



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 08:16 PM UTC

PDB ID : 8RM0 / pdb_00008rm0
EMDB ID : EMD-19347
Title : Cryo-EM structure of a Foamy Virus fusion glycoprotein stabilized in the pre-fusion conformation
Authors : Fernandez, I.; Backovic, M.
Deposited on : 2024-01-04
Resolution : 3.80 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:

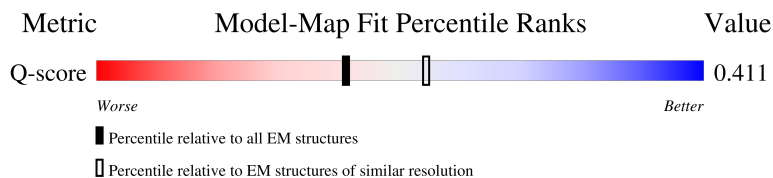
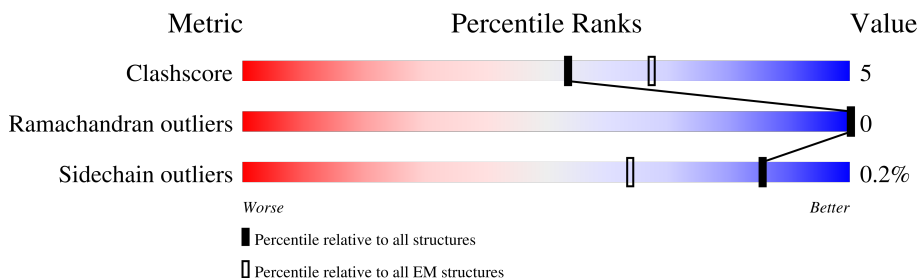
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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	890	68% (green), 10% (yellow), 22% (grey)
1	B	890	68% (green), 10% (yellow), 22% (grey)
1	C	890	68% (green), 10% (yellow), 22% (grey)
2	D	2	100% (green)

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Mol	Chain	Length	Quality of chain
2	E	2	 100%
2	G	2	 50% 50%
2	H	2	 100%
2	I	2	 100%
2	K	2	 50% 50%
2	L	2	 100%
2	M	2	 100%
2	O	2	 50% 50%
3	F	5	 40% 60%
3	J	5	 40% 60%
3	N	5	 40% 60%

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 16311 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 Envelope glycoprotein gp130.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	696	5222	3340	894	954	34	0	0
1	B	696	5222	3340	894	954	34	0	0
1	C	696	5222	3340	894	954	34	0	0

There are 237 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	126	ALA	ARG	engineered mutation	UNP K7YEW5
A	556K	GLY	-	linker	UNP K7YEW5
A	556L	GLY	-	linker	UNP K7YEW5
A	556M	GLY	-	linker	UNP K7YEW5
A	556N	GLY	-	linker	UNP K7YEW5
A	556O	SER	-	linker	UNP K7YEW5
A	556P	GLY	-	linker	UNP K7YEW5
A	556Q	GLY	-	linker	UNP K7YEW5
A	556R	GLY	-	linker	UNP K7YEW5
A	556S	GLY	-	linker	UNP K7YEW5
A	556T	SER	-	linker	UNP K7YEW5
A	630	PRO	GLU	engineered mutation	UNP K7YEW5
A	908	SER	-	expression tag	UNP K7YEW5
A	909	ALA	-	expression tag	UNP K7YEW5
A	910	ILE	-	expression tag	UNP K7YEW5
A	911	GLY	-	expression tag	UNP K7YEW5
A	912	GLY	-	expression tag	UNP K7YEW5
A	913	TYR	-	expression tag	UNP K7YEW5
A	914	ILE	-	expression tag	UNP K7YEW5
A	915	PRO	-	expression tag	UNP K7YEW5
A	916	GLU	-	expression tag	UNP K7YEW5
A	917	ALA	-	expression tag	UNP K7YEW5
A	918	PRO	-	expression tag	UNP K7YEW5
A	919	ARG	-	expression tag	UNP K7YEW5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	920	ASP	-	expression tag	UNP K7YEW5
A	921	GLY	-	expression tag	UNP K7YEW5
A	922	GLN	-	expression tag	UNP K7YEW5
A	923	ALA	-	expression tag	UNP K7YEW5
A	924	TYR	-	expression tag	UNP K7YEW5
A	925	VAL	-	expression tag	UNP K7YEW5
A	926	ARG	-	expression tag	UNP K7YEW5
A	927	LYS	-	expression tag	UNP K7YEW5
A	928	ASP	-	expression tag	UNP K7YEW5
A	929	GLY	-	expression tag	UNP K7YEW5
A	930	GLU	-	expression tag	UNP K7YEW5
A	931	TRP	-	expression tag	UNP K7YEW5
A	932	VAL	-	expression tag	UNP K7YEW5
A	933	LEU	-	expression tag	UNP K7YEW5
A	934	LEU	-	expression tag	UNP K7YEW5
A	935	SER	-	expression tag	UNP K7YEW5
A	936	THR	-	expression tag	UNP K7YEW5
A	937	PHE	-	expression tag	UNP K7YEW5
A	938	LEU	-	expression tag	UNP K7YEW5
A	939	GLY	-	expression tag	UNP K7YEW5
A	940	ASP	-	expression tag	UNP K7YEW5
A	941	ASP	-	expression tag	UNP K7YEW5
A	942	ASP	-	expression tag	UNP K7YEW5
A	943	ASP	-	expression tag	UNP K7YEW5
A	944	LYS	-	expression tag	UNP K7YEW5
A	945	ALA	-	expression tag	UNP K7YEW5
A	946	GLY	-	expression tag	UNP K7YEW5
A	947	TRP	-	expression tag	UNP K7YEW5
A	948	SER	-	expression tag	UNP K7YEW5
A	949	HIS	-	expression tag	UNP K7YEW5
A	950	PRO	-	expression tag	UNP K7YEW5
A	951	GLN	-	expression tag	UNP K7YEW5
A	952	PHE	-	expression tag	UNP K7YEW5
A	953	GLU	-	expression tag	UNP K7YEW5
A	954	LYS	-	expression tag	UNP K7YEW5
A	955	GLY	-	expression tag	UNP K7YEW5
A	956	GLY	-	expression tag	UNP K7YEW5
A	957	GLY	-	expression tag	UNP K7YEW5
A	958	SER	-	expression tag	UNP K7YEW5
A	959	GLY	-	expression tag	UNP K7YEW5
A	960	GLY	-	expression tag	UNP K7YEW5
A	961	GLY	-	expression tag	UNP K7YEW5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	962	SER	-	expression tag	UNP K7YEW5
A	963	GLY	-	expression tag	UNP K7YEW5
A	964	GLY	-	expression tag	UNP K7YEW5
A	965	GLY	-	expression tag	UNP K7YEW5
A	966	SER	-	expression tag	UNP K7YEW5
A	967	TRP	-	expression tag	UNP K7YEW5
A	968	SER	-	expression tag	UNP K7YEW5
A	969	HIS	-	expression tag	UNP K7YEW5
A	970	PRO	-	expression tag	UNP K7YEW5
A	971	GLN	-	expression tag	UNP K7YEW5
A	972	PHE	-	expression tag	UNP K7YEW5
A	973	GLU	-	expression tag	UNP K7YEW5
A	974	LYS	-	expression tag	UNP K7YEW5
B	126	ALA	ARG	engineered mutation	UNP K7YEW5
B	556K	GLY	-	linker	UNP K7YEW5
B	556L	GLY	-	linker	UNP K7YEW5
B	556M	GLY	-	linker	UNP K7YEW5
B	556N	GLY	-	linker	UNP K7YEW5
B	556O	SER	-	linker	UNP K7YEW5
B	556P	GLY	-	linker	UNP K7YEW5
B	556Q	GLY	-	linker	UNP K7YEW5
B	556R	GLY	-	linker	UNP K7YEW5
B	556S	GLY	-	linker	UNP K7YEW5
B	556T	SER	-	linker	UNP K7YEW5
B	630	PRO	GLU	engineered mutation	UNP K7YEW5
B	908	SER	-	expression tag	UNP K7YEW5
B	909	ALA	-	expression tag	UNP K7YEW5
B	910	ILE	-	expression tag	UNP K7YEW5
B	911	GLY	-	expression tag	UNP K7YEW5
B	912	GLY	-	expression tag	UNP K7YEW5
B	913	TYR	-	expression tag	UNP K7YEW5
B	914	ILE	-	expression tag	UNP K7YEW5
B	915	PRO	-	expression tag	UNP K7YEW5
B	916	GLU	-	expression tag	UNP K7YEW5
B	917	ALA	-	expression tag	UNP K7YEW5
B	918	PRO	-	expression tag	UNP K7YEW5
B	919	ARG	-	expression tag	UNP K7YEW5
B	920	ASP	-	expression tag	UNP K7YEW5
B	921	GLY	-	expression tag	UNP K7YEW5
B	922	GLN	-	expression tag	UNP K7YEW5
B	923	ALA	-	expression tag	UNP K7YEW5
B	924	TYR	-	expression tag	UNP K7YEW5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	925	VAL	-	expression tag	UNP K7YEW5
B	926	ARG	-	expression tag	UNP K7YEW5
B	927	LYS	-	expression tag	UNP K7YEW5
B	928	ASP	-	expression tag	UNP K7YEW5
B	929	GLY	-	expression tag	UNP K7YEW5
B	930	GLU	-	expression tag	UNP K7YEW5
B	931	TRP	-	expression tag	UNP K7YEW5
B	932	VAL	-	expression tag	UNP K7YEW5
B	933	LEU	-	expression tag	UNP K7YEW5
B	934	LEU	-	expression tag	UNP K7YEW5
B	935	SER	-	expression tag	UNP K7YEW5
B	936	THR	-	expression tag	UNP K7YEW5
B	937	PHE	-	expression tag	UNP K7YEW5
B	938	LEU	-	expression tag	UNP K7YEW5
B	939	GLY	-	expression tag	UNP K7YEW5
B	940	ASP	-	expression tag	UNP K7YEW5
B	941	ASP	-	expression tag	UNP K7YEW5
B	942	ASP	-	expression tag	UNP K7YEW5
B	943	ASP	-	expression tag	UNP K7YEW5
B	944	LYS	-	expression tag	UNP K7YEW5
B	945	ALA	-	expression tag	UNP K7YEW5
B	946	GLY	-	expression tag	UNP K7YEW5
B	947	TRP	-	expression tag	UNP K7YEW5
B	948	SER	-	expression tag	UNP K7YEW5
B	949	HIS	-	expression tag	UNP K7YEW5
B	950	PRO	-	expression tag	UNP K7YEW5
B	951	GLN	-	expression tag	UNP K7YEW5
B	952	PHE	-	expression tag	UNP K7YEW5
B	953	GLU	-	expression tag	UNP K7YEW5
B	954	LYS	-	expression tag	UNP K7YEW5
B	955	GLY	-	expression tag	UNP K7YEW5
B	956	GLY	-	expression tag	UNP K7YEW5
B	957	GLY	-	expression tag	UNP K7YEW5
B	958	SER	-	expression tag	UNP K7YEW5
B	959	GLY	-	expression tag	UNP K7YEW5
B	960	GLY	-	expression tag	UNP K7YEW5
B	961	GLY	-	expression tag	UNP K7YEW5
B	962	SER	-	expression tag	UNP K7YEW5
B	963	GLY	-	expression tag	UNP K7YEW5
B	964	GLY	-	expression tag	UNP K7YEW5
B	965	GLY	-	expression tag	UNP K7YEW5
B	966	SER	-	expression tag	UNP K7YEW5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	967	TRP	-	expression tag	UNP K7YEW5
B	968	SER	-	expression tag	UNP K7YEW5
B	969	HIS	-	expression tag	UNP K7YEW5
B	970	PRO	-	expression tag	UNP K7YEW5
B	971	GLN	-	expression tag	UNP K7YEW5
B	972	PHE	-	expression tag	UNP K7YEW5
B	973	GLU	-	expression tag	UNP K7YEW5
B	974	LYS	-	expression tag	UNP K7YEW5
C	126	ALA	ARG	engineered mutation	UNP K7YEW5
C	556K	GLY	-	linker	UNP K7YEW5
C	556L	GLY	-	linker	UNP K7YEW5
C	556M	GLY	-	linker	UNP K7YEW5
C	556N	GLY	-	linker	UNP K7YEW5
C	556O	SER	-	linker	UNP K7YEW5
C	556P	GLY	-	linker	UNP K7YEW5
C	556Q	GLY	-	linker	UNP K7YEW5
C	556R	GLY	-	linker	UNP K7YEW5
C	556S	GLY	-	linker	UNP K7YEW5
C	556T	SER	-	linker	UNP K7YEW5
C	630	PRO	GLU	engineered mutation	UNP K7YEW5
C	908	SER	-	expression tag	UNP K7YEW5
C	909	ALA	-	expression tag	UNP K7YEW5
C	910	ILE	-	expression tag	UNP K7YEW5
C	911	GLY	-	expression tag	UNP K7YEW5
C	912	GLY	-	expression tag	UNP K7YEW5
C	913	TYR	-	expression tag	UNP K7YEW5
C	914	ILE	-	expression tag	UNP K7YEW5
C	915	PRO	-	expression tag	UNP K7YEW5
C	916	GLU	-	expression tag	UNP K7YEW5
C	917	ALA	-	expression tag	UNP K7YEW5
C	918	PRO	-	expression tag	UNP K7YEW5
C	919	ARG	-	expression tag	UNP K7YEW5
C	920	ASP	-	expression tag	UNP K7YEW5
C	921	GLY	-	expression tag	UNP K7YEW5
C	922	GLN	-	expression tag	UNP K7YEW5
C	923	ALA	-	expression tag	UNP K7YEW5
C	924	TYR	-	expression tag	UNP K7YEW5
C	925	VAL	-	expression tag	UNP K7YEW5
C	926	ARG	-	expression tag	UNP K7YEW5
C	927	LYS	-	expression tag	UNP K7YEW5
C	928	ASP	-	expression tag	UNP K7YEW5
C	929	GLY	-	expression tag	UNP K7YEW5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	930	GLU	-	expression tag	UNP K7YEW5
C	931	TRP	-	expression tag	UNP K7YEW5
C	932	VAL	-	expression tag	UNP K7YEW5
C	933	LEU	-	expression tag	UNP K7YEW5
C	934	LEU	-	expression tag	UNP K7YEW5
C	935	SER	-	expression tag	UNP K7YEW5
C	936	THR	-	expression tag	UNP K7YEW5
C	937	PHE	-	expression tag	UNP K7YEW5
C	938	LEU	-	expression tag	UNP K7YEW5
C	939	GLY	-	expression tag	UNP K7YEW5
C	940	ASP	-	expression tag	UNP K7YEW5
C	941	ASP	-	expression tag	UNP K7YEW5
C	942	ASP	-	expression tag	UNP K7YEW5
C	943	ASP	-	expression tag	UNP K7YEW5
C	944	LYS	-	expression tag	UNP K7YEW5
C	945	ALA	-	expression tag	UNP K7YEW5
C	946	GLY	-	expression tag	UNP K7YEW5
C	947	TRP	-	expression tag	UNP K7YEW5
C	948	SER	-	expression tag	UNP K7YEW5
C	949	HIS	-	expression tag	UNP K7YEW5
C	950	PRO	-	expression tag	UNP K7YEW5
C	951	GLN	-	expression tag	UNP K7YEW5
C	952	PHE	-	expression tag	UNP K7YEW5
C	953	GLU	-	expression tag	UNP K7YEW5
C	954	LYS	-	expression tag	UNP K7YEW5
C	955	GLY	-	expression tag	UNP K7YEW5
C	956	GLY	-	expression tag	UNP K7YEW5
C	957	GLY	-	expression tag	UNP K7YEW5
C	958	SER	-	expression tag	UNP K7YEW5
C	959	GLY	-	expression tag	UNP K7YEW5
C	960	GLY	-	expression tag	UNP K7YEW5
C	961	GLY	-	expression tag	UNP K7YEW5
C	962	SER	-	expression tag	UNP K7YEW5
C	963	GLY	-	expression tag	UNP K7YEW5
C	964	GLY	-	expression tag	UNP K7YEW5
C	965	GLY	-	expression tag	UNP K7YEW5
C	966	SER	-	expression tag	UNP K7YEW5
C	967	TRP	-	expression tag	UNP K7YEW5
C	968	SER	-	expression tag	UNP K7YEW5
C	969	HIS	-	expression tag	UNP K7YEW5
C	970	PRO	-	expression tag	UNP K7YEW5
C	971	GLN	-	expression tag	UNP K7YEW5

