wwPDB EM Validation Summary Report

Dec 16, 2024 – 06:09 PM EST

PDB ID	:	5W9I
EMDB ID	:	EMD-8784
Title	:	MERS S ectodomain trimer in complex with variable domain of neutralizing antibody G4
Authors	:	Pallesen, J.; Ward, A.B.
Deposited on	:	2017-06-23
Resolution	:	3.60 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

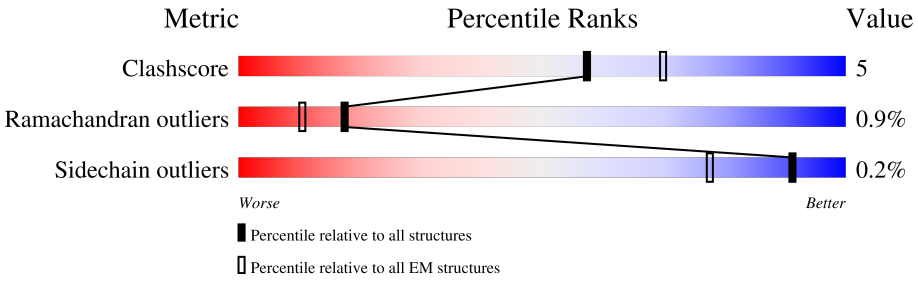
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 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 <=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	1329	32% · 65%
1	B	1329	36% · 61%
1	E	1329	33% · 65%
1	F	1329	36% · 61%
1	I	1329	32% · 65%
1	J	1329	35% · 61%
2	C	233	50% · 49%
2	G	233	49% · 49%

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Mol	Chain	Length	Quality of chain
2	K	233	49% 49%
3	D	218	9% 50% 49%
3	H	218	10% 50% 49%
3	L	218	9% 50% 49%
4	M	2	50% 50%
4	N	2	50% 50%
4	O	2	50% 50%
4	P	2	100%
4	Q	2	100%
4	R	2	50% 50%
4	S	2	50% 50%
4	T	2	50% 50%
4	U	2	50% 50%
4	V	2	100%
4	W	2	50% 50%
4	X	2	50% 50%
4	Y	2	100%
4	Z	2	100%
4	a	2	100%
4	b	2	100%
4	c	2	100%
4	d	2	50% 50%
4	e	2	50% 100%
4	f	2	100%
4	g	2	100%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 28896 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	463	Total	C	N	O	S	0	0
			3545	2243	600	685	17		
1	B	513	Total	C	N	O	S	0	0
			4010	2549	664	774	23		
1	E	463	Total	C	N	O	S	0	0
			3545	2243	600	685	17		
1	F	513	Total	C	N	O	S	0	0
			4010	2549	664	774	23		
1	I	463	Total	C	N	O	S	0	0
			3545	2243	600	685	17		
1	J	513	Total	C	N	O	S	0	0
			4010	2549	664	774	23		

There are 258 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	506	PHE	LEU	conflict	UNP W5ZZF5
A	748	ALA	ARG	conflict	UNP W5ZZF5
A	751	GLY	ARG	conflict	UNP W5ZZF5
A	1060	PRO	VAL	engineered mutation	UNP W5ZZF5
A	1061	PRO	LEU	engineered mutation	UNP W5ZZF5
A	1292	GLY	-	expression tag	UNP W5ZZF5
A	1293	SER	-	expression tag	UNP W5ZZF5
A	1294	GLY	-	expression tag	UNP W5ZZF5
A	1295	TYR	-	expression tag	UNP W5ZZF5
A	1296	ILE	-	expression tag	UNP W5ZZF5
A	1297	PRO	-	expression tag	UNP W5ZZF5
A	1298	GLU	-	expression tag	UNP W5ZZF5
A	1299	ALA	-	expression tag	UNP W5ZZF5
A	1300	PRO	-	expression tag	UNP W5ZZF5
A	1301	ARG	-	expression tag	UNP W5ZZF5
A	1302	ASP	-	expression tag	UNP W5ZZF5
A	1303	GLY	-	expression tag	UNP W5ZZF5
A	1304	GLN	-	expression tag	UNP W5ZZF5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1305	ALA	-	expression tag	UNP W5ZZF5
A	1306	TYR	-	expression tag	UNP W5ZZF5
A	1307	VAL	-	expression tag	UNP W5ZZF5
A	1308	ARG	-	expression tag	UNP W5ZZF5
A	1309	LYS	-	expression tag	UNP W5ZZF5
A	1310	ASP	-	expression tag	UNP W5ZZF5
A	1311	GLY	-	expression tag	UNP W5ZZF5
A	1312	GLU	-	expression tag	UNP W5ZZF5
A	1313	TRP	-	expression tag	UNP W5ZZF5
A	1314	VAL	-	expression tag	UNP W5ZZF5
A	1315	LEU	-	expression tag	UNP W5ZZF5
A	1316	LEU	-	expression tag	UNP W5ZZF5
A	1317	SER	-	expression tag	UNP W5ZZF5
A	1318	THR	-	expression tag	UNP W5ZZF5
A	1319	PHE	-	expression tag	UNP W5ZZF5
A	1320	LEU	-	expression tag	UNP W5ZZF5
A	1321	GLY	-	expression tag	UNP W5ZZF5
A	1322	ARG	-	expression tag	UNP W5ZZF5
A	1323	SER	-	expression tag	UNP W5ZZF5
A	1324	LEU	-	expression tag	UNP W5ZZF5
A	1325	GLU	-	expression tag	UNP W5ZZF5
A	1326	VAL	-	expression tag	UNP W5ZZF5
A	1327	LEU	-	expression tag	UNP W5ZZF5
A	1328	PHE	-	expression tag	UNP W5ZZF5
A	1329	GLN	-	expression tag	UNP W5ZZF5
B	506	PHE	LEU	conflict	UNP W5ZZF5
B	748	ALA	ARG	conflict	UNP W5ZZF5
B	751	GLY	ARG	conflict	UNP W5ZZF5
B	1060	PRO	VAL	engineered mutation	UNP W5ZZF5
B	1061	PRO	LEU	engineered mutation	UNP W5ZZF5
B	1292	GLY	-	expression tag	UNP W5ZZF5
B	1293	SER	-	expression tag	UNP W5ZZF5
B	1294	GLY	-	expression tag	UNP W5ZZF5
B	1295	TYR	-	expression tag	UNP W5ZZF5
B	1296	ILE	-	expression tag	UNP W5ZZF5
B	1297	PRO	-	expression tag	UNP W5ZZF5
B	1298	GLU	-	expression tag	UNP W5ZZF5
B	1299	ALA	-	expression tag	UNP W5ZZF5
B	1300	PRO	-	expression tag	UNP W5ZZF5
B	1301	ARG	-	expression tag	UNP W5ZZF5
B	1302	ASP	-	expression tag	UNP W5ZZF5
B	1303	GLY	-	expression tag	UNP W5ZZF5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1304	GLN	-	expression tag	UNP W5ZZF5
B	1305	ALA	-	expression tag	UNP W5ZZF5
B	1306	TYR	-	expression tag	UNP W5ZZF5
B	1307	VAL	-	expression tag	UNP W5ZZF5
B	1308	ARG	-	expression tag	UNP W5ZZF5
B	1309	LYS	-	expression tag	UNP W5ZZF5
B	1310	ASP	-	expression tag	UNP W5ZZF5
B	1311	GLY	-	expression tag	UNP W5ZZF5
B	1312	GLU	-	expression tag	UNP W5ZZF5
B	1313	TRP	-	expression tag	UNP W5ZZF5
B	1314	VAL	-	expression tag	UNP W5ZZF5
B	1315	LEU	-	expression tag	UNP W5ZZF5
B	1316	LEU	-	expression tag	UNP W5ZZF5
B	1317	SER	-	expression tag	UNP W5ZZF5
B	1318	THR	-	expression tag	UNP W5ZZF5
B	1319	PHE	-	expression tag	UNP W5ZZF5
B	1320	LEU	-	expression tag	UNP W5ZZF5
B	1321	GLY	-	expression tag	UNP W5ZZF5
B	1322	ARG	-	expression tag	UNP W5ZZF5
B	1323	SER	-	expression tag	UNP W5ZZF5
B	1324	LEU	-	expression tag	UNP W5ZZF5
B	1325	GLU	-	expression tag	UNP W5ZZF5
B	1326	VAL	-	expression tag	UNP W5ZZF5
B	1327	LEU	-	expression tag	UNP W5ZZF5
B	1328	PHE	-	expression tag	UNP W5ZZF5
B	1329	GLN	-	expression tag	UNP W5ZZF5
E	506	PHE	LEU	conflict	UNP W5ZZF5
E	748	ALA	ARG	conflict	UNP W5ZZF5
E	751	GLY	ARG	conflict	UNP W5ZZF5
E	1060	PRO	VAL	engineered mutation	UNP W5ZZF5
E	1061	PRO	LEU	engineered mutation	UNP W5ZZF5
E	1292	GLY	-	expression tag	UNP W5ZZF5
E	1293	SER	-	expression tag	UNP W5ZZF5
E	1294	GLY	-	expression tag	UNP W5ZZF5
E	1295	TYR	-	expression tag	UNP W5ZZF5
E	1296	ILE	-	expression tag	UNP W5ZZF5
E	1297	PRO	-	expression tag	UNP W5ZZF5
E	1298	GLU	-	expression tag	UNP W5ZZF5
E	1299	ALA	-	expression tag	UNP W5ZZF5
E	1300	PRO	-	expression tag	UNP W5ZZF5
E	1301	ARG	-	expression tag	UNP W5ZZF5
E	1302	ASP	-	expression tag	UNP W5ZZF5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1303	GLY	-	expression tag	UNP W5ZZF5
E	1304	GLN	-	expression tag	UNP W5ZZF5
E	1305	ALA	-	expression tag	UNP W5ZZF5
E	1306	TYR	-	expression tag	UNP W5ZZF5
E	1307	VAL	-	expression tag	UNP W5ZZF5
E	1308	ARG	-	expression tag	UNP W5ZZF5
E	1309	LYS	-	expression tag	UNP W5ZZF5
E	1310	ASP	-	expression tag	UNP W5ZZF5
E	1311	GLY	-	expression tag	UNP W5ZZF5
E	1312	GLU	-	expression tag	UNP W5ZZF5
E	1313	TRP	-	expression tag	UNP W5ZZF5
E	1314	VAL	-	expression tag	UNP W5ZZF5
E	1315	LEU	-	expression tag	UNP W5ZZF5
E	1316	LEU	-	expression tag	UNP W5ZZF5
E	1317	SER	-	expression tag	UNP W5ZZF5
E	1318	THR	-	expression tag	UNP W5ZZF5
E	1319	PHE	-	expression tag	UNP W5ZZF5
E	1320	LEU	-	expression tag	UNP W5ZZF5
E	1321	GLY	-	expression tag	UNP W5ZZF5
E	1322	ARG	-	expression tag	UNP W5ZZF5
E	1323	SER	-	expression tag	UNP W5ZZF5
E	1324	LEU	-	expression tag	UNP W5ZZF5
E	1325	GLU	-	expression tag	UNP W5ZZF5
E	1326	VAL	-	expression tag	UNP W5ZZF5
E	1327	LEU	-	expression tag	UNP W5ZZF5
E	1328	PHE	-	expression tag	UNP W5ZZF5
E	1329	GLN	-	expression tag	UNP W5ZZF5
F	506	PHE	LEU	conflict	UNP W5ZZF5
F	748	ALA	ARG	conflict	UNP W5ZZF5
F	751	GLY	ARG	conflict	UNP W5ZZF5
F	1060	PRO	VAL	engineered mutation	UNP W5ZZF5
F	1061	PRO	LEU	engineered mutation	UNP W5ZZF5
F	1292	GLY	-	expression tag	UNP W5ZZF5
F	1293	SER	-	expression tag	UNP W5ZZF5
F	1294	GLY	-	expression tag	UNP W5ZZF5
F	1295	TYR	-	expression tag	UNP W5ZZF5
F	1296	ILE	-	expression tag	UNP W5ZZF5
F	1297	PRO	-	expression tag	UNP W5ZZF5
F	1298	GLU	-	expression tag	UNP W5ZZF5
F	1299	ALA	-	expression tag	UNP W5ZZF5
F	1300	PRO	-	expression tag	UNP W5ZZF5
F	1301	ARG	-	expression tag	UNP W5ZZF5

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Chain	Residue	Modelled	Actual	Comment	Reference
F	1302	ASP	-	expression tag	UNP W5ZZF5
F	1303	GLY	-	expression tag	UNP W5ZZF5
F	1304	GLN	-	expression tag	UNP W5ZZF5
F	1305	ALA	-	expression tag	UNP W5ZZF5
F	1306	TYR	-	expression tag	UNP W5ZZF5
F	1307	VAL	-	expression tag	UNP W5ZZF5
F	1308	ARG	-	expression tag	UNP W5ZZF5
F	1309	LYS	-	expression tag	UNP W5ZZF5
F	1310	ASP	-	expression tag	UNP W5ZZF5
F	1311	GLY	-	expression tag	UNP W5ZZF5
F	1312	GLU	-	expression tag	UNP W5ZZF5
F	1313	TRP	-	expression tag	UNP W5ZZF5
F	1314	VAL	-	expression tag	UNP W5ZZF5
F	1315	LEU	-	expression tag	UNP W5ZZF5
F	1316	LEU	-	expression tag	UNP W5ZZF5
F	1317	SER	-	expression tag	UNP W5ZZF5
F	1318	THR	-	expression tag	UNP W5ZZF5
F	1319	PHE	-	expression tag	UNP W5ZZF5
F	1320	LEU	-	expression tag	UNP W5ZZF5
F	1321	GLY	-	expression tag	UNP W5ZZF5
F	1322	ARG	-	expression tag	UNP W5ZZF5
F	1323	SER	-	expression tag	UNP W5ZZF5
F	1324	LEU	-	expression tag	UNP W5ZZF5
F	1325	GLU	-	expression tag	UNP W5ZZF5
F	1326	VAL	-	expression tag	UNP W5ZZF5
F	1327	LEU	-	expression tag	UNP W5ZZF5
F	1328	PHE	-	expression tag	UNP W5ZZF5
F	1329	GLN	-	expression tag	UNP W5ZZF5
I	506	PHE	LEU	conflict	UNP W5ZZF5
I	748	ALA	ARG	conflict	UNP W5ZZF5
I	751	GLY	ARG	conflict	UNP W5ZZF5
I	1060	PRO	VAL	engineered mutation	UNP W5ZZF5
I	1061	PRO	LEU	engineered mutation	UNP W5ZZF5
I	1292	GLY	-	expression tag	UNP W5ZZF5
I	1293	SER	-	expression tag	UNP W5ZZF5
I	1294	GLY	-	expression tag	UNP W5ZZF5
I	1295	TYR	-	expression tag	UNP W5ZZF5
I	1296	ILE	-	expression tag	UNP W5ZZF5
I	1297	PRO	-	expression tag	UNP W5ZZF5
I	1298	GLU	-	expression tag	UNP W5ZZF5
I	1299	ALA	-	expression tag	UNP W5ZZF5
I	1300	PRO	-	expression tag	UNP W5ZZF5

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Chain	Residue	Modelled	Actual	Comment	Reference
I	1301	ARG	-	expression tag	UNP W5ZZF5
I	1302	ASP	-	expression tag	UNP W5ZZF5
I	1303	GLY	-	expression tag	UNP W5ZZF5
I	1304	GLN	-	expression tag	UNP W5ZZF5
I	1305	ALA	-	expression tag	UNP W5ZZF5
I	1306	TYR	-	expression tag	UNP W5ZZF5
I	1307	VAL	-	expression tag	UNP W5ZZF5
I	1308	ARG	-	expression tag	UNP W5ZZF5
I	1309	LYS	-	expression tag	UNP W5ZZF5
I	1310	ASP	-	expression tag	UNP W5ZZF5
I	1311	GLY	-	expression tag	UNP W5ZZF5
I	1312	GLU	-	expression tag	UNP W5ZZF5
I	1313	TRP	-	expression tag	UNP W5ZZF5
I	1314	VAL	-	expression tag	UNP W5ZZF5
I	1315	LEU	-	expression tag	UNP W5ZZF5
I	1316	LEU	-	expression tag	UNP W5ZZF5
I	1317	SER	-	expression tag	UNP W5ZZF5
I	1318	THR	-	expression tag	UNP W5ZZF5
I	1319	PHE	-	expression tag	UNP W5ZZF5
I	1320	LEU	-	expression tag	UNP W5ZZF5
I	1321	GLY	-	expression tag	UNP W5ZZF5
I	1322	ARG	-	expression tag	UNP W5ZZF5
I	1323	SER	-	expression tag	UNP W5ZZF5
I	1324	LEU	-	expression tag	UNP W5ZZF5
I	1325	GLU	-	expression tag	UNP W5ZZF5
I	1326	VAL	-	expression tag	UNP W5ZZF5
I	1327	LEU	-	expression tag	UNP W5ZZF5
I	1328	PHE	-	expression tag	UNP W5ZZF5
I	1329	GLN	-	expression tag	UNP W5ZZF5
J	506	PHE	LEU	conflict	UNP W5ZZF5
J	748	ALA	ARG	conflict	UNP W5ZZF5
J	751	GLY	ARG	conflict	UNP W5ZZF5
J	1060	PRO	VAL	engineered mutation	UNP W5ZZF5
J	1061	PRO	LEU	engineered mutation	UNP W5ZZF5
J	1292	GLY	-	expression tag	UNP W5ZZF5
J	1293	SER	-	expression tag	UNP W5ZZF5
J	1294	GLY	-	expression tag	UNP W5ZZF5
J	1295	TYR	-	expression tag	UNP W5ZZF5
J	1296	ILE	-	expression tag	UNP W5ZZF5
J	1297	PRO	-	expression tag	UNP W5ZZF5
J	1298	GLU	-	expression tag	UNP W5ZZF5
J	1299	ALA	-	expression tag	UNP W5ZZF5

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Chain	Residue	Modelled	Actual	Comment	Reference
J	1300	PRO	-	expression tag	UNP W5ZZF5
J	1301	ARG	-	expression tag	UNP W5ZZF5
J	1302	ASP	-	expression tag	UNP W5ZZF5
J	1303	GLY	-	expression tag	UNP W5ZZF5
J	1304	GLN	-	expression tag	UNP W5ZZF5
J	1305	ALA	-	expression tag	UNP W5ZZF5
J	1306	TYR	-	expression tag	UNP W5ZZF5
J	1307	VAL	-	expression tag	UNP W5ZZF5
J	1308	ARG	-	expression tag	UNP W5ZZF5
J	1309	LYS	-	expression tag	UNP W5ZZF5
J	1310	ASP	-	expression tag	UNP W5ZZF5
J	1311	GLY	-	expression tag	UNP W5ZZF5
J	1312	GLU	-	expression tag	UNP W5ZZF5
J	1313	TRP	-	expression tag	UNP W5ZZF5
J	1314	VAL	-	expression tag	UNP W5ZZF5
J	1315	LEU	-	expression tag	UNP W5ZZF5
J	1316	LEU	-	expression tag	UNP W5ZZF5
J	1317	SER	-	expression tag	UNP W5ZZF5
J	1318	THR	-	expression tag	UNP W5ZZF5
J	1319	PHE	-	expression tag	UNP W5ZZF5
J	1320	LEU	-	expression tag	UNP W5ZZF5
J	1321	GLY	-	expression tag	UNP W5ZZF5
J	1322	ARG	-	expression tag	UNP W5ZZF5
J	1323	SER	-	expression tag	UNP W5ZZF5
J	1324	LEU	-	expression tag	UNP W5ZZF5
J	1325	GLU	-	expression tag	UNP W5ZZF5
J	1326	VAL	-	expression tag	UNP W5ZZF5
J	1327	LEU	-	expression tag	UNP W5ZZF5
J	1328	PHE	-	expression tag	UNP W5ZZF5
J	1329	GLN	-	expression tag	UNP W5ZZF5

- Molecule 2 is a protein called G4 VH.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	119	Total	C	N	O	S	0	0
			948	602	156	185	5		
2	G	119	Total	C	N	O	S	0	0
			948	602	156	185	5		
2	K	119	Total	C	N	O	S	0	0
			948	602	156	185	5		

- Molecule 3 is a protein called G4 VL.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	111	Total	C	N	O	S	0	0
			835	522	143	166	4		
3	H	111	Total	C	N	O	S	0	0
			835	522	143	166	4		
3	L	111	Total	C	N	O	S	0	0
			835	522	143	166	4		

- Molecule 4 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
4	M	2	Total	C	N	O	0	0
			28	16	2	10		
4	N	2	Total	C	N	O	0	0
			28	16	2	10		
4	O	2	Total	C	N	O	0	0
			28	16	2	10		
4	P	2	Total	C	N	O	0	0
			28	16	2	10		
4	Q	2	Total	C	N	O	0	0
			28	16	2	10		
4	R	2	Total	C	N	O	0	0
			28	16	2	10		
4	S	2	Total	C	N	O	0	0
			28	16	2	10		
4	T	2	Total	C	N	O	0	0
			28	16	2	10		
4	U	2	Total	C	N	O	0	0
			28	16	2	10		
4	V	2	Total	C	N	O	0	0
			28	16	2	10		
4	W	2	Total	C	N	O	0	0
			28	16	2	10		
4	X	2	Total	C	N	O	0	0
			28	16	2	10		
4	Y	2	Total	C	N	O	0	0
			28	16	2	10		
4	Z	2	Total	C	N	O	0	0
			28	16	2	10		

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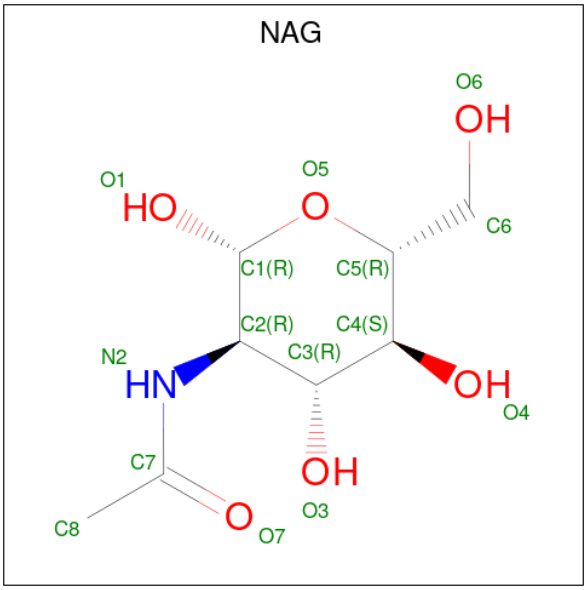
Mol	Chain	Residues	Atoms	AltConf	Trace
4	a	2	Total C N O 28 16 2 10	0	0
4	b	2	Total C N O 28 16 2 10	0	0
4	c	2	Total C N O 28 16 2 10	0	0
4	d	2	Total C N O 28 16 2 10	0	0
4	e	2	Total C N O 28 16 2 10	0	0
4	f	2	Total C N O 28 16 2 10	0	0
4	g	2	Total C N O 28 16 2 10	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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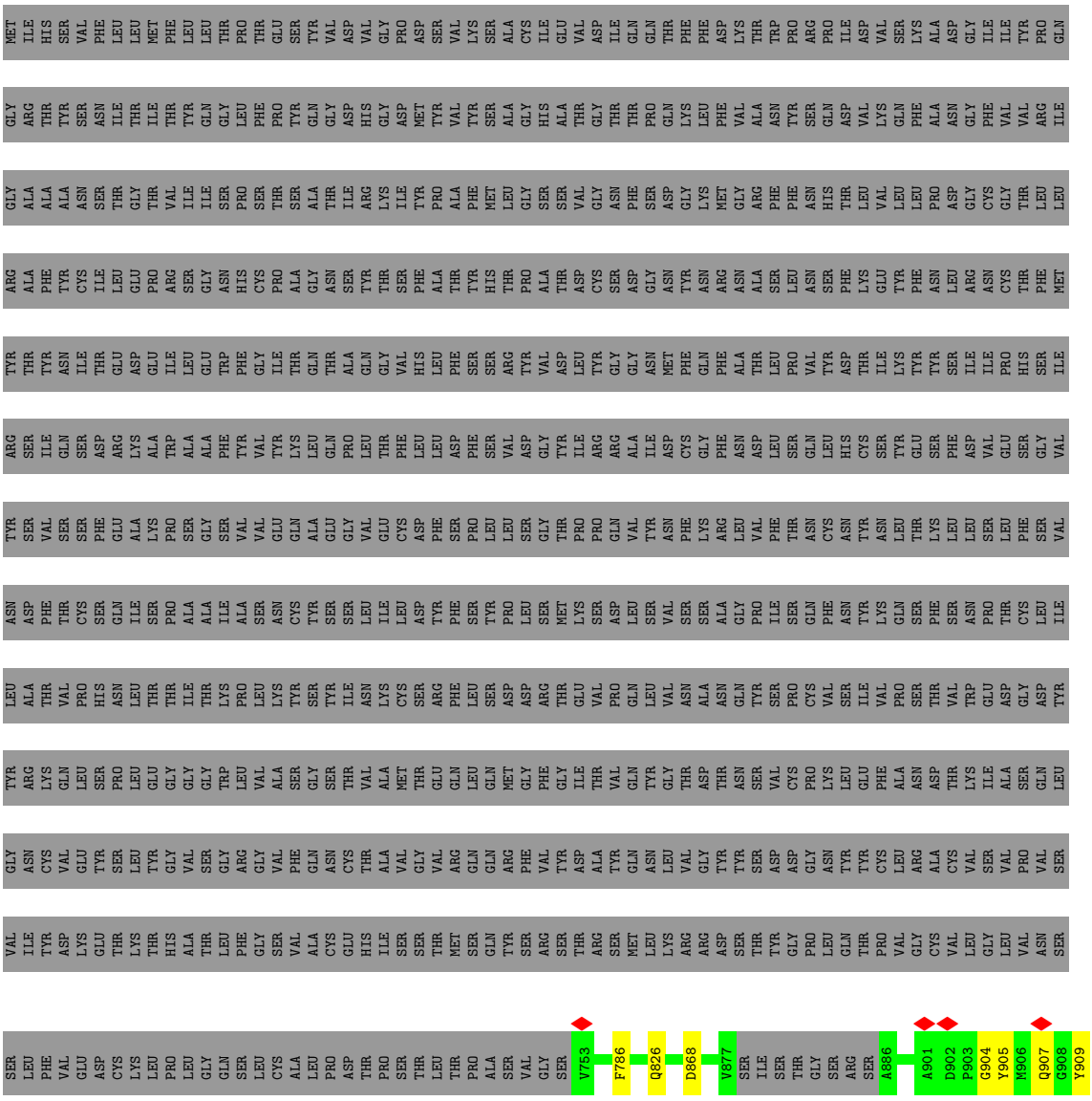
Mol	Chain	Residues	Atoms				AltConf
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	E	1	Total	C	N	O	0
			14	8	1	5	
5	F	1	Total	C	N	O	0
			14	8	1	5	
5	F	1	Total	C	N	O	0
			14	8	1	5	
5	F	1	Total	C	N	O	0
			14	8	1	5	
5	F	1	Total	C	N	O	0
			14	8	1	5	
5	F	1	Total	C	N	O	0
			14	8	1	5	
5	F	1	Total	C	N	O	0
			14	8	1	5	
5	I	1	Total	C	N	O	0
			14	8	1	5	
5	J	1	Total	C	N	O	0
			14	8	1	5	
5	J	1	Total	C	N	O	0
			14	8	1	5	
5	J	1	Total	C	N	O	0
			14	8	1	5	
5	J	1	Total	C	N	O	0
			14	8	1	5	
5	J	1	Total	C	N	O	0
			14	8	1	5	
5	J	1	Total	C	N	O	0
			14	8	1	5	

