Full wwPDB EM Validation Report

Mar 8, 2026 – 02:39 AM UTC

PDB ID	:	9B0Y / pdb_00009b0y
EMDB ID	:	EMD-44062
Title	:	SARS CoV-2 Spike protein Ectodomain with internal tag, all RBD-down conformation
Authors	:	Singh, S.; Hasan, S.S.
Deposited on	:	2024-03-12
Resolution	:	2.32 Å(reported)
Based on initial model	:	7KRQ

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 (i) 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 (1)) were used in the production of this report:

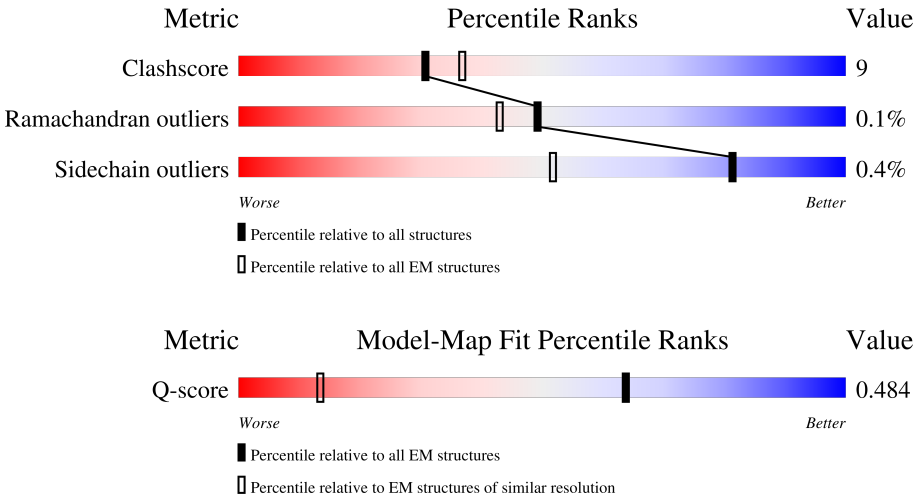
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.32 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	4359 (1.82 - 2.82)

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	1275	71% 12% 17%
1	B	1275	5% 70% 14% 16%
1	C	1275	66% 16% 17%
2	D	3	100%

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Mol	Chain	Length	Quality of chain
2	K	3	33% 67%
2	Q	3	33% 67%
3	E	2	50% 50% 50%
3	O	2	100%
3	V	2	100%
3	W	2	100%
3	a	2	50% 100%
4	F	3	33% 67%
4	G	3	33% 67%
4	I	3	100%
4	J	3	33% 67% 33%
4	P	3	100%
4	R	3	33% 67%
4	T	3	33% 67%
4	U	3	33% 67%
4	X	3	100%
4	Y	3	33% 33% 67%
4	b	3	33% 100%
4	c	3	33% 33% 67%
5	H	3	100%
5	L	3	33% 100%
5	M	3	100%
5	N	3	33% 67% 33%
5	S	3	33% 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FUC	D	3	X	-	-	-
2	FUC	K	3	X	-	-	-
2	FUC	Q	3	X	-	-	-
4	NAG	G	1	X	-	-	-
5	MAN	L	3	X	-	-	-
5	MAN	M	3	X	-	-	-
5	MAN	N	3	X	-	-	-
5	MAN	S	3	X	-	-	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 51135 atoms, of which 25122 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	1060	Total	C	H	N	O	S	0	0
			16311	5285	8040	1375	1573	38		
1	B	1074	Total	C	H	N	O	S	0	0
			16502	5346	8131	1391	1596	38		
1	C	1053	Total	C	H	N	O	S	0	0
			16193	5249	7977	1368	1561	38		

There are 219 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	SER	-	insertion	UNP P0DTC2
A	-19	ALA	-	insertion	UNP P0DTC2
A	-18	TRP	-	insertion	UNP P0DTC2
A	-17	SER	-	insertion	UNP P0DTC2
A	-16	HIS	-	insertion	UNP P0DTC2
A	-15	PRO	-	insertion	UNP P0DTC2
A	-14	GLN	-	insertion	UNP P0DTC2
A	-13	PHE	-	insertion	UNP P0DTC2
A	-12	GLU	-	insertion	UNP P0DTC2
A	-11	LYS	-	insertion	UNP P0DTC2
A	-10	GLY	-	insertion	UNP P0DTC2
A	-9	GLY	-	insertion	UNP P0DTC2
A	-8	GLY	-	insertion	UNP P0DTC2
A	-7	SER	-	insertion	UNP P0DTC2
A	-6	GLY	-	insertion	UNP P0DTC2
A	-5	GLY	-	insertion	UNP P0DTC2
A	-4	GLY	-	insertion	UNP P0DTC2
A	-3	SER	-	insertion	UNP P0DTC2
A	-2	GLY	-	insertion	UNP P0DTC2
A	-1	GLY	-	insertion	UNP P0DTC2
A	0	SER	-	insertion	UNP P0DTC2
A	1	SER	-	insertion	UNP P0DTC2
A	2	ALA	-	insertion	UNP P0DTC2
A	3	TRP	-	insertion	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	4	SER	-	insertion	UNP P0DTC2
A	5	HIS	-	insertion	UNP P0DTC2
A	6	PRO	-	insertion	UNP P0DTC2
A	7	GLN	-	insertion	UNP P0DTC2
A	8	PHE	-	insertion	UNP P0DTC2
A	9	GLU	-	insertion	UNP P0DTC2
A	10	LYS	-	insertion	UNP P0DTC2
A	11	SER	-	insertion	UNP P0DTC2
A	12	ALA	-	insertion	UNP P0DTC2
A	13	LEU	-	insertion	UNP P0DTC2
A	14	VAL	-	insertion	UNP P0DTC2
A	15	PRO	-	insertion	UNP P0DTC2
A	16	ARG	-	insertion	UNP P0DTC2
A	17	GLY	-	insertion	UNP P0DTC2
A	18	SER	-	insertion	UNP P0DTC2
A	614	GLY	ASP	variant	UNP P0DTC2
A	682	GLY	ARG	engineered mutation	UNP P0DTC2
A	683	SER	ARG	engineered mutation	UNP P0DTC2
A	685	SER	ARG	engineered mutation	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2
A	1209	GLY	-	expression tag	UNP P0DTC2
A	1210	SER	-	expression tag	UNP P0DTC2
A	1211	GLY	-	expression tag	UNP P0DTC2
A	1212	TYR	-	expression tag	UNP P0DTC2
A	1213	ILE	-	expression tag	UNP P0DTC2
A	1214	PRO	-	expression tag	UNP P0DTC2
A	1215	GLU	-	expression tag	UNP P0DTC2
A	1216	ALA	-	expression tag	UNP P0DTC2
A	1217	PRO	-	expression tag	UNP P0DTC2
A	1218	ARG	-	expression tag	UNP P0DTC2
A	1219	ASP	-	expression tag	UNP P0DTC2
A	1220	GLY	-	expression tag	UNP P0DTC2
A	1221	GLN	-	expression tag	UNP P0DTC2
A	1222	ALA	-	expression tag	UNP P0DTC2
A	1223	TYR	-	expression tag	UNP P0DTC2
A	1224	VAL	-	expression tag	UNP P0DTC2
A	1225	ARG	-	expression tag	UNP P0DTC2
A	1226	LYS	-	expression tag	UNP P0DTC2
A	1227	ASP	-	expression tag	UNP P0DTC2
A	1228	GLY	-	expression tag	UNP P0DTC2
A	1229	GLU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1230	TRP	-	expression tag	UNP P0DTC2
A	1231	VAL	-	expression tag	UNP P0DTC2
A	1232	LEU	-	expression tag	UNP P0DTC2
A	1233	LEU	-	expression tag	UNP P0DTC2
A	1234	SER	-	expression tag	UNP P0DTC2
A	1235	THR	-	expression tag	UNP P0DTC2
A	1236	PHE	-	expression tag	UNP P0DTC2
B	-20	SER	-	insertion	UNP P0DTC2
B	-19	ALA	-	insertion	UNP P0DTC2
B	-18	TRP	-	insertion	UNP P0DTC2
B	-17	SER	-	insertion	UNP P0DTC2
B	-16	HIS	-	insertion	UNP P0DTC2
B	-15	PRO	-	insertion	UNP P0DTC2
B	-14	GLN	-	insertion	UNP P0DTC2
B	-13	PHE	-	insertion	UNP P0DTC2
B	-12	GLU	-	insertion	UNP P0DTC2
B	-11	LYS	-	insertion	UNP P0DTC2
B	-10	GLY	-	insertion	UNP P0DTC2
B	-9	GLY	-	insertion	UNP P0DTC2
B	-8	GLY	-	insertion	UNP P0DTC2
B	-7	SER	-	insertion	UNP P0DTC2
B	-6	GLY	-	insertion	UNP P0DTC2
B	-5	GLY	-	insertion	UNP P0DTC2
B	-4	GLY	-	insertion	UNP P0DTC2
B	-3	SER	-	insertion	UNP P0DTC2
B	-2	GLY	-	insertion	UNP P0DTC2
B	-1	GLY	-	insertion	UNP P0DTC2
B	0	SER	-	insertion	UNP P0DTC2
B	1	SER	-	insertion	UNP P0DTC2
B	2	ALA	-	insertion	UNP P0DTC2
B	3	TRP	-	insertion	UNP P0DTC2
B	4	SER	-	insertion	UNP P0DTC2
B	5	HIS	-	insertion	UNP P0DTC2
B	6	PRO	-	insertion	UNP P0DTC2
B	7	GLN	-	insertion	UNP P0DTC2
B	8	PHE	-	insertion	UNP P0DTC2
B	9	GLU	-	insertion	UNP P0DTC2
B	10	LYS	-	insertion	UNP P0DTC2
B	11	SER	-	insertion	UNP P0DTC2
B	12	ALA	-	insertion	UNP P0DTC2
B	13	LEU	-	insertion	UNP P0DTC2
B	14	VAL	-	insertion	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	15	PRO	-	insertion	UNP P0DTC2
B	16	ARG	-	insertion	UNP P0DTC2
B	17	GLY	-	insertion	UNP P0DTC2
B	18	SER	-	insertion	UNP P0DTC2
B	614	GLY	ASP	variant	UNP P0DTC2
B	682	GLY	ARG	engineered mutation	UNP P0DTC2
B	683	SER	ARG	engineered mutation	UNP P0DTC2
B	685	SER	ARG	engineered mutation	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	1209	GLY	-	expression tag	UNP P0DTC2
B	1210	SER	-	expression tag	UNP P0DTC2
B	1211	GLY	-	expression tag	UNP P0DTC2
B	1212	TYR	-	expression tag	UNP P0DTC2
B	1213	ILE	-	expression tag	UNP P0DTC2
B	1214	PRO	-	expression tag	UNP P0DTC2
B	1215	GLU	-	expression tag	UNP P0DTC2
B	1216	ALA	-	expression tag	UNP P0DTC2
B	1217	PRO	-	expression tag	UNP P0DTC2
B	1218	ARG	-	expression tag	UNP P0DTC2
B	1219	ASP	-	expression tag	UNP P0DTC2
B	1220	GLY	-	expression tag	UNP P0DTC2
B	1221	GLN	-	expression tag	UNP P0DTC2
B	1222	ALA	-	expression tag	UNP P0DTC2
B	1223	TYR	-	expression tag	UNP P0DTC2
B	1224	VAL	-	expression tag	UNP P0DTC2
B	1225	ARG	-	expression tag	UNP P0DTC2
B	1226	LYS	-	expression tag	UNP P0DTC2
B	1227	ASP	-	expression tag	UNP P0DTC2
B	1228	GLY	-	expression tag	UNP P0DTC2
B	1229	GLU	-	expression tag	UNP P0DTC2
B	1230	TRP	-	expression tag	UNP P0DTC2
B	1231	VAL	-	expression tag	UNP P0DTC2
B	1232	LEU	-	expression tag	UNP P0DTC2
B	1233	LEU	-	expression tag	UNP P0DTC2
B	1234	SER	-	expression tag	UNP P0DTC2
B	1235	THR	-	expression tag	UNP P0DTC2
B	1236	PHE	-	expression tag	UNP P0DTC2
C	-20	SER	-	insertion	UNP P0DTC2
C	-19	ALA	-	insertion	UNP P0DTC2
C	-18	TRP	-	insertion	UNP P0DTC2
C	-17	SER	-	insertion	UNP P0DTC2

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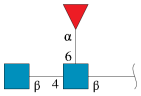
Chain	Residue	Modelled	Actual	Comment	Reference
C	-16	HIS	-	insertion	UNP P0DTC2
C	-15	PRO	-	insertion	UNP P0DTC2
C	-14	GLN	-	insertion	UNP P0DTC2
C	-13	PHE	-	insertion	UNP P0DTC2
C	-12	GLU	-	insertion	UNP P0DTC2
C	-11	LYS	-	insertion	UNP P0DTC2
C	-10	GLY	-	insertion	UNP P0DTC2
C	-9	GLY	-	insertion	UNP P0DTC2
C	-8	GLY	-	insertion	UNP P0DTC2
C	-7	SER	-	insertion	UNP P0DTC2
C	-6	GLY	-	insertion	UNP P0DTC2
C	-5	GLY	-	insertion	UNP P0DTC2
C	-4	GLY	-	insertion	UNP P0DTC2
C	-3	SER	-	insertion	UNP P0DTC2
C	-2	GLY	-	insertion	UNP P0DTC2
C	-1	GLY	-	insertion	UNP P0DTC2
C	0	SER	-	insertion	UNP P0DTC2
C	1	SER	-	insertion	UNP P0DTC2
C	2	ALA	-	insertion	UNP P0DTC2
C	3	TRP	-	insertion	UNP P0DTC2
C	4	SER	-	insertion	UNP P0DTC2
C	5	HIS	-	insertion	UNP P0DTC2
C	6	PRO	-	insertion	UNP P0DTC2
C	7	GLN	-	insertion	UNP P0DTC2
C	8	PHE	-	insertion	UNP P0DTC2
C	9	GLU	-	insertion	UNP P0DTC2
C	10	LYS	-	insertion	UNP P0DTC2
C	11	SER	-	insertion	UNP P0DTC2
C	12	ALA	-	insertion	UNP P0DTC2
C	13	LEU	-	insertion	UNP P0DTC2
C	14	VAL	-	insertion	UNP P0DTC2
C	15	PRO	-	insertion	UNP P0DTC2
C	16	ARG	-	insertion	UNP P0DTC2
C	17	GLY	-	insertion	UNP P0DTC2
C	18	SER	-	insertion	UNP P0DTC2
C	614	GLY	ASP	variant	UNP P0DTC2
C	682	GLY	ARG	engineered mutation	UNP P0DTC2
C	683	SER	ARG	engineered mutation	UNP P0DTC2
C	685	SER	ARG	engineered mutation	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	1209	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1210	SER	-	expression tag	UNP P0DTC2
C	1211	GLY	-	expression tag	UNP P0DTC2
C	1212	TYR	-	expression tag	UNP P0DTC2
C	1213	ILE	-	expression tag	UNP P0DTC2
C	1214	PRO	-	expression tag	UNP P0DTC2
C	1215	GLU	-	expression tag	UNP P0DTC2
C	1216	ALA	-	expression tag	UNP P0DTC2
C	1217	PRO	-	expression tag	UNP P0DTC2
C	1218	ARG	-	expression tag	UNP P0DTC2
C	1219	ASP	-	expression tag	UNP P0DTC2
C	1220	GLY	-	expression tag	UNP P0DTC2
C	1221	GLN	-	expression tag	UNP P0DTC2
C	1222	ALA	-	expression tag	UNP P0DTC2
C	1223	TYR	-	expression tag	UNP P0DTC2
C	1224	VAL	-	expression tag	UNP P0DTC2
C	1225	ARG	-	expression tag	UNP P0DTC2
C	1226	LYS	-	expression tag	UNP P0DTC2
C	1227	ASP	-	expression tag	UNP P0DTC2
C	1228	GLY	-	expression tag	UNP P0DTC2
C	1229	GLU	-	expression tag	UNP P0DTC2
C	1230	TRP	-	expression tag	UNP P0DTC2
C	1231	VAL	-	expression tag	UNP P0DTC2
C	1232	LEU	-	expression tag	UNP P0DTC2
C	1233	LEU	-	expression tag	UNP P0DTC2
C	1234	SER	-	expression tag	UNP P0DTC2
C	1235	THR	-	expression tag	UNP P0DTC2
C	1236	PHE	-	expression tag	UNP P0DTC2

- Molecule 2 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.



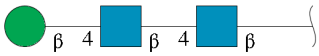
Mol	Chain	Residues	Atoms	AltConf	Trace
2	D	3	Total C N O 38 22 2 14	0	0
2	K	3	Total C H N O 72 22 34 2 14	0	0
2	Q	3	Total C H N O 71 22 33 2 14	0	0

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



Mol	Chain	Residues	Atoms					AltConf	Trace
3	a	2	Total	C	H	N	O	0	0
			53	16	25	2	10		
3	E	2	Total	C	H	N	O	0	0
			53	16	25	2	10		
3	O	2	Total	C	H	N	O	0	0
			53	16	25	2	10		
3	V	2	Total	C	H	N	O	0	0
			53	16	25	2	10		
3	W	2	Total	C	H	N	O	0	0
			53	16	25	2	10		

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



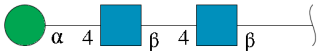
Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	3	Total	C	H	N	O	0	0
			73	22	34	2	15		
4	G	3	Total	C	H	N	O	0	0
			73	22	34	2	15		
4	I	3	Total	C	H	N	O	0	0
			73	22	34	2	15		
4	J	3	Total	C	H	N	O	0	0
			73	22	34	2	15		
4	b	3	Total	C	H	N	O	0	0
			73	22	34	2	15		
4	P	3	Total	C	H	N	O	0	0
			73	22	34	2	15		
4	R	3	Total	C	H	N	O	0	0
			73	22	34	2	15		
4	c	3	Total	C	H	N	O	0	0
			73	22	34	2	15		

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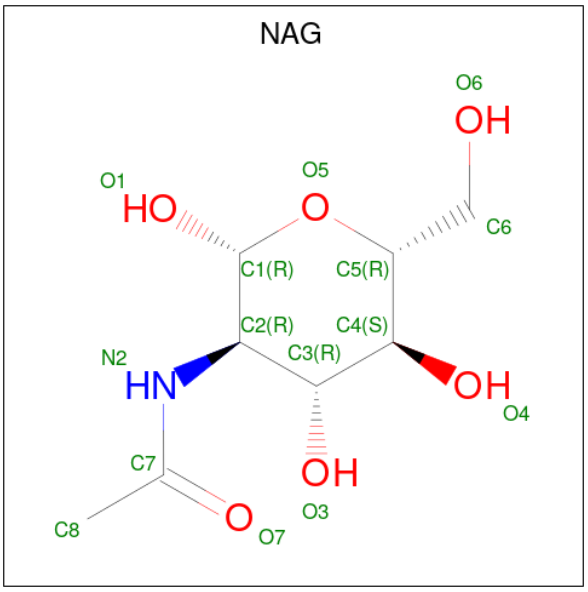
Mol	Chain	Residues	Atoms					AltConf	Trace
4	T	3	Total	C	H	N	O	0	0
			63	22	24	2	15		
4	U	3	Total	C	H	N	O	0	0
			73	22	34	2	15		
4	X	3	Total	C	H	N	O	0	0
			73	22	34	2	15		
4	Y	3	Total	C	H	N	O	0	0
			73	22	34	2	15		

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



Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	3	Total	C	H	N	O	0	0
			71	22	32	2	15		
5	L	3	Total	C	H	N	O	0	0
			72	22	33	2	15		
5	M	3	Total	C	H	N	O	0	0
			72	22	33	2	15		
5	N	3	Total	C	H	N	O	0	0
			72	22	33	2	15		
5	S	3	Total	C	H	N	O	0	0
			71	22	32	2	15		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	B	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	B	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	B	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	B	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	B	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	C	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	C	1	Total	C	H	N	O	0
			27	8	13	1	5	

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Mol	Chain	Residues	Atoms					AltConf
6	C	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	C	1	Total	C	H	N	O	0
			27	8	13	1	5	
6	C	1	Total	C	H	N	O	0
			27	8	13	1	5	

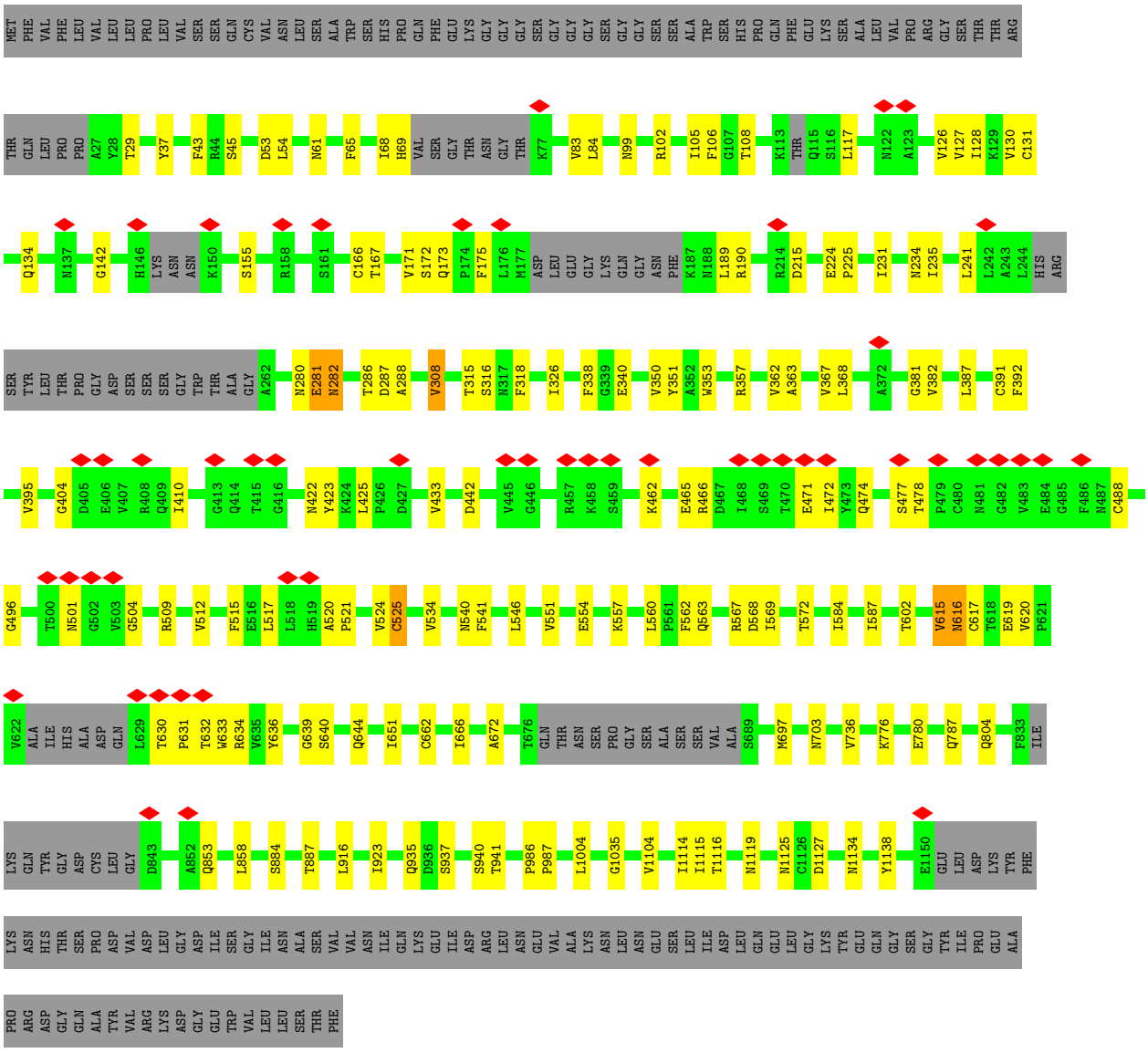
3 Residue-property plots (i)

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

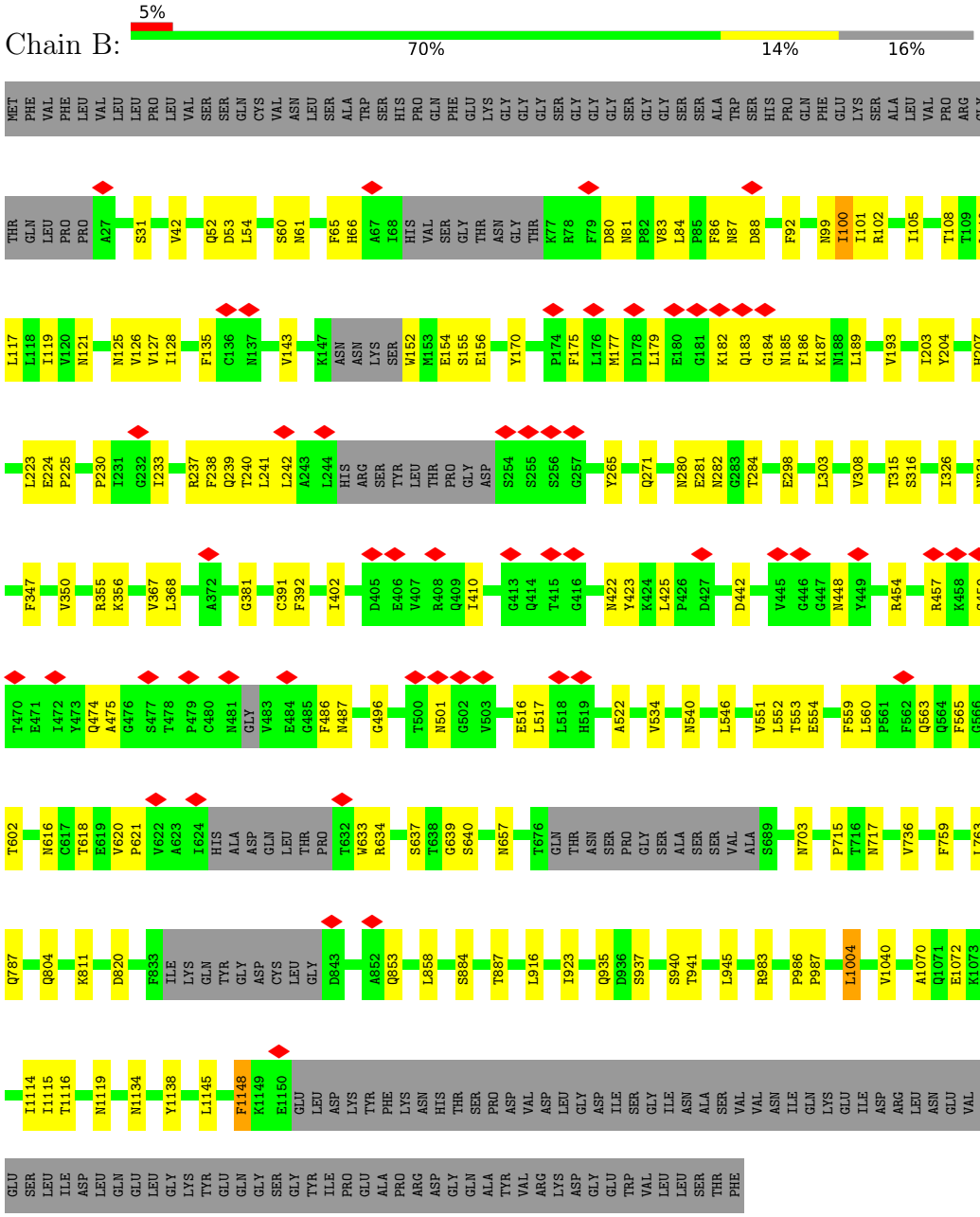
Chain A:





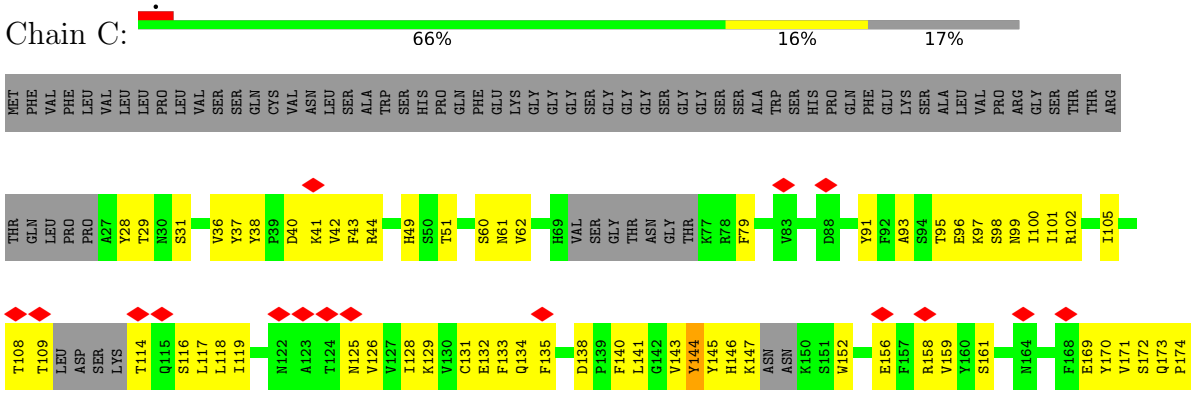
- Molecule 1: Spike glycoprotein

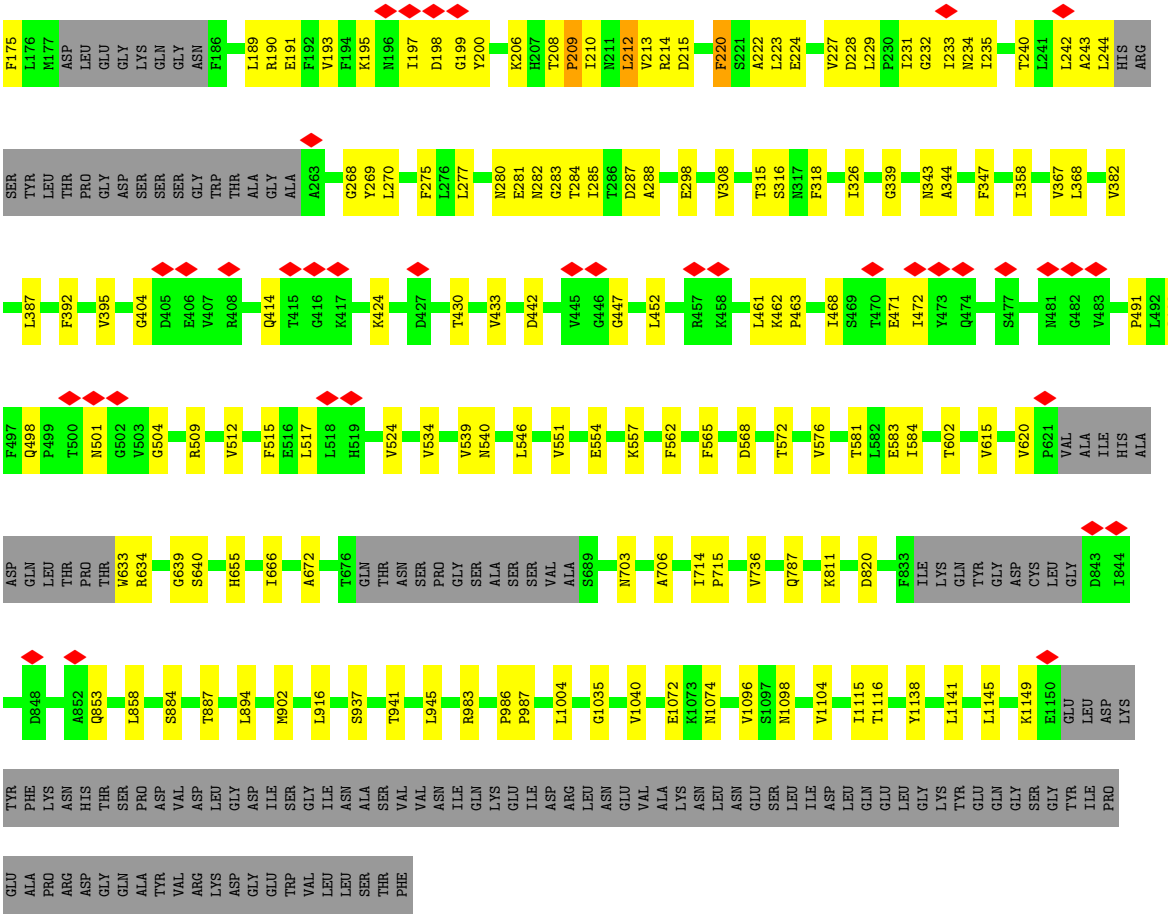
Chain B:



• Molecule 1: Spike glycoprotein

Chain C:





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

Chain D:





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

Chain K:





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

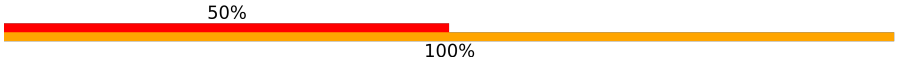
Chain Q:





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

Chain a:





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

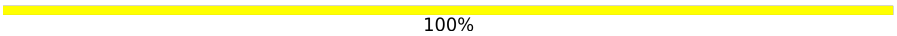
Chain E:





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

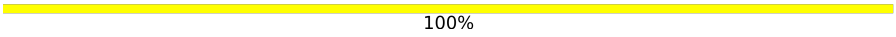
Chain O:





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

Chain V:





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

Chain W:





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

Chain F:





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

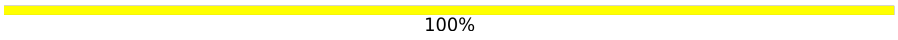
Chain G:





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

Chain I:





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

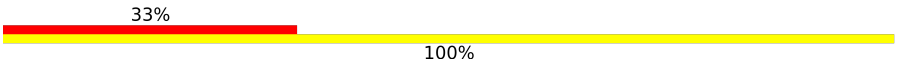
Chain J:





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

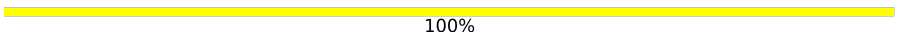
Chain b:





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

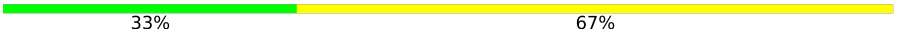
Chain P:





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

Chain R:





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

Chain c:





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

Chain T:





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

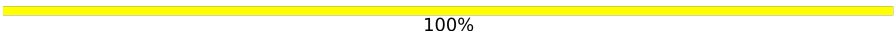
Chain U:





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

Chain X:





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

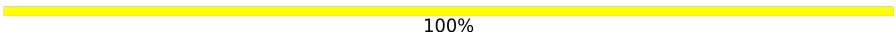
Chain Y:





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

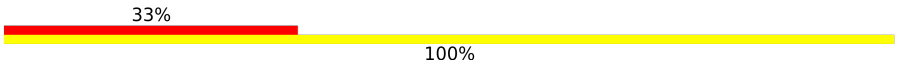
Chain H:





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

Chain L:





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

Chain M:





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

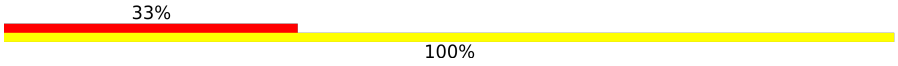
Chain N:





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

Chain S:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	157865	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	43.97	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	191780	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	1.099	Depositor
Minimum map value	-0.428	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.092	Depositor
Map size (Å)	377.00003, 377.00003, 377.00003	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.99210536, 0.99210536, 0.99210536	Depositor

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.13	0/8460	0.34	4/11510 (0.0%)
1	B	0.13	0/8562	0.29	0/11648
1	C	0.16	0/8404	0.33	1/11431 (0.0%)
All	All	0.14	0/25426	0.32	5/34589 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	525	CYS	CA-CB-SG	11.40	140.62	114.40
1	A	281	GLU	CA-C-N	8.73	137.03	121.66
1	A	281	GLU	C-N-CA	8.73	137.03	121.66
1	A	282	ASN	N-CA-CB	-6.80	99.83	110.44
1	C	209	PRO	CA-N-CD	-6.71	102.61	112.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8271	8040	8041	119	0
1	B	8371	8131	8134	150	0
1	C	8216	7977	7978	191	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	38	0	34	10	0
2	K	38	34	34	1	0
2	Q	38	33	34	3	0
3	E	28	25	25	2	0
3	O	28	25	25	0	0
3	V	28	25	25	0	0
3	W	28	25	25	1	0
3	a	28	25	25	2	0
4	F	39	34	34	2	0
4	G	39	34	33	2	0
4	I	39	34	34	0	0
4	J	39	34	34	2	0
4	P	39	34	34	0	0
4	R	39	34	34	0	0
4	T	39	24	34	2	0
4	U	39	34	34	1	0
4	X	39	34	34	0	0
4	Y	39	34	34	0	0
4	b	39	34	34	0	0
4	c	39	34	34	2	0
5	H	39	32	34	0	0
5	L	39	33	33	0	0
5	M	39	33	33	4	0
5	N	39	33	33	3	0
5	S	39	32	33	0	0
6	A	98	91	91	2	0
6	B	70	65	65	6	0
6	C	70	65	65	4	0
All	All	26013	25122	25174	456	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (456) 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:C:282:ASN:OD1	4:c:1:NAG:N2	1.91	1.02
1:B:616:ASN:OD1	1:B:618:THR:OG1	1.85	0.94
1:C:620:VAL:O	1:C:634:ARG:NH2	2.01	0.93
4:c:1:NAG:O3	4:c:2:NAG:N2	2.02	0.93
1:A:391:CYS:HA	1:A:525:CYS:HB2	1.51	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:THR:OG1	3:E:1:NAG:O6	1.89	0.91
1:B:1134:ASN:OD1	5:N:1:NAG:N2	2.05	0.90
1:C:99:ASN:OD1	1:C:102:ARG:NE	2.03	0.90
4:G:1:NAG:O6	4:G:2:NAG:N2	2.05	0.89
1:B:620:VAL:O	1:B:634:ARG:NH2	2.06	0.87
1:A:620:VAL:O	1:A:634:ARG:NH2	2.08	0.87
4:F:1:NAG:O3	4:F:2:NAG:N2	2.08	0.85
1:C:114:THR:N	1:C:132:GLU:OE1	2.11	0.82
1:C:1074:ASN:HD22	2:D:3:FUC:H5	1.45	0.81
1:A:381:GLY:O	1:B:983:ARG:NH1	2.14	0.80
1:A:1134:ASN:OD1	4:J:1:NAG:O3	1.99	0.79
3:W:1:NAG:O3	3:W:2:NAG:N2	2.15	0.79
1:B:99:ASN:O	1:B:101:ILE:N	2.15	0.78
1:C:706:ALA:HB2	2:D:1:NAG:H5	1.66	0.78
1:A:117:LEU:HD21	1:A:231:ILE:HD13	1.66	0.77
1:C:96:GLU:OE2	1:C:100:ILE:N	2.18	0.76
1:A:496:GLY:O	1:A:501:ASN:ND2	2.18	0.76
1:B:563:GLN:NE2	1:C:40:ASP:O	2.18	0.76
1:C:655:HIS:HB3	6:C:1304:NAG:H81	1.68	0.76
3:a:1:NAG:O3	3:a:2:NAG:N2	2.18	0.76
1:C:125:ASN:OD1	1:C:126:VAL:N	2.20	0.75
1:A:37:TYR:OH	1:A:53:ASP:OD2	2.03	0.75
1:C:191:GLU:O	1:C:223:LEU:HD22	1.87	0.74
1:A:29:THR:OG1	1:A:215:ASP:OD1	2.06	0.74
1:B:657:ASN:OD1	6:B:1305:NAG:N2	2.21	0.74
1:C:101:ILE:O	1:C:190:ARG:NH2	2.21	0.74
1:C:40:ASP:OD2	1:C:44:ARG:NH2	2.21	0.73
1:B:486:PHE:O	1:B:487:ASN:ND2	2.22	0.72
1:A:99:ASN:O	1:A:102:ARG:NH1	2.23	0.71
1:C:736:VAL:HG22	1:C:858:LEU:HD22	1.72	0.71
1:A:639:GLY:O	1:A:640:SER:OG	2.05	0.71
1:A:471:GLU:N	1:A:471:GLU:OE1	2.24	0.70
1:B:203:ILE:HG22	1:B:203:ILE:O	1.91	0.70
1:B:367:VAL:HG23	1:B:368:LEU:HD12	1.74	0.70
1:B:703:ASN:ND2	1:C:787:GLN:OE1	2.25	0.70
1:C:206:LYS:HB3	1:C:223:LEU:HD23	1.74	0.70
1:A:224:GLU:N	1:A:224:GLU:OE1	2.25	0.69
1:B:496:GLY:O	1:B:501:ASN:ND2	2.25	0.69
1:A:340:GLU:OE1	1:A:340:GLU:N	2.25	0.69
1:B:53:ASP:OD1	1:B:54:LEU:N	2.24	0.69
1:C:147:LYS:NZ	1:C:156:GLU:OE2	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:TRP:O	1:A:466:ARG:NE	2.23	0.68
1:C:224:GLU:N	1:C:224:GLU:OE1	2.26	0.68
1:B:215:ASP:OD1	1:B:216:LEU:N	2.27	0.67
1:B:105:ILE:N	1:B:239:GLN:O	2.26	0.67
1:A:884:SER:OG	1:A:887:THR:OG1	2.12	0.66
1:B:736:VAL:HG22	1:B:858:LEU:HD22	1.76	0.66
1:C:229:LEU:CD1	1:C:231:ILE:HG23	2.25	0.66
1:C:38:TYR:CE2	1:C:222:ALA:HB3	2.31	0.66
1:B:281:GLU:HG3	1:B:282:ASN:OD1	1.96	0.66
2:D:1:NAG:H61	2:D:2:NAG:N2	2.10	0.66
1:C:1074:ASN:ND2	2:D:3:FUC:H5	2.11	0.65
1:A:736:VAL:HG22	1:A:858:LEU:HD22	1.78	0.65
1:B:182:LYS:NZ	1:B:185:ASN:O	2.28	0.65
1:B:516:GLU:N	1:B:516:GLU:OE1	2.30	0.65
1:A:318:PHE:HZ	1:A:615:VAL:HG11	1.61	0.65
1:B:553:THR:O	1:B:586:ASP:N	2.29	0.64
1:C:37:TYR:HA	1:C:222:ALA:HB1	1.79	0.64
1:C:101:ILE:HG23	1:C:240:THR:OG1	1.97	0.64
1:C:116:SER:OG	1:C:133:PHE:O	2.16	0.64
1:B:108:THR:OG1	1:B:237:ARG:NH2	2.31	0.64
1:C:468:ILE:HG23	1:C:468:ILE:O	1.98	0.64
1:B:175:PHE:CE1	1:B:177:MET:HE2	2.32	0.63
1:A:560:LEU:HD23	1:B:225:PRO:HD2	1.79	0.63
1:A:557:LYS:HB3	1:A:584:ILE:HG21	1.79	0.63
1:B:381:GLY:O	1:C:983:ARG:NH1	2.31	0.63
1:C:129:LYS:NZ	1:C:161:SER:O	2.32	0.63
1:B:81:ASN:OD1	1:B:240:THR:OG1	2.15	0.63
1:A:61:ASN:OD1	6:A:1306:NAG:N2	2.32	0.62
1:C:193:VAL:HG22	1:C:270:LEU:HD11	1.80	0.62
1:B:1134:ASN:OD1	5:N:1:NAG:C7	2.47	0.62
1:B:127:VAL:HG23	1:B:127:VAL:O	1.99	0.62
1:C:99:ASN:OD1	1:C:99:ASN:O	2.17	0.62
1:C:173:GLN:NE2	1:C:174:PRO:O	2.32	0.62
1:C:308:VAL:HG22	1:C:602:THR:HG23	1.80	0.61
1:B:559:PHE:HA	1:C:43:PHE:CE1	2.35	0.61
1:C:318:PHE:HZ	1:C:615:VAL:HG11	1.65	0.61
1:C:128:ILE:HD12	1:C:170:TYR:CD2	2.36	0.61
1:A:391:CYS:HA	1:A:525:CYS:CB	2.28	0.61
1:C:496:GLY:O	1:C:501:ASN:ND2	2.33	0.60
1:A:546:LEU:O	1:A:546:LEU:HD23	2.01	0.60
1:B:203:ILE:O	1:B:203:ILE:CG2	2.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:414:GLN:O	1:C:424:LYS:NZ	2.35	0.59
1:A:422:ASN:OD1	1:A:423:TYR:N	2.35	0.59
1:C:706:ALA:CB	2:D:1:NAG:H5	2.32	0.59
1:B:884:SER:OG	1:B:887:THR:OG1	2.20	0.59
1:C:97:LYS:O	1:C:98:SER:OG	2.13	0.59
1:B:422:ASN:OD1	1:B:423:TYR:N	2.36	0.59
1:A:472:ILE:O	1:A:474:GLN:NE2	2.36	0.59
1:A:554:GLU:OE1	1:A:554:GLU:N	2.35	0.58
1:B:280:ASN:ND2	1:B:284:THR:OG1	2.36	0.58
1:B:568:ASP:N	1:B:572:THR:O	2.36	0.58
1:C:811:LYS:NZ	1:C:820:ASP:OD2	2.36	0.58
1:C:91:TYR:HB2	1:C:270:LEU:HD21	1.84	0.58
1:B:1114:ILE:O	1:B:1119:ASN:ND2	2.37	0.58
1:C:169:GLU:OE1	1:C:169:GLU:N	2.37	0.58
1:B:804:GLN:NE2	1:B:935:GLN:OE1	2.37	0.58
1:C:568:ASP:N	1:C:572:THR:O	2.37	0.58
1:B:189:LEU:HD22	1:B:210:ILE:HG21	1.85	0.57
1:B:546:LEU:HD23	1:B:546:LEU:O	2.03	0.57
1:B:567:ARG:NH1	1:B:571:ASP:OD1	2.37	0.57
1:A:568:ASP:N	1:A:572:THR:O	2.37	0.57
1:B:239:GLN:OE1	1:B:240:THR:N	2.36	0.57
1:B:554:GLU:N	1:B:554:GLU:OE1	2.37	0.57
1:A:287:ASP:OD1	1:A:288:ALA:N	2.36	0.57
1:C:318:PHE:CZ	1:C:615:VAL:HG11	2.39	0.57
1:A:318:PHE:CZ	1:A:615:VAL:HG11	2.39	0.57
1:C:229:LEU:HD13	1:C:231:ILE:HG23	1.84	0.56
1:A:1114:ILE:O	1:A:1119:ASN:ND2	2.38	0.56
4:U:2:NAG:O3	4:U:3:BMA:O5	2.21	0.56
1:A:117:LEU:HD11	1:A:231:ILE:HD11	1.87	0.56
1:B:83:VAL:HG12	1:B:239:GLN:HB2	1.87	0.56
1:A:367:VAL:HG23	1:A:368:LEU:HD12	1.87	0.56
1:A:916:LEU:HD12	1:A:923:ILE:HD13	1.88	0.56
1:C:101:ILE:HG23	1:C:240:THR:HG1	1.71	0.56
1:A:703:ASN:ND2	1:B:787:GLN:OE1	2.39	0.56
1:C:233:ILE:HG23	1:C:233:ILE:O	2.06	0.56
1:B:155:SER:OG	1:B:156:GLU:OE1	2.19	0.55
1:C:554:GLU:N	1:C:554:GLU:OE1	2.39	0.55
1:B:763:LEU:HD13	1:B:1004:LEU:HD22	1.89	0.55
1:C:281:GLU:OE1	1:C:281:GLU:N	2.34	0.55
1:A:126:VAL:HG21	1:A:175:PHE:CE1	2.42	0.55
1:B:117:LEU:HD11	1:B:233:ILE:HD11	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:ILE:HD11	1:A:241:LEU:HD21	1.89	0.55
1:C:736:VAL:HG13	1:C:858:LEU:HD23	1.89	0.55
1:A:616:ASN:C	1:A:616:ASN:OD1	2.49	0.55
1:B:101:ILE:HD12	1:B:241:LEU:O	2.05	0.55
1:A:166:CYS:SG	1:A:167:THR:N	2.80	0.54
1:B:187:LYS:O	1:B:207:HIS:NE2	2.38	0.54
1:C:118:LEU:HD23	1:C:118:LEU:O	2.06	0.54
1:C:126:VAL:HG23	1:C:126:VAL:O	2.07	0.54
1:A:617:CYS:N	1:A:644:GLN:OE1	2.41	0.54
1:B:189:LEU:CD2	1:B:210:ILE:HG21	2.38	0.54
1:C:430:THR:HG21	1:C:517:LEU:HD12	1.89	0.54
1:C:1098:ASN:OD1	1:C:1098:ASN:C	2.50	0.54
1:C:367:VAL:HG23	1:C:368:LEU:HD12	1.90	0.54
1:B:101:ILE:HD11	1:B:240:THR:OG1	2.07	0.54
1:A:619:GLU:OE1	1:A:620:VAL:N	2.42	0.53
1:C:326:ILE:HD12	1:C:539:VAL:HG21	1.90	0.53
1:A:61:ASN:OD1	6:A:1306:NAG:C7	2.57	0.53
1:A:106:PHE:HB3	1:A:235:ILE:HD13	1.91	0.53
1:A:937:SER:O	1:A:941:THR:HG22	2.09	0.53
1:B:111:ASP:O	1:B:113:LYS:NZ	2.35	0.53
1:C:736:VAL:HG13	1:C:858:LEU:CD2	2.39	0.53
1:B:462:LYS:N	1:B:465:GLU:OE1	2.37	0.53
1:B:563:GLN:OE1	1:C:43:PHE:CE1	2.62	0.53
1:C:102:ARG:HG3	1:C:141:LEU:HD13	1.91	0.53
1:B:454:ARG:NE	1:B:467:ASP:OD2	2.41	0.52
1:C:937:SER:O	1:C:941:THR:HG22	2.08	0.52
2:Q:1:NAG:H5	2:Q:2:NAG:H82	1.91	0.52
1:B:736:VAL:HG13	1:B:858:LEU:HD23	1.91	0.52
1:C:339:GLY:O	1:C:343:ASN:OD1	2.28	0.52
1:B:126:VAL:HG13	1:B:126:VAL:O	2.09	0.52
1:C:404:GLY:N	1:C:504:GLY:O	2.42	0.52
4:T:2:NAG:H61	4:T:3:BMA:H2	1.92	0.52
1:C:208:THR:HB	1:C:209:PRO:CD	2.40	0.52
1:A:142:GLY:O	1:A:155:SER:N	2.38	0.52
1:B:331:ASN:OD1	6:B:1301:NAG:N2	2.43	0.52
1:B:937:SER:O	1:B:941:THR:HG22	2.09	0.52
4:T:2:NAG:C6	4:T:3:BMA:H2	2.40	0.52
1:A:37:TYR:OH	1:A:54:LEU:O	2.28	0.52
1:A:462:LYS:N	1:A:465:GLU:OE1	2.40	0.52
1:A:45:SER:OG	1:A:281:GLU:HA	2.10	0.51
1:C:128:ILE:HD12	1:C:170:TYR:HD2	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:357:ARG:NH1	1:B:230:PRO:O	2.43	0.51
1:B:392:PHE:CE2	1:B:517:LEU:HD21	2.45	0.51
1:C:326:ILE:N	1:C:540:ASN:O	2.43	0.51
1:B:457:ARG:NE	1:B:459:SER:O	2.40	0.51
5:M:2:NAG:O3	5:M:3:MAN:O5	2.21	0.51
1:A:65:PHE:CZ	1:A:84:LEU:HD21	2.45	0.51
1:A:134:GLN:N	1:A:134:GLN:OE1	2.42	0.51
1:B:121:ASN:CG	1:B:126:VAL:HG23	2.36	0.51
1:C:344:ALA:HB3	1:C:347:PHE:CE1	2.46	0.51
1:C:581:THR:HG23	1:C:583:GLU:HG2	1.92	0.51
1:A:632:THR:O	1:A:632:THR:HG22	2.09	0.50
1:C:326:ILE:HD11	1:C:534:VAL:HB	1.93	0.50
1:B:410:ILE:O	1:B:425:LEU:HD12	2.12	0.50
1:C:128:ILE:HD13	1:C:229:LEU:CD2	2.41	0.50
1:C:902:MET:HB3	1:C:916:LEU:HD11	1.92	0.50
1:C:736:VAL:HG11	1:C:1004:LEU:HD11	1.94	0.50
1:B:86:PHE:HB2	1:B:238:PHE:HB3	1.93	0.50
1:B:100:ILE:HG22	1:B:242:LEU:HD11	1.94	0.50
1:B:125:ASN:OD1	1:B:127:VAL:HG13	2.12	0.50
1:C:105:ILE:HD12	1:C:105:ILE:O	2.11	0.50
1:A:477:SER:O	1:A:478:THR:OG1	2.26	0.49
1:A:410:ILE:O	1:A:425:LEU:HD12	2.12	0.49
1:C:140:PHE:CE1	1:C:244:LEU:HD22	2.47	0.49
1:C:546:LEU:O	1:C:546:LEU:HD23	2.13	0.49
6:C:1303:NAG:C1	6:C:1303:NAG:O7	2.59	0.49
1:B:99:ASN:HB2	1:B:179:LEU:HD22	1.93	0.49
1:C:275:PHE:CE2	1:C:288:ALA:HB1	2.47	0.49
1:B:811:LYS:NZ	1:B:820:ASP:OD2	2.45	0.49
1:C:119:ILE:HD12	1:C:119:ILE:H	1.77	0.49
1:A:804:GLN:NE2	1:A:935:GLN:OE1	2.40	0.49
1:B:128:ILE:N	1:B:170:TYR:O	2.45	0.49
1:C:128:ILE:HD13	1:C:229:LEU:HD22	1.94	0.49
1:C:128:ILE:HG21	1:C:229:LEU:HD22	1.95	0.49
1:C:36:VAL:HG11	1:C:220:PHE:CE2	2.48	0.49
1:C:231:ILE:HD13	1:C:235:ILE:HD11	1.95	0.48
1:A:517:LEU:HD13	1:B:983:ARG:CD	2.43	0.48
1:C:1074:ASN:HD22	2:D:3:FUC:C5	2.20	0.48
1:C:108:THR:CG2	1:C:114:THR:HG21	2.43	0.48
1:C:125:ASN:OD1	1:C:171:VAL:HG13	2.13	0.48
1:C:280:ASN:ND2	1:C:284:THR:OG1	2.42	0.48
1:C:298:GLU:OE1	1:C:633:TRP:NE1	2.40	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:ILE:O	1:A:69:HIS:C	2.56	0.48
1:C:135:PHE:O	1:C:135:PHE:CG	2.66	0.48
1:C:143:VAL:O	1:C:152:TRP:HA	2.13	0.48
1:C:392:PHE:CE2	1:C:517:LEU:HD21	2.48	0.48
1:A:280:ASN:ND2	1:A:286:THR:OG1	2.47	0.48
1:A:1116:THR:HG22	1:A:1138:TYR:HD2	1.79	0.48
1:C:195:LYS:HE2	1:C:197:ILE:HD11	1.95	0.48
1:C:546:LEU:HD13	1:C:565:PHE:CE2	2.48	0.48
1:B:193:VAL:HG23	1:B:223:LEU:CD2	2.44	0.48
1:C:62:VAL:HG12	1:C:268:GLY:HA2	1.95	0.48
1:C:79:PHE:HZ	1:C:243:ALA:O	1.97	0.48
1:A:308:VAL:HG22	1:A:602:THR:HG23	1.95	0.48
1:C:339:GLY:CA	1:C:343:ASN:OD1	2.62	0.48
1:B:341:VAL:HG22	1:B:356:LYS:HD3	1.96	0.48
1:B:546:LEU:HD13	1:B:565:PHE:CD1	2.49	0.48
1:B:1074:ASN:HB3	2:Q:1:NAG:N2	2.29	0.48
1:B:326:ILE:N	1:B:540:ASN:O	2.47	0.47
5:M:3:MAN:O6	5:M:3:MAN:O4	2.31	0.47
1:A:392:PHE:CE2	1:A:517:LEU:HD21	2.49	0.47
1:A:442:ASP:OD2	1:A:509:ARG:NH2	2.47	0.47
6:B:1304:NAG:H83	6:B:1304:NAG:H3	1.96	0.47
1:B:717:ASN:HB3	1:B:1070:ALA:HB3	1.95	0.47
1:C:212:LEU:HD13	1:C:213:VAL:H	1.79	0.47
1:B:517:LEU:HD22	1:C:983:ARG:HD3	1.95	0.47
1:C:138:ASP:HB3	1:C:140:PHE:O	2.14	0.47
1:B:203:ILE:O	1:B:204:TYR:C	2.57	0.47
1:C:557:LYS:HB3	1:C:584:ILE:HG21	1.96	0.47
1:B:81:ASN:O	1:B:239:GLN:NE2	2.42	0.47
1:B:119:ILE:HD12	1:B:128:ILE:HG13	1.96	0.47
1:A:326:ILE:HD11	1:A:534:VAL:HG22	1.97	0.47
1:C:170:TYR:CD1	1:C:171:VAL:N	2.83	0.47
1:A:524:VAL:O	1:A:525:CYS:HB3	2.14	0.47
4:F:1:NAG:HO3	4:F:2:NAG:HN2	1.63	0.47
1:B:101:ILE:O	1:B:102:ARG:C	2.58	0.47
2:Q:2:NAG:H83	2:Q:2:NAG:H3	1.97	0.47
1:B:224:GLU:N	1:B:224:GLU:OE1	2.48	0.46
1:B:121:ASN:OD1	1:B:126:VAL:HG23	2.15	0.46
1:C:118:LEU:N	1:C:129:LYS:O	2.48	0.46
1:C:277:LEU:HD22	1:C:285:ILE:HD13	1.96	0.46
1:A:567:ARG:HG2	1:B:42:VAL:HG21	1.97	0.46
1:C:96:GLU:OE1	1:C:97:LYS:O	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:884:SER:OG	1:C:887:THR:OG1	2.33	0.46
1:C:1116:THR:HG22	1:C:1138:TYR:HD2	1.80	0.46
1:A:474:GLN:HG3	1:A:488:CYS:HB3	1.97	0.46
1:B:776:LYS:NZ	1:B:780:GLU:OE2	2.48	0.46
1:C:315:THR:HG22	1:C:316:SER:N	2.30	0.46
1:B:620:VAL:HB	1:B:621:PRO:HD3	1.97	0.46
1:A:776:LYS:NZ	1:A:780:GLU:OE2	2.48	0.46
1:B:1116:THR:HG22	1:B:1138:TYR:HD2	1.81	0.46
1:C:51:THR:OG1	1:C:277:LEU:HD12	2.16	0.46
1:A:326:ILE:N	1:A:540:ASN:O	2.48	0.46
1:B:52:GLN:C	1:B:52:GLN:OE1	2.58	0.46
1:B:87:ASN:C	1:B:88:ASP:OD1	2.58	0.46
1:B:567:ARG:HB3	1:B:567:ARG:CZ	2.46	0.46
1:A:130:VAL:O	1:A:167:THR:OG1	2.32	0.46
1:A:1035:GLY:HA3	1:C:1040:VAL:HG21	1.98	0.46
1:C:280:ASN:OD1	1:C:283:GLY:N	2.48	0.46
1:A:131:CYS:HB3	1:A:166:CYS:HA	1.98	0.46
1:B:143:VAL:HG11	1:B:152:TRP:CZ2	2.51	0.46
1:C:277:LEU:CD2	1:C:285:ILE:HG21	2.46	0.46
1:B:560:LEU:HG	1:C:43:PHE:HZ	1.80	0.46
1:C:213:VAL:HG23	1:C:214:ARG:N	2.31	0.46
1:B:853:GLN:HB2	1:B:858:LEU:HD12	1.98	0.45
1:C:231:ILE:CD1	1:C:235:ILE:HG13	2.45	0.45
1:A:736:VAL:HG13	1:A:858:LEU:HD23	1.98	0.45
1:B:736:VAL:HG22	1:B:858:LEU:CD2	2.46	0.45
1:C:138:ASP:OD1	1:C:158:ARG:NH1	2.50	0.45
1:C:1145:LEU:O	1:C:1149:LYS:N	2.43	0.45
1:A:636:TYR:HB3	1:A:651:ILE:HG21	1.98	0.45
1:B:1098:ASN:OD1	5:M:1:NAG:C7	2.65	0.45
1:C:36:VAL:O	1:C:222:ALA:HA	2.17	0.45
1:C:79:PHE:CZ	1:C:242:LEU:HB3	2.52	0.45
1:C:639:GLY:O	1:C:640:SER:OG	2.24	0.45
2:D:1:NAG:O5	2:D:3:FUC:C1	2.64	0.45
1:A:433:VAL:HG22	1:A:512:VAL:HG23	1.98	0.45
1:A:1104:VAL:HG23	1:A:1115:ILE:HG12	1.98	0.45
1:B:101:ILE:HD11	1:B:240:THR:CB	2.47	0.45
1:C:339:GLY:HA2	1:C:343:ASN:OD1	2.16	0.45
1:C:231:ILE:HD12	1:C:232:GLY:N	2.32	0.45
1:A:630:THR:N	1:A:631:PRO:CD	2.79	0.45
1:A:736:VAL:HG11	1:A:1004:LEU:HD21	1.98	0.45
1:B:331:ASN:OD1	6:B:1301:NAG:C2	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:36:VAL:HG22	1:C:37:TYR:N	2.32	0.45
1:B:391:CYS:SG	1:B:522:ALA:HB1	2.57	0.45
1:C:95:THR:HG23	1:C:189:LEU:HD21	1.99	0.45
1:A:315:THR:HG22	1:A:316:SER:N	2.31	0.45
1:B:61:ASN:ND2	6:B:1303:NAG:O6	2.44	0.45
1:B:105:ILE:CG1	1:B:241:LEU:HD21	2.46	0.45
1:B:442:ASP:C	1:B:448:ASN:HD22	2.25	0.45
1:C:433:VAL:HG22	1:C:512:VAL:HG23	1.98	0.45
1:C:706:ALA:HA	2:D:2:NAG:H81	1.99	0.45
1:C:198:ASP:OD1	1:C:199:GLY:N	2.50	0.44
1:B:563:GLN:HG2	1:C:41:LYS:HA	1.99	0.44
6:C:1304:NAG:O6	6:C:1304:NAG:O4	2.26	0.44
1:A:172:SER:OG	1:A:173:GLN:N	2.51	0.44
1:A:128:ILE:N	1:A:128:ILE:HD12	2.31	0.44
1:A:404:GLY:N	1:A:504:GLY:O	2.51	0.44
1:B:31:SER:HG	1:B:60:SER:H	1.61	0.44
1:B:546:LEU:O	1:B:546:LEU:CD2	2.65	0.44
1:C:36:VAL:HG22	1:C:37:TYR:H	1.82	0.44
1:C:234:ASN:ND2	6:C:1303:NAG:O7	2.50	0.44
1:C:1104:VAL:HG23	1:C:1115:ILE:HG12	2.00	0.44
1:C:62:VAL:HG12	1:C:268:GLY:CA	2.47	0.44
1:C:145:TYR:O	1:C:146:HIS:ND1	2.50	0.44
1:C:229:LEU:HD11	1:C:231:ILE:HG12	2.00	0.44
1:C:1072:GLU:O	2:D:1:NAG:H81	2.18	0.44
1:A:225:PRO:HD2	1:C:562:PHE:CE1	2.53	0.44
1:B:271:GLN:N	1:B:271:GLN:OE1	2.51	0.44
1:B:567:ARG:HE	1:C:42:VAL:HG11	1.83	0.43
1:C:197:ILE:HD12	1:C:198:ASP:HB2	2.00	0.43
1:B:657:ASN:CG	6:B:1305:NAG:N2	2.76	0.43
1:B:986:PRO:N	1:B:987:PRO:HD2	2.32	0.43
1:C:551:VAL:HG13	1:C:551:VAL:O	2.18	0.43
1:B:183:GLN:O	1:B:184:GLY:C	2.60	0.43
1:C:49:HIS:O	1:C:277:LEU:N	2.52	0.43
1:C:159:VAL:HG23	1:C:159:VAL:O	2.18	0.43
1:A:391:CYS:CA	1:A:525:CYS:HB2	2.30	0.43
1:B:105:ILE:HD12	1:B:135:PHE:CZ	2.54	0.43
1:B:1134:ASN:OD1	5:N:1:NAG:C2	2.67	0.43
1:C:31:SER:OG	1:C:60:SER:N	2.44	0.43
1:C:565:PHE:CD2	1:C:576:VAL:HG23	2.53	0.43
1:B:315:THR:O	1:B:316:SER:C	2.62	0.43
1:C:118:LEU:O	1:C:119:ILE:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:315:THR:O	1:A:316:SER:C	2.61	0.43
1:C:29:THR:O	1:C:61:ASN:HA	2.19	0.43
1:B:143:VAL:HG12	1:B:154:GLU:HA	2.00	0.43
1:C:197:ILE:HD12	1:C:197:ILE:C	2.44	0.43
1:A:666:ILE:HD11	1:A:672:ALA:HB2	2.00	0.43
1:B:546:LEU:HD23	1:B:546:LEU:C	2.44	0.43
1:C:91:TYR:CE2	1:C:191:GLU:HB3	2.53	0.43
1:C:189:LEU:HB2	1:C:210:ILE:HG21	2.01	0.42
1:C:433:VAL:HG22	1:C:512:VAL:CG2	2.49	0.42
1:C:442:ASP:OD2	1:C:509:ARG:NH2	2.52	0.42
1:A:562:PHE:CE1	1:B:225:PRO:HG2	2.54	0.42
1:B:517:LEU:HD13	1:C:983:ARG:CD	2.49	0.42
1:A:127:VAL:HG12	1:A:171:VAL:HG13	2.02	0.42
1:A:280:ASN:C	1:A:282:ASN:H	2.26	0.42
1:A:517:LEU:HD13	1:B:983:ARG:HD2	2.02	0.42
1:A:1125:ASN:ND2	1:A:1127:ASP:OD2	2.51	0.42
1:B:303:LEU:HD12	1:B:308:VAL:HG12	2.00	0.42
1:B:454:ARG:NH1	1:B:469:SER:O	2.47	0.42
1:B:551:VAL:O	1:B:551:VAL:HG13	2.19	0.42
1:B:634:ARG:NE	1:B:637:SER:OG	2.52	0.42
1:B:1145:LEU:HA	1:B:1148:PHE:CE1	2.54	0.42
1:C:565:PHE:CE2	1:C:576:VAL:HG23	2.54	0.42
1:C:126:VAL:HG21	1:C:172:SER:HB3	2.00	0.42
1:A:362:VAL:HG13	1:A:525:CYS:O	2.19	0.42
1:A:619:GLU:CD	1:A:619:GLU:C	2.86	0.42
1:B:639:GLY:O	1:B:640:SER:OG	2.24	0.42
1:B:1098:ASN:OD1	5:M:1:NAG:N2	2.53	0.42
1:C:212:LEU:HD12	1:C:215:ASP:O	2.19	0.42
1:C:546:LEU:HD23	1:C:546:LEU:C	2.44	0.42
1:B:315:THR:HG22	1:B:316:SER:N	2.34	0.42
1:C:315:THR:O	1:C:316:SER:C	2.62	0.42
1:C:462:LYS:HB2	1:C:463:PRO:HD2	2.02	0.42
1:C:367:VAL:CG2	1:C:368:LEU:HD12	2.50	0.42
1:A:318:PHE:HA	1:A:630:THR:HB	2.02	0.42
1:A:551:VAL:O	1:A:551:VAL:HG13	2.20	0.42
1:A:633:TRP:HE3	1:A:633:TRP:O	2.02	0.42
1:A:736:VAL:HG13	1:A:858:LEU:CD2	2.50	0.42
1:B:110:LEU:N	1:B:110:LEU:HD12	2.35	0.42
1:C:37:TYR:HA	1:C:223:LEU:H	1.84	0.42
1:C:447:GLY:N	1:C:498:GLN:OE1	2.53	0.42
1:C:853:GLN:HB2	1:C:858:LEU:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:1:NAG:O5	2:K:3:FUC:C1	2.68	0.42
1:A:43:PHE:CE1	1:C:557:LYS:HD2	2.55	0.42
1:A:662:CYS:HB2	1:A:697:MET:HE3	2.01	0.42
1:A:940:SER:OG	1:A:941:THR:N	2.52	0.42
1:B:468:ILE:O	1:B:468:ILE:HG22	2.20	0.42
1:C:105:ILE:HG12	1:C:135:PHE:HB3	2.02	0.42
1:C:471:GLU:HB2	1:C:491:PRO:HB3	2.02	0.42
1:B:81:ASN:ND2	1:B:240:THR:O	2.48	0.41
1:C:277:LEU:HD22	1:C:285:ILE:HG21	2.02	0.41
1:A:853:GLN:HB2	1:A:858:LEU:HD12	2.03	0.41
1:A:127:VAL:C	1:A:128:ILE:HD12	2.46	0.41
1:B:940:SER:OG	1:B:941:THR:N	2.52	0.41
1:B:1040:VAL:HG21	1:C:1035:GLY:HA3	2.02	0.41
3:a:1:NAG:O3	3:a:2:NAG:C7	2.68	0.41
1:B:298:GLU:OE1	1:B:633:TRP:NE1	2.42	0.41
1:C:134:GLN:O	1:C:135:PHE:C	2.63	0.41
1:C:227:VAL:HG22	1:C:228:ASP:N	2.35	0.41
1:C:287:ASP:OD1	1:C:288:ALA:N	2.51	0.41
1:C:382:VAL:HG11	1:C:387:LEU:HD12	2.01	0.41
1:A:338:PHE:CZ	1:A:363:ALA:HB1	2.56	0.41
1:A:395:VAL:HG23	1:A:524:VAL:HG11	2.02	0.41
1:A:433:VAL:HG22	1:A:512:VAL:CG2	2.51	0.41
1:A:541:PHE:CE2	1:A:587:ILE:HD12	2.55	0.41
1:B:308:VAL:HG22	1:B:602:THR:HG23	2.03	0.41
1:B:344:ALA:HB3	1:B:347:PHE:CE1	2.56	0.41
1:B:552:LEU:O	1:B:553:THR:OG1	2.31	0.41
1:B:945:LEU:HD12	1:B:945:LEU:N	2.36	0.41
1:B:1104:VAL:HG23	1:B:1115:ILE:HG12	2.03	0.41
1:C:93:ALA:HB1	1:C:189:LEU:HD22	2.01	0.41
1:C:268:GLY:O	1:C:269:TYR:C	2.63	0.41
1:C:395:VAL:HG22	1:C:515:PHE:HB3	2.02	0.41
1:C:666:ILE:HD11	1:C:672:ALA:HB2	2.03	0.41
4:G:2:NAG:N2	4:G:2:NAG:O4	2.53	0.41
1:A:520:ALA:HB1	1:A:521:PRO:HD2	2.03	0.41
1:A:787:GLN:OE1	1:C:703:ASN:ND2	2.54	0.41
1:B:715:PRO:HA	1:B:1072:GLU:HA	2.03	0.41
1:C:126:VAL:HG13	1:C:175:PHE:CE2	2.56	0.41
1:C:395:VAL:HG23	1:C:524:VAL:HG11	2.03	0.41
1:A:83:VAL:HG13	1:A:83:VAL:O	2.20	0.41
1:A:189:LEU:HD12	1:A:190:ARG:N	2.36	0.41
1:A:382:VAL:HG11	1:A:387:LEU:HD21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:916:LEU:HD12	1:B:923:ILE:HD13	2.02	0.41
1:C:99:ASN:OD1	1:C:102:ARG:CZ	2.66	0.41
1:C:461:LEU:HD12	1:C:462:LYS:O	2.21	0.41
1:A:117:LEU:HD11	1:A:231:ILE:CD1	2.50	0.41
1:B:65:PHE:CE2	1:B:84:LEU:HD11	2.55	0.41
1:B:87:ASN:O	1:B:88:ASP:C	2.64	0.41
1:B:326:ILE:HD11	1:B:534:VAL:CG1	2.50	0.41
1:C:117:LEU:HD21	1:C:231:ILE:HD13	2.03	0.41
1:C:452:LEU:HD13	1:C:493:GLN:C	2.46	0.41
1:B:108:THR:O	1:B:237:ARG:NH1	2.54	0.40
1:C:108:THR:HG23	1:C:109:THR:N	2.36	0.40
1:C:706:ALA:CB	2:D:1:NAG:C5	2.97	0.40
1:C:1141:LEU:HD11	1:C:1145:LEU:HD11	2.03	0.40
1:A:560:LEU:HB2	1:A:563:GLN:HG3	2.04	0.40
1:A:568:ASP:OD1	1:A:569:ILE:N	2.48	0.40
1:A:986:PRO:N	1:A:987:PRO:HD2	2.36	0.40
1:C:28:TYR:CD1	1:C:61:ASN:OD1	2.74	0.40
1:C:143:VAL:O	1:C:144:TYR:C	2.64	0.40
1:C:468:ILE:O	1:C:468:ILE:CG2	2.68	0.40
1:B:335:LEU:N	1:B:335:LEU:HD23	2.36	0.40
1:C:358:ILE:HD12	1:C:358:ILE:N	2.36	0.40
1:C:715:PRO:HA	1:C:1072:GLU:HA	2.03	0.40
1:C:945:LEU:HD12	1:C:945:LEU:N	2.35	0.40
1:C:986:PRO:N	1:C:987:PRO:CD	2.85	0.40
1:A:234:ASN:ND2	3:E:1:NAG:H82	2.37	0.40
1:A:318:PHE:HZ	1:A:615:VAL:HG21	1.87	0.40
1:A:557:LYS:CB	1:A:584:ILE:HG21	2.49	0.40
1:B:80:ASP:O	1:B:265:TYR:OH	2.34	0.40
1:B:350:VAL:CG2	1:B:402:ILE:HG22	2.51	0.40
1:B:474:GLN:O	1:B:475:ALA:C	2.65	0.40
1:C:714:ILE:HD12	1:C:1096:VAL:HG11	2.02	0.40
1:A:350:VAL:HG13	1:A:351:TYR:N	2.36	0.40
1:A:395:VAL:HG22	1:A:515:PHE:HB3	2.04	0.40
1:A:1134:ASN:OD1	4:J:1:NAG:H2	2.21	0.40
1:B:92:PHE:CE2	1:B:101:ILE:HG21	2.56	0.40
1:B:117:LEU:CD1	1:B:233:ILE:HD11	2.51	0.40
1:B:355:ARG:NH1	1:C:200:TYR:OH	2.54	0.40
1:B:715:PRO:HD3	1:C:894:LEU:HD13	2.03	0.40
1:B:759:PHE:O	1:B:763:LEU:HG	2.22	0.40
1:C:131:CYS:HB3	1:C:133:PHE:CD2	2.56	0.40
1:C:145:TYR:O	1:C:147:LYS:HG3	2.22	0.40