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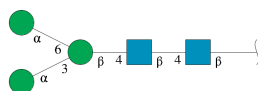
Chain	Residue	Modelled	Actual	Comment	Reference
C	972	PHE	-	expression tag	UNP K7YEW5
C	973	GLU	-	expression tag	UNP K7YEW5
C	974	LYS	-	expression tag	UNP K7YEW5

- Molecule 2 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		
2	D	2	28	16	2	10	0	0
2	E	2	28	16	2	10	0	0
2	G	2	28	16	2	10	0	0
2	H	2	28	16	2	10	0	0
2	I	2	28	16	2	10	0	0
2	K	2	28	16	2	10	0	0
2	L	2	28	16	2	10	0	0
2	M	2	28	16	2	10	0	0
2	O	2	28	16	2	10	0	0

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



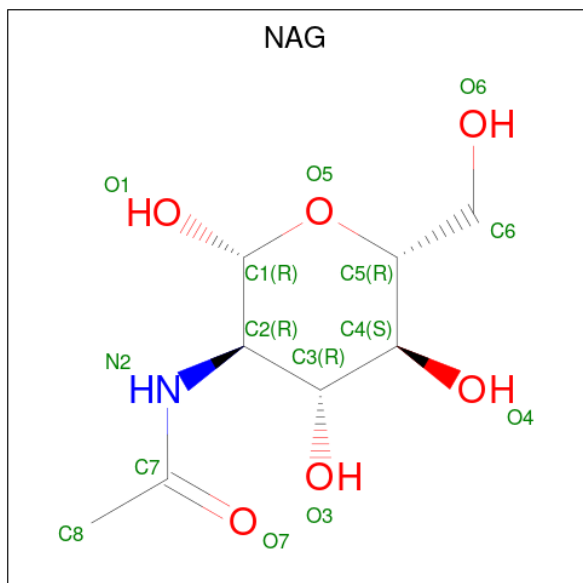
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	F	5	61	34	2	25	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	J	5	61	34	2	25	0	0
3	N	5	61	34	2	25	0	0

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



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

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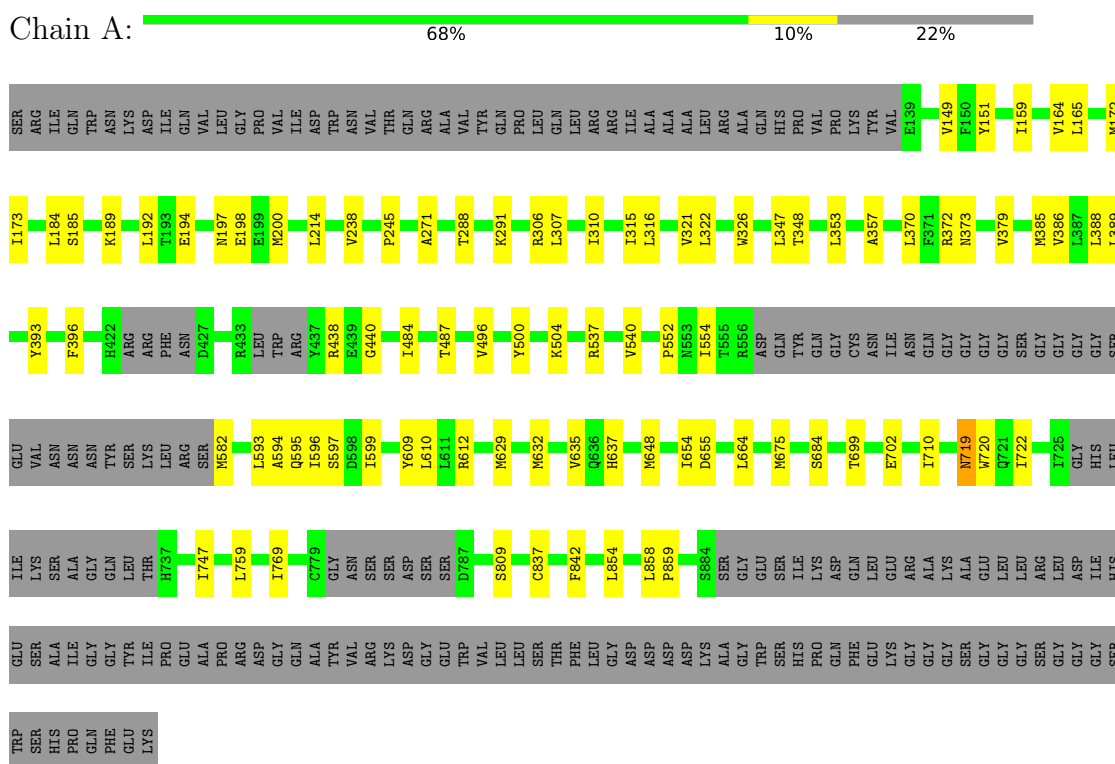
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Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
4	B	1	Total 14	8	1	5	0
4	C	1	Total 14	8	1	5	0
4	C	1	Total 14	8	1	5	0
4	C	1	Total 14	8	1	5	0
4	C	1	Total 14	8	1	5	0
4	C	1	Total 14	8	1	5	0

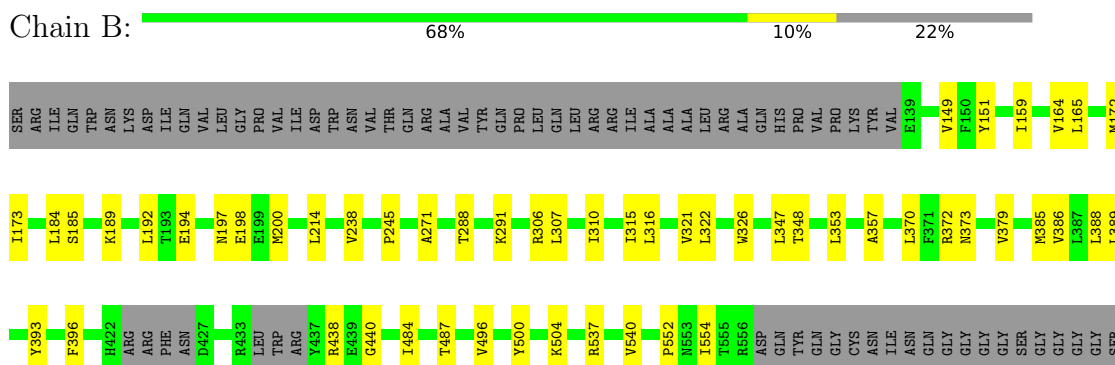
3 Residue-property plots [i](#)

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: Envelope glycoprotein gp130



- Molecule 1: Envelope glycoprotein gp130



MAG1
MAG2

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

Chain G:  50% 50%MAG1
MAG2

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

Chain H:  100%MAG1
MAG2

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

Chain I:  100%MAG1
MAG2

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

Chain K:  50% 50%MAG1
MAG2

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

Chain L:  100%MAG1
MAG2

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

Chain M:  100%MAG1
MAG2

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

Chain O:  50% 50%


MAG1
MAG2

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

Chain F:  40% 60%

MAG1
MAG2
BMA3
MAN4
MAN5

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

Chain J:  40% 60%

MAG1
MAG2
BMA3
MAN4
MAN5

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

Chain N:  40% 60%

MAG1
MAG2
BMA3
MAN4
MAN5

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15471	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.984	Depositor
Minimum map value	-0.003	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.0152	Depositor
Map size (Å)	304.0, 304.0, 304.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, 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	A	0.14	0/5354	0.38	0/7335
1	B	0.14	0/5354	0.38	0/7335
1	C	0.14	0/5354	0.38	0/7335
All	All	0.14	0/16062	0.38	0/22005

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

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	5222	0	4770	55	0
1	B	5222	0	4770	53	0
1	C	5222	0	4770	54	0
2	D	28	0	25	0	0
2	E	28	0	25	0	0
2	G	28	0	25	2	0
2	H	28	0	25	0	0
2	I	28	0	25	0	0
2	K	28	0	25	2	0
2	L	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	M	28	0	25	0	0
2	O	28	0	25	2	0
3	F	61	0	52	0	0
3	J	61	0	52	0	0
3	N	61	0	52	0	0
4	A	70	0	65	0	0
4	B	70	0	65	0	0
4	C	70	0	65	0	0
All	All	16311	0	14886	162	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 162 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:A:858:LEU:HD12	1:A:859:PRO:HD2	1.70	0.74
1:B:858:LEU:HD12	1:B:859:PRO:HD2	1.70	0.72
1:C:858:LEU:HD12	1:C:859:PRO:HD2	1.70	0.72
1:C:722:ILE:HD11	1:C:747:ILE:HG23	1.72	0.72
1:B:722:ILE:HD11	1:B:747:ILE:HG23	1.71	0.71

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	684/890 (77%)	661 (97%)	23 (3%)	0	100 100
1	B	684/890 (77%)	661 (97%)	23 (3%)	0	100 100
1	C	684/890 (77%)	660 (96%)	24 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	2052/2670 (77%)	1982 (97%)	70 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	522/794 (66%)	521 (100%)	1 (0%)	87	87
1	B	522/794 (66%)	521 (100%)	1 (0%)	87	87
1	C	522/794 (66%)	521 (100%)	1 (0%)	87	87
All	All	1566/2382 (66%)	1563 (100%)	3 (0%)	85	87

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	719	ASN
1	B	719	ASN
1	C	719	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	336	ASN
1	C	862	GLN
1	C	624	HIS
1	C	719	ASN
1	B	154	HIS

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](#)

33 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
2	NAG	D	1	2,1	14,14,15	0.21	0	17,19,21	0.47	0
2	NAG	D	2	2	14,14,15	0.29	0	17,19,21	0.54	0
2	NAG	E	1	2,1	14,14,15	0.21	0	17,19,21	0.45	0
2	NAG	E	2	2	14,14,15	0.22	0	17,19,21	0.44	0
3	NAG	F	1	3,1	14,14,15	0.35	0	17,19,21	0.70	1 (5%)
3	NAG	F	2	3	14,14,15	0.23	0	17,19,21	0.59	0
3	BMA	F	3	3	11,11,12	0.89	0	15,15,17	0.79	0
3	MAN	F	4	3	11,11,12	0.62	0	15,15,17	0.98	2 (13%)
3	MAN	F	5	3	11,11,12	0.81	0	15,15,17	1.27	2 (13%)
2	NAG	G	1	2,1	14,14,15	0.37	0	17,19,21	1.39	2 (11%)
2	NAG	G	2	2	14,14,15	0.51	0	17,19,21	0.44	0
2	NAG	H	1	2,1	14,14,15	0.22	0	17,19,21	0.47	0
2	NAG	H	2	2	14,14,15	0.29	0	17,19,21	0.54	0
2	NAG	I	1	2,1	14,14,15	0.21	0	17,19,21	0.46	0
2	NAG	I	2	2	14,14,15	0.21	0	17,19,21	0.44	0
3	NAG	J	1	3,1	14,14,15	0.33	0	17,19,21	0.69	1 (5%)
3	NAG	J	2	3	14,14,15	0.23	0	17,19,21	0.58	0
3	BMA	J	3	3	11,11,12	0.88	0	15,15,17	0.79	0
3	MAN	J	4	3	11,11,12	0.62	0	15,15,17	0.98	2 (13%)
3	MAN	J	5	3	11,11,12	0.81	0	15,15,17	1.27	2 (13%)
2	NAG	K	1	2,1	14,14,15	0.37	0	17,19,21	1.38	2 (11%)
2	NAG	K	2	2	14,14,15	0.51	0	17,19,21	0.44	0
2	NAG	L	1	2,1	14,14,15	0.21	0	17,19,21	0.47	0
2	NAG	L	2	2	14,14,15	0.30	0	17,19,21	0.55	0
2	NAG	M	1	2,1	14,14,15	0.22	0	17,19,21	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	M	2	2	14,14,15	0.22	0	17,19,21	0.44	0
3	NAG	N	1	3,1	14,14,15	0.35	0	17,19,21	0.69	1 (5%)
3	NAG	N	2	3	14,14,15	0.24	0	17,19,21	0.59	0
3	BMA	N	3	3	11,11,12	0.88	0	15,15,17	0.79	0
3	MAN	N	4	3	11,11,12	0.61	0	15,15,17	0.99	2 (13%)
3	MAN	N	5	3	11,11,12	0.82	0	15,15,17	1.27	2 (13%)
2	NAG	O	1	2,1	14,14,15	0.37	0	17,19,21	1.38	2 (11%)
2	NAG	O	2	2	14,14,15	0.53	0	17,19,21	0.44	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
2	NAG	D	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	NAG	E	1	2,1	-	3/6/23/26	0/1/1/1
2	NAG	E	2	2	-	4/6/23/26	0/1/1/1
3	NAG	F	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	4/6/23/26	0/1/1/1
3	BMA	F	3	3	-	0/2/19/22	0/1/1/1
3	MAN	F	4	3	-	0/2/19/22	0/1/1/1
3	MAN	F	5	3	-	0/2/19/22	0/1/1/1
2	NAG	G	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	G	2	2	-	3/6/23/26	0/1/1/1
2	NAG	H	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	H	2	2	-	2/6/23/26	0/1/1/1
2	NAG	I	1	2,1	-	3/6/23/26	0/1/1/1
2	NAG	I	2	2	-	4/6/23/26	0/1/1/1
3	NAG	J	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	J	2	3	-	4/6/23/26	0/1/1/1
3	BMA	J	3	3	-	0/2/19/22	0/1/1/1
3	MAN	J	4	3	-	0/2/19/22	0/1/1/1
3	MAN	J	5	3	-	0/2/19/22	0/1/1/1
2	NAG	K	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	K	2	2	-	3/6/23/26	0/1/1/1
2	NAG	L	1	2,1	-	4/6/23/26	0/1/1/1

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

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	1	NAG	C2-N2-C7	4.63	129.11	122.90
2	K	1	NAG	C2-N2-C7	4.62	129.09	122.90
2	O	1	NAG	C2-N2-C7	4.61	129.08	122.90
3	J	5	MAN	C1-O5-C5	3.54	116.93	112.19
3	N	5	MAN	C1-O5-C5	3.52	116.91	112.19

There are no chirality outliers.