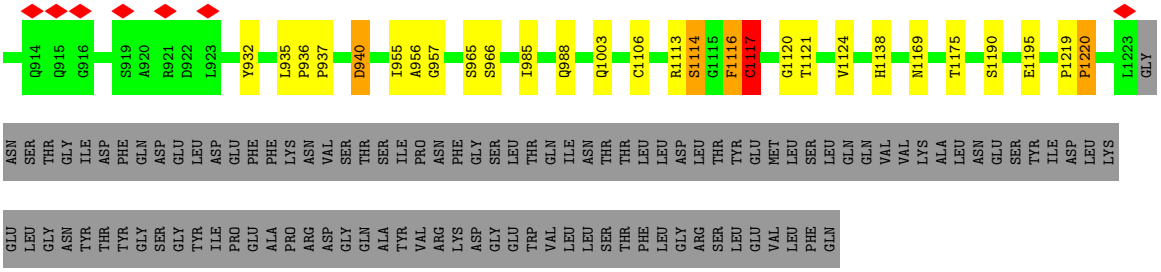
3 Residue-property plots (i)

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: Spike glycoprotein

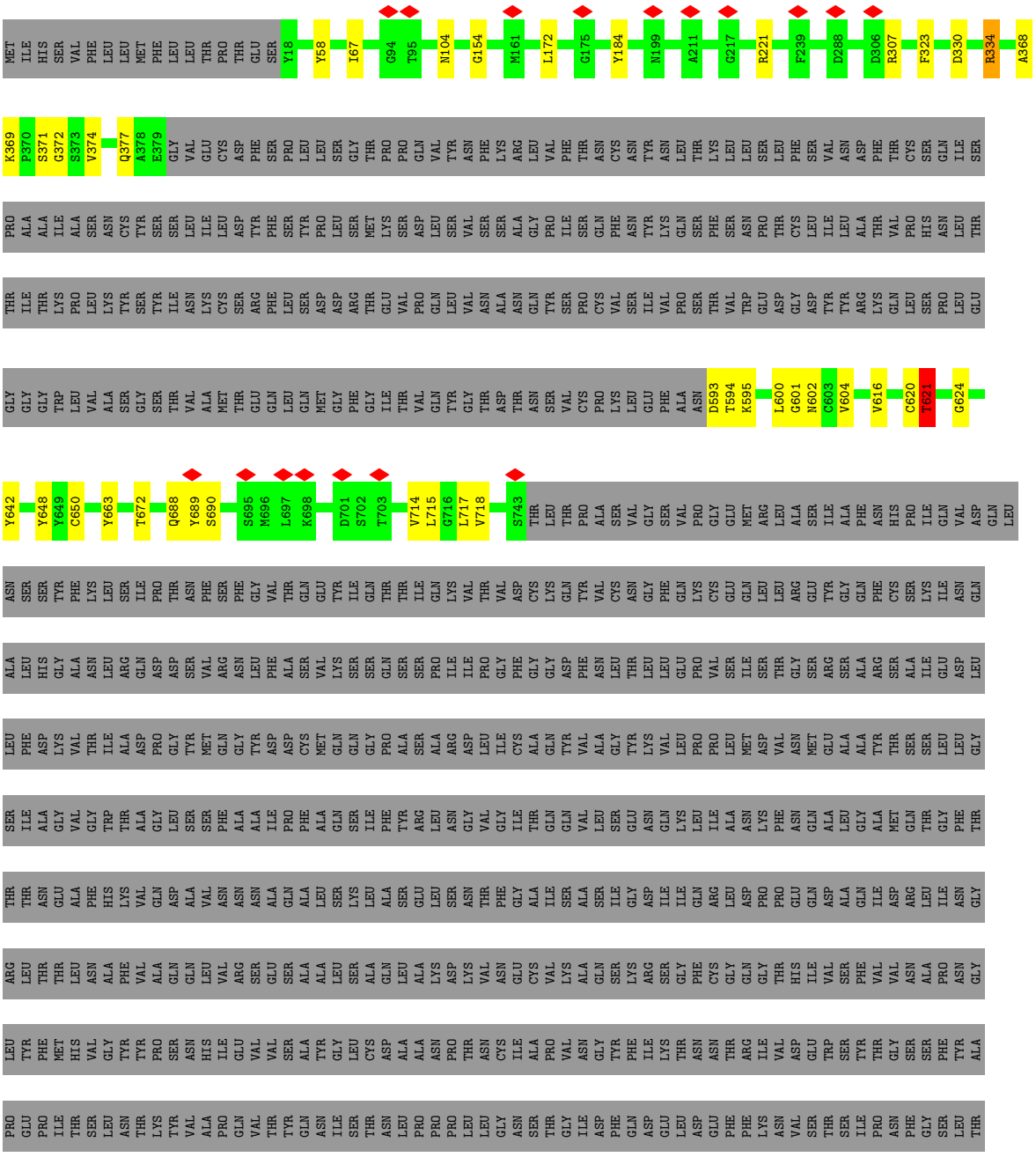
Chain A:

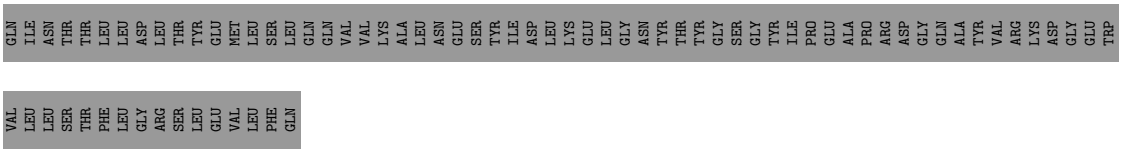




- Molecule 1: Spike glycoprotein

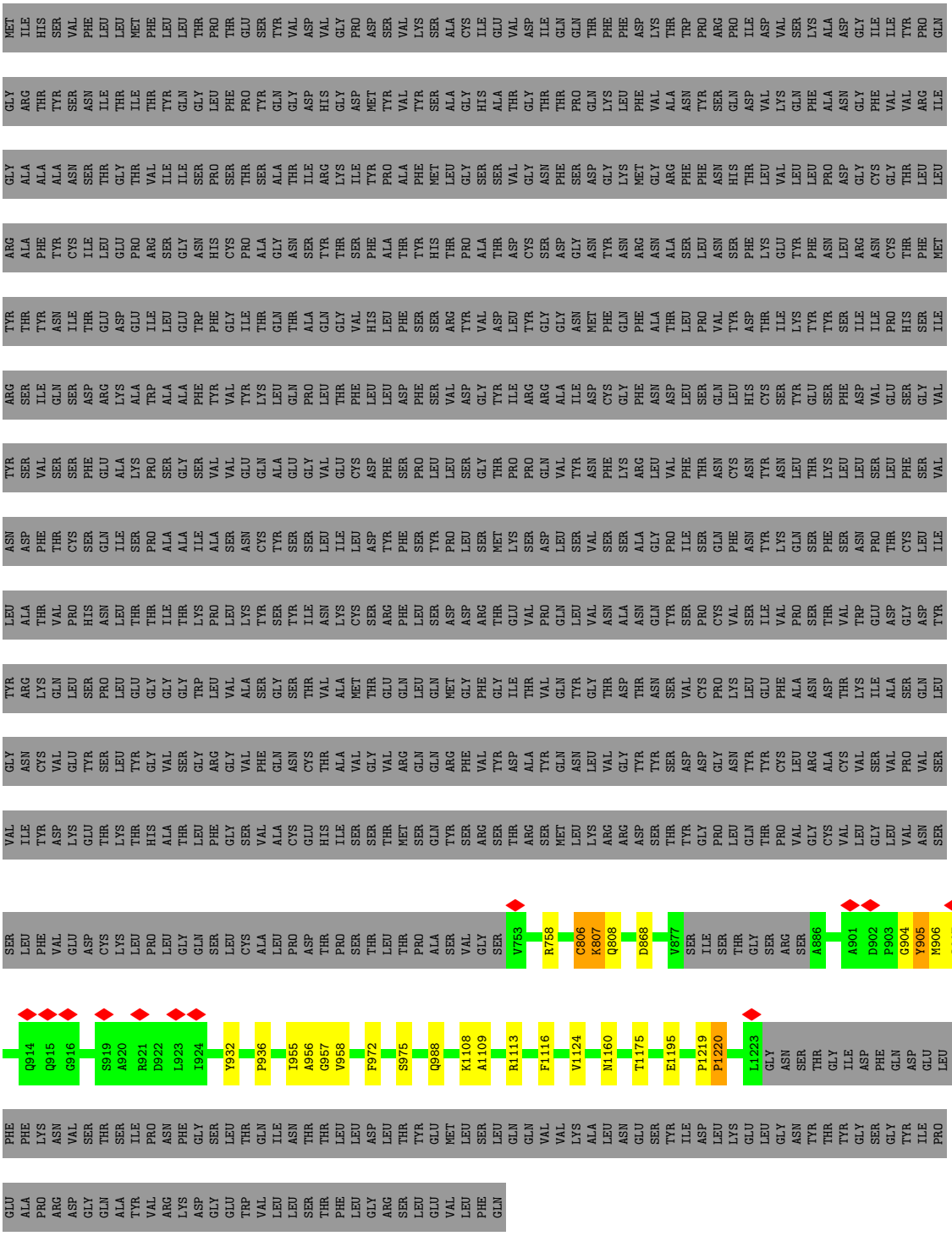
Chain B:





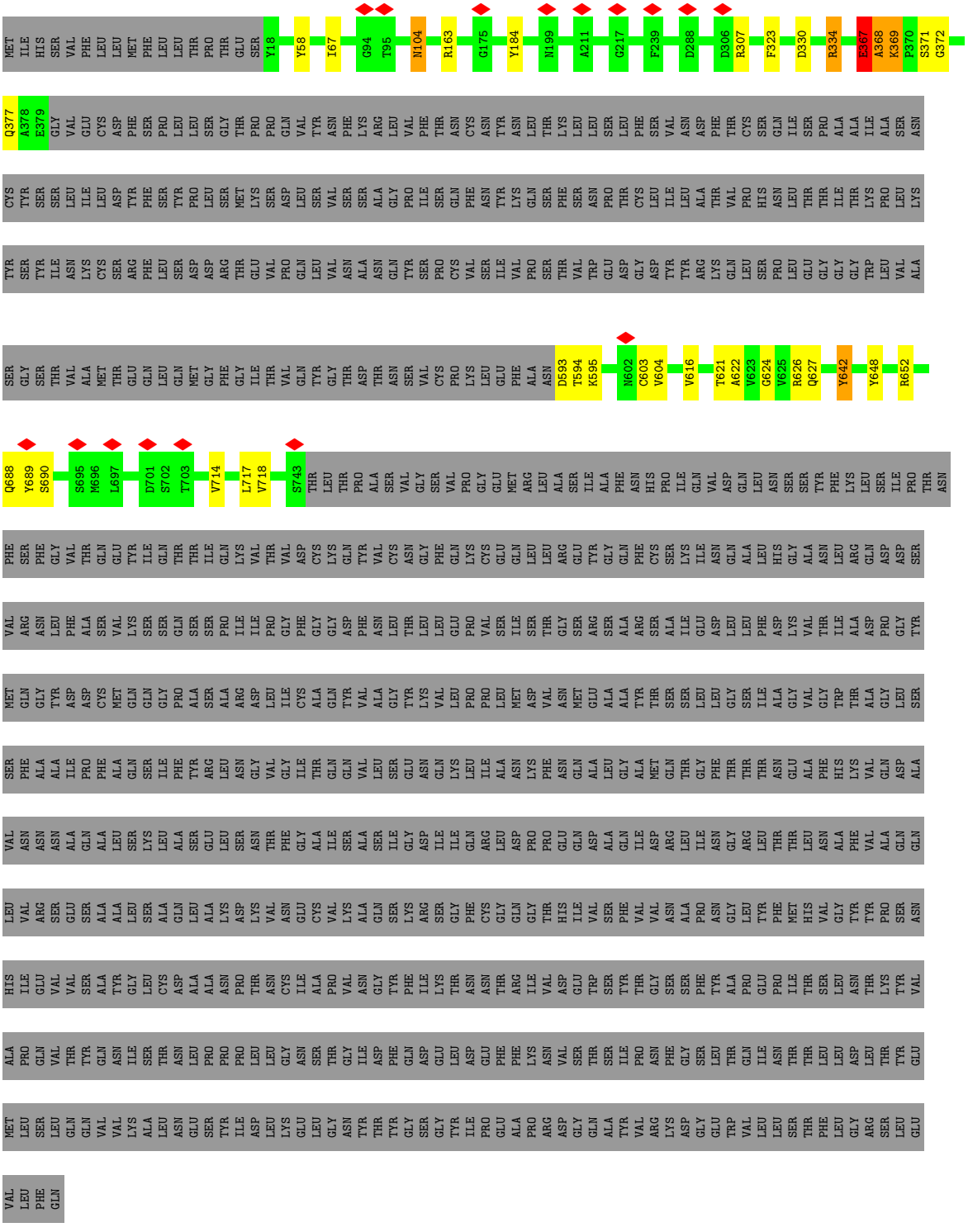
• Molecule 1: Spike glycoprotein

Chain E:



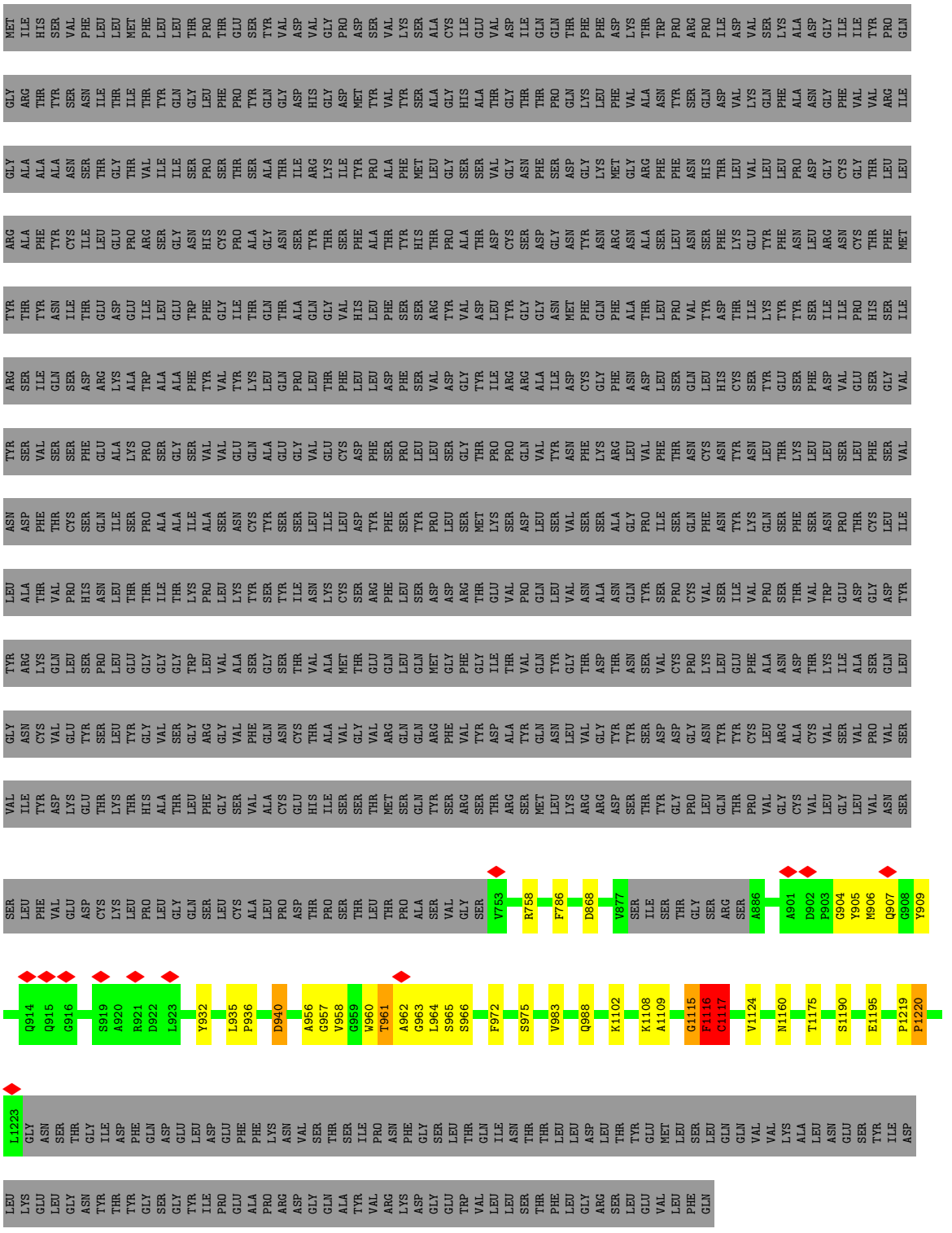
• Molecule 1: Spike glycoprotein

Chain F:



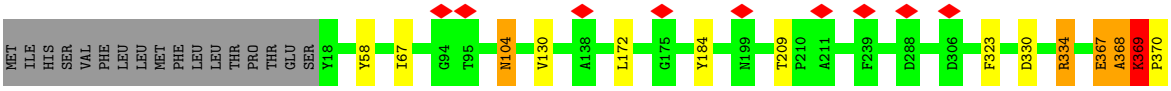
• Molecule 1: Spike glycoprotein

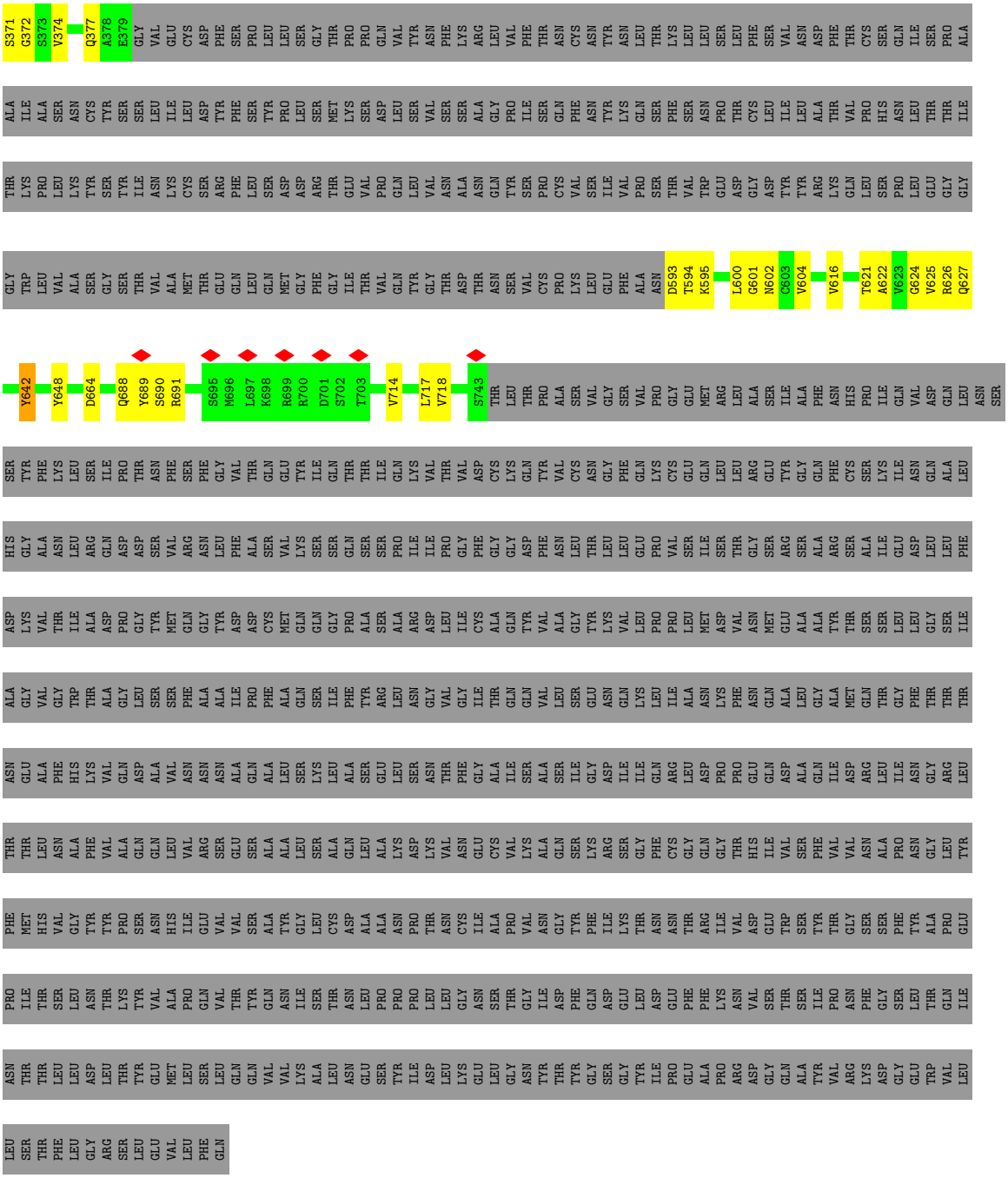
Chain I:



• Molecule 1: Spike glycoprotein

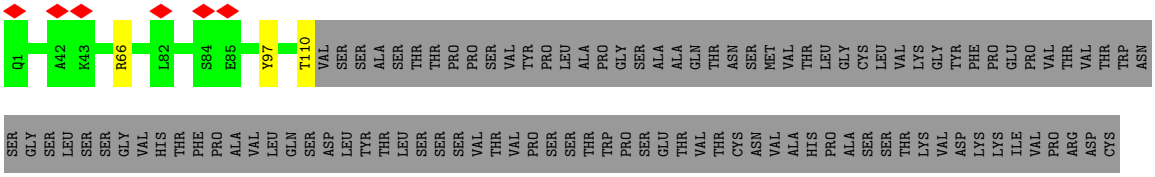
Chain J:





