



Full wwPDB EM Validation Report ⓘ

Nov 10, 2024 – 12:00 pm GMT

PDB ID : 7Q9F
EMDB ID : EMD-13868
Title : Beta-50 fab in complex with SARS-CoV-2 beta-Spike glycoprotein
Authors : Duyvesteyn, H.M.E.; Ren, J.; Stuart, D.I.
Deposited on : 2021-11-12
Resolution : 3.60 Å (reported)
Based on initial model : 7Q0H

This is a Full wwPDB EM Validation 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.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

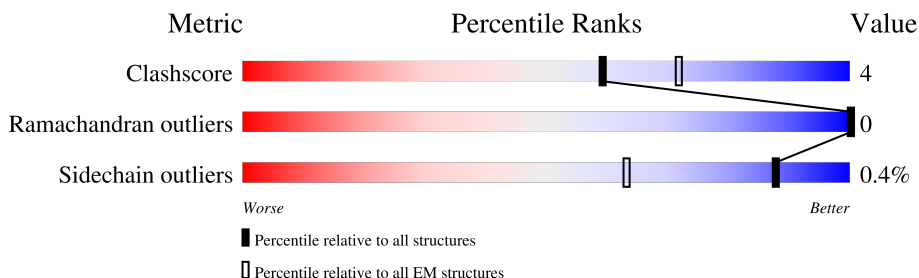
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY


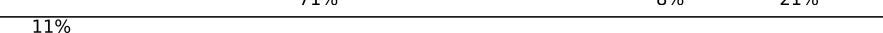
The reported resolution of this entry is 3.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.






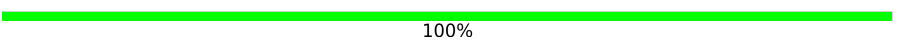

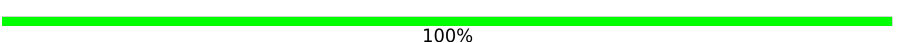
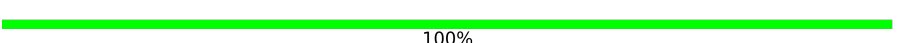
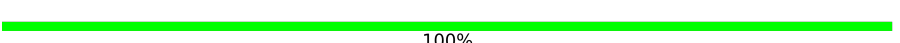
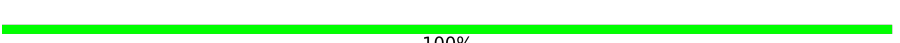
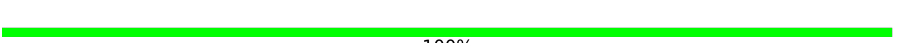

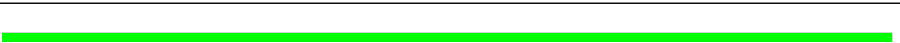



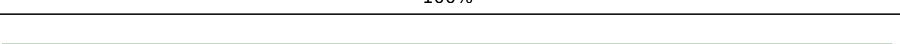
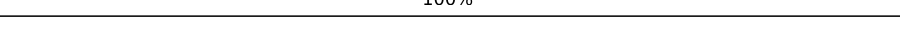
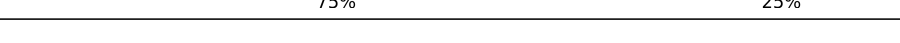
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	1285	
1	B	1285	
1	C	1285	
2	F	217	
2	K	217	
2	L	217	
3	E	223	
3	H	223	

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Mol	Chain	Length	Quality of chain
3	J	223	
4	D	3	
5	G	2	
5	I	2	
5	M	2	
5	N	2	
5	O	2	
5	Q	2	
5	R	2	
5	S	2	
5	T	2	
5	U	2	
5	W	2	
5	X	2	
5	Y	2	
5	Z	2	
6	P	4	
6	V	4	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 34264 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1009	Total	C	N	O	S	0	0
			7874	5030	1308	1501	35		
1	B	1005	Total	C	N	O	S	0	0
			7848	5015	1304	1494	35		
1	C	1014	Total	C	N	O	S	0	0
			7926	5063	1318	1509	36		

There are 291 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	18	PHE	LEU	variant	UNP P0DTC2
A	80	ALA	ASP	variant	UNP P0DTC2
A	215	GLY	ASP	variant	UNP P0DTC2
A	?	-	LEU	deletion	UNP P0DTC2
A	?	-	ALA	deletion	UNP P0DTC2
A	?	-	LEU	deletion	UNP P0DTC2
A	243	ILE	ARG	variant	UNP P0DTC2
A	414	ASN	LYS	variant	UNP P0DTC2
A	481	LYS	GLU	variant	UNP P0DTC2
A	498	TYR	ASN	variant	UNP P0DTC2
A	611	GLY	ASP	variant	UNP P0DTC2
A	679	GLY	ARG	conflict	UNP P0DTC2
A	680	SER	ARG	conflict	UNP P0DTC2
A	682	SER	ARG	conflict	UNP P0DTC2
A	698	VAL	ALA	variant	UNP P0DTC2
A	983	PRO	LYS	conflict	UNP P0DTC2
A	984	PRO	VAL	conflict	UNP P0DTC2
A	1206	GLY	-	expression tag	UNP P0DTC2
A	1207	SER	-	expression tag	UNP P0DTC2
A	1208	GLY	-	expression tag	UNP P0DTC2
A	1209	TYR	-	expression tag	UNP P0DTC2
A	1210	ILE	-	expression tag	UNP P0DTC2
A	1211	PRO	-	expression tag	UNP P0DTC2
A	1212	GLU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1213	ALA	-	expression tag	UNP P0DTC2
A	1214	PRO	-	expression tag	UNP P0DTC2
A	1215	ARG	-	expression tag	UNP P0DTC2
A	1216	ASP	-	expression tag	UNP P0DTC2
A	1217	GLY	-	expression tag	UNP P0DTC2
A	1218	GLN	-	expression tag	UNP P0DTC2
A	1219	ALA	-	expression tag	UNP P0DTC2
A	1220	TYR	-	expression tag	UNP P0DTC2
A	1221	VAL	-	expression tag	UNP P0DTC2
A	1222	ARG	-	expression tag	UNP P0DTC2
A	1223	LYS	-	expression tag	UNP P0DTC2
A	1224	ASP	-	expression tag	UNP P0DTC2
A	1225	GLY	-	expression tag	UNP P0DTC2
A	1226	GLU	-	expression tag	UNP P0DTC2
A	1227	TRP	-	expression tag	UNP P0DTC2
A	1228	VAL	-	expression tag	UNP P0DTC2
A	1229	LEU	-	expression tag	UNP P0DTC2
A	1230	LEU	-	expression tag	UNP P0DTC2
A	1231	SER	-	expression tag	UNP P0DTC2
A	1232	THR	-	expression tag	UNP P0DTC2
A	1233	PHE	-	expression tag	UNP P0DTC2
A	1234	LEU	-	expression tag	UNP P0DTC2
A	1235	GLY	-	expression tag	UNP P0DTC2
A	1236	ARG	-	expression tag	UNP P0DTC2
A	1237	SER	-	expression tag	UNP P0DTC2
A	1238	LEU	-	expression tag	UNP P0DTC2
A	1239	GLU	-	expression tag	UNP P0DTC2
A	1240	VAL	-	expression tag	UNP P0DTC2
A	1241	LEU	-	expression tag	UNP P0DTC2
A	1242	PHE	-	expression tag	UNP P0DTC2
A	1243	GLN	-	expression tag	UNP P0DTC2
A	1244	GLY	-	expression tag	UNP P0DTC2
A	1245	PRO	-	expression tag	UNP P0DTC2
A	1246	GLY	-	expression tag	UNP P0DTC2
A	1247	HIS	-	expression tag	UNP P0DTC2
A	1248	HIS	-	expression tag	UNP P0DTC2
A	1249	HIS	-	expression tag	UNP P0DTC2
A	1250	HIS	-	expression tag	UNP P0DTC2
A	1251	HIS	-	expression tag	UNP P0DTC2
A	1252	HIS	-	expression tag	UNP P0DTC2
A	1253	HIS	-	expression tag	UNP P0DTC2
A	1254	HIS	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1255	GLY	-	expression tag	UNP P0DTC2
A	1256	SER	-	expression tag	UNP P0DTC2
A	1257	ALA	-	expression tag	UNP P0DTC2
A	1258	TRP	-	expression tag	UNP P0DTC2
A	1259	SER	-	expression tag	UNP P0DTC2
A	1260	HIS	-	expression tag	UNP P0DTC2
A	1261	PRO	-	expression tag	UNP P0DTC2
A	1262	GLN	-	expression tag	UNP P0DTC2
A	1263	PHE	-	expression tag	UNP P0DTC2
A	1264	GLU	-	expression tag	UNP P0DTC2
A	1265	LYS	-	expression tag	UNP P0DTC2
A	1266	GLY	-	expression tag	UNP P0DTC2
A	1267	GLY	-	expression tag	UNP P0DTC2
A	1268	GLY	-	expression tag	UNP P0DTC2
A	1269	SER	-	expression tag	UNP P0DTC2
A	1270	GLY	-	expression tag	UNP P0DTC2
A	1271	GLY	-	expression tag	UNP P0DTC2
A	1272	GLY	-	expression tag	UNP P0DTC2
A	1273	SER	-	expression tag	UNP P0DTC2
A	1274	GLY	-	expression tag	UNP P0DTC2
A	1275	GLY	-	expression tag	UNP P0DTC2
A	1276	SER	-	expression tag	UNP P0DTC2
A	1277	ALA	-	expression tag	UNP P0DTC2
A	1278	TRP	-	expression tag	UNP P0DTC2
A	1279	SER	-	expression tag	UNP P0DTC2
A	1280	HIS	-	expression tag	UNP P0DTC2
A	1281	PRO	-	expression tag	UNP P0DTC2
A	1282	GLN	-	expression tag	UNP P0DTC2
A	1283	PHE	-	expression tag	UNP P0DTC2
A	1284	GLU	-	expression tag	UNP P0DTC2
A	1285	LYS	-	expression tag	UNP P0DTC2
B	18	PHE	LEU	variant	UNP P0DTC2
B	80	ALA	ASP	variant	UNP P0DTC2
B	215	GLY	ASP	variant	UNP P0DTC2
B	?	-	LEU	deletion	UNP P0DTC2
B	?	-	ALA	deletion	UNP P0DTC2
B	?	-	LEU	deletion	UNP P0DTC2
B	243	ILE	ARG	variant	UNP P0DTC2
B	414	ASN	LYS	variant	UNP P0DTC2
B	481	LYS	GLU	variant	UNP P0DTC2
B	498	TYR	ASN	variant	UNP P0DTC2
B	611	GLY	ASP	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	679	GLY	ARG	conflict	UNP P0DTC2
B	680	SER	ARG	conflict	UNP P0DTC2
B	682	SER	ARG	conflict	UNP P0DTC2
B	698	VAL	ALA	variant	UNP P0DTC2
B	983	PRO	LYS	conflict	UNP P0DTC2
B	984	PRO	VAL	conflict	UNP P0DTC2
B	1206	GLY	-	expression tag	UNP P0DTC2
B	1207	SER	-	expression tag	UNP P0DTC2
B	1208	GLY	-	expression tag	UNP P0DTC2
B	1209	TYR	-	expression tag	UNP P0DTC2
B	1210	ILE	-	expression tag	UNP P0DTC2
B	1211	PRO	-	expression tag	UNP P0DTC2
B	1212	GLU	-	expression tag	UNP P0DTC2
B	1213	ALA	-	expression tag	UNP P0DTC2
B	1214	PRO	-	expression tag	UNP P0DTC2
B	1215	ARG	-	expression tag	UNP P0DTC2
B	1216	ASP	-	expression tag	UNP P0DTC2
B	1217	GLY	-	expression tag	UNP P0DTC2
B	1218	GLN	-	expression tag	UNP P0DTC2
B	1219	ALA	-	expression tag	UNP P0DTC2
B	1220	TYR	-	expression tag	UNP P0DTC2
B	1221	VAL	-	expression tag	UNP P0DTC2
B	1222	ARG	-	expression tag	UNP P0DTC2
B	1223	LYS	-	expression tag	UNP P0DTC2
B	1224	ASP	-	expression tag	UNP P0DTC2
B	1225	GLY	-	expression tag	UNP P0DTC2
B	1226	GLU	-	expression tag	UNP P0DTC2
B	1227	TRP	-	expression tag	UNP P0DTC2
B	1228	VAL	-	expression tag	UNP P0DTC2
B	1229	LEU	-	expression tag	UNP P0DTC2
B	1230	LEU	-	expression tag	UNP P0DTC2
B	1231	SER	-	expression tag	UNP P0DTC2
B	1232	THR	-	expression tag	UNP P0DTC2
B	1233	PHE	-	expression tag	UNP P0DTC2
B	1234	LEU	-	expression tag	UNP P0DTC2
B	1235	GLY	-	expression tag	UNP P0DTC2
B	1236	ARG	-	expression tag	UNP P0DTC2
B	1237	SER	-	expression tag	UNP P0DTC2
B	1238	LEU	-	expression tag	UNP P0DTC2
B	1239	GLU	-	expression tag	UNP P0DTC2
B	1240	VAL	-	expression tag	UNP P0DTC2
B	1241	LEU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1242	PHE	-	expression tag	UNP P0DTC2
B	1243	GLN	-	expression tag	UNP P0DTC2
B	1244	GLY	-	expression tag	UNP P0DTC2
B	1245	PRO	-	expression tag	UNP P0DTC2
B	1246	GLY	-	expression tag	UNP P0DTC2
B	1247	HIS	-	expression tag	UNP P0DTC2
B	1248	HIS	-	expression tag	UNP P0DTC2
B	1249	HIS	-	expression tag	UNP P0DTC2
B	1250	HIS	-	expression tag	UNP P0DTC2
B	1251	HIS	-	expression tag	UNP P0DTC2
B	1252	HIS	-	expression tag	UNP P0DTC2
B	1253	HIS	-	expression tag	UNP P0DTC2
B	1254	HIS	-	expression tag	UNP P0DTC2
B	1255	GLY	-	expression tag	UNP P0DTC2
B	1256	SER	-	expression tag	UNP P0DTC2
B	1257	ALA	-	expression tag	UNP P0DTC2
B	1258	TRP	-	expression tag	UNP P0DTC2
B	1259	SER	-	expression tag	UNP P0DTC2
B	1260	HIS	-	expression tag	UNP P0DTC2
B	1261	PRO	-	expression tag	UNP P0DTC2
B	1262	GLN	-	expression tag	UNP P0DTC2
B	1263	PHE	-	expression tag	UNP P0DTC2
B	1264	GLU	-	expression tag	UNP P0DTC2
B	1265	LYS	-	expression tag	UNP P0DTC2
B	1266	GLY	-	expression tag	UNP P0DTC2
B	1267	GLY	-	expression tag	UNP P0DTC2
B	1268	GLY	-	expression tag	UNP P0DTC2
B	1269	SER	-	expression tag	UNP P0DTC2
B	1270	GLY	-	expression tag	UNP P0DTC2
B	1271	GLY	-	expression tag	UNP P0DTC2
B	1272	GLY	-	expression tag	UNP P0DTC2
B	1273	SER	-	expression tag	UNP P0DTC2
B	1274	GLY	-	expression tag	UNP P0DTC2
B	1275	GLY	-	expression tag	UNP P0DTC2
B	1276	SER	-	expression tag	UNP P0DTC2
B	1277	ALA	-	expression tag	UNP P0DTC2
B	1278	TRP	-	expression tag	UNP P0DTC2
B	1279	SER	-	expression tag	UNP P0DTC2
B	1280	HIS	-	expression tag	UNP P0DTC2
B	1281	PRO	-	expression tag	UNP P0DTC2
B	1282	GLN	-	expression tag	UNP P0DTC2
B	1283	PHE	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1284	GLU	-	expression tag	UNP P0DTC2
B	1285	LYS	-	expression tag	UNP P0DTC2
C	18	PHE	LEU	variant	UNP P0DTC2
C	80	ALA	ASP	variant	UNP P0DTC2
C	215	GLY	ASP	variant	UNP P0DTC2
C	?	-	LEU	deletion	UNP P0DTC2
C	?	-	ALA	deletion	UNP P0DTC2
C	?	-	LEU	deletion	UNP P0DTC2
C	243	ILE	ARG	variant	UNP P0DTC2
C	414	ASN	LYS	variant	UNP P0DTC2
C	481	LYS	GLU	variant	UNP P0DTC2
C	498	TYR	ASN	variant	UNP P0DTC2
C	611	GLY	ASP	variant	UNP P0DTC2
C	679	GLY	ARG	conflict	UNP P0DTC2
C	680	SER	ARG	conflict	UNP P0DTC2
C	682	SER	ARG	conflict	UNP P0DTC2
C	698	VAL	ALA	variant	UNP P0DTC2
C	983	PRO	LYS	conflict	UNP P0DTC2
C	984	PRO	VAL	conflict	UNP P0DTC2
C	1206	GLY	-	expression tag	UNP P0DTC2
C	1207	SER	-	expression tag	UNP P0DTC2
C	1208	GLY	-	expression tag	UNP P0DTC2
C	1209	TYR	-	expression tag	UNP P0DTC2
C	1210	ILE	-	expression tag	UNP P0DTC2
C	1211	PRO	-	expression tag	UNP P0DTC2
C	1212	GLU	-	expression tag	UNP P0DTC2
C	1213	ALA	-	expression tag	UNP P0DTC2
C	1214	PRO	-	expression tag	UNP P0DTC2
C	1215	ARG	-	expression tag	UNP P0DTC2
C	1216	ASP	-	expression tag	UNP P0DTC2
C	1217	GLY	-	expression tag	UNP P0DTC2
C	1218	GLN	-	expression tag	UNP P0DTC2
C	1219	ALA	-	expression tag	UNP P0DTC2
C	1220	TYR	-	expression tag	UNP P0DTC2
C	1221	VAL	-	expression tag	UNP P0DTC2
C	1222	ARG	-	expression tag	UNP P0DTC2
C	1223	LYS	-	expression tag	UNP P0DTC2
C	1224	ASP	-	expression tag	UNP P0DTC2
C	1225	GLY	-	expression tag	UNP P0DTC2
C	1226	GLU	-	expression tag	UNP P0DTC2
C	1227	TRP	-	expression tag	UNP P0DTC2
C	1228	VAL	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1229	LEU	-	expression tag	UNP P0DTC2
C	1230	LEU	-	expression tag	UNP P0DTC2
C	1231	SER	-	expression tag	UNP P0DTC2
C	1232	THR	-	expression tag	UNP P0DTC2
C	1233	PHE	-	expression tag	UNP P0DTC2
C	1234	LEU	-	expression tag	UNP P0DTC2
C	1235	GLY	-	expression tag	UNP P0DTC2
C	1236	ARG	-	expression tag	UNP P0DTC2
C	1237	SER	-	expression tag	UNP P0DTC2
C	1238	LEU	-	expression tag	UNP P0DTC2
C	1239	GLU	-	expression tag	UNP P0DTC2
C	1240	VAL	-	expression tag	UNP P0DTC2
C	1241	LEU	-	expression tag	UNP P0DTC2
C	1242	PHE	-	expression tag	UNP P0DTC2
C	1243	GLN	-	expression tag	UNP P0DTC2
C	1244	GLY	-	expression tag	UNP P0DTC2
C	1245	PRO	-	expression tag	UNP P0DTC2
C	1246	GLY	-	expression tag	UNP P0DTC2
C	1247	HIS	-	expression tag	UNP P0DTC2
C	1248	HIS	-	expression tag	UNP P0DTC2
C	1249	HIS	-	expression tag	UNP P0DTC2
C	1250	HIS	-	expression tag	UNP P0DTC2
C	1251	HIS	-	expression tag	UNP P0DTC2
C	1252	HIS	-	expression tag	UNP P0DTC2
C	1253	HIS	-	expression tag	UNP P0DTC2
C	1254	HIS	-	expression tag	UNP P0DTC2
C	1255	GLY	-	expression tag	UNP P0DTC2
C	1256	SER	-	expression tag	UNP P0DTC2
C	1257	ALA	-	expression tag	UNP P0DTC2
C	1258	TRP	-	expression tag	UNP P0DTC2
C	1259	SER	-	expression tag	UNP P0DTC2
C	1260	HIS	-	expression tag	UNP P0DTC2
C	1261	PRO	-	expression tag	UNP P0DTC2
C	1262	GLN	-	expression tag	UNP P0DTC2
C	1263	PHE	-	expression tag	UNP P0DTC2
C	1264	GLU	-	expression tag	UNP P0DTC2
C	1265	LYS	-	expression tag	UNP P0DTC2
C	1266	GLY	-	expression tag	UNP P0DTC2
C	1267	GLY	-	expression tag	UNP P0DTC2
C	1268	GLY	-	expression tag	UNP P0DTC2
C	1269	SER	-	expression tag	UNP P0DTC2
C	1270	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1271	GLY	-	expression tag	UNP P0DTC2
C	1272	GLY	-	expression tag	UNP P0DTC2
C	1273	SER	-	expression tag	UNP P0DTC2
C	1274	GLY	-	expression tag	UNP P0DTC2
C	1275	GLY	-	expression tag	UNP P0DTC2
C	1276	SER	-	expression tag	UNP P0DTC2
C	1277	ALA	-	expression tag	UNP P0DTC2
C	1278	TRP	-	expression tag	UNP P0DTC2
C	1279	SER	-	expression tag	UNP P0DTC2
C	1280	HIS	-	expression tag	UNP P0DTC2
C	1281	PRO	-	expression tag	UNP P0DTC2
C	1282	GLN	-	expression tag	UNP P0DTC2
C	1283	PHE	-	expression tag	UNP P0DTC2
C	1284	GLU	-	expression tag	UNP P0DTC2
C	1285	LYS	-	expression tag	UNP P0DTC2

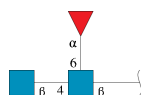
- Molecule 2 is a protein called Beta-50 light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	216	Total	C	N	O	S	2	0
			1668	1045	282	334	7		
2	F	216	Total	C	N	O	S	2	0
			1668	1045	282	334	7		
2	K	216	Total	C	N	O	S	2	0
			1668	1045	282	334	7		

- Molecule 3 is a protein called Beta-50 heavy chain.