5 of 78 torsion outliers are listed below:

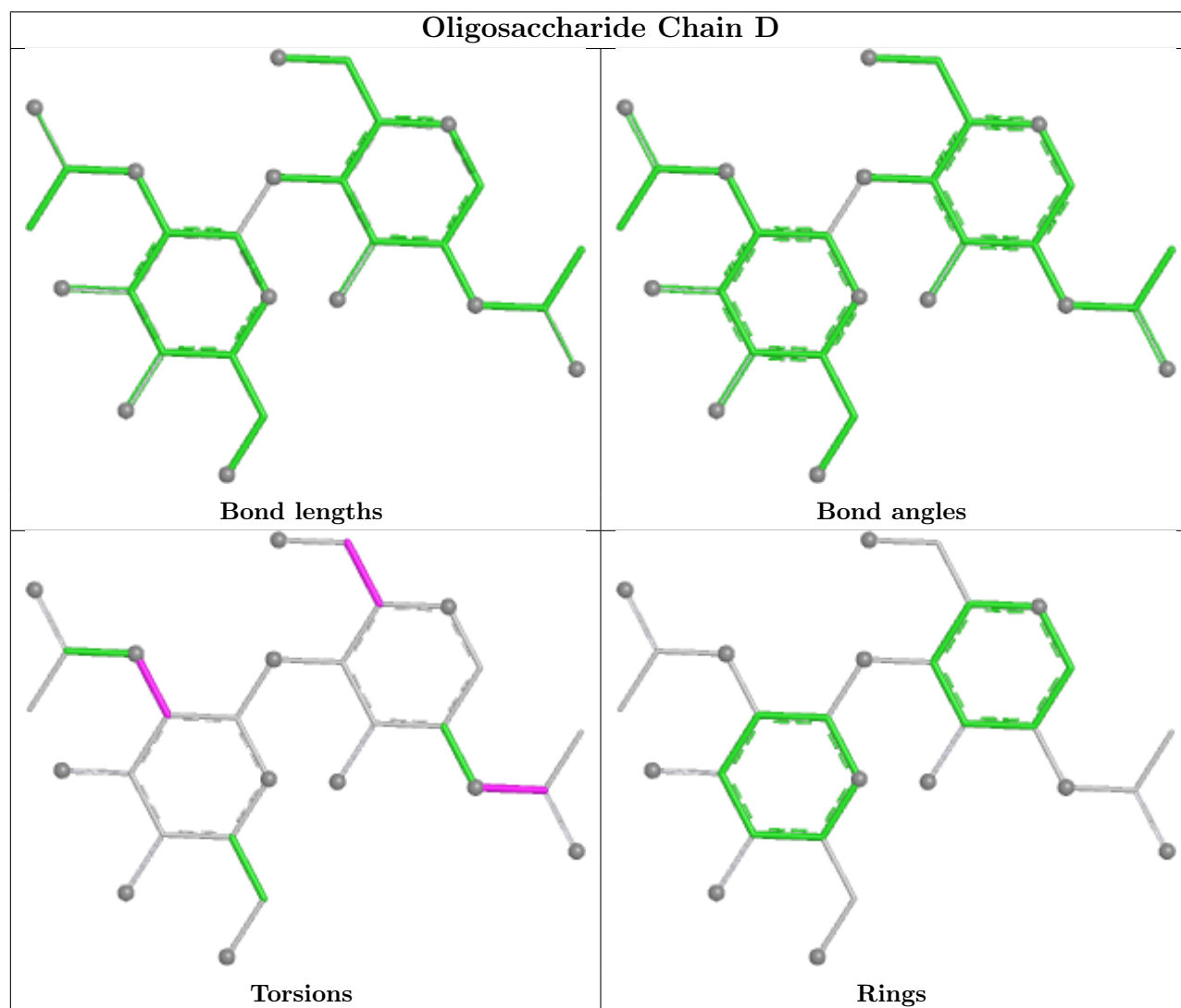
Mol	Chain	Res	Type	Atoms
2	D	1	NAG	O5-C5-C6-O6
2	G	2	NAG	O5-C5-C6-O6
2	H	1	NAG	O5-C5-C6-O6
2	K	2	NAG	O5-C5-C6-O6
2	L	1	NAG	O5-C5-C6-O6

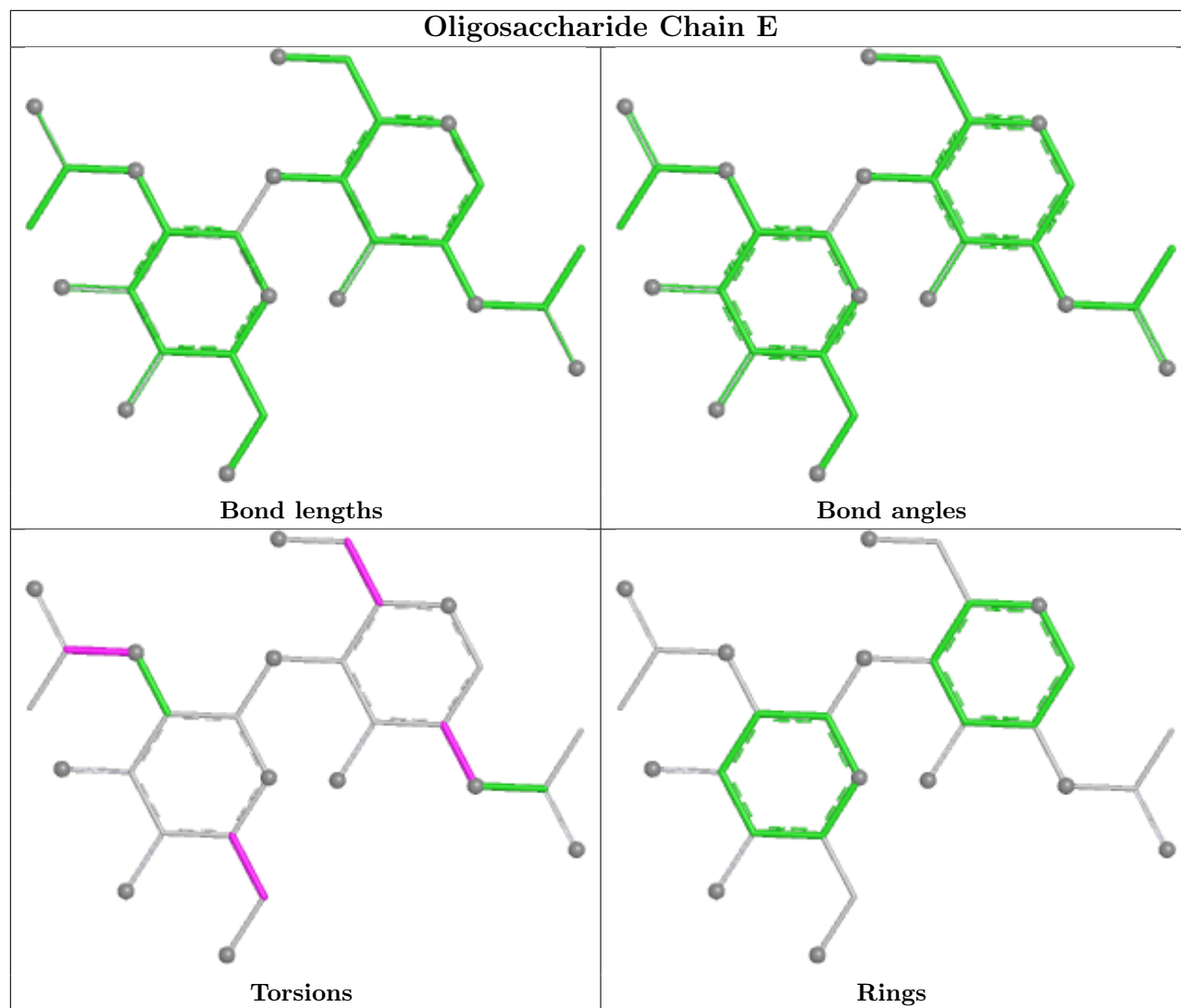
There are no ring outliers.

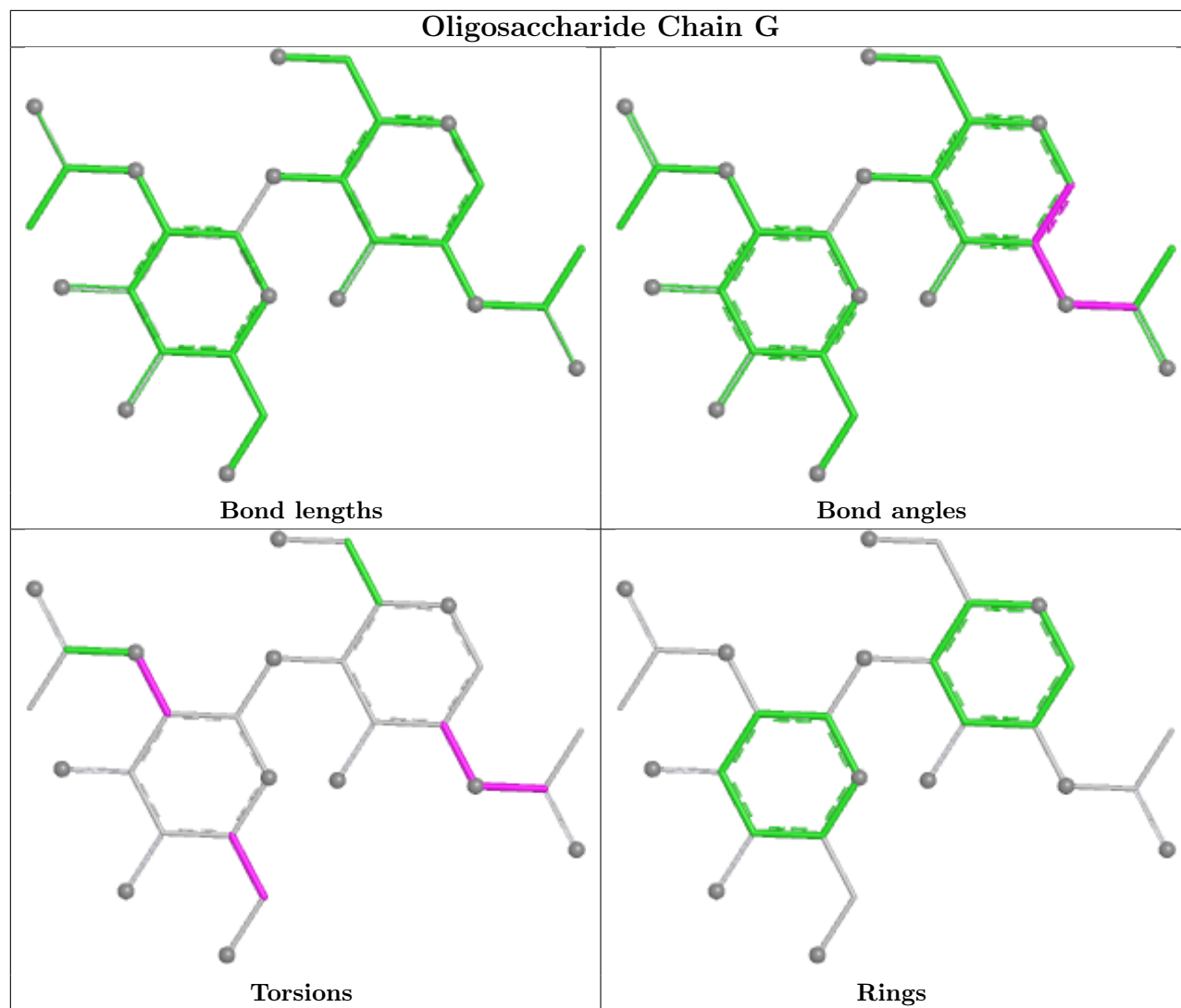
3 monomers are involved in 6 short contacts:

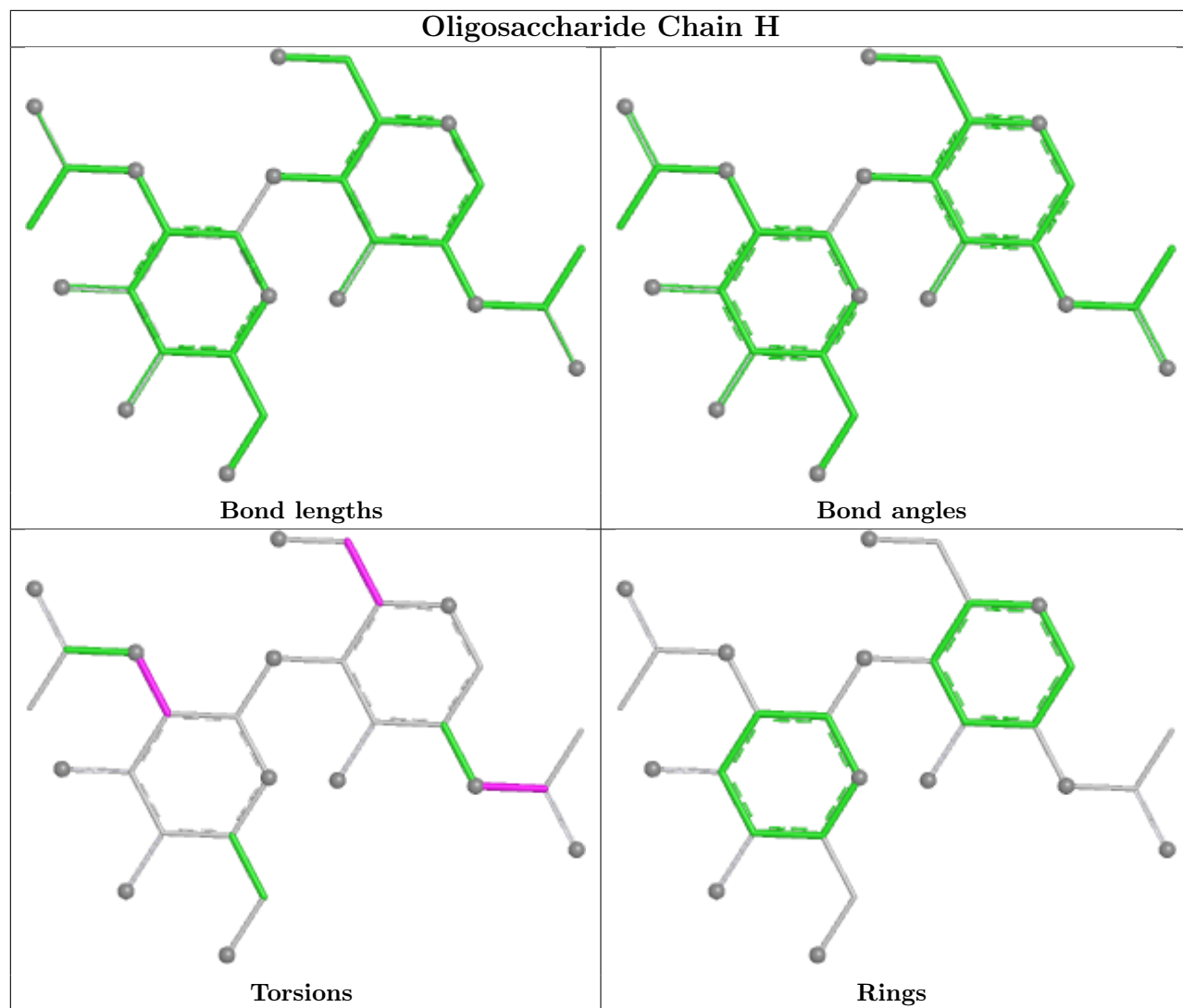
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	1	NAG	2	0
2	K	1	NAG	2	0
2	O	1	NAG	2	0

