conflict	UNP P42212
C	553	GLY	-	linker	UNP P42212
C	554	ARG	-	linker	UNP P42212
C	555	ALA	-	linker	UNP P42212
C	556	ALA	-	linker	UNP P42212
C	584	SER	-	expression tag	UNP P28472
C	585	ARG	-	expression tag	UNP P28472
C	586	GLU	-	expression tag	UNP P28472
C	587	ASN	-	expression tag	UNP P28472
C	588	LEU	-	expression tag	UNP P28472
C	589	TYR	-	expression tag	UNP P28472
C	590	PHE	-	expression tag	UNP P28472
C	591	GLN	-	expression tag	UNP P28472
C	592	ALA	-	expression tag	UNP P28472
C	593	HIS	-	expression tag	UNP P28472
C	594	HIS	-	expression tag	UNP P28472
C	595	HIS	-	expression tag	UNP P28472
C	596	HIS	-	expression tag	UNP P28472
C	597	HIS	-	expression tag	UNP P28472
C	598	HIS	-	expression tag	UNP P28472
E	308	SER	-	linker	UNP P28472
E	309	GLN	-	linker	UNP P28472
E	310	PRO	-	linker	UNP P28472
E	311	GLY	-	linker	UNP P28472
E	312	ARG	-	linker	UNP P28472
E	313	ALA	-	linker	UNP P28472
E	314	MET	-	linker	UNP P28472
E	315	VAL	-	linker	UNP P28472

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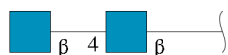
Chain	Residue	Modelled	Actual	Comment	Reference
E	332	MET	LEU	conflict	UNP P42212
E	339	ARG	HIS	conflict	UNP P42212
E	344	ARG	SER	conflict	UNP P42212
E	346	VAL	GLU	conflict	UNP P42212
E	353	HIS	TYR	conflict	UNP P42212
E	364	SER	THR	conflict	UNP P42212
E	378	LEU	PHE	conflict	UNP P42212
E	419	SER	ASN	conflict	UNP P42212
E	438	VAL	GLU	conflict	UNP P42212
E	442	THR	ILE	conflict	UNP P42212
E	459	MET	TYR	conflict	UNP P42212
E	461	VAL	SER	conflict	UNP P42212
E	462	GLY	HIS	conflict	UNP P42212
E	467	THR	MET	conflict	UNP P42212
E	477	ALA	VAL	conflict	UNP P42212
E	480	GLU	LYS	conflict	UNP P42212
E	485	VAL	ILE	conflict	UNP P42212
E	489	GLY	SER	conflict	UNP P42212
E	506	SER	PRO	conflict	UNP P42212
E	517	VAL	THR	conflict	UNP P42212
E	519	VAL	SER	conflict	UNP P42212
E	520	LYS	ALA	conflict	UNP P42212
E	538	ARG	VAL	conflict	UNP P42212
E	545	PRO	HIS	conflict	UNP P42212
E	553	GLY	-	linker	UNP P42212
E	554	ARG	-	linker	UNP P42212
E	555	ALA	-	linker	UNP P42212
E	556	ALA	-	linker	UNP P42212
E	584	SER	-	expression tag	UNP P28472
E	585	ARG	-	expression tag	UNP P28472
E	586	GLU	-	expression tag	UNP P28472
E	587	ASN	-	expression tag	UNP P28472
E	588	LEU	-	expression tag	UNP P28472
E	589	TYR	-	expression tag	UNP P28472
E	590	PHE	-	expression tag	UNP P28472
E	591	GLN	-	expression tag	UNP P28472
E	592	ALA	-	expression tag	UNP P28472
E	593	HIS	-	expression tag	UNP P28472
E	594	HIS	-	expression tag	UNP P28472
E	595	HIS	-	expression tag	UNP P28472
E	596	HIS	-	expression tag	UNP P28472
E	597	HIS	-	expression tag	UNP P28472

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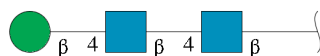
Chain	Residue	Modelled	Actual	Comment	Reference
E	598	HIS	-	expression tag	UNP P28472

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



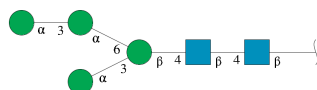
Mol	Chain	Residues	Atoms				AltConf	Trace
3	F	2	Total	C	N	O	0	0
			28	16	2	10		

- 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.



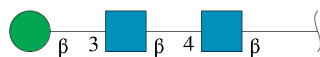
Mol	Chain	Residues	Atoms				AltConf	Trace
4	G	3	Total	C	N	O	0	0
			39	22	2	15		
4	I	3	Total	C	N	O	0	0
			39	22	2	15		
4	N	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



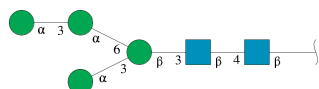
Mol	Chain	Residues	Atoms				AltConf	Trace
5	H	6	Total	C	N	O	0	0
			72	40	2	30		
5	M	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 6 is an oligosaccharide called beta-D-mannopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



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

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



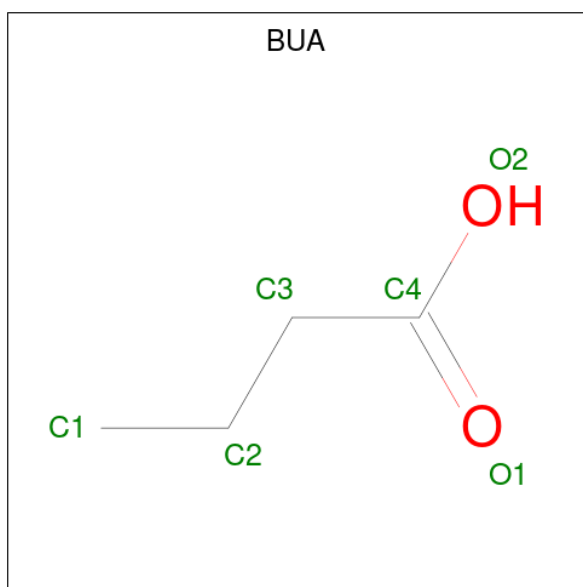
Mol	Chain	Residues	Atoms				AltConf	Trace
7	K	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 8 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



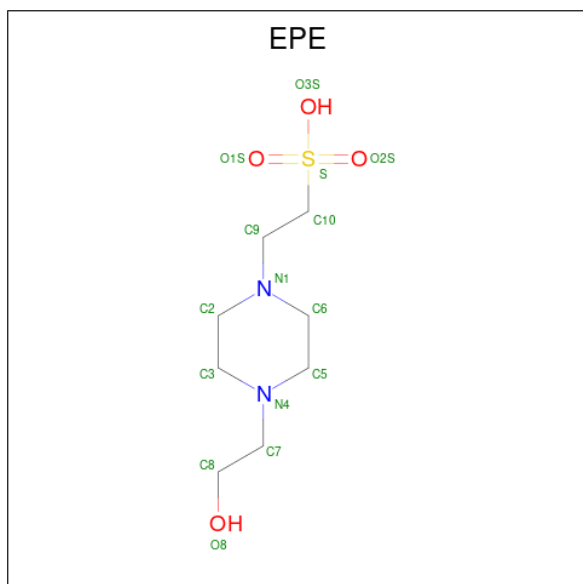
Mol	Chain	Residues	Atoms				AltConf	Trace
8	L	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 9 is butanoic acid (CCD ID: BUA) (formula: C₄H₈O₂).



Mol	Chain	Residues	Atoms			AltConf
9	B	1	Total	C	O	0
			6	4	2	
9	E	1	Total	C	O	0
			6	4	2	

- Molecule 10 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).

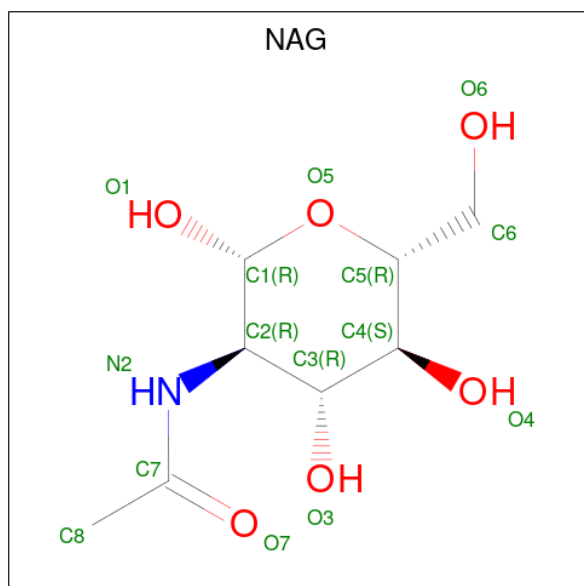


Mol	Chain	Residues	Atoms					AltConf
10	B	1	Total	C	N	O	S	0
			15	8	2	4	1	

- Molecule 11 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms			AltConf
11	B	1	Total	Zn		0
			1	1		

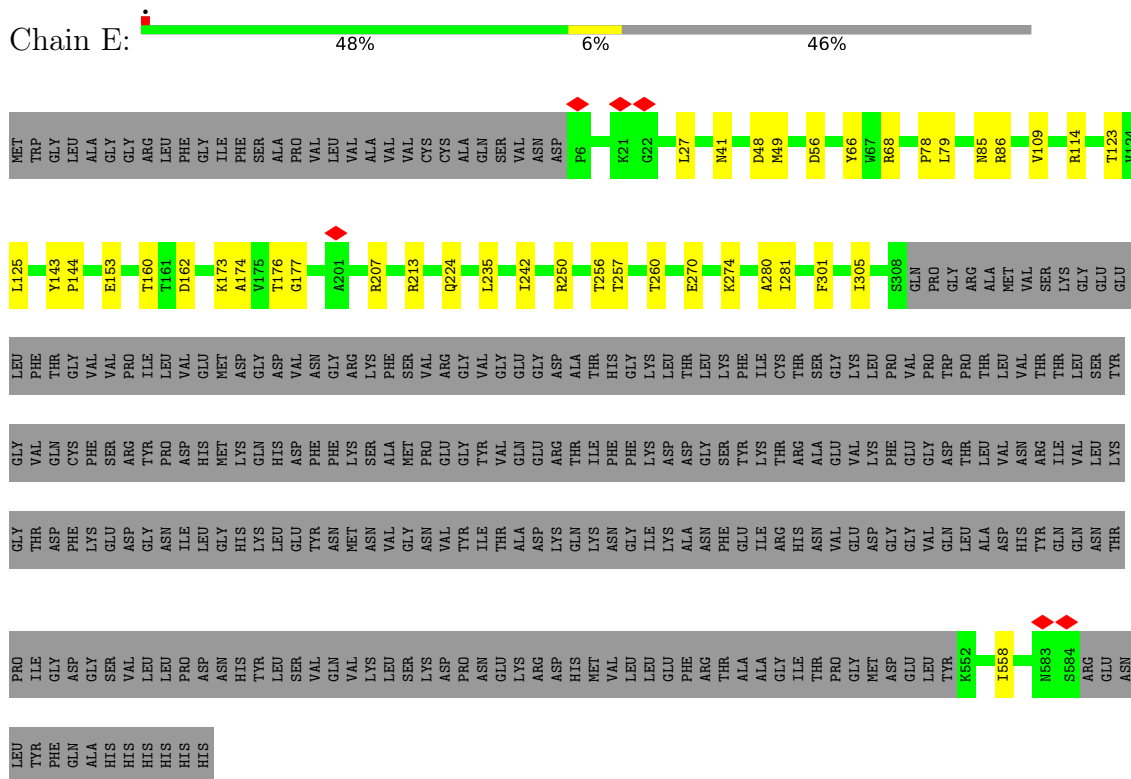
- Molecule 12 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



