



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 10:55 AM UTC

PDB ID : 7RDH / pdb_00007rdh
Title : Crystal structure of the de novo designed binding protein H3mb in complex with the 1968 influenza A virus hemagglutinin
Authors : Kadam, R.U.; Wilson, I.A.
Deposited on : 2021-07-09
Resolution : 2.75 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

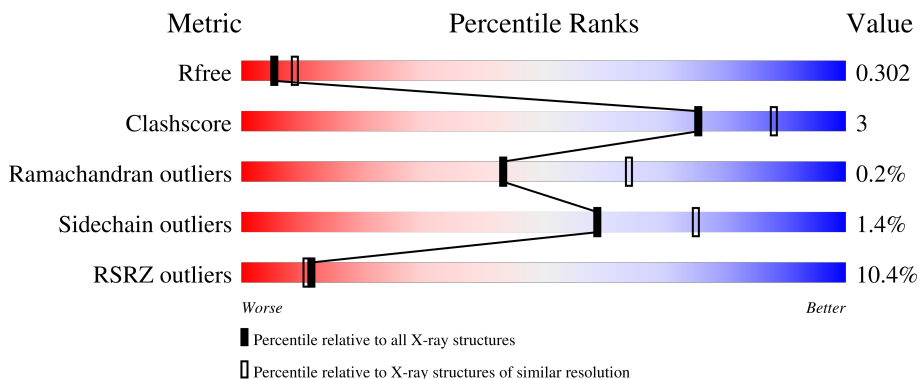
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	323	 13% 89% 9%
1	C	323	 9% 90% 7%
1	E	323	 11% 88% 10%
2	B	239	 5% 65% 6% 28%
2	D	239	 5% 71% 7% 23%

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Mol	Chain	Length	Quality of chain
2	F	239	<p>7% 65% 7% 28%</p>
3	G	77	<p>5% 68% 5% 26%</p>
3	H	77	<p>16% 68% 6% 26%</p>
4	I	2	<p>100%</p>
4	J	2	<p>50% 50%</p>
4	K	2	<p>100%</p>
4	M	2	<p>100%</p>
4	O	2	<p>100%</p>
5	L	3	<p>67% 33%</p>
5	N	3	<p>100%</p>

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 12887 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Hemagglutinin HA1 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	316	Total 2463	C 1545	N 431	O 473	S 14	0	6	0
1	C	316	Total 2461	C 1543	N 432	O 472	S 14	0	4	0
1	E	317	Total 2450	C 1532	N 431	O 473	S 14	0	3	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	ALA	-	expression tag	UNP Q91MA7
A	8	ASP	-	expression tag	UNP Q91MA7
A	9	PRO	-	expression tag	UNP Q91MA7
A	10	GLY	-	expression tag	UNP Q91MA7
C	7	ALA	-	expression tag	UNP Q91MA7
C	8	ASP	-	expression tag	UNP Q91MA7
C	9	PRO	-	expression tag	UNP Q91MA7
C	10	GLY	-	expression tag	UNP Q91MA7
E	7	ALA	-	expression tag	UNP Q91MA7
E	8	ASP	-	expression tag	UNP Q91MA7
E	9	PRO	-	expression tag	UNP Q91MA7
E	10	GLY	-	expression tag	UNP Q91MA7

- Molecule 2 is a protein called Hemagglutinin HA2 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	172	Total 1422	C 885	N 248	O 282	S 7	0	5	0
2	D	185	Total 1495	C 927	N 261	O 300	S 7	0	3	0
2	F	171	Total 1427	C 889	N 247	O 285	S 6	0	6	0