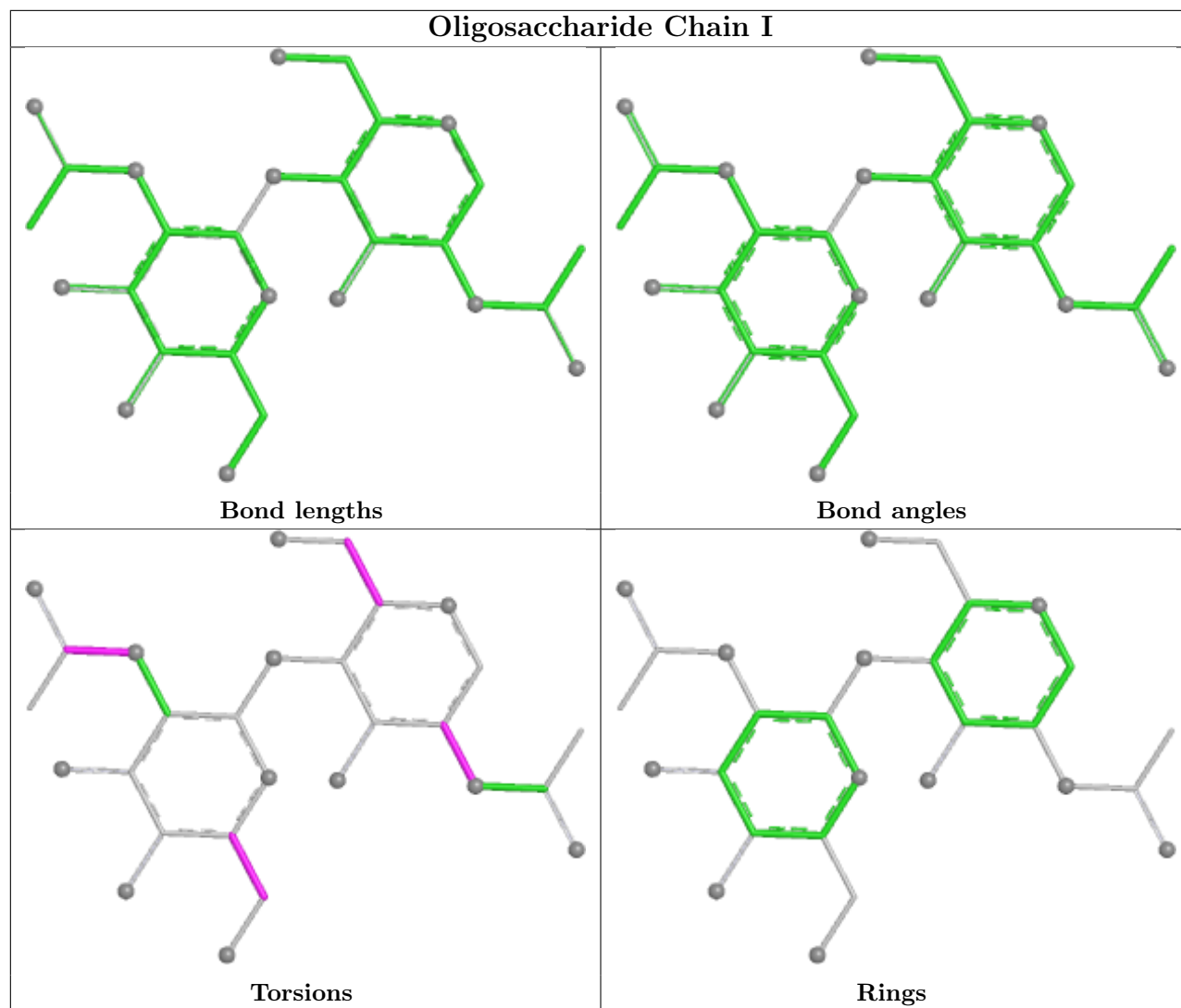
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