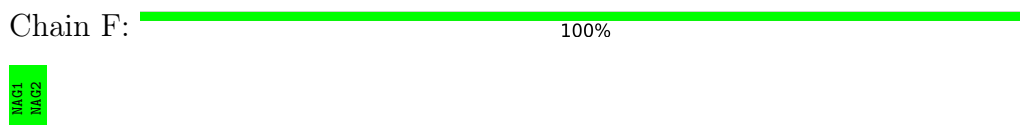
Mol	Chain	Residues	Atoms				AltConf
12	D	1	Total	C	N	O	0
			14	8	1	5	



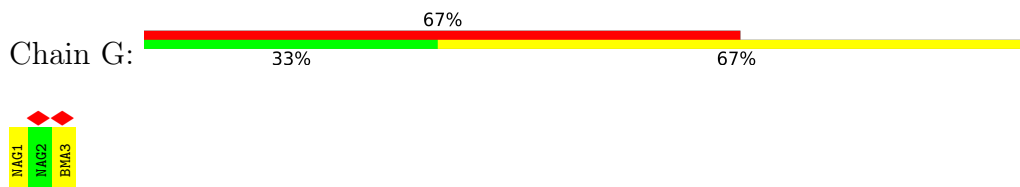
- Molecule 2: Gamma-aminobutyric acid receptor subunit beta-3, Green fluorescent protein



- Molecule 3: 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



- 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



- Molecule 5: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: beta-D-mannopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 7: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  100%

MAG1
MAG2
BGA3
MAN4
MAN5
MAN6

- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  50%  50%

MAG1
MAG2

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	68589	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58.65	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	39.451	Depositor
Minimum map value	-25.209	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.5	Depositor
Map size (Å)	286.0, 286.0, 286.0	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.65, 0.65, 0.65	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: ZN, EPE, NAG, BUA, BMA, MAN

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	0.15	0/2818	0.40	0/3833
1	D	0.15	0/2786	0.40	0/3788
2	B	0.15	0/2859	0.40	0/3887
2	C	0.16	0/2859	0.40	0/3887
2	E	0.15	0/2820	0.41	0/3834
All	All	0.15	0/14142	0.40	0/19229

There are no bond length outliers.

There are no bond angle outliers.

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	A	2750	0	2724	36	0
1	D	2719	0	2700	32	0
2	B	2785	0	2776	9	0
2	C	2785	0	2776	20	0
2	E	2747	0	2742	31	0
3	F	28	0	25	0	0
4	G	39	0	34	0	0
4	I	39	0	34	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	N	39	0	34	1	0
5	H	72	0	61	0	0
5	M	72	0	61	0	0
6	J	39	0	34	0	0
7	K	72	0	61	0	0
8	L	28	0	25	1	0
9	B	6	0	7	0	0
9	E	6	0	7	1	0
10	B	15	0	18	0	0
11	B	1	0	0	0	0
12	D	14	0	13	0	0
All	All	14256	0	14132	115	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 4.

The worst 5 of 115 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:116:THR:CG2	1:D:117:PRO:HD2	2.05	0.86
1:D:116:THR:HG22	1:D:117:PRO:HD2	1.66	0.76
1:D:116:THR:CG2	1:D:117:PRO:CD	2.65	0.75
1:D:133:MET:HE2	1:D:135:LEU:HD21	1.70	0.73
2:C:68:ARG:NH1	2:C:121:ASP:OD2	2.22	0.73

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	339/679 (50%)	333 (98%)	6 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	335/679 (49%)	325 (97%)	10 (3%)	0	100	100
2	B	336/623 (54%)	332 (99%)	4 (1%)	0	100	100
2	C	336/623 (54%)	330 (98%)	6 (2%)	0	100	100
2	E	332/623 (53%)	328 (99%)	4 (1%)	0	100	100
All	All	1678/3227 (52%)	1648 (98%)	30 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	306/589 (52%)	306 (100%)	0	100	100
1	D	302/589 (51%)	301 (100%)	1 (0%)	86	85
2	B	304/544 (56%)	304 (100%)	0	100	100
2	C	304/544 (56%)	304 (100%)	0	100	100
2	E	300/544 (55%)	300 (100%)	0	100	100
All	All	1516/2810 (54%)	1515 (100%)	1 (0%)	87	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	175	ASN

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	218	HIS
1	D	90	ASN
1	D	218	HIS
2	E	54	ASN

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Mol	Chain	Res	Type
2	E	303	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

34 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	$\# Z > 2$
3	NAG	F	1	3,1	14,14,15	0.74	0	17,19,21	0.87	0
3	NAG	F	2	3	14,14,15	0.72	0	17,19,21	0.88	0
4	NAG	G	1	4,1	14,14,15	0.70	0	17,19,21	0.96	1 (5%)
4	NAG	G	2	4	14,14,15	0.74	0	17,19,21	0.76	0
4	BMA	G	3	4	11,11,12	0.87	0	15,15,17	3.22	7 (46%)
5	NAG	H	1	5,2	14,14,15	0.76	0	17,19,21	0.96	0
5	NAG	H	2	5	14,14,15	0.75	0	17,19,21	0.96	0
5	BMA	H	3	5	11,11,12	0.86	0	15,15,17	2.24	4 (26%)
5	MAN	H	4	5	11,11,12	0.67	0	15,15,17	1.20	1 (6%)
5	MAN	H	5	5	11,11,12	0.71	0	15,15,17	1.10	1 (6%)
5	MAN	H	6	5	11,11,12	0.67	0	15,15,17	1.26	1 (6%)
4	NAG	I	1	4,2	14,14,15	0.74	0	17,19,21	0.96	1 (5%)
4	NAG	I	2	4	14,14,15	0.73	0	17,19,21	0.88	0
4	BMA	I	3	4	11,11,12	0.87	0	15,15,17	3.15	7 (46%)
6	NAG	J	1	6,2	14,14,15	0.71	0	17,19,21	1.11	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	J	2	6	14,14,15	0.71	0	17,19,21	1.15	1 (5%)
6	BMA	J	3	6	11,11,12	0.87	0	15,15,17	2.98	7 (46%)
7	NAG	K	1	7,2	14,14,15	0.69	0	17,19,21	2.12	4 (23%)
7	NAG	K	2	7	14,14,15	0.86	0	17,19,21	1.17	1 (5%)
7	BMA	K	3	7	11,11,12	0.94	0	15,15,17	2.65	7 (46%)
7	MAN	K	4	7	11,11,12	0.68	0	15,15,17	1.66	2 (13%)
7	MAN	K	5	7	11,11,12	0.74	0	15,15,17	0.97	1 (6%)
7	MAN	K	6	7	11,11,12	0.66	0	15,15,17	1.44	1 (6%)
8	NAG	L	1	8,1	14,14,15	0.72	0	17,19,21	0.92	0
8	NAG	L	2	8	14,14,15	0.71	0	17,19,21	0.86	0
5	NAG	M	1	5,2	14,14,15	0.74	0	17,19,21	0.88	0
5	NAG	M	2	5	14,14,15	0.74	0	17,19,21	0.95	0
5	BMA	M	3	5	11,11,12	0.86	0	15,15,17	2.23	4 (26%)
5	MAN	M	4	5	11,11,12	0.65	0	15,15,17	1.26	1 (6%)
5	MAN	M	5	5	11,11,12	0.73	0	15,15,17	1.02	1 (6%)
5	MAN	M	6	5	11,11,12	0.71	0	15,15,17	1.05	1 (6%)
4	NAG	N	1	4,2	14,14,15	0.81	0	17,19,21	1.03	1 (5%)
4	NAG	N	2	4	14,14,15	0.78	0	17,19,21	1.32	2 (11%)
4	BMA	N	3	4	11,11,12	0.89	0	15,15,17	2.93	6 (40%)

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
3	NAG	F	1	3,1	-	1/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
4	NAG	G	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	G	2	4	-	0/6/23/26	0/1/1/1
4	BMA	G	3	4	-	0/2/19/22	0/1/1/1
5	NAG	H	1	5,2	-	0/6/23/26	0/1/1/1
5	NAG	H	2	5	-	0/6/23/26	0/1/1/1
5	BMA	H	3	5	-	0/2/19/22	0/1/1/1
5	MAN	H	4	5	-	0/2/19/22	0/1/1/1
5	MAN	H	5	5	-	0/2/19/22	0/1/1/1
5	MAN	H	6	5	-	1/2/19/22	0/1/1/1
4	NAG	I	1	4,2	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BMA	I	3	4	-	0/2/19/22	0/1/1/1
6	NAG	J	1	6,2	-	0/6/23/26	0/1/1/1
6	NAG	J	2	6	-	0/6/23/26	0/1/1/1
6	BMA	J	3	6	-	1/2/19/22	0/1/1/1
7	NAG	K	1	7,2	-	0/6/23/26	0/1/1/1
7	NAG	K	2	7	-	0/6/23/26	0/1/1/1
7	BMA	K	3	7	-	1/2/19/22	0/1/1/1
7	MAN	K	4	7	-	1/2/19/22	0/1/1/1
7	MAN	K	5	7	-	0/2/19/22	0/1/1/1
7	MAN	K	6	7	-	0/2/19/22	0/1/1/1
8	NAG	L	1	8,1	-	1/6/23/26	0/1/1/1
8	NAG	L	2	8	-	0/6/23/26	0/1/1/1
5	NAG	M	1	5,2	-	0/6/23/26	0/1/1/1
5	NAG	M	2	5	-	0/6/23/26	0/1/1/1
5	BMA	M	3	5	-	0/2/19/22	0/1/1/1
5	MAN	M	4	5	-	0/2/19/22	0/1/1/1
5	MAN	M	5	5	-	0/2/19/22	0/1/1/1
5	MAN	M	6	5	-	0/2/19/22	0/1/1/1
4	NAG	N	1	4,2	-	1/6/23/26	0/1/1/1
4	NAG	N	2	4	-	2/6/23/26	0/1/1/1
4	BMA	N	3	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	3	BMA	C1-O5-C5	9.79	125.46	112.19
4	I	3	BMA	C1-O5-C5	9.08	124.49	112.19
4	N	3	BMA	C1-O5-C5	8.74	124.03	112.19
6	J	3	BMA	C1-O5-C5	8.61	123.86	112.19
7	K	3	BMA	C1-O5-C5	6.64	121.19	112.19