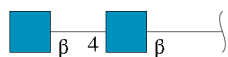
Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	212	Total	C	N	O	S	0	0
			1578	1002	258	311	7		
3	E	212	Total	C	N	O	S	0	0
			1578	1002	258	311	7		
3	J	212	Total	C	N	O	S	0	0
			1578	1002	258	311	7		

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



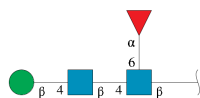
Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



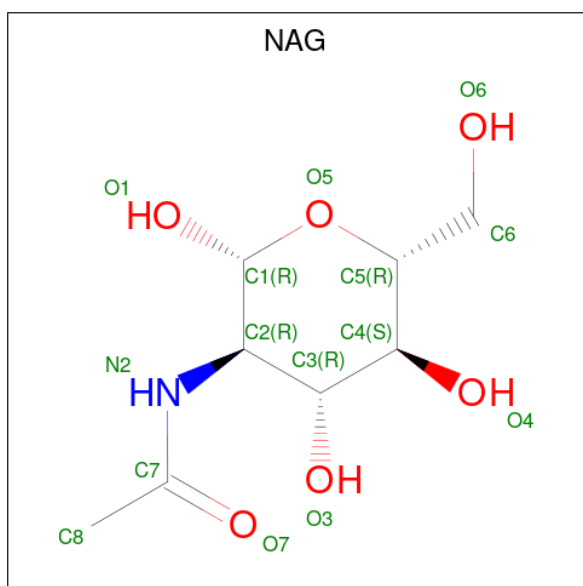
Mol	Chain	Residues	Atoms				AltConf	Trace
5	G	2	Total	C	N	O	0	0
			28	16	2	10		
5	I	2	Total	C	N	O	0	0
			28	16	2	10		
5	M	2	Total	C	N	O	0	0
			28	16	2	10		
5	N	2	Total	C	N	O	0	0
			28	16	2	10		
5	O	2	Total	C	N	O	0	0
			28	16	2	10		
5	Q	2	Total	C	N	O	0	0
			28	16	2	10		
5	R	2	Total	C	N	O	0	0
			28	16	2	10		
5	S	2	Total	C	N	O	0	0
			28	16	2	10		
5	T	2	Total	C	N	O	0	0
			28	16	2	10		
5	U	2	Total	C	N	O	0	0
			28	16	2	10		
5	W	2	Total	C	N	O	0	0
			28	16	2	10		
5	X	2	Total	C	N	O	0	0
			28	16	2	10		
5	Y	2	Total	C	N	O	0	0
			28	16	2	10		
5	Z	2	Total	C	N	O	0	0
			28	16	2	10		

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



Mol	Chain	Residues	Atoms				AltConf	Trace
6	P	4	Total	C	N	O	0	0
			49	28	2	19		
6	V	4	Total	C	N	O	0	0
			49	28	2	19		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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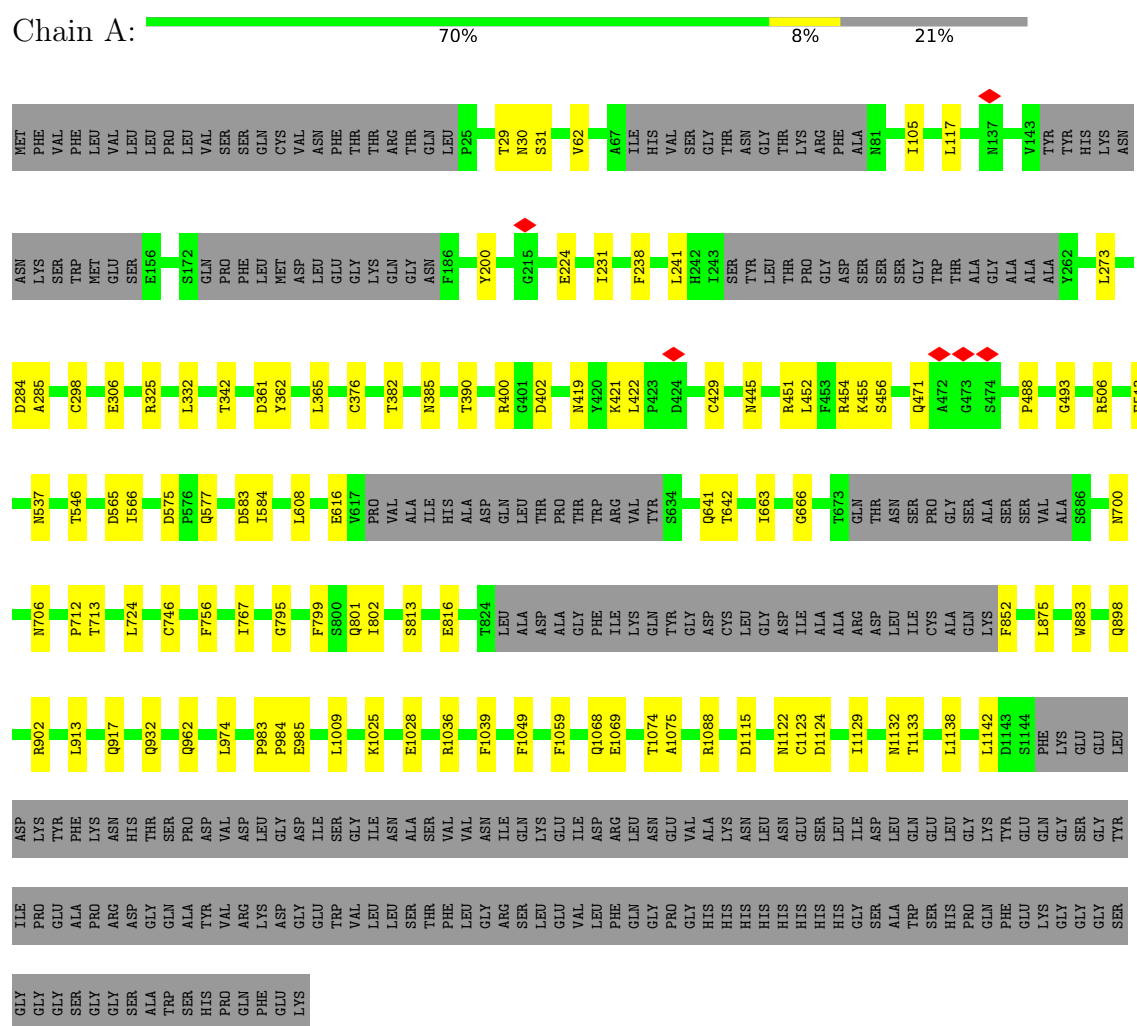
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Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C	N	O	0
			14	8	1	5	
7	B	1	Total	C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

3 Residue-property plots

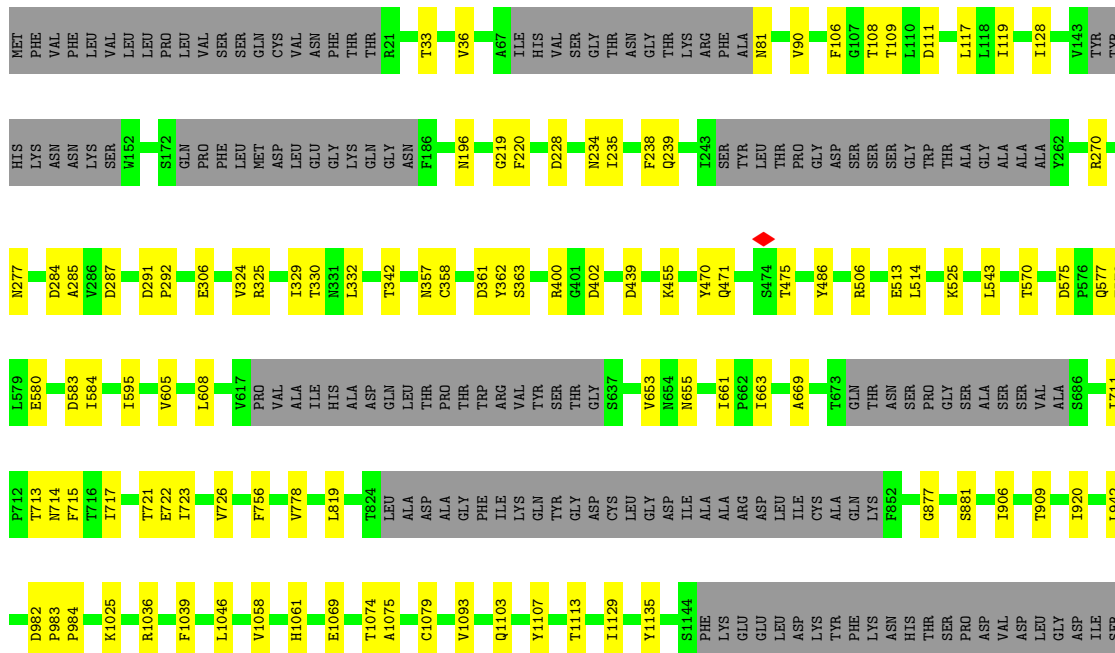
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Spike glycoprotein



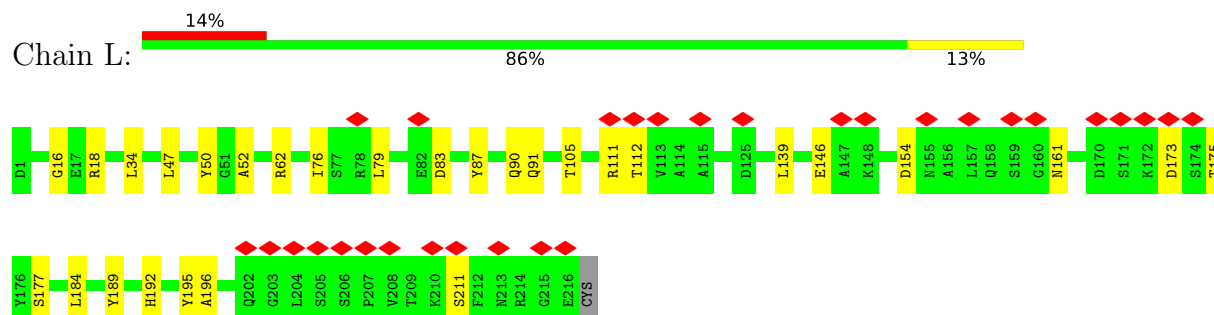
• Molecule 1: Spike glycoprotein



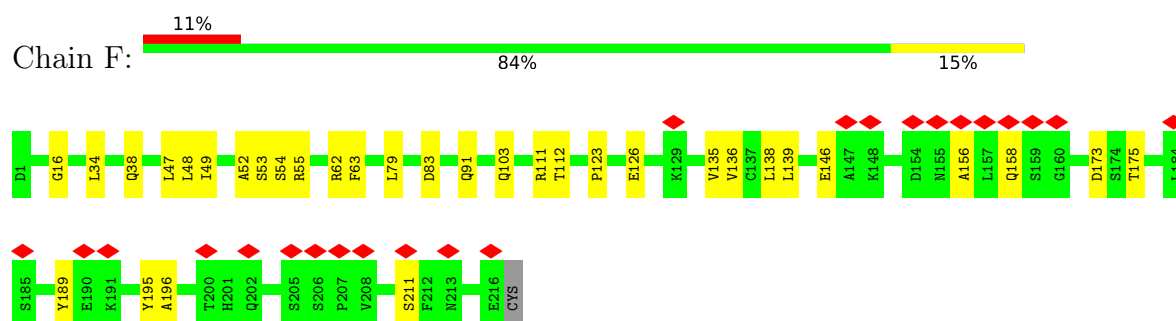


GLY	ILE	ASN	ALA	SER	THR	PHE	VAL	VAL	ASN	ILE	GLN	LYS	GLU	ASP	ARG	ASN	GLY	GLU	VAL	ALA	LYS	ASN	LEU	GLU	SER	ASP	GLN	GLY	LEU	TRP	SER	GLU	LEU	GLY	LYS	GLN	TYR	GLU	GLN	GLY	SER	GLY	TYR	ILE	PRO	GLY	ALA	PRO	GLY	ASP	ASP	GLY	GLN	TRP	ALA	TRP	GLN	SER	VAL	TYR	HIS	PRO	GLN	ARG	LYS	ASP	GLY	GLU	TRP	LYS
VAL	LEU	SER	ALA	SER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

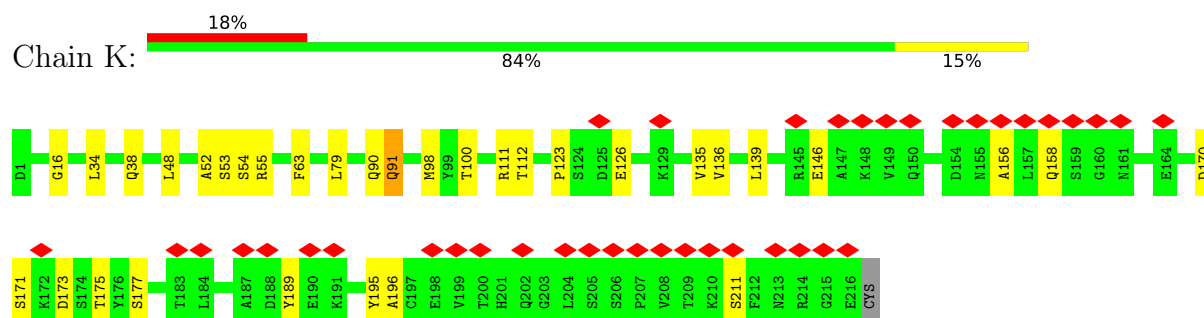
• Molecule 2: Beta-50 light chain



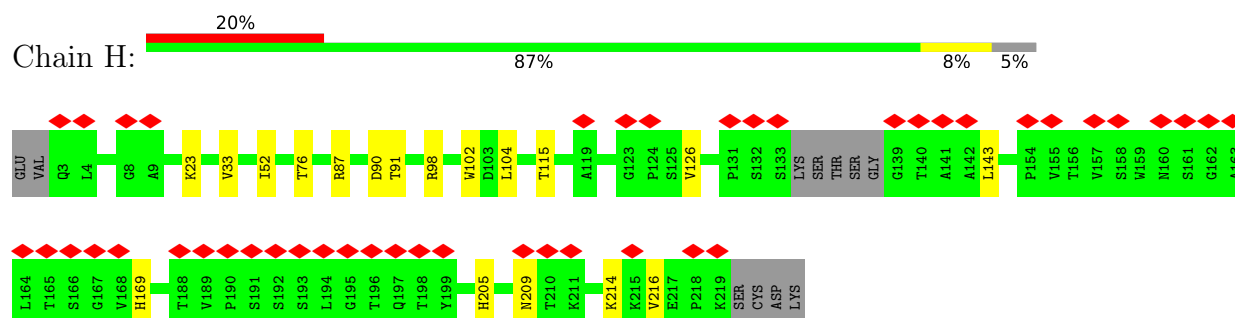
• Molecule 2: Beta-50 light chain



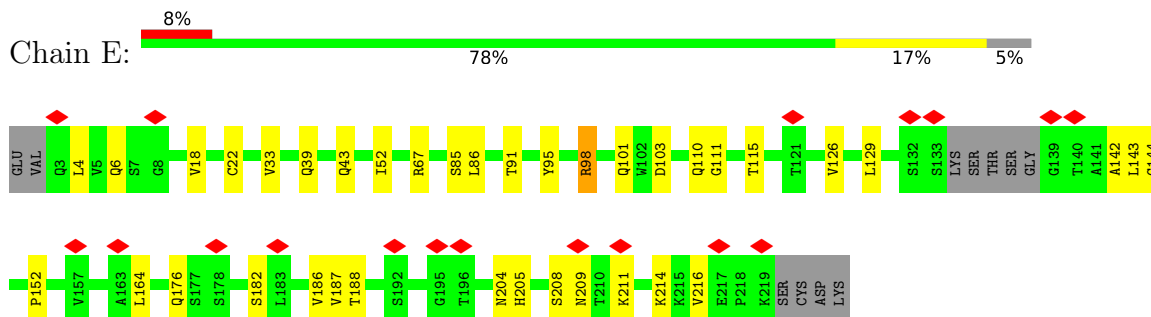
• Molecule 2: Beta-50 light chain



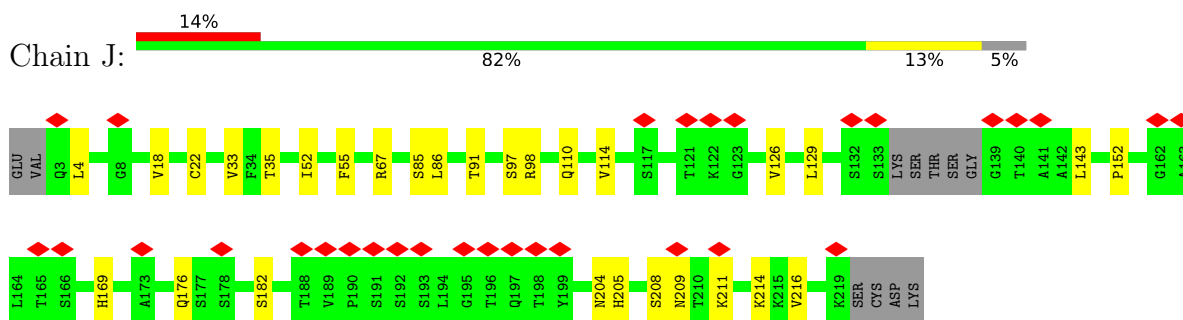
• Molecule 3: Beta-50 heavy chain



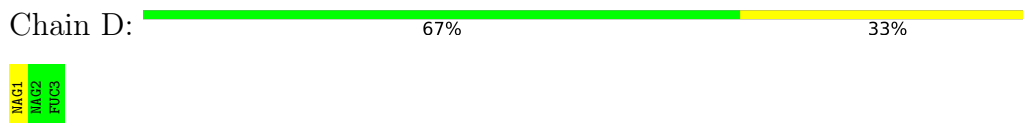
- Molecule 3: Beta-50 heavy chain



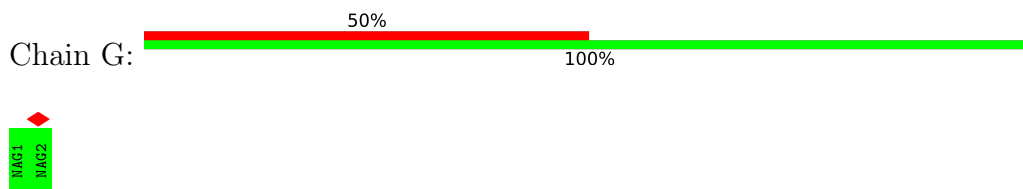
- Molecule 3: Beta-50 heavy chain



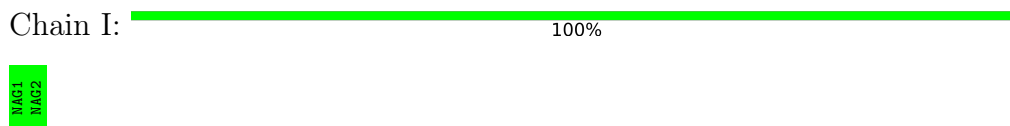
- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:  50% 50%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  100%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  100%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Q:  100%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain R:  100%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S:  100%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain T:  100%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain U:  100%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain W:  100%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain X:  100%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y:  100%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z:  100%



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

Chain P:  75% 25%



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

Chain V:  100%

MAG1
MAG2
BMA3
FUC4

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	40869	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	38.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.815	Depositor
Minimum map value	-0.440	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.0917	Depositor
Map size (\AA)	344.4, 344.4, 344.4	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.82, 0.82, 0.82	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: FUC, 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	0.28	0/8054	0.47	0/10960
1	B	0.28	0/8028	0.47	0/10925
1	C	0.28	0/8108	0.47	0/11034
2	F	0.26	0/1711	0.49	0/2323
2	K	0.26	0/1711	0.48	0/2323
2	L	0.26	0/1711	0.48	0/2323
3	E	0.25	0/1617	0.46	0/2208
3	H	0.25	0/1617	0.46	0/2208
3	J	0.25	0/1617	0.46	0/2208
All	All	0.27	0/34174	0.47	0/46512

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	7874	0	7672	64	0
1	B	7848	0	7642	73	0
1	C	7926	0	7717	63	0
2	F	1668	0	1622	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	K	1668	0	1622	23	0
2	L	1668	0	1622	19	0
3	E	1578	0	1534	26	0
3	H	1578	0	1534	11	0
3	J	1578	0	1534	19	0
4	D	38	0	34	1	0
5	G	28	0	25	0	0
5	I	28	0	25	0	0
5	M	28	0	25	1	0
5	N	28	0	25	0	0
5	O	28	0	25	0	0
5	Q	28	0	25	0	0
5	R	28	0	25	0	0
5	S	28	0	25	0	0
5	T	28	0	25	0	0
5	U	28	0	25	0	0
5	W	28	0	25	0	0
5	X	28	0	25	0	0
5	Y	28	0	25	0	0
5	Z	28	0	25	0	0
6	P	49	0	43	0	0
6	V	49	0	43	0	0
7	A	112	0	104	0	0
7	B	126	0	117	0	0
7	C	112	0	104	1	0
All	All	34264	0	33294	294	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.