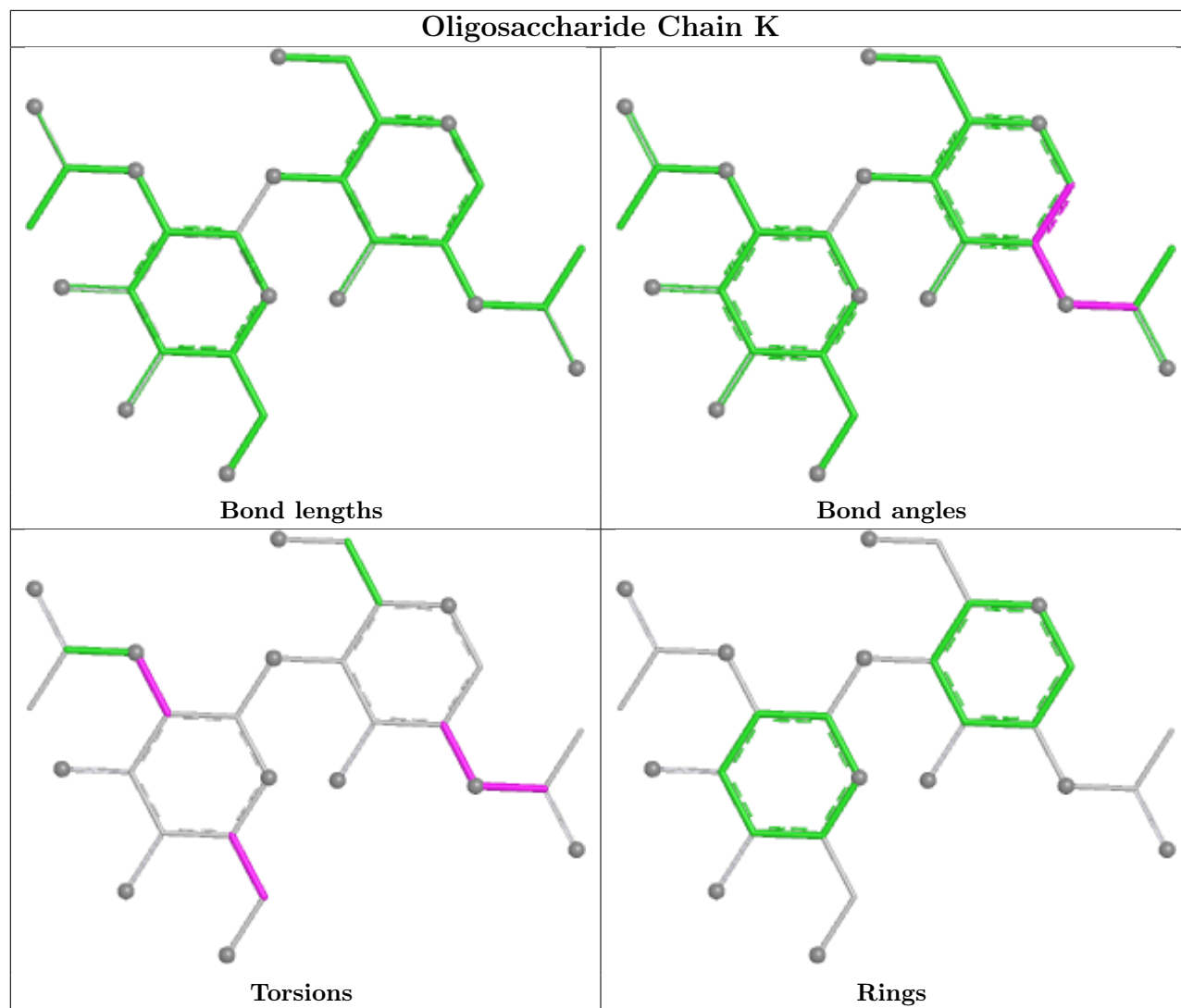


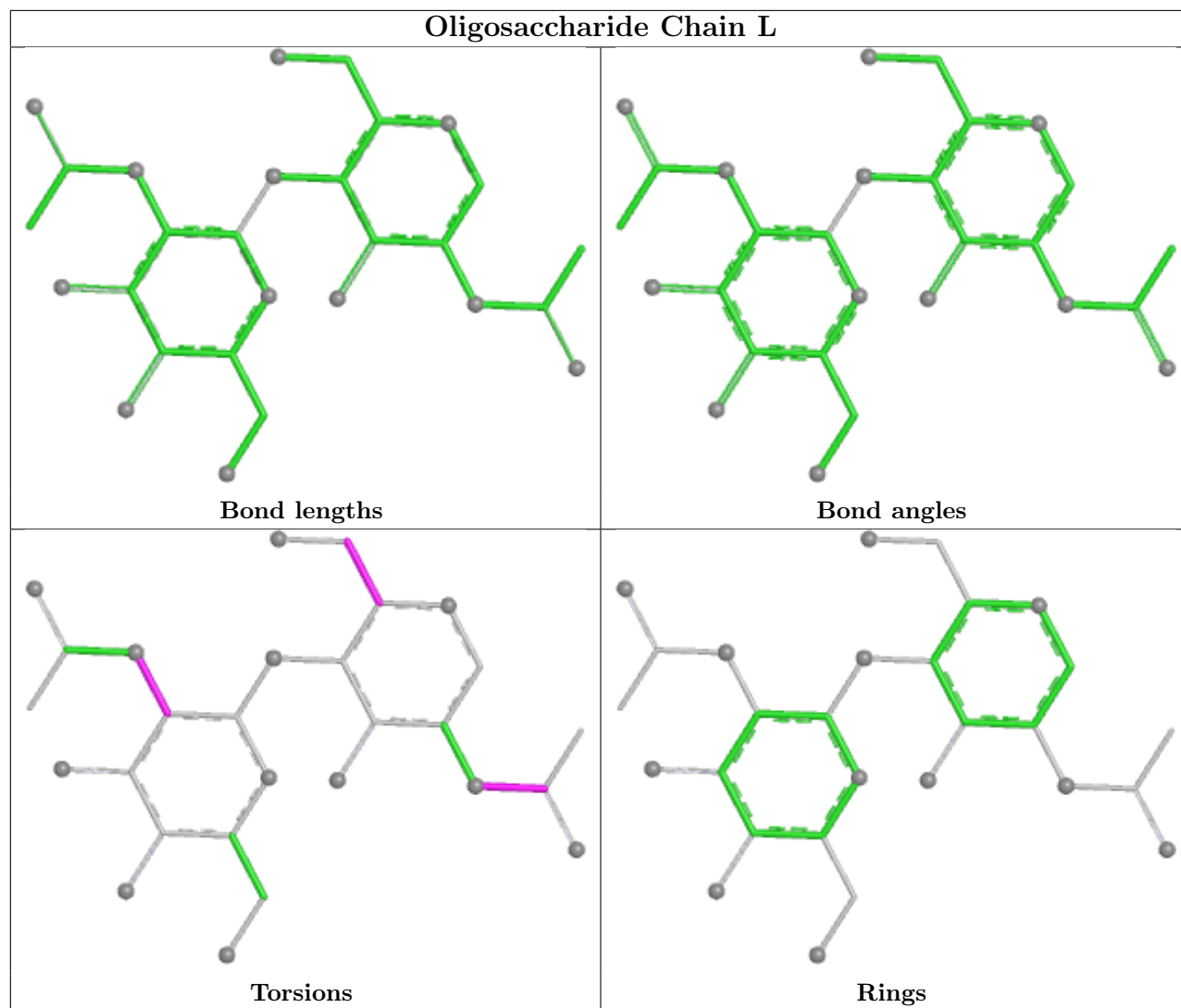


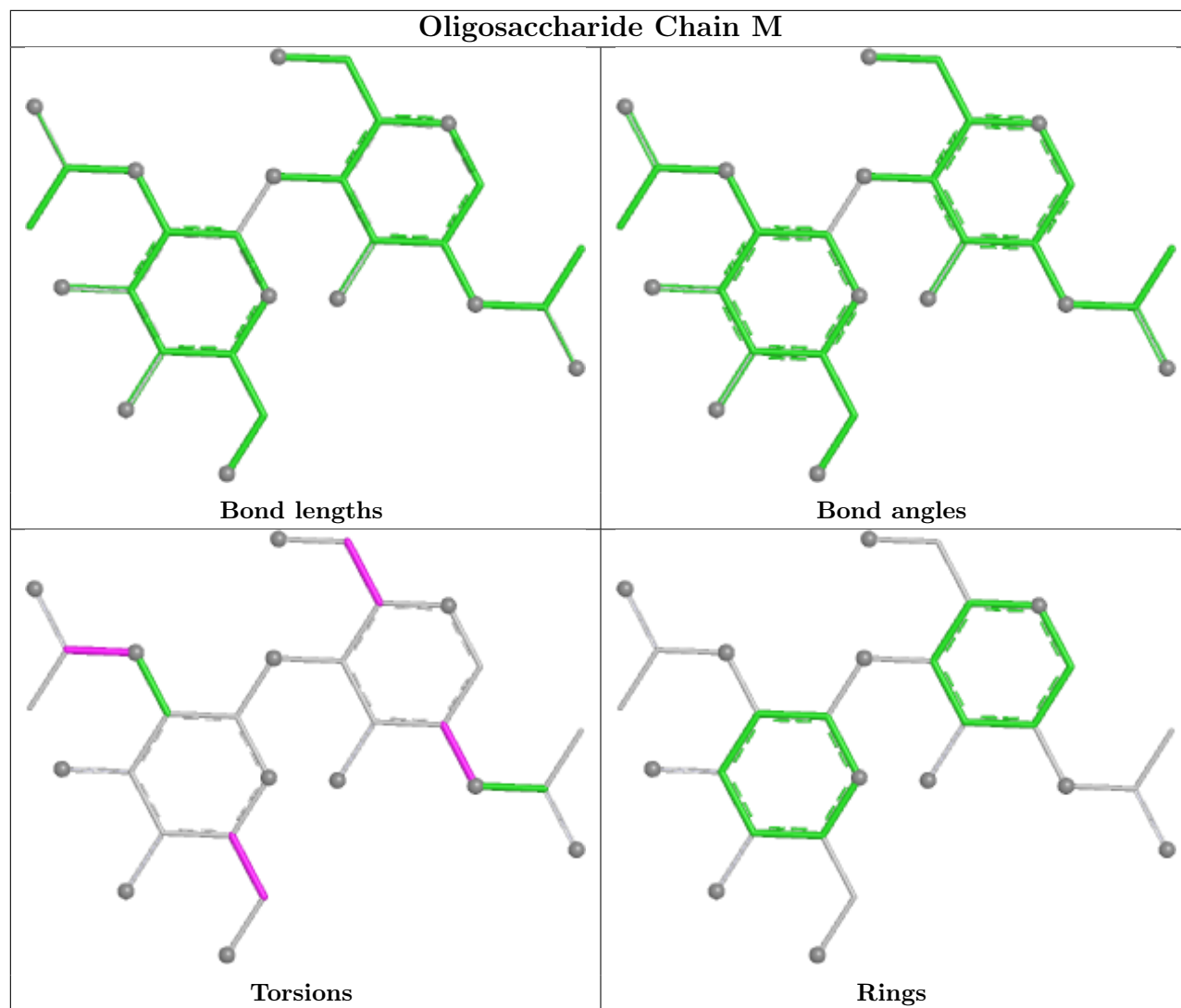


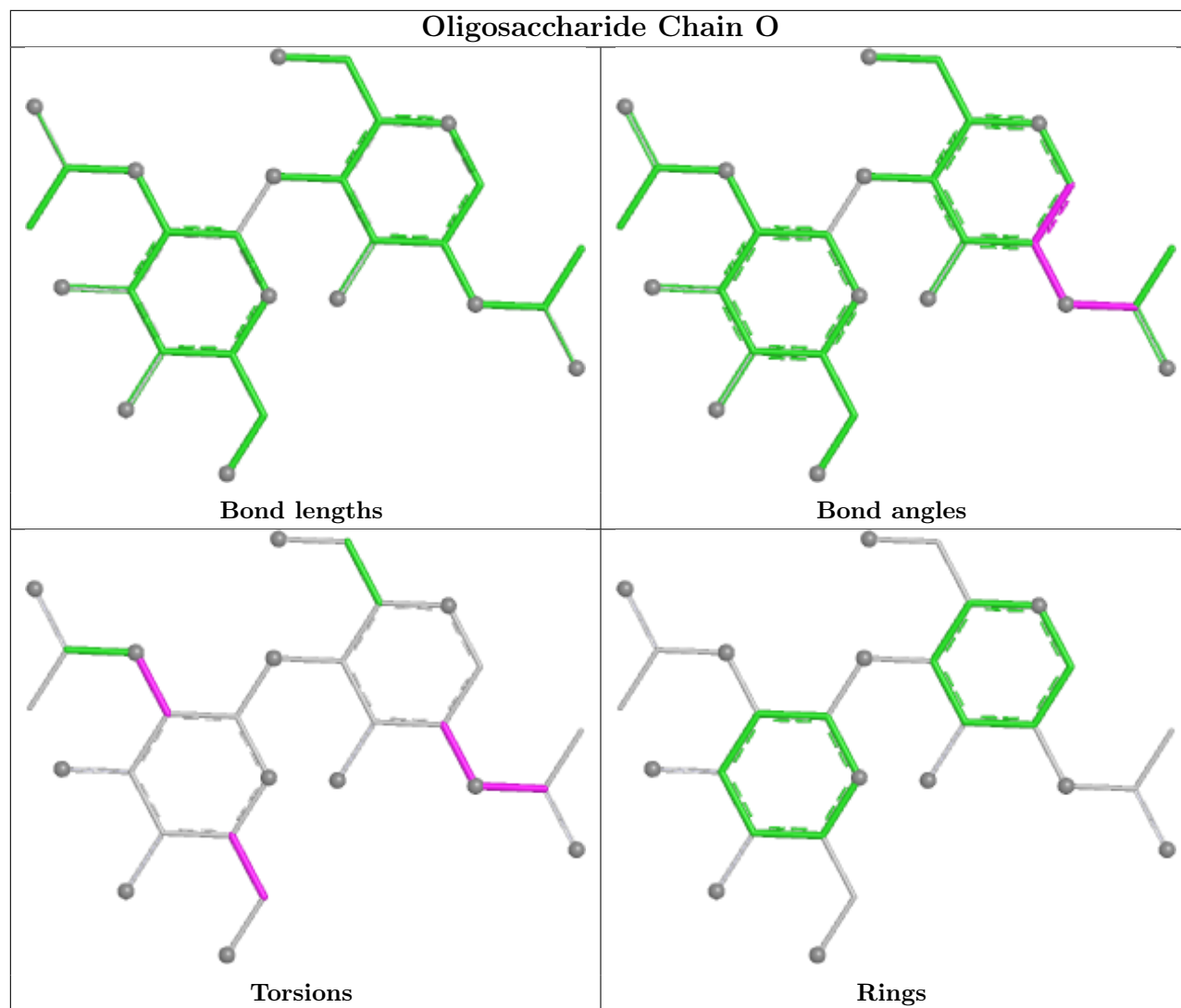


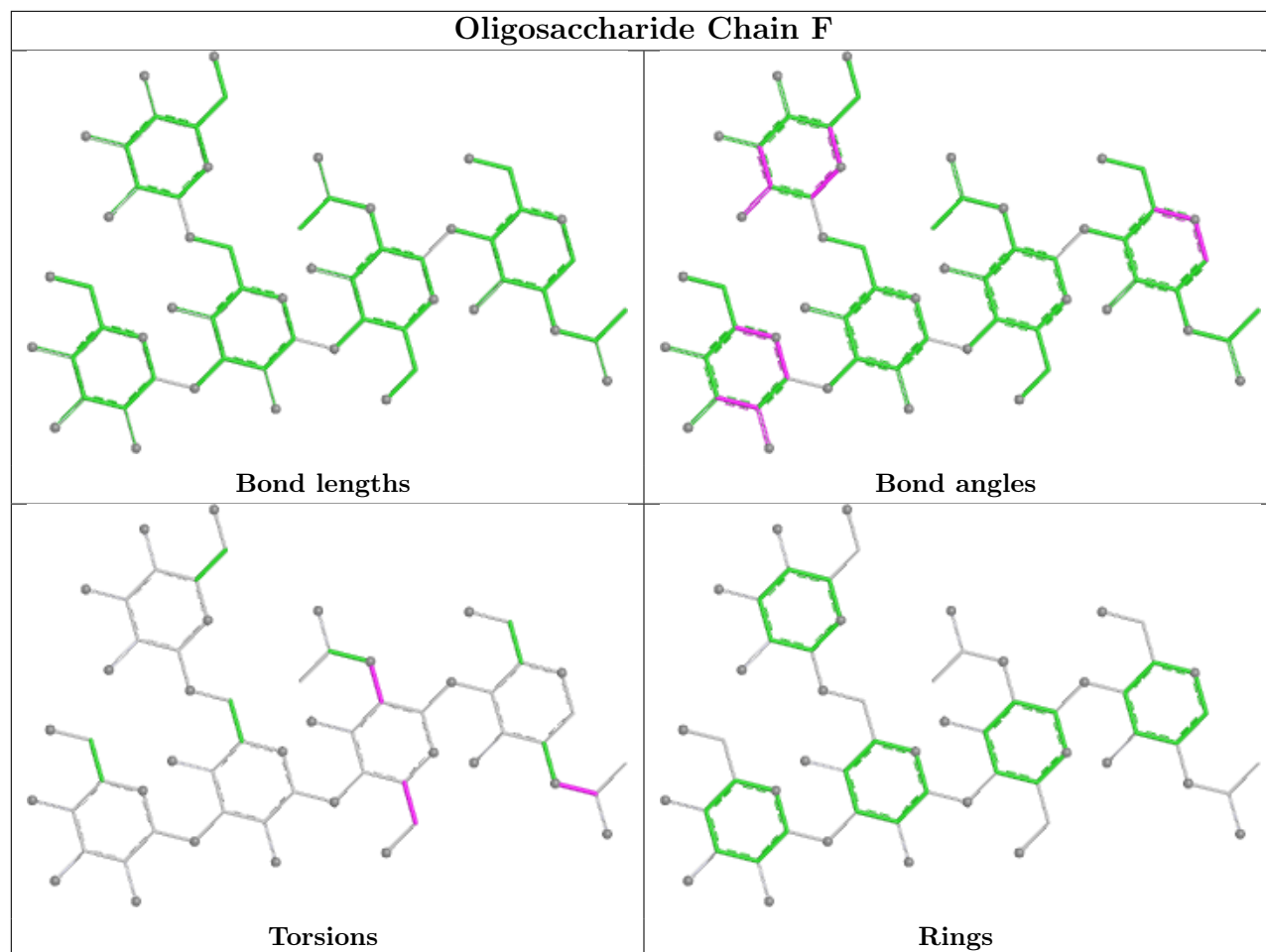


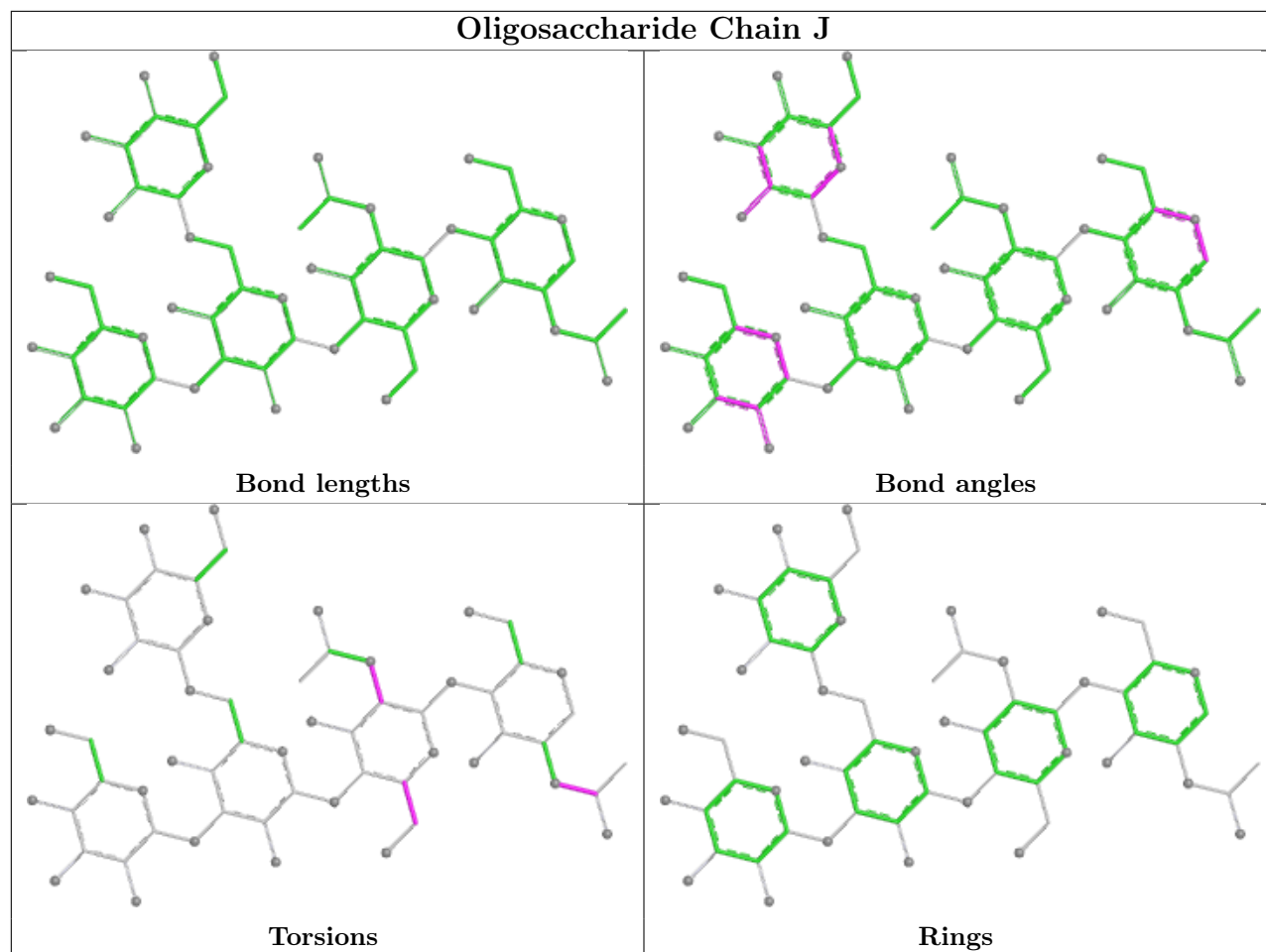


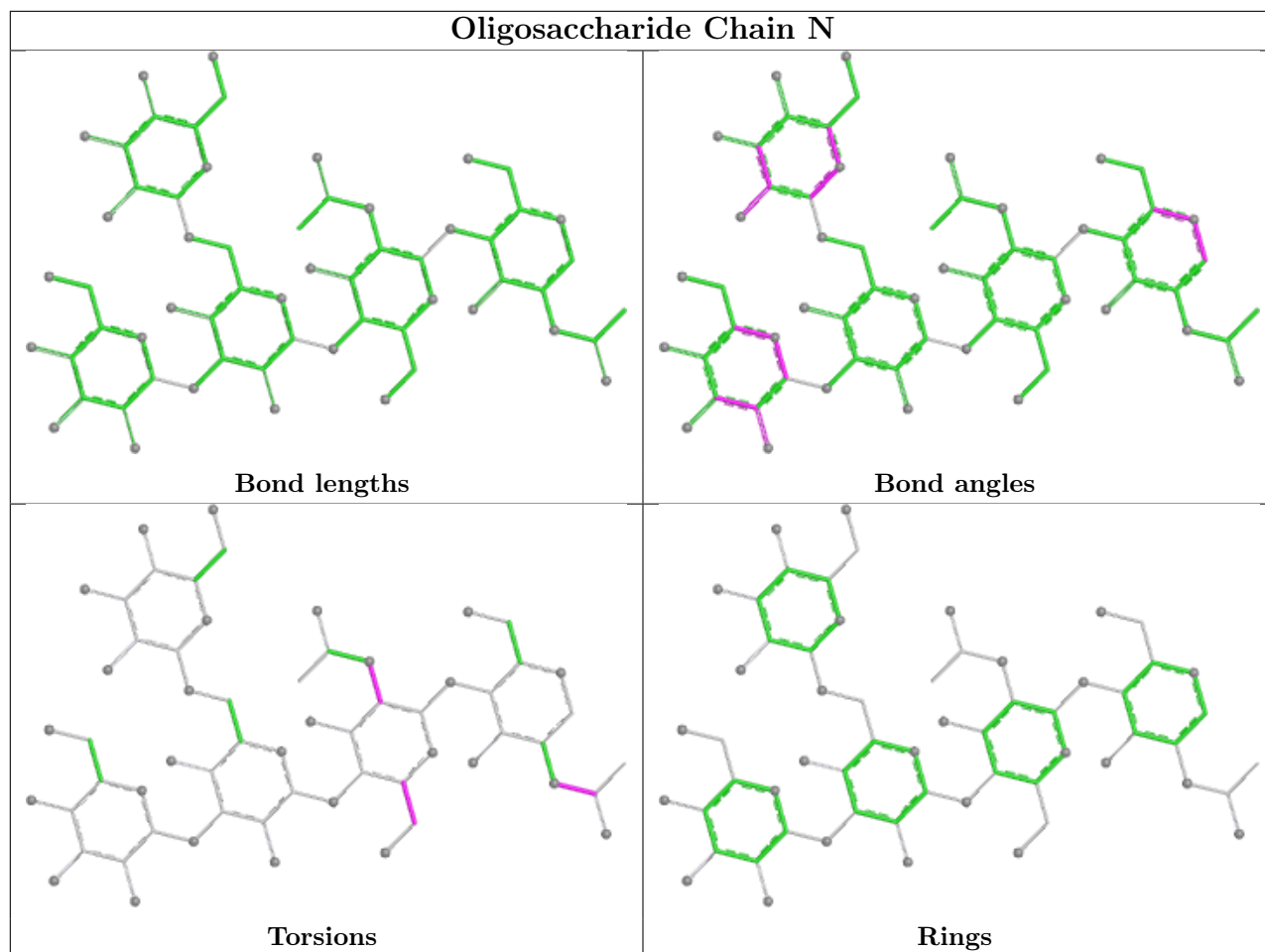












5.6 Ligand geometry [i](#)

15 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	C	1002	1	14,14,15	0.25	0	17,19,21	0.55	0
4	NAG	A	1002	1	14,14,15	0.24	0	17,19,21	0.56	0
4	NAG	A	1005	1	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	C	1004	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	B	1003	1	14,14,15	0.25	0	17,19,21	0.45	0
4	NAG	A	1001	1	14,14,15	0.19	0	17,19,21	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	A	1004	1	14,14,15	0.22	0	17,19,21	0.44	0
4	NAG	C	1005	1	14,14,15	0.23	0	17,19,21	0.44	0
4	NAG	B	1002	1	14,14,15	0.26	0	17,19,21	0.55	0
4	NAG	B	1005	1	14,14,15	0.24	0	17,19,21	0.44	0
4	NAG	A	1003	1	14,14,15	0.27	0	17,19,21	0.44	0
4	NAG	C	1001	1	14,14,15	0.20	0	17,19,21	0.36	0
4	NAG	B	1001	1	14,14,15	0.19	0	17,19,21	0.37	0
4	NAG	B	1004	1	14,14,15	0.22	0	17,19,21	0.45	0
4	NAG	C	1003	1	14,14,15	0.25	0	17,19,21	0.45	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	C	1002	1	-	4/6/23/26	0/1/1/1
4	NAG	A	1002	1	-	4/6/23/26	0/1/1/1
4	NAG	A	1005	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1004	1	-	4/6/23/26	0/1/1/1
4	NAG	B	1003	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1001	1	-	1/6/23/26	0/1/1/1
4	NAG	A	1004	1	-	4/6/23/26	0/1/1/1
4	NAG	C	1005	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1002	1	-	4/6/23/26	0/1/1/1