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	1042/1275 (82%)	994 (95%)	48 (5%)	0	100	100
1	B	1058/1275 (83%)	989 (94%)	68 (6%)	1 (0%)	48	59
1	C	1035/1275 (81%)	944 (91%)	90 (9%)	1 (0%)	48	59
All	All	3135/3825 (82%)	2927 (93%)	206 (7%)	2 (0%)	49	59

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	100	ILE
1	C	472	ILE

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	919/1101 (84%)	916 (100%)	3 (0%)	86	92
1	B	928/1101 (84%)	924 (100%)	4 (0%)	84	91
1	C	911/1101 (83%)	908 (100%)	3 (0%)	86	92
All	All	2758/3303 (84%)	2748 (100%)	10 (0%)	81	91

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	308	VAL
1	A	615	VAL
1	A	616	ASN
1	B	66	HIS
1	B	186	PHE
1	B	1004	LEU
1	B	1148	PHE
1	C	144	TYR
1	C	212	LEU
1	C	220	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	ASN
1	A	99	ASN
1	A	173	GLN
1	A	211	ASN
1	A	519	HIS
1	A	762	GLN
1	A	1113	GLN
1	B	61	ASN
1	B	134	GLN
1	B	493	GLN
1	B	580	GLN
1	B	762	GLN
1	B	913	GLN
1	B	957	GLN
1	B	1071	GLN
1	B	1083	HIS
1	B	1113	GLN
1	C	519	HIS
1	C	536	ASN
1	C	580	GLN
1	C	644	GLN
1	C	762	GLN
1	C	1002	GLN
1	C	1036	GLN
1	C	1119	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

70 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	D	1	1,2	14,14,15	2.17	4 (28%)	17,19,21	2.50	6 (35%)
2	NAG	D	2	2	14,14,15	1.98	4 (28%)	17,19,21	1.05	1 (5%)
2	FUC	D	3	2	10,10,11	1.44	1 (10%)	14,14,16	0.85	1 (7%)
3	NAG	E	1	3,1	14,14,15	2.02	4 (28%)	17,19,21	2.24	8 (47%)
3	NAG	E	2	3	14,14,15	2.08	4 (28%)	17,19,21	1.12	1 (5%)
4	NAG	F	1	4,1	14,14,15	1.96	3 (21%)	17,19,21	1.26	2 (11%)
4	NAG	F	2	4	14,14,15	2.16	4 (28%)	17,19,21	1.26	3 (17%)
4	BMA	F	3	4	11,11,12	0.70	0	15,15,17	0.84	1 (6%)
4	NAG	G	1	4,1	14,14,15	2.17	6 (42%)	17,19,21	6.11	9 (52%)
4	NAG	G	2	4	14,14,15	2.13	5 (35%)	17,19,21	1.49	3 (17%)
4	BMA	G	3	4	11,11,12	0.81	0	15,15,17	0.77	0
5	NAG	H	1	5,1	14,14,15	1.98	3 (21%)	17,19,21	1.15	1 (5%)
5	NAG	H	2	5	14,14,15	2.13	4 (28%)	17,19,21	1.38	4 (23%)
5	MAN	H	3	5	11,11,12	1.46	2 (18%)	15,15,17	2.11	2 (13%)
4	NAG	I	1	4,1	14,14,15	1.94	4 (28%)	17,19,21	1.40	4 (23%)
4	NAG	I	2	4	14,14,15	2.05	5 (35%)	17,19,21	1.35	3 (17%)
4	BMA	I	3	4	11,11,12	0.64	0	15,15,17	0.85	1 (6%)
4	NAG	J	1	4,1	14,14,15	2.09	4 (28%)	17,19,21	1.74	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	NAG	J	2	4	14,14,15	2.04	4 (28%)	17,19,21	2.47	4 (23%)
4	BMA	J	3	4	11,11,12	0.60	0	15,15,17	0.85	1 (6%)
2	NAG	K	1	1,2	14,14,15	1.93	4 (28%)	17,19,21	2.13	3 (17%)
2	NAG	K	2	2	14,14,15	2.05	4 (28%)	17,19,21	1.32	3 (17%)
2	FUC	K	3	2	10,10,11	0.93	1 (10%)	14,14,16	0.86	0
5	NAG	L	1	5,1	14,14,15	1.91	3 (21%)	17,19,21	1.54	3 (17%)
5	NAG	L	2	5	14,14,15	2.07	4 (28%)	17,19,21	1.31	3 (17%)
5	MAN	L	3	5	11,11,12	0.93	1 (9%)	15,15,17	2.63	4 (26%)
5	NAG	M	1	5,1	14,14,15	1.96	3 (21%)	17,19,21	1.44	1 (5%)
5	NAG	M	2	5	14,14,15	2.04	4 (28%)	17,19,21	1.27	2 (11%)
5	MAN	M	3	5	11,11,12	0.95	1 (9%)	15,15,17	2.65	4 (26%)
5	NAG	N	1	5,1	14,14,15	2.22	5 (35%)	17,19,21	1.56	3 (17%)
5	NAG	N	2	5	14,14,15	2.08	4 (28%)	17,19,21	1.30	3 (17%)
5	MAN	N	3	5	11,11,12	0.96	1 (9%)	15,15,17	2.65	4 (26%)
3	NAG	O	1	3,1	14,14,15	1.95	3 (21%)	17,19,21	1.10	1 (5%)
3	NAG	O	2	3	14,14,15	2.03	4 (28%)	17,19,21	1.26	3 (17%)
4	NAG	P	1	4,1	14,14,15	1.96	4 (28%)	17,19,21	1.55	5 (29%)
4	NAG	P	2	4	14,14,15	2.04	4 (28%)	17,19,21	1.32	3 (17%)
4	BMA	P	3	4	11,11,12	0.61	0	15,15,17	0.85	1 (6%)
2	NAG	Q	1	1,2	14,14,15	1.88	3 (21%)	17,19,21	1.90	4 (23%)
2	NAG	Q	2	2	14,14,15	2.15	3 (21%)	17,19,21	1.81	4 (23%)
2	FUC	Q	3	2	10,10,11	0.76	0	14,14,16	0.79	0
4	NAG	R	1	4,1	14,14,15	2.07	4 (28%)	17,19,21	1.94	4 (23%)
4	NAG	R	2	4	14,14,15	2.27	5 (35%)	17,19,21	1.35	1 (5%)
4	BMA	R	3	4	11,11,12	0.82	0	15,15,17	0.86	0
5	NAG	S	1	5,1	14,14,15	1.86	3 (21%)	17,19,21	1.44	3 (17%)
5	NAG	S	2	5	14,14,15	2.05	4 (28%)	17,19,21	1.20	2 (11%)
5	MAN	S	3	5	11,11,12	0.88	0	15,15,17	2.63	4 (26%)
4	NAG	T	1	4	14,14,15	1.87	3 (21%)	17,19,21	1.75	4 (23%)
4	NAG	T	2	4	14,14,15	2.13	4 (28%)	17,19,21	1.62	5 (29%)
4	BMA	T	3	4	11,11,12	0.83	1 (9%)	15,15,17	1.08	2 (13%)
4	NAG	U	1	4,1	14,14,15	1.98	5 (35%)	17,19,21	1.04	2 (11%)
4	NAG	U	2	4	14,14,15	2.06	5 (35%)	17,19,21	1.24	3 (17%)
4	BMA	U	3	4	11,11,12	0.70	0	15,15,17	0.85	1 (6%)
3	NAG	V	1	3,1	14,14,15	1.92	5 (35%)	17,19,21	1.40	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	NAG	V	2	3	14,14,15	2.03	4 (28%)	17,19,21	1.32	3 (17%)
3	NAG	W	1	3,1	14,14,15	2.29	5 (35%)	17,19,21	1.89	4 (23%)
3	NAG	W	2	3	14,14,15	2.17	4 (28%)	17,19,21	1.06	1 (5%)
4	NAG	X	1	4,1	14,14,15	1.91	3 (21%)	17,19,21	1.18	2 (11%)
4	NAG	X	2	4	14,14,15	2.02	4 (28%)	17,19,21	1.41	3 (17%)
4	BMA	X	3	4	11,11,12	0.61	0	15,15,17	0.83	1 (6%)
4	NAG	Y	1	4,1	14,14,15	2.34	5 (35%)	17,19,21	1.76	5 (29%)
4	NAG	Y	2	4	14,14,15	2.09	4 (28%)	17,19,21	1.29	3 (17%)
4	BMA	Y	3	4	11,11,12	0.78	0	15,15,17	0.81	0
3	NAG	a	1	3,1	14,14,15	1.97	3 (21%)	17,19,21	1.19	2 (11%)
3	NAG	a	2	3	14,14,15	2.10	3 (21%)	17,19,21	1.28	2 (11%)
4	NAG	b	1	4,1	14,14,15	2.20	4 (28%)	17,19,21	1.49	4 (23%)
4	NAG	b	2	4	14,14,15	2.11	4 (28%)	17,19,21	1.04	1 (5%)
4	BMA	b	3	4	11,11,12	0.69	0	15,15,17	0.83	1 (6%)
4	NAG	c	1	4,1	14,14,15	2.13	6 (42%)	17,19,21	1.19	2 (11%)
4	NAG	c	2	4	14,14,15	2.14	4 (28%)	17,19,21	1.14	2 (11%)
4	BMA	c	3	4	11,11,12	0.55	0	15,15,17	1.01	2 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
2	FUC	D	3	2	1/1/4/5	-	0/1/1/1
3	NAG	E	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	E	2	3	-	3/6/23/26	0/1/1/1
4	NAG	F	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
4	BMA	F	3	4	-	0/2/19/22	0/1/1/1
4	NAG	G	1	4,1	1/1/6/7	3/6/23/26	0/1/1/1
4	NAG	G	2	4	-	3/6/23/26	0/1/1/1
4	BMA	G	3	4	-	0/2/19/22	0/1/1/1
5	NAG	H	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	H	2	5	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MAN	H	3	5	-	0/2/19/22	0/1/1/1
4	NAG	I	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	I	2	4	-	0/6/23/26	0/1/1/1
4	BMA	I	3	4	-	0/2/19/22	0/1/1/1
4	NAG	J	1	4,1	-	3/6/23/26	0/1/1/1
4	NAG	J	2	4	-	4/6/23/26	0/1/1/1
4	BMA	J	3	4	-	0/2/19/22	0/1/1/1
2	NAG	K	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	K	2	2	-	1/6/23/26	0/1/1/1
2	FUC	K	3	2	1/1/4/5	-	0/1/1/1
5	NAG	L	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	L	2	5	-	0/6/23/26	0/1/1/1
5	MAN	L	3	5	1/1/4/5	1/2/19/22	0/1/1/1
5	NAG	M	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	M	2	5	-	0/6/23/26	0/1/1/1
5	MAN	M	3	5	1/1/4/5	1/2/19/22	0/1/1/1
5	NAG	N	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	N	2	5	-	0/6/23/26	0/1/1/1
5	MAN	N	3	5	1/1/4/5	0/2/19/22	0/1/1/1
3	NAG	O	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	O	2	3	-	0/6/23/26	0/1/1/1
4	NAG	P	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	P	2	4	-	2/6/23/26	0/1/1/1
4	BMA	P	3	4	-	0/2/19/22	0/1/1/1
2	NAG	Q	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	Q	2	2	-	4/6/23/26	0/1/1/1
2	FUC	Q	3	2	1/1/4/5	-	0/1/1/1
4	NAG	R	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	R	2	4	-	3/6/23/26	0/1/1/1
4	BMA	R	3	4	-	1/2/19/22	0/1/1/1
5	NAG	S	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	S	2	5	-	0/6/23/26	0/1/1/1
5	MAN	S	3	5	1/1/4/5	1/2/19/22	0/1/1/1
4	NAG	T	1	4	-	1/6/23/26	0/1/1/1
4	NAG	T	2	4	-	0/6/23/26	0/1/1/1
4	BMA	T	3	4	-	1/2/19/22	0/1/1/1
4	NAG	U	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	U	2	4	-	0/6/23/26	0/1/1/1
4	BMA	U	3	4	-	1/2/19/22	0/1/1/1
3	NAG	V	1	3,1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	V	2	3	-	0/6/23/26	0/1/1/1
3	NAG	W	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	W	2	3	-	0/6/23/26	0/1/1/1
4	NAG	X	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	X	2	4	-	0/6/23/26	0/1/1/1
4	BMA	X	3	4	-	1/2/19/22	0/1/1/1
4	NAG	Y	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	Y	2	4	-	1/6/23/26	0/1/1/1
4	BMA	Y	3	4	-	1/2/19/22	0/1/1/1
3	NAG	a	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	a	2	3	-	2/6/23/26	0/1/1/1
4	NAG	b	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	b	2	4	-	1/6/23/26	0/1/1/1
4	BMA	b	3	4	-	0/2/19/22	0/1/1/1
4	NAG	c	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	c	2	4	-	0/6/23/26	0/1/1/1
4	BMA	c	3	4	-	0/2/19/22	0/1/1/1

All (209) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	R	2	NAG	O5-C1	5.37	1.52	1.43
3	W	1	NAG	O5-C1	5.37	1.52	1.43
3	W	2	NAG	O5-C1	5.15	1.52	1.43
2	D	1	NAG	O5-C1	5.13	1.52	1.43
4	F	2	NAG	O5-C1	4.94	1.52	1.43
4	Y	2	NAG	O5-C1	4.77	1.51	1.43
4	b	1	NAG	O5-C1	4.77	1.51	1.43
4	T	2	NAG	O5-C1	4.76	1.51	1.43
4	b	2	NAG	O5-C1	4.73	1.51	1.43
4	J	1	NAG	O5-C1	4.70	1.51	1.43
5	H	2	NAG	O5-C1	4.69	1.51	1.43
2	Q	2	NAG	O5-C1	4.65	1.51	1.43
3	a	2	NAG	O5-C1	4.64	1.51	1.43
5	N	1	NAG	O5-C1	4.64	1.51	1.43
4	c	2	NAG	O5-C1	4.63	1.51	1.43
3	E	2	NAG	O5-C1	4.56	1.51	1.43
4	G	2	NAG	O5-C1	4.54	1.51	1.43
4	R	1	NAG	O5-C1	4.54	1.51	1.43
5	N	2	NAG	O5-C1	4.53	1.51	1.43
3	V	2	NAG	O5-C1	4.53	1.51	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	U	2	NAG	O5-C1	4.53	1.51	1.43
2	K	1	NAG	O5-C1	4.51	1.51	1.43
4	Y	1	NAG	O5-C1	4.49	1.51	1.43
5	S	2	NAG	O5-C1	4.48	1.51	1.43
5	L	2	NAG	O5-C1	4.45	1.51	1.43
2	K	2	NAG	O5-C1	4.42	1.51	1.43
3	O	2	NAG	O5-C1	4.42	1.51	1.43
4	I	2	NAG	O5-C1	4.42	1.51	1.43
4	c	1	NAG	O5-C1	4.41	1.51	1.43
5	M	2	NAG	O5-C1	4.41	1.51	1.43
4	P	2	NAG	O5-C1	4.40	1.51	1.43
4	J	2	NAG	O5-C1	4.38	1.51	1.43
4	X	2	NAG	O5-C1	4.37	1.51	1.43
4	P	1	NAG	O5-C1	4.37	1.51	1.43
4	Y	1	NAG	C7-N2	4.35	1.48	1.34
4	G	1	NAG	C1-C2	4.34	1.58	1.52
2	D	2	NAG	O5-C1	4.31	1.50	1.43
4	F	1	NAG	O5-C1	4.30	1.50	1.43
5	N	1	NAG	C7-N2	4.27	1.48	1.34
3	O	1	NAG	O5-C1	4.27	1.50	1.43
4	b	1	NAG	C7-N2	4.22	1.48	1.34
2	Q	2	NAG	C7-N2	4.18	1.47	1.34
4	U	1	NAG	O5-C1	4.12	1.50	1.43
3	V	1	NAG	O5-C1	4.10	1.50	1.43
3	E	1	NAG	C7-N2	4.07	1.47	1.34
4	X	1	NAG	O5-C1	4.07	1.50	1.43
4	G	2	NAG	C7-N2	4.05	1.47	1.34
5	L	1	NAG	O5-C1	4.05	1.50	1.43
5	H	1	NAG	O5-C1	4.02	1.50	1.43
4	R	1	NAG	C7-N2	4.02	1.47	1.34
3	a	1	NAG	O5-C1	4.02	1.50	1.43
5	H	1	NAG	C7-N2	4.02	1.47	1.34
4	c	2	NAG	C7-N2	4.01	1.47	1.34
3	a	2	NAG	C7-N2	4.01	1.47	1.34
4	R	2	NAG	C7-N2	4.01	1.47	1.34
5	M	1	NAG	C7-N2	3.99	1.47	1.34
4	c	1	NAG	C7-N2	3.96	1.47	1.34
3	a	1	NAG	C7-N2	3.96	1.47	1.34
4	F	2	NAG	C7-N2	3.95	1.47	1.34
2	Q	1	NAG	O5-C1	3.93	1.50	1.43
4	J	1	NAG	C7-N2	3.93	1.47	1.34
5	S	1	NAG	O5-C1	3.93	1.50	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	b	2	NAG	C7-N2	3.92	1.47	1.34
4	J	2	NAG	C7-N2	3.92	1.47	1.34
3	E	1	NAG	O5-C1	3.92	1.50	1.43
4	I	1	NAG	O5-C1	3.92	1.50	1.43
3	E	2	NAG	C7-N2	3.91	1.47	1.34
5	L	1	NAG	C7-N2	3.91	1.47	1.34
4	T	1	NAG	C7-N2	3.91	1.47	1.34
4	Y	2	NAG	C7-N2	3.91	1.47	1.34
4	T	2	NAG	C7-N2	3.89	1.46	1.34
2	K	2	NAG	C7-N2	3.89	1.46	1.34
5	M	1	NAG	O5-C1	3.88	1.50	1.43
3	O	2	NAG	C7-N2	3.87	1.46	1.34
4	I	1	NAG	C7-N2	3.87	1.46	1.34
5	L	2	NAG	C7-N2	3.86	1.46	1.34
4	U	1	NAG	C7-N2	3.85	1.46	1.34
3	V	2	NAG	C7-N2	3.85	1.46	1.34
4	X	1	NAG	C7-N2	3.85	1.46	1.34
5	S	2	NAG	C7-N2	3.85	1.46	1.34
2	Q	1	NAG	C7-N2	3.85	1.46	1.34
3	W	2	NAG	C7-N2	3.84	1.46	1.34
4	F	1	NAG	C7-N2	3.84	1.46	1.34
4	U	2	NAG	C7-N2	3.84	1.46	1.34
5	S	1	NAG	C7-N2	3.84	1.46	1.34
5	N	2	NAG	C7-N2	3.83	1.46	1.34
5	H	2	NAG	C7-N2	3.83	1.46	1.34
3	W	1	NAG	C7-N2	3.83	1.46	1.34
4	I	2	NAG	C7-N2	3.83	1.46	1.34
5	M	2	NAG	C7-N2	3.83	1.46	1.34
3	O	1	NAG	C7-N2	3.83	1.46	1.34
4	X	2	NAG	C7-N2	3.81	1.46	1.34
4	P	1	NAG	C7-N2	3.80	1.46	1.34
4	P	2	NAG	C7-N2	3.80	1.46	1.34
2	D	2	NAG	C7-N2	3.75	1.46	1.34
2	K	1	NAG	C7-N2	3.72	1.46	1.34
2	D	1	NAG	C7-N2	3.70	1.46	1.34
4	Y	1	NAG	C2-N2	3.70	1.52	1.46
3	V	1	NAG	C7-N2	3.69	1.46	1.34
2	D	3	FUC	O5-C1	-3.69	1.37	1.43
5	H	3	MAN	O5-C5	3.56	1.50	1.43
4	T	1	NAG	O5-C1	3.56	1.49	1.43
4	G	1	NAG	O5-C5	3.50	1.50	1.43
4	G	1	NAG	C7-N2	3.47	1.45	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1	NAG	O5-C5	3.05	1.49	1.43
3	E	1	NAG	C2-N2	2.91	1.51	1.46
3	W	1	NAG	O5-C5	2.81	1.48	1.43
2	Q	2	NAG	C2-N2	2.81	1.50	1.46
4	G	2	NAG	C2-N2	2.76	1.50	1.46
4	b	1	NAG	C2-N2	2.73	1.50	1.46
4	c	1	NAG	C2-N2	2.73	1.50	1.46
4	T	1	NAG	C2-N2	2.72	1.50	1.46
5	H	2	NAG	O5-C5	2.72	1.48	1.43
4	R	1	NAG	C2-N2	2.71	1.50	1.46
4	J	2	NAG	C2-N2	2.71	1.50	1.46
4	G	1	NAG	O5-C1	2.67	1.48	1.43
4	c	2	NAG	C2-N2	2.67	1.50	1.46
3	W	1	NAG	C2-N2	2.63	1.50	1.46
3	a	2	NAG	C2-N2	2.60	1.50	1.46
4	T	2	NAG	O5-C5	2.60	1.48	1.43
3	a	1	NAG	C2-N2	2.59	1.50	1.46
5	N	1	NAG	C2-N2	2.57	1.50	1.46
4	b	2	NAG	C2-N2	2.54	1.50	1.46
3	E	2	NAG	C2-N2	2.53	1.50	1.46
5	M	1	NAG	C2-N2	2.52	1.50	1.46
5	H	1	NAG	C2-N2	2.52	1.50	1.46
5	L	2	NAG	C2-N2	2.51	1.50	1.46
5	N	2	NAG	O5-C5	2.51	1.48	1.43
4	I	2	NAG	O5-C5	2.50	1.48	1.43
5	N	1	NAG	O5-C5	2.49	1.48	1.43
2	K	2	NAG	C2-N2	2.48	1.50	1.46
4	T	2	NAG	C2-N2	2.48	1.50	1.46
5	L	2	NAG	O5-C5	2.48	1.48	1.43
4	J	1	NAG	C2-N2	2.46	1.50	1.46
4	R	2	NAG	C2-N2	2.46	1.50	1.46
5	N	2	NAG	C2-N2	2.45	1.50	1.46
4	U	2	NAG	O5-C5	2.45	1.48	1.43
2	Q	1	NAG	C2-N2	2.44	1.50	1.46
3	O	2	NAG	C2-N2	2.44	1.50	1.46
5	H	2	NAG	C2-N2	2.44	1.50	1.46
4	I	1	NAG	C2-N2	2.43	1.50	1.46
5	S	2	NAG	C2-N2	2.43	1.50	1.46
4	P	2	NAG	C2-N2	2.43	1.50	1.46
5	S	1	NAG	C2-N2	2.43	1.50	1.46
4	X	2	NAG	C2-N2	2.42	1.50	1.46
5	M	2	NAG	C2-N2	2.41	1.50	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	1	NAG	C2-N2	2.40	1.50	1.46
3	E	2	NAG	O5-C5	2.39	1.48	1.43
4	P	2	NAG	O5-C5	2.39	1.48	1.43
5	M	2	NAG	O5-C5	2.38	1.48	1.43
3	E	1	NAG	O5-C5	2.37	1.48	1.43
2	K	3	FUC	O5-C1	-2.37	1.39	1.43
4	T	3	BMA	O2-C2	-2.37	1.38	1.43
4	F	2	NAG	C2-N2	2.37	1.50	1.46
4	Y	2	NAG	O5-C5	2.37	1.48	1.43
4	U	2	NAG	C2-N2	2.37	1.50	1.46
4	I	2	NAG	C2-N2	2.36	1.50	1.46
3	V	2	NAG	C2-N2	2.34	1.50	1.46
3	W	2	NAG	C2-N2	2.33	1.50	1.46
2	K	2	NAG	O5-C5	2.33	1.48	1.43
2	D	2	NAG	C2-N2	2.33	1.50	1.46
5	N	1	NAG	C1-C2	2.33	1.55	1.52
3	O	1	NAG	C2-N2	2.32	1.50	1.46
4	X	1	NAG	C2-N2	2.32	1.50	1.46
4	F	2	NAG	O5-C5	2.31	1.47	1.43
3	W	2	NAG	O5-C5	2.31	1.47	1.43
4	P	1	NAG	O5-C5	2.30	1.47	1.43
4	R	2	NAG	O5-C5	2.30	1.47	1.43
4	R	1	NAG	O5-C5	2.30	1.47	1.43
4	b	1	NAG	O5-C5	2.29	1.47	1.43
5	S	2	NAG	O5-C5	2.29	1.47	1.43
4	X	2	NAG	O5-C5	2.29	1.47	1.43
4	R	2	NAG	C1-C2	2.28	1.55	1.52
4	Y	2	NAG	C2-N2	2.28	1.50	1.46
3	O	2	NAG	O5-C5	2.27	1.47	1.43
3	V	2	NAG	O5-C5	2.26	1.47	1.43
4	F	1	NAG	C2-N2	2.26	1.50	1.46
2	D	1	NAG	C2-N2	2.26	1.50	1.46
4	U	1	NAG	C2-N2	2.24	1.50	1.46
2	K	1	NAG	O5-C5	2.21	1.47	1.43
4	G	1	NAG	C2-N2	2.21	1.49	1.46
4	U	1	NAG	O5-C5	2.20	1.47	1.43
3	W	1	NAG	C1-C2	2.19	1.55	1.52
4	J	1	NAG	O5-C5	2.19	1.47	1.43
4	b	2	NAG	O5-C5	2.18	1.47	1.43
4	J	2	NAG	O5-C5	2.18	1.47	1.43
5	N	3	MAN	C1-C2	2.18	1.57	1.52
4	G	2	NAG	C1-C2	2.17	1.55	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	NAG	O5-C5	2.16	1.47	1.43
3	V	1	NAG	C2-N2	2.16	1.49	1.46
4	c	1	NAG	C3-C2	-2.15	1.48	1.52
4	Y	1	NAG	C3-C2	-2.15	1.48	1.52
4	Y	1	NAG	O5-C5	2.13	1.47	1.43
4	G	1	NAG	O7-C7	-2.11	1.18	1.23
5	H	3	MAN	C4-C5	2.10	1.57	1.53
4	c	1	NAG	C1-C2	2.10	1.55	1.52
4	c	1	NAG	O5-C5	2.10	1.47	1.43
3	V	1	NAG	O5-C5	2.10	1.47	1.43
5	M	3	MAN	C1-C2	2.07	1.57	1.52
4	P	1	NAG	C2-N2	2.07	1.49	1.46
4	c	2	NAG	C1-C2	2.05	1.55	1.52
5	L	3	MAN	C1-C2	2.05	1.57	1.52
4	I	1	NAG	O5-C5	2.04	1.47	1.43
3	V	1	NAG	C3-C2	-2.03	1.48	1.52
4	U	1	NAG	C3-C2	-2.03	1.48	1.52
2	K	1	NAG	C2-N2	2.03	1.49	1.46
4	U	2	NAG	C3-C2	-2.03	1.48	1.52
4	I	2	NAG	C3-C2	-2.02	1.48	1.52
4	G	2	NAG	C3-C2	-2.00	1.48	1.52