All (294) 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:390:THR:OG1	1:A:513:GLU:O	1.94	0.85
1:B:361:ASP:OD1	1:B:362:TYR:N	2.11	0.82
1:C:361:ASP:OD1	1:C:362:TYR:N	2.13	0.82
1:B:390:THR:OG1	1:B:513:GLU:O	2.01	0.78
1:A:700:ASN:ND2	1:B:784:GLN:OE1	2.17	0.78
1:A:325:ARG:NH1	1:A:575:ASP:OD2	2.18	0.76
1:A:361:ASP:OD1	1:A:362:TYR:N	2.18	0.76
1:A:985:GLU:OE1	1:A:985:GLU:N	2.18	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:356:SER:OG	1:B:391:ASN:OD1	2.04	0.75
1:A:616:GLU:N	1:A:616:GLU:OE1	2.22	0.72
2:F:189:TYR:O	2:F:195:TYR:OH	2.06	0.72
1:B:325:ARG:NH1	1:B:575:ASP:OD2	2.23	0.72
1:A:799:PHE:HD1	1:A:802:ILE:HD11	1.56	0.70
3:E:205:HIS:O	3:E:209:ASN:N	2.25	0.70
1:B:361:ASP:OD1	1:B:363:SER:N	2.21	0.70
1:C:722:GLU:OE1	1:C:1061:HIS:NE2	2.25	0.70
1:B:717:ILE:HD12	1:B:920:ILE:HG23	1.74	0.69
3:J:205:HIS:O	3:J:209:ASN:N	2.26	0.69
1:B:106:PHE:HB3	1:B:235:ILE:HD13	1.77	0.66
1:C:329:ILE:HD11	1:C:358:CYS:N	2.10	0.66
3:H:126:VAL:O	3:H:214:LYS:NZ	2.29	0.65
2:L:189:TYR:O	2:L:195:TYR:OH	2.14	0.65
1:B:278:GLU:N	1:B:278:GLU:OE1	2.30	0.65
1:C:717:ILE:HD12	1:C:920:ILE:HG23	1.79	0.65
2:K:91:GLN:OE1	2:K:100:THR:N	2.30	0.65
1:B:193:VAL:HG23	1:B:223:LEU:HD22	1.79	0.65
1:C:1025:LYS:NZ	1:C:1039:PHE:O	2.29	0.65
2:F:111:ARG:NH1	2:F:112:THR:OG1	2.30	0.64
1:B:382:THR:OG1	1:C:982:ASP:OD1	2.15	0.64
1:C:575:ASP:OD2	1:C:578:THR:N	2.31	0.63
1:C:284:ASP:OD1	1:C:285:ALA:N	2.30	0.63
1:B:81:ASN:O	1:B:239:GLN:NE2	2.31	0.63
1:B:490:GLN:OE1	1:B:491:SER:N	2.31	0.63
1:A:224:GLU:N	1:A:224:GLU:OE1	2.32	0.62
3:J:126:VAL:O	3:J:214:LYS:NZ	2.32	0.62
1:C:325:ARG:NH2	1:C:577:GLN:OE1	2.32	0.62
3:E:126:VAL:O	3:E:214:LYS:NZ	2.33	0.61
2:F:173:ASP:OD2	2:F:175:THR:OG1	2.12	0.61
1:A:400:ARG:NH1	1:A:402:ASP:OD2	2.35	0.60
1:A:455:LYS:NZ	1:A:471:GLN:O	2.35	0.59
3:H:33:VAL:HG22	3:H:52:ILE:HG12	1.84	0.59
3:E:176:GLN:OE1	3:E:182:SER:OG	2.21	0.58
1:C:108:THR:OG1	1:C:234:ASN:O	2.21	0.58
1:C:306:GLU:OE1	1:C:306:GLU:N	2.36	0.58
1:C:342:THR:HG21	2:K:53:SER:OG	2.02	0.58
1:A:325:ARG:NH2	1:A:577:GLN:OE1	2.36	0.58
3:H:23:LYS:NZ	3:H:76:THR:O	2.37	0.58
1:A:1025:LYS:NZ	1:A:1039:PHE:O	2.38	0.57
1:A:306:GLU:N	1:A:306:GLU:OE1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:146:GLU:OE1	2:F:146:GLU:N	2.37	0.57
1:C:361:ASP:OD1	1:C:363:SER:N	2.38	0.57
1:C:342:THR:HG22	2:K:54:SER:HB2	1.86	0.57
1:B:781:GLN:OE1	1:B:1027:SER:OG	2.22	0.56
1:B:540:PHE:CE2	1:B:573:VAL:HG21	2.41	0.56
1:C:723:ILE:HD13	1:C:942:LEU:HD13	1.88	0.56
2:K:173:ASP:OD2	2:K:175:THR:OG1	2.17	0.56
2:L:173:ASP:OD2	2:L:175:THR:OG1	2.19	0.55
3:J:110:GLN:OE1	3:J:110:GLN:N	2.38	0.55
1:B:119:ILE:HG23	1:B:128:ILE:HG12	1.88	0.55
3:J:35:THR:OG1	3:J:97:SER:OG	2.25	0.55
1:B:616:GLU:OE1	1:B:616:GLU:N	2.40	0.55
3:E:67:ARG:NH1	3:E:85:SER:O	2.40	0.55
1:B:332:LEU:HD13	3:E:52:ILE:HD13	1.88	0.54
1:B:819:LEU:HD22	1:B:942:LEU:HD11	1.89	0.54
1:A:419:ASN:OD1	1:A:451:ARG:N	2.37	0.54
1:C:723:ILE:HG12	1:C:1058:VAL:HG22	1.88	0.54
2:L:111:ARG:NH1	2:L:112:THR:OG1	2.41	0.54
2:K:126:GLU:OE1	3:J:214:LYS:NZ	2.39	0.54
3:J:176:GLN:OE1	3:J:182:SER:OG	2.25	0.54
3:E:103:ASP:N	3:E:103:ASP:OD1	2.40	0.54
2:K:111:ARG:NH1	2:K:112:THR:OG1	2.41	0.54
3:J:205:HIS:CG	3:J:208:SER:HG	2.24	0.54
1:B:306:GLU:OE1	1:B:306:GLU:N	2.40	0.53
3:E:110:GLN:N	3:E:110:GLN:OE1	2.40	0.53
2:F:62:ARG:NH2	2:F:83:ASP:OD1	2.40	0.53
3:E:39:GLN:NE2	3:E:43:GLN:O	2.39	0.53
1:B:608:LEU:HD22	1:B:663:ILE:HG23	1.90	0.53
1:B:767:ILE:HD11	1:B:1009:LEU:HD23	1.91	0.53
1:B:822:LYS:NZ	1:B:938:THR:O	2.36	0.53
1:A:1123:CYS:SG	1:A:1129:ILE:HD13	2.49	0.53
1:B:400:ARG:NH1	1:B:403:GLU:OE2	2.42	0.53
2:F:38:GLN:HB2	2:F:48:LEU:HD11	1.89	0.53
1:B:722:GLU:OE1	1:B:1061:HIS:NE2	2.35	0.53
1:A:712:PRO:HD3	1:B:891:LEU:HD13	1.90	0.52
1:B:724:LEU:HD11	1:B:1025:LYS:HD2	1.91	0.52
2:F:123:PRO:HD3	2:F:135:VAL:HG22	1.91	0.52
1:B:711:ILE:HD12	1:B:1093:VAL:HG11	1.90	0.52
1:B:342:THR:HG22	2:F:54:SER:HB2	1.92	0.52
3:J:204:ASN:OD1	3:J:211:LYS:NZ	2.39	0.52
3:H:205:HIS:O	3:H:209:ASN:N	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:595:ILE:HG23	1:B:661:ILE:HG21	1.92	0.52
2:K:91:GLN:NE2	2:K:98:MET:O	2.43	0.52
1:B:1025:LYS:NZ	1:B:1039:PHE:O	2.43	0.51
2:K:146:GLU:OE1	2:K:146:GLU:N	2.42	0.51
1:C:332:LEU:HD11	3:J:52:ILE:HD13	1.92	0.51
1:B:932:GLN:O	1:B:936:SER:N	2.42	0.51
1:C:400:ARG:NH1	1:C:402:ASP:OD2	2.43	0.51
1:C:1079:CYS:SG	1:C:1129:ILE:HD13	2.50	0.51
2:F:126:GLU:OE1	3:E:214:LYS:NZ	2.42	0.51
1:A:801:GLN:NE2	1:A:932:GLN:OE1	2.44	0.51
1:B:119:ILE:HG12	1:B:128:ILE:HG23	1.93	0.51
1:C:109:THR:OG1	1:C:111:ASP:OD1	2.27	0.51
2:K:91:GLN:CD	2:K:100:THR:HG1	2.15	0.51
1:B:27:ALA:HB3	1:B:64:TRP:HB3	1.93	0.50
1:A:1074:THR:OG1	1:A:1075:ALA:N	2.45	0.50
1:B:1090:GLY:O	1:B:1104:ARG:NH1	2.44	0.50
1:A:1138:LEU:HG	1:A:1142:LEU:HD13	1.94	0.50
2:K:111:ARG:NH1	2:K:112:THR:O	2.42	0.50
1:C:819:LEU:HD22	1:C:942:LEU:HD11	1.93	0.50
1:B:723:ILE:HG12	1:B:1058:VAL:HG22	1.94	0.50
1:B:801:GLN:OE1	1:B:932:GLN:NE2	2.43	0.50
1:C:711:ILE:HD12	1:C:1093:VAL:HG11	1.94	0.49
1:C:877:GLY:O	1:C:881:SER:OG	2.21	0.49
2:L:87:TYR:N	2:L:105:THR:O	2.40	0.49
2:F:138:LEU:HD22	3:E:186:VAL:HG21	1.95	0.49
2:F:103:GLN:OE1	2:F:103:GLN:N	2.41	0.49
1:B:356:SER:HA	1:B:521:VAL:HG23	1.95	0.49
1:C:714:ASN:OD1	1:C:715:PHE:N	2.46	0.49
1:A:608:LEU:HD22	1:A:663:ILE:HG23	1.95	0.49
1:B:170:TYR:HE2	1:B:172:SER:HG	1.61	0.49
3:E:33:VAL:HG13	3:E:52:ILE:HG12	1.94	0.48
1:C:81:ASN:ND2	1:C:239:GLN:OE1	2.41	0.48
1:C:1074:THR:OG1	1:C:1075:ALA:N	2.46	0.48
2:F:16:GLY:N	2:F:79:LEU:O	2.40	0.48
3:E:4:LEU:HD13	3:E:22:CYS:SG	2.53	0.48
2:L:62:ARG:NE	2:L:83:ASP:OD2	2.47	0.48
3:J:152:PRO:O	3:J:205:HIS:NE2	2.39	0.48
1:A:284:ASP:OD1	1:A:285:ALA:N	2.46	0.48
1:C:653:VAL:HG12	1:C:655:ASN:H	1.79	0.48
1:B:342:THR:HG21	2:F:53:SER:HB3	1.96	0.47
2:L:111:ARG:NH1	2:L:112:THR:O	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:506:ARG:HH12	4:D:1:NAG:H81	1.79	0.47
1:C:470:TYR:N	1:C:486:TYR:O	2.43	0.47
2:L:146:GLU:OE1	2:L:146:GLU:N	2.44	0.47
2:K:34:LEU:HD12	2:K:90:GLN:O	2.15	0.47
1:A:641:GLN:NE2	1:A:642:THR:O	2.43	0.47
1:A:795:GLY:O	1:A:917:GLN:NE2	2.44	0.47
1:C:33:THR:OG1	1:C:219:GLY:O	2.31	0.47
3:H:87:ARG:N	3:H:90:ASP:OD2	2.42	0.47
2:F:34:LEU:HB3	2:F:52:ALA:HB2	1.96	0.47
1:A:875:LEU:HD21	1:A:1049:PHE:HB3	1.97	0.47
1:A:898:GLN:O	1:A:902:ARG:HG2	2.15	0.47
1:A:962:GLN:OE1	1:B:755:SER:OG	2.28	0.47
1:A:1028:GLU:OE2	1:C:1036:ARG:NH2	2.47	0.47
3:E:18:VAL:HG12	3:E:86:LEU:HD21	1.96	0.47
3:J:4:LEU:HD13	3:J:22:CYS:SG	2.55	0.47
2:L:62:ARG:NH2	2:L:83:ASP:OD1	2.45	0.47
1:C:906:ILE:HD13	1:C:1046:LEU:HD21	1.97	0.46
1:A:117:LEU:HD22	1:A:231:ILE:HD13	1.97	0.46
1:C:713:THR:HG22	1:C:1107:TYR:HB3	1.97	0.46
1:B:560:GLN:O	1:B:561:GLN:NE2	2.49	0.46
1:B:1088:ARG:NH1	1:B:1115:ASP:O	2.46	0.46
1:A:29:THR:HG22	1:A:30:ASN:N	2.30	0.46
1:A:382:THR:O	1:A:385:ASN:ND2	2.46	0.46
1:B:1115:ASP:OD1	1:B:1115:ASP:N	2.48	0.46
2:F:55:ARG:NE	2:F:63:PHE:O	2.49	0.46
1:A:1132:ASN:OD1	1:A:1133:THR:N	2.49	0.46
1:A:724:LEU:HD11	1:A:1025:LYS:HD2	1.98	0.45
1:C:595:ILE:HG23	1:C:661:ILE:HG21	1.98	0.45
1:C:663:ILE:HD11	1:C:669:ALA:HB2	1.99	0.45
1:C:292:PRO:HB2	1:C:605:VAL:HG21	1.98	0.45
1:C:1069:GLU:N	1:C:1069:GLU:OE1	2.49	0.45
1:A:706:ASN:OD1	1:A:706:ASN:N	2.47	0.45
1:C:909:THR:OG1	1:C:1103:GLN:NE2	2.49	0.45
1:A:712:PRO:HA	1:A:1069:GLU:HA	1.99	0.45
1:A:801:GLN:OE1	5:M:1:NAG:O6	2.32	0.45
1:B:718:SER:OG	1:B:1063:THR:OG1	2.34	0.45
2:L:154:ASP:OD2	2:L:192:HIS:ND1	2.49	0.45
3:E:205:HIS:CG	3:E:208:SER:HG	2.28	0.45
1:A:1088:ARG:NE	1:A:1115:ASP:O	2.38	0.45
1:C:583:ASP:OD1	1:C:584:ILE:N	2.49	0.45
2:K:16:GLY:N	2:K:79:LEU:O	2.38	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:201:PHE:HE2	1:B:203:ILE:HD11	1.82	0.45
1:B:942:LEU:HD12	1:B:945:LEU:HD12	1.99	0.45
1:B:210:ILE:HG21	1:B:217:PRO:HG2	1.97	0.45
1:C:291:ASP:N	1:C:291:ASP:OD1	2.49	0.45
1:C:475:THR:HG23	3:H:23:LYS:HE2	1.99	0.45
1:A:273:LEU:HD22	1:A:298:CYS:HA	2.00	0.44
1:A:565:ASP:OD1	1:A:566:ILE:N	2.44	0.44
1:B:1079:CYS:SG	1:B:1129:ILE:HD13	2.58	0.44
2:F:136:VAL:HG21	3:E:129:LEU:HD13	1.99	0.44
1:C:608:LEU:HD22	1:C:663:ILE:HG23	1.99	0.44
2:L:139:LEU:HD12	2:L:139:LEU:N	2.32	0.44
2:F:34:LEU:O	2:F:52:ALA:N	2.51	0.44
3:E:6:GLN:OE1	3:E:111:GLY:N	2.44	0.44
2:K:139:LEU:N	2:K:139:LEU:HD12	2.33	0.44
1:B:385:ASN:O	1:B:523:GLY:HA3	2.18	0.44
1:B:1138:LEU:HG	1:B:1142:LEU:HD13	1.99	0.44
1:C:455:LYS:NZ	1:C:471:GLN:O	2.51	0.44
1:C:726:VAL:HG13	1:C:778:VAL:HG21	2.00	0.44
2:L:161:ASN:HD22	2:L:184:LEU:HD21	1.83	0.44
1:A:445:ASN:N	1:A:493:GLY:O	2.50	0.44
1:A:913:LEU:C	1:A:913:LEU:HD13	2.38	0.44
1:C:329:ILE:HD11	1:C:357:ASN:C	2.38	0.44
2:K:55:ARG:NE	2:K:63:PHE:O	2.51	0.44
1:B:464:ASP:OD1	1:B:465:ILE:N	2.51	0.44
1:B:609:TYR:HE2	1:B:648:ILE:HD12	1.83	0.44
3:E:4:LEU:HD21	3:E:98:ARG:HG2	1.99	0.44
3:H:91:THR:HG23	3:H:115:THR:HA	1.99	0.43
3:E:91:THR:HG23	3:E:115:THR:HA	1.99	0.43
3:E:143:LEU:HB2	3:E:216:VAL:HG11	2.00	0.43
1:B:390:THR:O	1:B:520:THR:OG1	2.36	0.43
1:B:1124:ASP:N	1:B:1124:ASP:OD1	2.50	0.43
1:A:365:LEU:HD11	3:H:102:TRP:CZ3	2.53	0.43
3:E:18:VAL:HB	3:E:86:LEU:HD11	2.01	0.43
2:K:156:ALA:O	2:K:158:GLN:NE2	2.51	0.43
1:B:333:CYS:SG	1:B:360:ALA:HB2	2.59	0.43
1:B:898:GLN:O	1:B:902:ARG:HG2	2.19	0.43
2:K:136:VAL:HG21	3:J:129:LEU:HD13	2.00	0.43
1:B:723:ILE:HD13	1:B:942:LEU:HD13	2.00	0.43
1:A:1036:ARG:NH2	1:B:1028:GLU:OE2	2.50	0.43
1:C:119:ILE:HG23	1:C:128:ILE:HG12	2.01	0.43
2:L:177:SER:HG	3:H:169:HIS:CE1	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:452:LEU:N	1:A:488:PRO:O	2.44	0.42
1:A:746:CYS:SG	1:A:974:LEU:HD21	2.59	0.42
3:E:204:ASN:OD1	3:E:211:LYS:NZ	2.42	0.42
3:J:143:LEU:HB2	3:J:216:VAL:HG11	2.01	0.42
1:A:713:THR:N	1:A:1068:GLN:O	2.42	0.42
1:A:767:ILE:HD11	1:A:1009:LEU:HD23	2.00	0.42
1:C:270:ARG:NH1	1:C:287:ASP:OD2	2.52	0.42
2:F:111:ARG:NH1	2:F:112:THR:O	2.44	0.42
1:C:543:LEU:HD21	1:C:570:THR:HG21	2.01	0.42
1:C:228:ASP:OD1	1:C:228:ASP:N	2.53	0.42
2:L:34:LEU:HD12	2:L:90:GLN:O	2.19	0.42
3:J:67:ARG:NH1	3:J:85:SER:O	2.51	0.42
1:B:323:ILE:O	1:B:539:ASN:N	2.53	0.42
1:C:90:VAL:HG11	1:C:238:PHE:CZ	2.53	0.42
2:K:123:PRO:HD3	2:K:135:VAL:HG22	2.02	0.42
1:C:983:PRO:N	1:C:984:PRO:CD	2.83	0.42
1:A:799:PHE:CD1	1:A:802:ILE:HD11	2.46	0.42
1:A:983:PRO:N	1:A:984:PRO:CD	2.83	0.42
1:C:196:ASN:HD21	1:C:235:ILE:HD12	1.84	0.42
1:A:421:LYS:NZ	1:A:422:LEU:O	2.53	0.42
1:C:117:LEU:HD11	1:C:128:ILE:HG23	2.01	0.42
2:F:196:ALA:HB2	2:F:211:SER:CB	2.50	0.42
1:C:277:ASN:ND2	7:C:1302:NAG:H81	2.35	0.42
1:C:439:ASP:OD2	1:C:506:ARG:NE	2.46	0.42
3:H:143:LEU:HB2	3:H:216:VAL:HG11	2.02	0.42
3:J:18:VAL:HG12	3:J:86:LEU:HD21	2.01	0.42
3:E:142:ALA:HB2	3:E:188:THR:HG22	2.02	0.41
1:B:730:LYS:HE3	1:B:768:ALA:HB1	2.02	0.41
2:K:196:ALA:HB2	2:K:211:SER:CB	2.50	0.41
1:C:514:LEU:HD23	1:C:514:LEU:O	2.19	0.41
1:C:578:THR:O	1:C:580:GLU:N	2.51	0.41
3:J:33:VAL:HG22	3:J:52:ILE:HG12	2.02	0.41
1:B:540:PHE:CD2	1:B:573:VAL:HG21	2.54	0.41
3:E:152:PRO:O	3:E:205:HIS:NE2	2.42	0.41
1:A:454:ARG:NH1	1:A:456:SER:O	2.43	0.41
1:A:666:GLY:N	1:B:861:LEU:O	2.52	0.41
1:A:813:SER:N	1:A:816:GLU:OE1	2.44	0.41
2:L:16:GLY:N	2:L:79:LEU:O	2.41	0.41
1:A:105:ILE:HG13	1:A:241:LEU:HD11	2.02	0.41
1:A:1036:ARG:NE	1:B:1028:GLU:OE2	2.52	0.41
1:A:1122:ASN:ND2	1:A:1124:ASP:OD2	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:357:ASN:H	1:B:520:THR:HB	1.84	0.41
2:L:154:ASP:CG	2:L:192:HIS:HD1	2.24	0.41
1:A:31:SER:HB3	1:A:62:VAL:HG13	2.03	0.41
1:B:767:ILE:HD11	1:B:1009:LEU:HA	2.03	0.41
2:K:177:SER:HG	3:J:169:HIS:CE1	2.38	0.41
1:C:1113:THR:HA	1:C:1135:TYR:O	2.21	0.41
3:E:164:LEU:HD21	3:E:187:VAL:HG21	2.02	0.41
1:A:342:THR:O	1:A:506:ARG:NH2	2.53	0.41
1:B:721:THR:HG23	1:B:1058:VAL:HG13	2.01	0.41
1:C:36:VAL:HG21	1:C:220:PHE:CZ	2.56	0.41
1:C:324:VAL:HG21	1:C:525:LYS:HE2	2.03	0.41
1:C:721:THR:HG23	1:C:1058:VAL:HG13	2.03	0.41
2:L:18:ARG:HA	2:L:76:ILE:O	2.21	0.41
2:L:47:LEU:HD21	2:L:50:TYR:HB3	2.02	0.41
2:K:189:TYR:O	2:K:195:TYR:OH	2.36	0.41
1:A:583:ASP:OD1	1:A:584:ILE:N	2.54	0.41
1:C:330:THR:HA	3:J:55:PHE:CE1	2.56	0.41
2:L:34:LEU:HB3	2:L:52:ALA:HB2	2.02	0.41
2:K:38:GLN:HB2	2:K:48:LEU:HD11	2.03	0.41
3:J:91:THR:HA	3:J:114:VAL:O	2.21	0.41
1:A:200:TYR:OH	1:C:513:GLU:OE1	2.36	0.40
1:B:700:ASN:OD1	1:B:701:SER:N	2.54	0.40
1:C:106:PHE:HB3	1:C:235:ILE:HD13	2.03	0.40
1:B:333:CYS:N	3:E:101:GLN:OE1	2.54	0.40
2:L:196:ALA:HB2	2:L:211:SER:CB	2.52	0.40
2:F:47:LEU:HD11	2:F:49:ILE:O	2.21	0.40
1:A:332:LEU:HD13	3:H:52:ILE:HD13	2.04	0.40
1:B:596:THR:O	1:B:596:THR:HG23	2.22	0.40
2:F:139:LEU:N	2:F:139:LEU:HD12	2.37	0.40
2:F:156:ALA:O	2:F:158:GLN:NE2	2.47	0.40
2:F:173:ASP:OD1	2:F:173:ASP:N	2.48	0.40
3:E:144:GLY:HA3	3:E:186:VAL:HG12	2.02	0.40
2:K:34:LEU:HB3	2:K:52:ALA:HB2	2.02	0.40
2:K:170:ASP:OD1	2:K:171:SER:N	2.55	0.40
1:A:537:ASN:OD1	1:A:546:THR:OG1	2.39	0.40
1:B:593:SER:OG	1:B:610:GLN:NE2	2.53	0.40
1:B:983:PRO:N	1:B:984:PRO:CD	2.84	0.40
1:A:376:CYS:HA	1:A:429:CYS:HA	2.03	0.40
1:A:724:LEU:HD12	1:A:1059:PHE:HE2	1.86	0.40
1:B:115:GLN:OE1	1:B:115:GLN:N	2.49	0.40