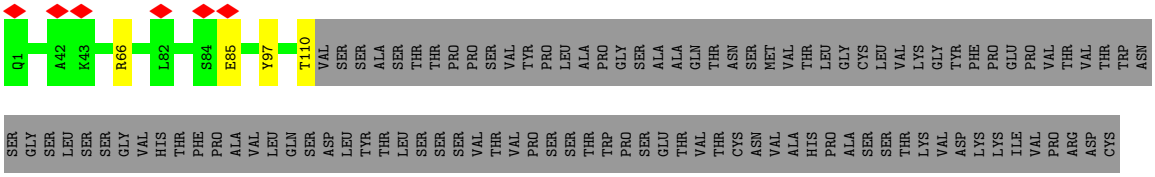
• Molecule 2: G4 VH

Chain C:



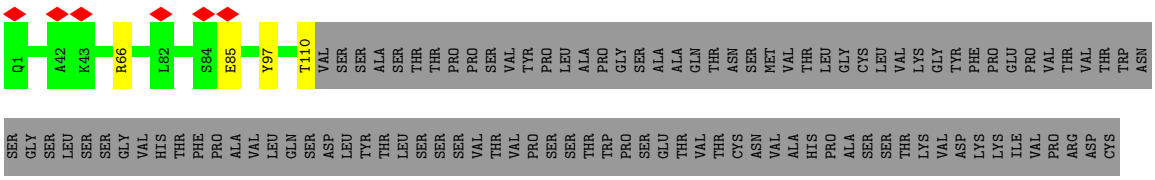
• Molecule 2: G4 VH

Chain G:



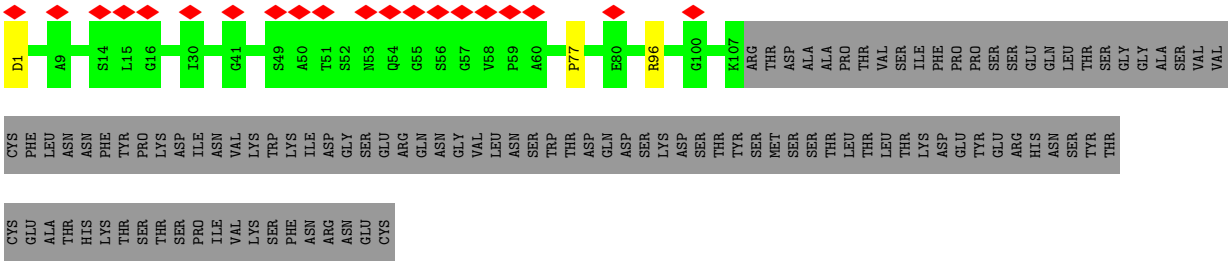
• Molecule 2: G4 VH

Chain K:



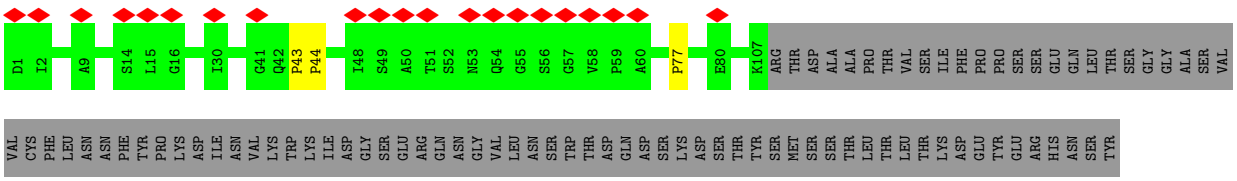
• Molecule 3: G4 VL

Chain D:



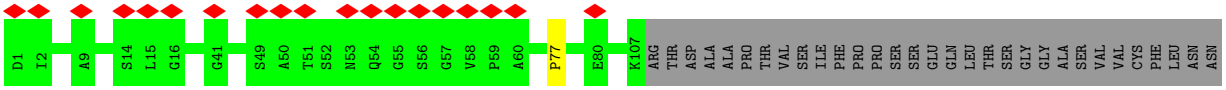
• Molecule 3: G4 VL

Chain H:



• Molecule 3: G4 VL

Chain L:



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

Chain M:

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

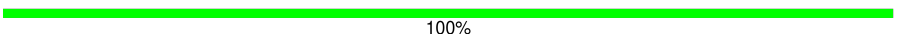
Chain N:

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

Chain O:

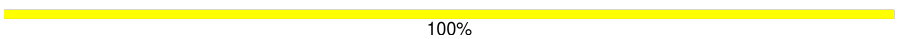
• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:



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

Chain Q:



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

Chain R:

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

Chain S:

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

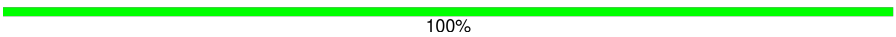
Chain T:

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

Chain U:

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

Chain V:



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

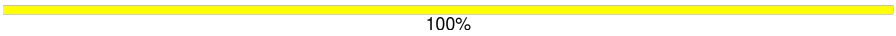
Chain W:

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

Chain X:

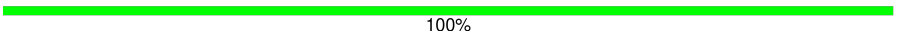
• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Y:



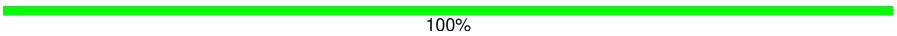
• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain Z:



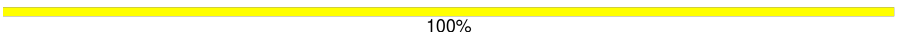
• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain a:



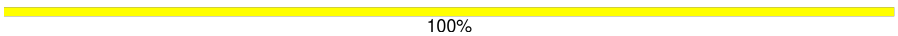
• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain b:



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

Chain c:

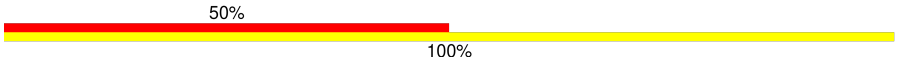


• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain d:

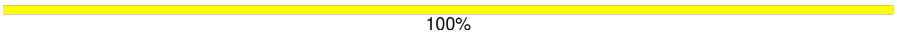
• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain e:



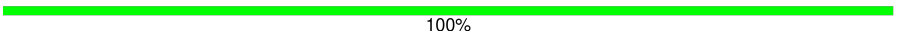
• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain f:



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

Chain g:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	37180	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 ($e^-/Å^2$)	1.89	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	29000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.124	Depositor
Minimum map value	-0.059	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	310.08, 310.08, 310.08	wwPDB
Map dimensions	304, 304, 304	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.02, 1.02, 1.02	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.75	0/3618	0.84	6/4921 (0.1%)
1	B	0.72	0/4112	0.90	9/5590 (0.2%)
1	E	0.75	0/3618	0.81	2/4921 (0.0%)
1	F	0.71	0/4112	0.90	10/5590 (0.2%)
1	I	0.76	0/3618	0.84	6/4921 (0.1%)
1	J	0.72	0/4112	0.89	8/5590 (0.1%)
2	C	0.72	0/972	0.88	2/1317 (0.2%)
2	G	0.71	0/972	0.87	2/1317 (0.2%)
2	K	0.71	0/972	0.87	2/1317 (0.2%)
3	D	0.73	0/852	0.88	1/1153 (0.1%)
3	H	0.74	0/852	0.87	0/1153
3	L	0.74	0/852	0.86	0/1153
All	All	0.73	0/28662	0.87	48/38943 (0.1%)

There are no bond length outliers.

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	642	TYR	CB-CG-CD1	-8.74	115.75	121.00
1	B	642	TYR	CB-CG-CD1	-8.61	115.83	121.00
1	J	334	ARG	NE-CZ-NH2	-8.57	116.02	120.30
1	F	334	ARG	NE-CZ-NH2	-8.56	116.02	120.30
1	B	334	ARG	NE-CZ-NH2	-8.18	116.21	120.30

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	3545	0	3467	38	0
1	B	4010	0	3808	38	0
1	E	3545	0	3467	39	0
1	F	4010	0	3808	42	0
1	I	3545	0	3467	45	0
1	J	4010	0	3810	67	0
2	C	948	0	904	1	0
2	G	948	0	904	2	0
2	K	948	0	904	2	0
3	D	835	0	816	1	0
3	H	835	0	816	1	0
3	L	835	0	816	0	0
4	M	28	0	25	1	0
4	N	28	0	25	0	0
4	O	28	0	25	0	0
4	P	28	0	25	0	0
4	Q	28	0	25	0	0
4	R	28	0	25	1	0
4	S	28	0	25	0	0
4	T	28	0	25	0	0
4	U	28	0	25	0	0
4	V	28	0	25	0	0
4	W	28	0	25	0	0
4	X	28	0	25	0	0
4	Y	28	0	24	0	0
4	Z	28	0	25	0	0
4	a	28	0	25	0	0
4	b	28	0	25	0	0
4	c	28	0	25	0	0
4	d	28	0	25	0	0
4	e	28	0	25	0	0
4	f	28	0	25	0	0
4	g	28	0	25	0	0
5	A	14	0	13	0	0
5	B	84	0	78	1	0
5	E	14	0	13	0	0
5	F	84	0	78	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	I	14	0	13	0	0
5	J	84	0	75	0	0
All	All	28896	0	27781	259	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 259 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:905:TYR:OH	1:A:936:PRO:CA	1.68	1.41
1:E:905:TYR:OH	1:E:936:PRO:CA	1.70	1.39
1:I:905:TYR:OH	1:I:936:PRO:HA	1.26	1.34
1:I:905:TYR:OH	1:I:936:PRO:CA	1.75	1.32
1:A:905:TYR:OH	1:A:936:PRO:HA	1.13	1.24

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	459/1329 (34%)	441 (96%)	14 (3%)	4 (1%)	14	48
1	B	509/1329 (38%)	478 (94%)	27 (5%)	4 (1%)	16	51
1	E	459/1329 (34%)	435 (95%)	20 (4%)	4 (1%)	14	48
1	F	509/1329 (38%)	475 (93%)	29 (6%)	5 (1%)	13	46
1	I	459/1329 (34%)	438 (95%)	14 (3%)	7 (2%)	8	39
1	J	509/1329 (38%)	475 (93%)	30 (6%)	4 (1%)	16	51
2	C	117/233 (50%)	115 (98%)	2 (2%)	0	100	100
2	G	117/233 (50%)	115 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	K	117/233 (50%)	115 (98%)	2 (2%)	0	100	100
3	D	109/218 (50%)	105 (96%)	3 (3%)	1 (1%)	14	48
3	H	109/218 (50%)	105 (96%)	3 (3%)	1 (1%)	14	48
3	L	109/218 (50%)	105 (96%)	3 (3%)	1 (1%)	14	48
All	All	3582/9327 (38%)	3402 (95%)	149 (4%)	31 (1%)	17	48

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1114	SER
1	A	1117	CYS
1	E	806	CYS
1	E	807	LYS
1	F	367	GLU

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	388/1148 (34%)	387 (100%)	1 (0%)	91	96
1	B	442/1148 (38%)	441 (100%)	1 (0%)	92	96
1	E	388/1148 (34%)	388 (100%)	0	100	100
1	F	442/1148 (38%)	440 (100%)	2 (0%)	86	93
1	I	388/1148 (34%)	387 (100%)	1 (0%)	91	96
1	J	442/1148 (38%)	441 (100%)	1 (0%)	92	96
2	C	102/202 (50%)	102 (100%)	0	100	100
2	G	102/202 (50%)	102 (100%)	0	100	100
2	K	102/202 (50%)	102 (100%)	0	100	100
3	D	93/192 (48%)	93 (100%)	0	100	100
3	H	93/192 (48%)	93 (100%)	0	100	100
3	L	93/192 (48%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3075/8070 (38%)	3069 (100%)	6 (0%)	91 96

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	367	GLU
1	I	1116	PHE
1	J	104	ASN
1	B	621	THR
1	A	1116	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1003	GLN
1	I	1169	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

42 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	M	1	4,1	14,14,15	0.46	0	17,19,21	0.87	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	NAG	M	2	4	14,14,15	0.63	0	17,19,21	0.94	1 (5%)
4	NAG	N	1	4,1	14,14,15	0.78	1 (7%)	17,19,21	0.51	0
4	NAG	N	2	4	14,14,15	0.25	0	17,19,21	0.58	0
4	NAG	O	1	4,1	14,14,15	0.33	0	17,19,21	0.47	0
4	NAG	O	2	4	14,14,15	0.34	0	17,19,21	0.64	1 (5%)
4	NAG	P	1	4,1	14,14,15	0.39	0	17,19,21	0.59	0
4	NAG	P	2	4	14,14,15	0.30	0	17,19,21	0.44	0
4	NAG	Q	1	4,1	14,14,15	0.92	1 (7%)	17,19,21	0.71	0
4	NAG	Q	2	4	14,14,15	0.19	0	17,19,21	0.70	1 (5%)
4	NAG	R	1	4,1	14,14,15	1.30	1 (7%)	17,19,21	1.27	2 (11%)
4	NAG	R	2	4	14,14,15	0.65	1 (7%)	17,19,21	0.50	0
4	NAG	S	1	4,1	14,14,15	1.44	3 (21%)	17,19,21	1.48	2 (11%)
4	NAG	S	2	4	14,14,15	0.60	0	17,19,21	0.72	0
4	NAG	T	1	4,1	14,14,15	0.60	0	17,19,21	0.83	0
4	NAG	T	2	4	14,14,15	0.84	1 (7%)	17,19,21	2.38	3 (17%)
4	NAG	U	1	4,1	14,14,15	0.51	0	17,19,21	1.12	1 (5%)
4	NAG	U	2	4	14,14,15	0.21	0	17,19,21	0.51	0
4	NAG	V	1	4,1	14,14,15	0.44	0	17,19,21	0.69	0
4	NAG	V	2	4	14,14,15	0.28	0	17,19,21	0.53	0
4	NAG	W	1	4,1	14,14,15	0.33	0	17,19,21	0.90	0
4	NAG	W	2	4	14,14,15	0.66	1 (7%)	17,19,21	0.65	1 (5%)
4	NAG	X	1	4,1	14,14,15	0.46	0	17,19,21	1.46	3 (17%)
4	NAG	X	2	4	14,14,15	0.27	0	17,19,21	0.61	0
4	NAG	Y	1	4,1	14,14,15	0.70	1 (7%)	17,19,21	1.09	1 (5%)
4	NAG	Y	2	4	14,14,15	0.64	0	17,19,21	1.00	1 (5%)
4	NAG	Z	1	4,1	14,14,15	0.32	0	17,19,21	0.60	0
4	NAG	Z	2	4	14,14,15	0.36	0	17,19,21	0.55	0
4	NAG	a	1	4,1	14,14,15	0.30	0	17,19,21	0.68	0
4	NAG	a	2	4	14,14,15	0.50	0	17,19,21	0.57	0
4	NAG	b	1	4,1	14,14,15	1.09	1 (7%)	17,19,21	0.69	1 (5%)
4	NAG	b	2	4	14,14,15	0.42	0	17,19,21	0.75	1 (5%)
4	NAG	c	1	4,1	14,14,15	0.21	0	17,19,21	1.17	2 (11%)
4	NAG	c	2	4	14,14,15	0.42	0	17,19,21	1.09	1 (5%)
4	NAG	d	1	4,1	14,14,15	0.54	0	17,19,21	0.74	1 (5%)
4	NAG	d	2	4	14,14,15	0.26	0	17,19,21	0.57	0
4	NAG	e	1	4,1	14,14,15	0.80	1 (7%)	17,19,21	1.24	2 (11%)
4	NAG	e	2	4	14,14,15	0.73	0	17,19,21	0.98	1 (5%)
4	NAG	f	1	4,1	14,14,15	0.77	1 (7%)	17,19,21	1.20	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	NAG	f	2	4	14,14,15	1.76	2 (14%)	17,19,21	1.38	1 (5%)
4	NAG	g	1	4,1	14,14,15	0.19	0	17,19,21	0.61	0
4	NAG	g	2	4	14,14,15	0.29	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
4	NAG	M	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	M	2	4	-	3/6/23/26	0/1/1/1
4	NAG	N	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	N	2	4	-	0/6/23/26	0/1/1/1
4	NAG	O	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	O	2	4	-	2/6/23/26	0/1/1/1
4	NAG	P	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	P	2	4	-	2/6/23/26	0/1/1/1
4	NAG	Q	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	4/6/23/26	0/1/1/1
4	NAG	R	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	R	2	4	-	1/6/23/26	0/1/1/1
4	NAG	S	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	S	2	4	-	3/6/23/26	0/1/1/1
4	NAG	T	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	T	2	4	-	5/6/23/26	0/1/1/1
4	NAG	U	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	U	2	4	-	2/6/23/26	0/1/1/1
4	NAG	V	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	V	2	4	-	2/6/23/26	0/1/1/1
4	NAG	W	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	W	2	4	-	2/6/23/26	0/1/1/1
4	NAG	X	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	X	2	4	-	3/6/23/26	0/1/1/1
4	NAG	Y	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	Y	2	4	-	3/6/23/26	0/1/1/1
4	NAG	Z	1	4,1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	Z	2	4	-	2/6/23/26	0/1/1/1
4	NAG	a	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	a	2	4	-	2/6/23/26	0/1/1/1
4	NAG	b	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	b	2	4	-	2/6/23/26	0/1/1/1
4	NAG	c	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	c	2	4	-	4/6/23/26	0/1/1/1
4	NAG	d	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	d	2	4	-	0/6/23/26	0/1/1/1
4	NAG	e	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	e	2	4	-	3/6/23/26	0/1/1/1
4	NAG	f	1	4,1	-	3/6/23/26	0/1/1/1
4	NAG	f	2	4	-	4/6/23/26	0/1/1/1
4	NAG	g	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	g	2	4	-	1/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	f	2	NAG	O5-C1	5.26	1.52	1.43
4	R	1	NAG	O5-C1	-4.63	1.35	1.43
4	b	1	NAG	O5-C1	-3.70	1.37	1.43
4	f	2	NAG	C1-C2	3.69	1.57	1.52
4	S	1	NAG	O5-C1	-3.63	1.37	1.43

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	T	2	NAG	C2-N2-C7	8.34	134.07	122.90
4	f	2	NAG	C1-O5-C5	5.09	119.01	112.19
4	S	1	NAG	C4-C3-C2	4.36	117.41	111.02
4	T	2	NAG	C1-C2-N2	3.90	116.58	110.43
4	X	1	NAG	C1-O5-C5	3.86	117.35	112.19

There are no chirality outliers.

5 of 96 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	X	1	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	Z	2	NAG	O5-C5-C6-O6
4	U	2	NAG	C4-C5-C6-O6
4	P	1	NAG	O5-C5-C6-O6
4	c	1	NAG	O5-C5-C6-O6

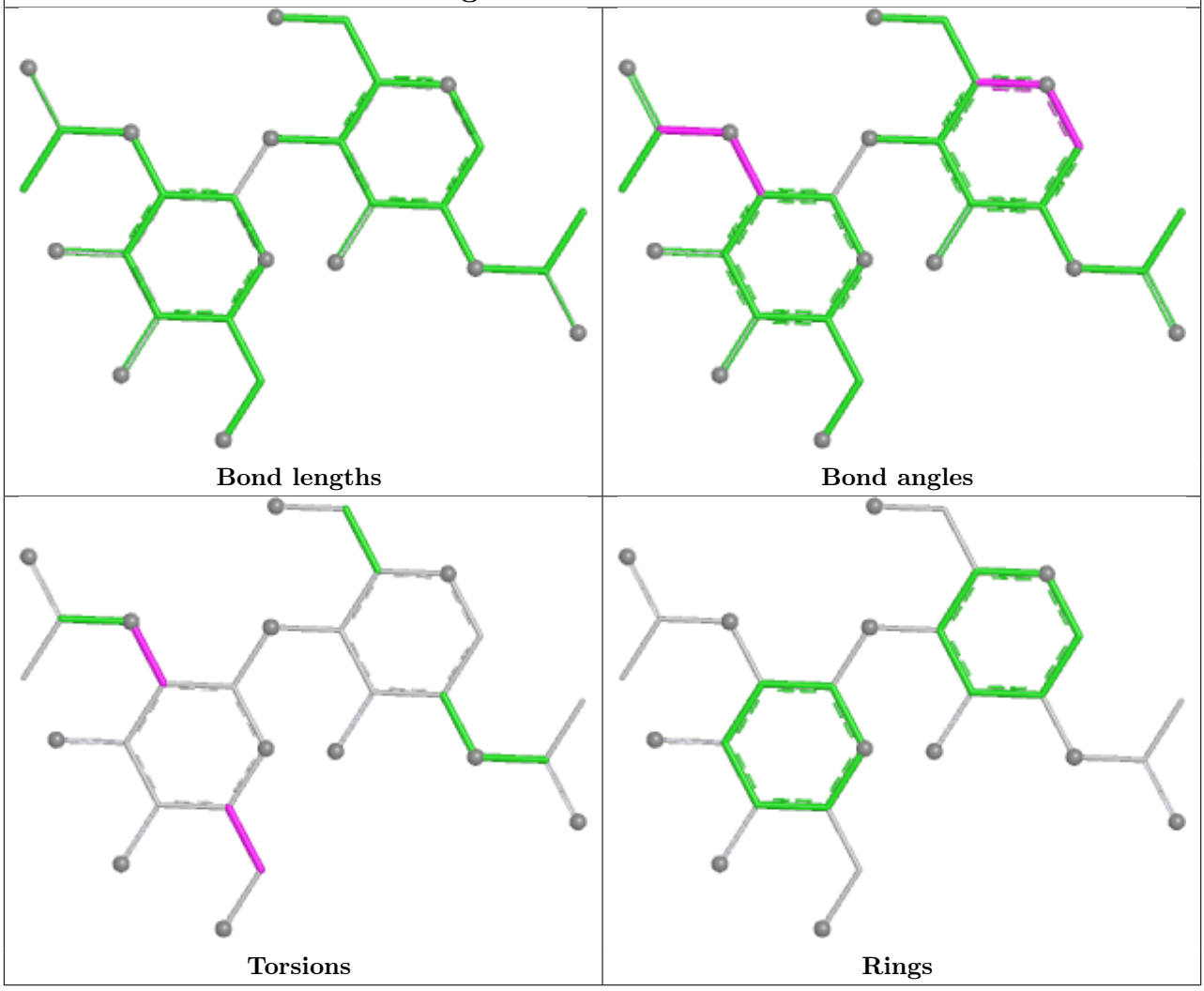
There are no ring outliers.