There are 192 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	123	GLY	ARG	engineered mutation	UNP Q91MA7
B	177	SER	-	expression tag	UNP Q91MA7
B	178	GLY	-	expression tag	UNP Q91MA7
B	179	GLY	-	expression tag	UNP Q91MA7
B	180	GLY	-	expression tag	UNP Q91MA7
B	181	GLY	-	expression tag	UNP Q91MA7
B	182	LEU	-	expression tag	UNP Q91MA7
B	183	ASN	-	expression tag	UNP Q91MA7
B	184	ASP	-	expression tag	UNP Q91MA7
B	185	ILE	-	expression tag	UNP Q91MA7
B	186	PHE	-	expression tag	UNP Q91MA7
B	187	GLU	-	expression tag	UNP Q91MA7
B	188	ALA	-	expression tag	UNP Q91MA7
B	189	GLN	-	expression tag	UNP Q91MA7
B	190	LYS	-	expression tag	UNP Q91MA7
B	191	ILE	-	expression tag	UNP Q91MA7
B	192	GLU	-	expression tag	UNP Q91MA7
B	193	TRP	-	expression tag	UNP Q91MA7
B	194	HIS	-	expression tag	UNP Q91MA7
B	195	GLU	-	expression tag	UNP Q91MA7
B	196	ARG	-	expression tag	UNP Q91MA7
B	197	LEU	-	expression tag	UNP Q91MA7
B	198	VAL	-	expression tag	UNP Q91MA7
B	199	PRO	-	expression tag	UNP Q91MA7
B	200	ARG	-	expression tag	UNP Q91MA7
B	201	GLY	-	expression tag	UNP Q91MA7
B	202	SER	-	expression tag	UNP Q91MA7
B	203	PRO	-	expression tag	UNP Q91MA7
B	204	GLY	-	expression tag	UNP Q91MA7
B	205	SER	-	expression tag	UNP Q91MA7
B	206	GLY	-	expression tag	UNP Q91MA7
B	207	TYR	-	expression tag	UNP Q91MA7
B	208	ILE	-	expression tag	UNP Q91MA7
B	209	PRO	-	expression tag	UNP Q91MA7
B	210	GLU	-	expression tag	UNP Q91MA7
B	211	ALA	-	expression tag	UNP Q91MA7
B	212	PRO	-	expression tag	UNP Q91MA7
B	213	ARG	-	expression tag	UNP Q91MA7
B	214	ASP	-	expression tag	UNP Q91MA7
B	215	GLY	-	expression tag	UNP Q91MA7
B	216	GLN	-	expression tag	UNP Q91MA7
B	217	ALA	-	expression tag	UNP Q91MA7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	218	TYR	-	expression tag	UNP Q91MA7
B	219	VAL	-	expression tag	UNP Q91MA7
B	220	ARG	-	expression tag	UNP Q91MA7
B	221	LYS	-	expression tag	UNP Q91MA7
B	222	ASP	-	expression tag	UNP Q91MA7
B	223	GLY	-	expression tag	UNP Q91MA7
B	224	GLU	-	expression tag	UNP Q91MA7
B	225	TRP	-	expression tag	UNP Q91MA7
B	226	VAL	-	expression tag	UNP Q91MA7
B	227	LEU	-	expression tag	UNP Q91MA7
B	228	LEU	-	expression tag	UNP Q91MA7
B	229	SER	-	expression tag	UNP Q91MA7
B	230	THR	-	expression tag	UNP Q91MA7
B	231	PHE	-	expression tag	UNP Q91MA7
B	232	LEU	-	expression tag	UNP Q91MA7
B	233	GLY	-	expression tag	UNP Q91MA7
B	234	HIS	-	expression tag	UNP Q91MA7
B	235	HIS	-	expression tag	UNP Q91MA7
B	236	HIS	-	expression tag	UNP Q91MA7
B	237	HIS	-	expression tag	UNP Q91MA7
B	238	HIS	-	expression tag	UNP Q91MA7
B	239	HIS	-	expression tag	UNP Q91MA7
D	123	GLY	ARG	engineered mutation	UNP Q91MA7
D	177	SER	-	expression tag	UNP Q91MA7
D	178	GLY	-	expression tag	UNP Q91MA7
D	179	GLY	-	expression tag	UNP Q91MA7