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

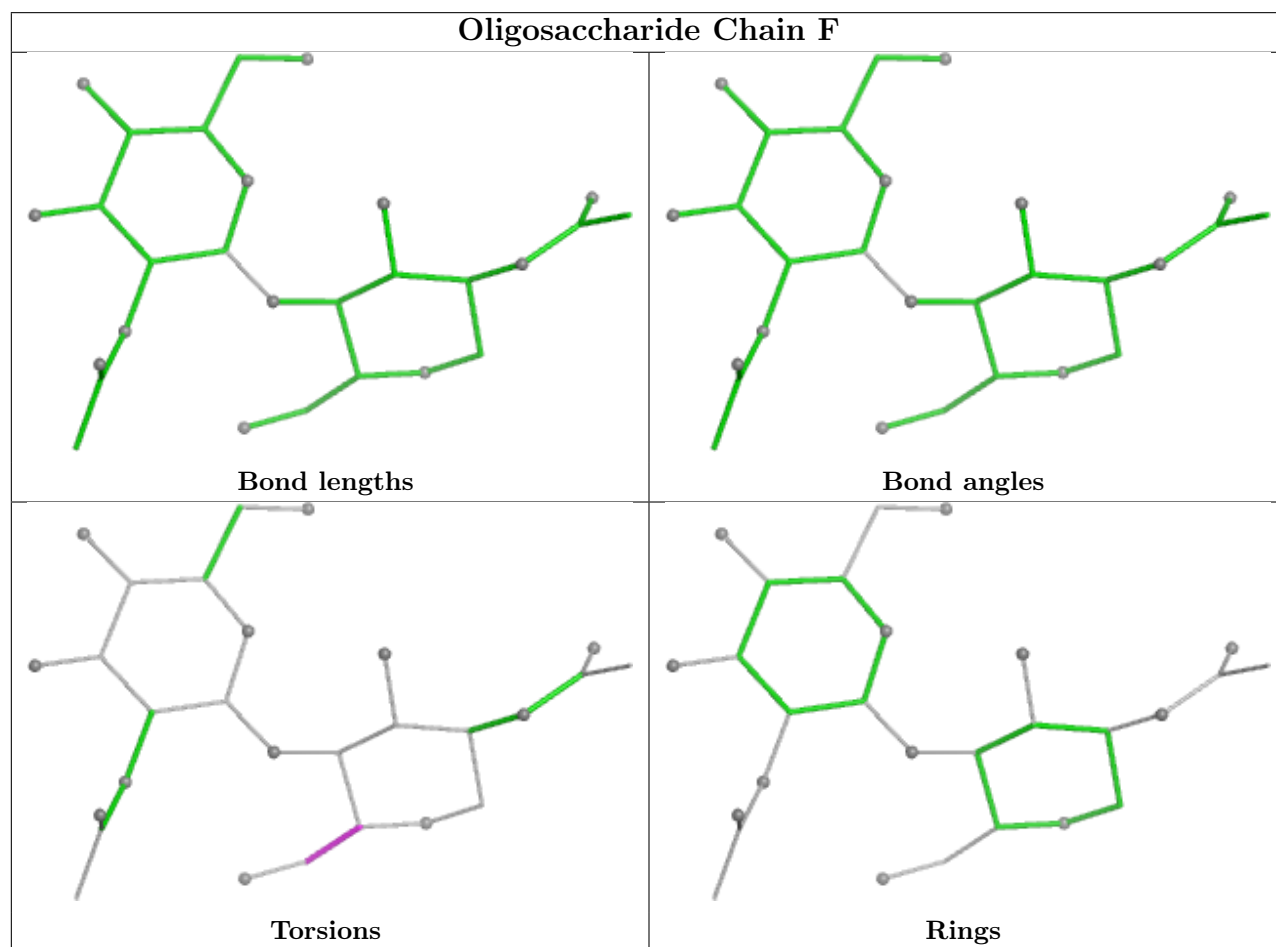
Mol	Chain	Res	Type	Atoms
6	J	3	BMA	O5-C5-C6-O6
7	K	4	MAN	O5-C5-C6-O6
3	F	1	NAG	O5-C5-C6-O6
4	N	1	NAG	O5-C5-C6-O6
5	H	6	MAN	O5-C5-C6-O6

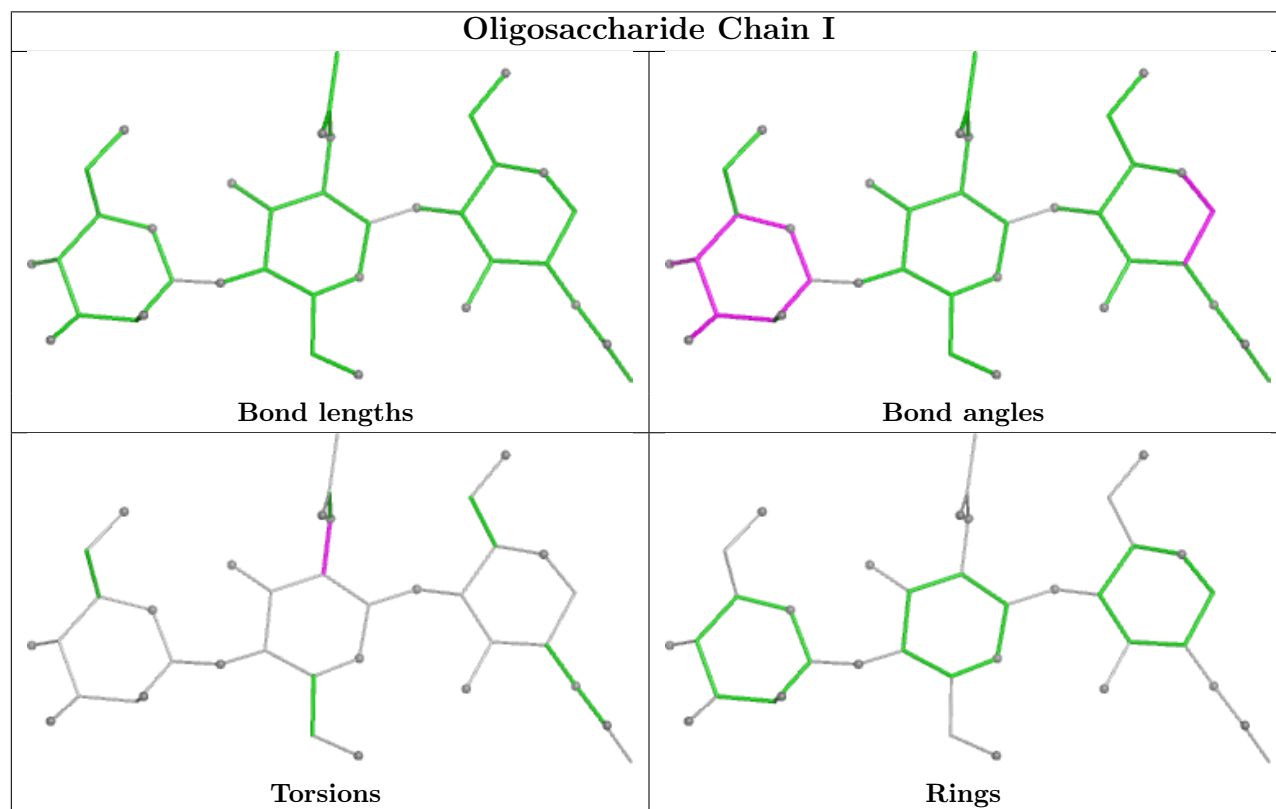
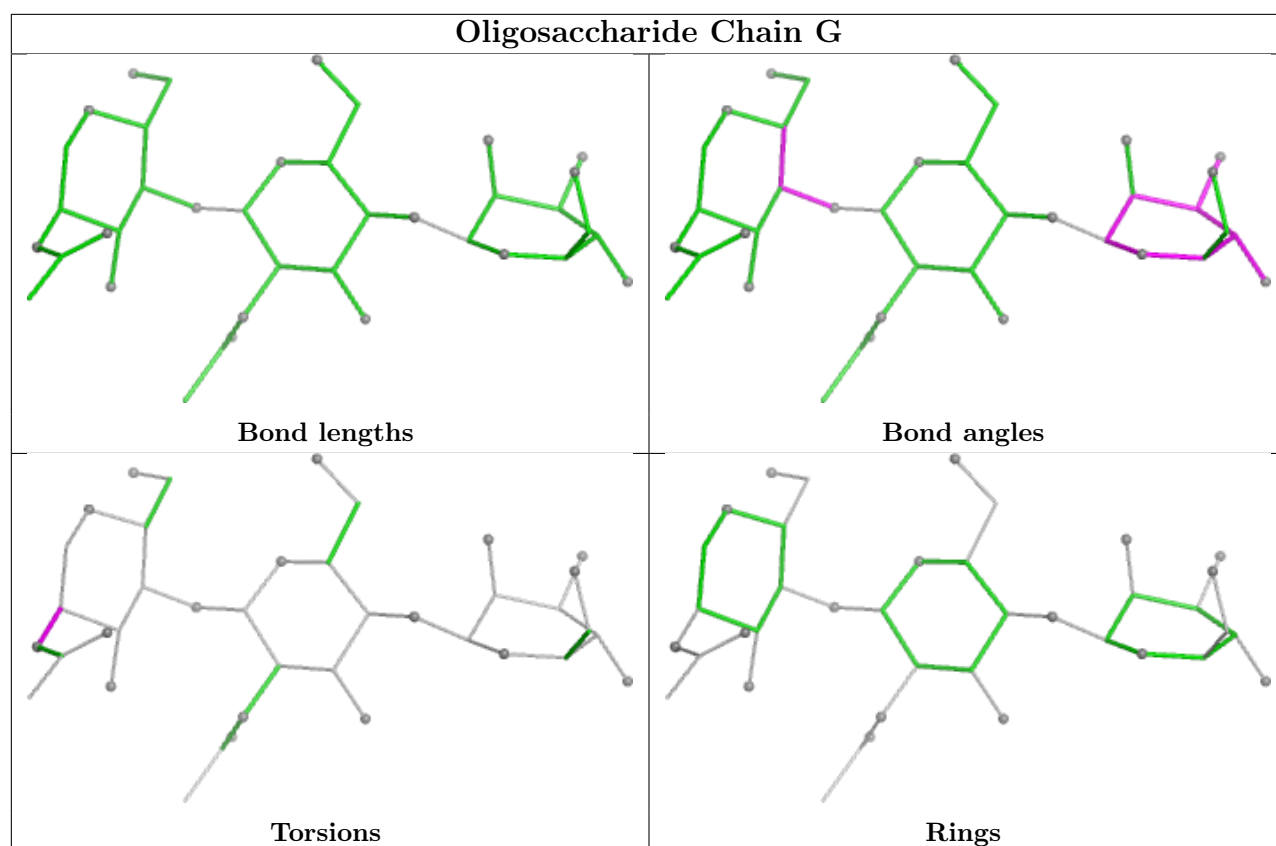
There are no ring outliers.

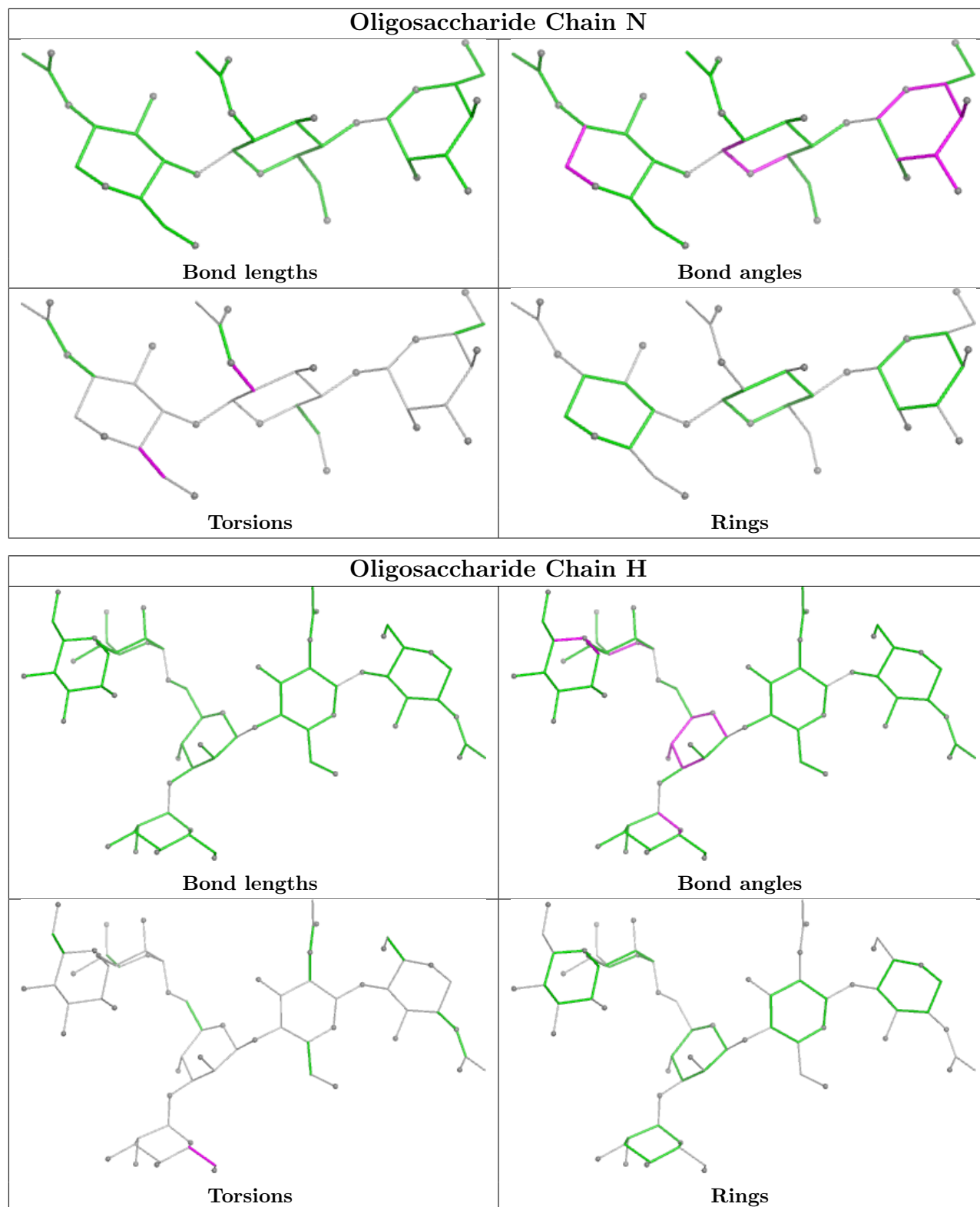
3 monomers are involved in 2 short contacts:

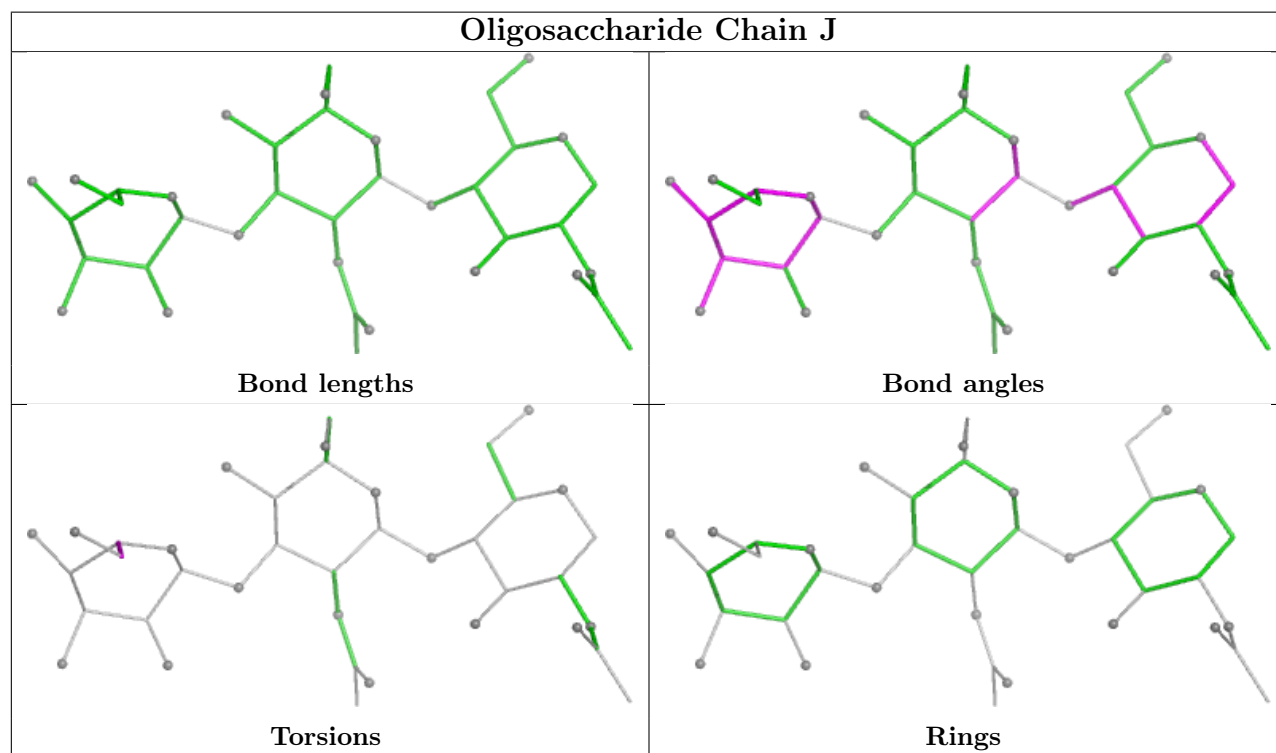
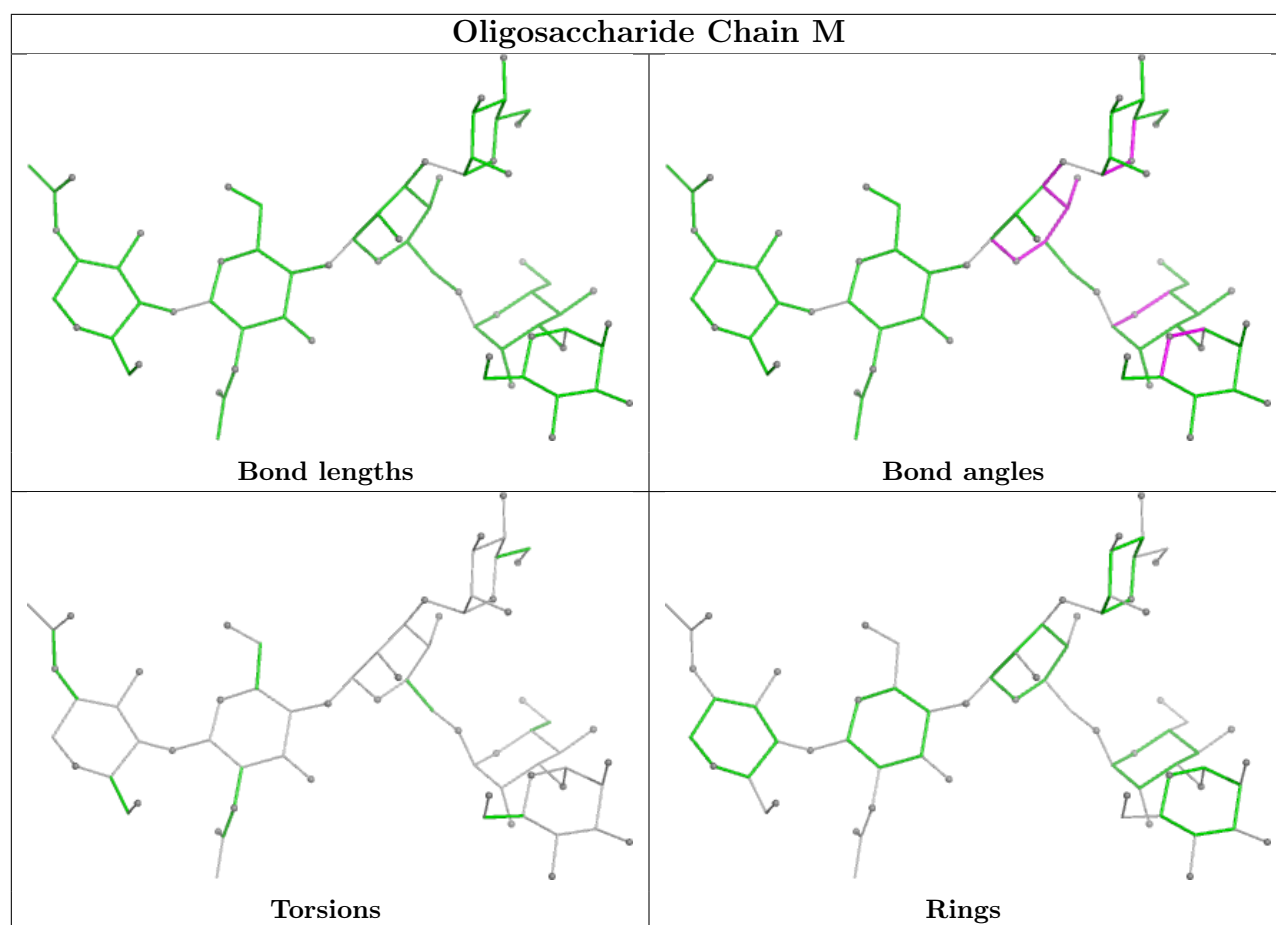
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	L	1	NAG	1	0
4	N	2	NAG	1	0
4	N	1	NAG	1	0

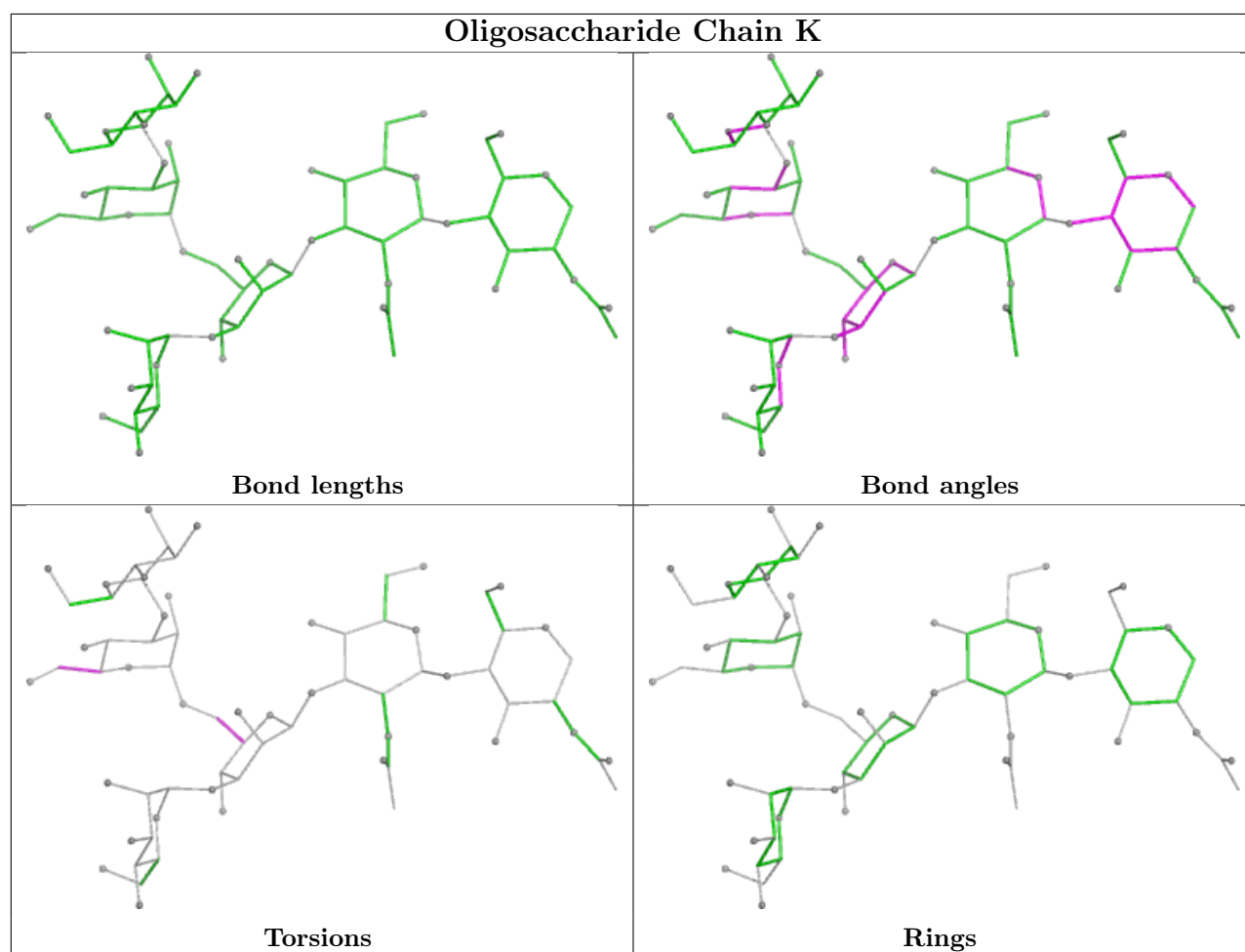
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