2 monomers are involved in 2 short contacts:

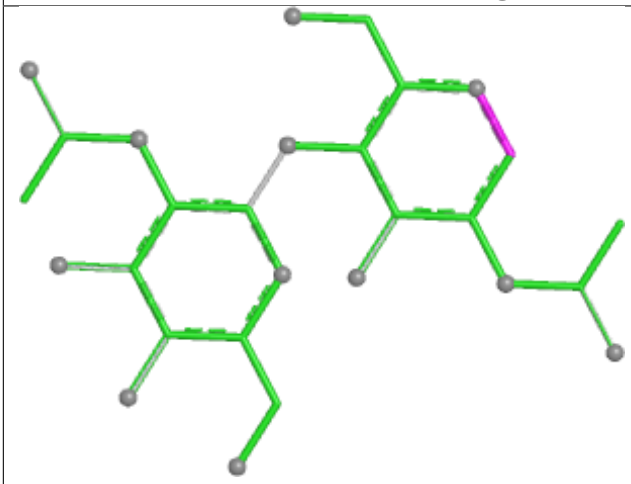
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	R	1	NAG	1	0
4	M	2	NAG	1	0

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

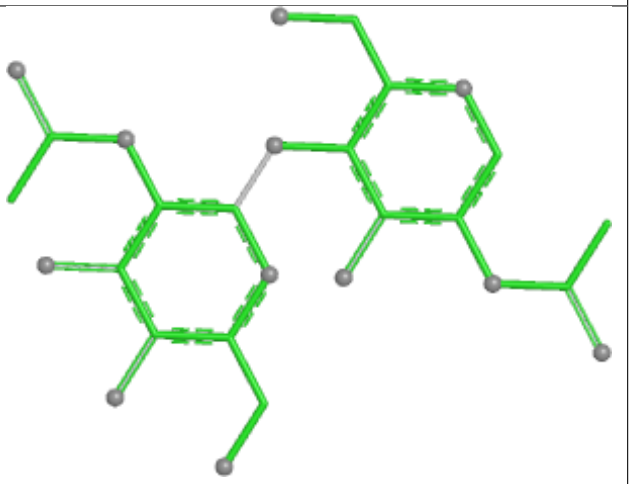
Oligosaccharide Chain M



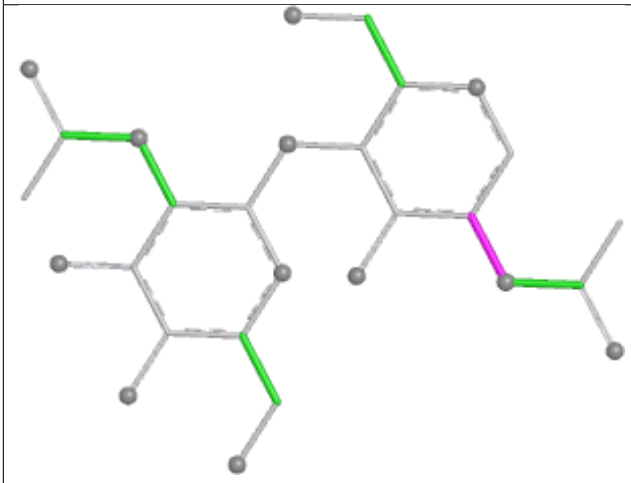
Oligosaccharide Chain N



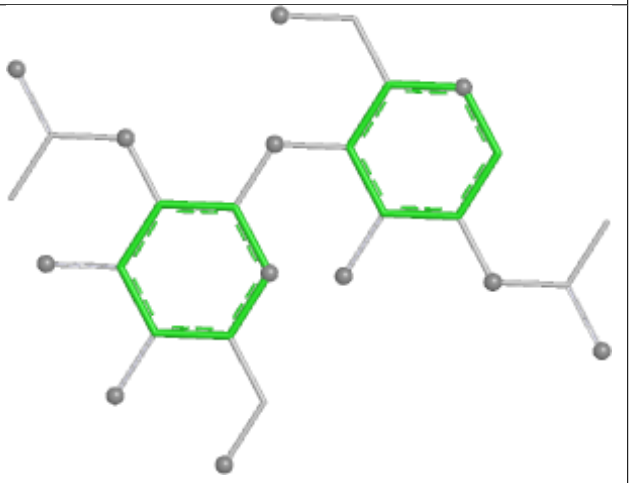
Bond lengths



Bond angles

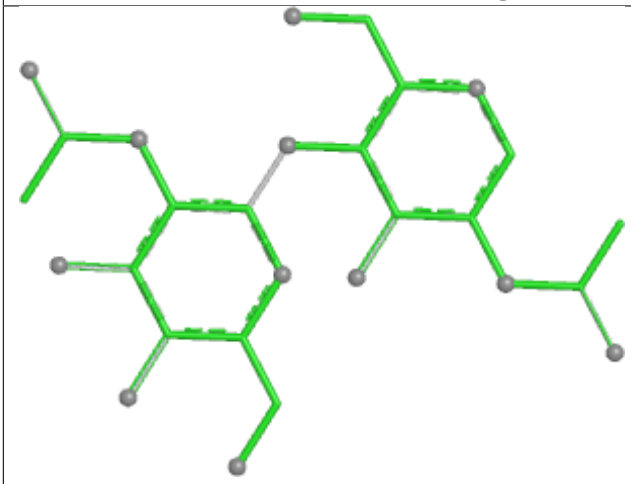


Torsions

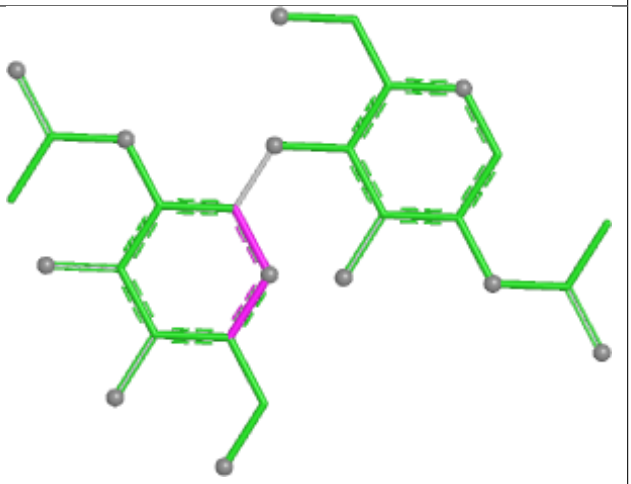


Rings

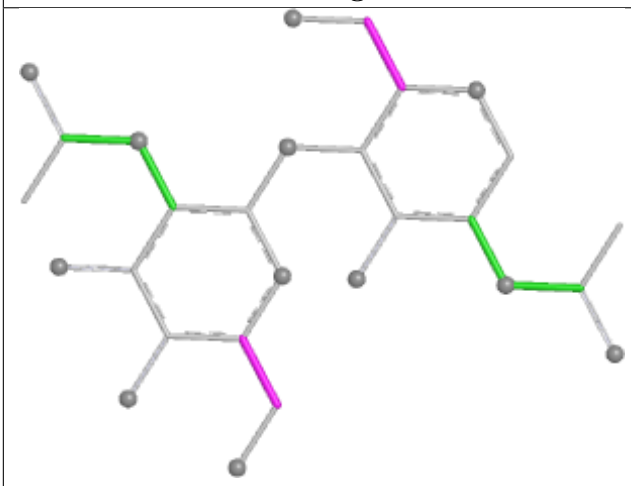
Oligosaccharide Chain O



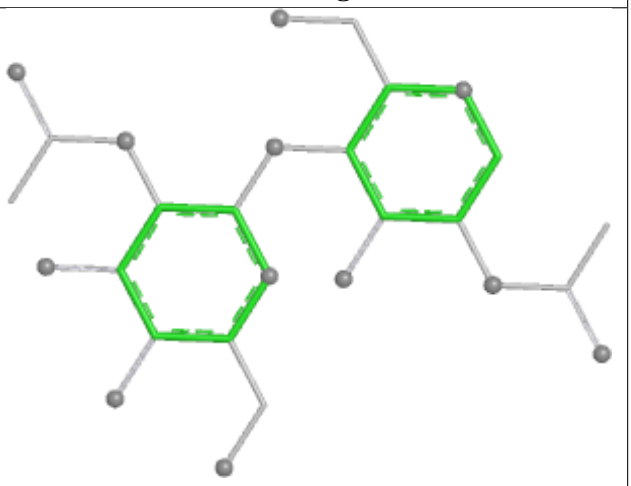
Bond lengths



Bond angles

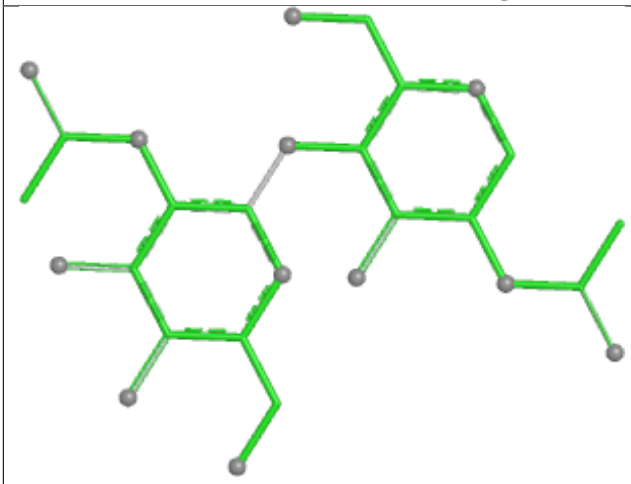


Torsions

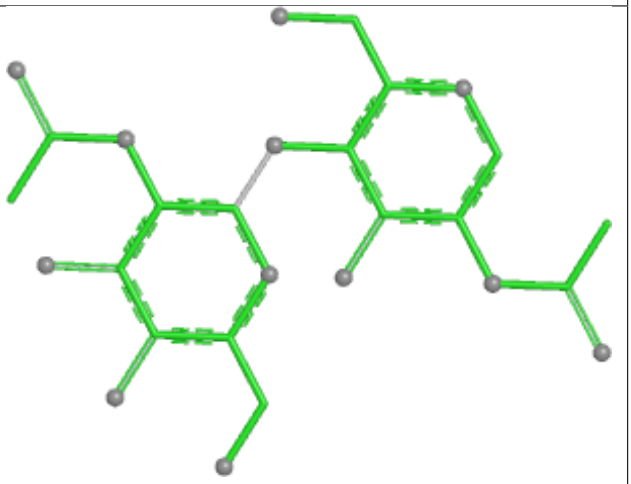


Rings

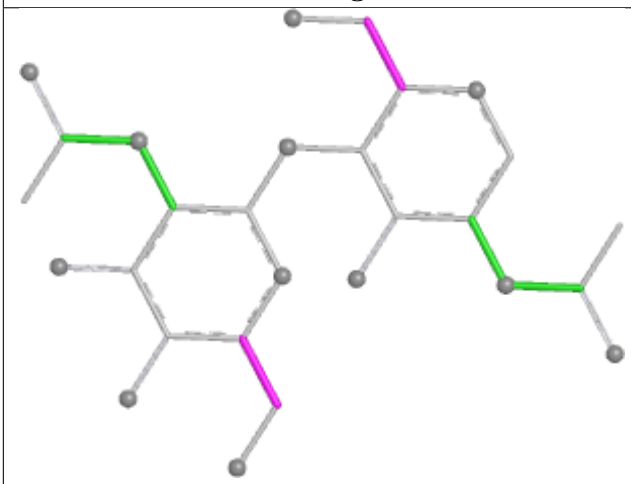
Oligosaccharide Chain P



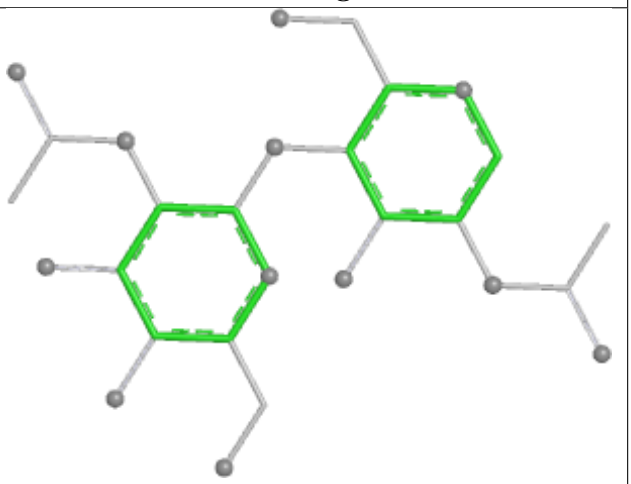
Bond lengths



Bond angles

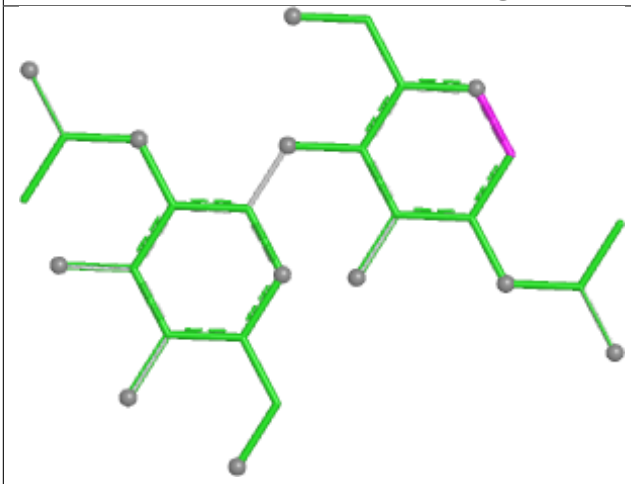


Torsions

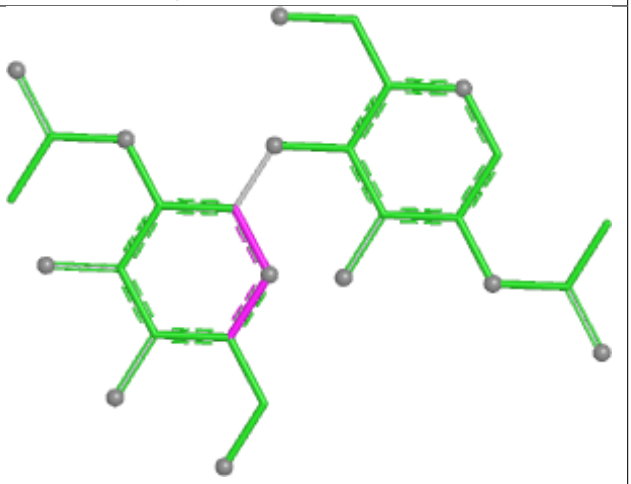


Rings

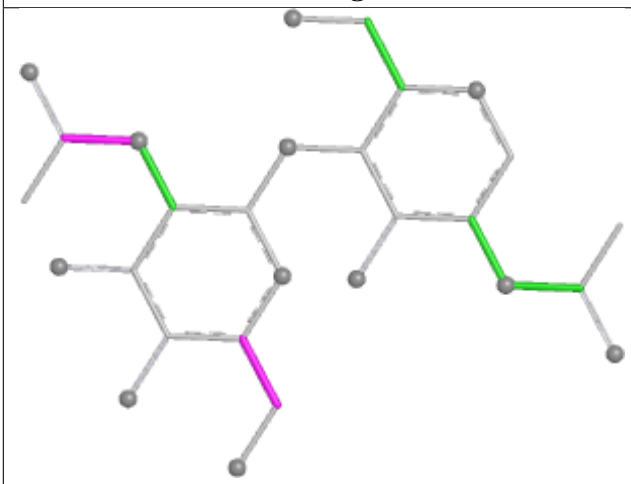
Oligosaccharide Chain Q



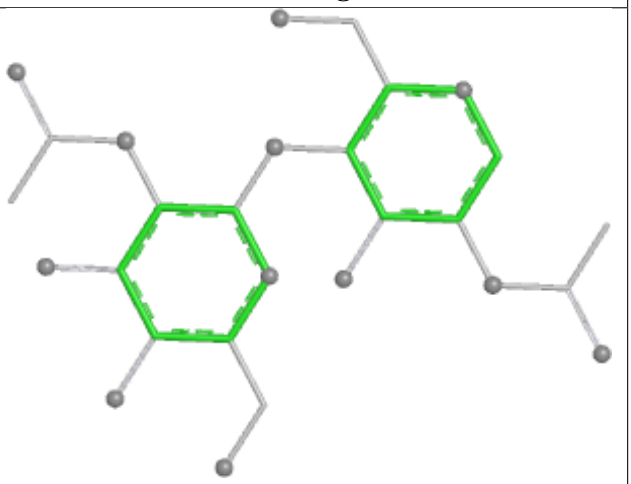
Bond lengths



Bond angles

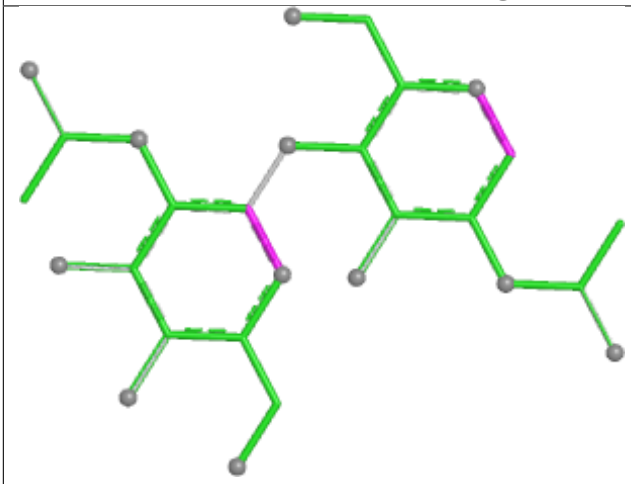


Torsions

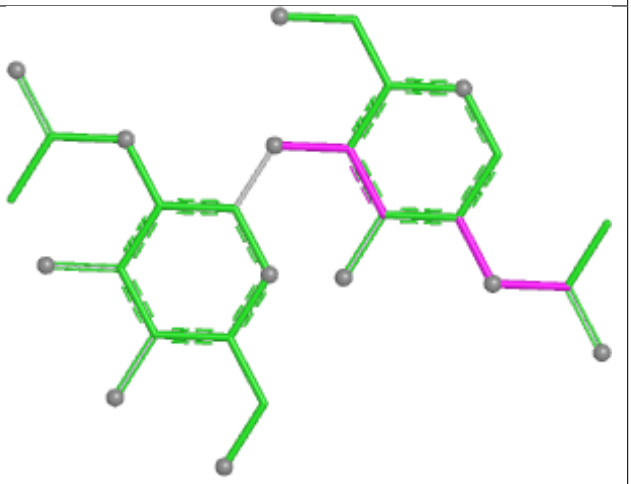


Rings

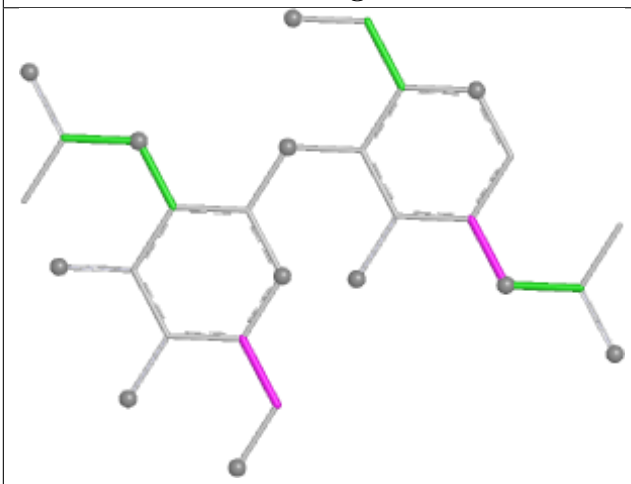
Oligosaccharide Chain R



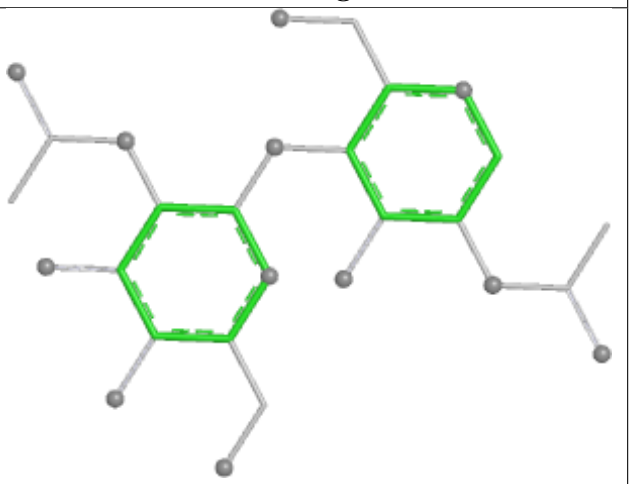
Bond lengths



Bond angles

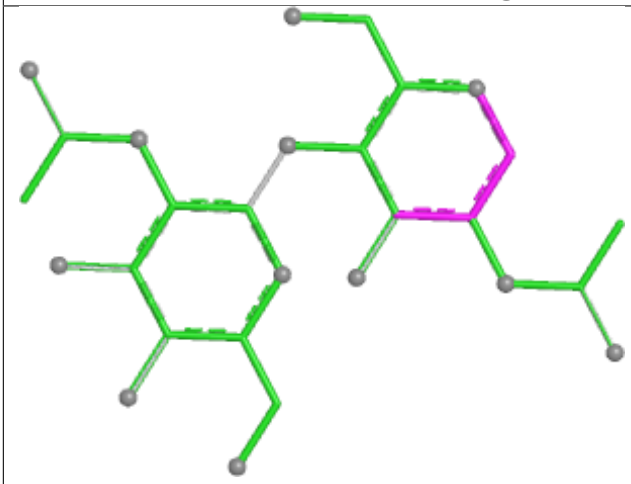


Torsions



Rings

Oligosaccharide Chain S



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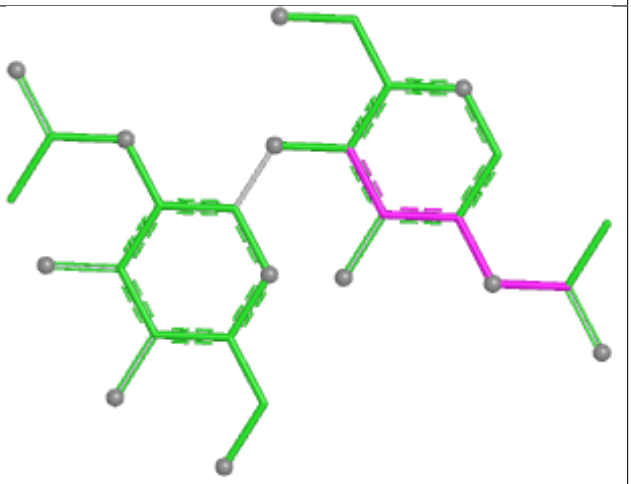

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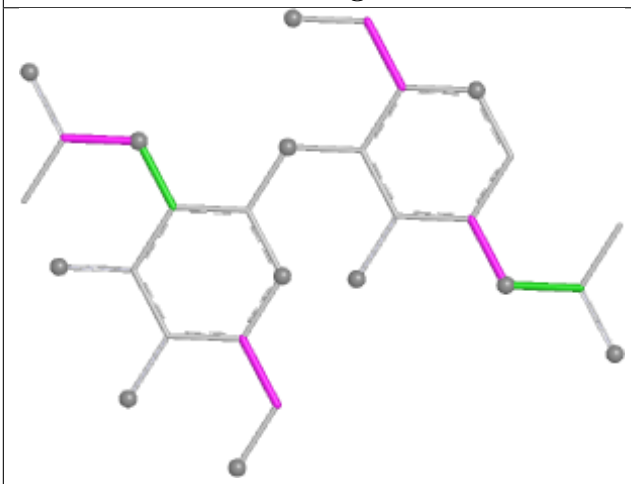

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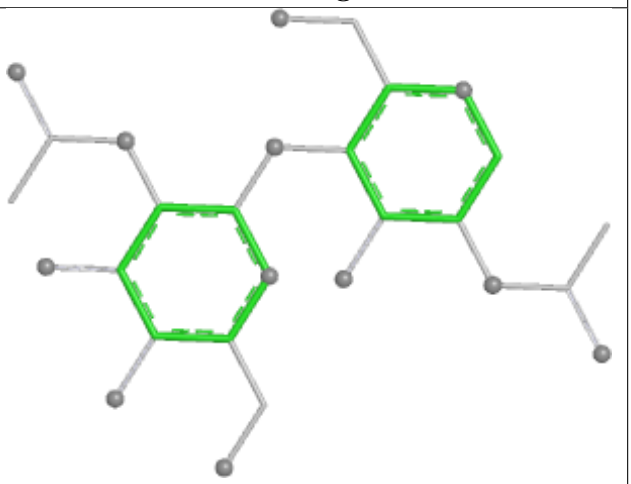
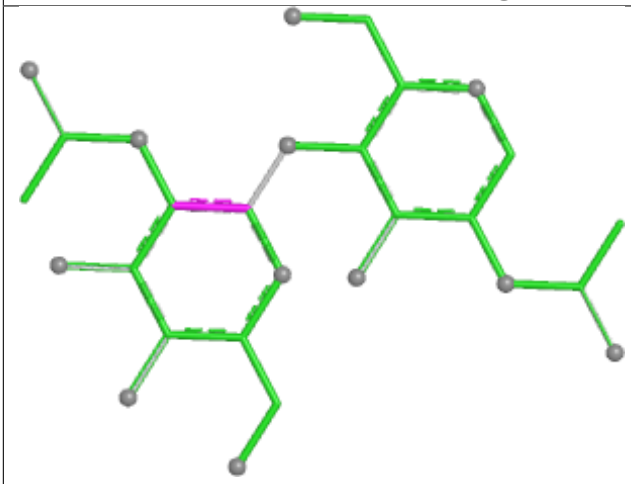


Rings

Oligosaccharide Chain T



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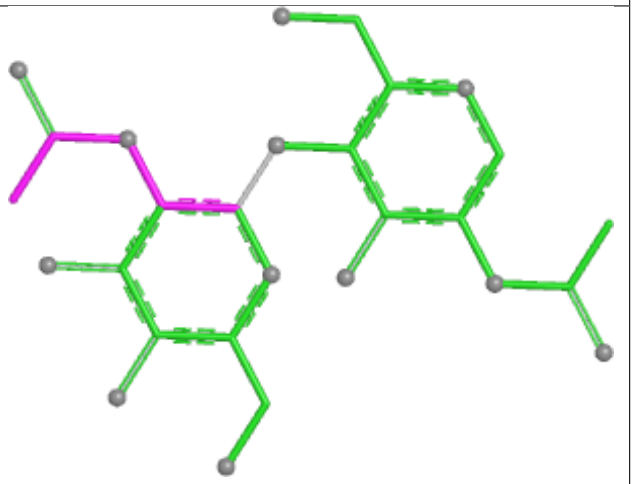

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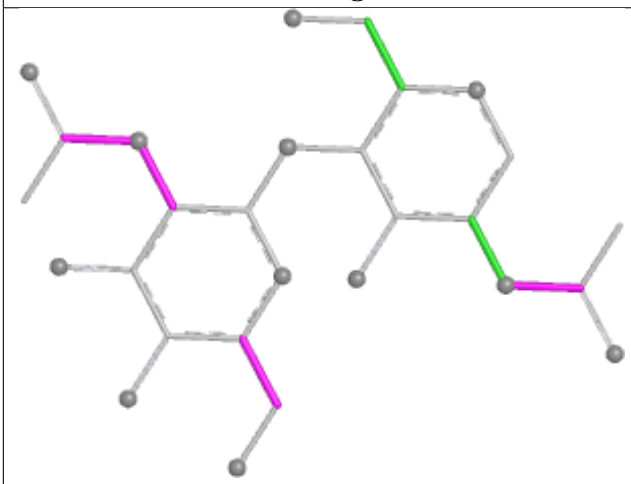