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	993/1285 (77%)	951 (96%)	42 (4%)	0	100	100
1	B	989/1285 (77%)	942 (95%)	47 (5%)	0	100	100
1	C	998/1285 (78%)	948 (95%)	50 (5%)	0	100	100
2	F	216/217 (100%)	214 (99%)	2 (1%)	0	100	100
2	K	216/217 (100%)	209 (97%)	7 (3%)	0	100	100
2	L	216/217 (100%)	212 (98%)	4 (2%)	0	100	100
3	E	208/223 (93%)	203 (98%)	5 (2%)	0	100	100
3	H	208/223 (93%)	204 (98%)	4 (2%)	0	100	100
3	J	208/223 (93%)	202 (97%)	6 (3%)	0	100	100
All	All	4252/5175 (82%)	4085 (96%)	167 (4%)	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	883/1109 (80%)	879 (100%)	4 (0%)	86	93
1	B	879/1109 (79%)	876 (100%)	3 (0%)	91	96
1	C	888/1109 (80%)	887 (100%)	1 (0%)	92	97
2	F	188/188 (100%)	187 (100%)	1 (0%)	86	93
2	K	188/188 (100%)	187 (100%)	1 (0%)	86	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	L	188/188 (100%)	187 (100%)	1 (0%)	86	93
3	E	177/190 (93%)	175 (99%)	2 (1%)	70	83
3	H	177/190 (93%)	175 (99%)	2 (1%)	70	83
3	J	177/190 (93%)	176 (99%)	1 (1%)	84	92
All	All	3745/4461 (84%)	3729 (100%)	16 (0%)	88	95

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	238	PHE
1	A	756	PHE
1	A	852	PHE
1	A	883	TRP
1	B	207	HIS
1	B	814	PHE
1	B	875	LEU
1	C	756	PHE
2	L	91	GLN
3	H	98	ARG
3	H	104	LEU
2	F	91	GLN
3	E	95	TYR
3	E	98	ARG
2	K	91	GLN
3	J	98	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	H	176	GLN

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 ⓘ

39 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	D	1	4,1	14,14,15	0.34	0	17,19,21	0.50	0
4	NAG	D	2	4	14,14,15	0.22	0	17,19,21	0.46	0
4	FUC	D	3	4	10,10,11	0.81	0	14,14,16	0.80	0
5	NAG	G	1	5,1	14,14,15	0.19	0	17,19,21	0.37	0
5	NAG	G	2	5	14,14,15	0.20	0	17,19,21	0.41	0
5	NAG	I	1	5,1	14,14,15	0.25	0	17,19,21	0.39	0
5	NAG	I	2	5	14,14,15	0.18	0	17,19,21	0.42	0
5	NAG	M	1	5,1	14,14,15	0.20	0	17,19,21	0.42	0
5	NAG	M	2	5	14,14,15	0.19	0	17,19,21	0.40	0
5	NAG	N	1	5,1	14,14,15	0.25	0	17,19,21	0.41	0
5	NAG	N	2	5	14,14,15	0.20	0	17,19,21	0.40	0
5	NAG	O	1	5,1	14,14,15	0.18	0	17,19,21	0.41	0
5	NAG	O	2	5	14,14,15	0.19	0	17,19,21	0.40	0
6	NAG	P	1	6,1	14,14,15	0.29	0	17,19,21	0.70	1 (5%)
6	NAG	P	2	6	14,14,15	0.24	0	17,19,21	0.43	0
6	BMA	P	3	6	11,11,12	0.55	0	15,15,17	0.79	0
6	FUC	P	4	6	10,10,11	0.80	0	14,14,16	0.74	0
5	NAG	Q	1	5,1	14,14,15	0.21	0	17,19,21	0.40	0
5	NAG	Q	2	5	14,14,15	0.18	0	17,19,21	0.44	0
5	NAG	R	1	5,1	14,14,15	0.22	0	17,19,21	0.42	0
5	NAG	R	2	5	14,14,15	0.19	0	17,19,21	0.43	0
5	NAG	S	1	5,1	14,14,15	0.28	0	17,19,21	0.38	0
5	NAG	S	2	5	14,14,15	0.19	0	17,19,21	0.41	0
5	NAG	T	1	5,1	14,14,15	0.25	0	17,19,21	0.41	0
5	NAG	T	2	5	14,14,15	0.20	0	17,19,21	0.40	0
5	NAG	U	1	5,1	14,14,15	0.19	0	17,19,21	0.48	0
5	NAG	U	2	5	14,14,15	0.18	0	17,19,21	0.42	0
6	NAG	V	1	6,1	14,14,15	0.22	0	17,19,21	0.53	0
6	NAG	V	2	6	14,14,15	0.21	0	17,19,21	0.39	0
6	BMA	V	3	6	11,11,12	0.51	0	15,15,17	0.84	0
6	FUC	V	4	6	10,10,11	0.67	0	14,14,16	0.78	0
5	NAG	W	1	5,1	14,14,15	0.22	0	17,19,21	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	W	2	5	14,14,15	0.19	0	17,19,21	0.41	0
5	NAG	X	1	5,1	14,14,15	0.33	0	17,19,21	0.37	0
5	NAG	X	2	5	14,14,15	0.18	0	17,19,21	0.42	0
5	NAG	Y	1	5,1	14,14,15	0.23	0	17,19,21	0.45	0
5	NAG	Y	2	5	14,14,15	0.21	0	17,19,21	0.40	0
5	NAG	Z	1	5,1	14,14,15	0.24	0	17,19,21	0.40	0
5	NAG	Z	2	5	14,14,15	0.19	0	17,19,21	0.40	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	D	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1
4	FUC	D	3	4	-	-	0/1/1/1
5	NAG	G	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	G	2	5	-	1/6/23/26	0/1/1/1
5	NAG	I	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	I	2	5	-	2/6/23/26	0/1/1/1
5	NAG	M	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	M	2	5	-	2/6/23/26	0/1/1/1
5	NAG	N	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	N	2	5	-	2/6/23/26	0/1/1/1
5	NAG	O	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	O	2	5	-	2/6/23/26	0/1/1/1
6	NAG	P	1	6,1	-	2/6/23/26	0/1/1/1
6	NAG	P	2	6	-	1/6/23/26	0/1/1/1
6	BMA	P	3	6	-	0/2/19/22	0/1/1/1
6	FUC	P	4	6	-	-	0/1/1/1
5	NAG	Q	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	Q	2	5	-	2/6/23/26	0/1/1/1
5	NAG	R	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	R	2	5	-	2/6/23/26	0/1/1/1
5	NAG	S	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	S	2	5	-	2/6/23/26	0/1/1/1
5	NAG	T	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	T	2	5	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	U	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	U	2	5	-	2/6/23/26	0/1/1/1
6	NAG	V	1	6,1	-	2/6/23/26	0/1/1/1
6	NAG	V	2	6	-	2/6/23/26	0/1/1/1
6	BMA	V	3	6	-	0/2/19/22	0/1/1/1
6	FUC	V	4	6	-	-	0/1/1/1
5	NAG	W	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	W	2	5	-	2/6/23/26	0/1/1/1
5	NAG	X	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	X	2	5	-	1/6/23/26	0/1/1/1
5	NAG	Y	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	Y	2	5	-	2/6/23/26	0/1/1/1
5	NAG	Z	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	Z	2	5	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	P	1	NAG	C1-O5-C5	2.40	115.44	112.19

There are no chirality outliers.

All (55) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	O	2	NAG	C4-C5-C6-O6
5	S	2	NAG	O5-C5-C6-O6
5	T	2	NAG	O5-C5-C6-O6
5	Z	1	NAG	O5-C5-C6-O6
5	O	2	NAG	O5-C5-C6-O6
5	N	2	NAG	C4-C5-C6-O6
5	Y	1	NAG	C4-C5-C6-O6
6	V	1	NAG	O5-C5-C6-O6
5	S	1	NAG	O5-C5-C6-O6
5	Z	1	NAG	C4-C5-C6-O6
5	O	1	NAG	O5-C5-C6-O6
5	T	2	NAG	C4-C5-C6-O6
5	U	2	NAG	O5-C5-C6-O6
5	W	2	NAG	O5-C5-C6-O6

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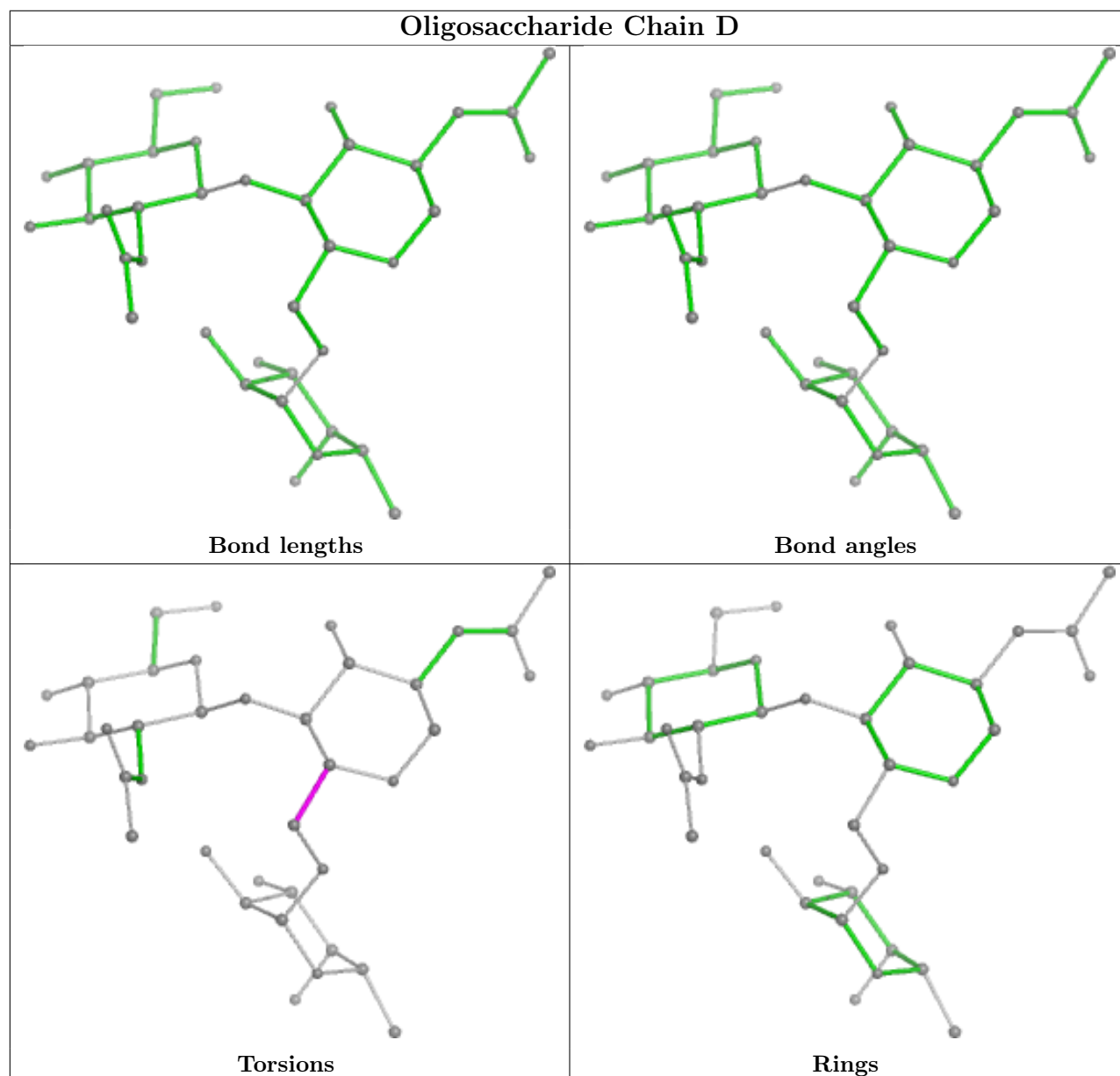
Mol	Chain	Res	Type	Atoms
5	N	2	NAG	O5-C5-C6-O6
5	X	1	NAG	O5-C5-C6-O6
5	S	2	NAG	C4-C5-C6-O6
5	S	1	NAG	C4-C5-C6-O6
5	O	1	NAG	C4-C5-C6-O6
5	W	2	NAG	C4-C5-C6-O6
6	V	1	NAG	C4-C5-C6-O6
5	U	2	NAG	C4-C5-C6-O6
5	Y	1	NAG	O5-C5-C6-O6
4	D	1	NAG	O5-C5-C6-O6
5	X	1	NAG	C4-C5-C6-O6
5	U	1	NAG	O5-C5-C6-O6
6	P	1	NAG	O5-C5-C6-O6
6	V	2	NAG	O5-C5-C6-O6
4	D	1	NAG	C4-C5-C6-O6
5	U	1	NAG	C4-C5-C6-O6
6	P	1	NAG	C4-C5-C6-O6
5	Y	2	NAG	C4-C5-C6-O6
5	M	2	NAG	O5-C5-C6-O6
5	N	1	NAG	O5-C5-C6-O6
5	M	2	NAG	C4-C5-C6-O6
5	N	1	NAG	C4-C5-C6-O6
5	M	1	NAG	C4-C5-C6-O6
5	X	2	NAG	O5-C5-C6-O6
6	P	2	NAG	O5-C5-C6-O6
5	Y	2	NAG	O5-C5-C6-O6
5	G	1	NAG	C4-C5-C6-O6
5	Q	2	NAG	C4-C5-C6-O6
5	M	1	NAG	O5-C5-C6-O6
5	Q	2	NAG	O5-C5-C6-O6
6	V	2	NAG	C4-C5-C6-O6
5	I	2	NAG	C4-C5-C6-O6
5	G	1	NAG	O5-C5-C6-O6
5	G	2	NAG	O5-C5-C6-O6
5	R	2	NAG	C4-C5-C6-O6
5	Q	1	NAG	C3-C2-N2-C7
5	T	1	NAG	C4-C5-C6-O6
5	I	2	NAG	O5-C5-C6-O6
5	Q	1	NAG	C1-C2-N2-C7
5	R	2	NAG	O5-C5-C6-O6
5	W	1	NAG	C4-C5-C6-O6

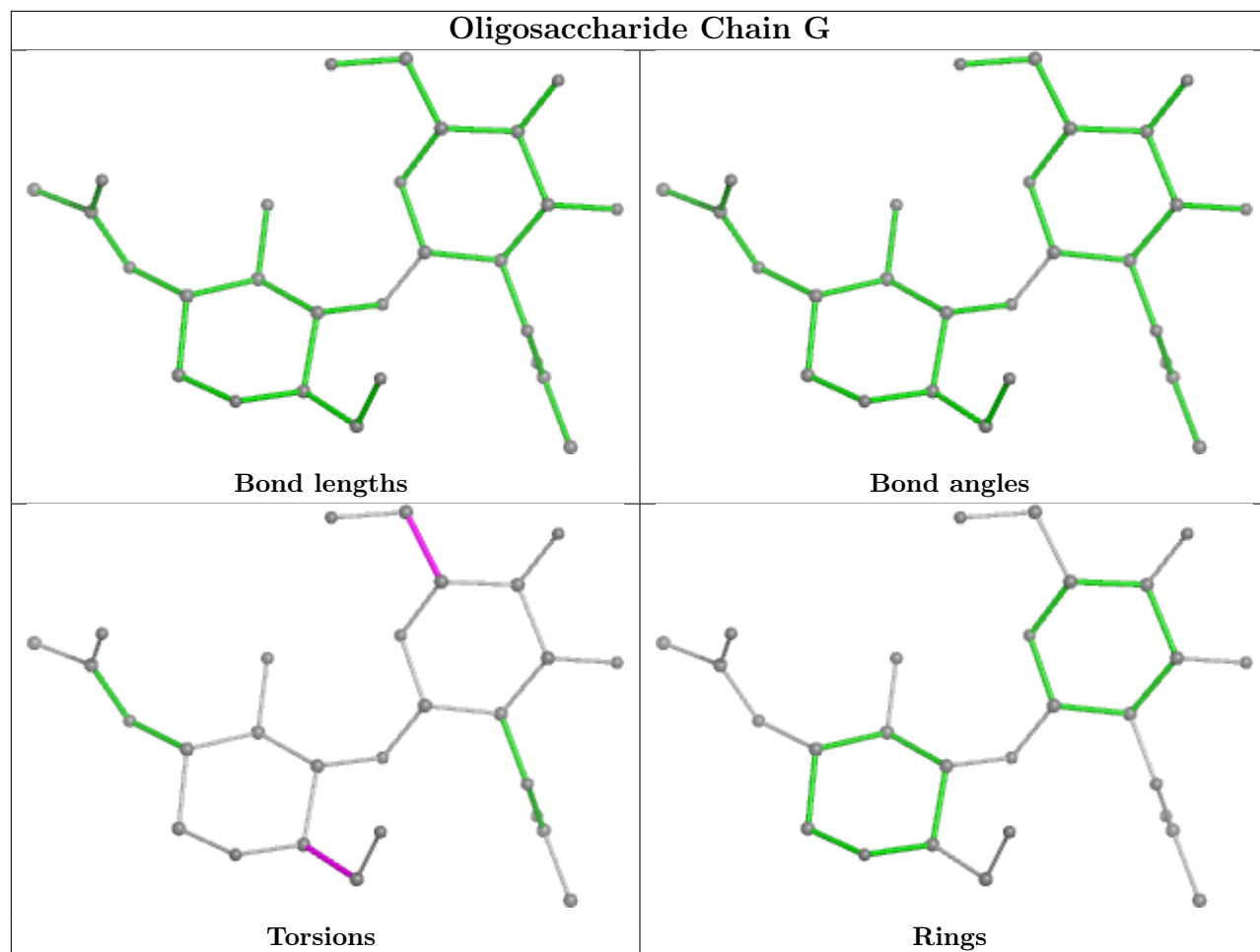
There are no ring outliers.