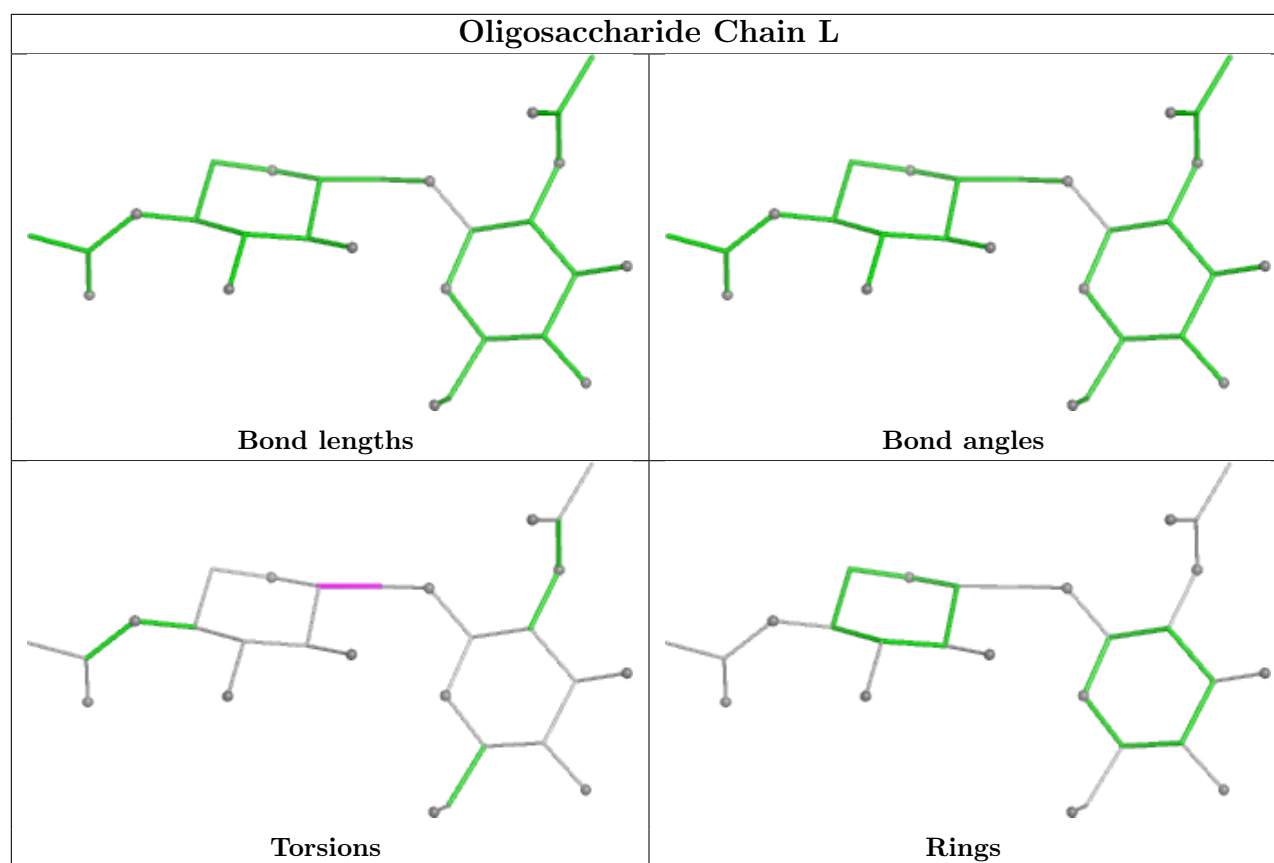












5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 for Mogul analysis.

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	$\# Z > 2$
9	BUA	E	601	-	5,5,5	1.09	0	5,5,5	0.91	0
12	NAG	D	401	1	14,14,15	0.69	0	17,19,21	0.92	0
9	BUA	B	601	-	5,5,5	1.08	0	5,5,5	0.93	0
10	EPE	B	602	-	15,15,15	0.82	1 (6%)	18,20,20	1.03	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
9	BUA	E	601	-	-	2/3/3/3	-
12	NAG	D	401	1	-	1/6/23/26	0/1/1/1
9	BUA	B	601	-	-	0/3/3/3	-
10	EPE	B	602	-	-	0/9/19/19	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	602	EPE	C10-S	2.37	1.80	1.77

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	D	401	NAG	O5-C5-C6-O6
9	E	601	BUA	C2-C3-C4-O1
9	E	601	BUA	C2-C3-C4-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	E	601	BUA	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.

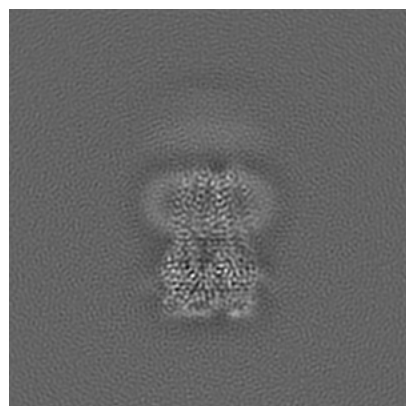
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51980. These allow visual inspection of the internal detail of the map and identification of artifacts.

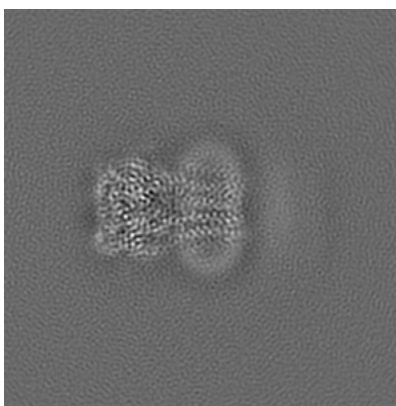
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

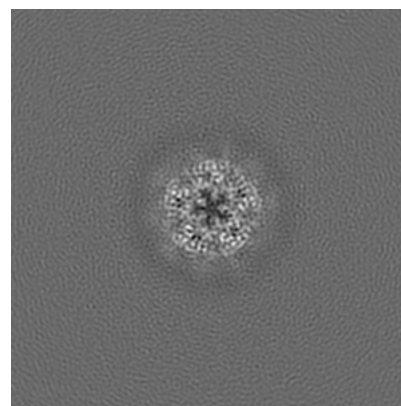
6.1.1 Primary map



X

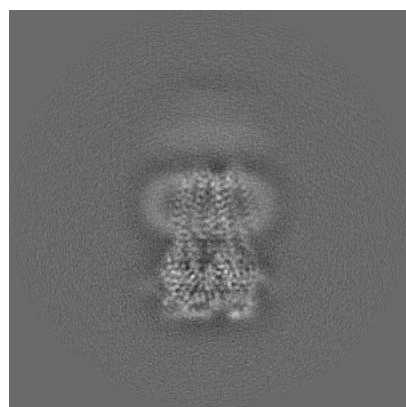


Y

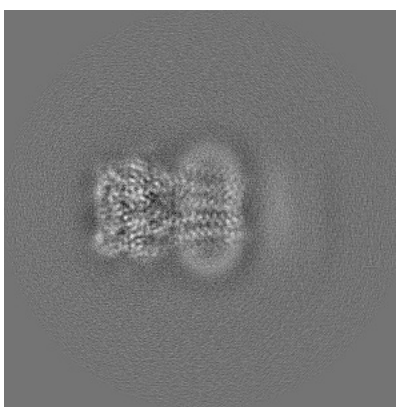


Z

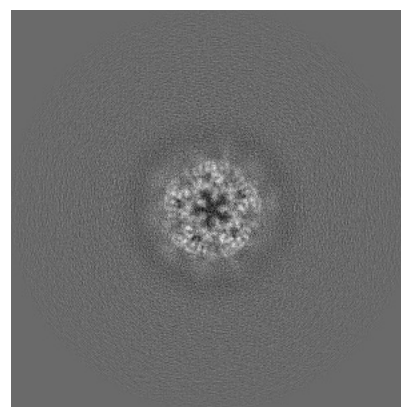
6.1.2 Raw map



X



Y

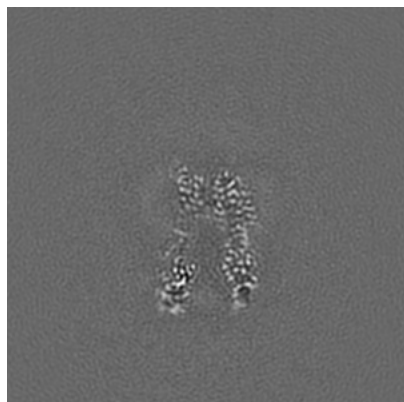


Z

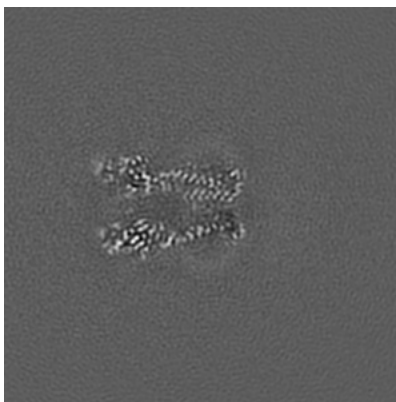
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

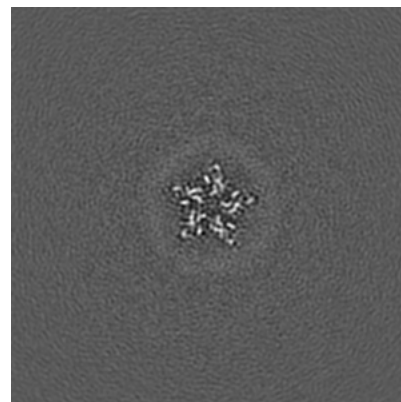
6.2.1 Primary map



X Index: 220

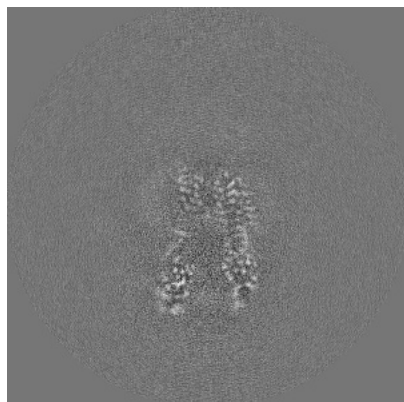


Y Index: 220

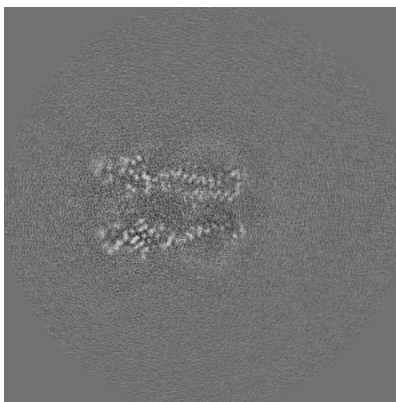


Z Index: 220

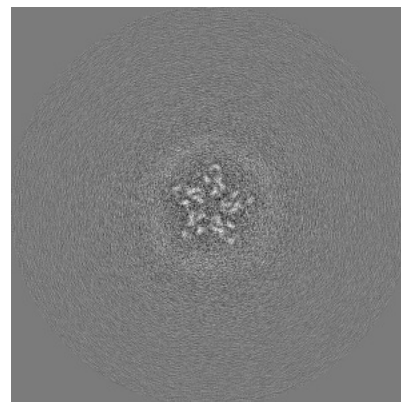
6.2.2 Raw map



X Index: 220



Y Index: 220

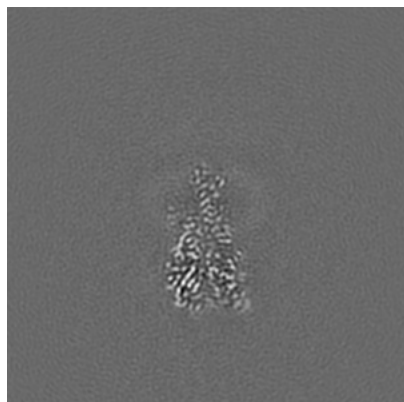


Z Index: 220

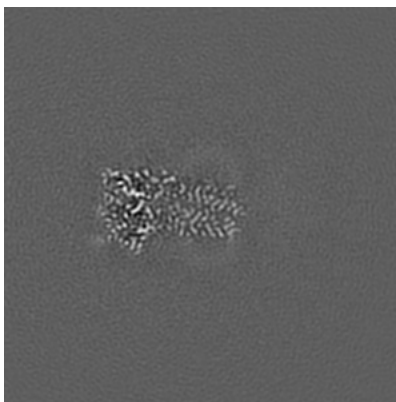
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