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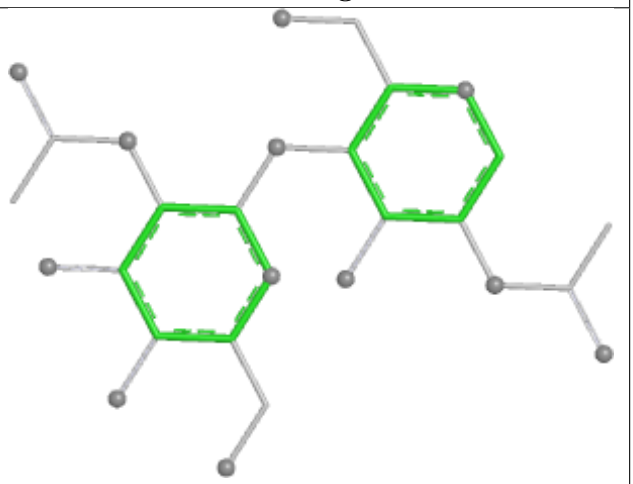
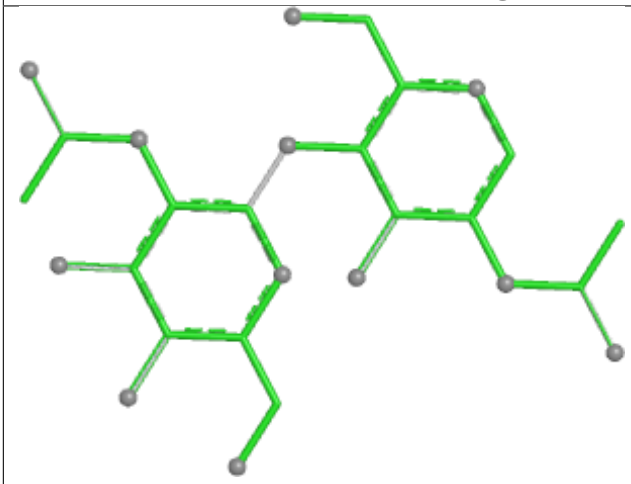


Rings

Oligosaccharide Chain U



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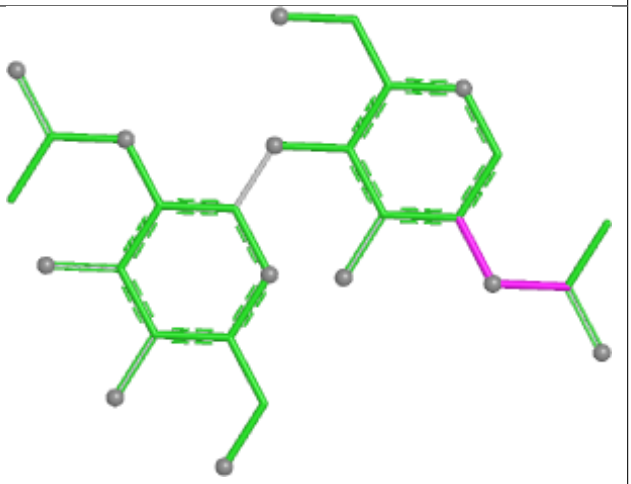

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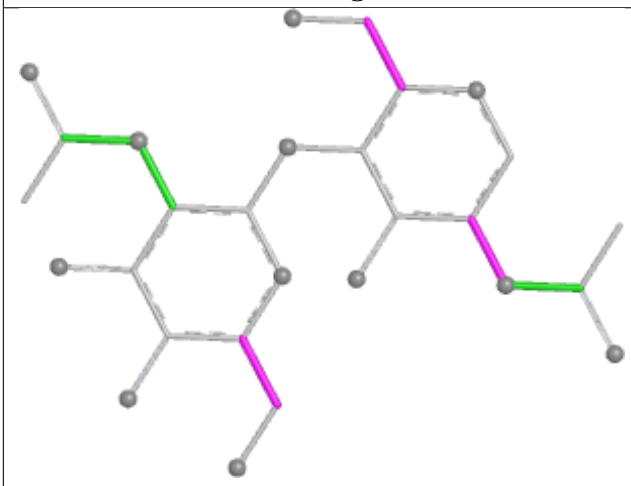

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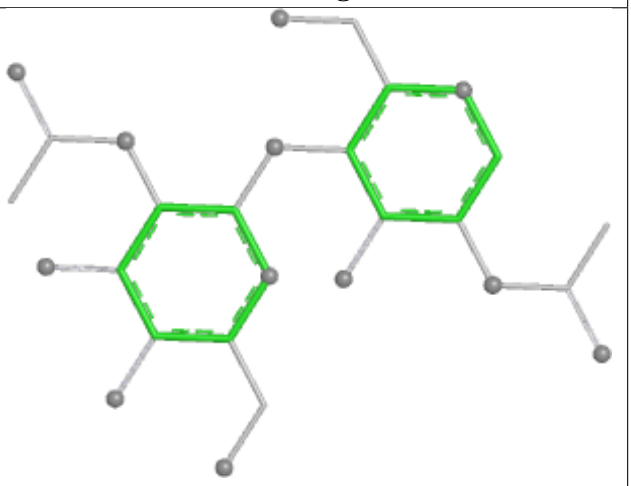
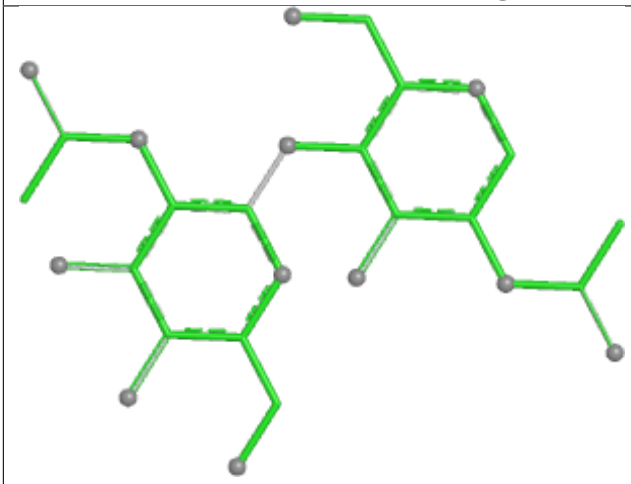


Rings

Oligosaccharide Chain V



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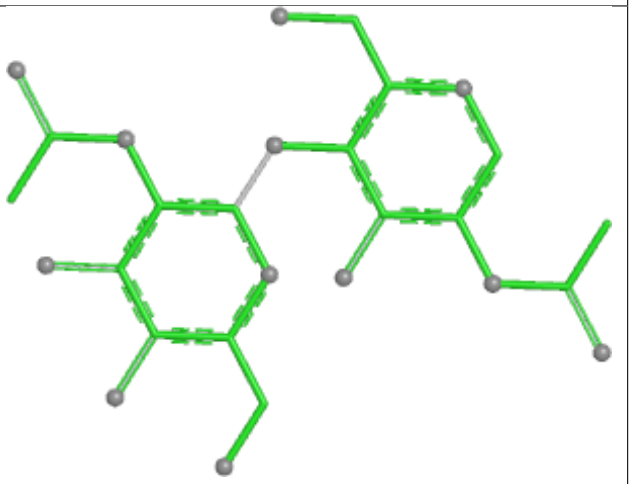

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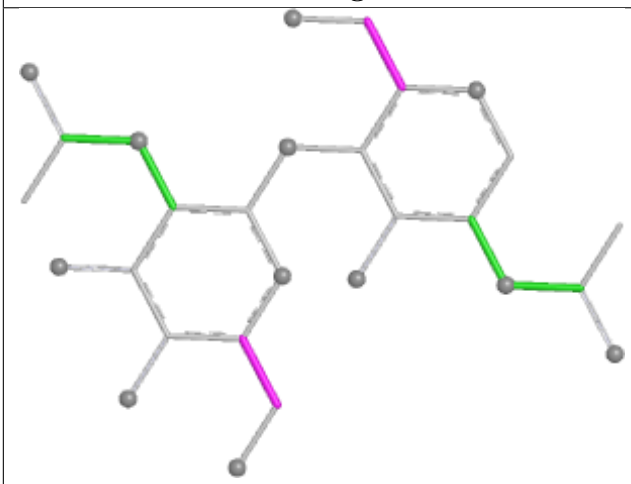

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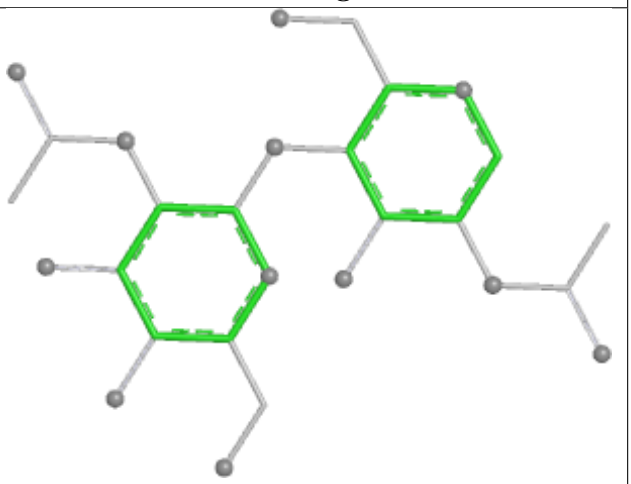
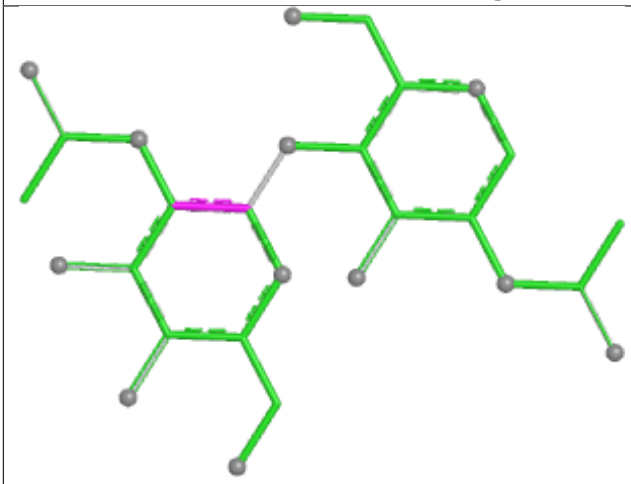


Rings

Oligosaccharide Chain W



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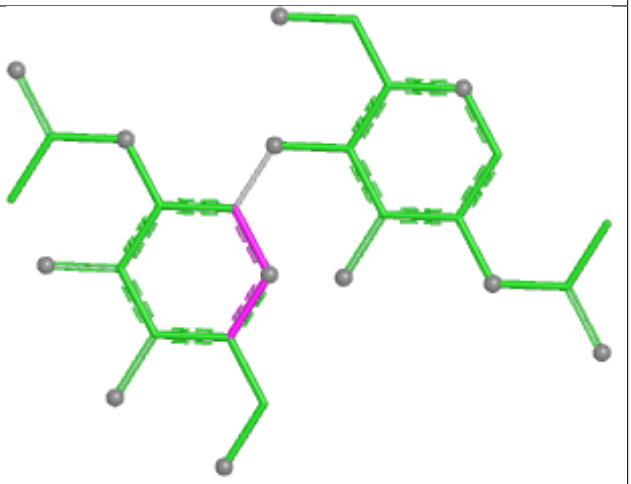

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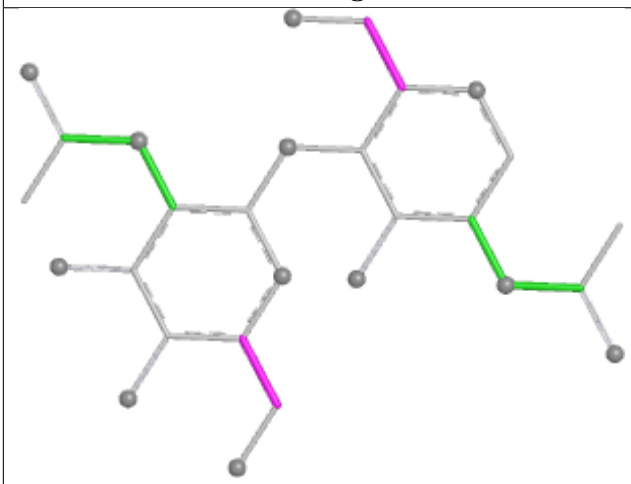

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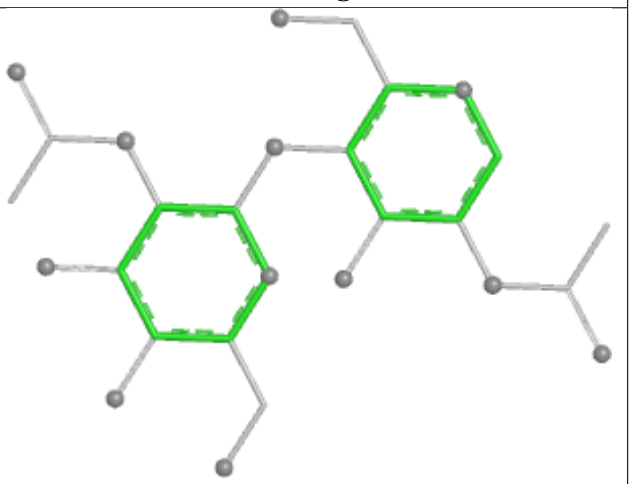
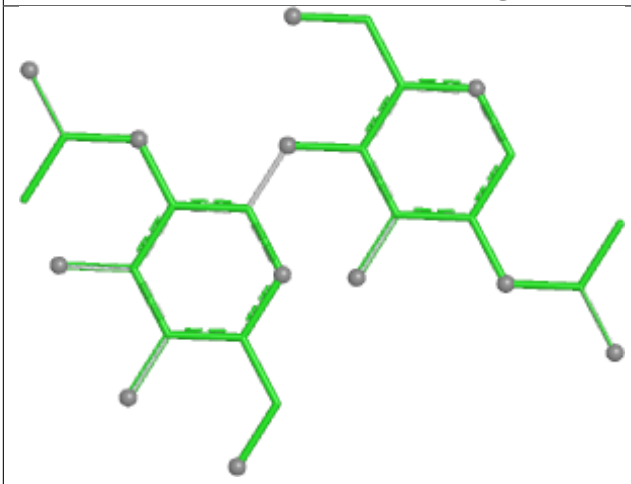


Rings

Oligosaccharide Chain X



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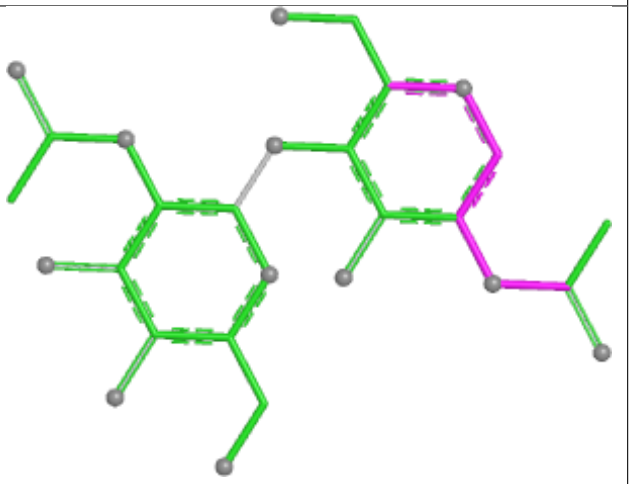

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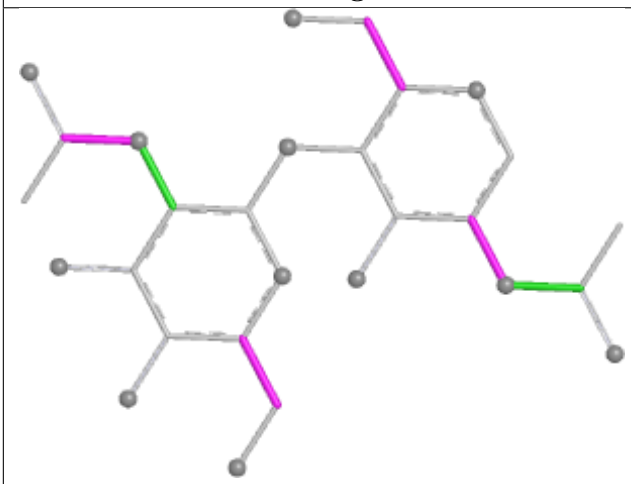

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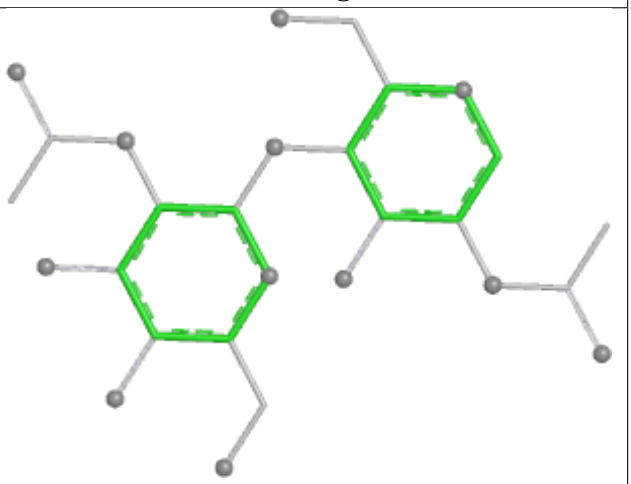

Rings

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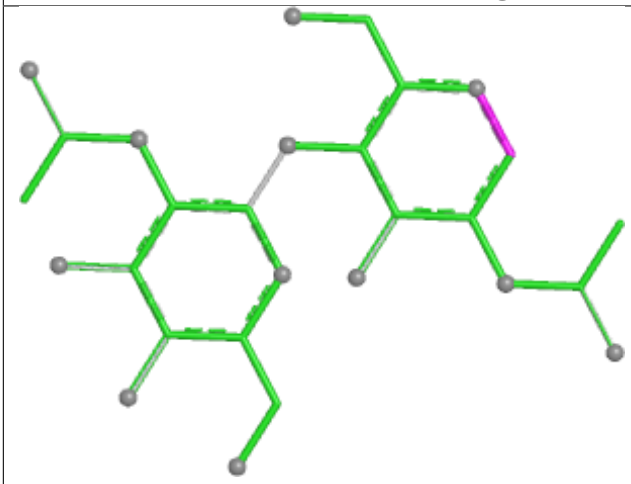

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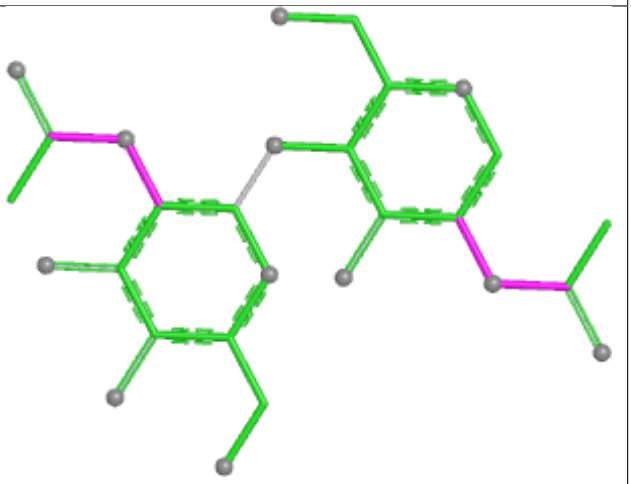

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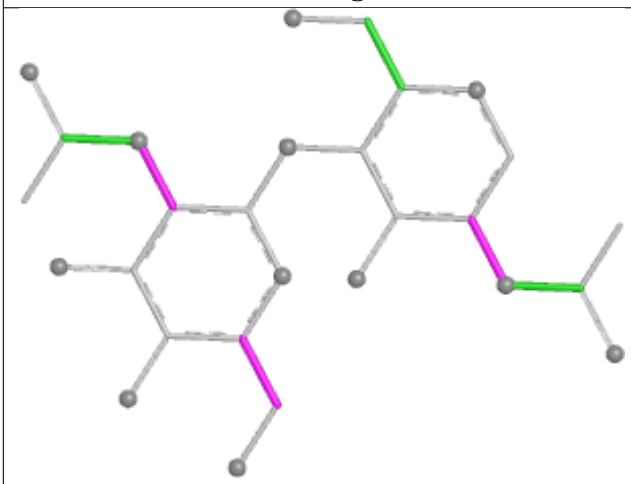

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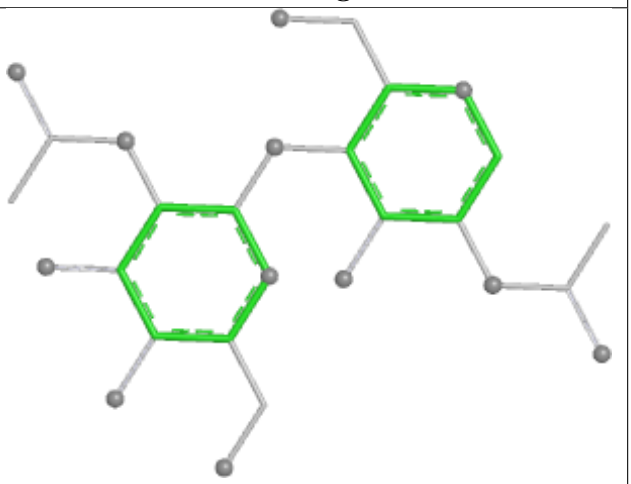
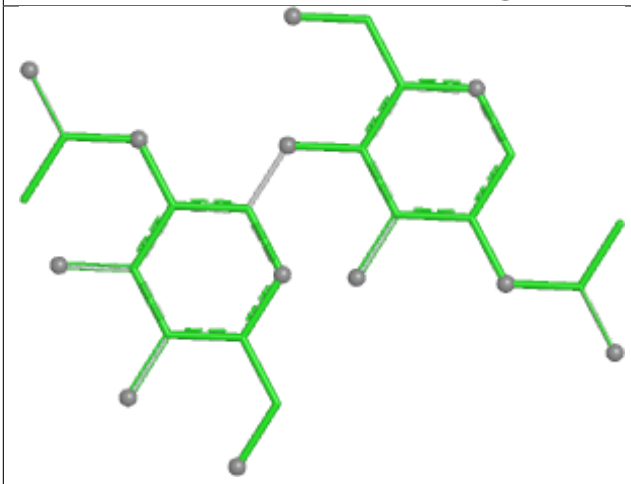


Rings

Oligosaccharide Chain Z



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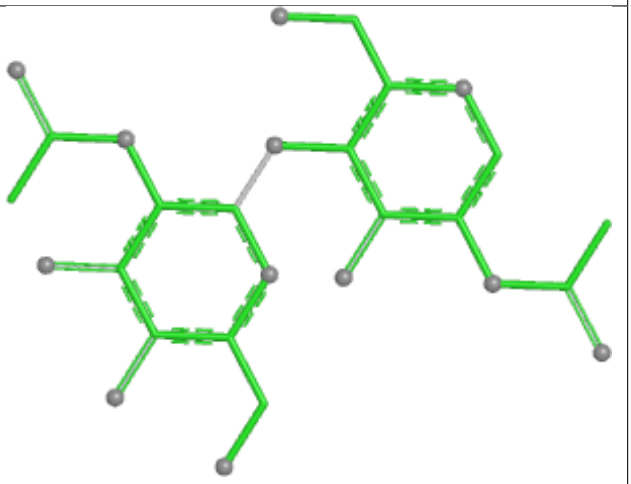

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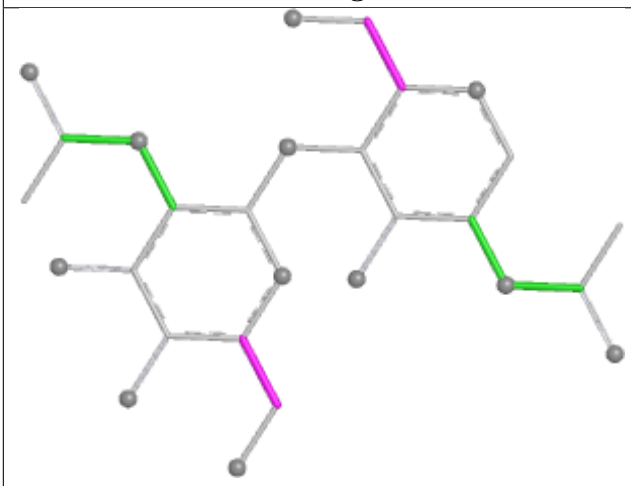