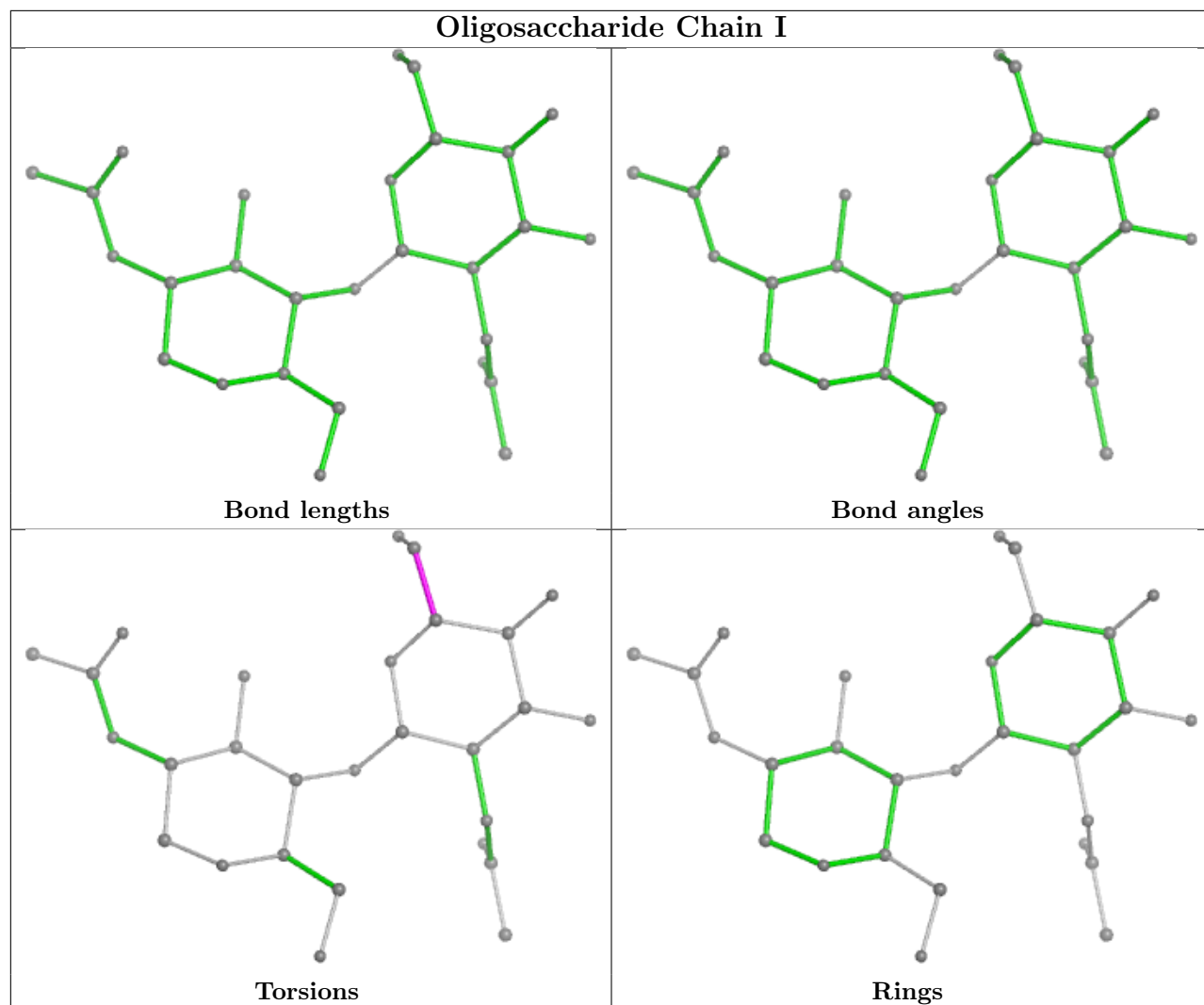
2 monomers are involved in 2 short contacts:

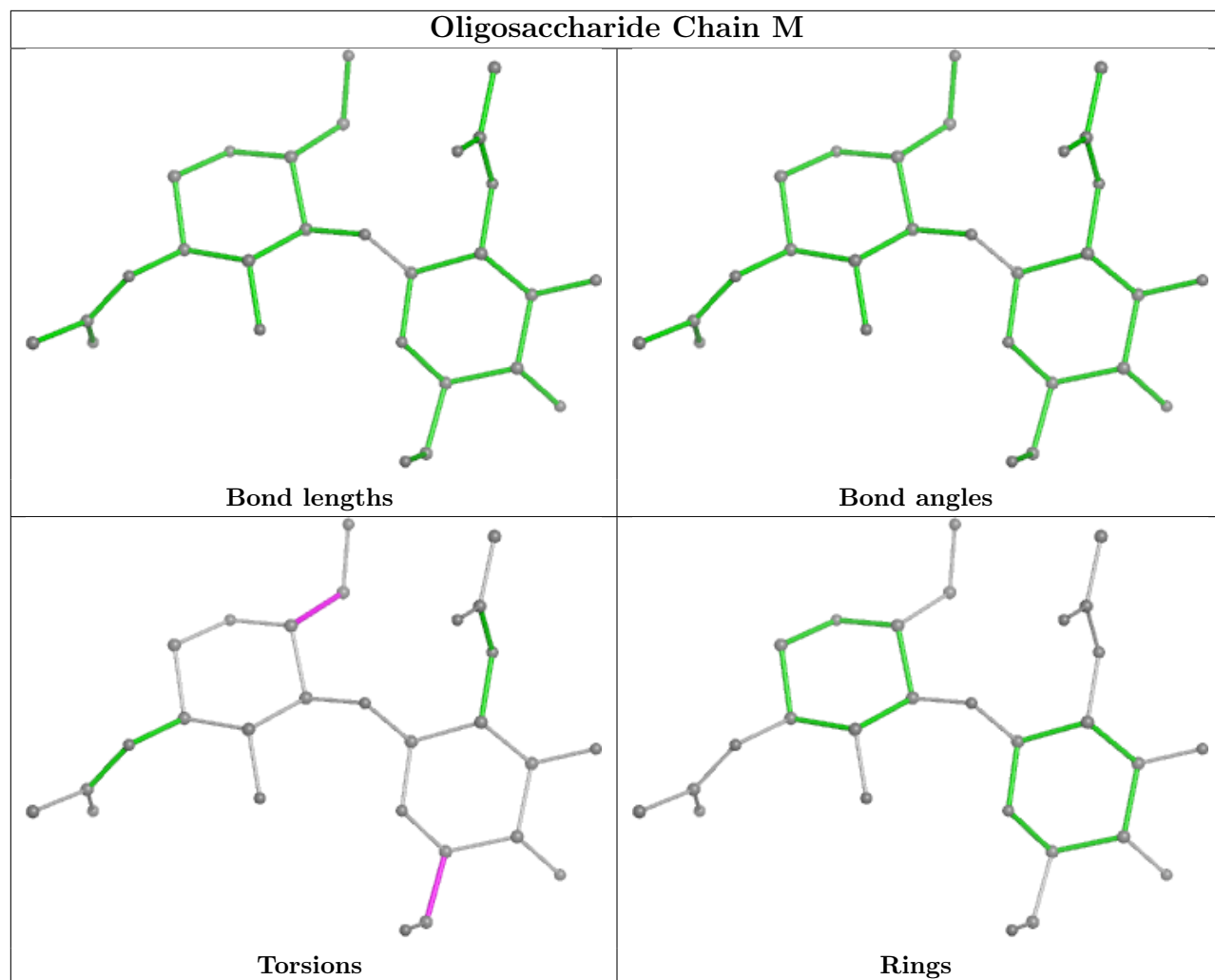
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	1	NAG	1	0
5	M	1	NAG	1	0

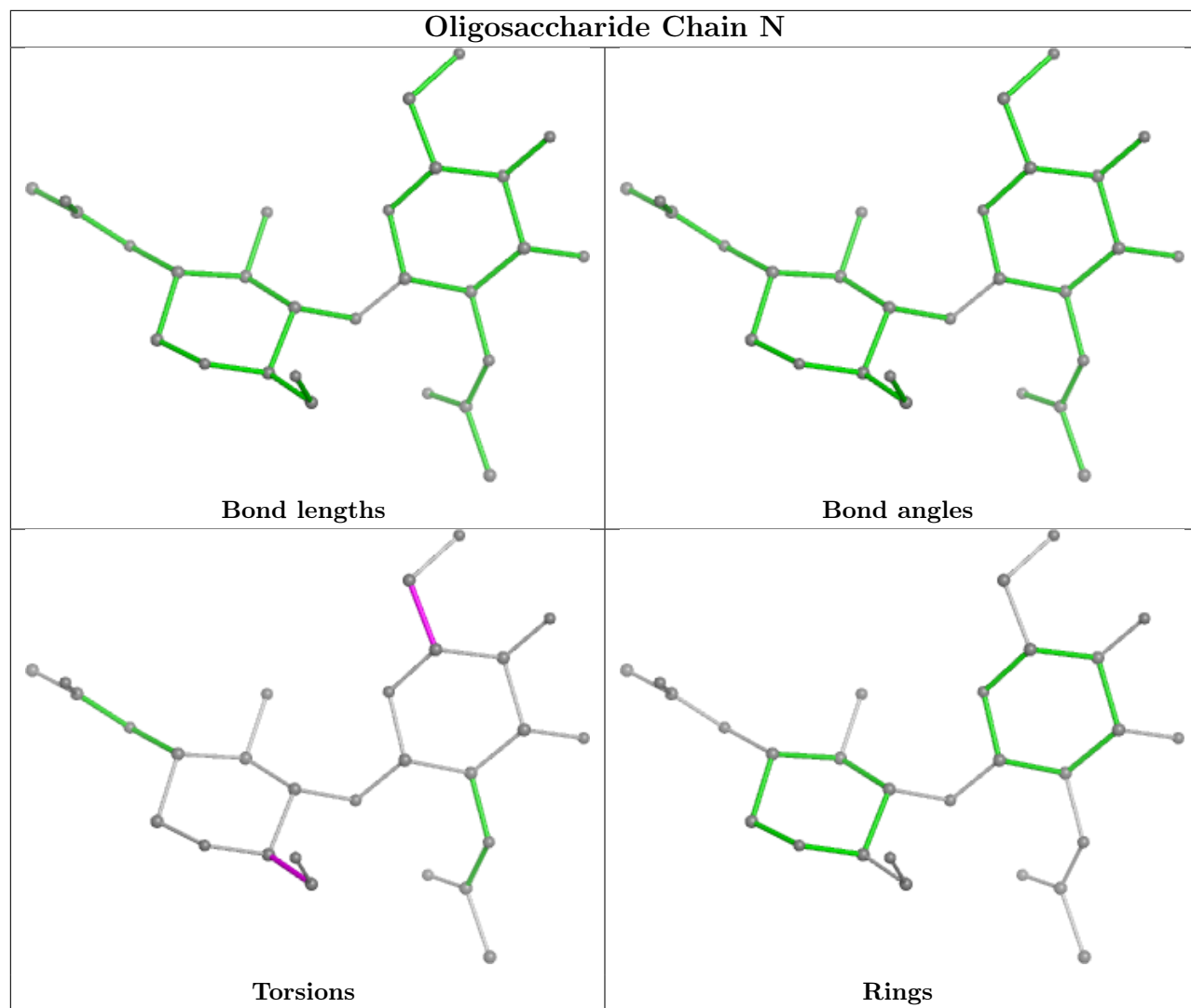
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