All (185) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	G	1	NAG	O5-C1-C2	-22.38	76.66	111.29
2	D	1	NAG	C1-O5-C5	6.86	121.38	112.19
5	N	3	MAN	C1-C2-C3	6.34	118.87	109.64
5	L	3	MAN	C1-C2-C3	6.28	118.78	109.64
5	M	3	MAN	C1-C2-C3	6.26	118.76	109.64
5	S	3	MAN	C1-C2-C3	6.26	118.76	109.64
5	N	3	MAN	O2-C2-C1	6.20	123.41	109.22
5	M	3	MAN	O2-C2-C1	6.18	123.37	109.22
4	J	2	NAG	O5-C1-C2	-6.18	101.74	111.29
5	L	3	MAN	O2-C2-C1	6.17	123.34	109.22
5	S	3	MAN	O2-C2-C1	6.17	123.34	109.22
5	H	3	MAN	C1-O5-C5	5.93	120.13	112.19
3	W	1	NAG	C1-O5-C5	5.90	120.09	112.19
4	G	1	NAG	O5-C5-C6	5.79	118.94	107.66
2	Q	1	NAG	C4-C3-C2	5.75	119.44	111.02
4	J	2	NAG	C1-O5-C5	-5.68	104.57	112.19
2	K	1	NAG	C1-O5-C5	5.34	119.34	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	Q	2	NAG	C8-C7-N2	5.15	124.66	116.12
4	G	1	NAG	O5-C5-C4	-5.14	98.32	110.83
4	G	1	NAG	C3-C4-C5	-4.90	101.35	110.23
3	E	1	NAG	C8-C7-N2	4.66	123.85	116.12
5	H	3	MAN	O2-C2-C3	-4.61	100.61	110.15
3	E	1	NAG	C3-C4-C5	4.30	118.02	110.23
4	G	1	NAG	C1-O5-C5	-4.27	106.46	112.19
5	M	1	NAG	C4-C3-C2	4.19	117.15	111.02
2	K	1	NAG	C1-C2-N2	-4.14	103.90	110.43
4	R	1	NAG	C4-C3-C2	3.92	116.77	111.02
4	G	2	NAG	C8-C7-N2	3.69	122.23	116.12
2	D	1	NAG	C4-C3-C2	3.58	116.27	111.02
4	T	1	NAG	C4-C3-C2	3.54	116.20	111.02
4	J	2	NAG	C3-C4-C5	3.49	116.57	110.23
4	R	1	NAG	C1-O5-C5	-3.41	107.61	112.19
5	S	1	NAG	C4-C3-C2	3.41	116.01	111.02
5	N	1	NAG	C1-O5-C5	3.39	116.73	112.19
5	M	3	MAN	C1-O5-C5	3.38	116.71	112.19
5	S	3	MAN	O2-C2-C3	3.36	117.12	110.15
5	L	3	MAN	O2-C2-C3	3.34	117.07	110.15
5	M	3	MAN	O2-C2-C3	3.31	117.02	110.15
5	N	3	MAN	C1-O5-C5	3.30	116.61	112.19
4	F	1	NAG	C8-C7-N2	3.30	121.59	116.12
4	Y	1	NAG	O5-C1-C2	3.29	116.38	111.29
5	L	1	NAG	C4-C3-C2	3.29	115.83	111.02
5	L	3	MAN	C1-O5-C5	3.28	116.58	112.19
2	K	1	NAG	C4-C3-C2	3.28	115.82	111.02
5	N	3	MAN	O2-C2-C3	3.27	116.93	110.15
4	R	1	NAG	C8-C7-N2	3.25	121.50	116.12
4	R	2	NAG	C8-C7-N2	3.24	121.49	116.12
3	V	1	NAG	C1-C2-N2	-3.22	105.36	110.43
5	S	3	MAN	C1-O5-C5	3.20	116.47	112.19
4	T	2	NAG	C1-O5-C5	-3.15	107.97	112.19
4	J	1	NAG	C1-O5-C5	3.15	116.40	112.19
4	R	1	NAG	C3-C4-C5	3.14	115.92	110.23
4	T	1	NAG	C3-C4-C5	3.06	115.78	110.23
2	D	1	NAG	O5-C1-C2	3.03	115.97	111.29
4	J	1	NAG	C2-N2-C7	-3.03	118.85	122.90
4	Y	1	NAG	C8-C7-N2	2.96	121.02	116.12
4	T	1	NAG	C1-C2-N2	-2.95	105.78	110.43
4	Y	1	NAG	O7-C7-C8	-2.95	116.80	122.05
3	W	1	NAG	O5-C1-C2	2.91	115.79	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	N	1	NAG	C6-C5-C4	-2.87	105.97	113.02
2	D	1	NAG	C1-C2-N2	-2.85	105.94	110.43
3	E	1	NAG	O5-C1-C2	-2.85	106.88	111.29
4	b	1	NAG	O5-C1-C2	2.85	115.70	111.29
4	I	1	NAG	C4-C3-C2	2.84	115.18	111.02
4	c	1	NAG	C1-C2-N2	2.83	114.90	110.43
4	G	1	NAG	C8-C7-N2	2.79	120.74	116.12
4	T	2	NAG	C1-C2-N2	-2.78	106.05	110.43
4	G	2	NAG	C1-O5-C5	-2.75	108.50	112.19
4	P	1	NAG	C2-N2-C7	-2.75	119.22	122.90
4	J	1	NAG	C1-C2-N2	-2.73	106.14	110.43
4	P	1	NAG	C1-C2-N2	-2.72	106.15	110.43
3	a	1	NAG	C1-O5-C5	-2.71	108.56	112.19
4	J	1	NAG	C8-C7-N2	2.71	120.61	116.12
4	Y	1	NAG	C1-C2-N2	2.67	114.65	110.43
4	T	2	NAG	C8-C7-N2	2.66	120.53	116.12
5	L	1	NAG	C8-C7-N2	2.66	120.53	116.12
5	H	2	NAG	C2-N2-C7	-2.65	119.35	122.90
2	Q	2	NAG	O7-C7-C8	-2.65	117.34	122.05
4	X	2	NAG	C1-O5-C5	-2.64	108.65	112.19
2	D	1	NAG	O5-C5-C4	2.64	117.25	110.83
5	N	2	NAG	O5-C1-C2	-2.63	107.22	111.29
5	H	2	NAG	C8-C7-N2	2.61	120.44	116.12
4	b	1	NAG	C1-O5-C5	-2.58	108.72	112.19
3	a	2	NAG	C8-C7-N2	2.58	120.39	116.12
4	I	2	NAG	O5-C1-C2	-2.55	107.35	111.29
4	G	1	NAG	C1-C2-N2	-2.54	106.43	110.43
4	c	1	NAG	C1-O5-C5	-2.53	108.80	112.19
4	G	1	NAG	C4-C3-C2	2.50	114.69	111.02
4	P	1	NAG	C8-C7-N2	2.48	120.24	116.12
4	T	3	BMA	O2-C2-C3	-2.48	105.02	110.15
5	L	2	NAG	C8-C7-N2	2.48	120.22	116.12
4	c	3	BMA	C1-O5-C5	2.47	115.50	112.19
4	T	1	NAG	C8-C7-N2	2.46	120.20	116.12
4	F	2	NAG	C1-O5-C5	2.46	115.48	112.19
4	b	1	NAG	C8-C7-N2	2.46	120.19	116.12
4	P	2	NAG	C8-C7-N2	2.46	120.19	116.12
2	K	2	NAG	C8-C7-N2	2.44	120.17	116.12
5	L	2	NAG	O5-C1-C2	-2.44	107.51	111.29
3	a	2	NAG	C2-N2-C7	-2.43	119.64	122.90
4	X	1	NAG	C8-C7-N2	2.42	120.14	116.12
5	L	2	NAG	C2-N2-C7	-2.42	119.66	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	P	2	NAG	O5-C1-C2	-2.40	107.57	111.29
4	Y	1	NAG	C4-C3-C2	-2.39	107.51	111.02
2	Q	1	NAG	C8-C7-N2	2.38	120.07	116.12
2	K	2	NAG	O5-C1-C2	-2.38	107.61	111.29
5	S	2	NAG	C8-C7-N2	2.38	120.06	116.12
4	T	2	NAG	C2-N2-C7	-2.36	119.73	122.90
5	M	2	NAG	O5-C1-C2	-2.36	107.64	111.29
3	a	1	NAG	C8-C7-N2	2.36	120.03	116.12
5	H	2	NAG	O5-C1-C2	-2.36	107.64	111.29
4	X	2	NAG	O5-C1-C2	-2.35	107.65	111.29
2	Q	1	NAG	C3-C4-C5	2.35	114.50	110.23
3	E	1	NAG	C1-O5-C5	-2.35	109.03	112.19
4	I	1	NAG	C3-C4-C5	2.34	114.48	110.23
4	J	2	NAG	C4-C3-C2	2.33	114.44	111.02
3	O	2	NAG	O5-C1-C2	-2.33	107.68	111.29
4	c	2	NAG	C8-C7-N2	2.33	119.98	116.12
4	J	1	NAG	C3-C4-C5	2.31	114.43	110.23
4	Y	2	NAG	C8-C7-N2	2.30	119.93	116.12
5	N	2	NAG	C8-C7-N2	2.30	119.93	116.12
4	F	1	NAG	C1-O5-C5	2.30	115.26	112.19
3	V	2	NAG	C2-N2-C7	-2.29	119.83	122.90
2	Q	2	NAG	C4-C3-C2	2.29	114.37	111.02
4	P	1	NAG	C1-O5-C5	2.29	115.25	112.19
3	E	2	NAG	C8-C7-N2	2.28	119.91	116.12
4	P	2	NAG	C2-N2-C7	-2.27	119.86	122.90
4	U	2	NAG	O5-C1-C2	-2.27	107.78	111.29
3	O	2	NAG	C8-C7-N2	2.27	119.88	116.12
4	b	2	NAG	C8-C7-N2	2.26	119.87	116.12
5	N	2	NAG	C2-N2-C7	-2.26	119.87	122.90
2	D	1	NAG	C3-C4-C5	2.26	114.33	110.23
2	Q	2	NAG	O7-C7-N2	-2.26	118.00	121.98
4	G	2	NAG	O5-C1-C2	-2.25	107.81	111.29
4	Y	2	NAG	C3-C4-C5	2.25	114.31	110.23
4	U	2	NAG	C8-C7-N2	2.25	119.85	116.12
3	E	1	NAG	O7-C7-N2	-2.24	118.02	121.98
5	M	2	NAG	C8-C7-N2	2.24	119.83	116.12
5	H	2	NAG	C4-C3-C2	-2.24	107.74	111.02
3	E	1	NAG	C6-C5-C4	-2.24	107.53	113.02
4	X	2	NAG	C8-C7-N2	2.23	119.82	116.12
4	I	2	NAG	C8-C7-N2	2.23	119.82	116.12
4	F	3	BMA	O2-C2-C3	-2.22	105.54	110.15
2	Q	1	NAG	C2-N2-C7	-2.22	119.92	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	V	2	NAG	C8-C7-N2	2.22	119.81	116.12
4	b	1	NAG	O7-C7-C8	-2.22	118.10	122.05
5	S	2	NAG	C2-N2-C7	-2.21	119.93	122.90
3	E	1	NAG	O7-C7-C8	-2.20	118.13	122.05
5	S	1	NAG	C8-C7-N2	2.20	119.77	116.12
4	T	3	BMA	C1-O5-C5	2.19	115.12	112.19
4	U	3	BMA	O2-C2-C3	-2.18	105.63	110.15
3	E	1	NAG	O5-C5-C4	2.17	116.11	110.83
4	Y	2	NAG	C2-N2-C7	-2.17	120.00	122.90
5	S	1	NAG	C3-C4-C5	2.16	114.16	110.23
2	D	2	NAG	C8-C7-N2	2.16	119.70	116.12
2	K	2	NAG	C2-N2-C7	-2.16	120.01	122.90
4	P	3	BMA	O2-C2-C3	-2.15	105.70	110.15
4	X	1	NAG	C2-N2-C7	-2.15	120.02	122.90
3	V	2	NAG	O5-C1-C2	-2.14	107.97	111.29
4	F	2	NAG	C8-C7-N2	2.13	119.65	116.12
4	I	3	BMA	O2-C2-C3	-2.12	105.76	110.15
4	G	1	NAG	C6-C5-C4	-2.12	107.82	113.02
4	J	3	BMA	O2-C2-C3	-2.11	105.78	110.15
3	W	1	NAG	O5-C5-C6	2.11	111.77	107.66
4	I	2	NAG	C2-N2-C7	-2.11	120.08	122.90
5	H	1	NAG	C8-C7-N2	2.10	119.60	116.12
4	F	2	NAG	C2-N2-C7	-2.09	120.10	122.90
4	X	3	BMA	O2-C2-C3	-2.08	105.85	110.15
4	T	2	NAG	O5-C5-C6	2.07	111.70	107.66
4	c	3	BMA	O2-C2-C3	-2.07	105.86	110.15
5	N	1	NAG	C8-C7-N2	2.07	119.55	116.12
4	b	3	BMA	O2-C2-C3	-2.07	105.87	110.15
3	V	1	NAG	C8-C7-N2	2.06	119.54	116.12
4	I	1	NAG	C6-C5-C4	-2.06	107.95	113.02
3	O	1	NAG	C8-C7-N2	2.06	119.54	116.12
4	c	2	NAG	C1-O5-C5	2.06	114.95	112.19
4	U	2	NAG	C2-N2-C7	-2.05	120.16	122.90
3	W	1	NAG	C6-C5-C4	-2.04	108.00	113.02
4	I	1	NAG	C8-C7-N2	2.04	119.50	116.12
3	W	2	NAG	C2-N2-C7	-2.04	120.17	122.90
4	U	1	NAG	C6-C5-C4	-2.04	108.02	113.02
4	P	1	NAG	C6-C5-C4	-2.03	108.04	113.02
2	D	3	FUC	O2-C2-C3	-2.02	105.96	110.15
3	O	2	NAG	C2-N2-C7	-2.01	120.20	122.90
5	L	1	NAG	C1-C2-N2	-2.01	107.27	110.43
4	U	1	NAG	C8-C7-N2	2.00	119.44	116.12

All (8) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	D	3	FUC	C1
2	K	3	FUC	C1
2	Q	3	FUC	C1
4	G	1	NAG	C1
5	L	3	MAN	C2
5	M	3	MAN	C2
5	N	3	MAN	C2
5	S	3	MAN	C2

All (74) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	a	1	NAG	C1-C2-N2-C7
3	E	1	NAG	C1-C2-N2-C7
4	Y	1	NAG	C3-C2-N2-C7
5	L	1	NAG	O5-C5-C6-O6
3	a	1	NAG	O5-C5-C6-O6
4	J	2	NAG	C4-C5-C6-O6
4	X	1	NAG	O5-C5-C6-O6
5	L	1	NAG	C4-C5-C6-O6
4	R	1	NAG	O5-C5-C6-O6
3	a	1	NAG	C4-C5-C6-O6
4	R	1	NAG	C4-C5-C6-O6
4	J	2	NAG	O5-C5-C6-O6
5	S	1	NAG	O5-C5-C6-O6
5	N	1	NAG	O5-C5-C6-O6
3	W	1	NAG	C4-C5-C6-O6
5	N	1	NAG	C4-C5-C6-O6
2	Q	2	NAG	C8-C7-N2-C2
2	Q	2	NAG	O7-C7-N2-C2
3	E	1	NAG	C8-C7-N2-C2
3	E	1	NAG	O7-C7-N2-C2
4	F	1	NAG	C8-C7-N2-C2
4	F	1	NAG	O7-C7-N2-C2
4	G	1	NAG	C8-C7-N2-C2
4	G	1	NAG	O7-C7-N2-C2
4	G	2	NAG	C8-C7-N2-C2
4	G	2	NAG	O7-C7-N2-C2
4	R	1	NAG	C8-C7-N2-C2
4	R	1	NAG	O7-C7-N2-C2
4	R	2	NAG	C8-C7-N2-C2
4	R	2	NAG	O7-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
3	W	1	NAG	O5-C5-C6-O6
3	V	1	NAG	C4-C5-C6-O6
4	F	2	NAG	C4-C5-C6-O6
4	X	1	NAG	C4-C5-C6-O6
5	S	1	NAG	C4-C5-C6-O6
5	H	2	NAG	C4-C5-C6-O6
5	S	3	MAN	O5-C5-C6-O6
4	J	1	NAG	O5-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
4	G	1	NAG	O5-C5-C6-O6
4	G	2	NAG	O5-C5-C6-O6
2	Q	1	NAG	C4-C5-C6-O6
4	F	2	NAG	O5-C5-C6-O6
4	R	3	BMA	O5-C5-C6-O6
3	V	1	NAG	O5-C5-C6-O6
5	H	1	NAG	C4-C5-C6-O6
4	T	3	BMA	O5-C5-C6-O6
4	X	3	BMA	O5-C5-C6-O6
3	a	2	NAG	O5-C5-C6-O6
5	H	2	NAG	O5-C5-C6-O6
5	M	3	MAN	O5-C5-C6-O6
4	Y	3	BMA	O5-C5-C6-O6
4	U	3	BMA	O5-C5-C6-O6
5	L	3	MAN	O5-C5-C6-O6
2	K	2	NAG	O5-C5-C6-O6
4	R	2	NAG	O5-C5-C6-O6
4	b	2	NAG	O5-C5-C6-O6
4	P	2	NAG	C4-C5-C6-O6
2	Q	2	NAG	C1-C2-N2-C7
3	E	2	NAG	C1-C2-N2-C7
4	J	1	NAG	C1-C2-N2-C7
2	Q	1	NAG	O5-C5-C6-O6
2	Q	2	NAG	C3-C2-N2-C7
4	J	2	NAG	C3-C2-N2-C7
4	b	1	NAG	C3-C2-N2-C7
4	P	2	NAG	O5-C5-C6-O6
5	H	1	NAG	O5-C5-C6-O6
4	J	2	NAG	C1-C2-N2-C7
4	b	1	NAG	C1-C2-N2-C7
4	Y	2	NAG	C1-C2-N2-C7
3	a	2	NAG	C3-C2-N2-C7
3	E	2	NAG	C3-C2-N2-C7

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Mol	Chain	Res	Type	Atoms
4	J	1	NAG	C3-C2-N2-C7
4	T	1	NAG	C4-C5-C6-O6

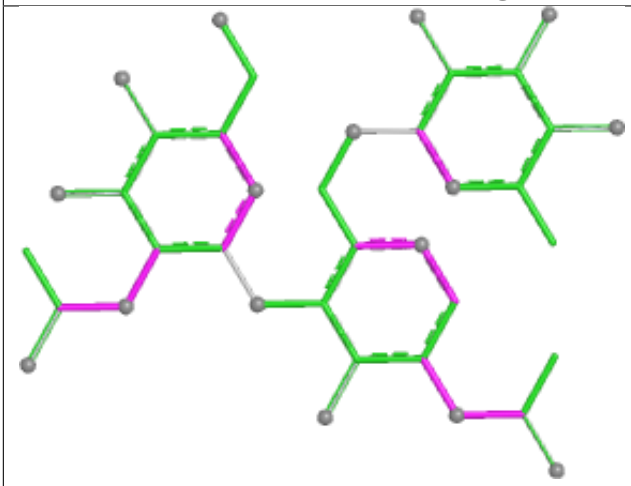
There are no ring outliers.

27 monomers are involved in 37 short contacts:

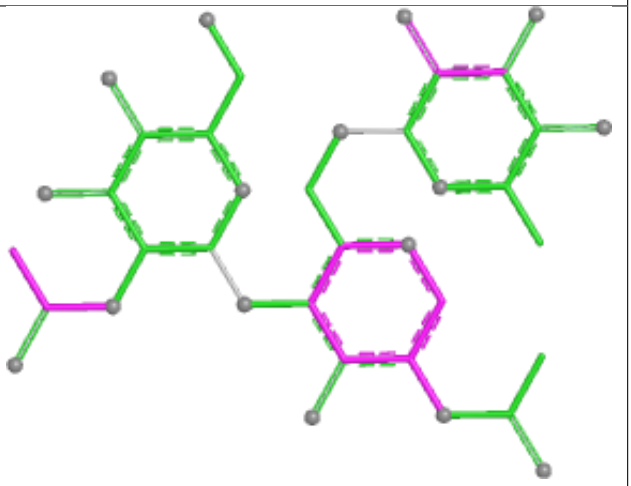
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	3	FUC	1	0
4	G	2	NAG	2	0
4	c	1	NAG	2	0
5	N	1	NAG	3	0
3	a	2	NAG	2	0
2	D	2	NAG	2	0
4	U	3	BMA	1	0
5	M	2	NAG	1	0
3	W	2	NAG	1	0
2	Q	1	NAG	2	0
4	c	2	NAG	1	0
4	F	2	NAG	2	0
4	U	2	NAG	1	0
4	G	1	NAG	1	0
2	Q	2	NAG	2	0
4	F	1	NAG	2	0
5	M	3	MAN	2	0
2	D	3	FUC	4	0
3	W	1	NAG	1	0
4	J	1	NAG	2	0
2	D	1	NAG	6	0
3	a	1	NAG	2	0
4	T	3	BMA	2	0
5	M	1	NAG	2	0
2	K	1	NAG	1	0
4	T	2	NAG	2	0
3	E	1	NAG	2	0