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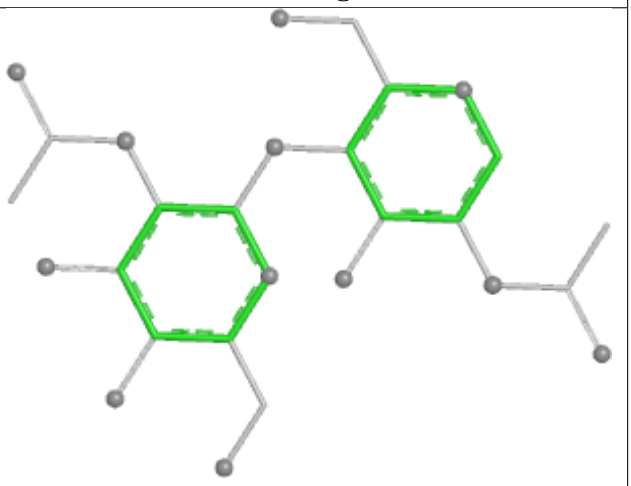
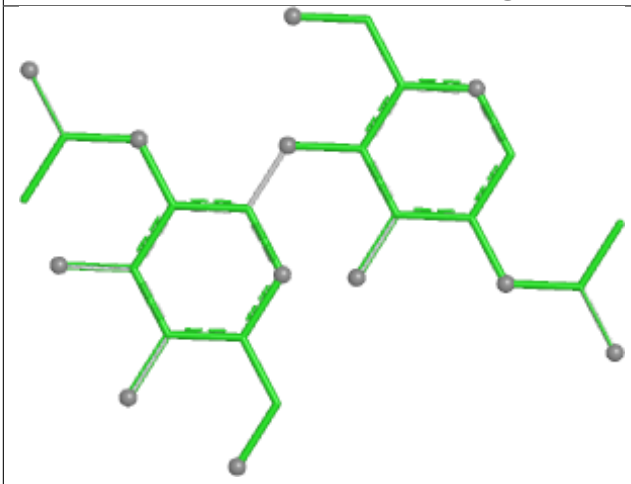


Rings

Oligosaccharide Chain a



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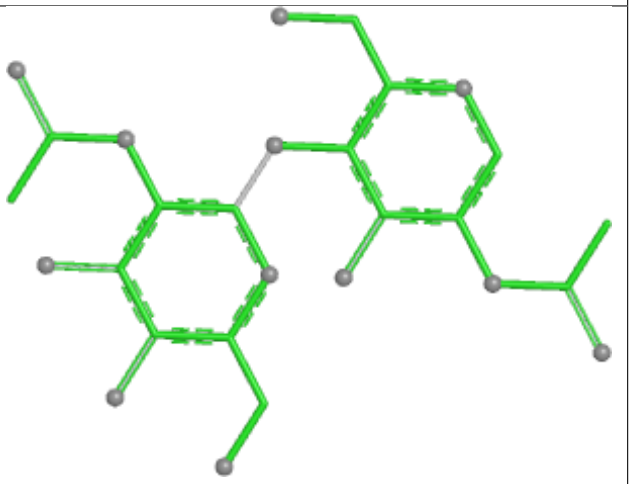

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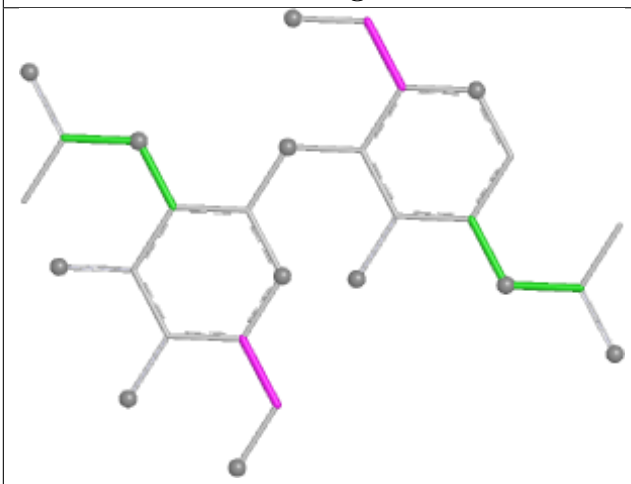

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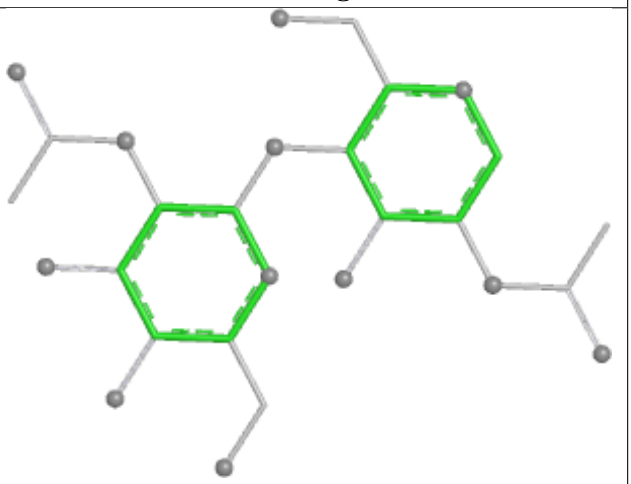
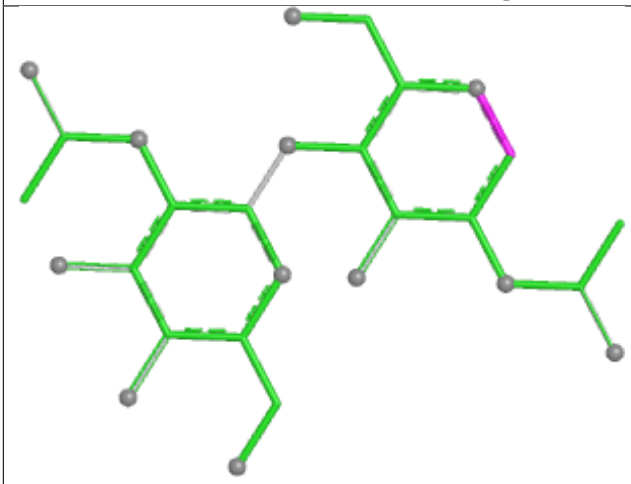


Rings

Oligosaccharide Chain b



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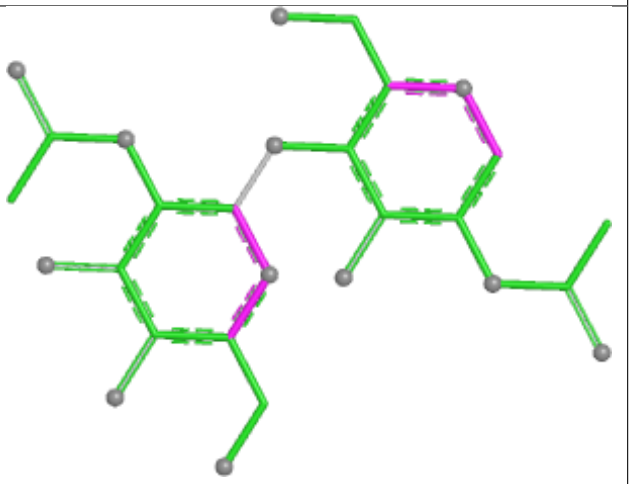

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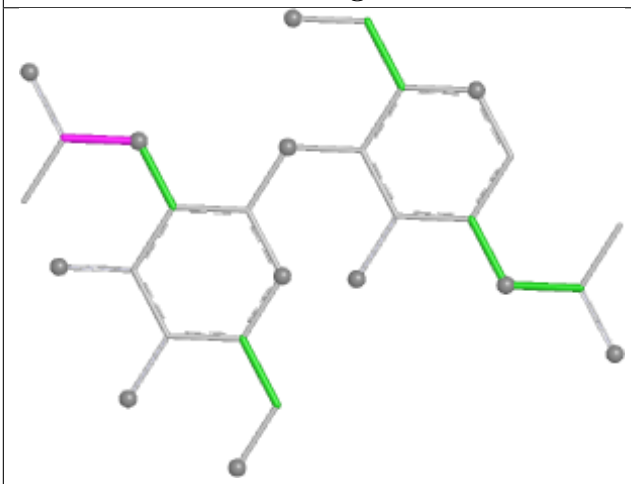

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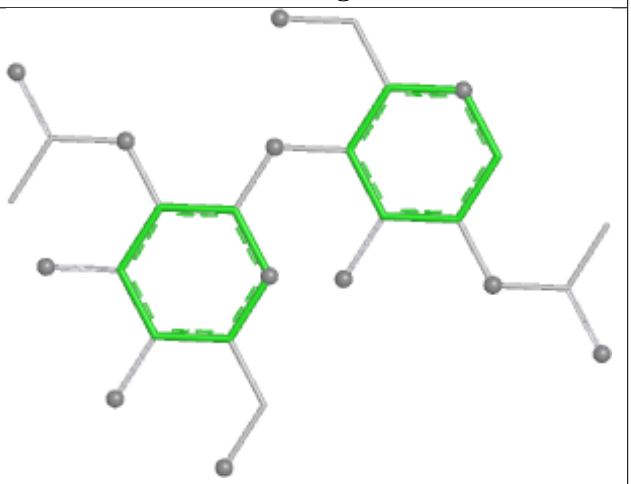
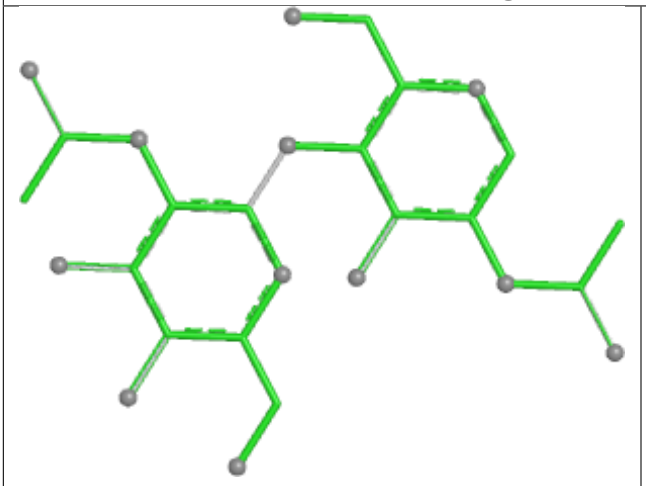


Rings

Oligosaccharide Chain c



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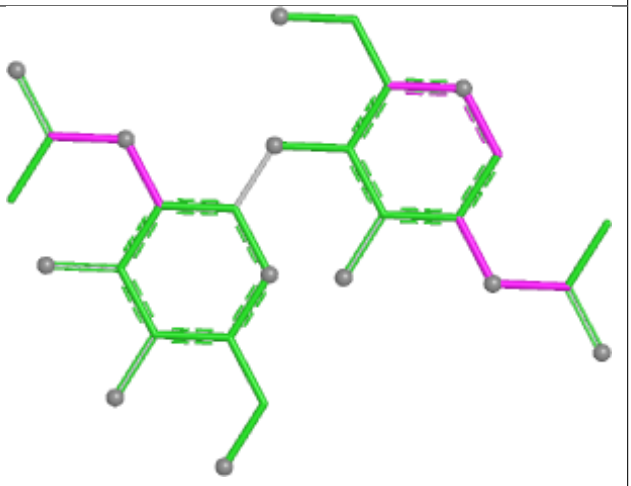
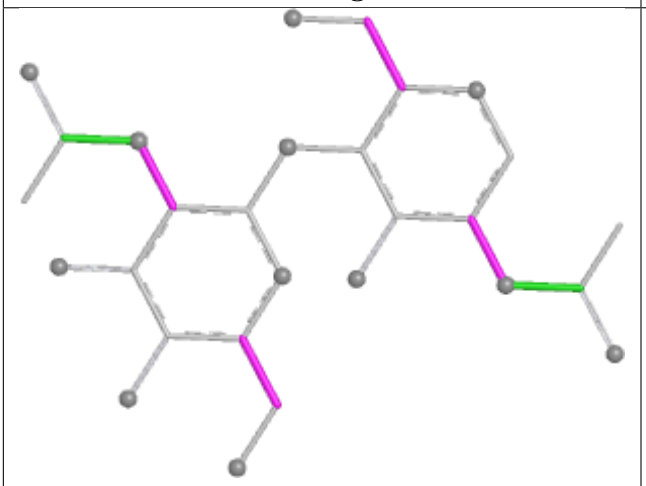


Bond angles



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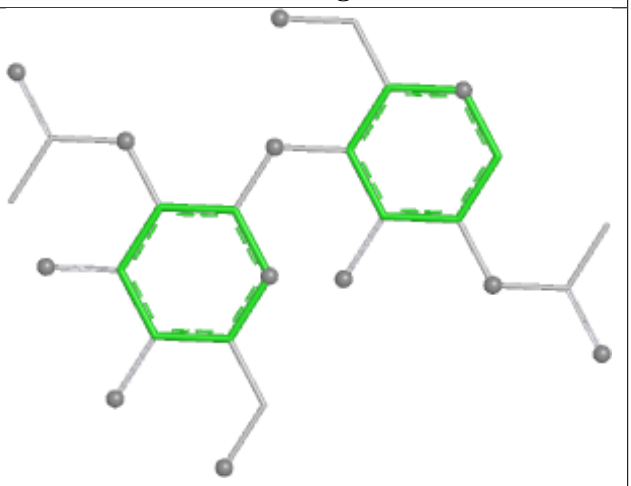
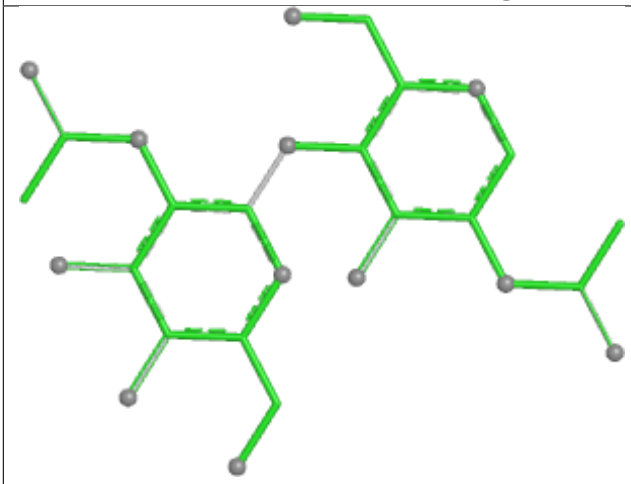


Rings

Oligosaccharide Chain d



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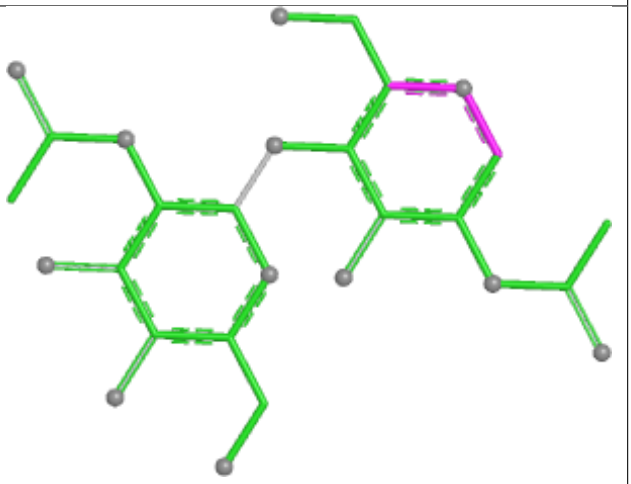
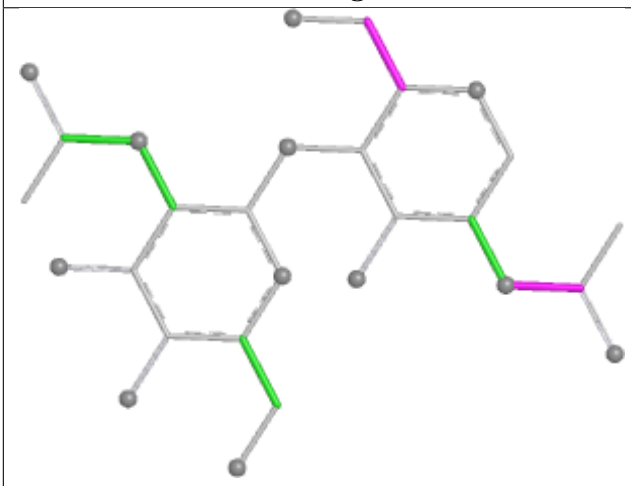


Bond angles



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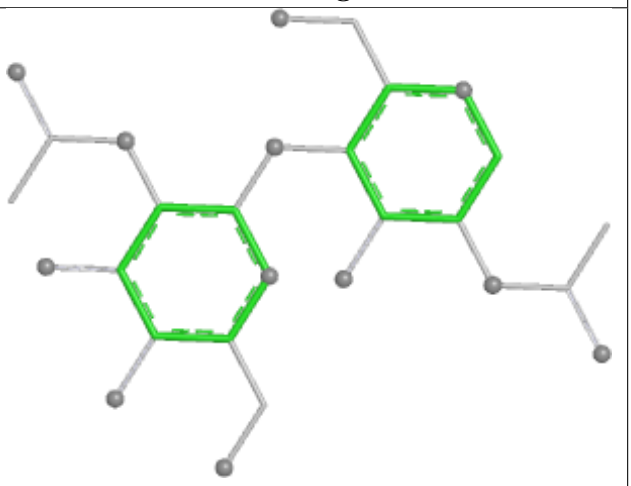
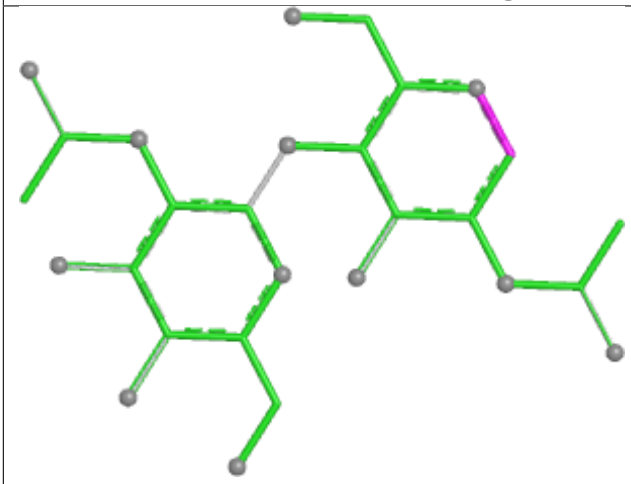


Rings

Oligosaccharide Chain e



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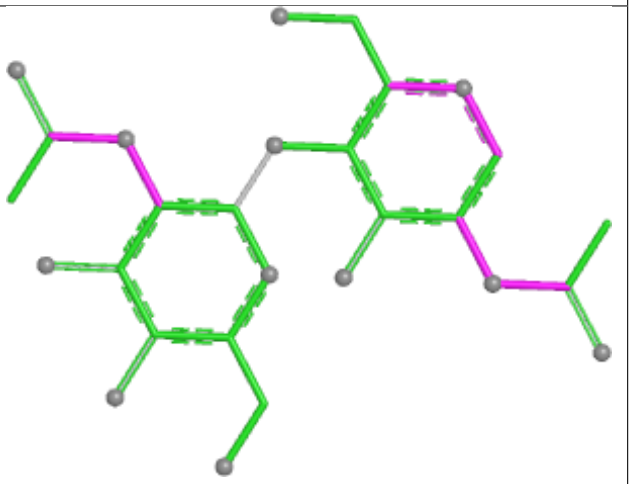
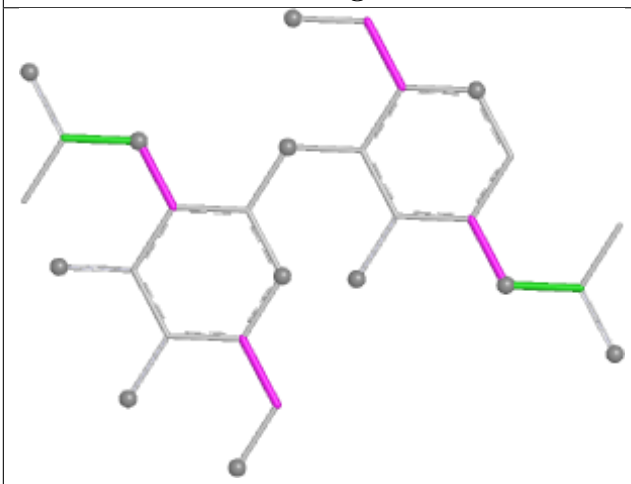


Bond angles



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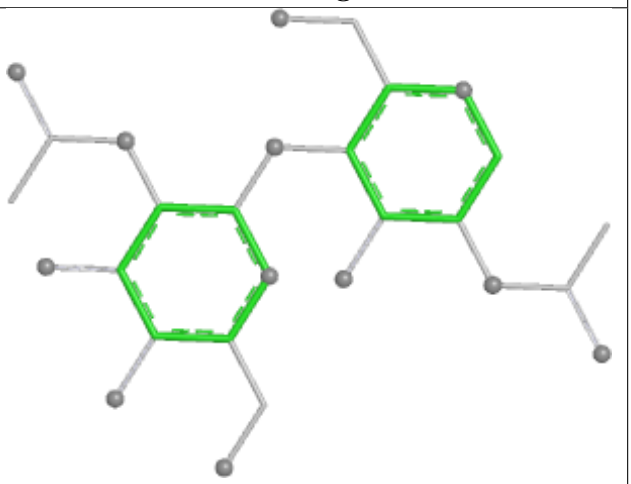
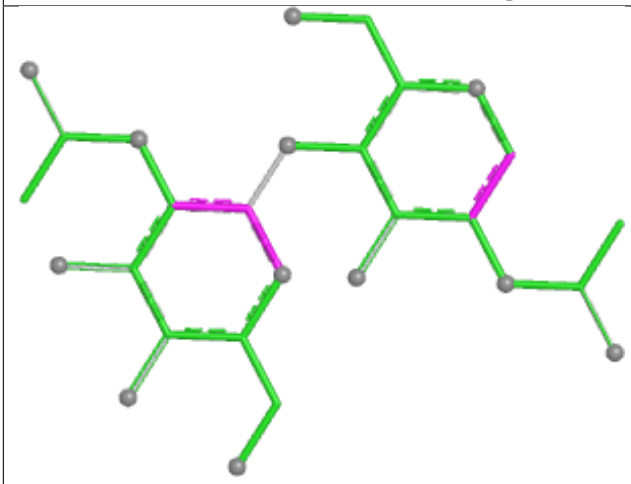
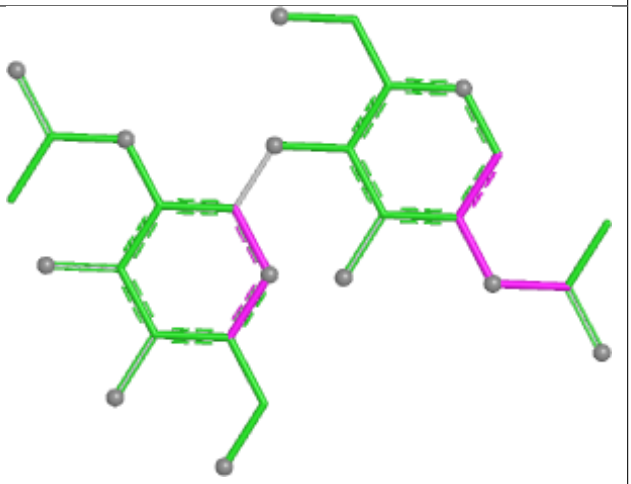