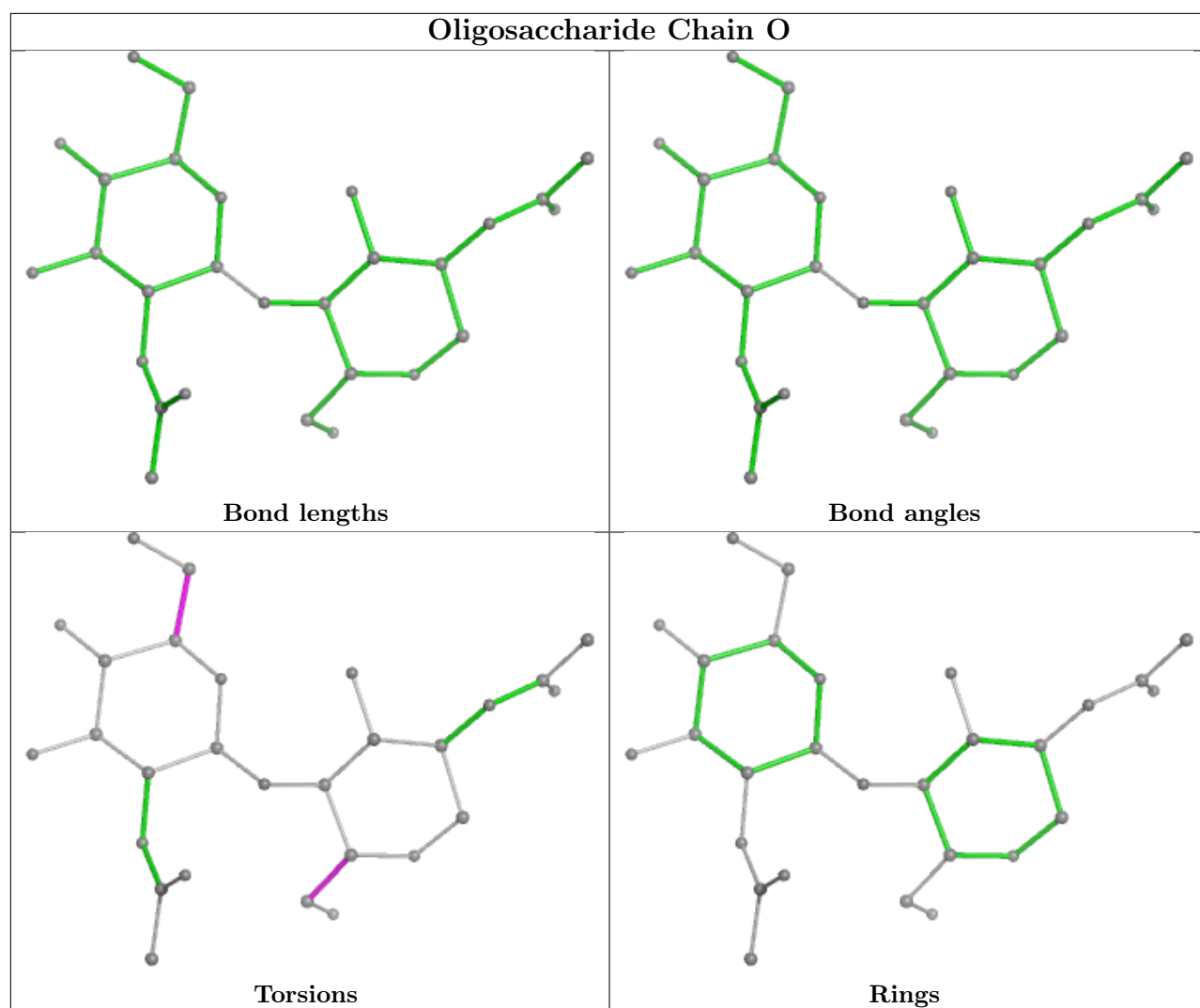


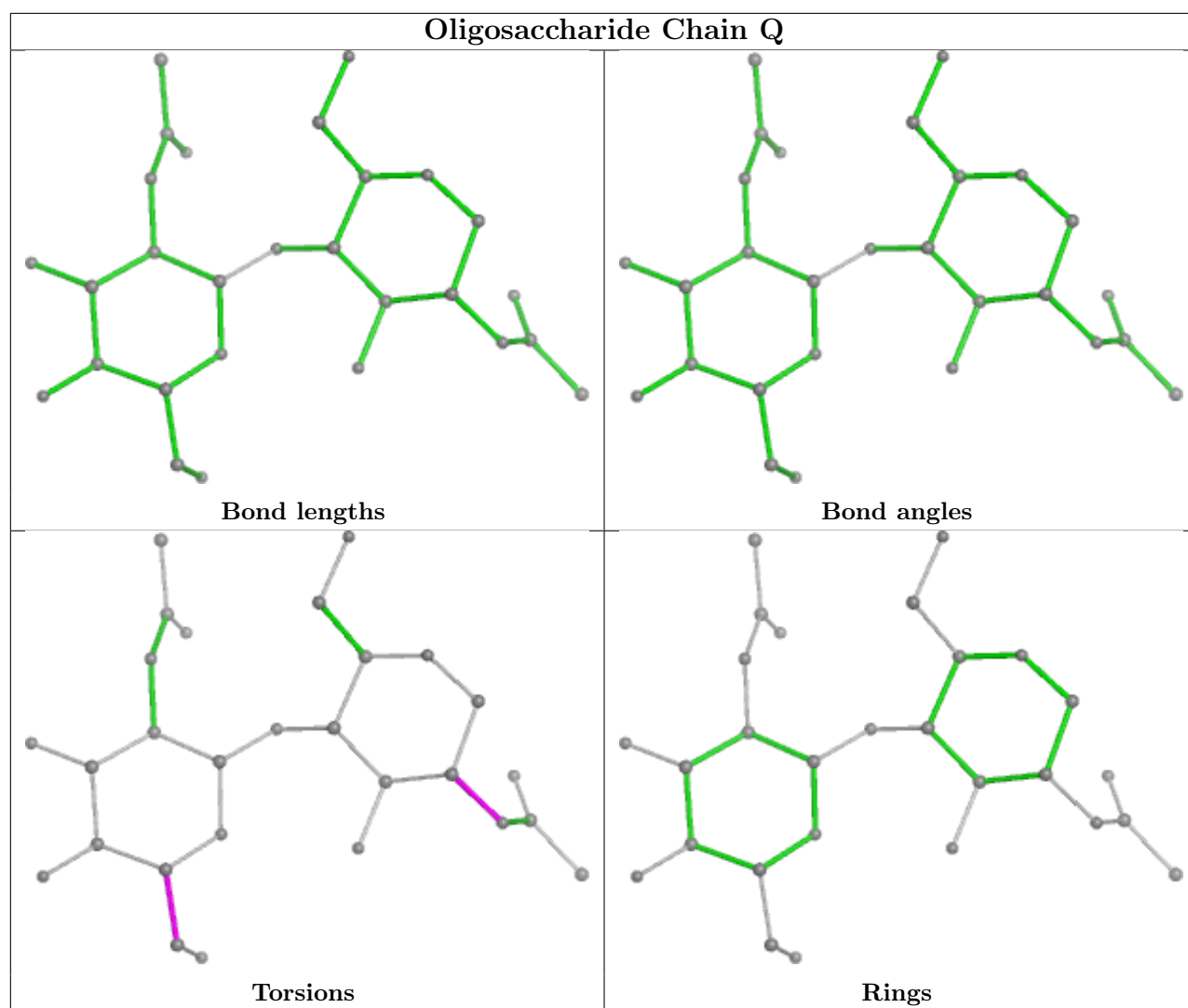


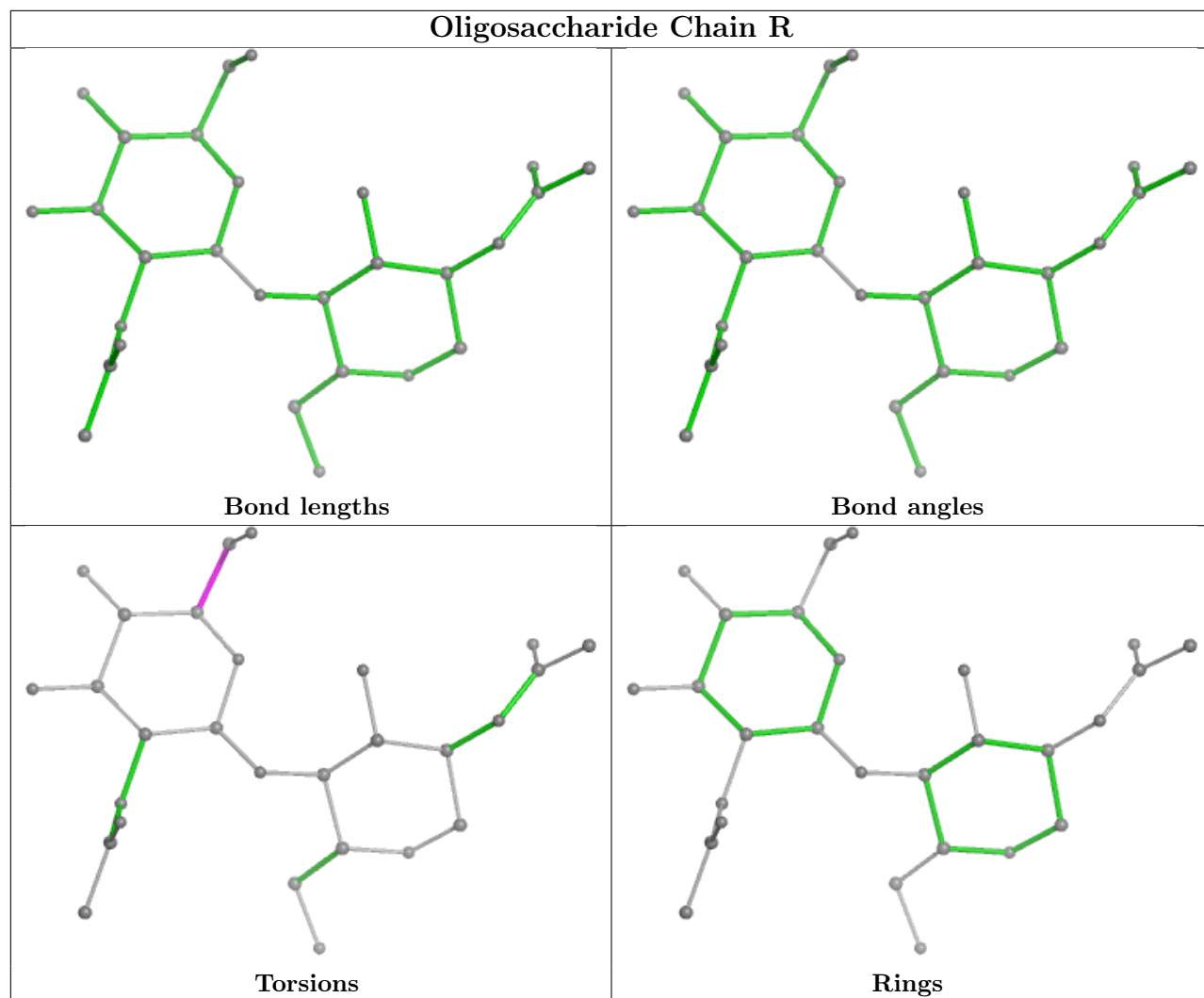


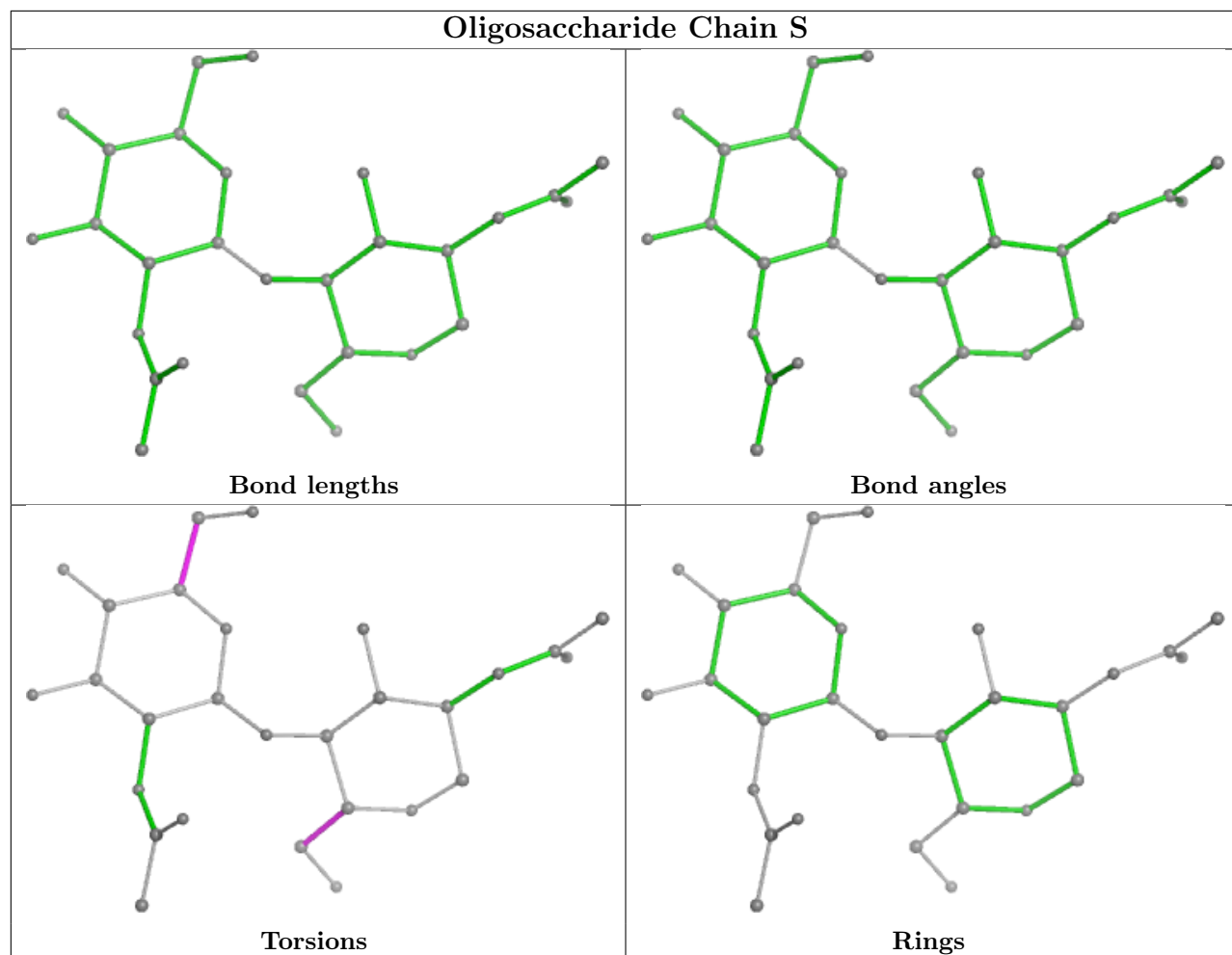


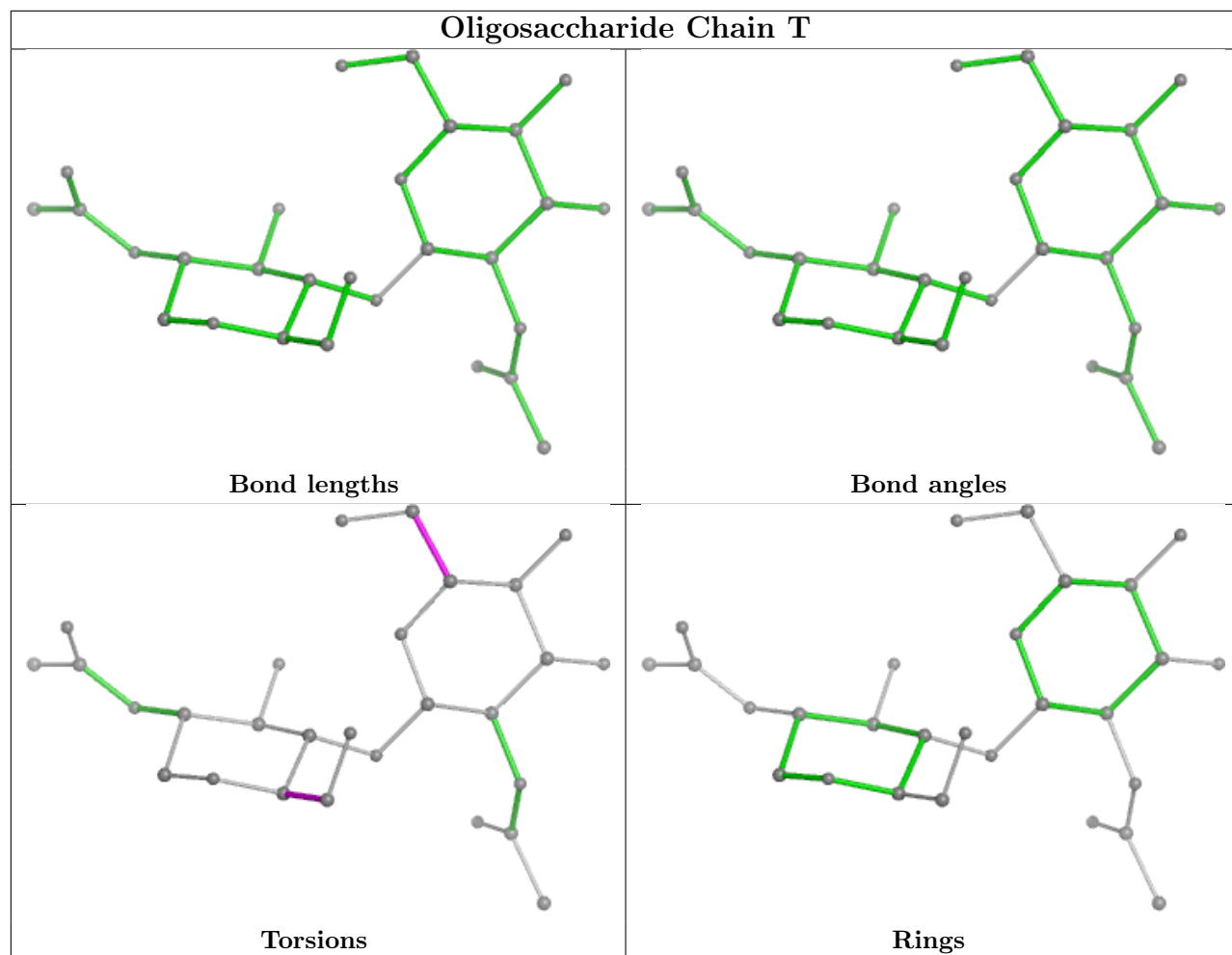


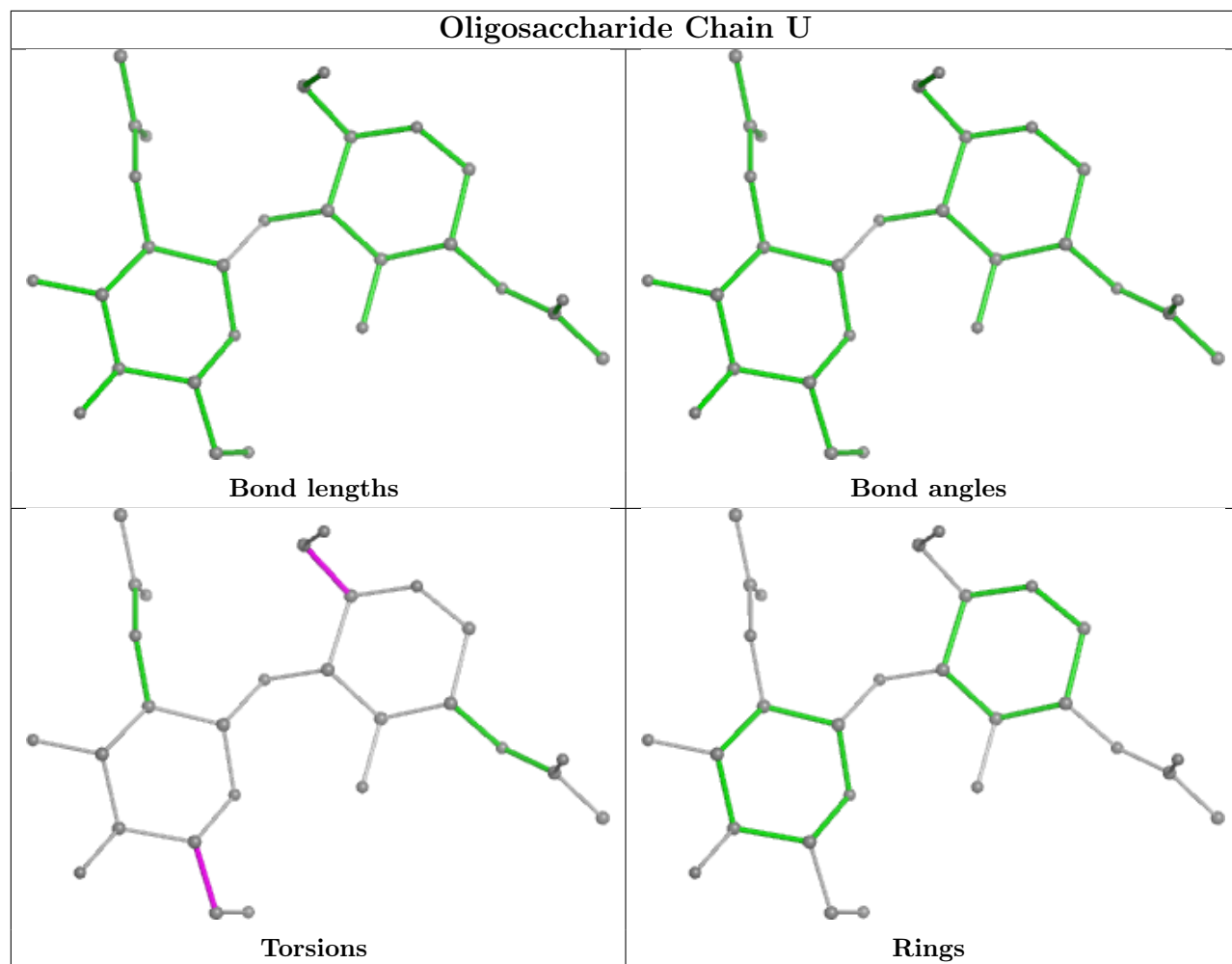


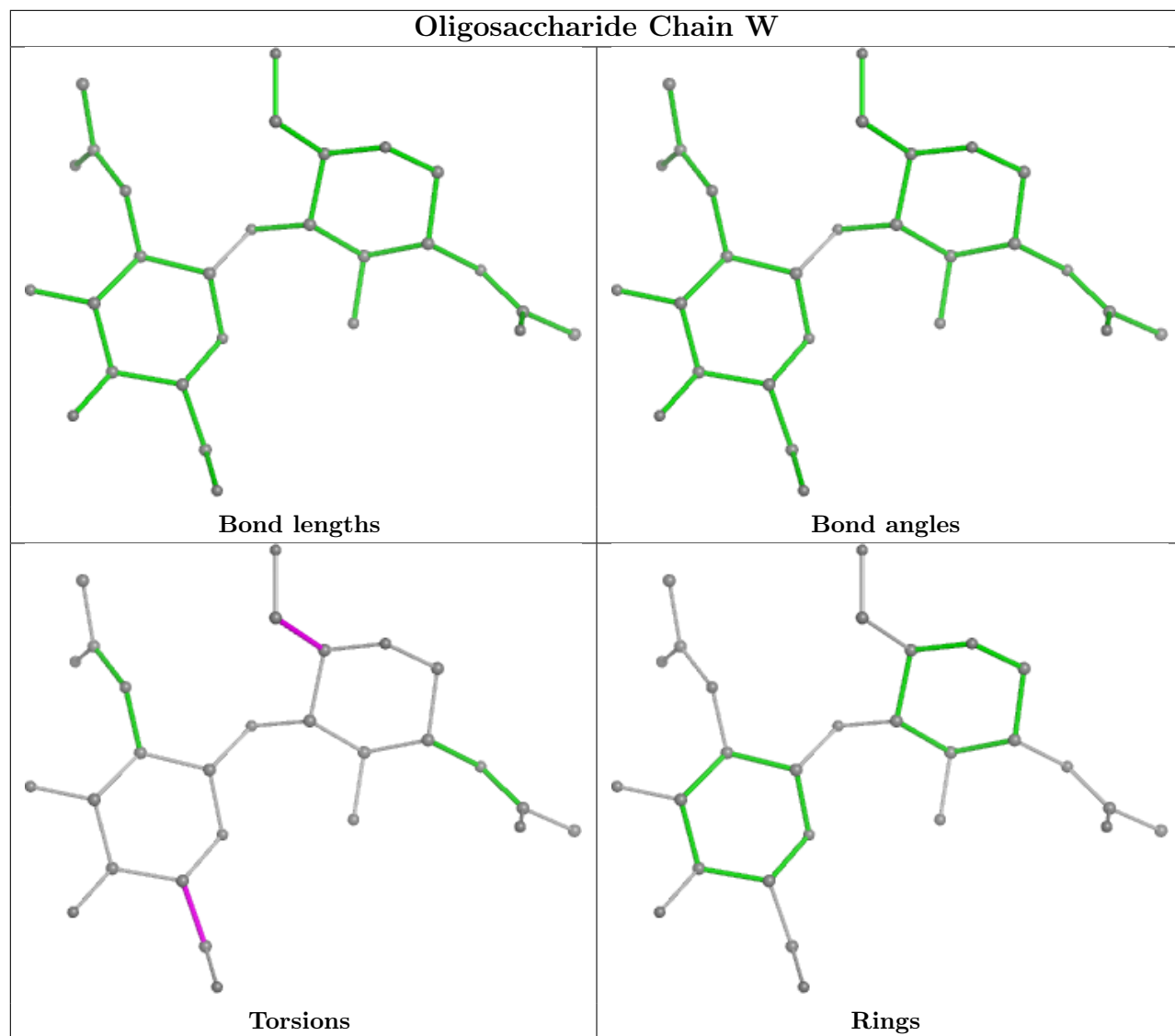


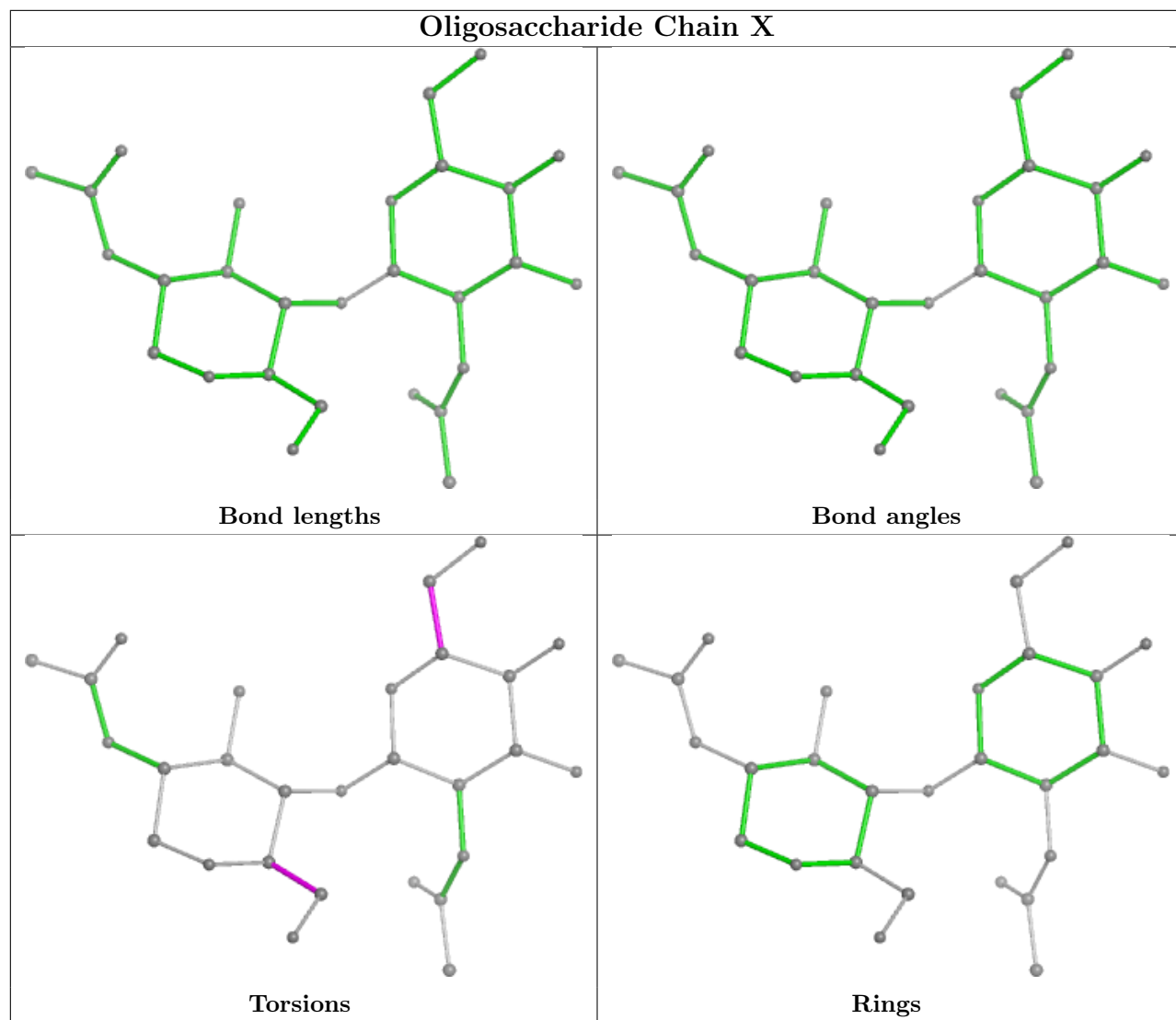


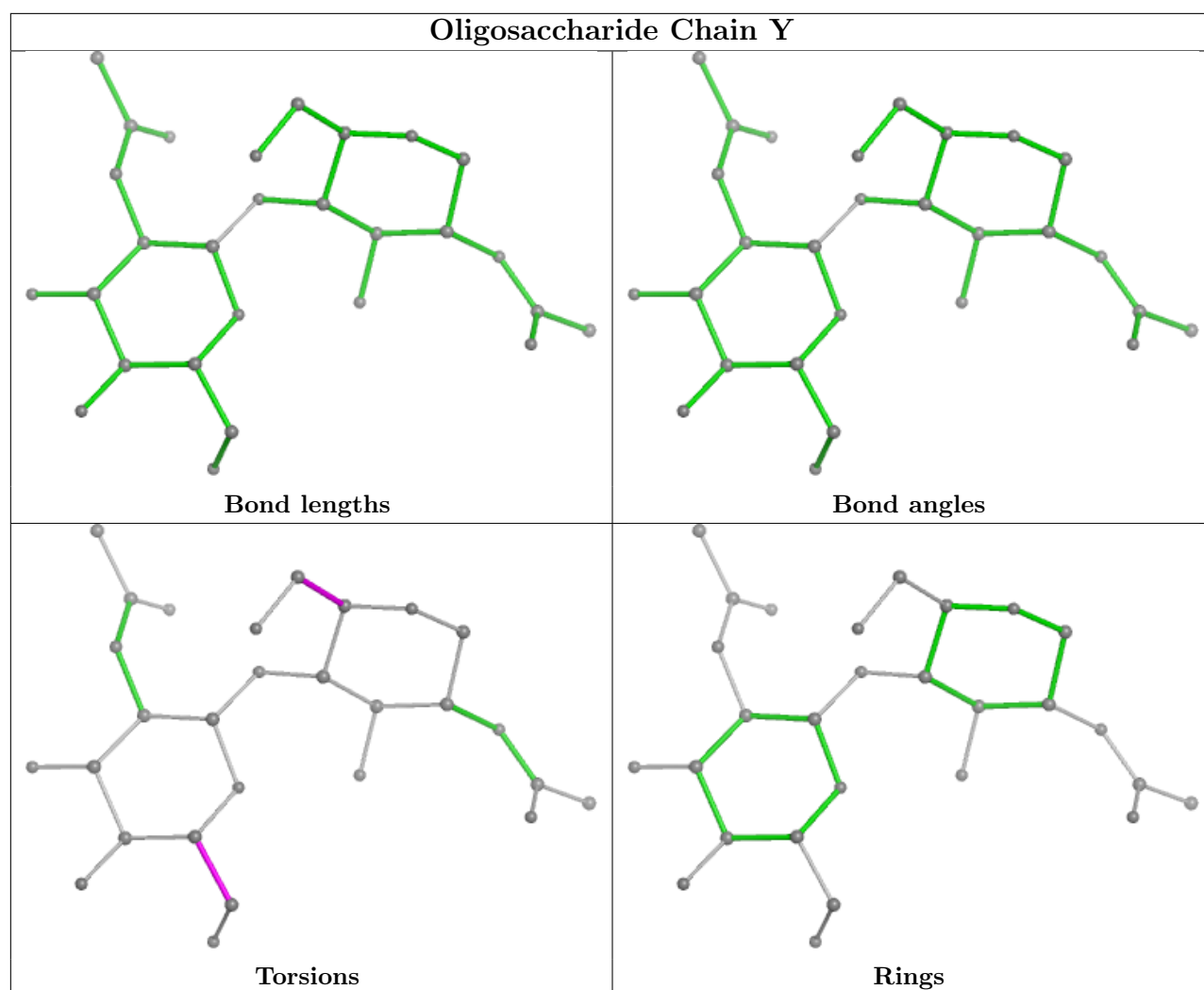


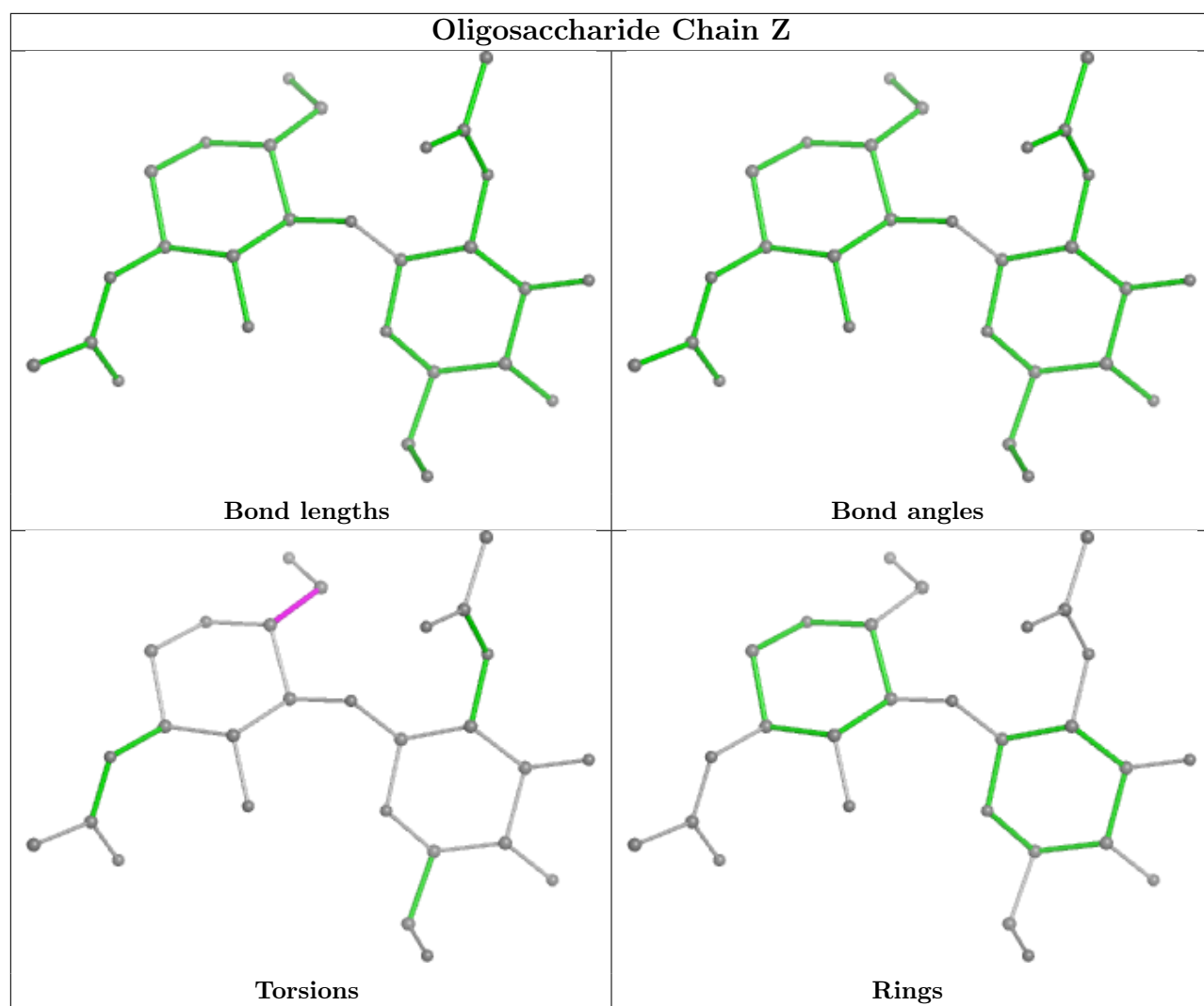


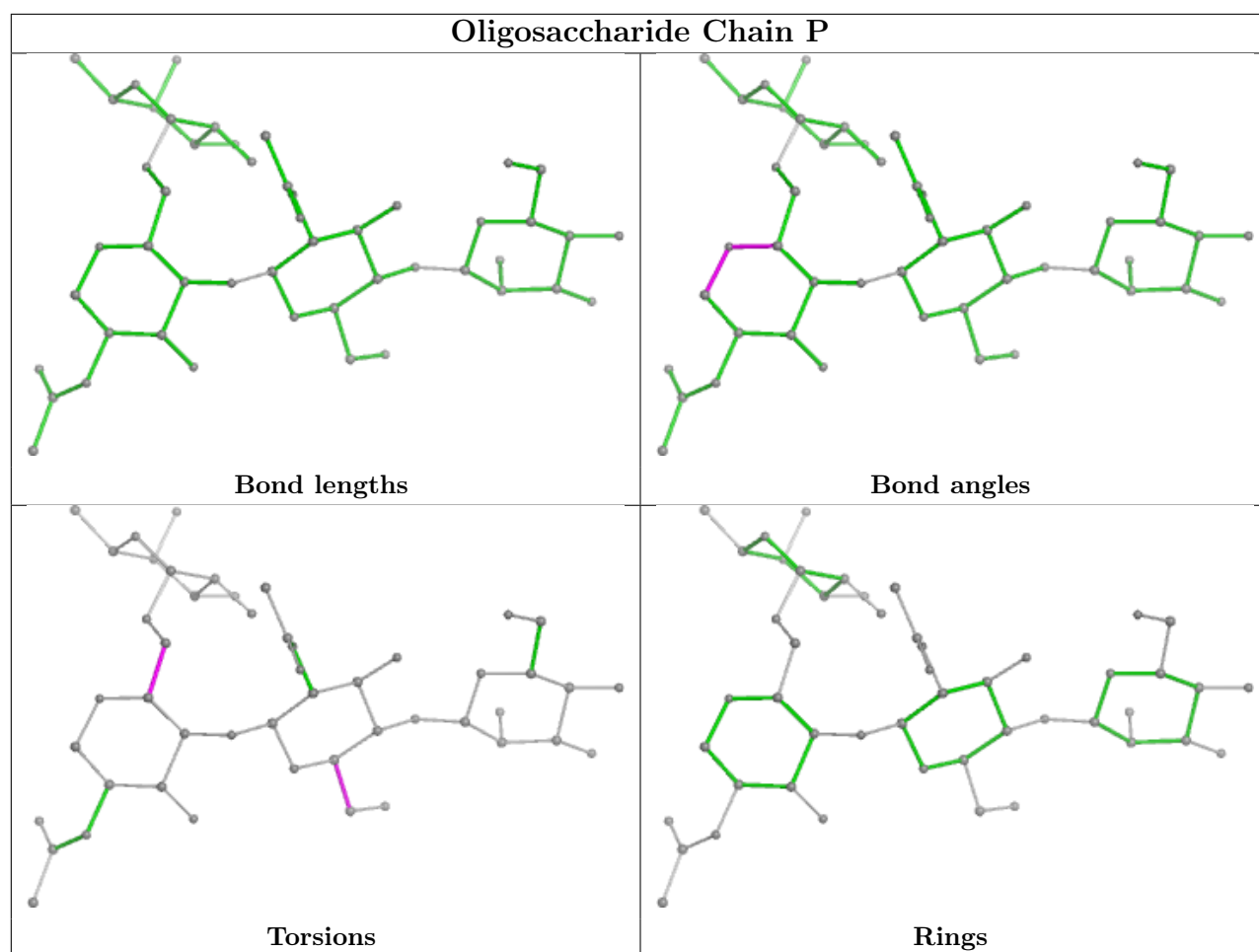


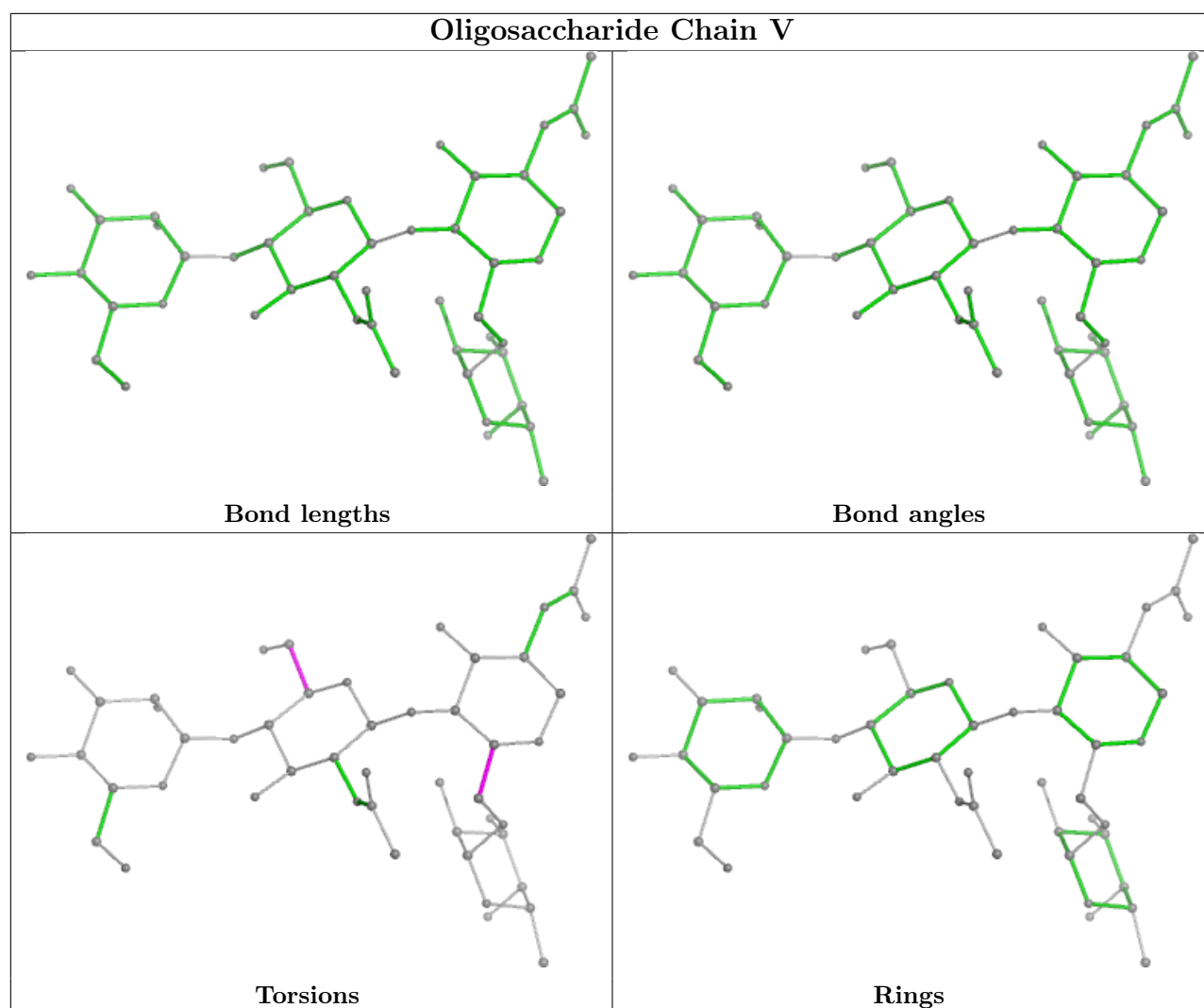












5.6 Ligand geometry [i](#)

25 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	$\# Z > 2$
7	NAG	A	1307	1	14,14,15	0.22	0	17,19,21	0.45	0
7	NAG	B	1309	1	14,14,15	0.22	0	17,19,21	0.57	0
7	NAG	C	1303	1	14,14,15	0.21	0	17,19,21	0.38	0
7	NAG	C	1306	1	14,14,15	0.19	0	17,19,21	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	A	1303	1	14,14,15	0.23	0	17,19,21	0.40	0
7	NAG	B	1307	1	14,14,15	0.22	0	17,19,21	0.38	0
7	NAG	A	1304	1	14,14,15	0.17	0	17,19,21	0.45	0
7	NAG	B	1304	1	14,14,15	0.20	0	17,19,21	0.38	0
7	NAG	C	1304	1	14,14,15	0.18	0	17,19,21	0.41	0
7	NAG	A	1301	1	14,14,15	0.25	0	17,19,21	0.46	0
7	NAG	B	1303	1	14,14,15	0.23	0	17,19,21	0.45	0
7	NAG	C	1302	1	14,14,15	0.21	0	17,19,21	0.44	0
7	NAG	A	1306	1	14,14,15	0.22	0	17,19,21	0.41	0
7	NAG	A	1302	1	14,14,15	0.20	0	17,19,21	0.40	0
7	NAG	B	1306	1	14,14,15	0.22	0	17,19,21	0.42	0
7	NAG	B	1305	1	14,14,15	0.21	0	17,19,21	0.42	0
7	NAG	B	1301	1	14,14,15	0.20	0	17,19,21	0.43	0
7	NAG	A	1308	1	14,14,15	0.21	0	17,19,21	0.42	0
7	NAG	C	1307	1	14,14,15	0.24	0	17,19,21	0.46	0
7	NAG	B	1302	1	14,14,15	0.20	0	17,19,21	0.42	0
7	NAG	C	1301	1	14,14,15	0.23	0	17,19,21	0.49	0
7	NAG	B	1308	1	14,14,15	0.21	0	17,19,21	0.46	0
7	NAG	C	1308	1	14,14,15	0.18	0	17,19,21	0.46	0
7	NAG	A	1305	1	14,14,15	0.23	0	17,19,21	0.40	0
7	NAG	C	1305	1	14,14,15	0.18	0	17,19,21	0.43	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
7	NAG	A	1307	1	-	4/6/23/26	0/1/1/1
7	NAG	B	1309	1	-	0/6/23/26	0/1/1/1
7	NAG	C	1303	1	-	2/6/23/26	0/1/1/1
7	NAG	C	1306	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1303	1	-	0/6/23/26	0/1/1/1
7	NAG	B	1307	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1304	1	-	2/6/23/26	0/1/1/1
7	NAG	B	1304	1	-	2/6/23/26	0/1/1/1
7	NAG	C	1304	1	-	0/6/23/26	0/1/1/1
7	NAG	A	1301	1	-	2/6/23/26	0/1/1/1
7	NAG	B	1303	1	-	2/6/23/26	0/1/1/1
7	NAG	C	1302	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1306	1	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	A	1302	1	-	0/6/23/26	0/1/1/1
7	NAG	B	1306	1	-	2/6/23/26	0/1/1/1
7	NAG	B	1305	1	-	2/6/23/26	0/1/1/1