4	NAG	B	1005	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1003	1	-	2/6/23/26	0/1/1/1
4	NAG	C	1001	1	-	1/6/23/26	0/1/1/1
4	NAG	B	1001	1	-	1/6/23/26	0/1/1/1
4	NAG	B	1004	1	-	4/6/23/26	0/1/1/1
4	NAG	C	1003	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1003	NAG	O5-C5-C6-O6
4	B	1003	NAG	O5-C5-C6-O6
4	C	1003	NAG	O5-C5-C6-O6
4	B	1003	NAG	C4-C5-C6-O6
4	C	1003	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19347. These allow visual inspection of the internal detail of the map and identification of artifacts.

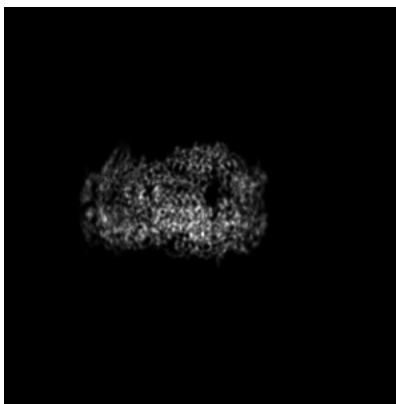
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

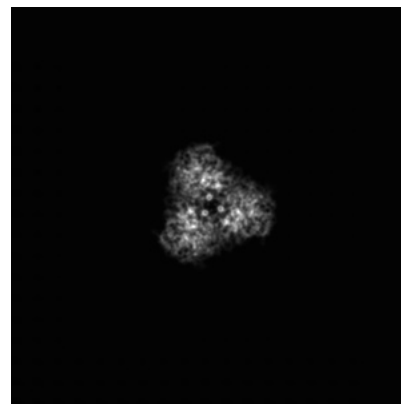
6.1.1 Primary map



X

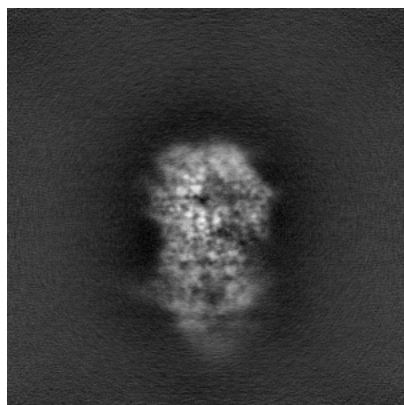


Y

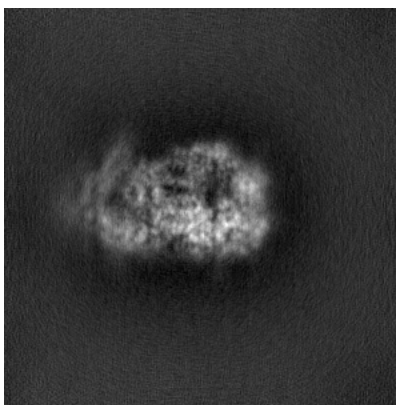


Z

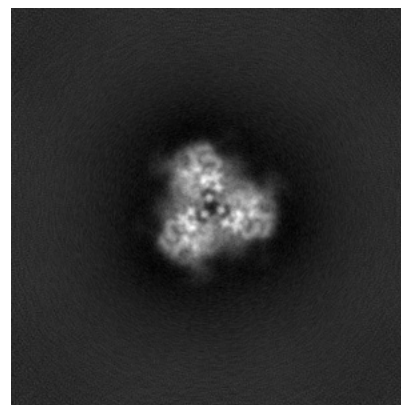
6.1.2 Raw map



X



Y



Z

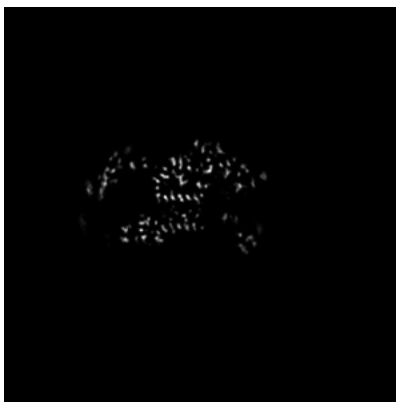
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 160

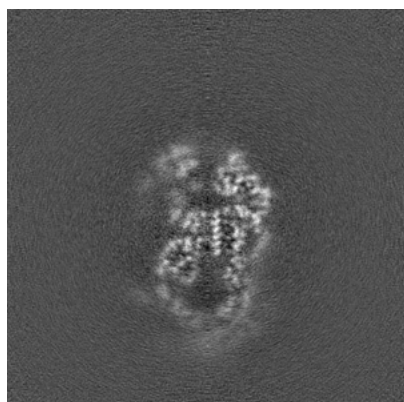


Y Index: 160

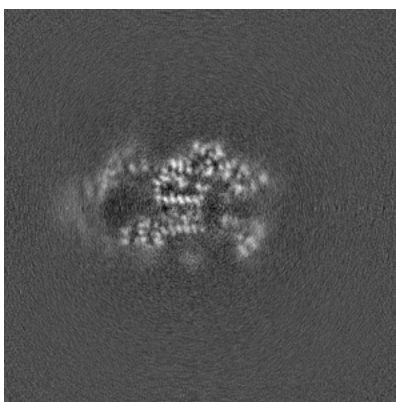


Z Index: 160

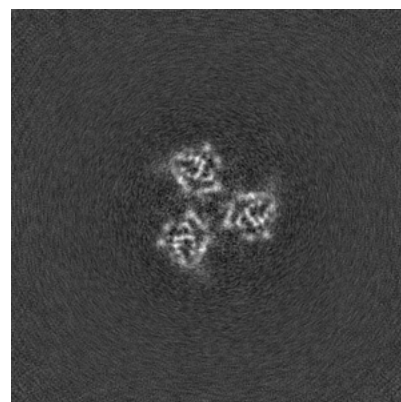
6.2.2 Raw map



X Index: 160



Y Index: 160



Z Index: 160

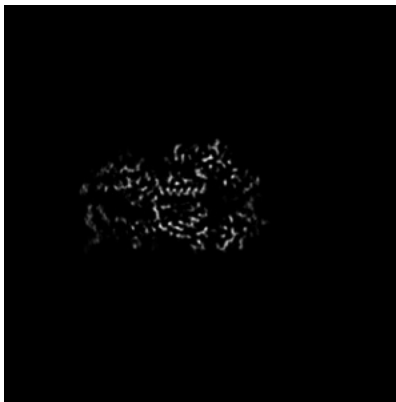
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 146

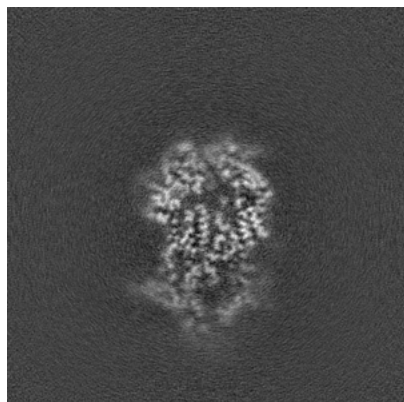


Y Index: 147

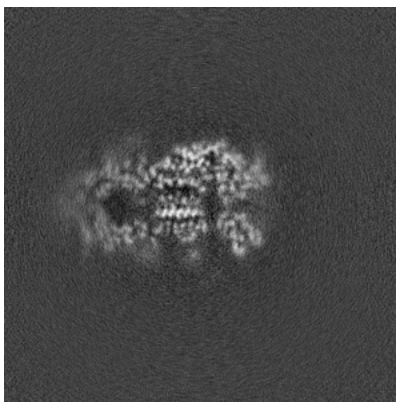


Z Index: 149

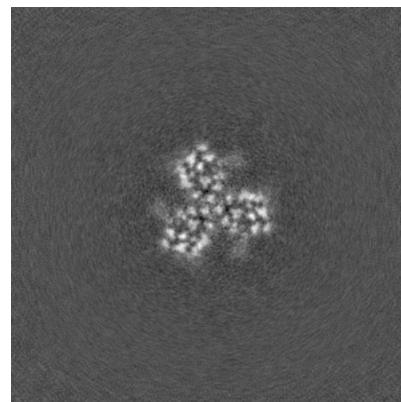
6.3.2 Raw map



X Index: 146



Y Index: 154

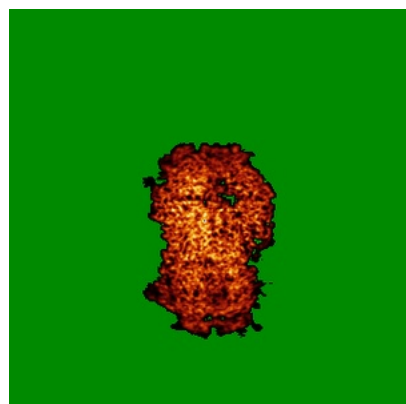


Z Index: 149

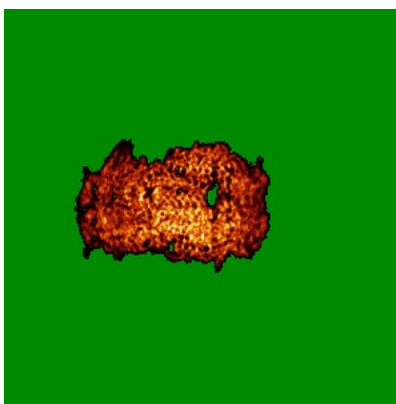
The images above show the largest variance slices of the map in three orthogonal directions.