Rings

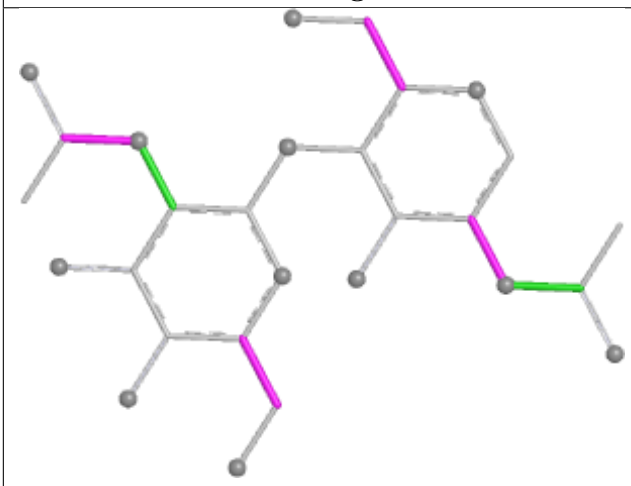
Oligosaccharide Chain f



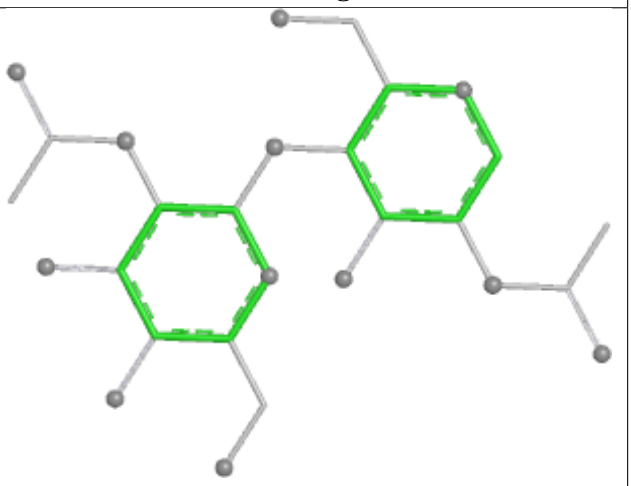
Bond lengths



Bond angles

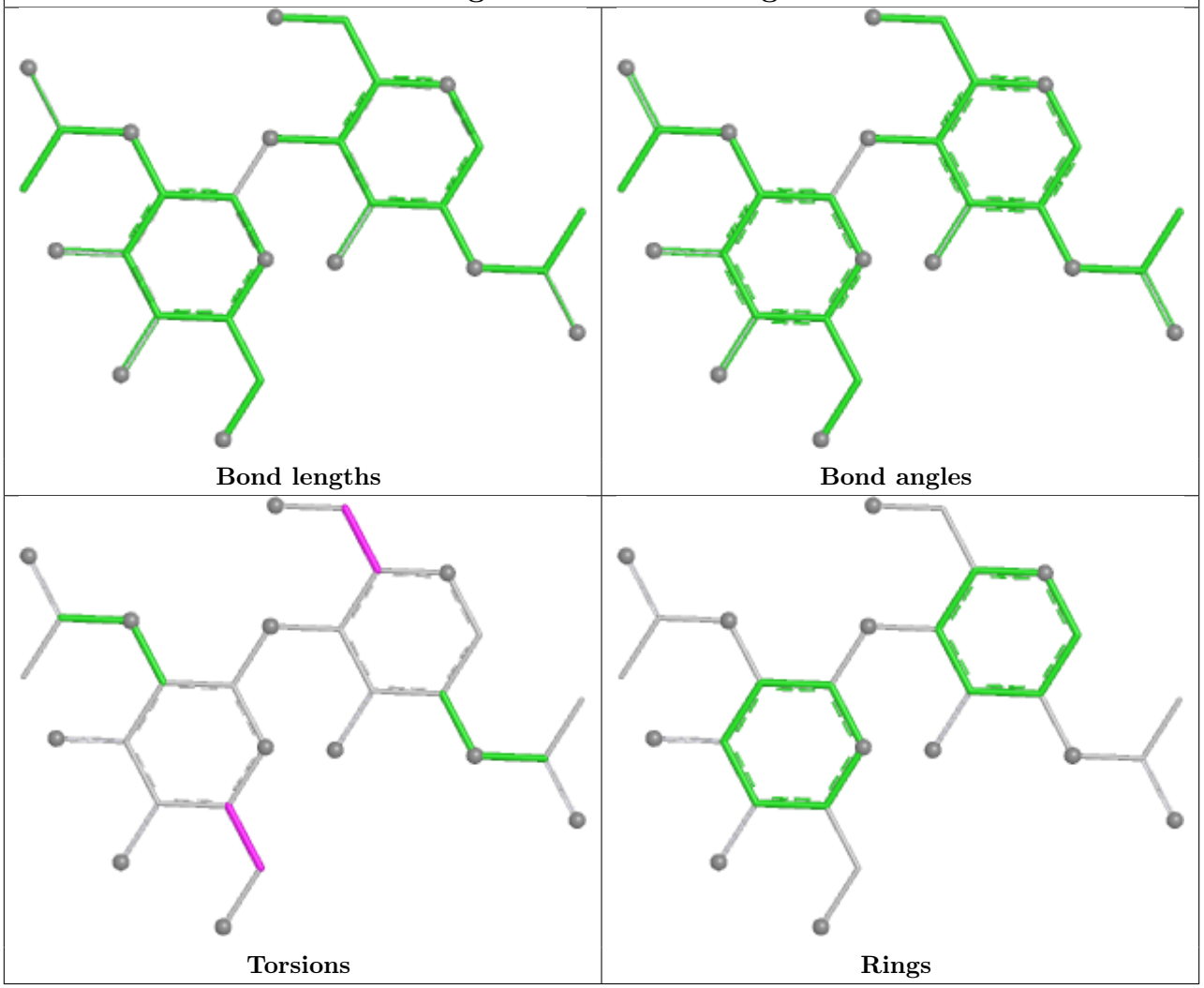


Torsions



Rings

Oligosaccharide Chain g



5.6 Ligand geometry (i)

21 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	NAG	J	1404	1	14,14,15	0.47	0	17,19,21	0.44	0
5	NAG	F	1402	1	14,14,15	0.28	0	17,19,21	0.67	1 (5%)
5	NAG	F	1403	1	14,14,15	1.28	1 (7%)	17,19,21	2.31	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
5	NAG	B	1405	1	14,14,15	0.69	0	17,19,21	0.65	0
5	NAG	J	1402	1	14,14,15	0.34	0	17,19,21	0.81	1 (5%)
5	NAG	J	1403	1	14,14,15	0.43	0	17,19,21	0.57	0
5	NAG	F	1404	1	14,14,15	0.55	0	17,19,21	0.76	1 (5%)
5	NAG	J	1406	1	14,14,15	0.60	0	17,19,21	0.64	0
5	NAG	B	1401	1	14,14,15	1.99	1 (7%)	17,19,21	1.99	3 (17%)
5	NAG	B	1402	1	14,14,15	0.47	0	17,19,21	0.66	1 (5%)
5	NAG	J	1401	1	14,14,15	0.70	0	17,19,21	0.79	1 (5%)
5	NAG	A	1401	1	14,14,15	0.61	0	17,19,21	1.10	1 (5%)
5	NAG	F	1405	1	14,14,15	0.71	0	17,19,21	0.65	0
5	NAG	J	1405	1	14,14,15	0.22	0	17,19,21	0.57	0
5	NAG	B	1403	1	14,14,15	0.77	1 (7%)	17,19,21	1.02	1 (5%)
5	NAG	I	1401	1	14,14,15	0.32	0	17,19,21	0.80	1 (5%)
5	NAG	B	1406	1	14,14,15	0.50	0	17,19,21	0.70	0
5	NAG	F	1406	1	14,14,15	0.64	0	17,19,21	0.76	1 (5%)
5	NAG	B	1404	1	14,14,15	0.75	1 (7%)	17,19,21	1.18	3 (17%)
5	NAG	E	1401	1	14,14,15	0.37	0	17,19,21	0.92	1 (5%)
5	NAG	F	1401	1	14,14,15	0.51	0	17,19,21	1.04	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	J	1404	1	-	2/6/23/26	0/1/1/1
5	NAG	F	1402	1	-	3/6/23/26	0/1/1/1
5	NAG	F	1403	1	-	6/6/23/26	0/1/1/1
5	NAG	B	1405	1	-	2/6/23/26	0/1/1/1
5	NAG	J	1402	1	-	4/6/23/26	0/1/1/1
5	NAG	J	1403	1	-	1/6/23/26	0/1/1/1
5	NAG	F	1404	1	-	4/6/23/26	0/1/1/1
5	NAG	J	1406	1	-	2/6/23/26	0/1/1/1
5	NAG	B	1401	1	-	3/6/23/26	0/1/1/1
5	NAG	B	1402	1	-	0/6/23/26	0/1/1/1
5	NAG	J	1401	1	-	2/6/23/26	0/1/1/1
5	NAG	A	1401	1	-	4/6/23/26	0/1/1/1

Continued on next page...

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	F	1405	1	-	3/6/23/26	0/1/1/1
5	NAG	J	1405	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1403	1	-	4/6/23/26	0/1/1/1
5	NAG	I	1401	1	-	4/6/23/26	0/1/1/1
5	NAG	B	1406	1	-	3/6/23/26	0/1/1/1
5	NAG	F	1406	1	-	1/6/23/26	0/1/1/1
5	NAG	B	1404	1	-	3/6/23/26	0/1/1/1
5	NAG	E	1401	1	-	2/6/23/26	0/1/1/1
5	NAG	F	1401	1	-	2/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1401	NAG	C1-C2	7.16	1.62	1.52
5	F	1403	NAG	C1-C2	4.12	1.58	1.52
5	B	1403	NAG	C1-C2	2.42	1.55	1.52
5	B	1404	NAG	O5-C1	2.26	1.47	1.43

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	F	1403	NAG	C2-N2-C7	8.19	133.88	122.90
5	B	1401	NAG	C2-N2-C7	6.26	131.29	122.90
5	E	1401	NAG	C1-O5-C5	3.42	116.78	112.19
5	A	1401	NAG	C2-N2-C7	3.30	127.32	122.90
5	F	1401	NAG	C2-N2-C7	3.26	127.28	122.90

There are no chirality outliers.

5 of 55 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	J	1402	NAG	O5-C5-C6-O6
5	B	1403	NAG	O5-C5-C6-O6
5	A	1401	NAG	C4-C5-C6-O6
5	J	1401	NAG	O5-C5-C6-O6
5	J	1404	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1402	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.

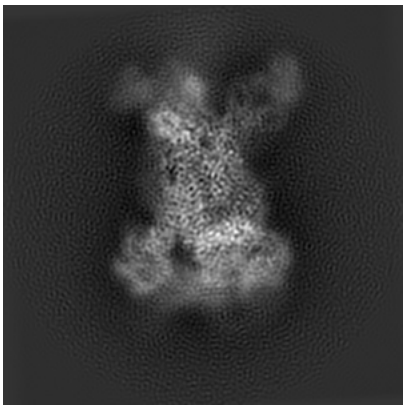
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-8784. These allow visual inspection of the internal detail of the map and identification of artifacts.

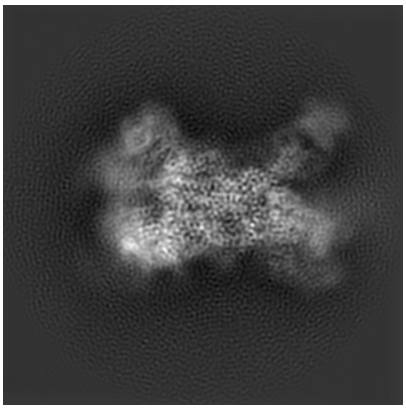
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

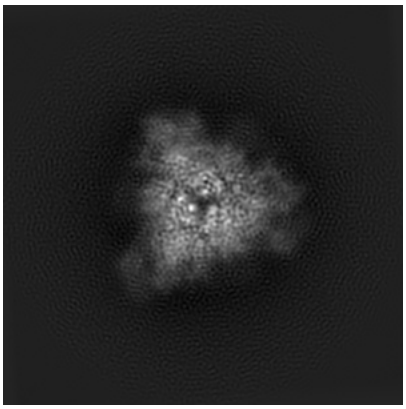
6.1.1 Primary map



X

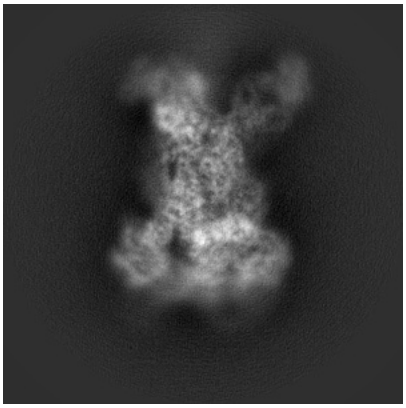


Y

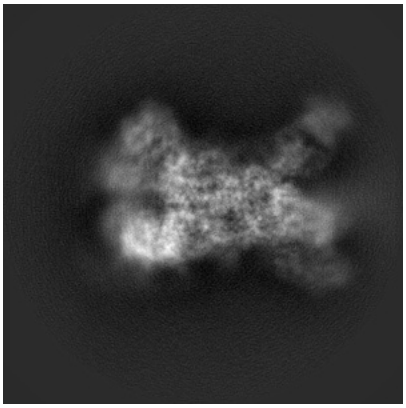


Z

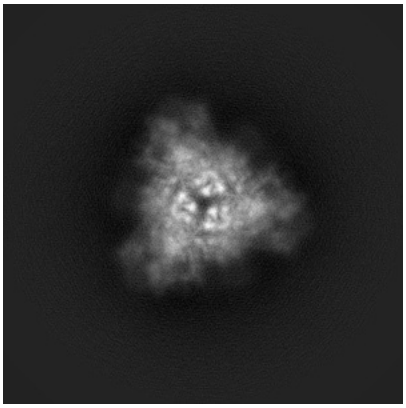
6.1.2 Raw map



X



Y

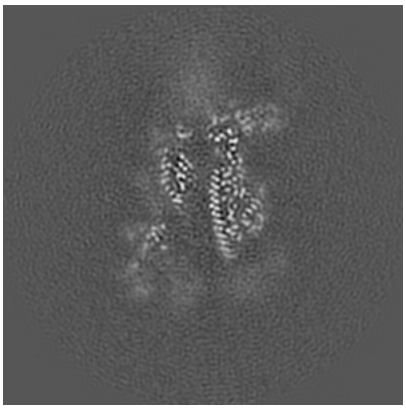


Z

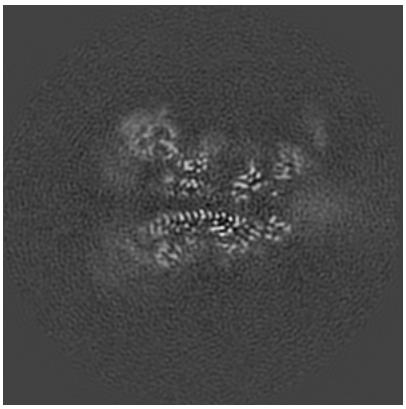
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

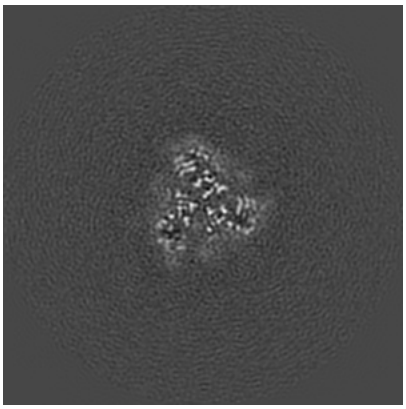
6.2.1 Primary map



X Index: 152

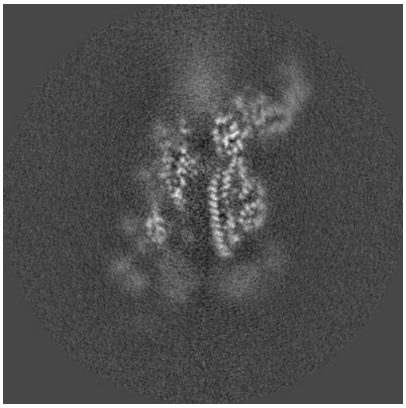


Y Index: 152

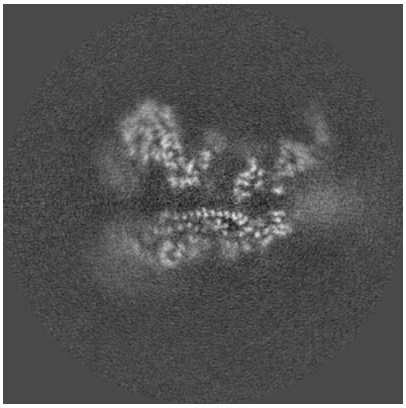


Z Index: 152

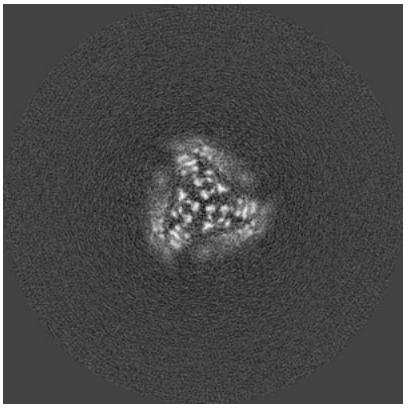
6.2.2 Raw map



X Index: 152



Y Index: 152

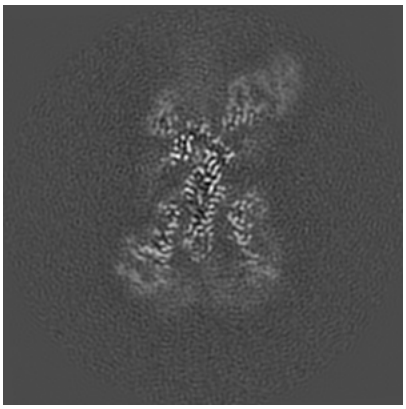


Z Index: 152

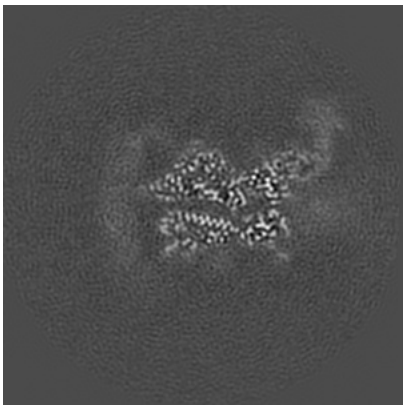
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

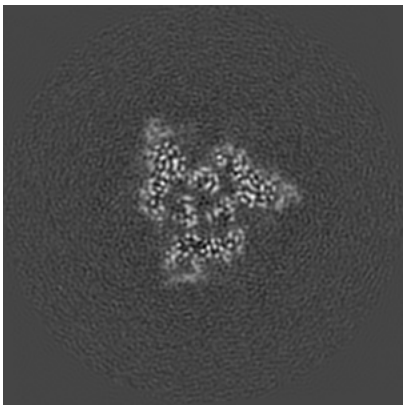
6.3.1 Primary map



X Index: 136

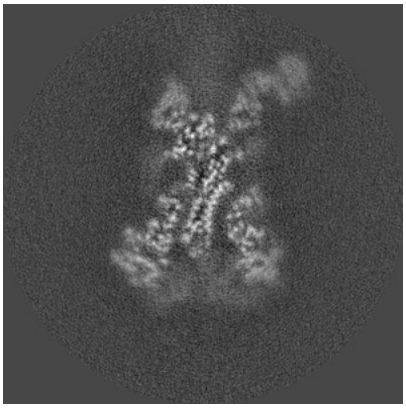


Y Index: 141

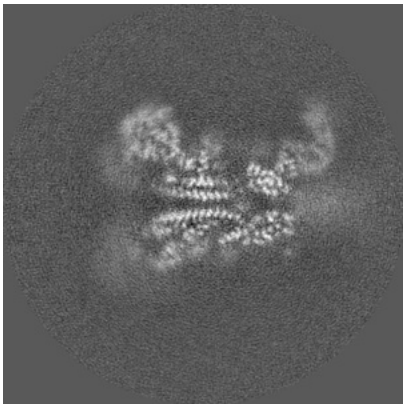


Z Index: 126

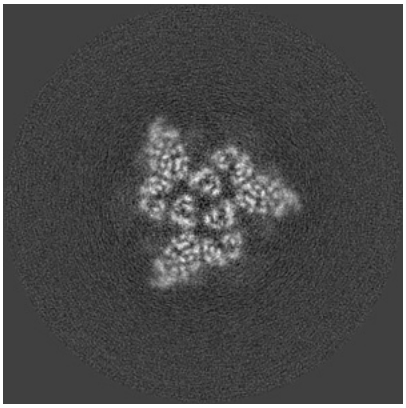
6.3.2 Raw map



X Index: 135



Y Index: 148

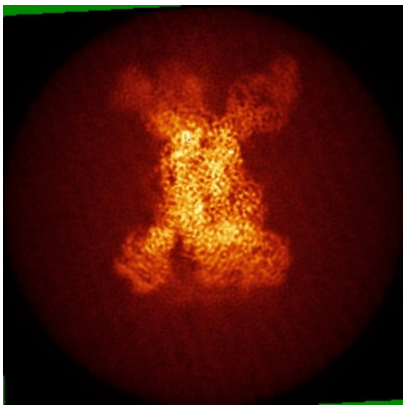


Z Index: 127

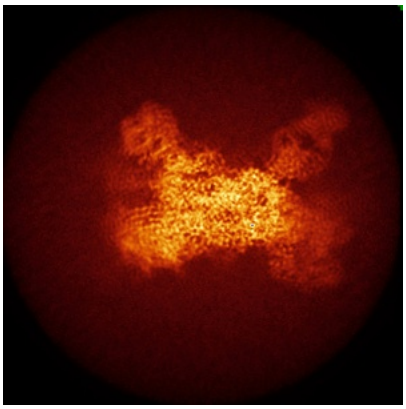
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

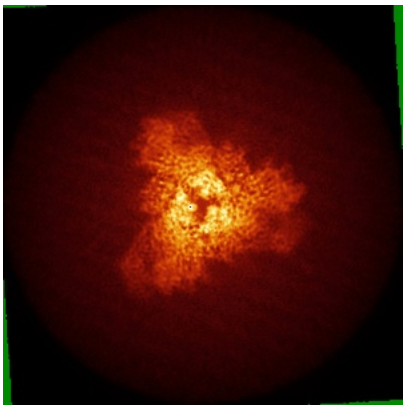
6.4.1 Primary map



X

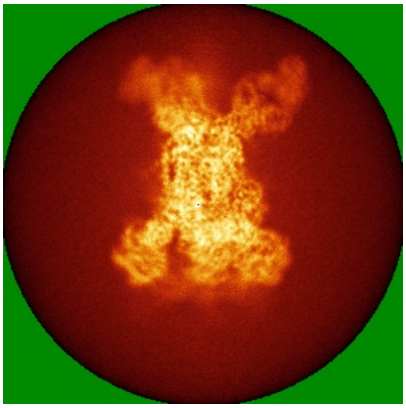


Y

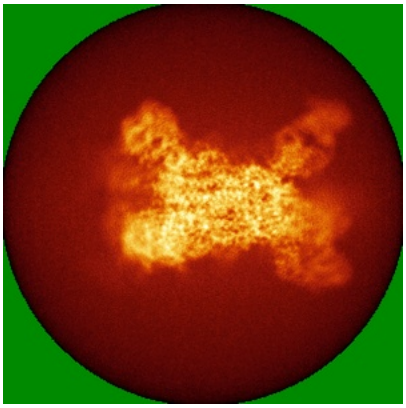


Z

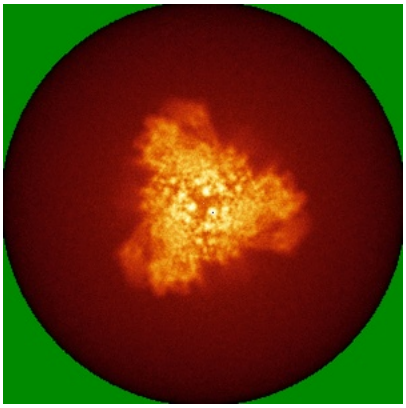
6.4.2 Raw map



X



Y

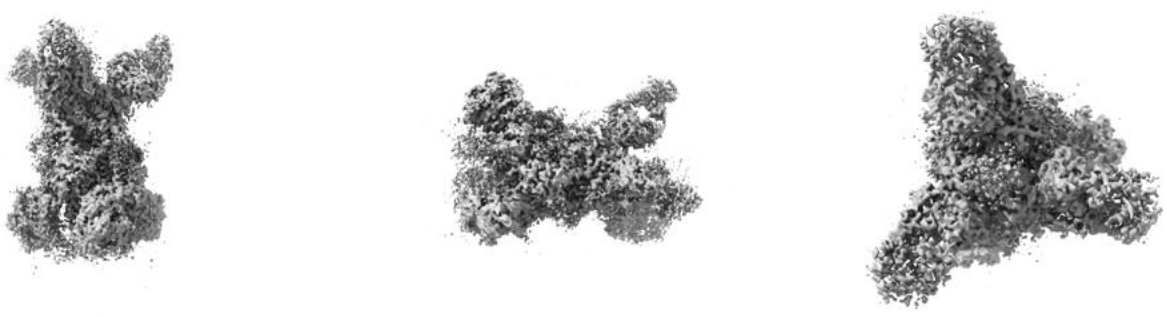


Z

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)

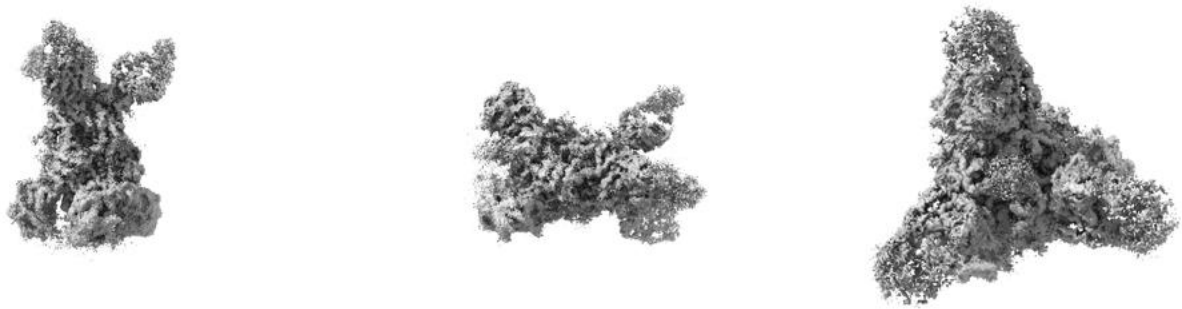
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. 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