7	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1308	1	-	2/6/23/26	0/1/1/1
7	NAG	C	1307	1	-	3/6/23/26	0/1/1/1
7	NAG	B	1302	1	-	0/6/23/26	0/1/1/1
7	NAG	C	1301	1	-	2/6/23/26	0/1/1/1
7	NAG	B	1308	1	-	2/6/23/26	0/1/1/1
7	NAG	C	1308	1	-	2/6/23/26	0/1/1/1
7	NAG	A	1305	1	-	1/6/23/26	0/1/1/1
7	NAG	C	1305	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.

All (41) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	B	1304	NAG	O5-C5-C6-O6
7	C	1303	NAG	O5-C5-C6-O6
7	C	1302	NAG	C4-C5-C6-O6
7	A	1304	NAG	C4-C5-C6-O6
7	A	1307	NAG	C4-C5-C6-O6
7	B	1305	NAG	O5-C5-C6-O6
7	C	1303	NAG	C4-C5-C6-O6
7	C	1306	NAG	O5-C5-C6-O6
7	C	1308	NAG	O5-C5-C6-O6
7	B	1304	NAG	C4-C5-C6-O6
7	B	1305	NAG	C4-C5-C6-O6
7	C	1305	NAG	O5-C5-C6-O6
7	C	1302	NAG	O5-C5-C6-O6
7	A	1307	NAG	O5-C5-C6-O6
7	B	1303	NAG	O5-C5-C6-O6
7	C	1305	NAG	C4-C5-C6-O6
7	C	1308	NAG	C4-C5-C6-O6
7	B	1306	NAG	O5-C5-C6-O6
7	B	1303	NAG	C4-C5-C6-O6
7	A	1304	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
7	C	1301	NAG	O5-C5-C6-O6
7	C	1307	NAG	O5-C5-C6-O6
7	B	1301	NAG	O5-C5-C6-O6
7	B	1308	NAG	C4-C5-C6-O6
7	A	1306	NAG	O5-C5-C6-O6
7	B	1306	NAG	C4-C5-C6-O6
7	A	1301	NAG	O5-C5-C6-O6
7	C	1306	NAG	C4-C5-C6-O6
7	B	1307	NAG	O5-C5-C6-O6
7	C	1301	NAG	C4-C5-C6-O6
7	B	1308	NAG	O5-C5-C6-O6
7	C	1307	NAG	C1-C2-N2-C7
7	A	1308	NAG	C4-C5-C6-O6
7	B	1301	NAG	C4-C5-C6-O6
7	A	1308	NAG	O5-C5-C6-O6
7	A	1307	NAG	C1-C2-N2-C7
7	A	1301	NAG	C4-C5-C6-O6
7	B	1307	NAG	C4-C5-C6-O6
7	A	1305	NAG	O5-C5-C6-O6
7	A	1307	NAG	C3-C2-N2-C7
7	C	1307	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	1302	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

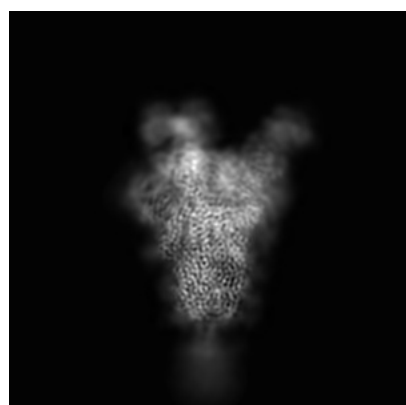
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13868. These allow visual inspection of the internal detail of the map and identification of artifacts.

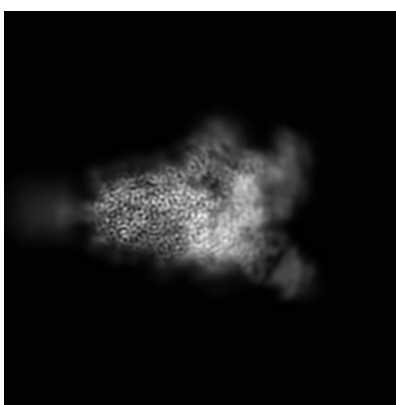
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

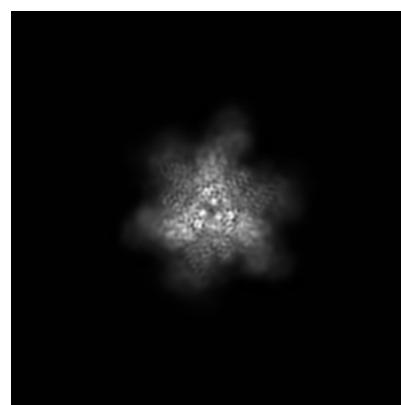
6.1.1 Primary map



X



Y

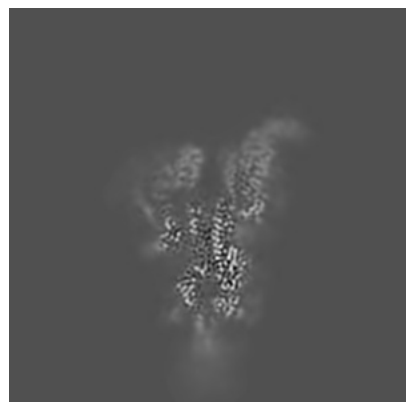


Z

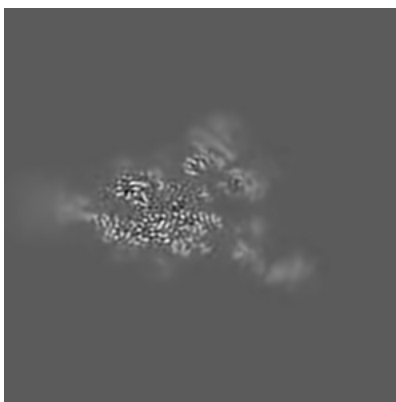
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 210



Y Index: 210

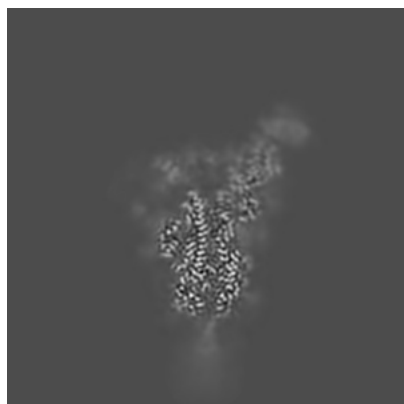


Z Index: 210

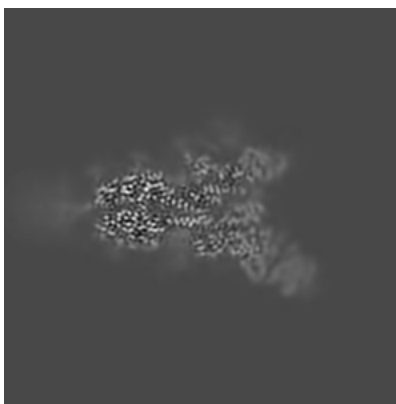
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

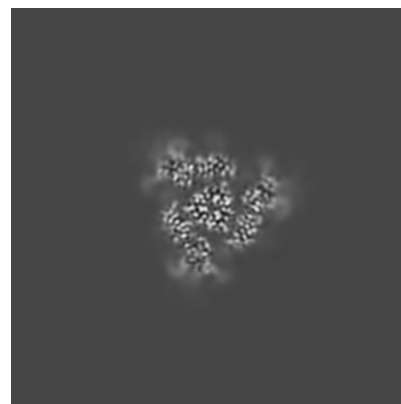
6.3.1 Primary map



X Index: 219



Y Index: 196

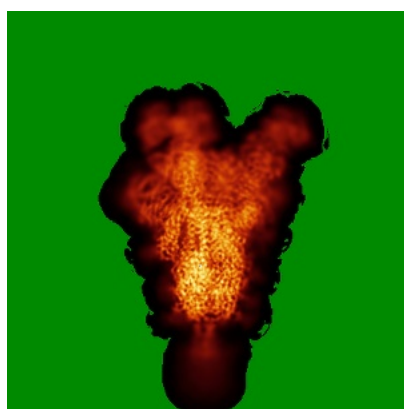


Z Index: 206

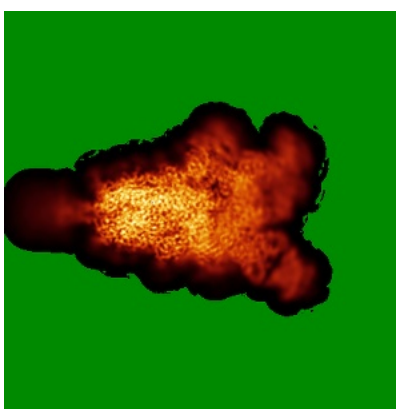
The images above show the largest variance slices of the map in three orthogonal directions.