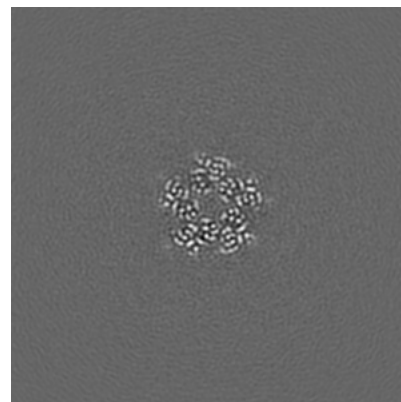
6.3.1 Primary map



X Index: 250

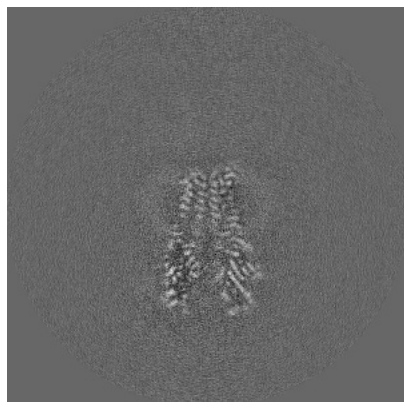


Y Index: 192

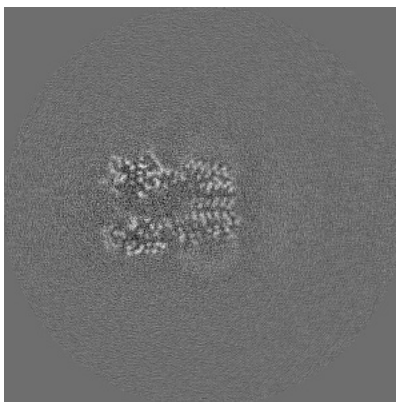


Z Index: 151

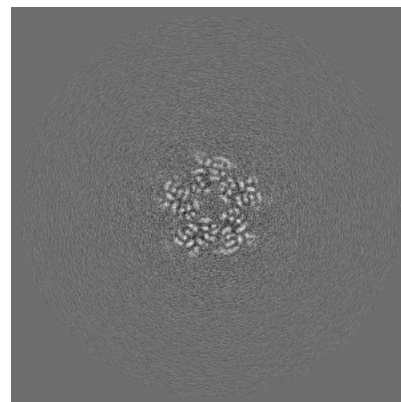
6.3.2 Raw map



X Index: 207



Y Index: 230

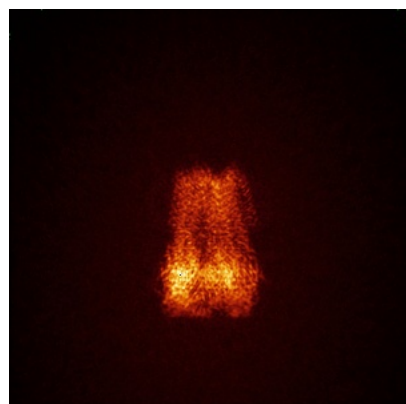


Z Index: 151

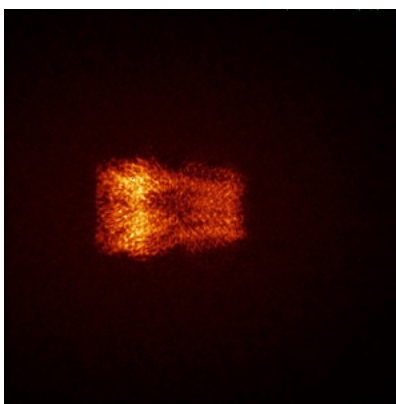
The images above show the largest variance slices of the map in three orthogonal directions.

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

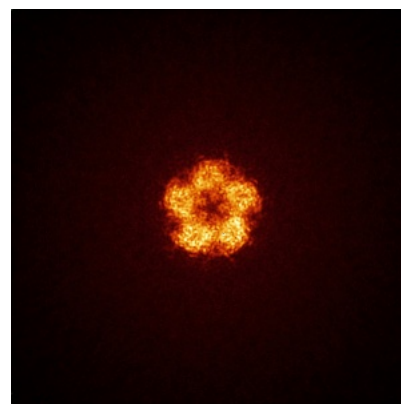
6.4.1 Primary map



X

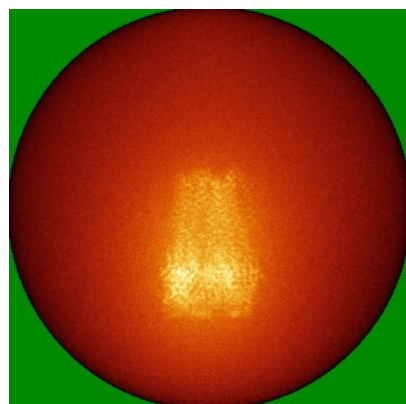


Y

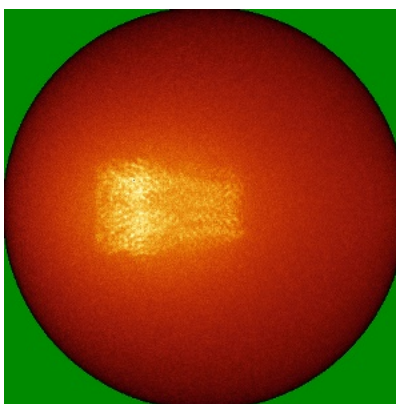


Z

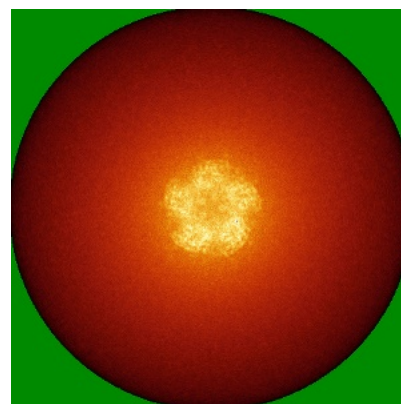
6.4.2 Raw map



X



Y

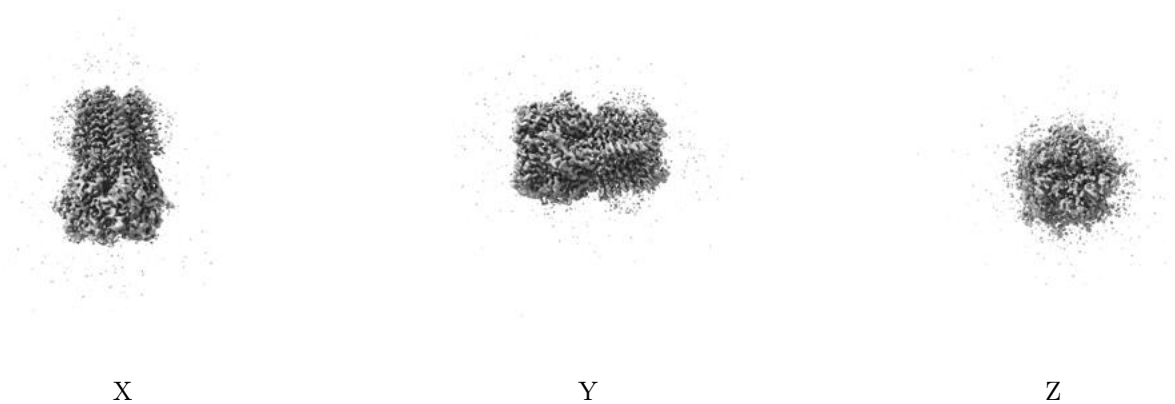


Z

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.

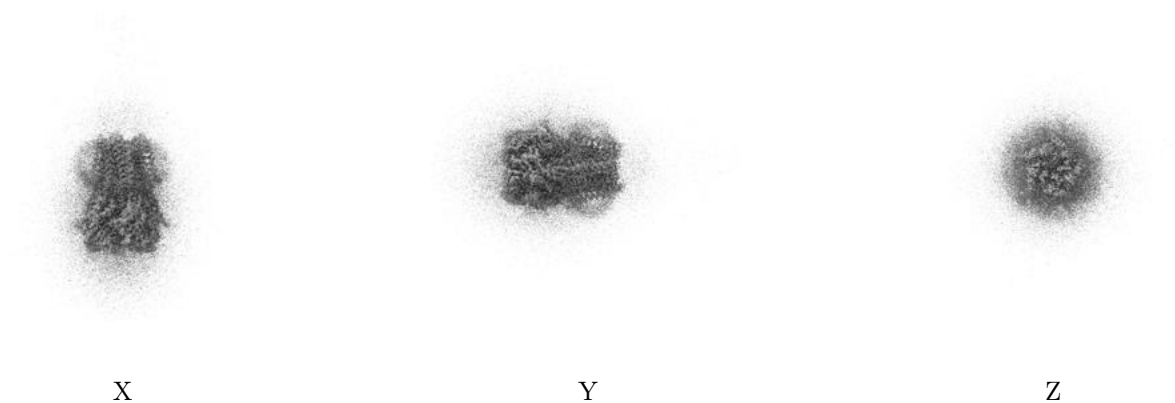
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