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

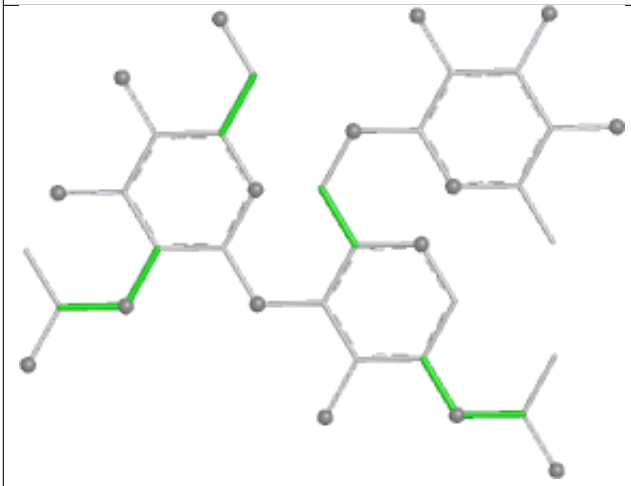
Oligosaccharide Chain D



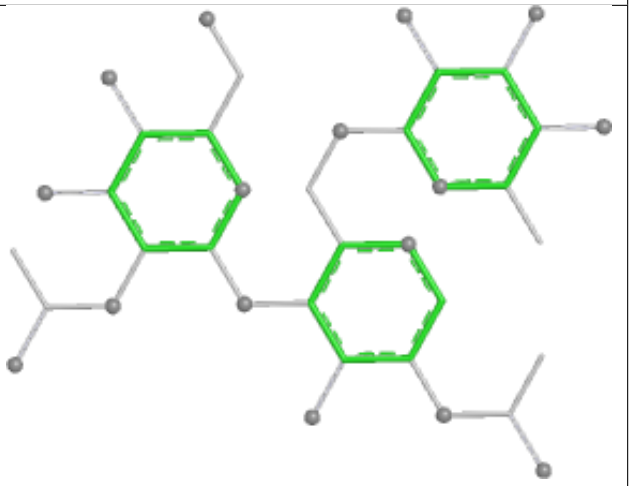
Bond lengths



Bond angles

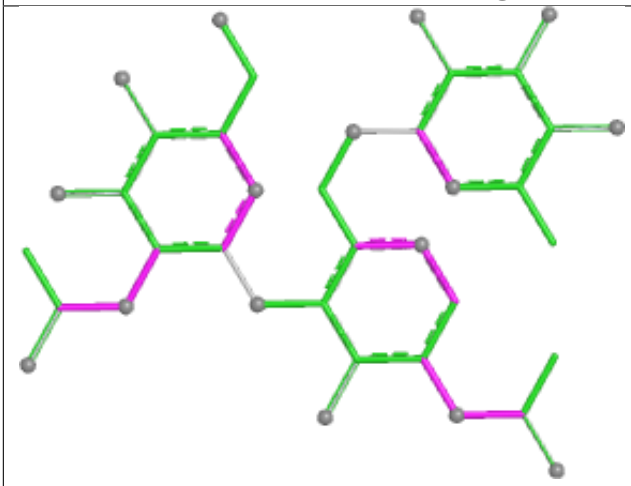


Torsions

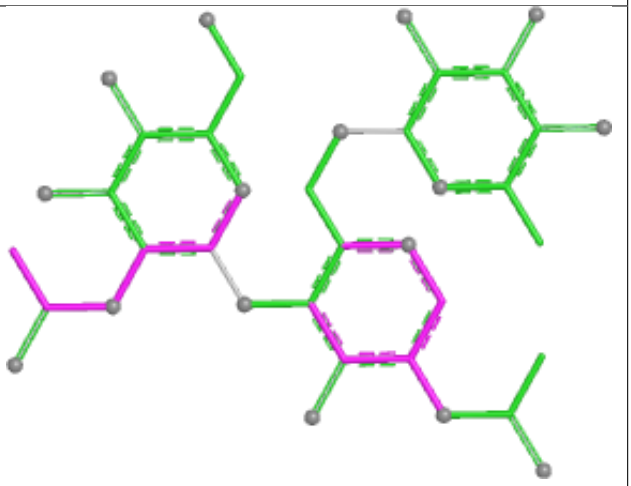


Rings

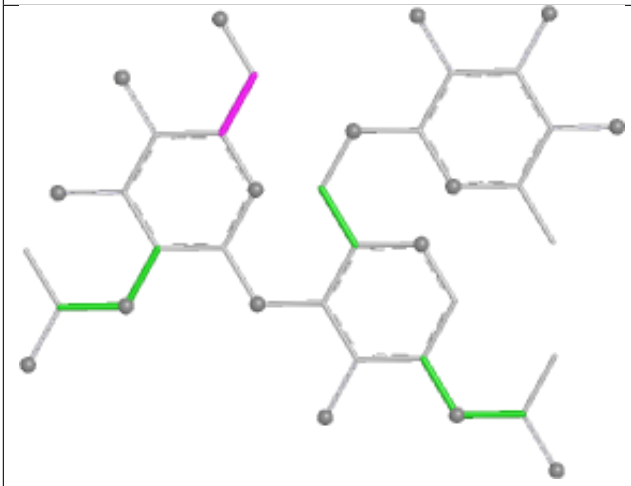
Oligosaccharide Chain K



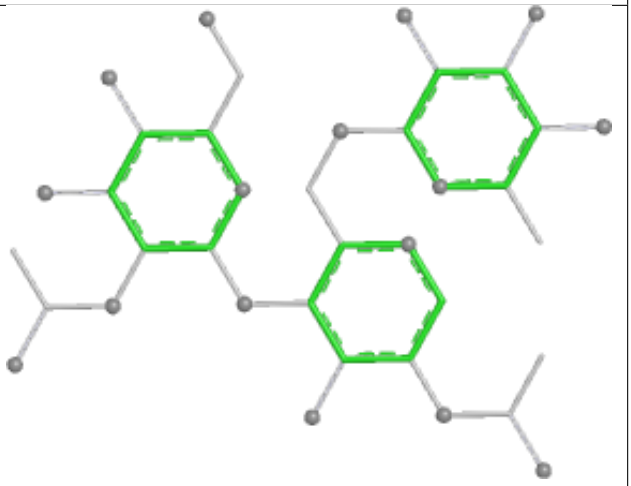
Bond lengths



Bond angles

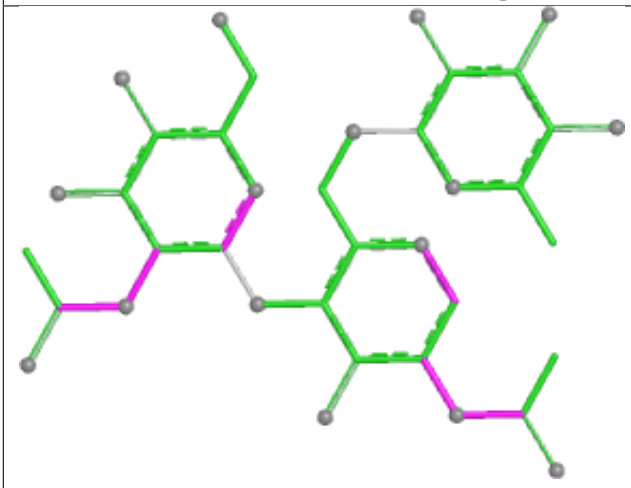


Torsions

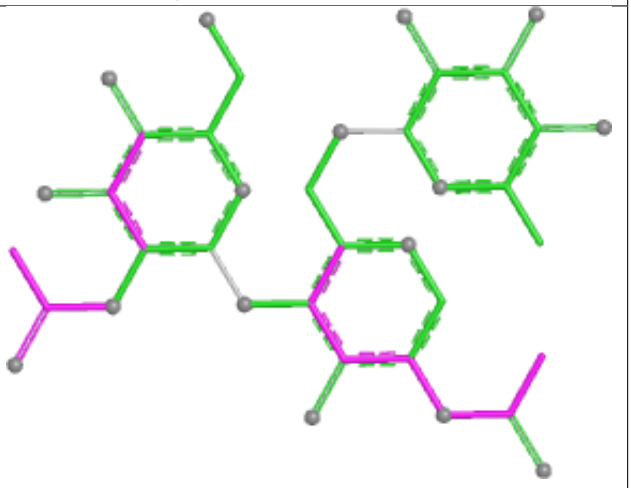


Rings

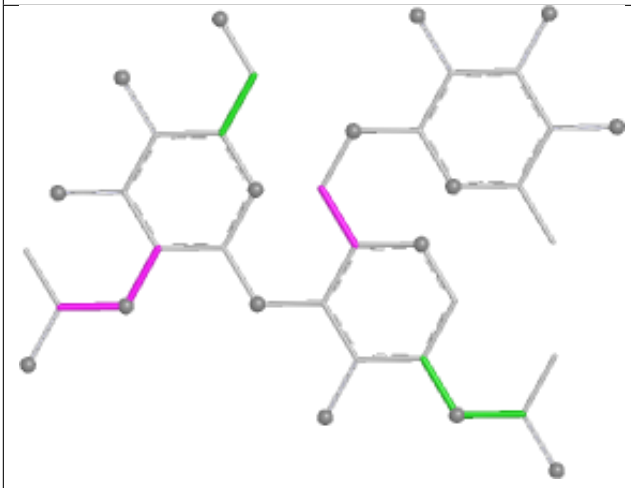
Oligosaccharide Chain Q



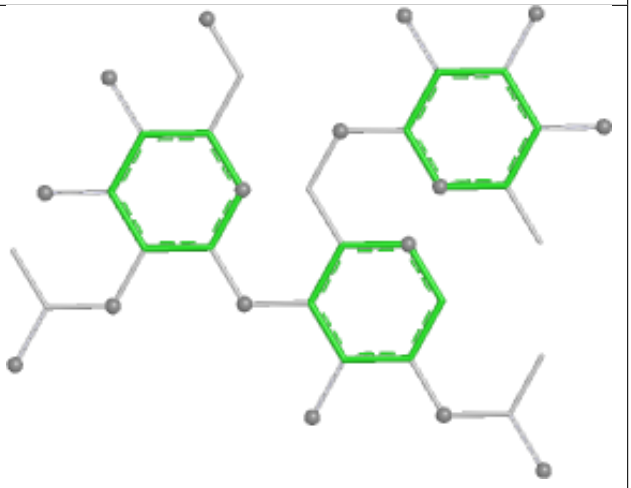
Bond lengths



Bond angles

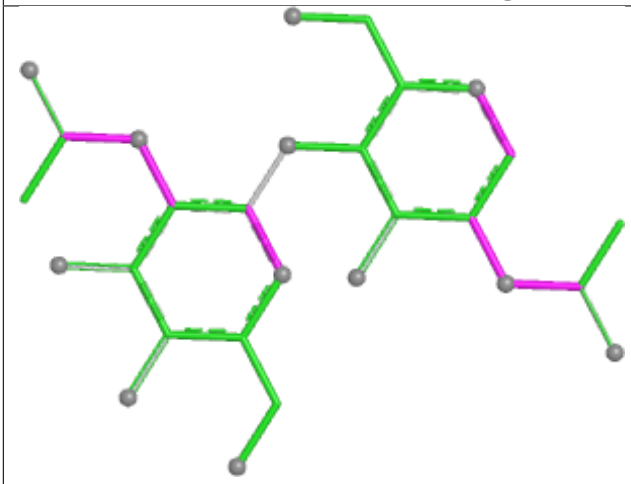


Torsions

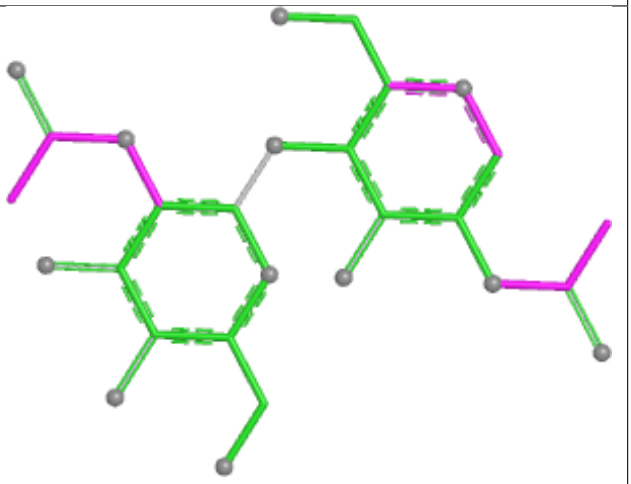


Rings

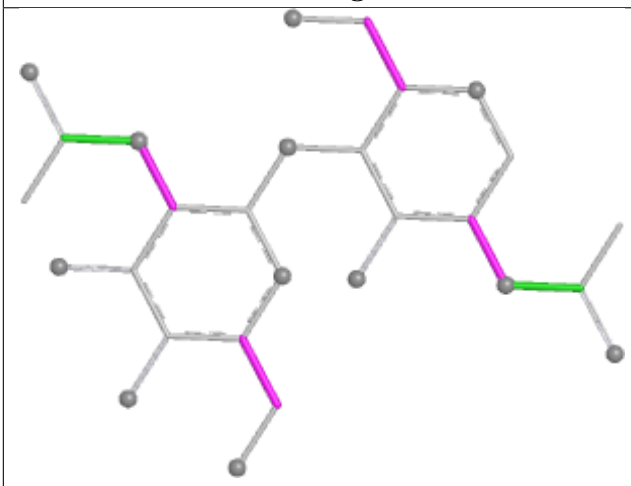
Oligosaccharide Chain a



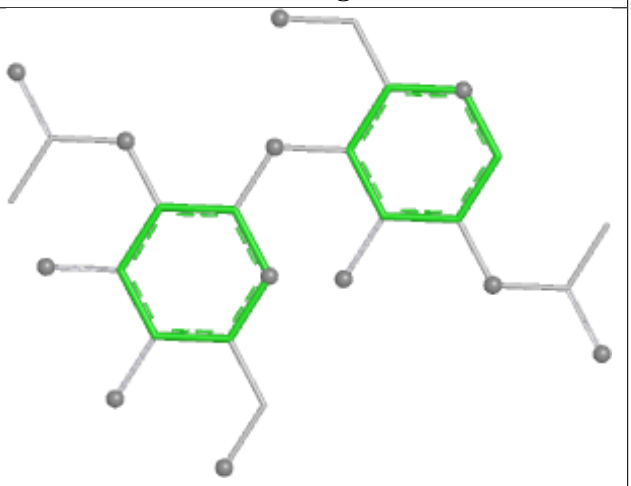
Bond lengths



Bond angles

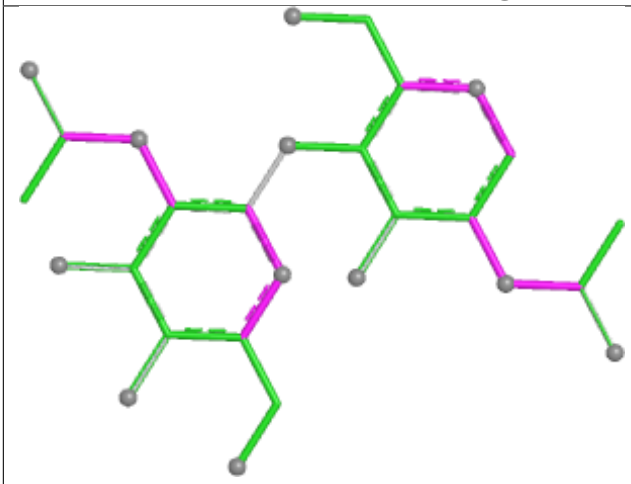


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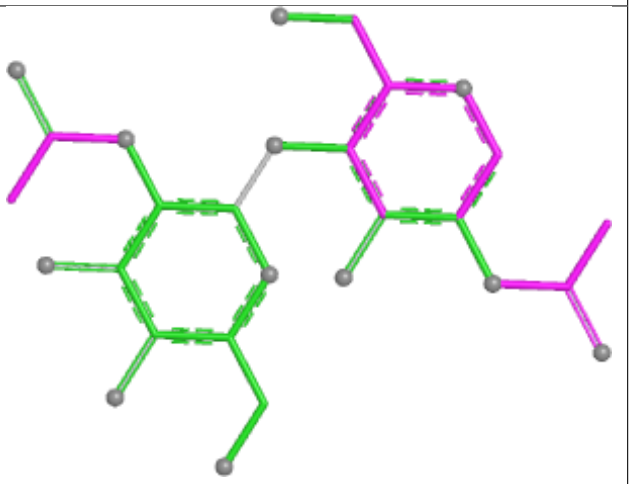


Rings

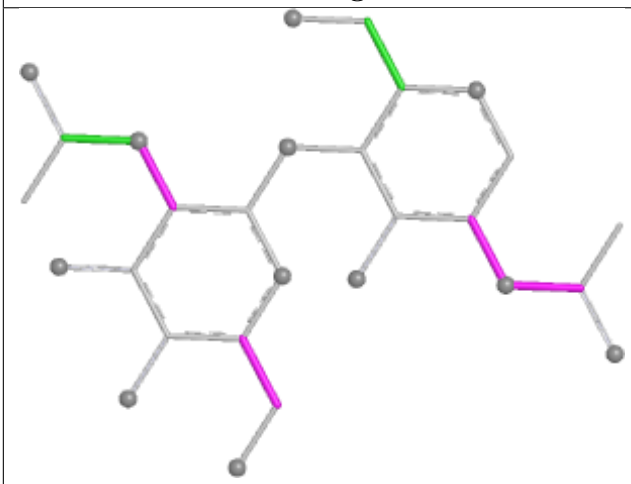
Oligosaccharide Chain E



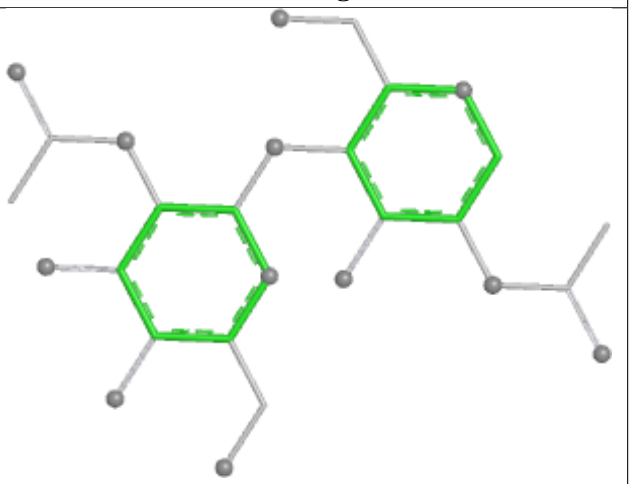
Bond lengths



Bond angles

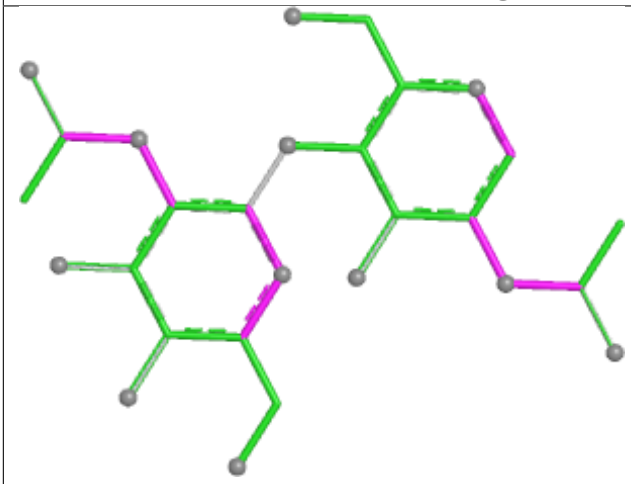


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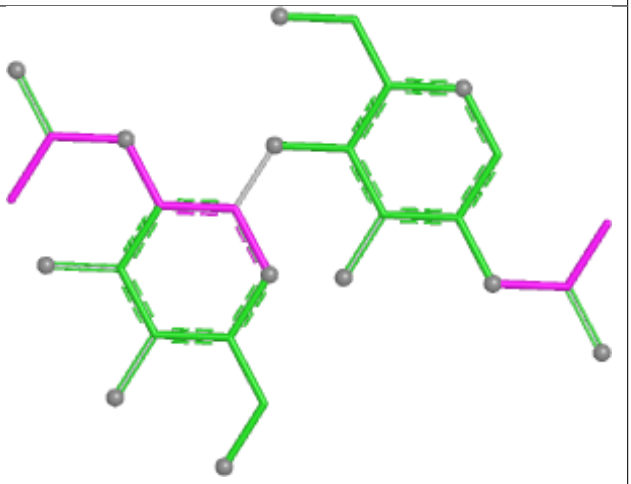


Rings

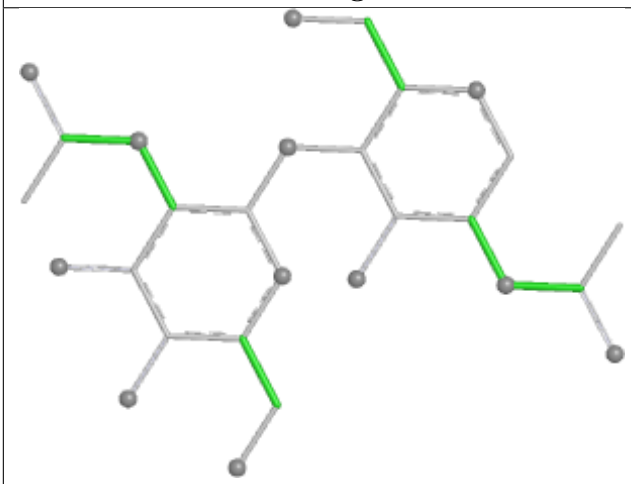
Oligosaccharide Chain O



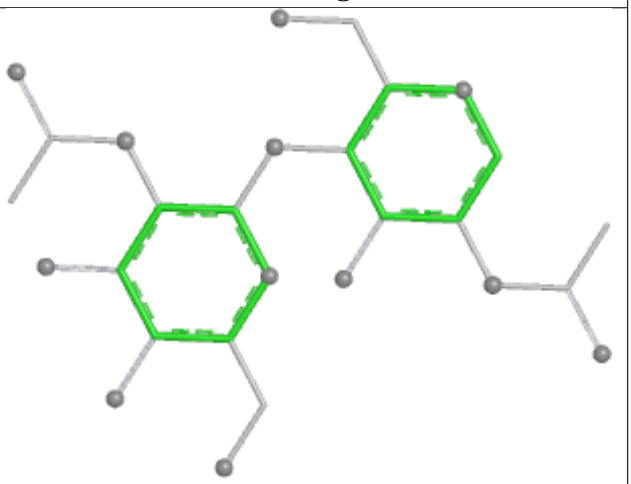
Bond lengths



Bond angles

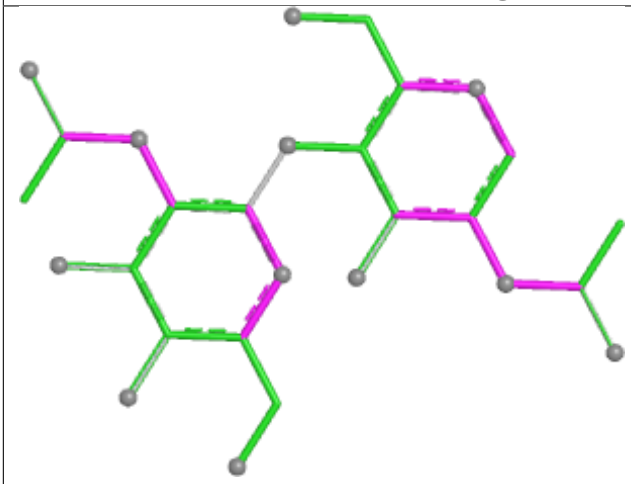


Torsions

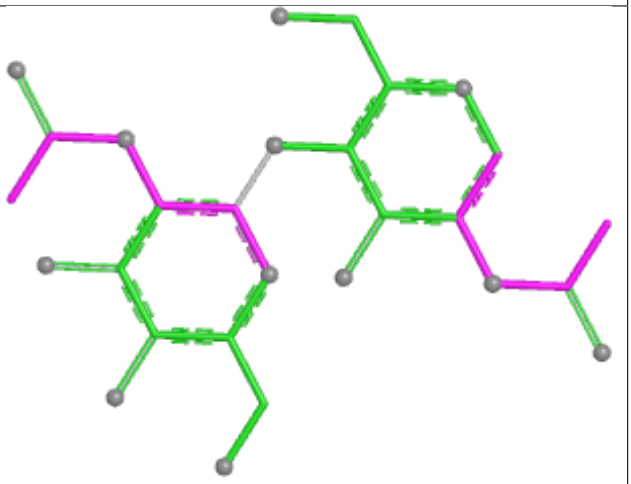


Rings

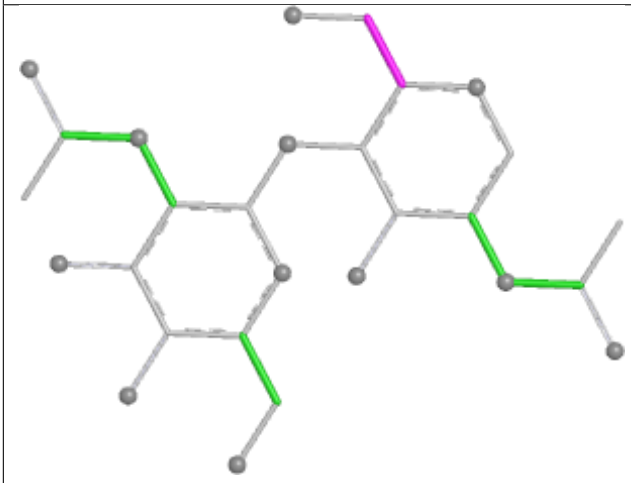
Oligosaccharide Chain V



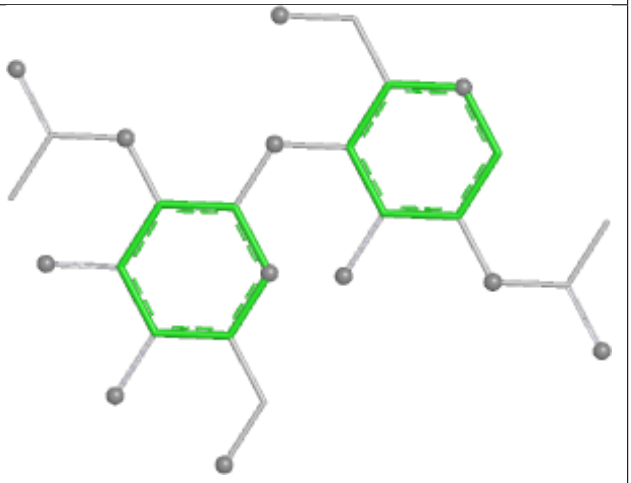
Bond lengths



Bond angles

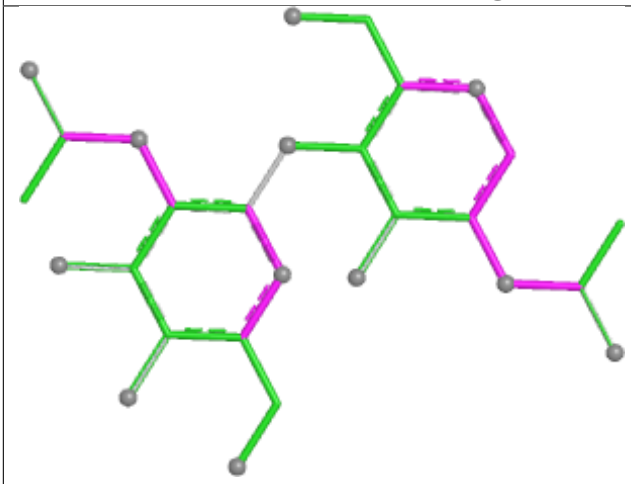


Torsions

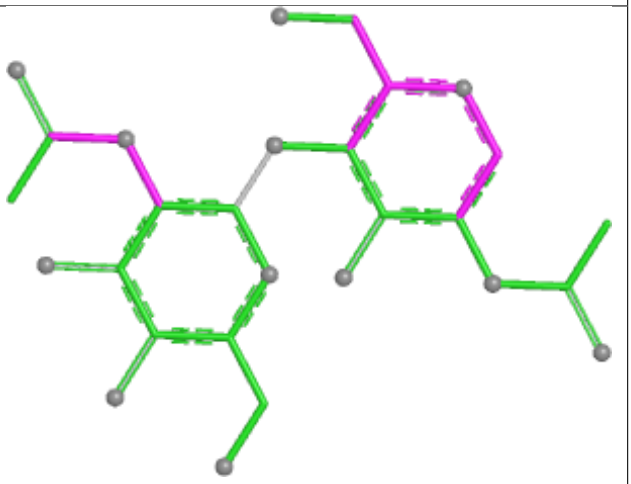


Rings

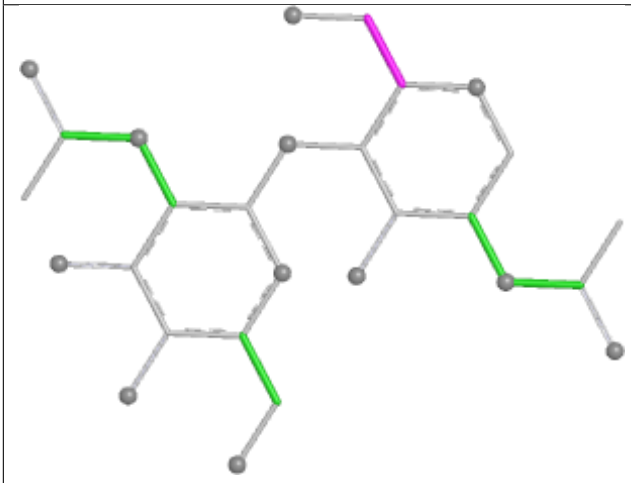
Oligosaccharide Chain W



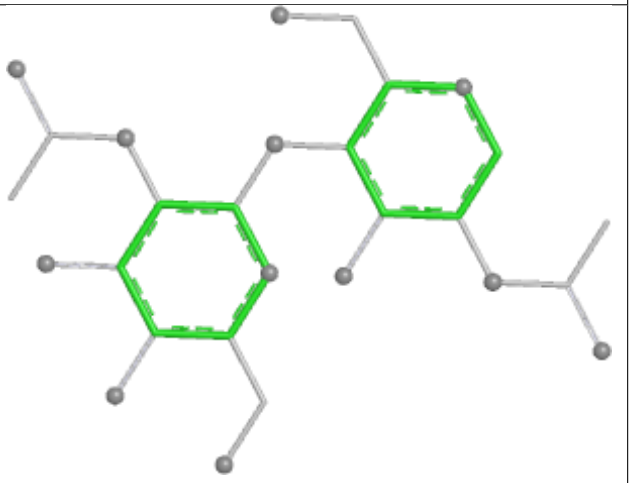
Bond lengths



Bond angles

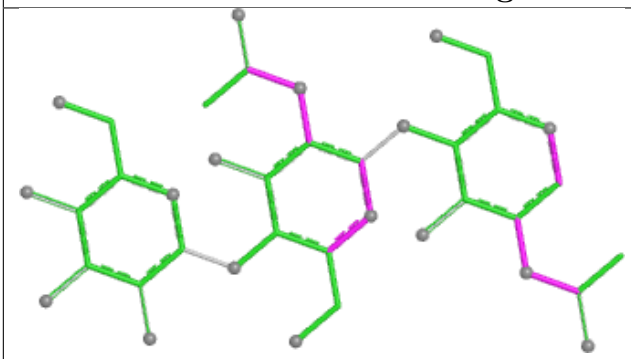


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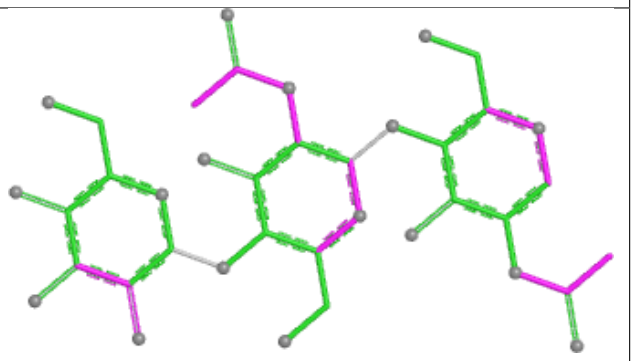


Rings

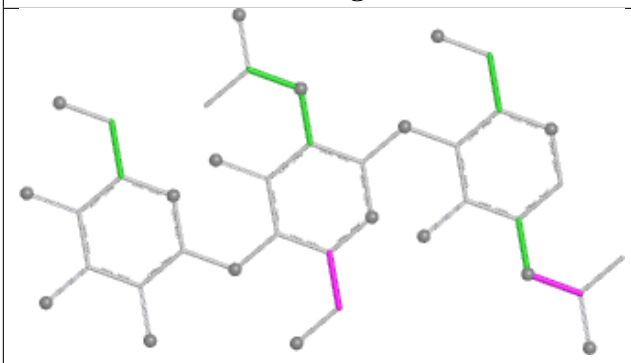
Oligosaccharide Chain F



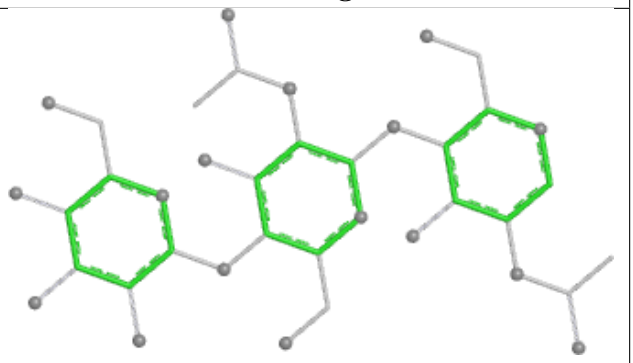
Bond lengths



Bond angles

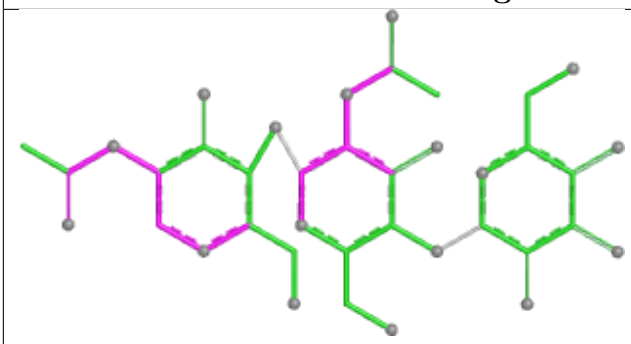


Torsions

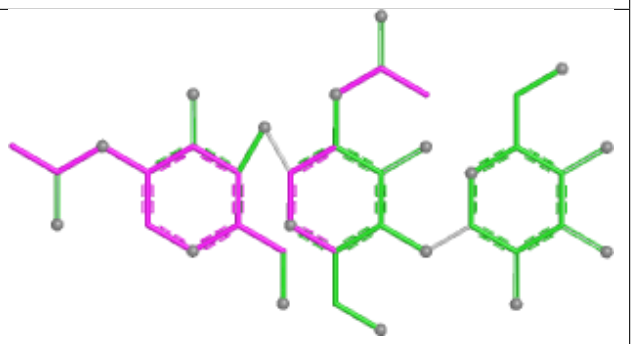


Rings

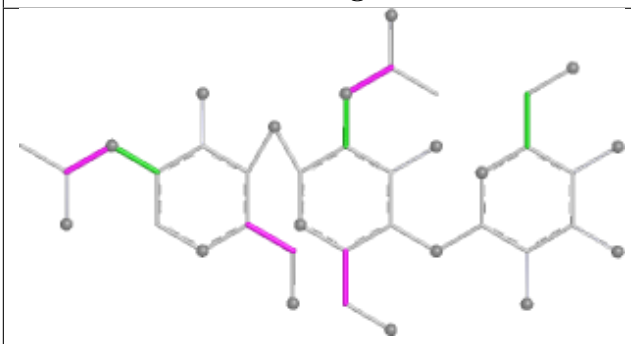
Oligosaccharide Chain G



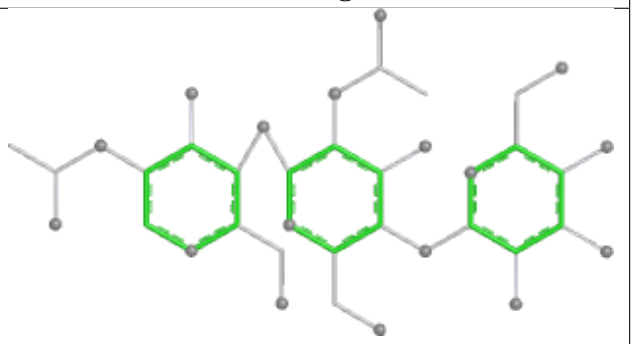
Bond lengths



Bond angles

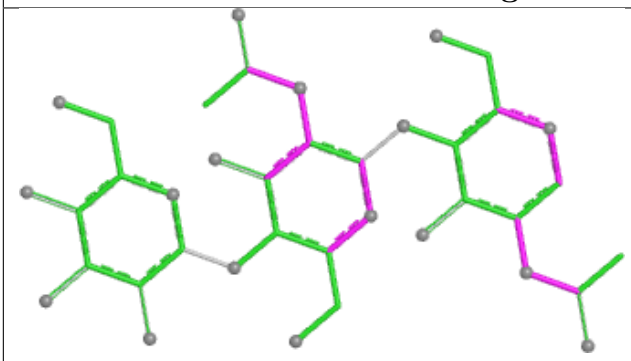


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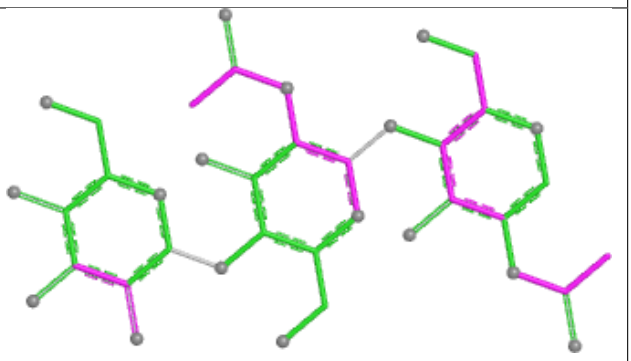