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

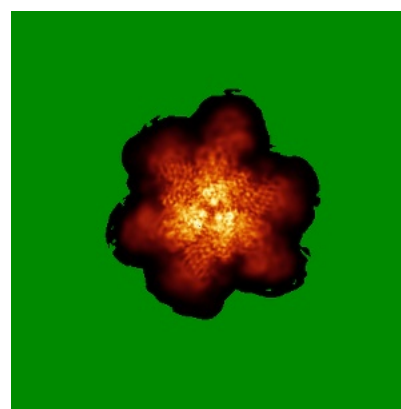
6.4.1 Primary map



X



Y



Z

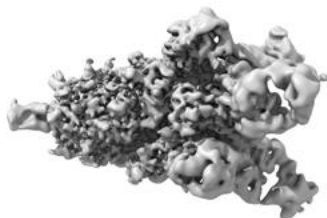
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

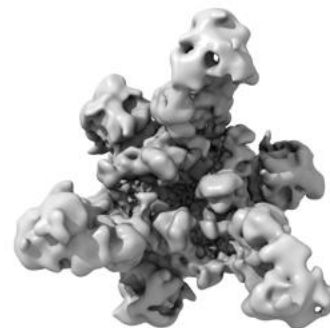
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0917. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

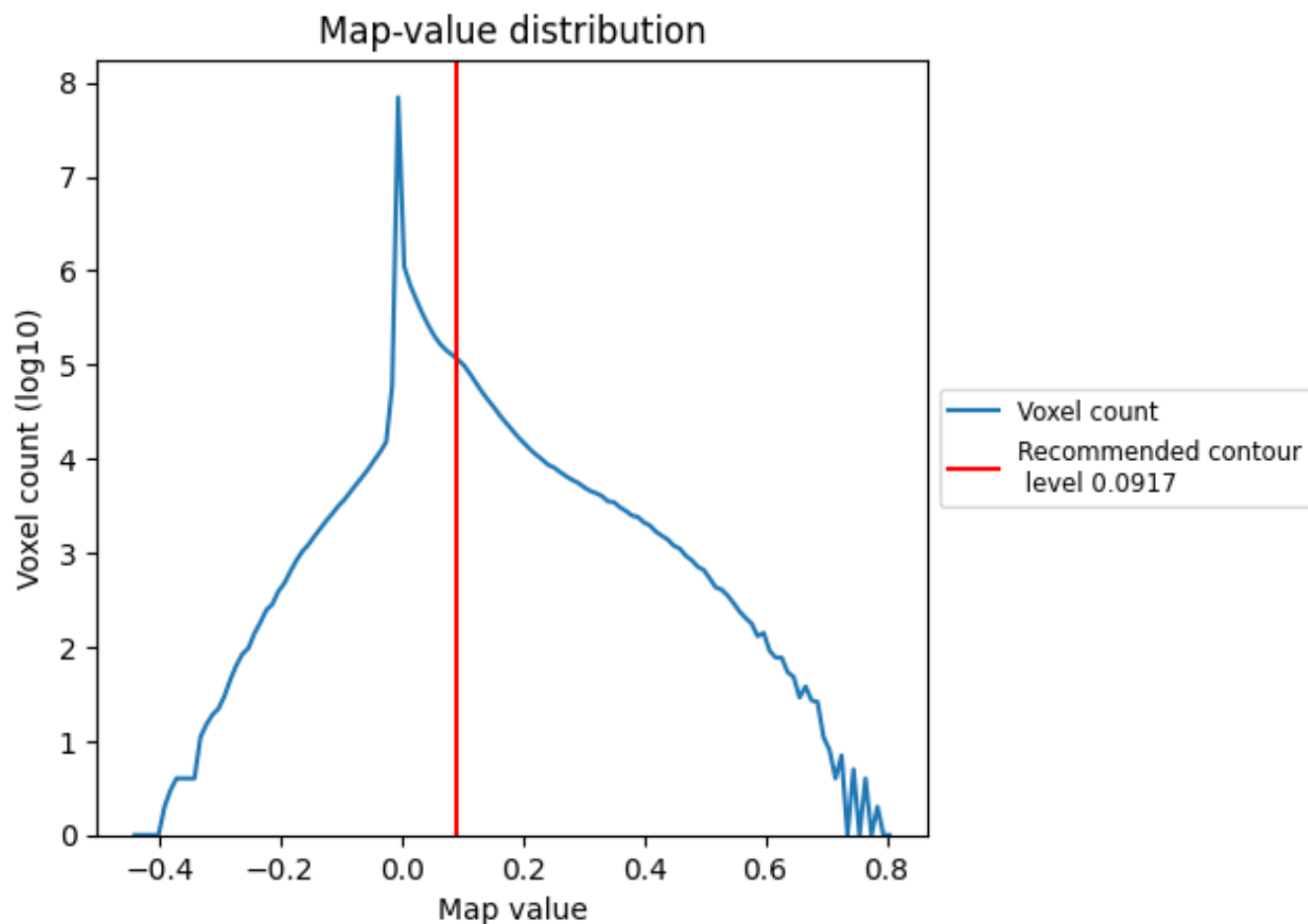
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

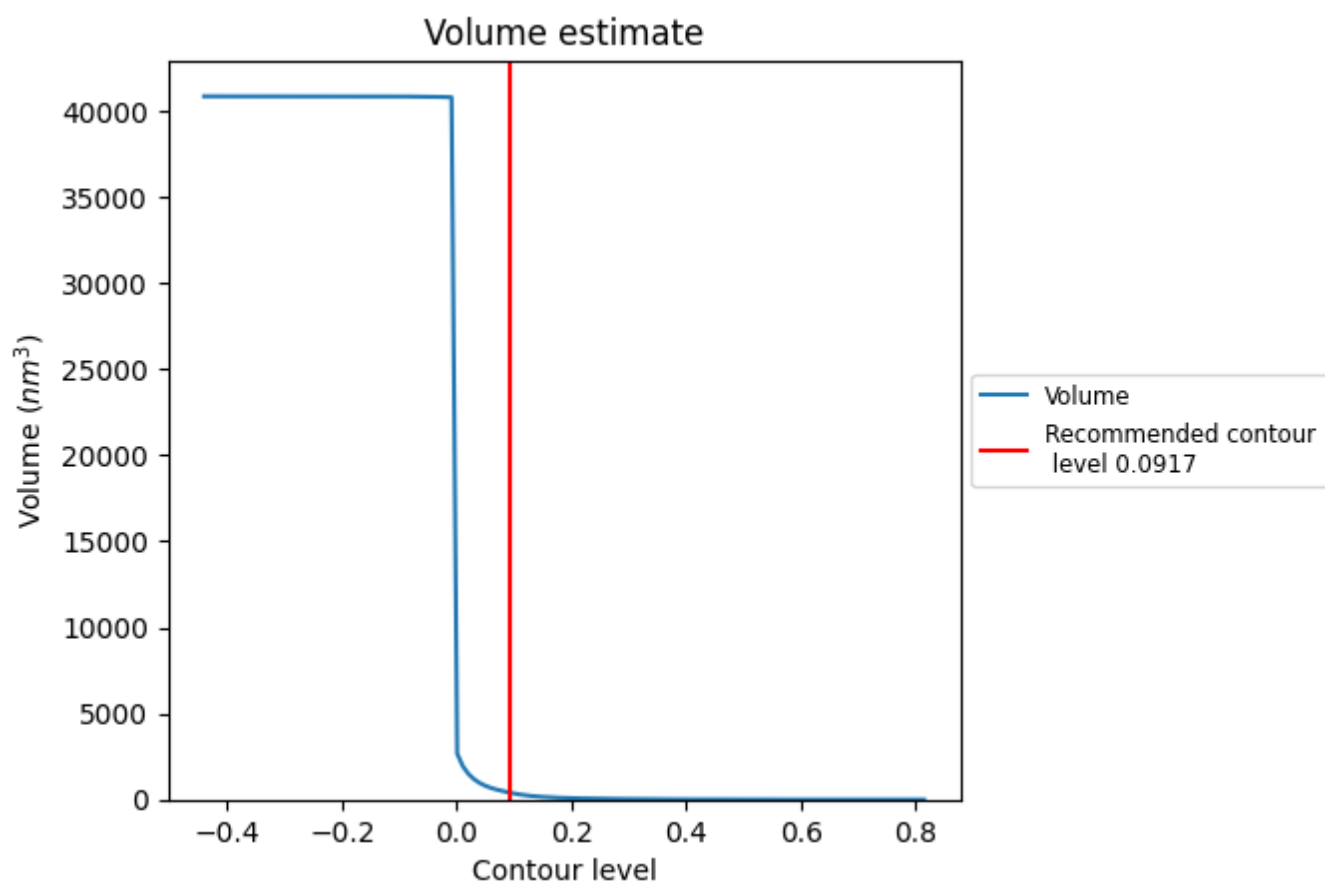
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

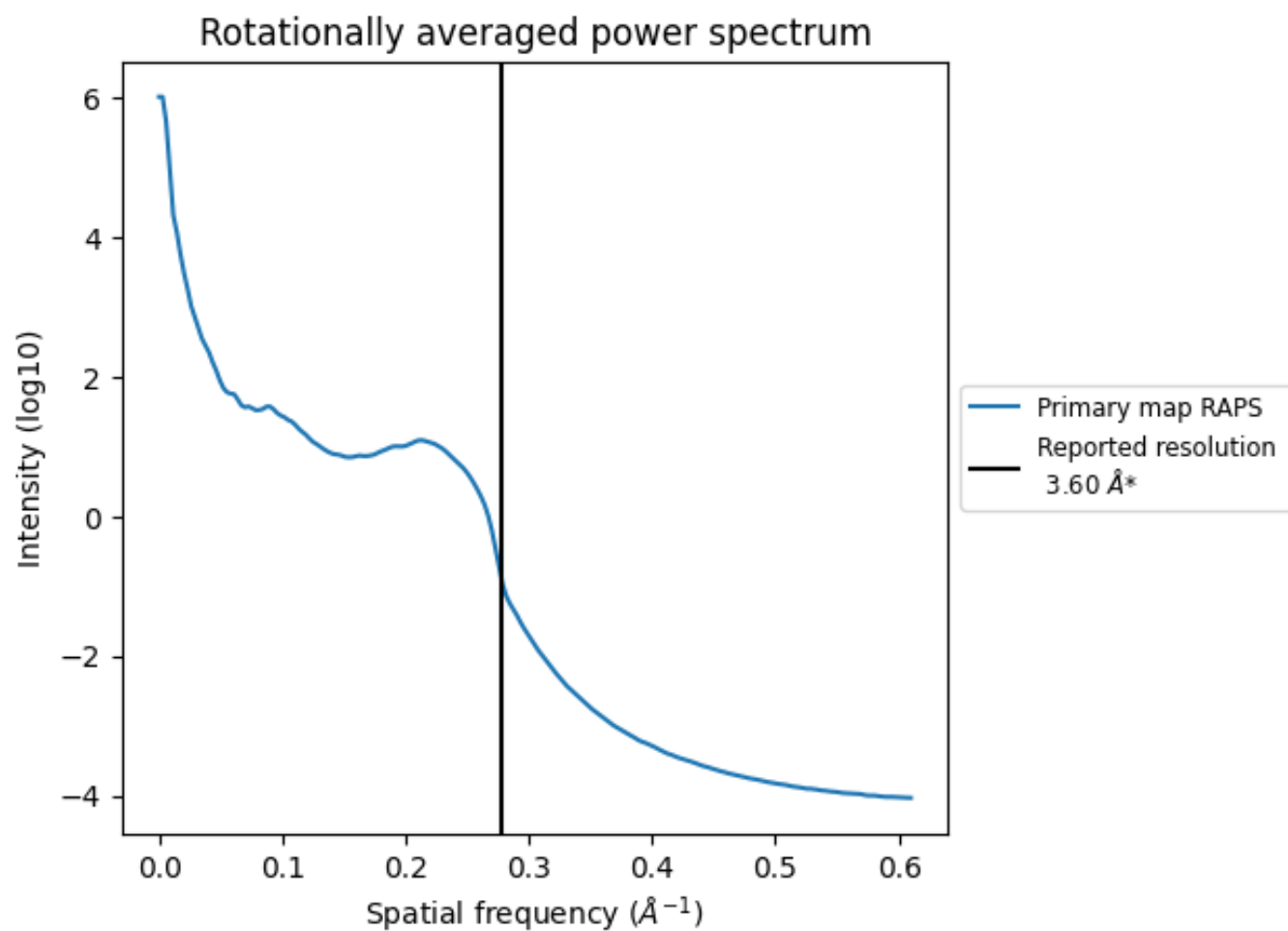
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 408 nm^3 ; this corresponds to an approximate mass of 368 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 0.278 Å⁻¹

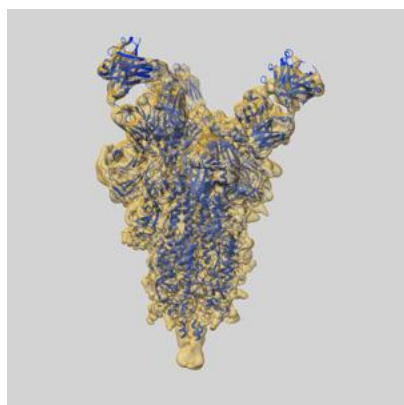
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

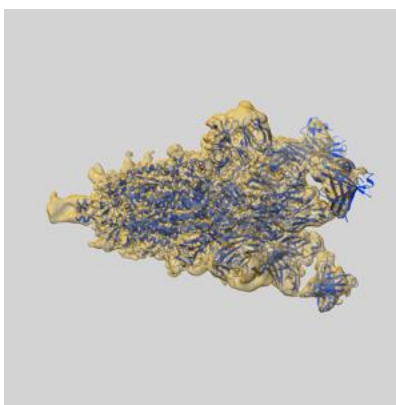
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13868 and PDB model 7Q9F. Per-residue inclusion information can be found in section 3 on page 15.

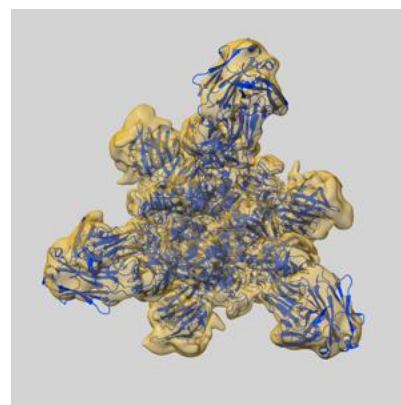
9.1 Map-model overlay [i](#)



X



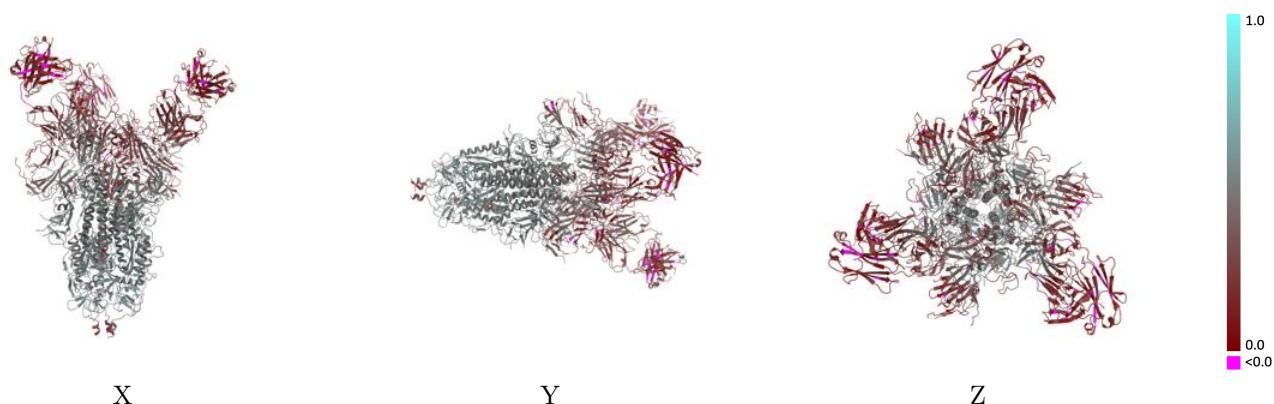
Y



Z

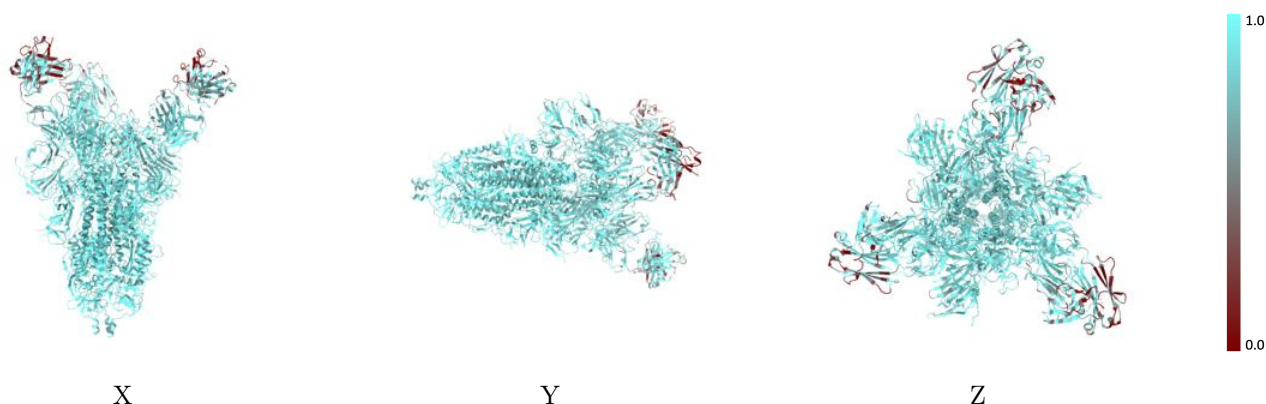
The images above show the 3D surface view of the map at the recommended contour level 0.0917 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



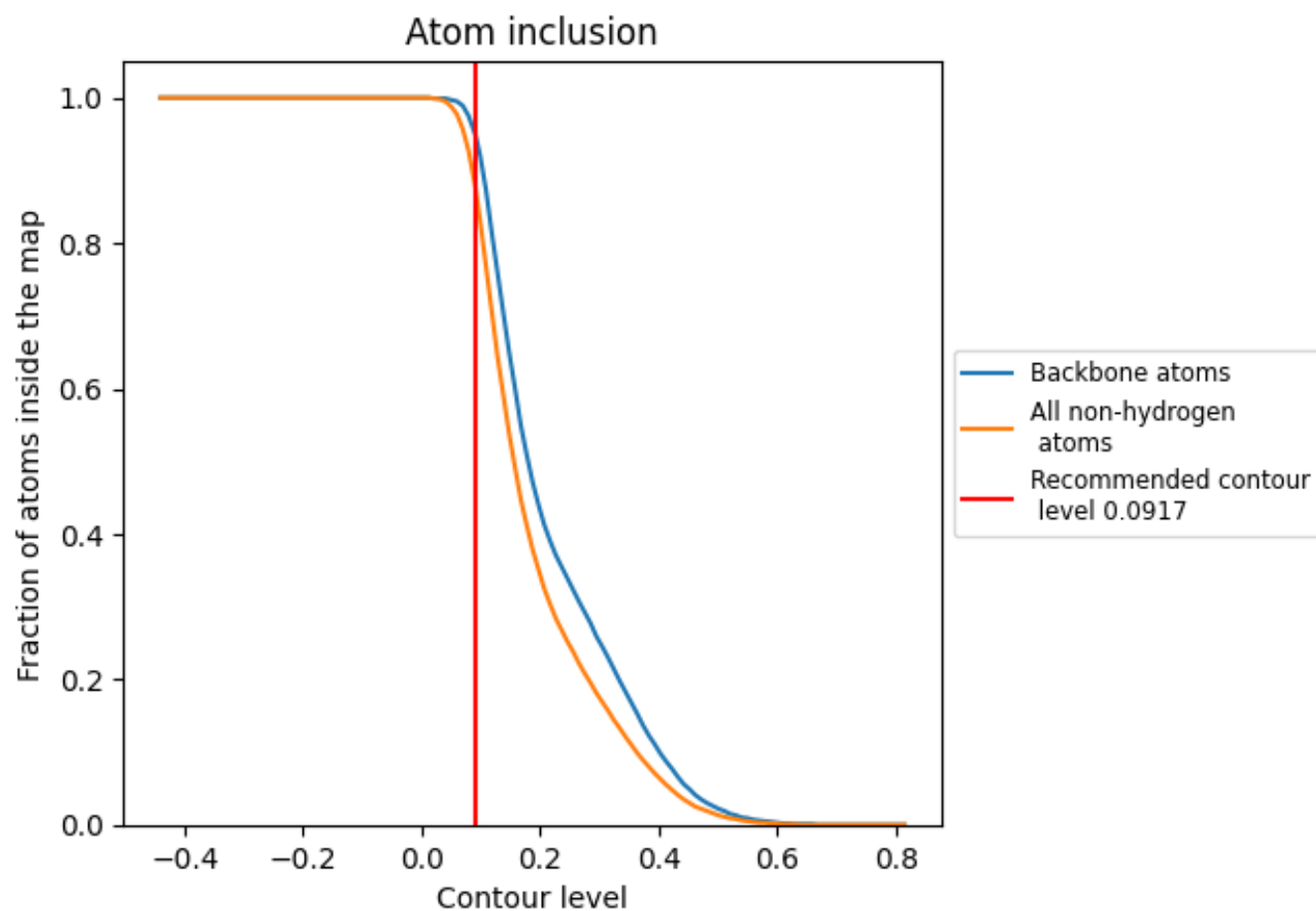
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0917).























































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 87% 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 (0.0917) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8730	 0.3660
A	 0.9170	 0.4170
B	 0.9310	 0.4310
C	 0.9250	 0.4270
D	 0.9470	 0.3780
E	 0.8050	 0.2280
F	 0.7910	 0.2200
G	 0.5000	 0.3080
H	 0.6920	 0.2280
I	 0.8930	 0.4750
J	 0.7450	 0.2270
K	 0.7210	 0.2180
L	 0.7180	 0.1950
M	 0.8210	 0.4040
N	 0.8930	 0.4220
O	 0.7860	 0.3800
P	 0.9390	 0.3960
Q	 0.6790	 0.3530
R	 1.0000	 0.5160
S	 0.9290	 0.4530
T	 0.9290	 0.4150
U	 0.8930	 0.4180
V	 0.9390	 0.4140
W	 0.9640	 0.4890
X	 0.8930	 0.4050
Y	 0.8570	 0.4060
Z	 0.8930	 0.4530