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

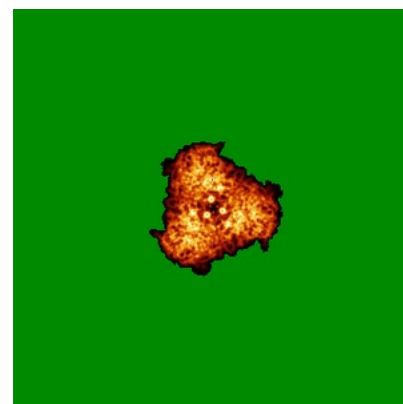
6.4.1 Primary map



X

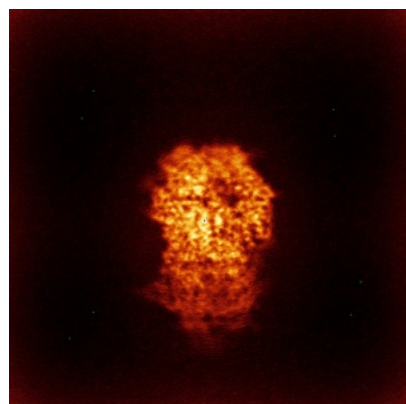


Y

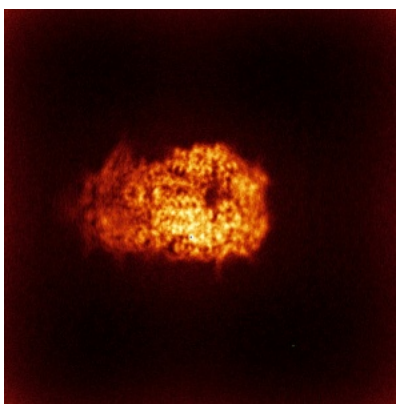


Z

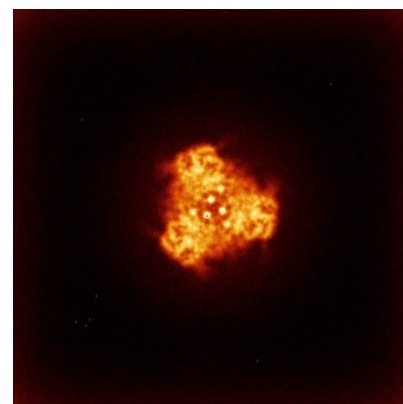
6.4.2 Raw map



X



Y

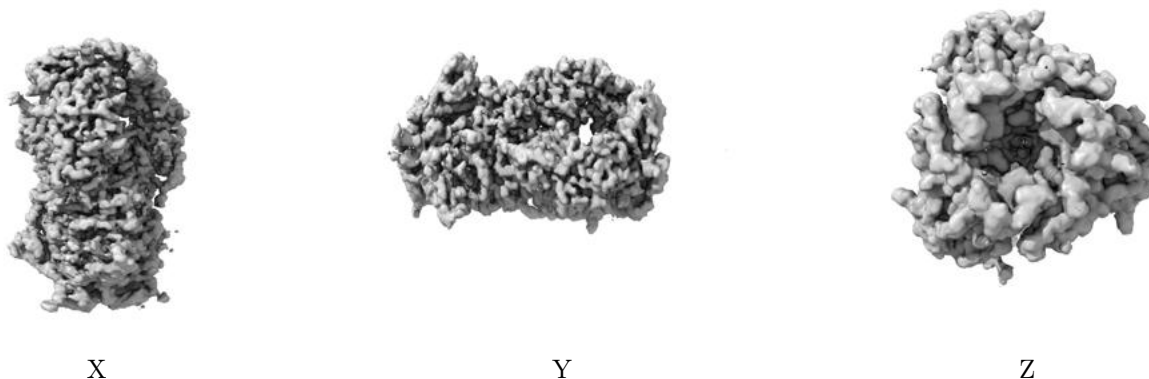


Z

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.

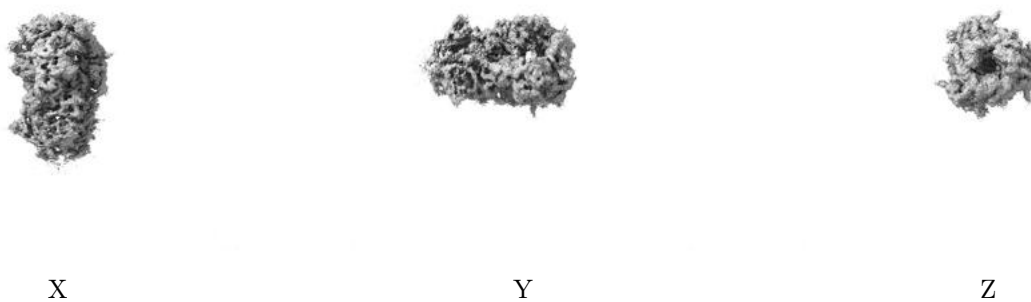
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0152. 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.

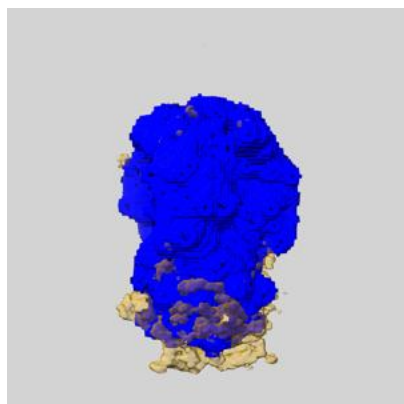
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

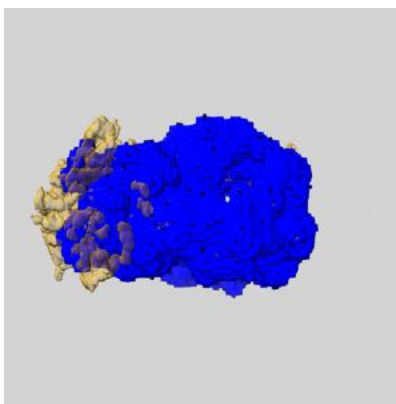
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

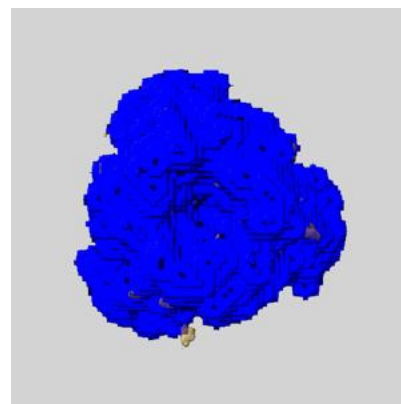
6.6.1 emd_19347_msk_1.map [i](#)



X



Y

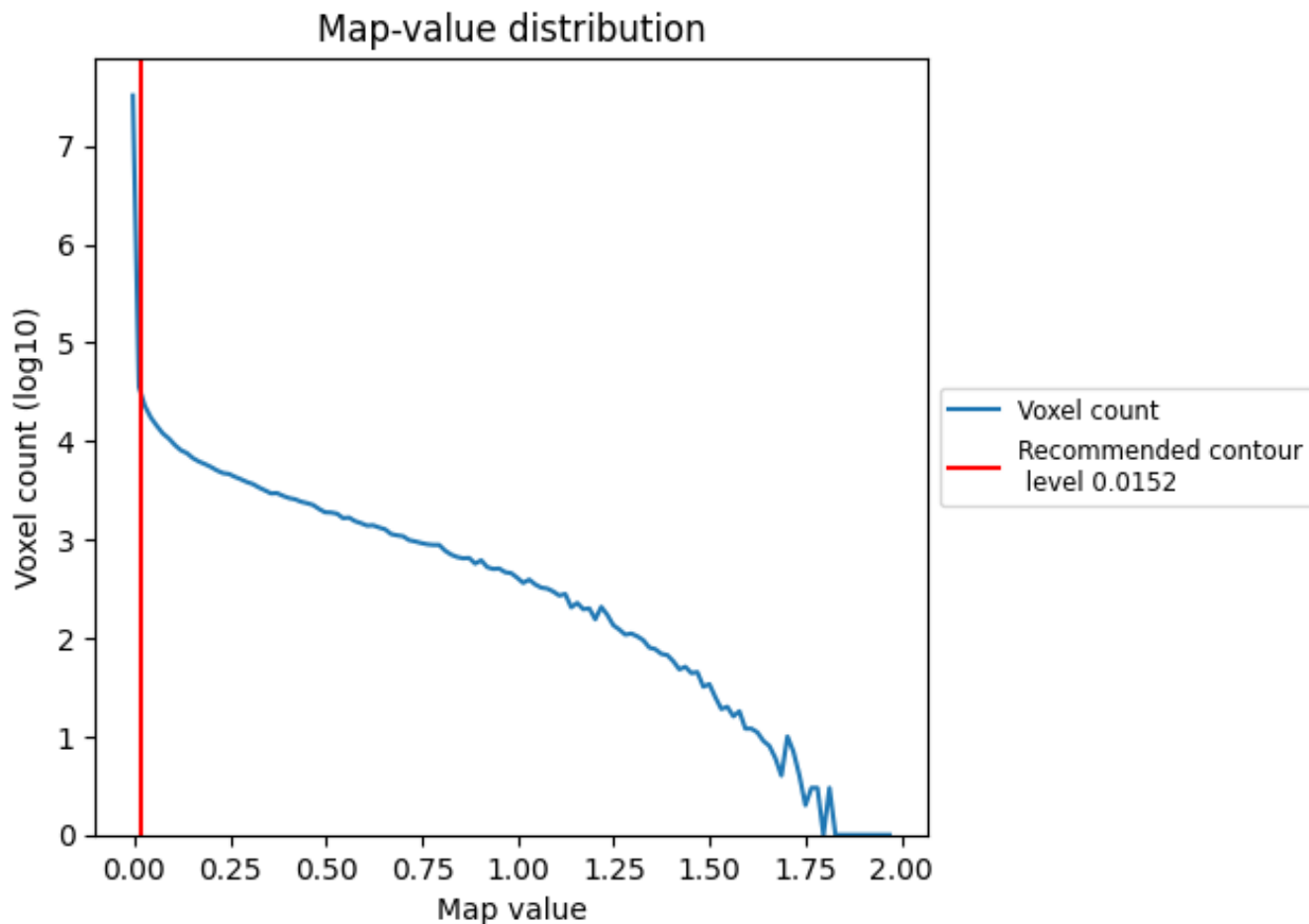


Z

7 Map analysis [i](#)

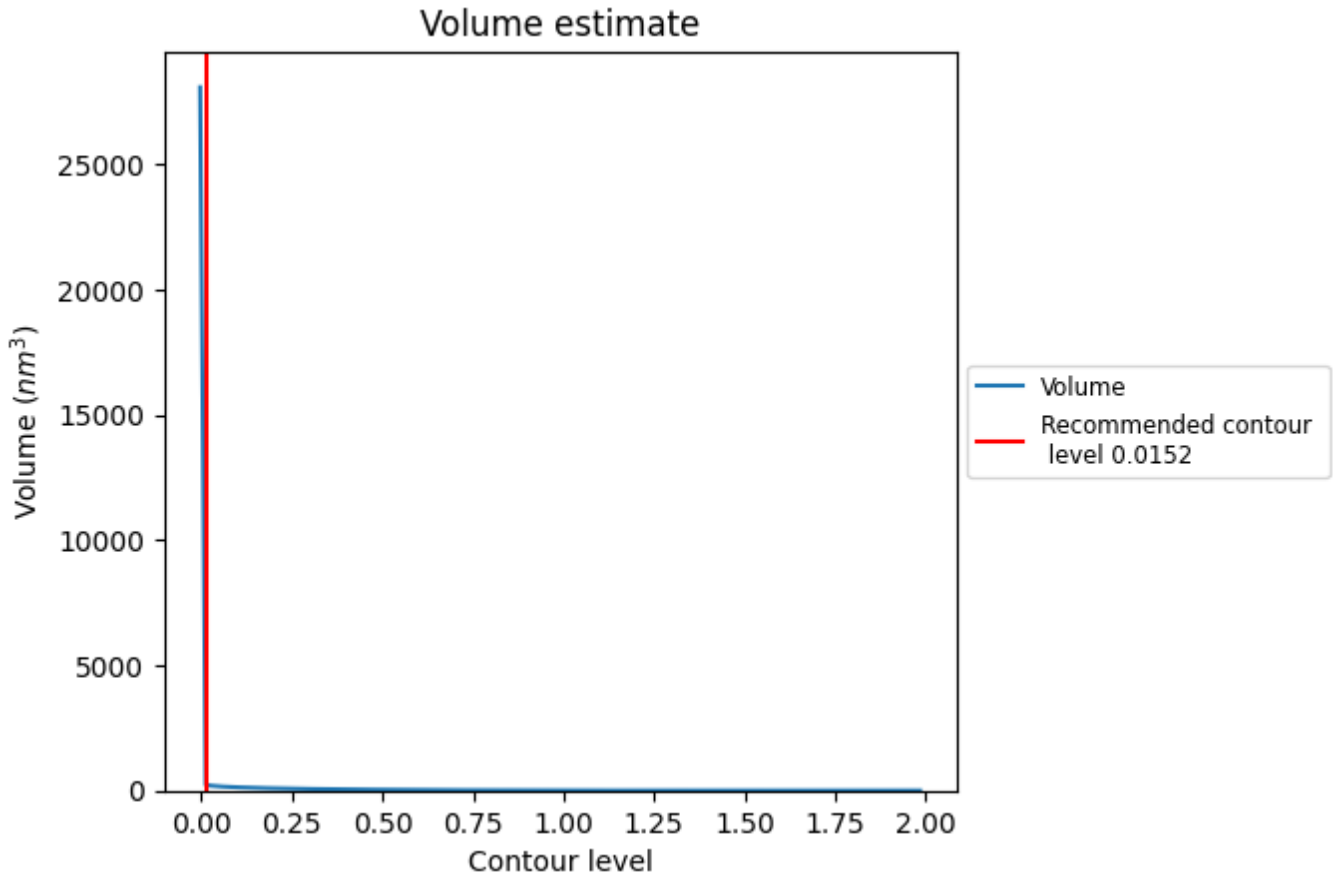
This section contains the results of statistical analysis of the map.

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.

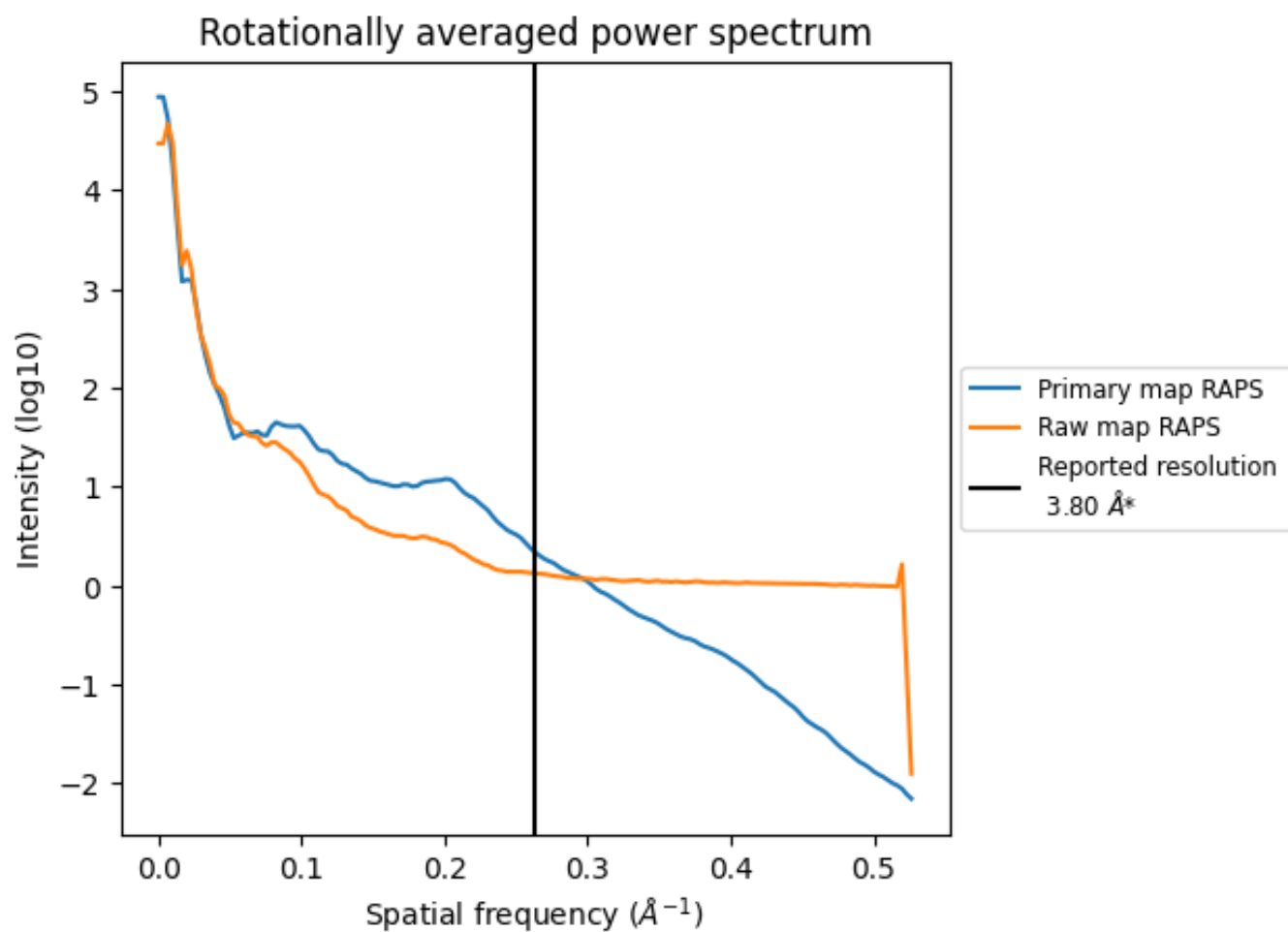
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 218 nm^3 ; this corresponds to an approximate mass of 197 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