Rings

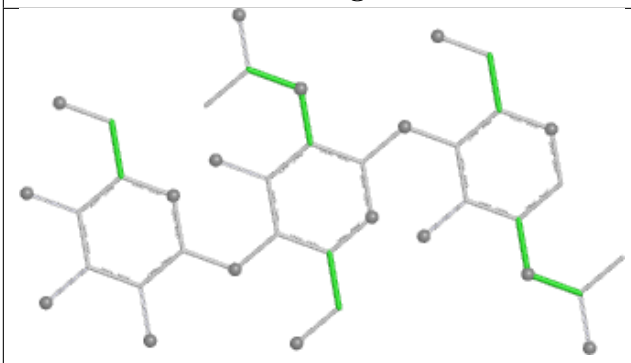
Oligosaccharide Chain I



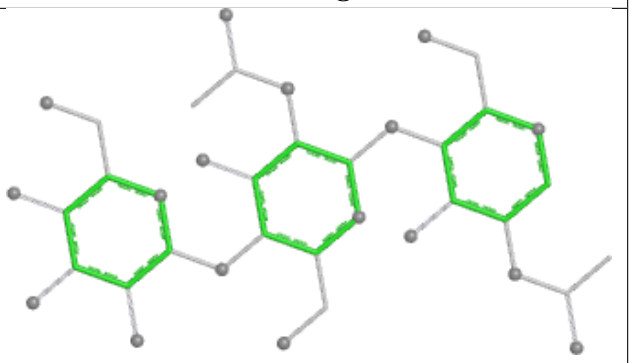
Bond lengths



Bond angles

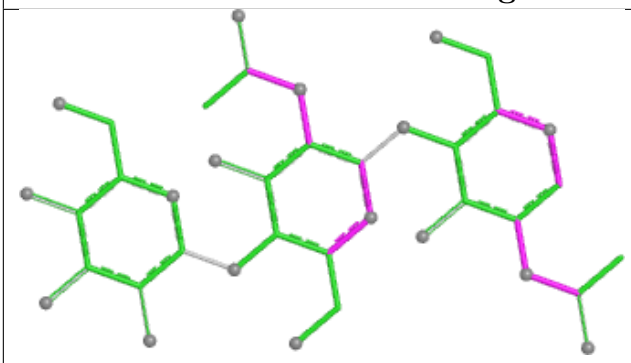


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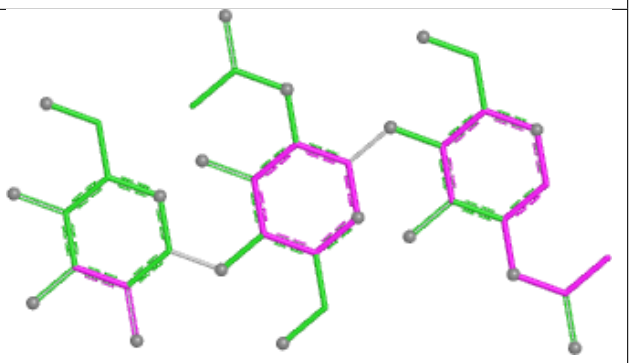


Rings

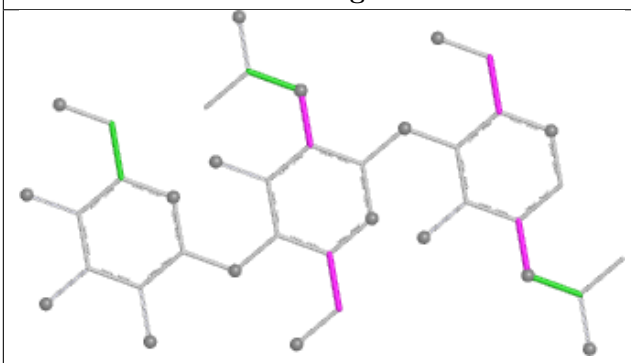
Oligosaccharide Chain J



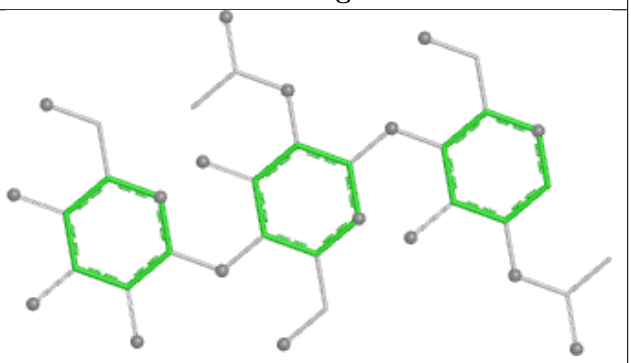
Bond lengths



Bond angles

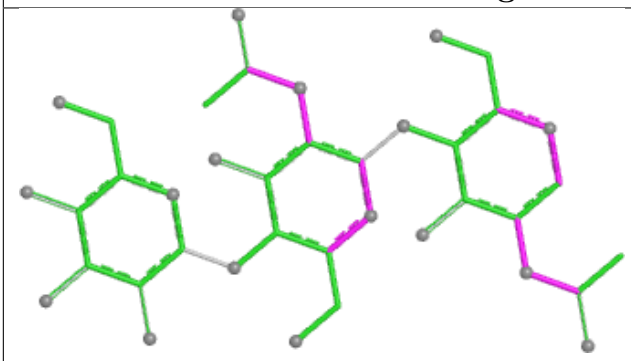


Torsions

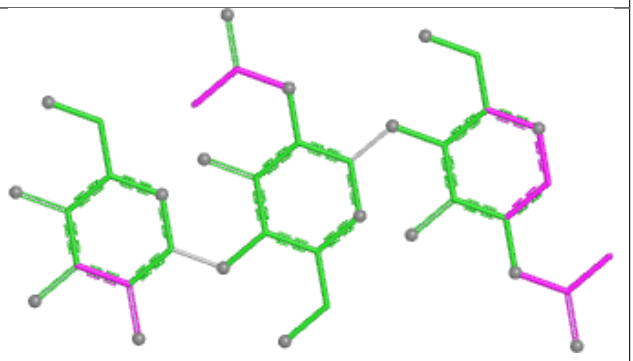


Rings

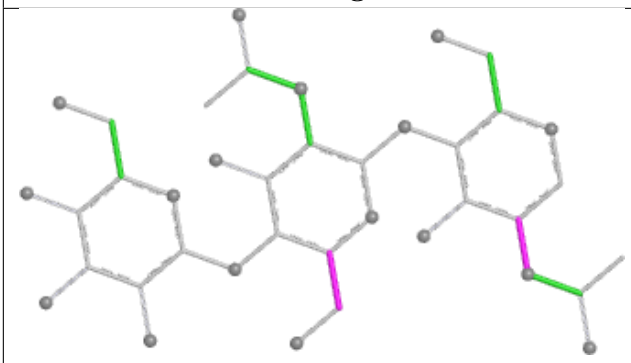
Oligosaccharide Chain b



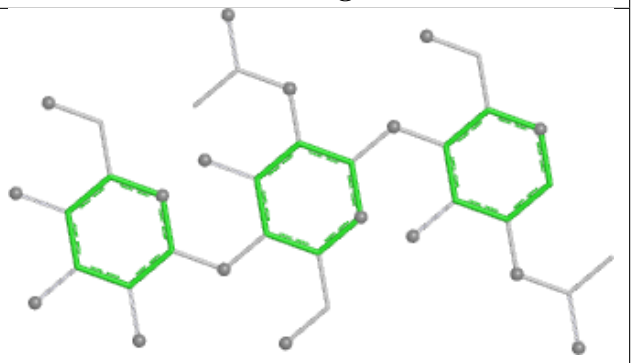
Bond lengths



Bond angles

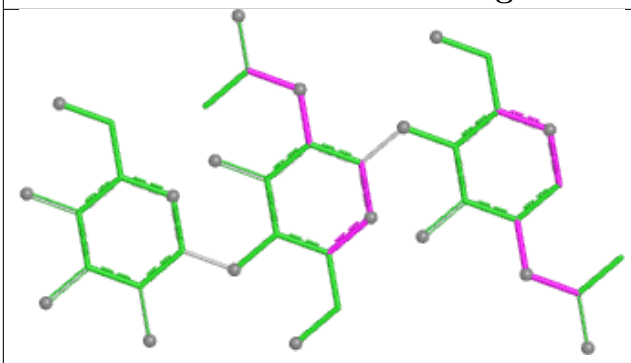


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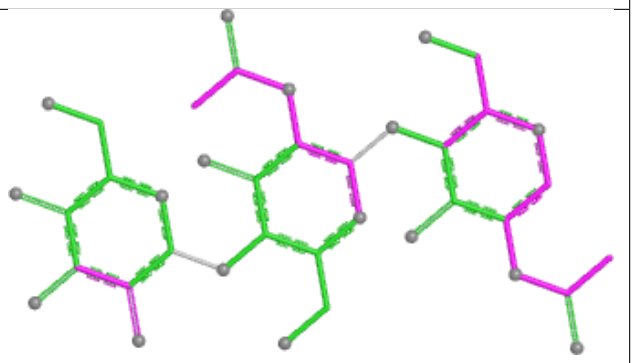


Rings

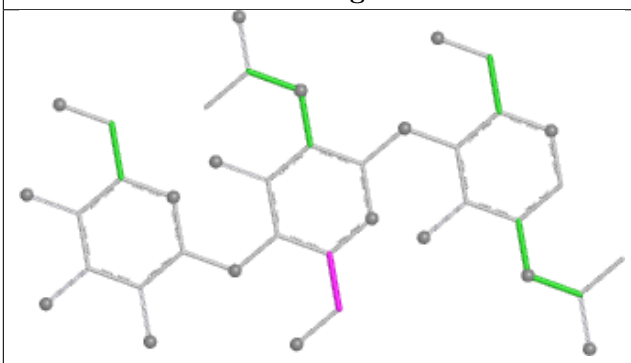
Oligosaccharide Chain P



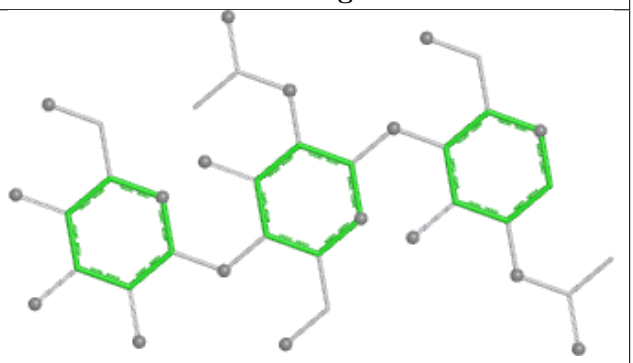
Bond lengths



Bond angles

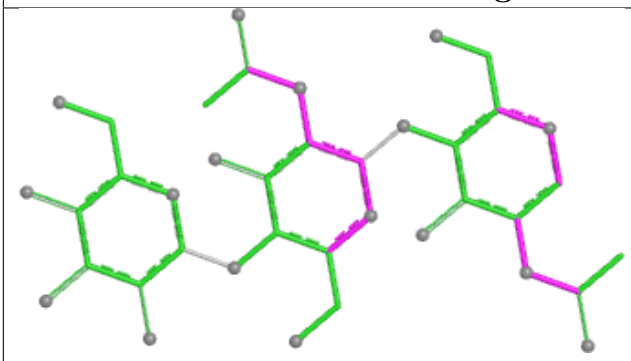


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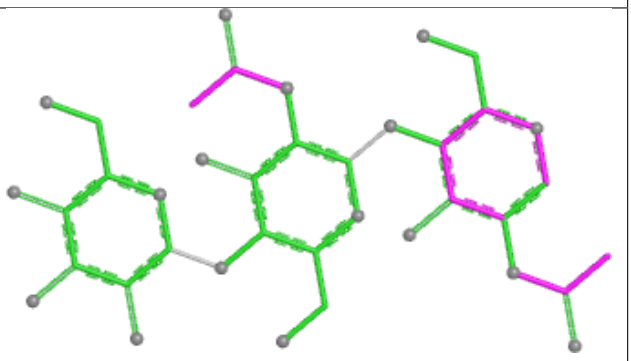


Rings

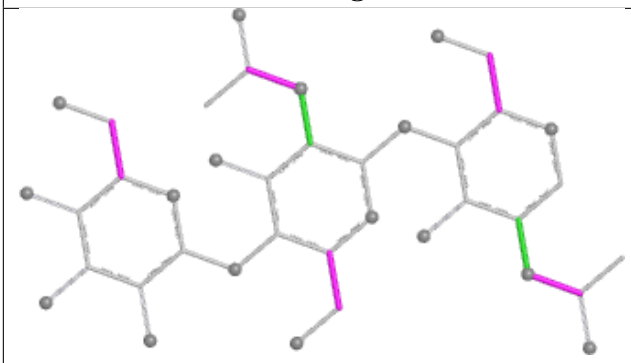
Oligosaccharide Chain R



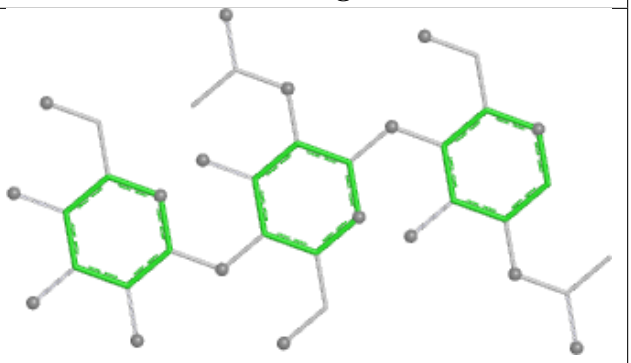
Bond lengths



Bond angles

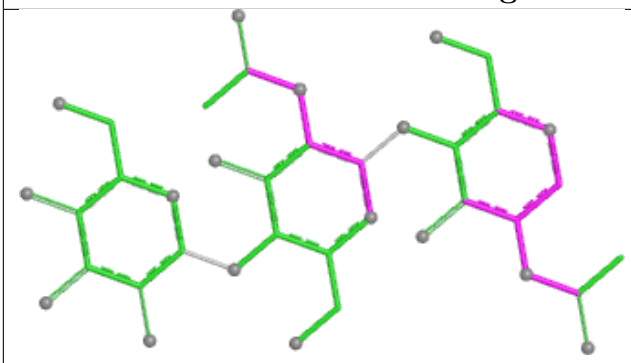


Torsions

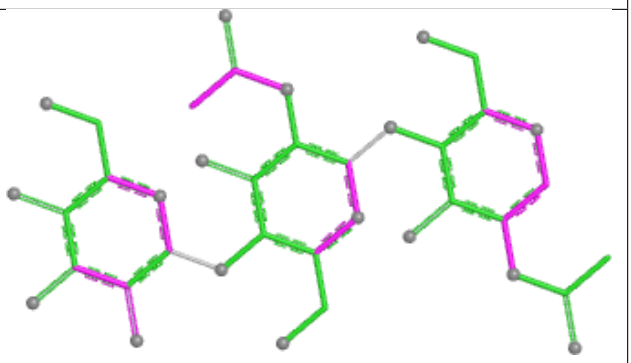


Rings

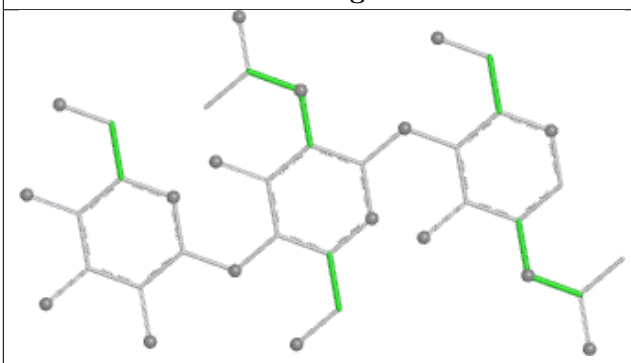
Oligosaccharide Chain c



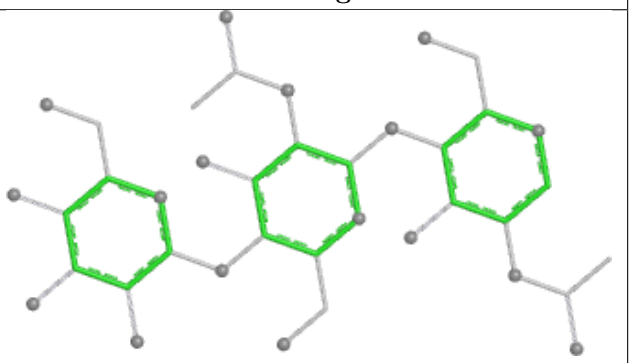
Bond lengths



Bond angles

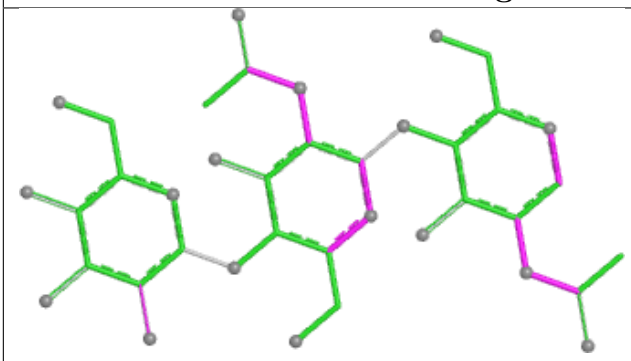


Torsions

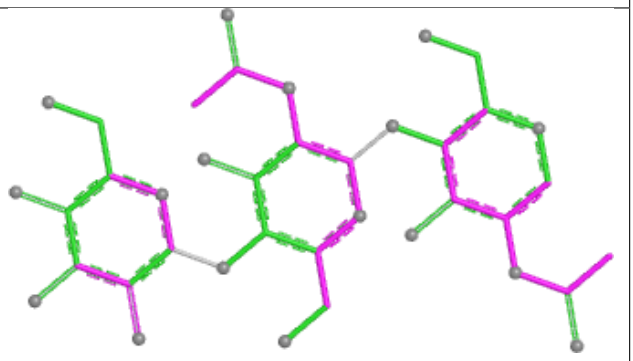


Rings

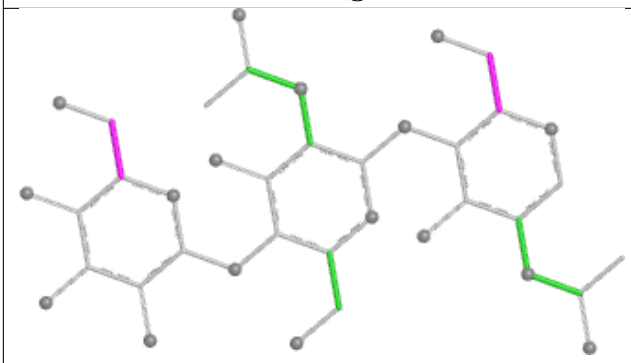
Oligosaccharide Chain T



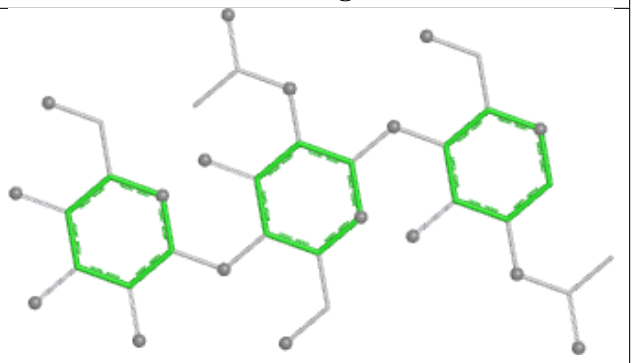
Bond lengths



Bond angles

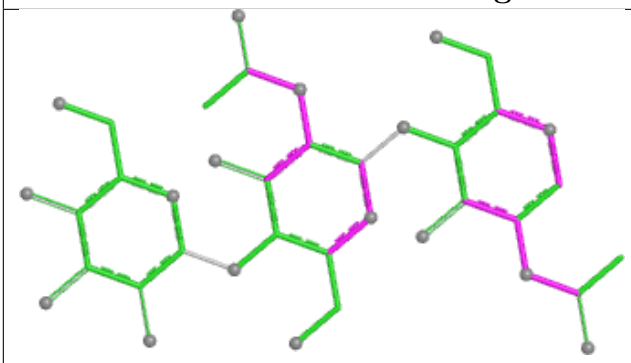


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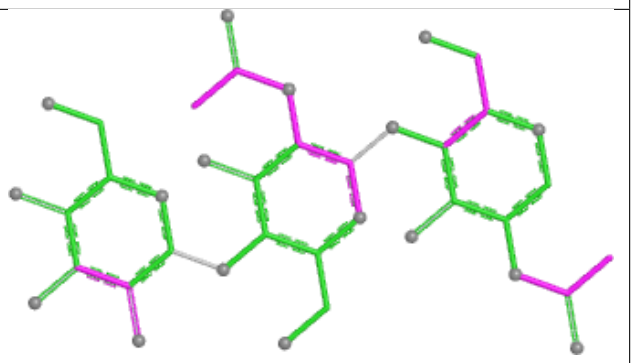


Rings

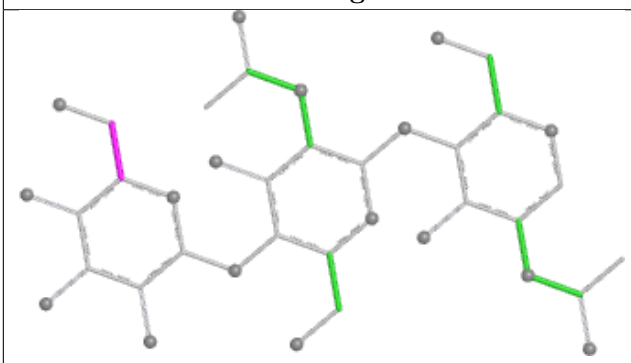
Oligosaccharide Chain U



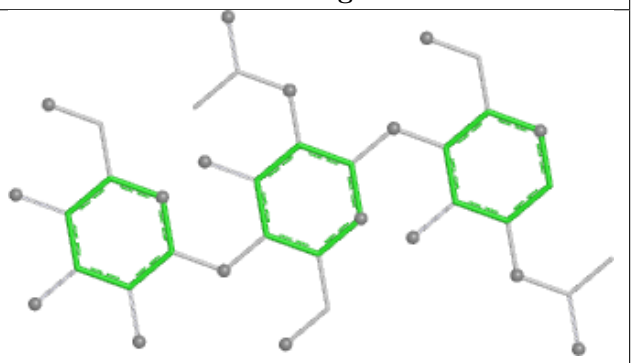
Bond lengths



Bond angles

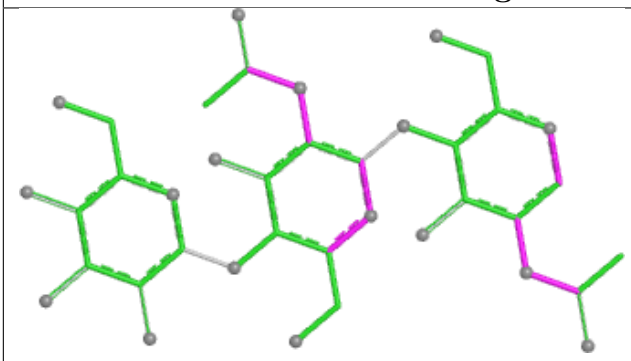


Torsions

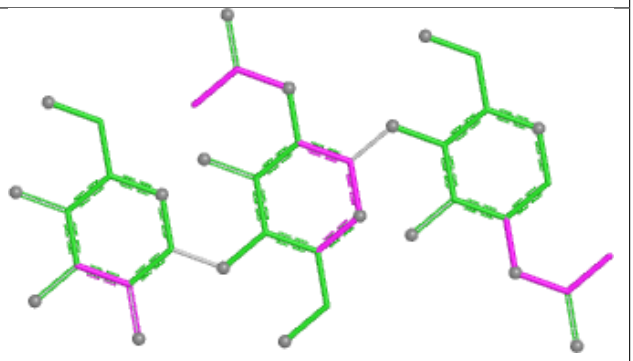


Rings

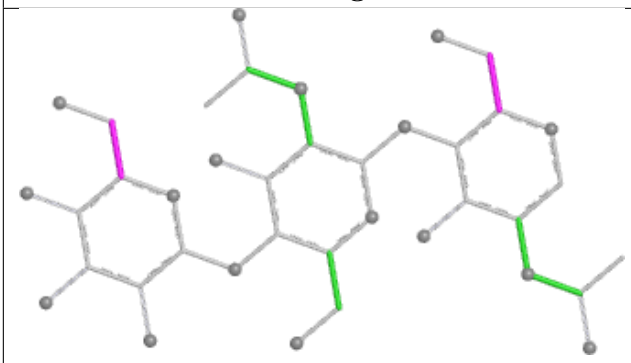
Oligosaccharide Chain X



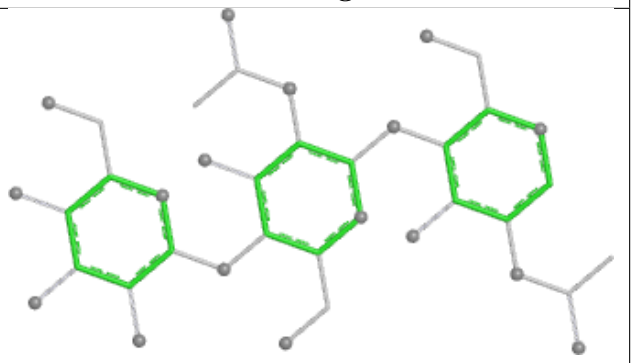
Bond lengths



Bond angles

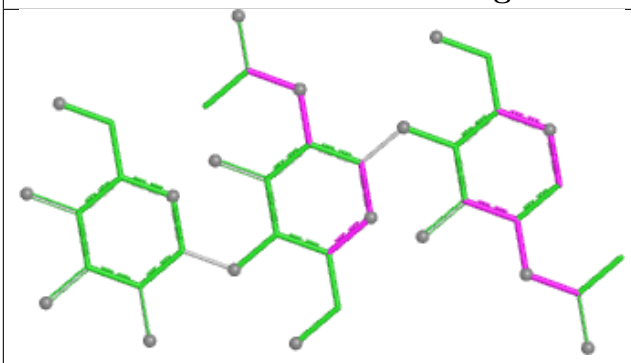


Torsions

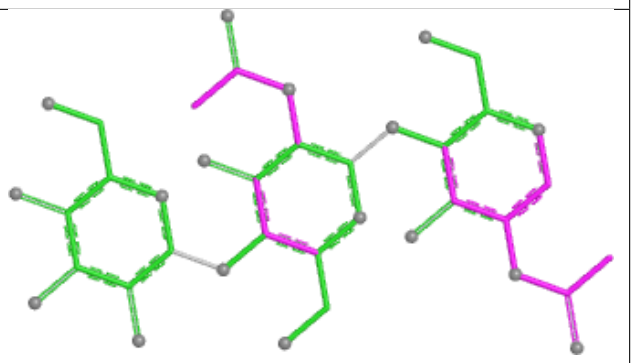


Rings

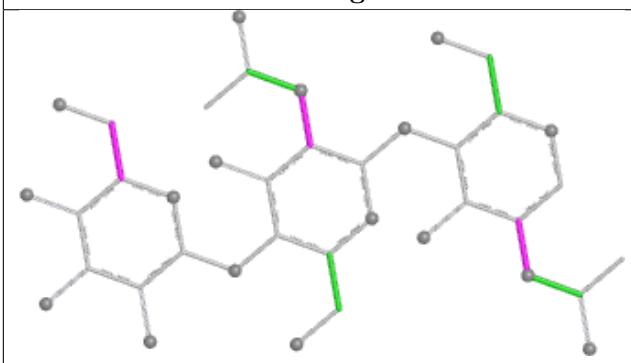
Oligosaccharide Chain Y



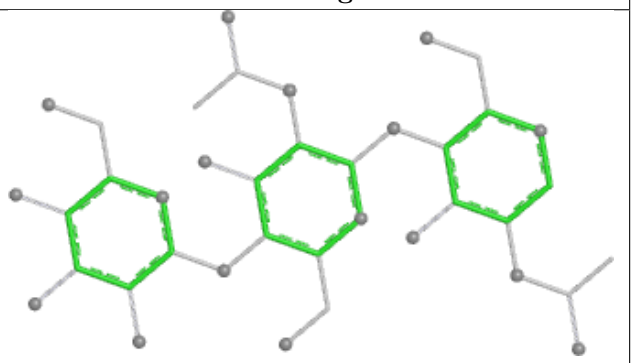
Bond lengths



Bond angles

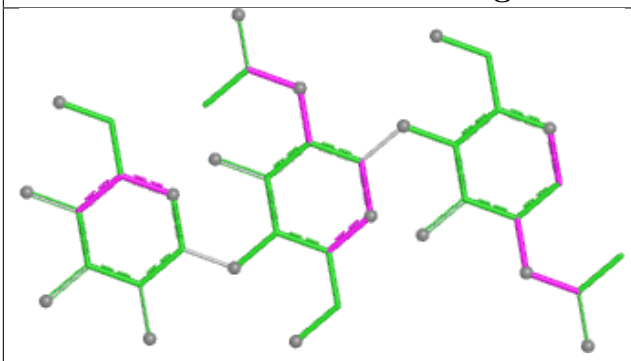


Torsions

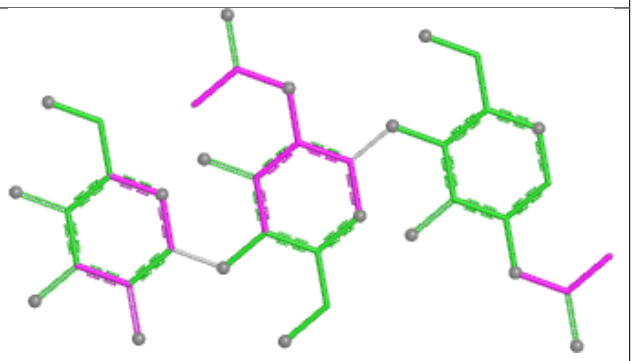


Rings

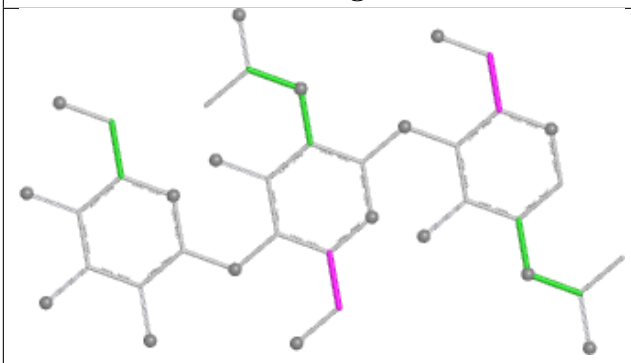
Oligosaccharide Chain H



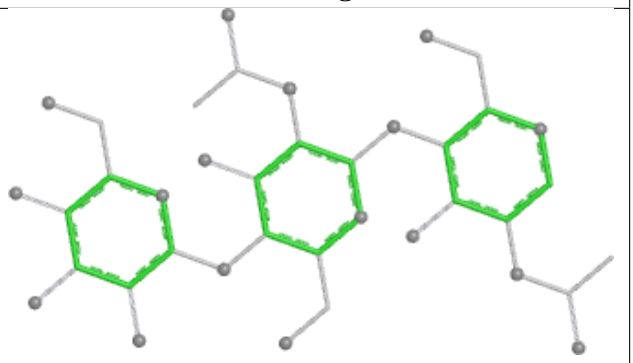
Bond lengths



Bond angles

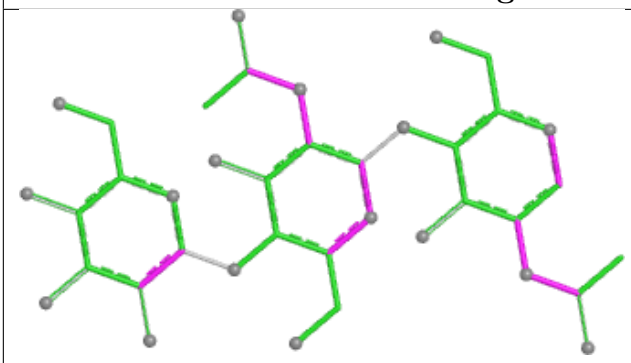


Torsions

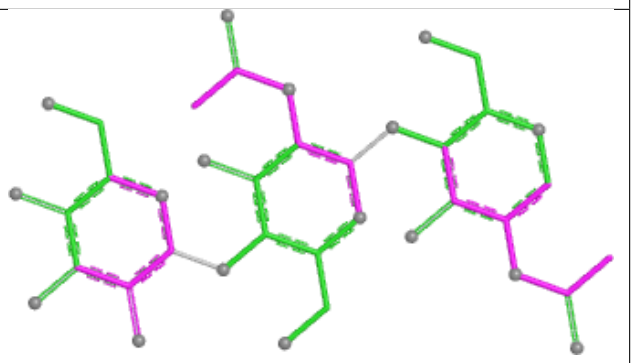


Rings

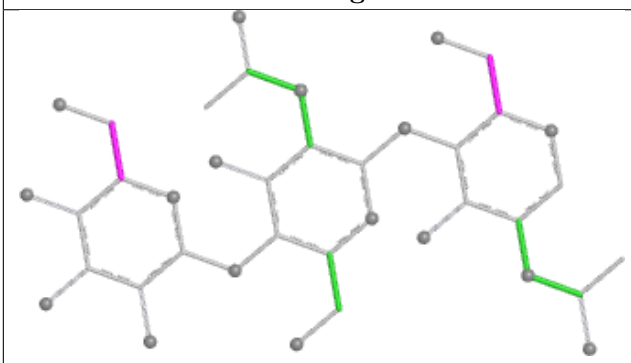
Oligosaccharide Chain L



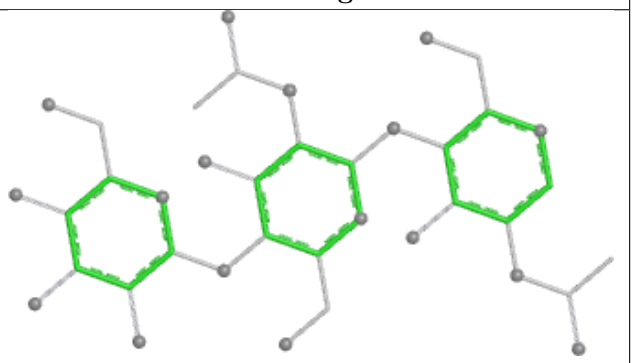
Bond lengths



Bond angles

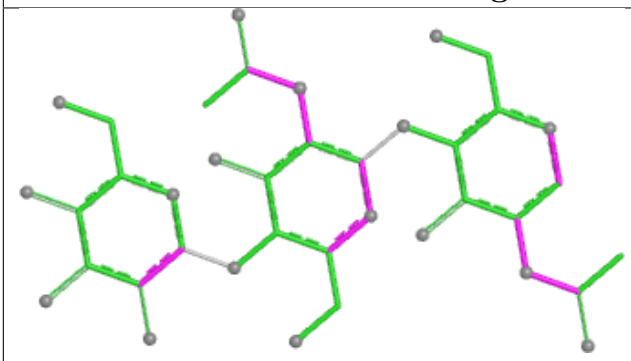


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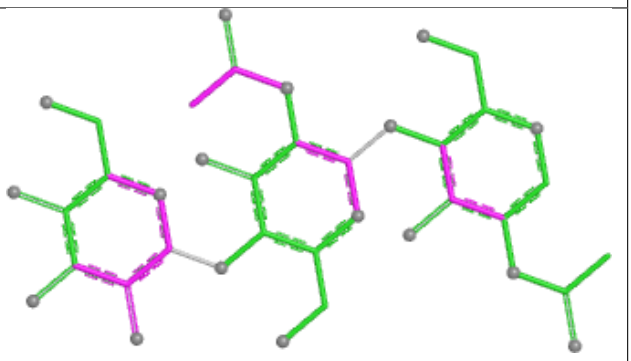