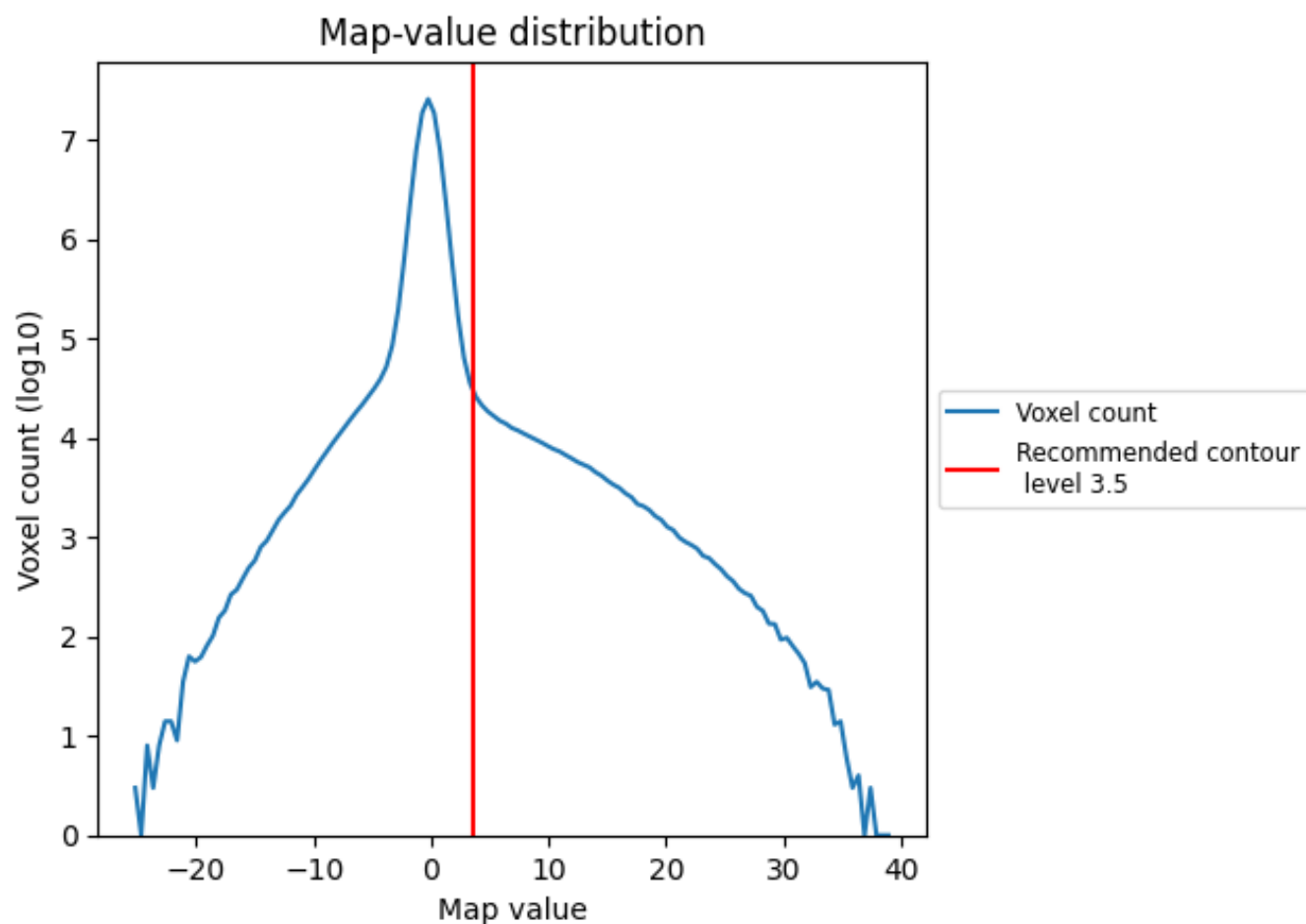
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

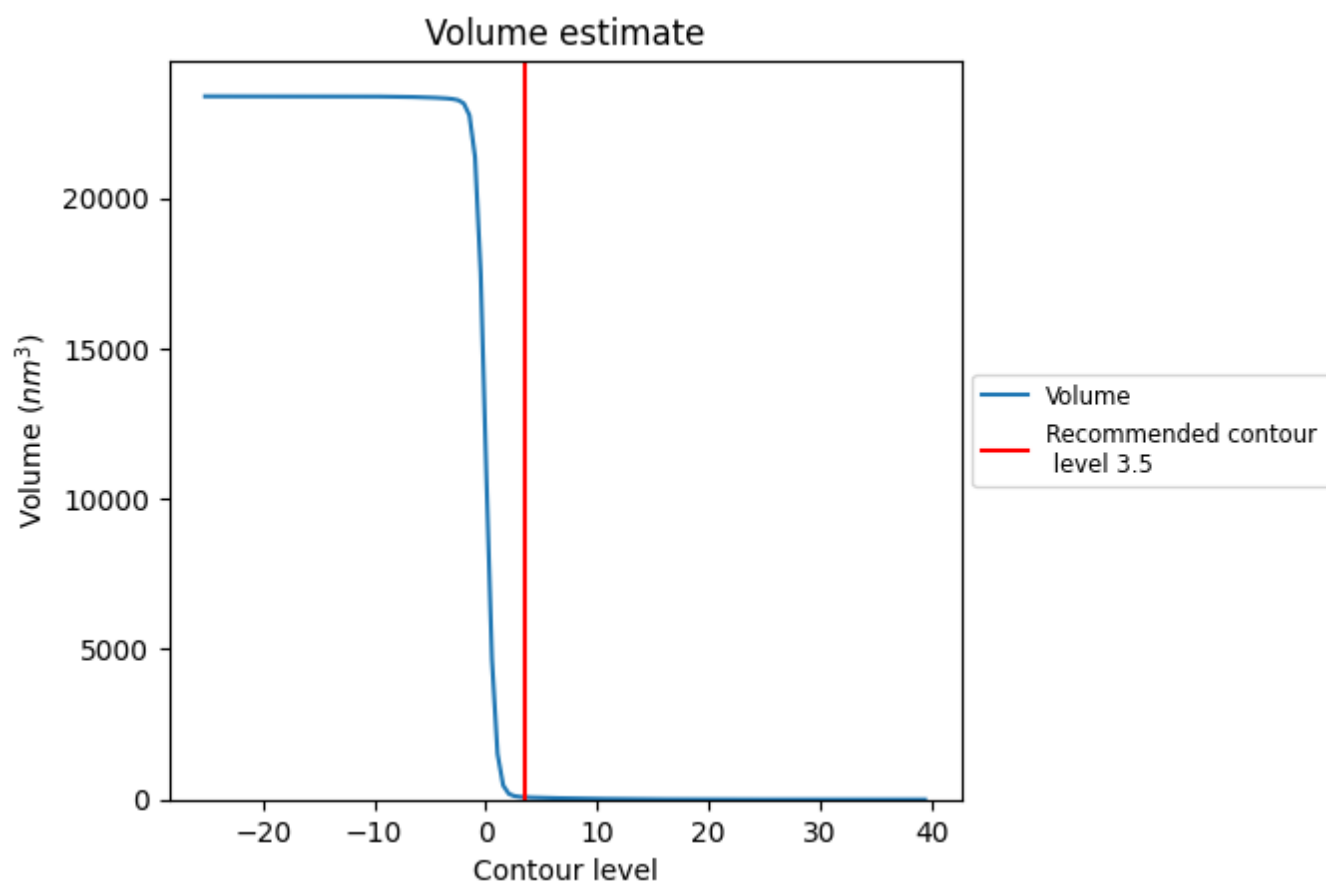
This section contains the results of statistical analysis of the map.

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.

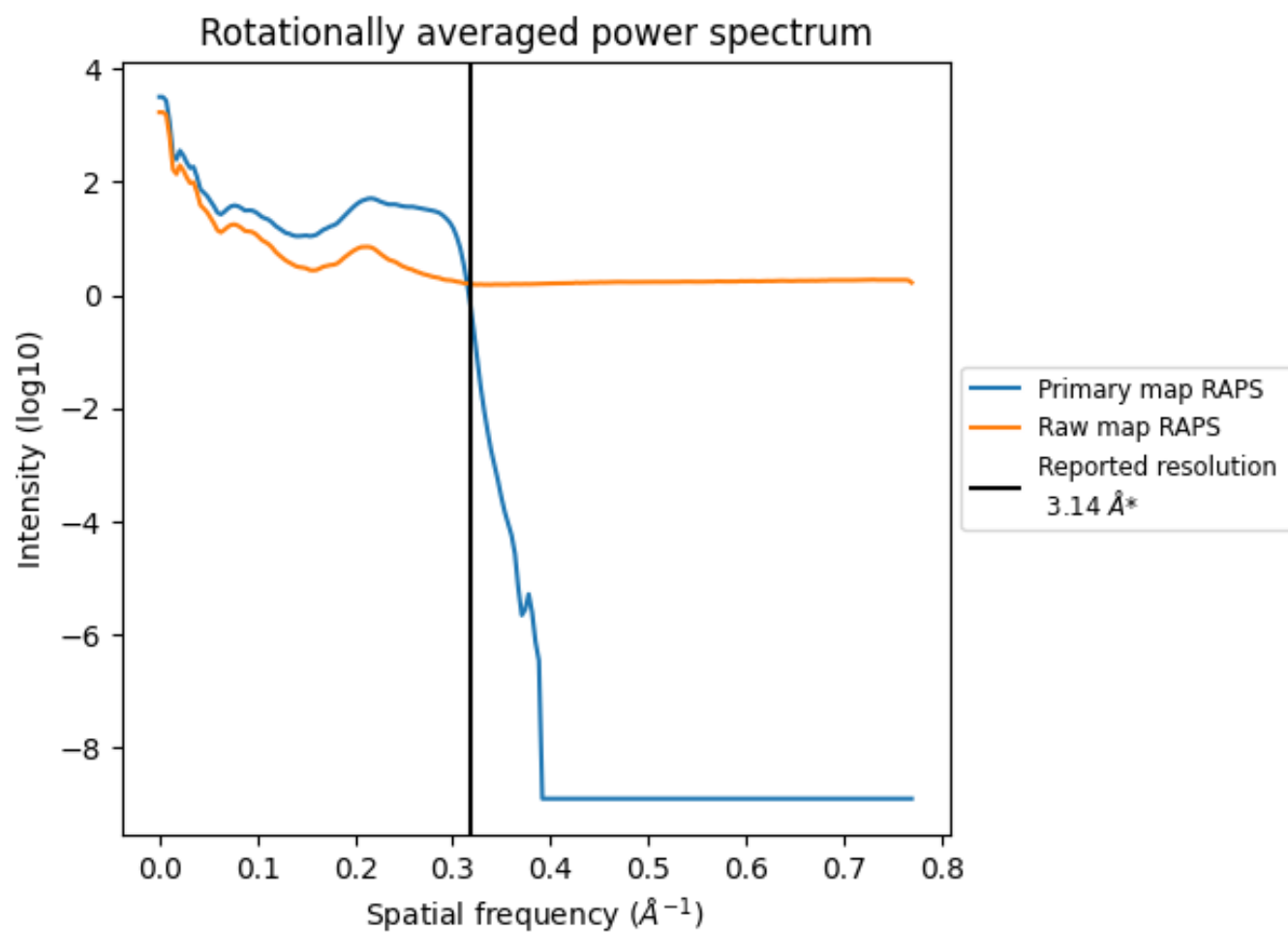
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 80 nm^3 ; this corresponds to an approximate mass of 73 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 ⓘ