X Y Z

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

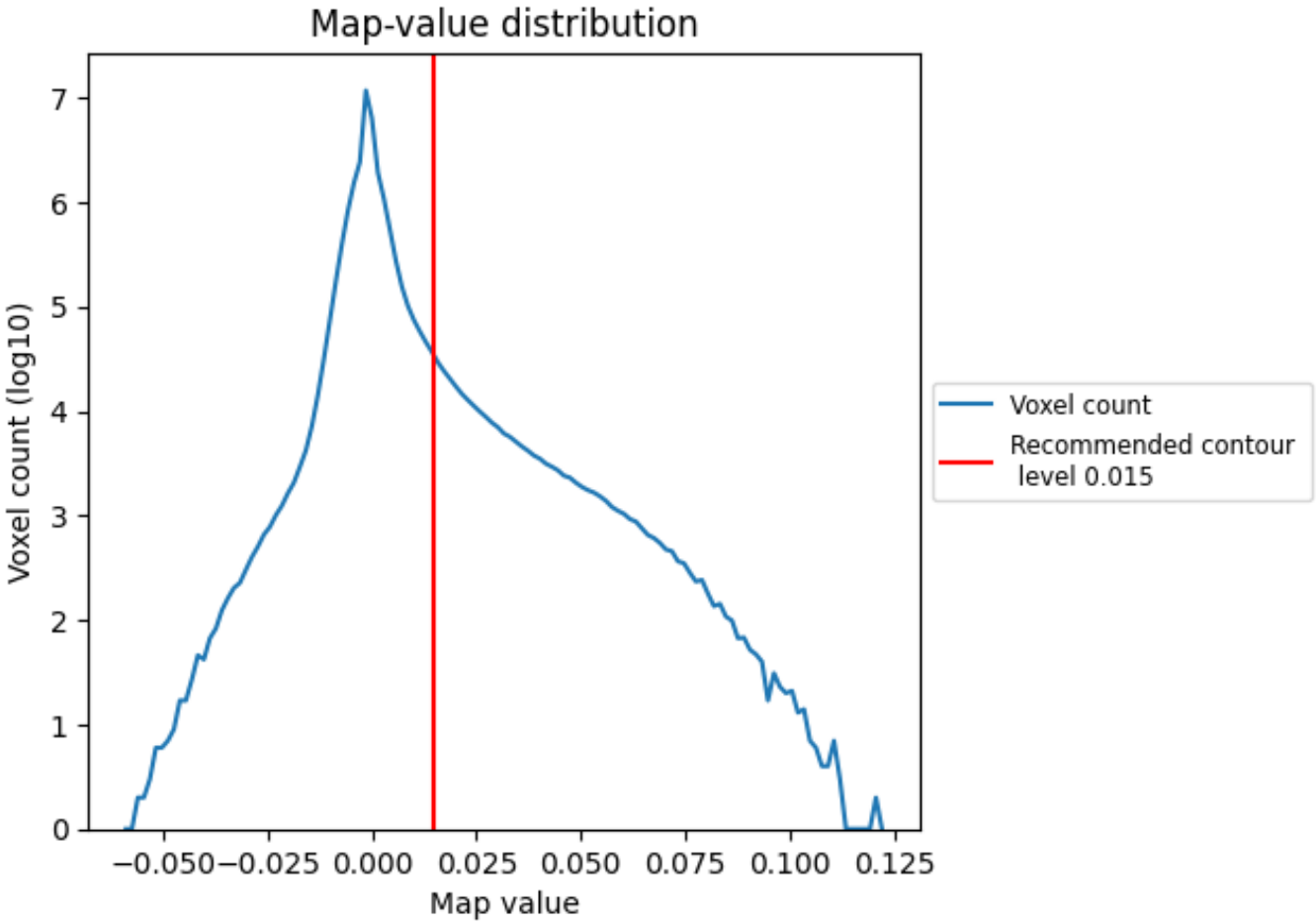
6.6 Mask visualisation (i)

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

7 Map analysis

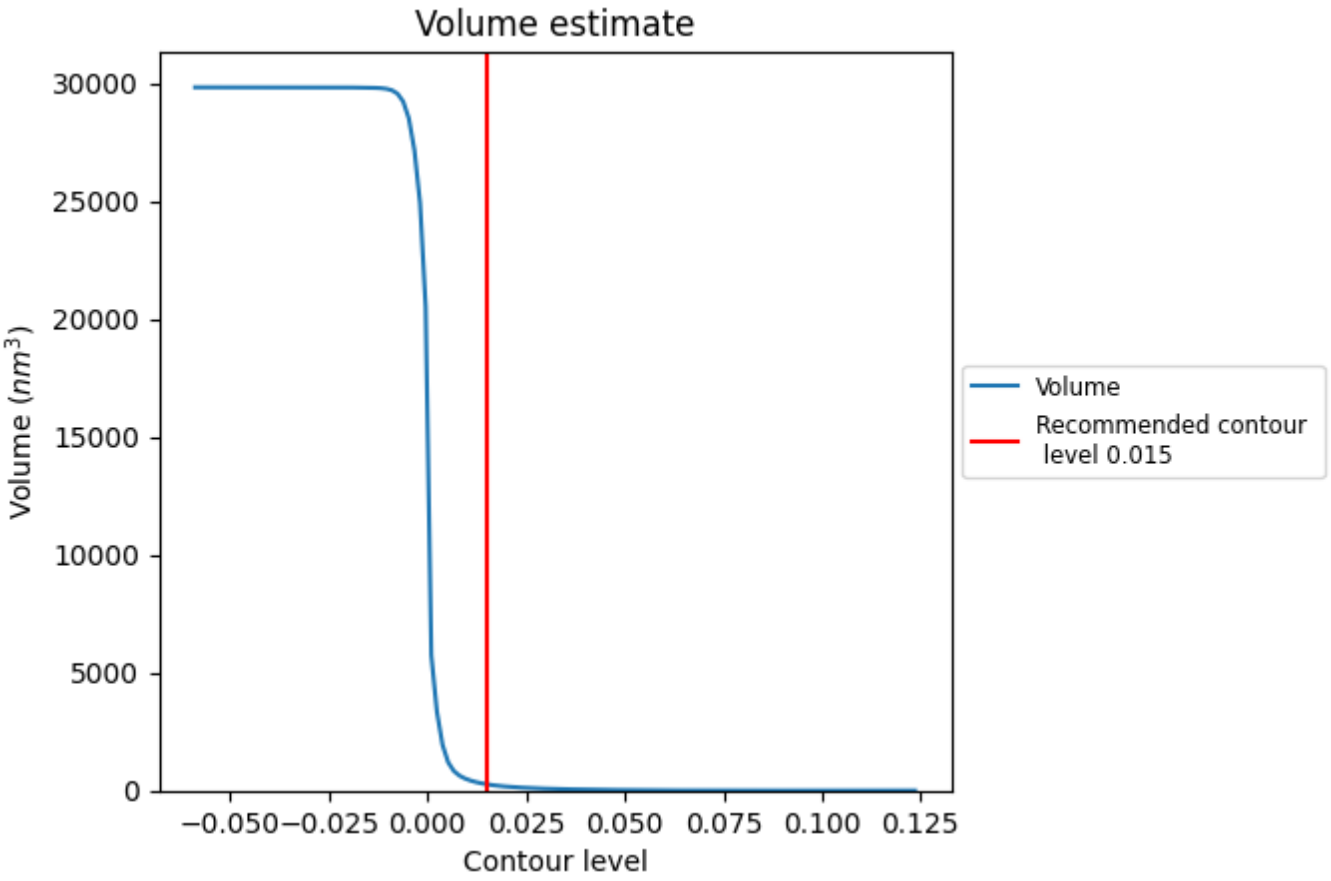
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

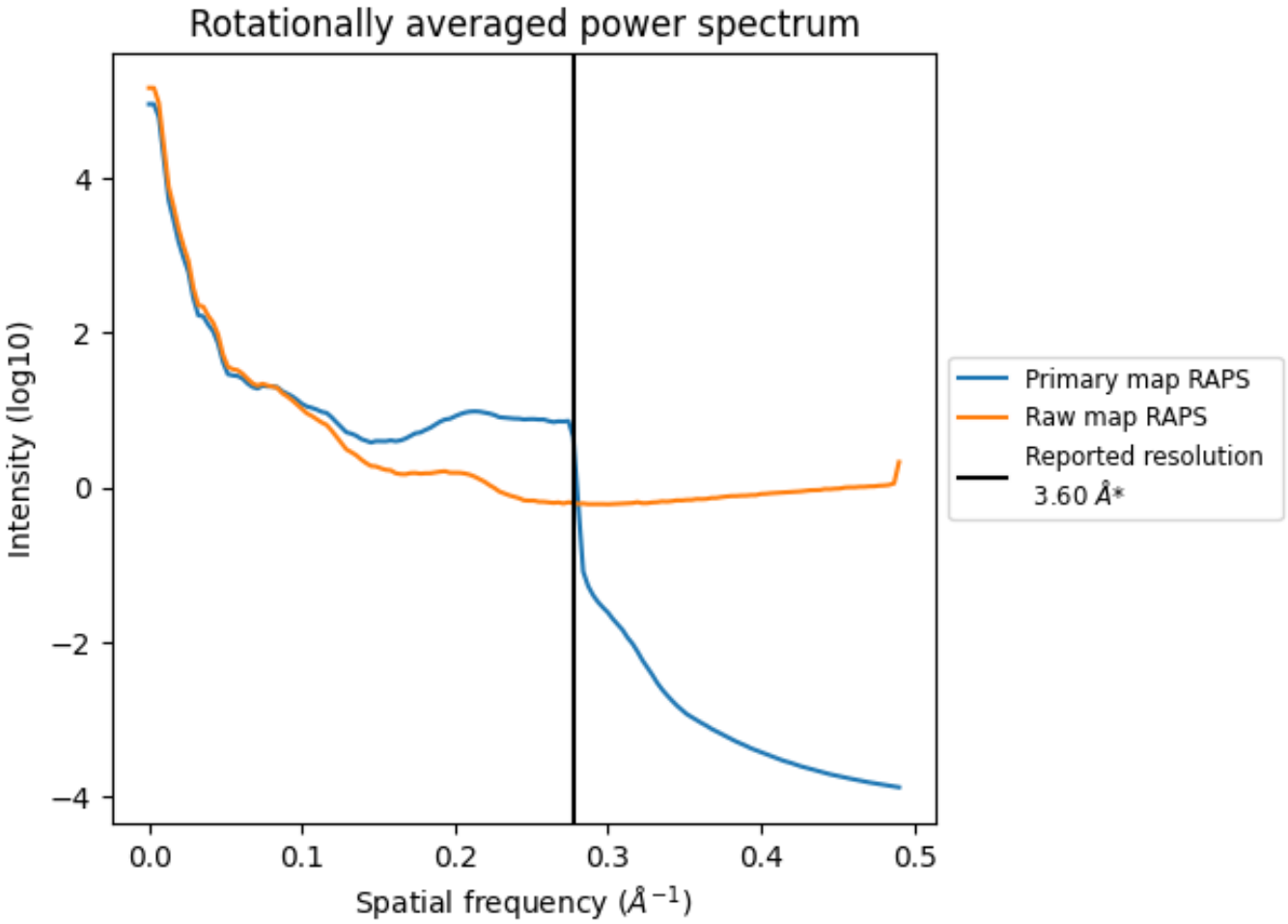
7.2 Volume estimate (i)



The volume at the recommended contour level is 266 nm^3; this corresponds to an approximate mass of 241 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)

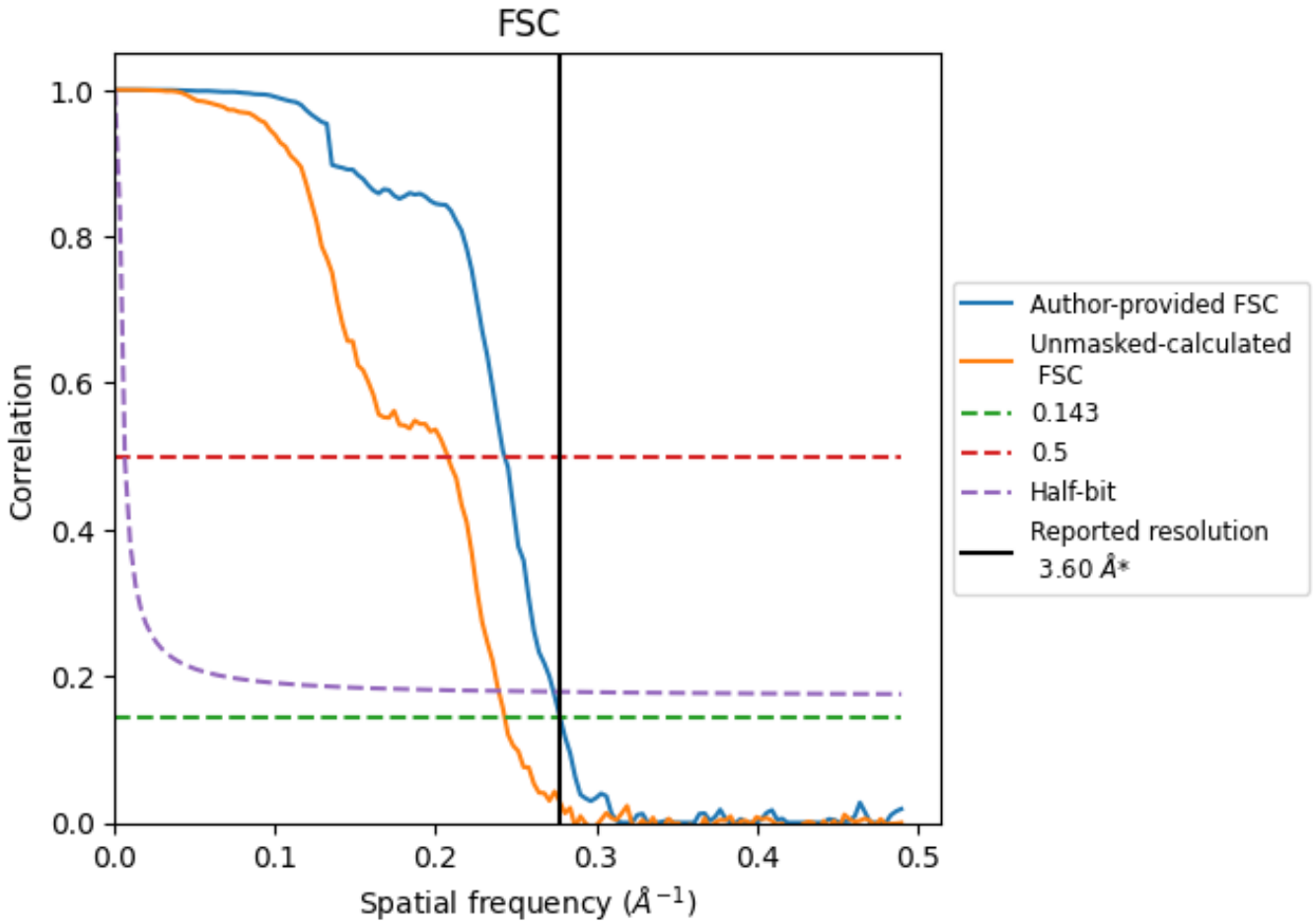


*Reported resolution corresponds to spatial frequency of 0.278 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.278 Å^{-1}

8.2 Resolution estimates (i)

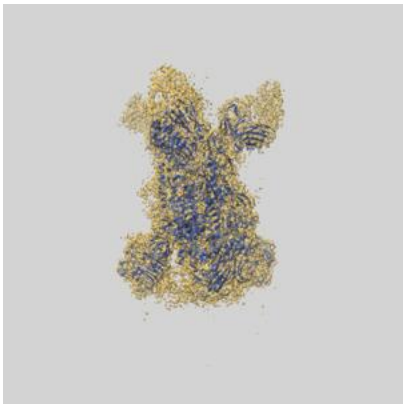
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.60	4.12	3.66
Unmasked-calculated*	4.11	4.82	4.18

*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 4.11 differs from the reported value 3.6 by more than 10 %

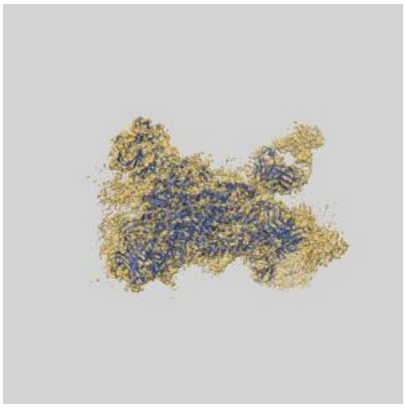
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-8784 and PDB model 5W9I. Per-residue inclusion information can be found in section 3 on page 14.

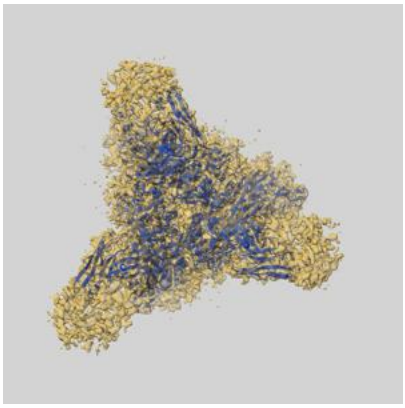
9.1 Map-model overlay



X



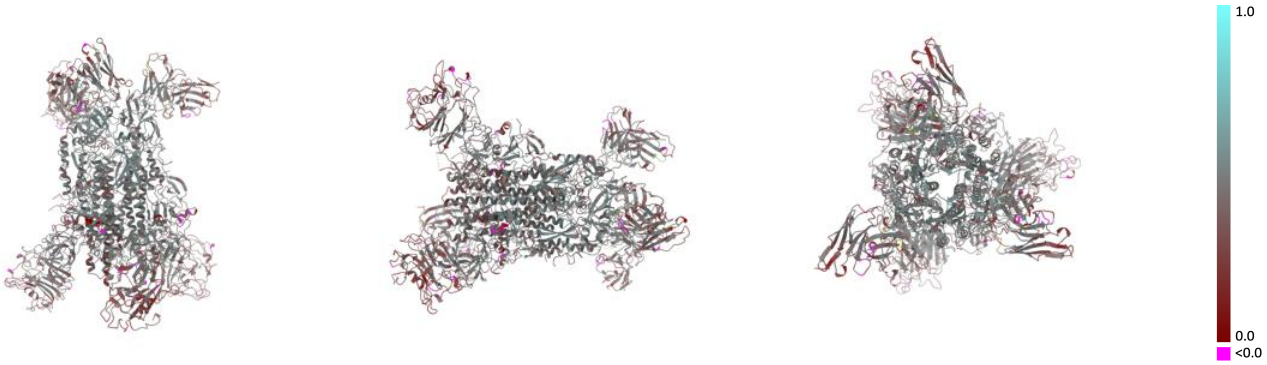
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015 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.

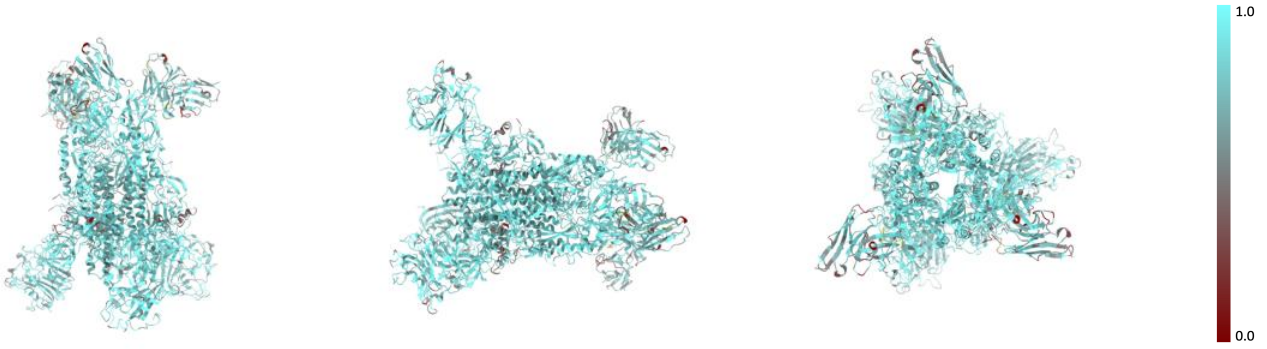
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

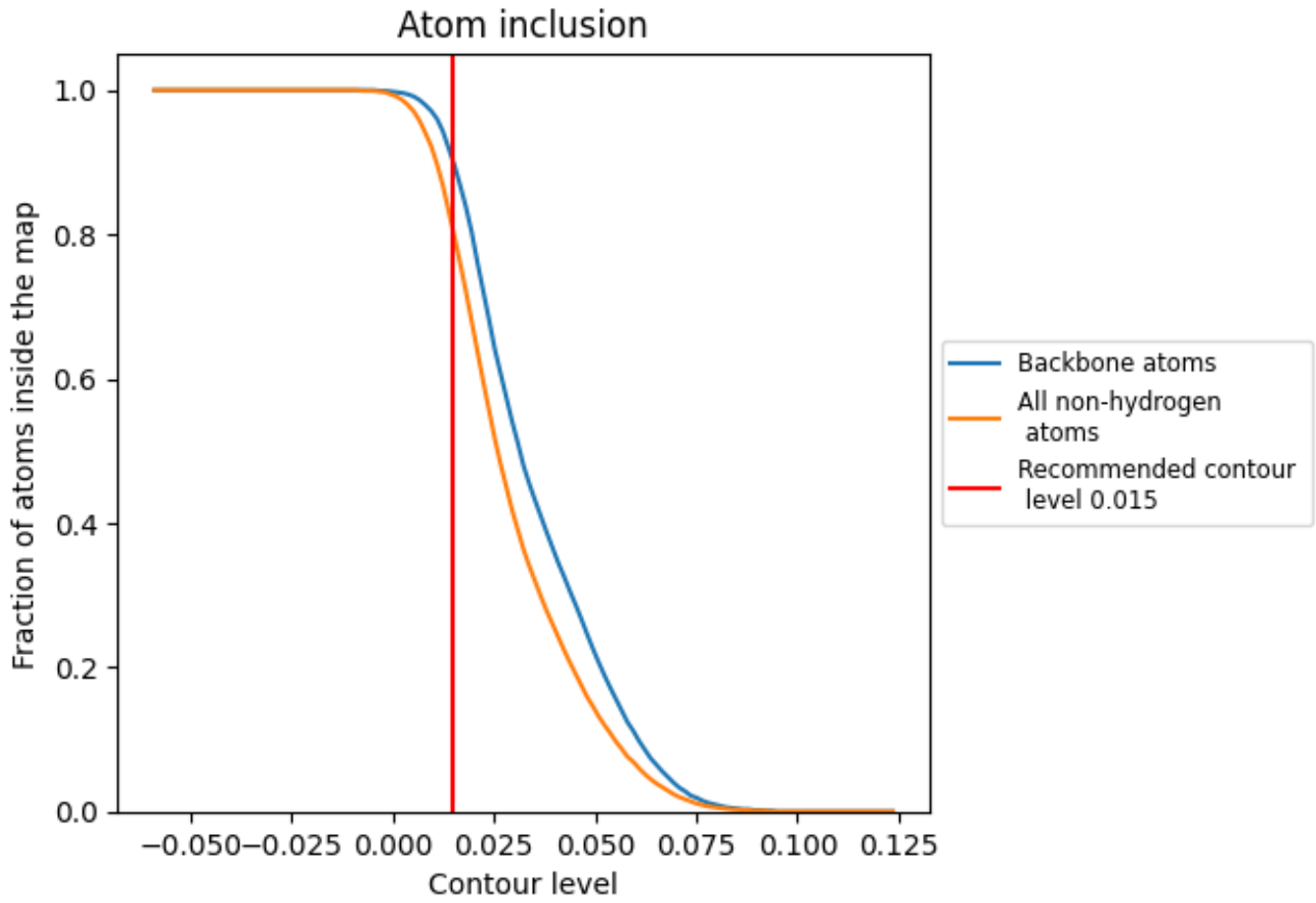
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.015).

9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 80% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8030	0.4140
A	0.8450	0.4580
B	0.8230	0.3930
C	0.7450	0.4070
D	0.6300	0.3480
E	0.8440	0.4600
F	0.8240	0.3950
G	0.7400	0.4010
H	0.6260	0.3460
I	0.8440	0.4620
J	0.8230	0.3930
K	0.7380	0.4090
L	0.6320	0.3490
M	0.6430	0.3210
N	0.6070	0.3020
O	0.7860	0.4420
P	0.7860	0.4600
Q	0.6070	0.3100
R	0.6430	0.3240
S	0.8570	0.3380
T	0.5710	0.2840
U	0.7860	0.3840
V	0.6430	0.3240
W	0.6790	0.3760
X	0.5710	0.3490
Y	0.5360	0.2730
Z	0.7140	0.3030
a	0.7140	0.4280
b	0.6070	0.2610
c	0.6070	0.3170
d	0.7860	0.4620
e	0.3210	0.2230
f	0.5710	0.3510
g	0.8210	0.3460