Rings

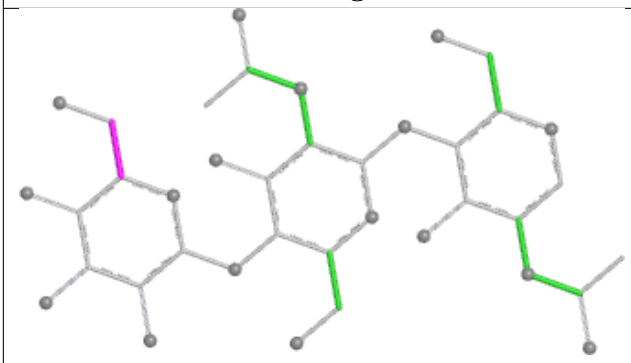
Oligosaccharide Chain M



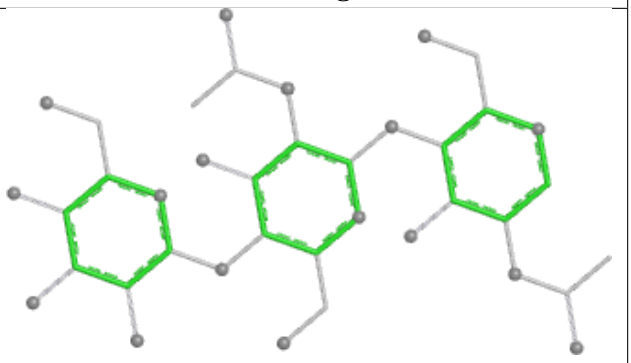
Bond lengths



Bond angles

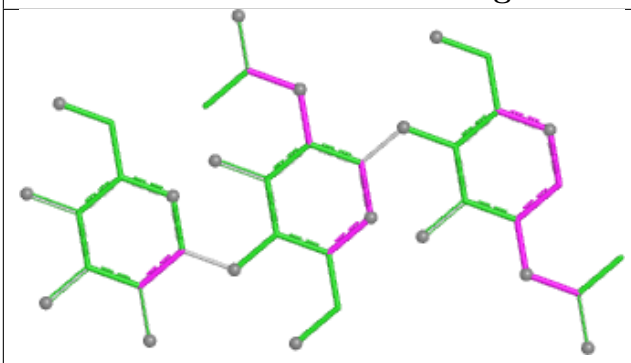


Torsions

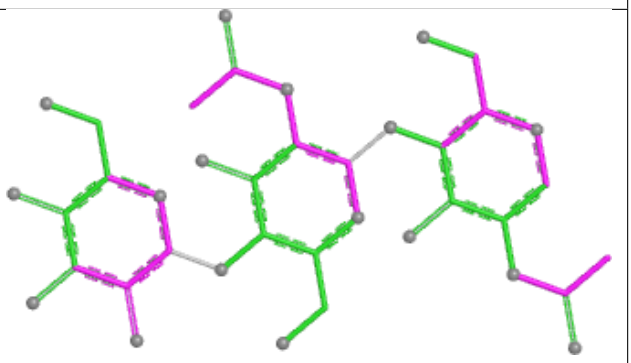


Rings

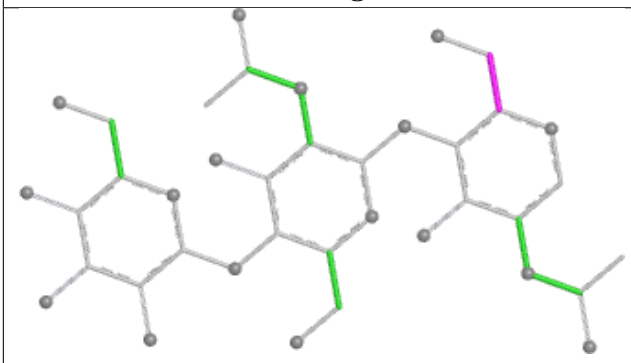
Oligosaccharide Chain N



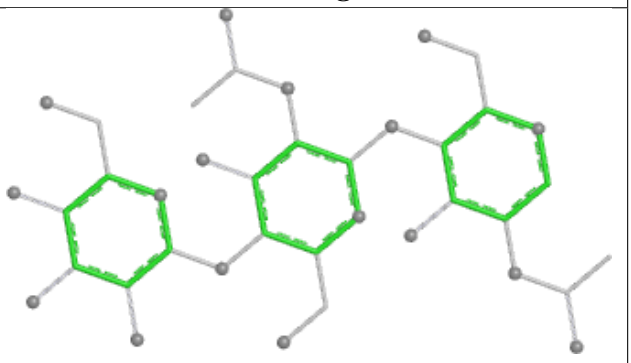
Bond lengths



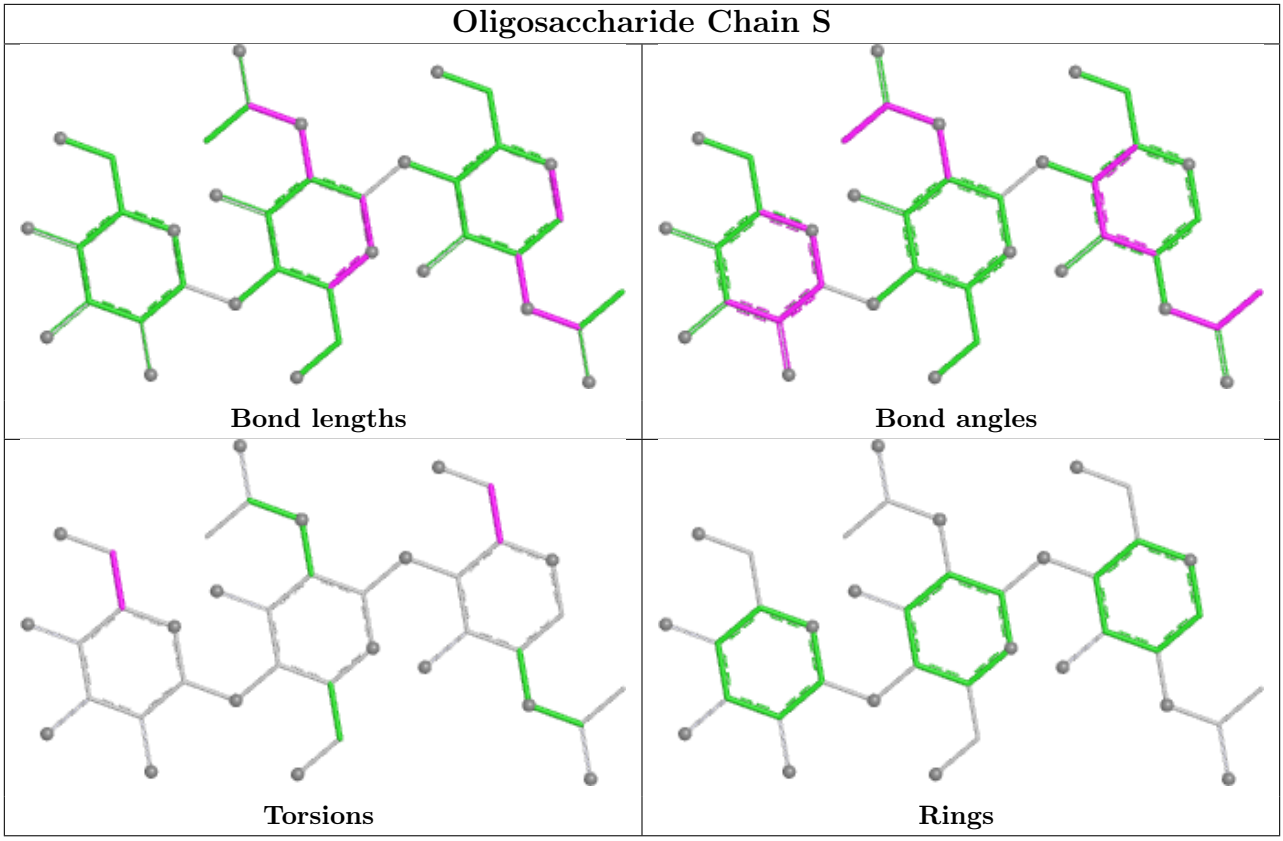
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

17 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	$\#\|Z\| > 2$
6	NAG	C	1301	1	14,14,15	1.99	4 (28%)	17,19,21	1.11	2 (11%)
6	NAG	A	1303	1	14,14,15	1.95	4 (28%)	17,19,21	1.18	2 (11%)
6	NAG	B	1301	1	14,14,15	2.03	4 (28%)	17,19,21	1.06	2 (11%)
6	NAG	B	1303	1	14,14,15	2.03	4 (28%)	17,19,21	1.50	4 (23%)
6	NAG	B	1305	1	14,14,15	2.13	5 (35%)	17,19,21	1.13	1 (5%)
6	NAG	C	1305	1	14,14,15	2.01	4 (28%)	17,19,21	1.46	4 (23%)
6	NAG	A	1307	1	14,14,15	2.06	4 (28%)	17,19,21	1.27	2 (11%)
6	NAG	A	1301	1	14,14,15	1.99	4 (28%)	17,19,21	1.12	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
6	NAG	B	1302	1	14,14,15	1.98	4 (28%)	17,19,21	1.13	2 (11%)
6	NAG	C	1303	1	14,14,15	2.03	4 (28%)	17,19,21	1.23	2 (11%)
6	NAG	A	1306	1	14,14,15	2.19	4 (28%)	17,19,21	1.37	2 (11%)
6	NAG	A	1305	1	14,14,15	2.00	4 (28%)	17,19,21	1.19	2 (11%)
6	NAG	B	1304	1	14,14,15	2.15	4 (28%)	17,19,21	1.65	4 (23%)
6	NAG	A	1304	1	14,14,15	2.02	4 (28%)	17,19,21	1.15	1 (5%)
6	NAG	C	1304	1	14,14,15	2.07	3 (21%)	17,19,21	3.93	5 (29%)
6	NAG	C	1302	1	14,14,15	1.95	4 (28%)	17,19,21	1.17	2 (11%)
6	NAG	A	1302	1	14,14,15	2.11	4 (28%)	17,19,21	1.76	2 (11%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	C	1301	1	-	2/6/23/26	0/1/1/1
6	NAG	A	1303	1	-	2/6/23/26	0/1/1/1
6	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
6	NAG	B	1303	1	-	2/6/23/26	0/1/1/1
6	NAG	B	1305	1	-	1/6/23/26	0/1/1/1
6	NAG	C	1305	1	-	2/6/23/26	0/1/1/1
6	NAG	A	1307	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1301	1	-	2/6/23/26	0/1/1/1
6	NAG	B	1302	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1303	1	-	3/6/23/26	0/1/1/1
6	NAG	A	1306	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1305	1	-	1/6/23/26	0/1/1/1
6	NAG	B	1304	1	-	4/6/23/26	0/1/1/1
6	NAG	A	1304	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1304	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1302	1	-	2/6/23/26	0/1/1/1
6	NAG	A	1302	1	-	2/6/23/26	0/1/1/1

All (68) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1306	NAG	O5-C1	4.92	1.52	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1304	NAG	C7-N2	4.90	1.50	1.34
6	A	1302	NAG	O5-C1	4.89	1.51	1.43
6	A	1304	NAG	O5-C1	4.86	1.51	1.43
6	B	1304	NAG	O5-C1	4.79	1.51	1.43
6	A	1307	NAG	O5-C1	4.46	1.51	1.43
6	B	1305	NAG	O5-C1	4.44	1.51	1.43
6	B	1301	NAG	O5-C1	4.39	1.51	1.43
6	B	1303	NAG	O5-C1	4.35	1.51	1.43
6	C	1303	NAG	O5-C1	4.28	1.50	1.43
6	C	1305	NAG	O5-C1	4.28	1.50	1.43
6	B	1302	NAG	O5-C1	4.28	1.50	1.43
6	A	1301	NAG	O5-C1	4.27	1.50	1.43
6	A	1305	NAG	O5-C1	4.24	1.50	1.43
6	C	1301	NAG	O5-C1	4.24	1.50	1.43
6	A	1303	NAG	O5-C1	4.23	1.50	1.43
6	C	1302	NAG	O5-C1	4.22	1.50	1.43
6	C	1303	NAG	C7-N2	4.06	1.47	1.34
6	B	1305	NAG	C7-N2	3.97	1.47	1.34
6	A	1306	NAG	C7-N2	3.94	1.47	1.34
6	B	1303	NAG	C7-N2	3.93	1.47	1.34
6	A	1302	NAG	C7-N2	3.92	1.47	1.34
6	A	1305	NAG	C7-N2	3.91	1.47	1.34
6	B	1304	NAG	C7-N2	3.90	1.46	1.34
6	B	1301	NAG	C7-N2	3.90	1.46	1.34
6	C	1301	NAG	C7-N2	3.89	1.46	1.34
6	A	1301	NAG	C7-N2	3.87	1.46	1.34
6	B	1302	NAG	C7-N2	3.85	1.46	1.34
6	C	1302	NAG	C7-N2	3.84	1.46	1.34
6	A	1303	NAG	C7-N2	3.84	1.46	1.34
6	C	1305	NAG	C7-N2	3.81	1.46	1.34
6	C	1304	NAG	C2-N2	3.79	1.52	1.46
6	A	1307	NAG	C7-N2	3.78	1.46	1.34
6	A	1304	NAG	C7-N2	3.75	1.46	1.34
6	C	1304	NAG	O5-C1	3.48	1.49	1.43
6	B	1304	NAG	C2-N2	2.87	1.51	1.46
6	C	1303	NAG	C2-N2	2.85	1.51	1.46
6	A	1307	NAG	O5-C5	2.67	1.48	1.43
6	A	1306	NAG	O5-C5	2.65	1.48	1.43
6	B	1305	NAG	C2-N2	2.63	1.50	1.46
6	A	1307	NAG	C2-N2	2.57	1.50	1.46
6	B	1304	NAG	O5-C5	2.56	1.48	1.43
6	B	1301	NAG	C2-N2	2.54	1.50	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1305	NAG	C2-N2	2.50	1.50	1.46
6	C	1305	NAG	C2-N2	2.48	1.50	1.46
6	B	1303	NAG	C2-N2	2.48	1.50	1.46
6	B	1303	NAG	O5-C5	2.48	1.48	1.43
6	C	1301	NAG	C2-N2	2.47	1.50	1.46
6	A	1301	NAG	C2-N2	2.45	1.50	1.46
6	A	1306	NAG	C2-N2	2.43	1.50	1.46
6	B	1302	NAG	C2-N2	2.42	1.50	1.46
6	C	1302	NAG	C2-N2	2.42	1.50	1.46
6	A	1303	NAG	C2-N2	2.41	1.50	1.46
6	B	1305	NAG	O5-C5	2.41	1.48	1.43
6	A	1302	NAG	O5-C5	2.36	1.48	1.43
6	C	1305	NAG	O5-C5	2.34	1.48	1.43
6	A	1302	NAG	C2-N2	2.33	1.50	1.46
6	A	1305	NAG	O5-C5	2.26	1.47	1.43
6	B	1301	NAG	O5-C5	2.20	1.47	1.43
6	C	1301	NAG	O5-C5	2.19	1.47	1.43
6	A	1304	NAG	C2-N2	2.17	1.49	1.46
6	A	1301	NAG	O5-C5	2.16	1.47	1.43
6	A	1304	NAG	O5-C5	2.15	1.47	1.43
6	B	1302	NAG	O5-C5	2.15	1.47	1.43
6	C	1302	NAG	O5-C5	2.08	1.47	1.43
6	A	1303	NAG	O5-C5	2.06	1.47	1.43
6	C	1303	NAG	O5-C5	2.03	1.47	1.43
6	B	1305	NAG	C3-C2	-2.00	1.48	1.52

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	C	1304	NAG	C2-N2-C7	10.33	136.75	122.90
6	C	1304	NAG	C8-C7-N2	-8.21	102.50	116.12
6	C	1304	NAG	O7-C7-N2	6.89	134.15	121.98
6	A	1302	NAG	C1-O5-C5	5.31	119.30	112.19
6	C	1304	NAG	C1-O5-C5	-4.35	106.36	112.19
6	B	1304	NAG	C8-C7-N2	4.28	123.21	116.12
6	C	1304	NAG	O5-C1-C2	3.77	117.13	111.29
6	A	1306	NAG	C1-O5-C5	3.63	117.05	112.19
6	A	1307	NAG	C1-O5-C5	-3.55	107.42	112.19
6	A	1304	NAG	C1-C2-N2	-2.75	106.09	110.43
6	C	1305	NAG	C3-C4-C5	2.74	115.21	110.23
6	C	1303	NAG	C1-O5-C5	-2.64	108.64	112.19
6	C	1305	NAG	C1-C2-N2	-2.61	106.32	110.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	1301	NAG	C8-C7-N2	2.53	120.31	116.12
6	C	1305	NAG	C8-C7-N2	2.50	120.27	116.12
6	C	1301	NAG	C8-C7-N2	2.48	120.23	116.12
6	A	1301	NAG	C2-N2-C7	-2.47	119.58	122.90
6	B	1301	NAG	C8-C7-N2	2.46	120.19	116.12
6	C	1305	NAG	C2-N2-C7	-2.44	119.64	122.90
6	A	1302	NAG	C8-C7-N2	2.42	120.12	116.12
6	A	1305	NAG	C8-C7-N2	2.39	120.08	116.12
6	B	1303	NAG	C1-O5-C5	-2.38	109.00	112.19
6	C	1301	NAG	C2-N2-C7	-2.37	119.73	122.90
6	A	1306	NAG	C6-C5-C4	-2.33	107.30	113.02
6	B	1302	NAG	C8-C7-N2	2.33	119.98	116.12
6	B	1301	NAG	C2-N2-C7	-2.29	119.83	122.90
6	B	1303	NAG	C6-C5-C4	-2.25	107.50	113.02
6	B	1302	NAG	C2-N2-C7	-2.24	119.90	122.90
6	B	1303	NAG	C8-C7-N2	2.23	119.81	116.12
6	C	1303	NAG	O7-C7-C8	-2.22	118.10	122.05
6	C	1302	NAG	C8-C7-N2	2.20	119.76	116.12
6	B	1305	NAG	C6-C5-C4	-2.19	107.63	113.02
6	A	1303	NAG	C8-C7-N2	2.19	119.74	116.12
6	B	1304	NAG	O5-C1-C2	-2.18	107.92	111.29
6	A	1307	NAG	O5-C5-C6	2.17	111.88	107.66
6	B	1303	NAG	C1-C2-N2	-2.08	107.15	110.43
6	A	1303	NAG	C2-N2-C7	-2.05	120.15	122.90
6	B	1304	NAG	O7-C7-C8	-2.05	118.41	122.05
6	B	1304	NAG	O7-C7-N2	-2.04	118.38	121.98
6	C	1302	NAG	C2-N2-C7	-2.03	120.18	122.90
6	A	1305	NAG	C2-N2-C7	-2.02	120.19	122.90

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	1303	NAG	C1-C2-N2-C7
6	C	1303	NAG	C1-C2-N2-C7
6	C	1304	NAG	C1-C2-N2-C7
6	A	1301	NAG	O5-C5-C6-O6
6	C	1301	NAG	O5-C5-C6-O6
6	B	1301	NAG	O5-C5-C6-O6
6	C	1305	NAG	O5-C5-C6-O6
6	C	1302	NAG	O5-C5-C6-O6
6	C	1302	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
6	C	1301	NAG	C4-C5-C6-O6
6	C	1303	NAG	C4-C5-C6-O6
6	A	1301	NAG	C4-C5-C6-O6
6	A	1303	NAG	C4-C5-C6-O6
6	C	1303	NAG	O5-C5-C6-O6
6	B	1301	NAG	C4-C5-C6-O6
6	A	1302	NAG	O5-C5-C6-O6
6	A	1303	NAG	O5-C5-C6-O6
6	B	1304	NAG	C8-C7-N2-C2
6	B	1304	NAG	O7-C7-N2-C2
6	B	1305	NAG	O5-C5-C6-O6
6	C	1304	NAG	O5-C5-C6-O6
6	C	1305	NAG	C4-C5-C6-O6
6	A	1302	NAG	C4-C5-C6-O6
6	A	1305	NAG	O5-C5-C6-O6
6	B	1304	NAG	C1-C2-N2-C7
6	B	1303	NAG	C3-C2-N2-C7
6	B	1304	NAG	C3-C2-N2-C7

There are no ring outliers.

7 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	1301	NAG	2	0
6	B	1303	NAG	1	0
6	B	1305	NAG	2	0
6	C	1303	NAG	2	0
6	A	1306	NAG	2	0
6	B	1304	NAG	1	0
6	C	1304	NAG	2	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.

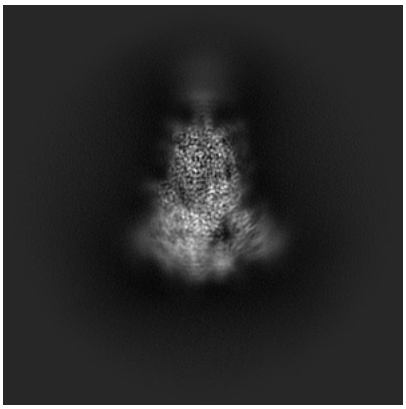
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-44062. These allow visual inspection of the internal detail of the map and identification of artifacts.

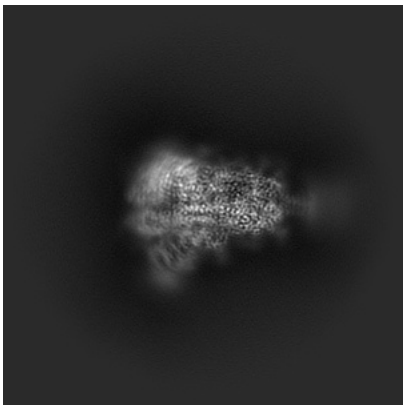
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

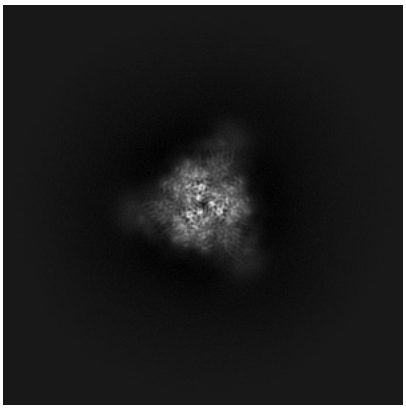
6.1.1 Primary map



X

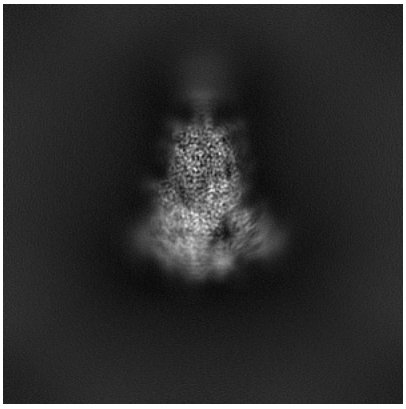


Y

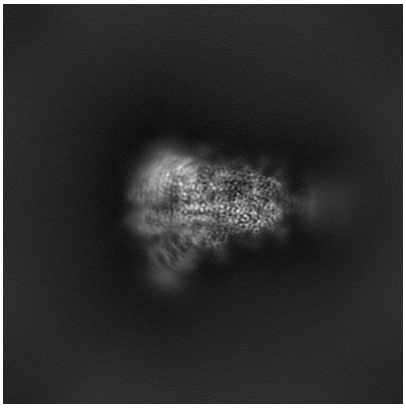


Z

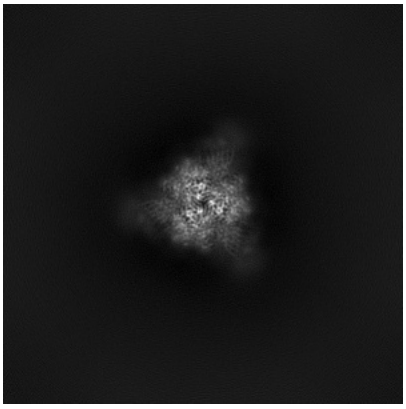
6.1.2 Raw map



X



Y

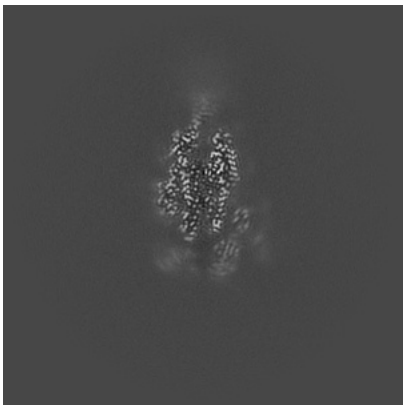


Z

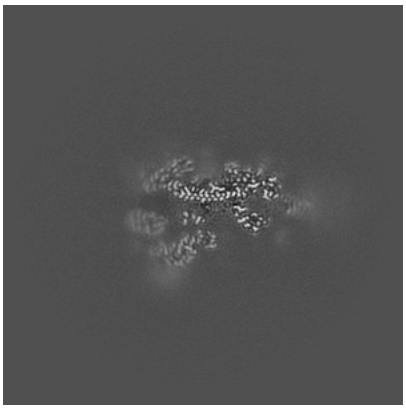
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

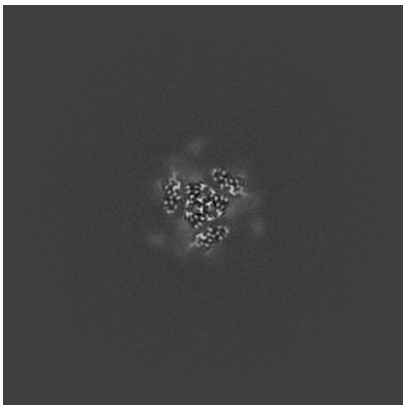
6.2.1 Primary map



X Index: 190

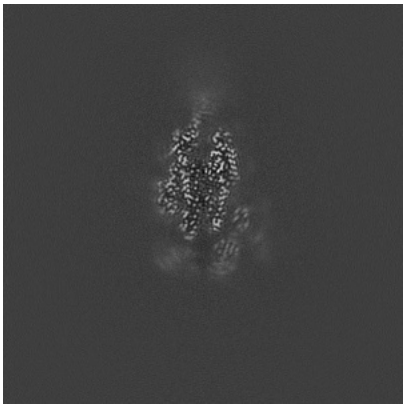


Y Index: 190

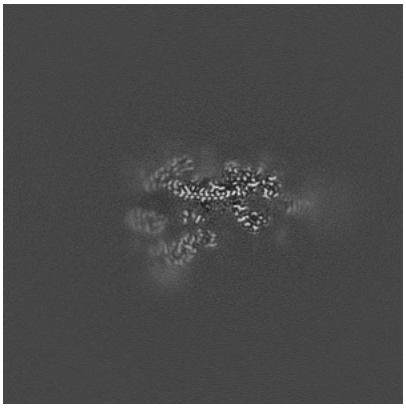


Z Index: 190

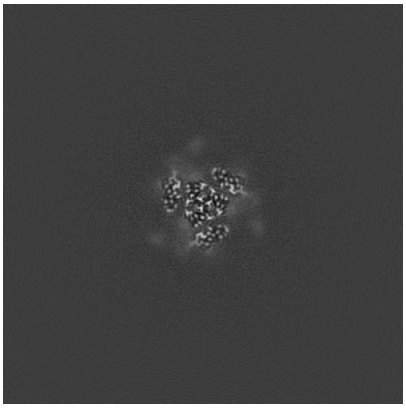
6.2.2 Raw map



X Index: 190



Y Index: 190

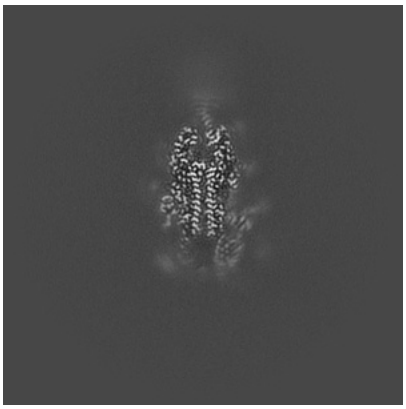


Z Index: 190

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

6.3 Largest variance slices (i)

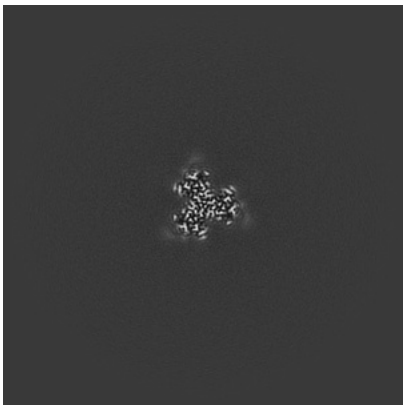
6.3.1 Primary map



X Index: 185

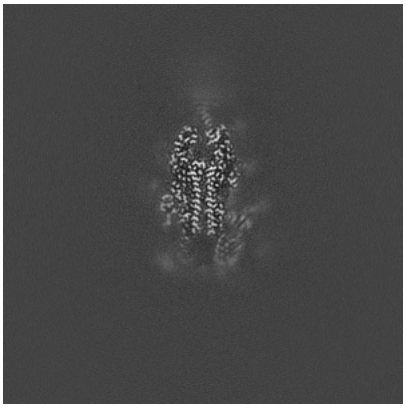


Y Index: 183



Z Index: 222

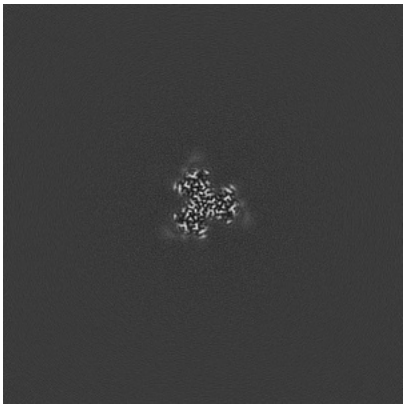
6.3.2 Raw map



X Index: 185



Y Index: 183

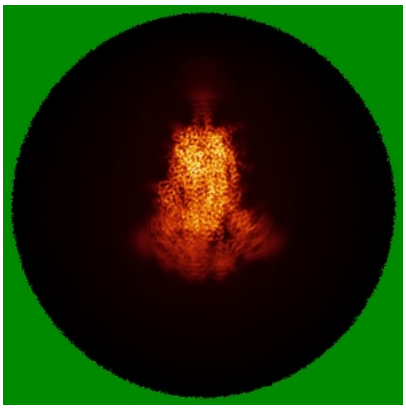


Z Index: 222

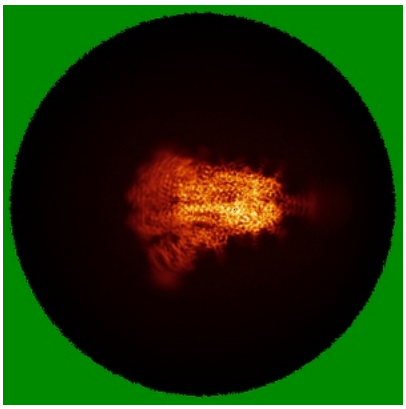
The images above show the largest variance slices of the map in three orthogonal directions.