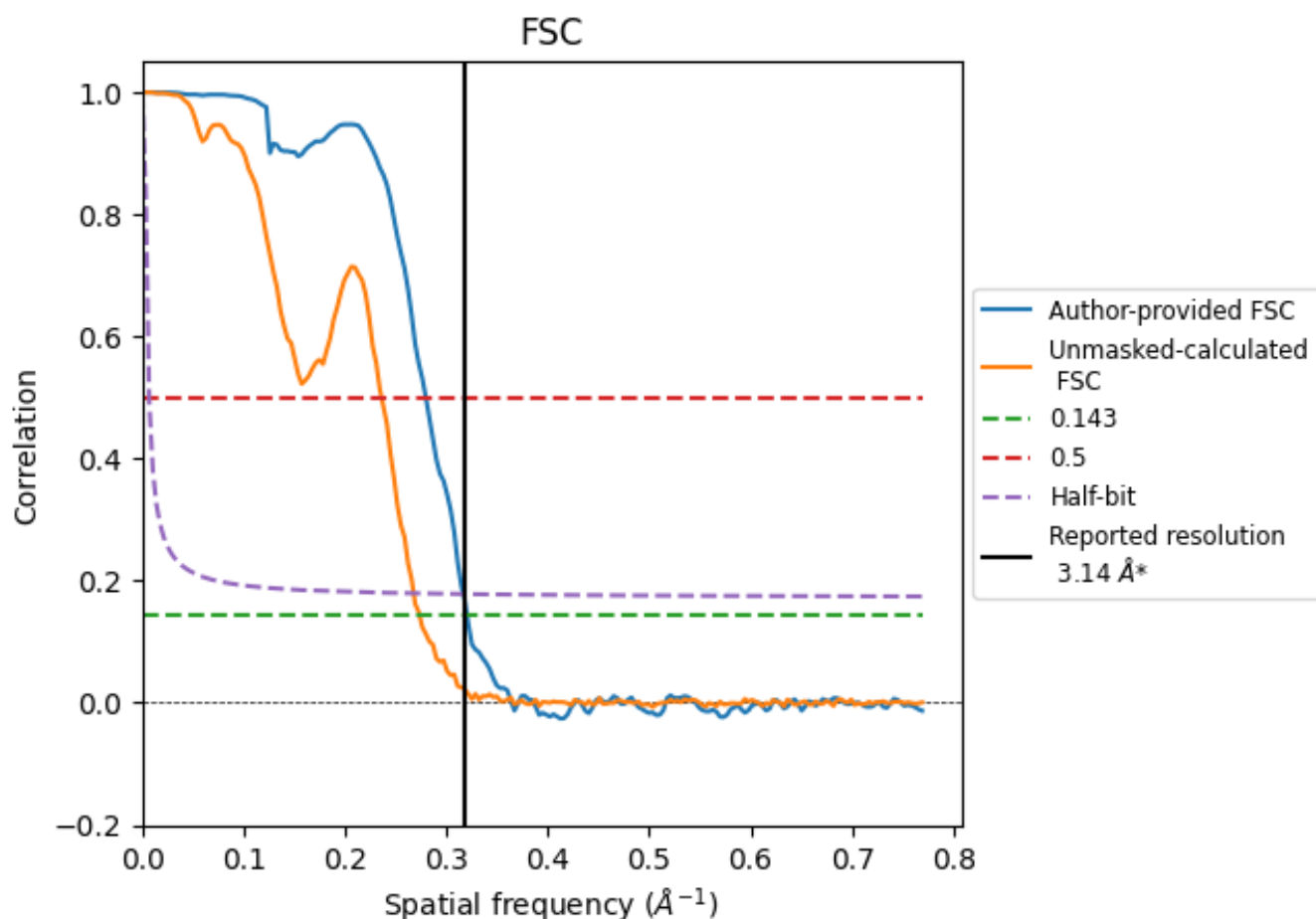


*Reported resolution corresponds to spatial frequency of 0.318 $\text{\AA}^{-1}$

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 0.318 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

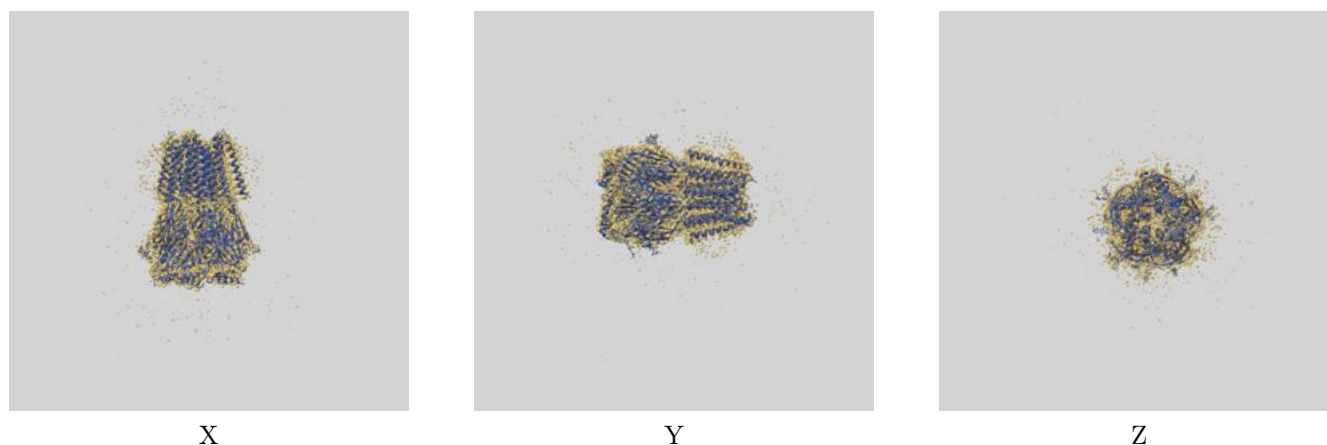
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.14	-	-
Author-provided FSC curve	3.12	3.57	3.16
Unmasked-calculated*	3.66	4.24	3.74

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.66 differs from the reported value 3.14 by more than 10 %

9 Map-model fit [i](#)

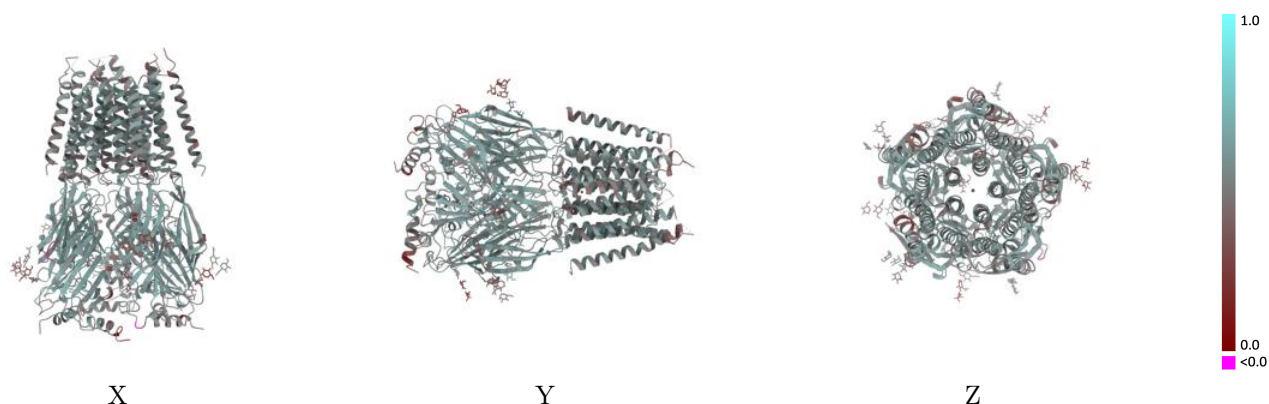
This section contains information regarding the fit between EMDB map EMD-51980 and PDB model 9HAA. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



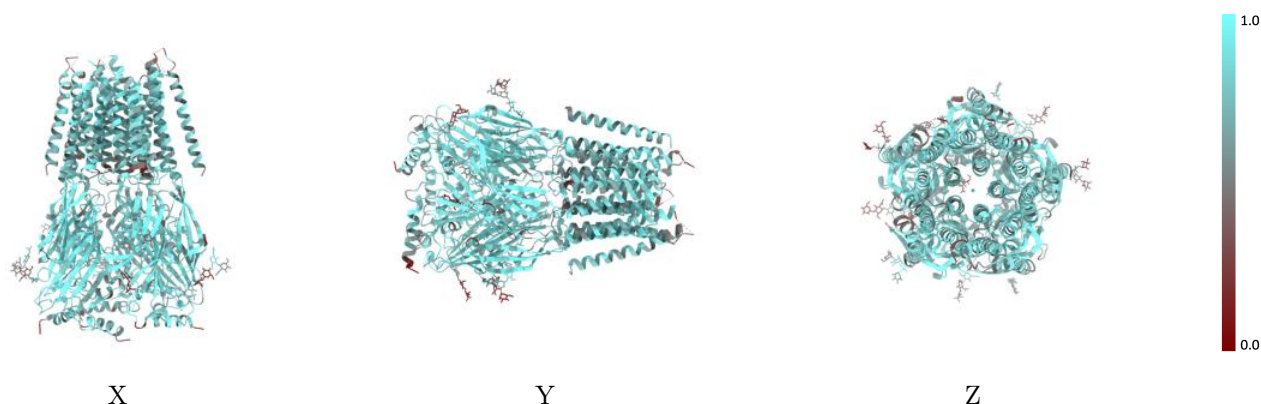
The images above show the 3D surface view of the map at the recommended contour level 3.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



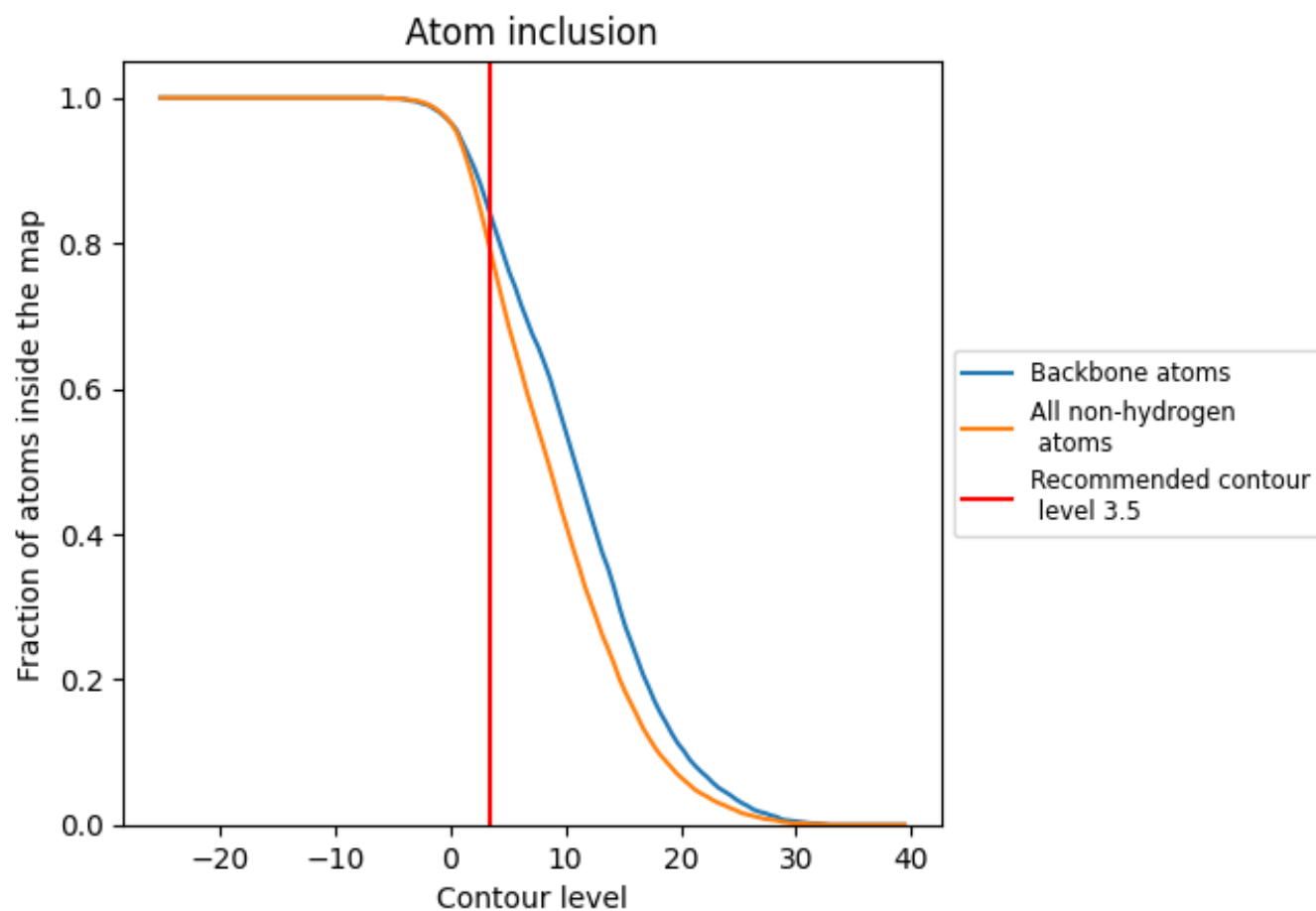
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 79% 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 (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7860	 0.5210
A	 0.7730	 0.5120
B	 0.7850	 0.5270
C	 0.8100	 0.5340
D	 0.7960	 0.5230
E	 0.8100	 0.5310
F	 0.6430	 0.4630
G	 0.2050	 0.2600
H	 0.4860	 0.4610
I	 0.2820	 0.3170
J	 0.4870	 0.2780
K	 0.7500	 0.4630
L	 0.5360	 0.4120
M	 0.5830	 0.3680
N	 0.3590	 0.3270