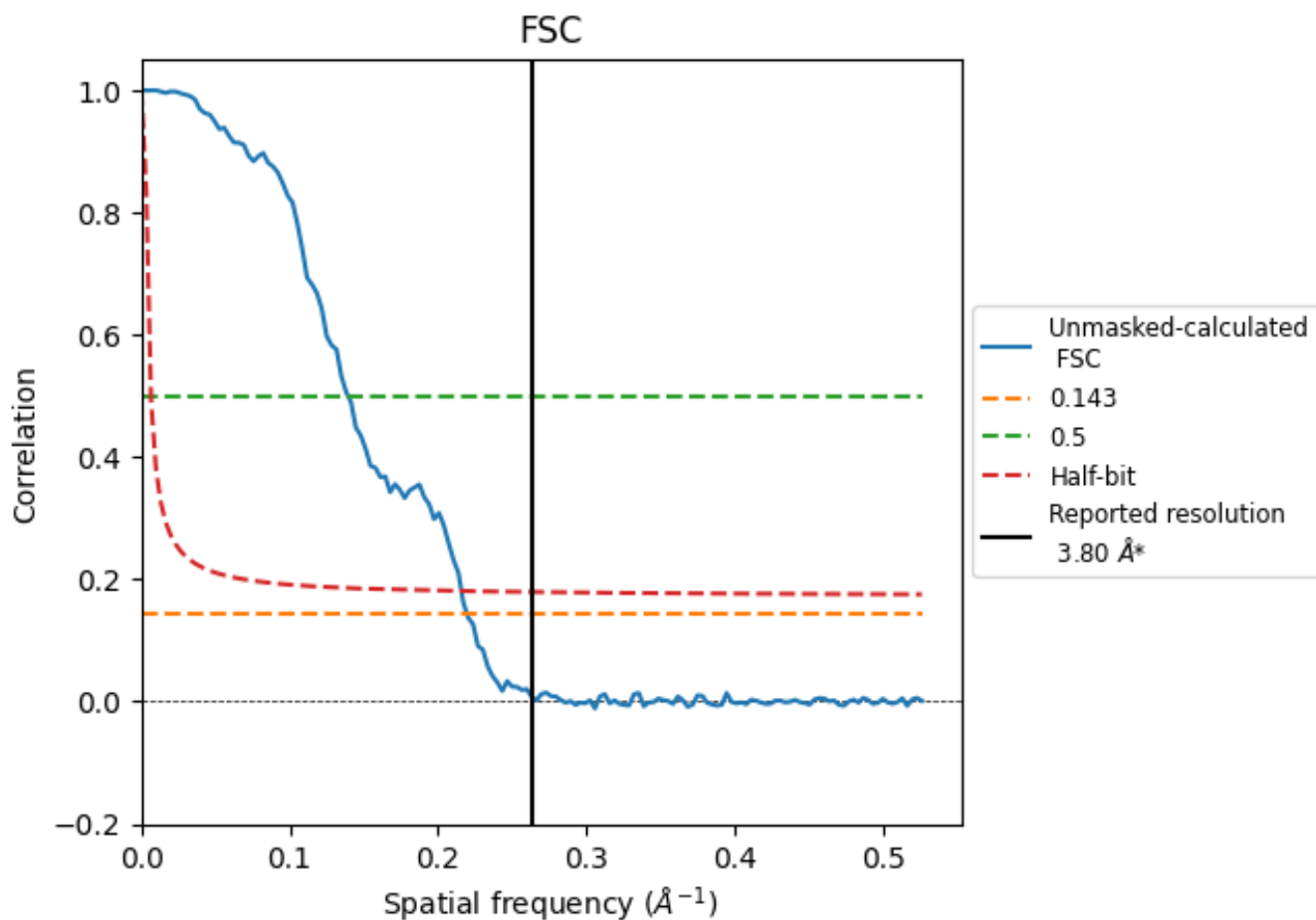


*Reported resolution corresponds to spatial frequency of 0.263 \AA^{-1}

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 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

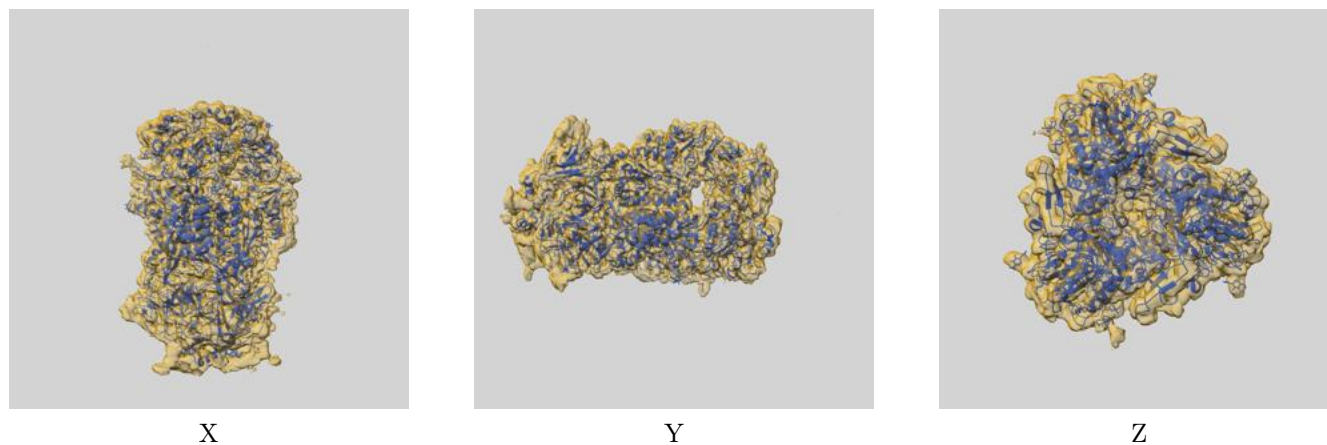
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.55	7.18	4.63

*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 4.55 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

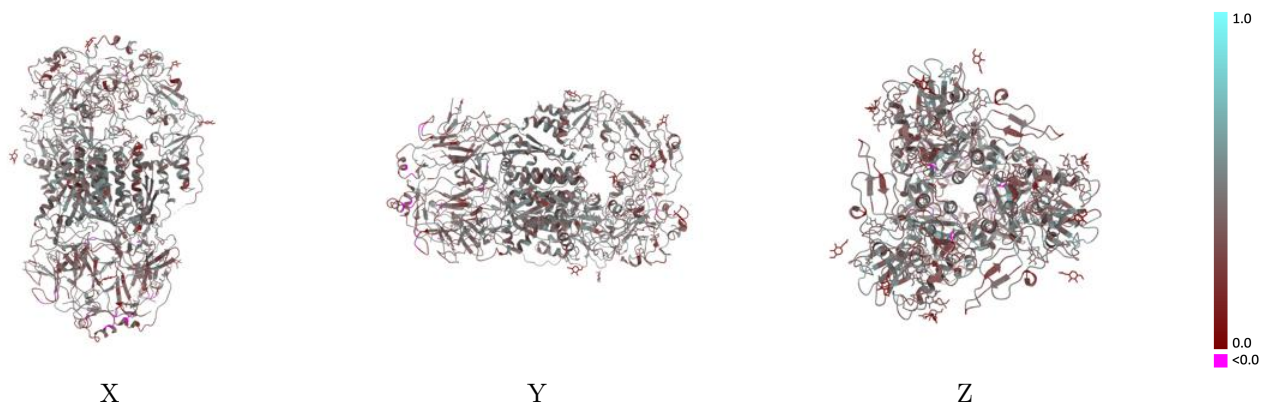
This section contains information regarding the fit between EMDB map EMD-19347 and PDB model 8RM0. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



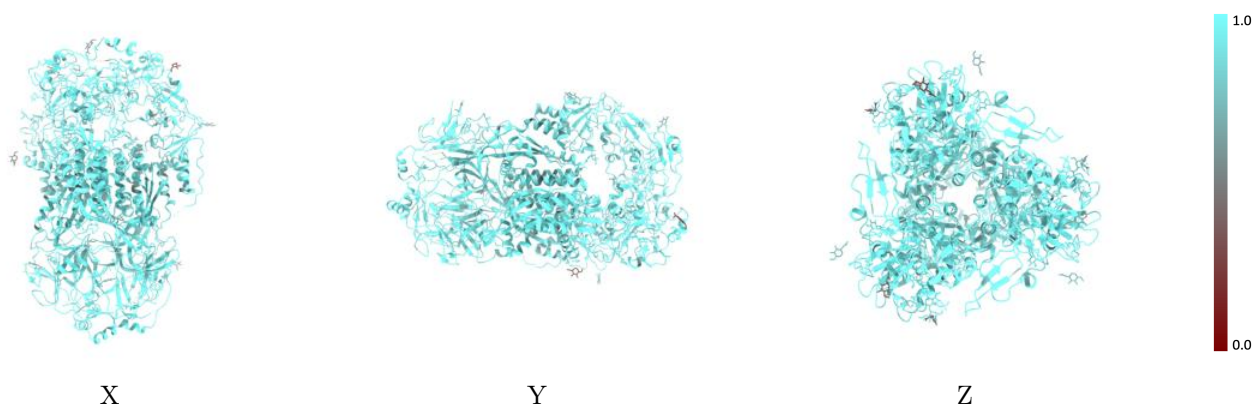
The images above show the 3D surface view of the map at the recommended contour level 0.0152 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



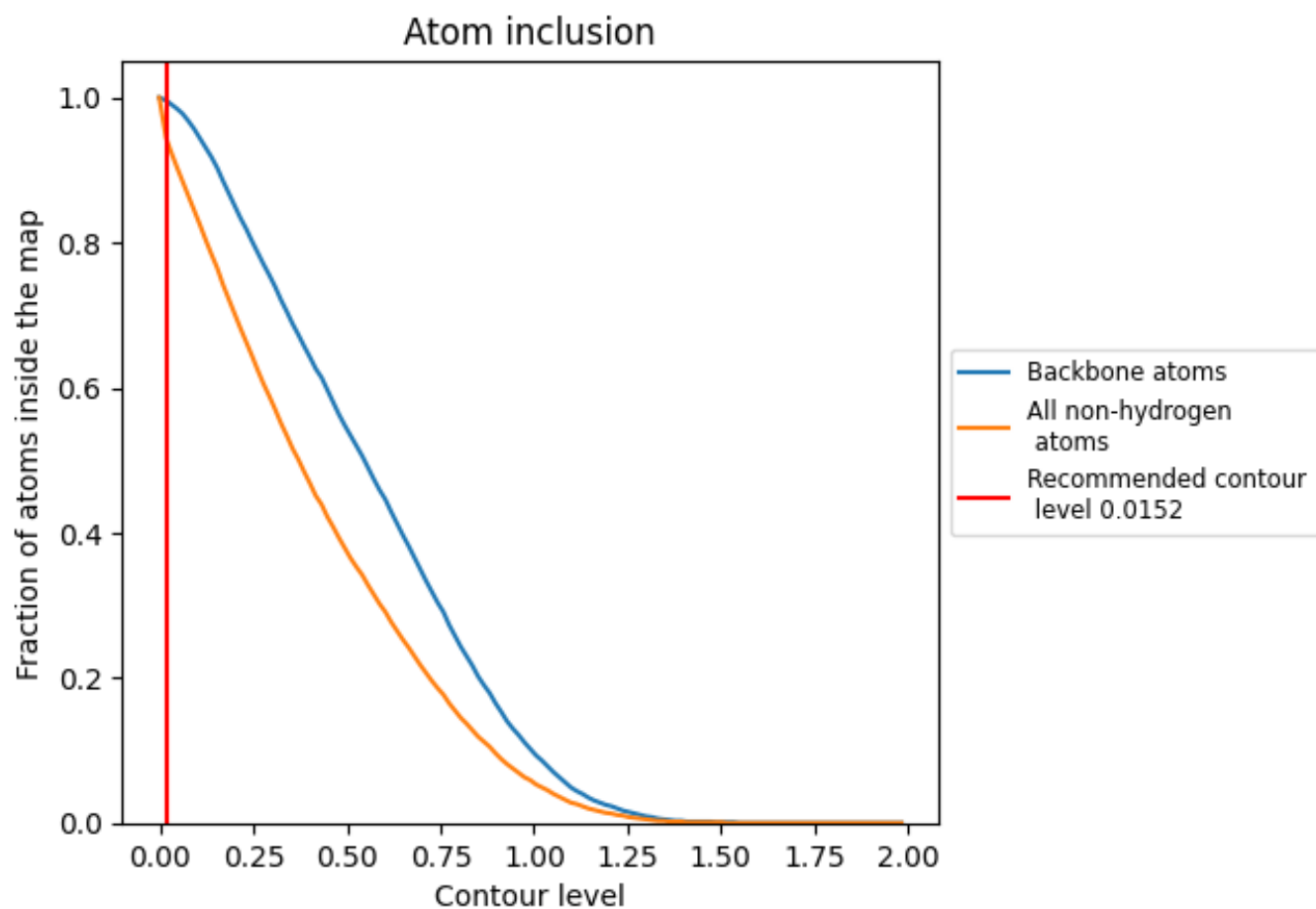
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0152).

































9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 94% 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 (0.0152) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.4110
A	 0.9450	 0.4120
B	 0.9430	 0.4110
C	 0.9450	 0.4100
D	 0.9290	 0.4170
E	 0.8930	 0.3630
F	 0.9840	 0.4080
G	 0.9290	 0.4220
H	 0.9290	 0.4080
I	 0.8930	 0.3660
J	 0.9840	 0.4230
K	 0.9290	 0.4310
L	 0.9290	 0.4200
M	 0.8930	 0.3370
N	 0.9840	 0.4080
O	 0.9640	 0.4330