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

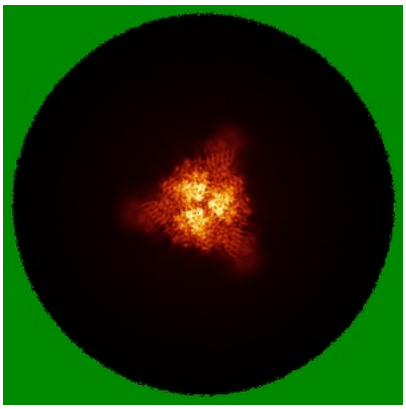
6.4.1 Primary map



X

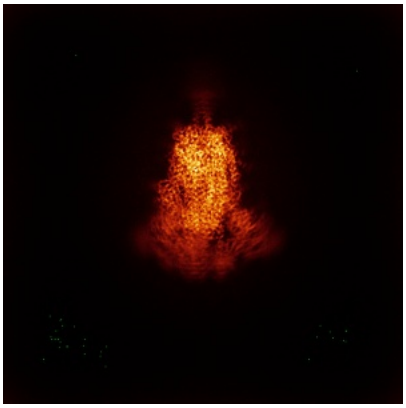


Y

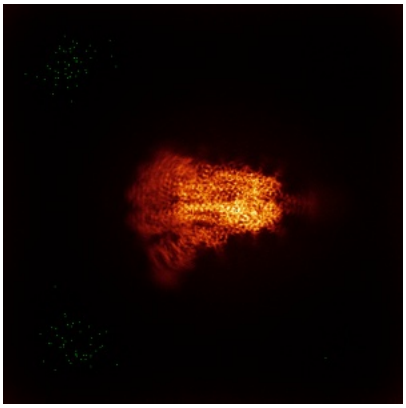


Z

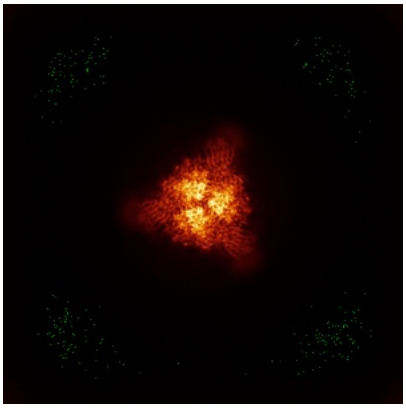
6.4.2 Raw map



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)

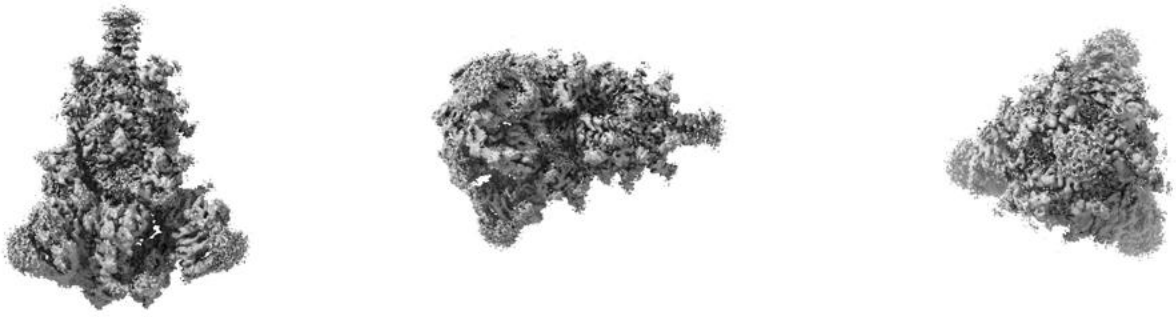
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.092. 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.

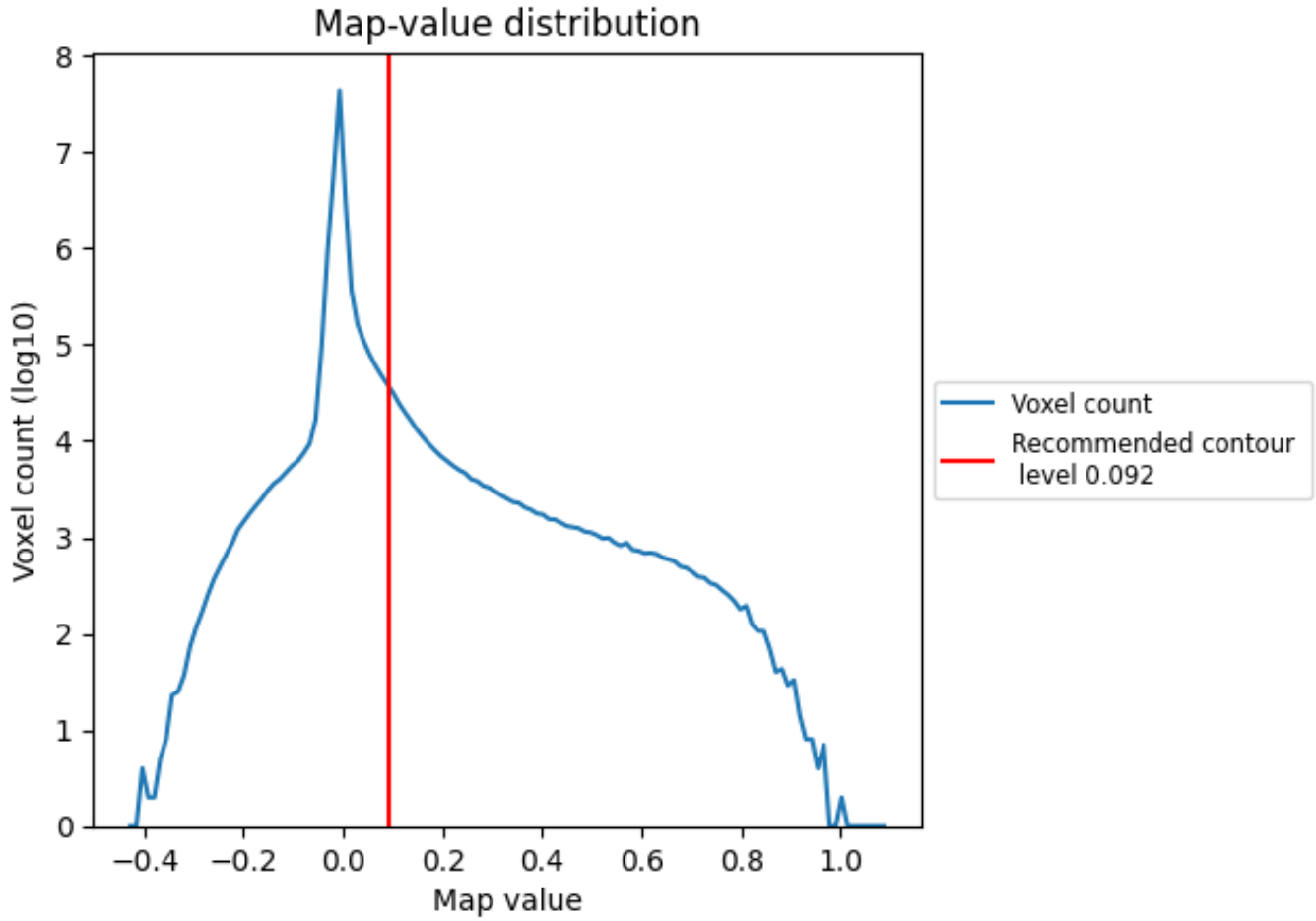
6.6 Mask visualisation (i)

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

7 Map analysis

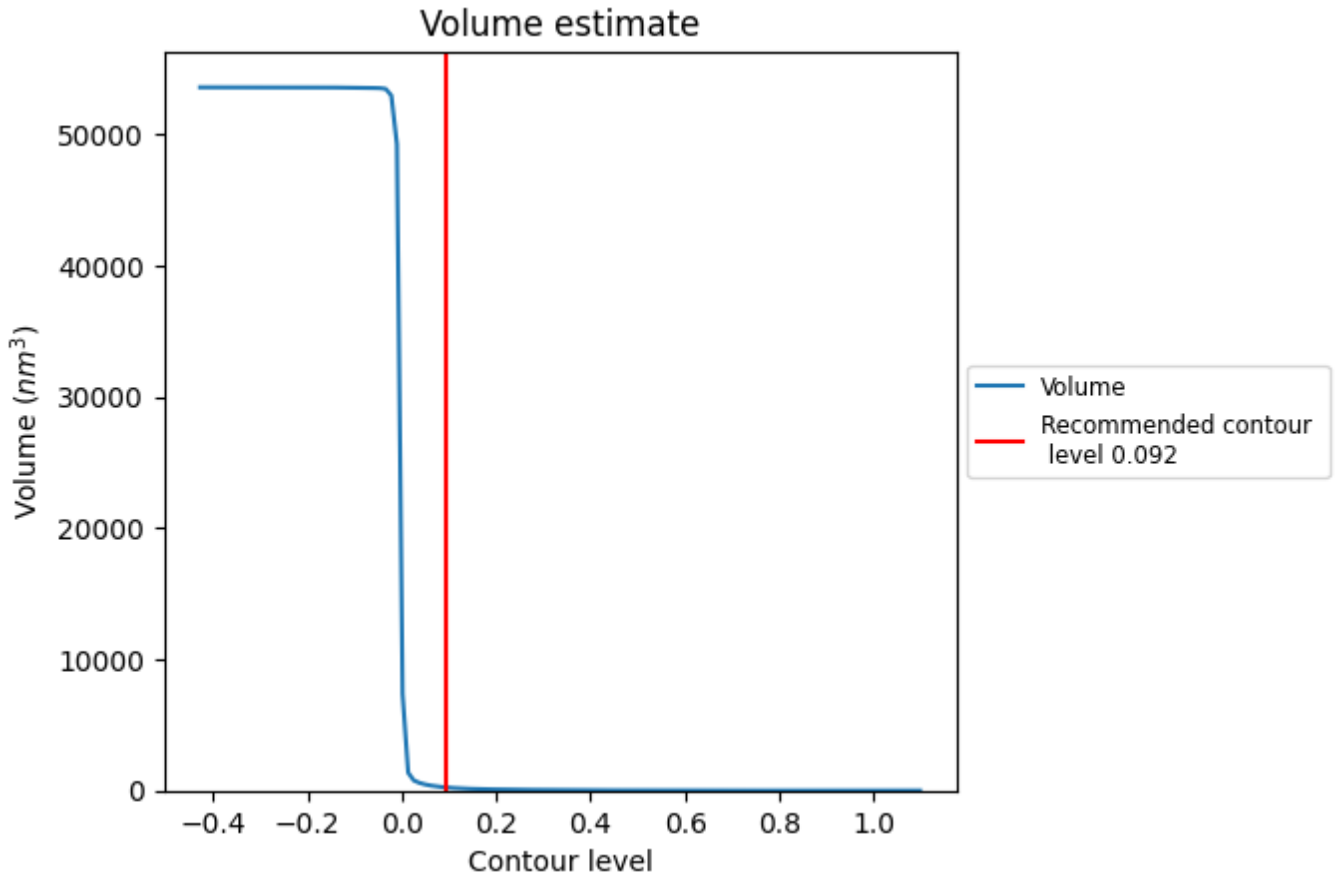
This section contains the results of statistical analysis of the map.

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.

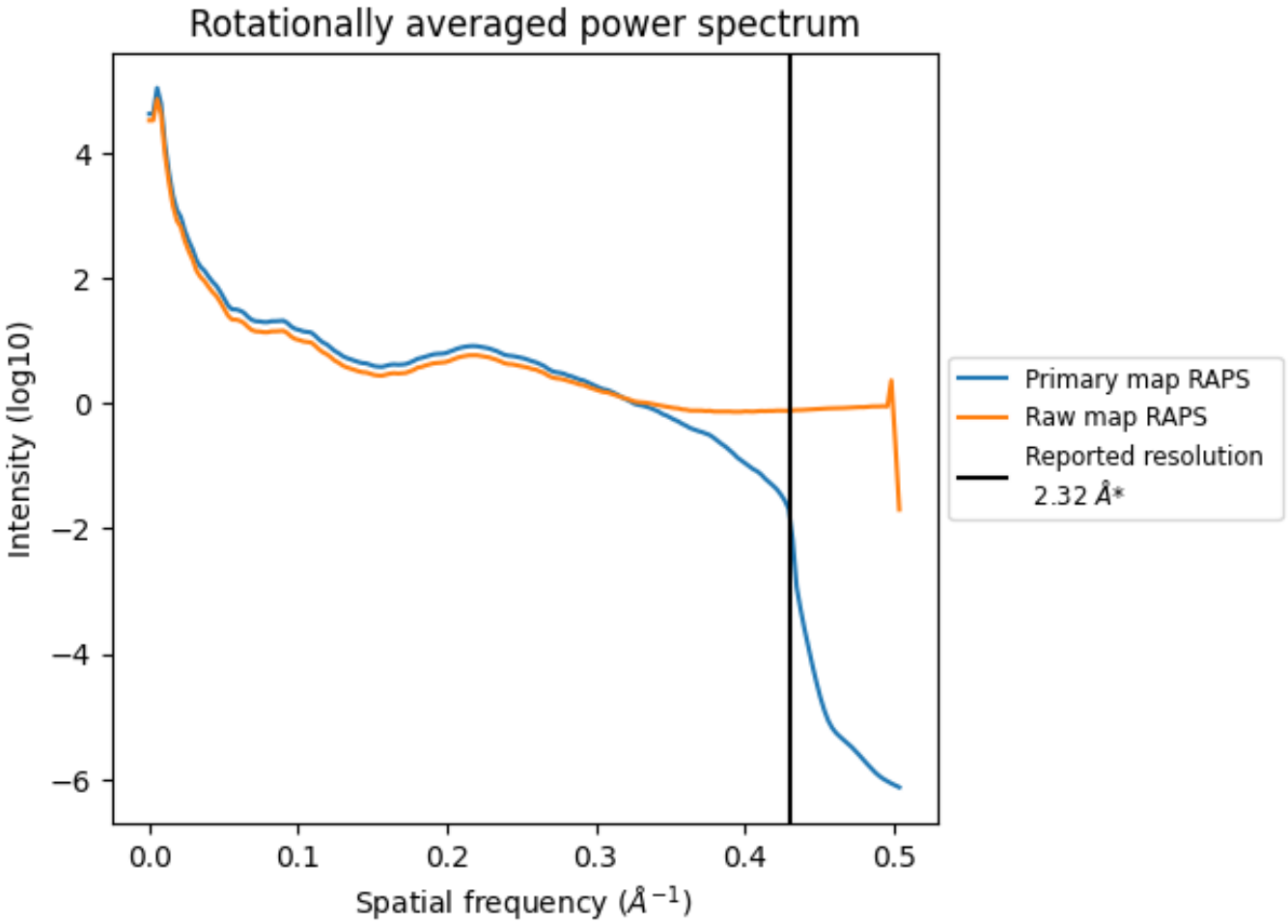
7.2 Volume estimate



The volume at the recommended contour level is 245 nm^3; this corresponds to an approximate mass of 221 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)

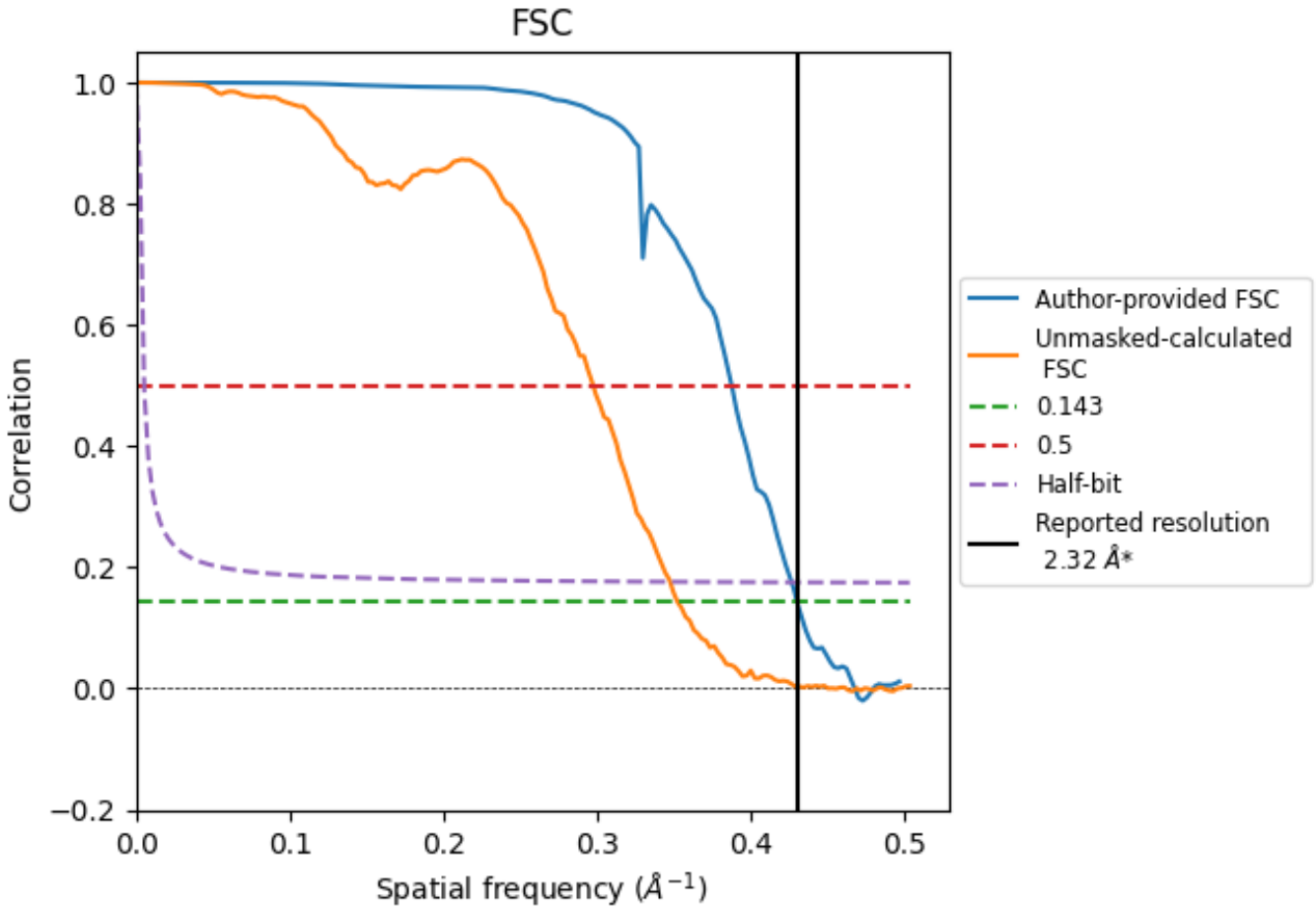


*Reported resolution corresponds to spatial frequency of 0.431 Å^{-1}

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 0.431 Å^{-1}

8.2 Resolution estimates (i)

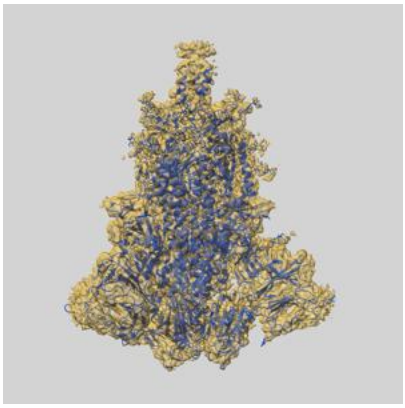
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.32	-	-
Author-provided FSC curve	2.32	2.58	2.34
Unmasked-calculated*	2.84	3.36	2.87

*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 2.84 differs from the reported value 2.32 by more than 10 %

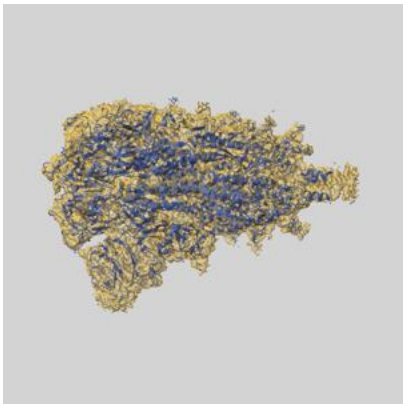
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-44062 and PDB model 9B0Y. Per-residue inclusion information can be found in section 3 on page 15.

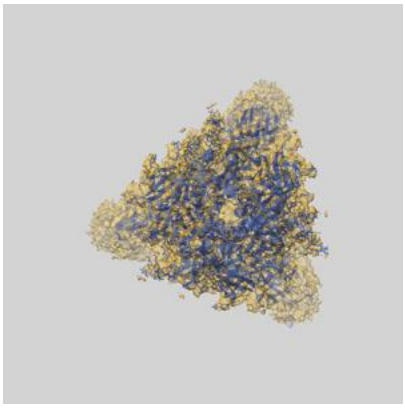
9.1 Map-model overlay



X



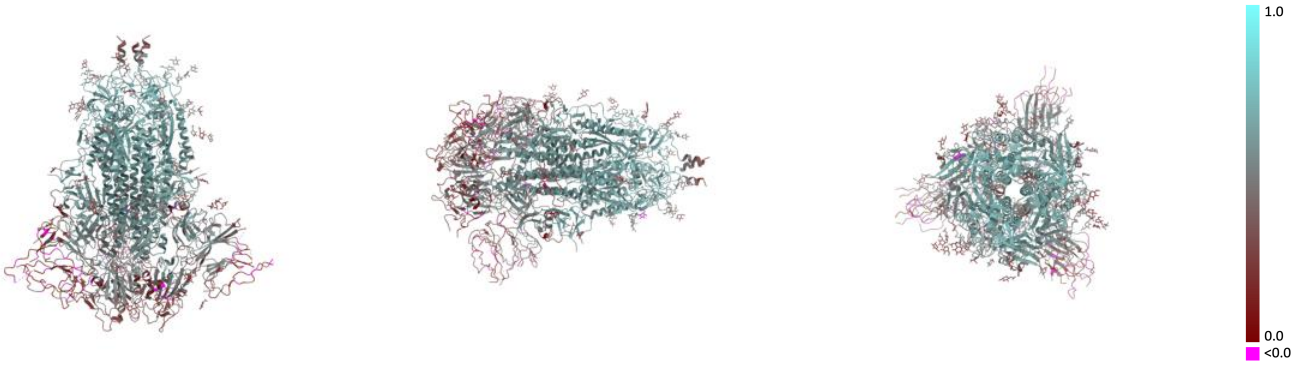
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.092 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.

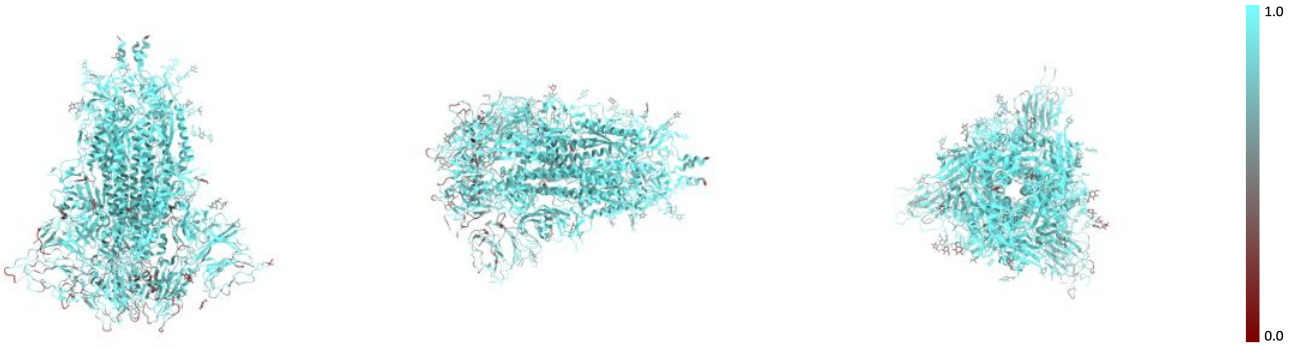
9.2 Q-score mapped to coordinate model (i)



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.

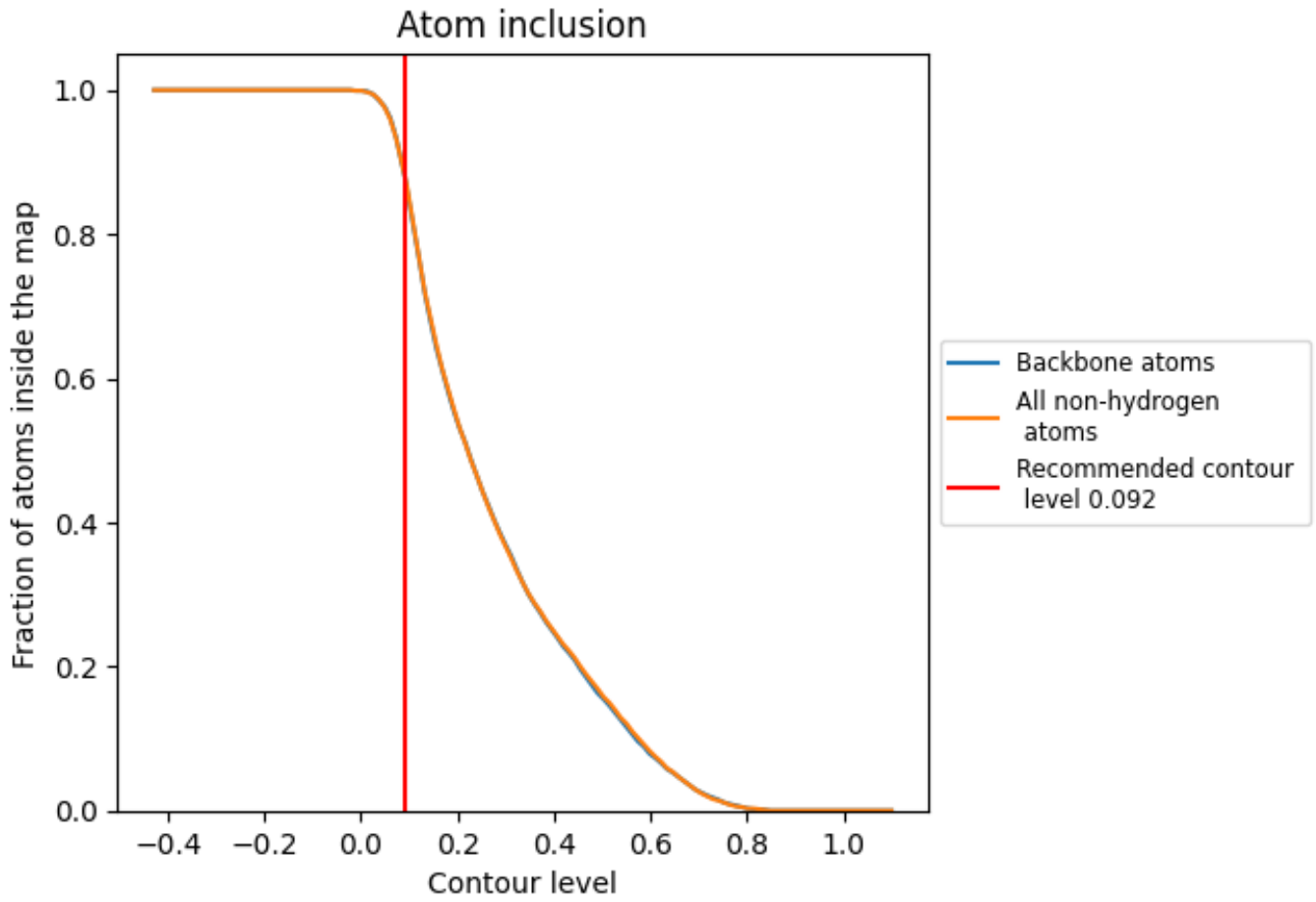
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.092).

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 88% 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 (0.092) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8780	0.4840
A	0.8930	0.4980
B	0.8820	0.4840
C	0.8870	0.4850
D	0.7110	0.3670
E	0.2860	0.2700
F	0.8210	0.3260
G	0.5640	0.1980
H	0.8720	0.4640
I	0.9490	0.4910
J	0.6410	0.2930
K	0.7630	0.4660
L	0.7440	0.4030
M	0.9230	0.4580
N	0.7180	0.3820
O	0.7860	0.4070
P	0.9740	0.5160
Q	0.6050	0.3200
R	0.5900	0.2300
S	0.7440	0.3970
T	0.8460	0.4070
U	0.8720	0.4260
V	0.7860	0.4250
W	0.5000	0.1190
X	0.8720	0.4900
Y	0.4870	0.2240
a	0.6790	0.3420
b	0.5130	0.3270
c	0.6150	0.1810