D	180	GLY	-	expression tag	UNP Q91MA7
D	181	GLY	-	expression tag	UNP Q91MA7
D	182	LEU	-	expression tag	UNP Q91MA7
D	183	ASN	-	expression tag	UNP Q91MA7
D	184	ASP	-	expression tag	UNP Q91MA7
D	185	ILE	-	expression tag	UNP Q91MA7
D	186	PHE	-	expression tag	UNP Q91MA7
D	187	GLU	-	expression tag	UNP Q91MA7
D	188	ALA	-	expression tag	UNP Q91MA7
D	189	GLN	-	expression tag	UNP Q91MA7
D	190	LYS	-	expression tag	UNP Q91MA7
D	191	ILE	-	expression tag	UNP Q91MA7
D	192	GLU	-	expression tag	UNP Q91MA7
D	193	TRP	-	expression tag	UNP Q91MA7
D	194	HIS	-	expression tag	UNP Q91MA7
D	195	GLU	-	expression tag	UNP Q91MA7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	196	ARG	-	expression tag	UNP Q91MA7
D	197	LEU	-	expression tag	UNP Q91MA7
D	198	VAL	-	expression tag	UNP Q91MA7
D	199	PRO	-	expression tag	UNP Q91MA7
D	200	ARG	-	expression tag	UNP Q91MA7
D	201	GLY	-	expression tag	UNP Q91MA7
D	202	SER	-	expression tag	UNP Q91MA7
D	203	PRO	-	expression tag	UNP Q91MA7
D	204	GLY	-	expression tag	UNP Q91MA7
D	205	SER	-	expression tag	UNP Q91MA7
D	206	GLY	-	expression tag	UNP Q91MA7
D	207	TYR	-	expression tag	UNP Q91MA7
D	208	ILE	-	expression tag	UNP Q91MA7
D	209	PRO	-	expression tag	UNP Q91MA7
D	210	GLU	-	expression tag	UNP Q91MA7
D	211	ALA	-	expression tag	UNP Q91MA7
D	212	PRO	-	expression tag	UNP Q91MA7
D	213	ARG	-	expression tag	UNP Q91MA7
D	214	ASP	-	expression tag	UNP Q91MA7
D	215	GLY	-	expression tag	UNP Q91MA7
D	216	GLN	-	expression tag	UNP Q91MA7
D	217	ALA	-	expression tag	UNP Q91MA7
D	218	TYR	-	expression tag	UNP Q91MA7
D	219	VAL	-	expression tag	UNP Q91MA7
D	220	ARG	-	expression tag	UNP Q91MA7
D	221	LYS	-	expression tag	UNP Q91MA7
D	222	ASP	-	expression tag	UNP Q91MA7
D	223	GLY	-	expression tag	UNP Q91MA7
D	224	GLU	-	expression tag	UNP Q91MA7
D	225	TRP	-	expression tag	UNP Q91MA7
D	226	VAL	-	expression tag	UNP Q91MA7
D	227	LEU	-	expression tag	UNP Q91MA7
D	228	LEU	-	expression tag	UNP Q91MA7
D	229	SER	-	expression tag	UNP Q91MA7
D	230	THR	-	expression tag	UNP Q91MA7
D	231	PHE	-	expression tag	UNP Q91MA7
D	232	LEU	-	expression tag	UNP Q91MA7
D	233	GLY	-	expression tag	UNP Q91MA7
D	234	HIS	-	expression tag	UNP Q91MA7
D	235	HIS	-	expression tag	UNP Q91MA7
D	236	HIS	-	expression tag	UNP Q91MA7
D	237	HIS	-	expression tag	UNP Q91MA7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	238	HIS	-	expression tag	UNP Q91MA7
D	239	HIS	-	expression tag	UNP Q91MA7
F	123	GLY	ARG	engineered mutation	UNP Q91MA7
F	177	SER	-	expression tag	UNP Q91MA7
F	178	GLY	-	expression tag	UNP Q91MA7
F	179	GLY	-	expression tag	UNP Q91MA7
F	180	GLY	-	expression tag	UNP Q91MA7
F	181	GLY	-	expression tag	UNP Q91MA7
F	182	LEU	-	expression tag	UNP Q91MA7
F	183	ASN	-	expression tag	UNP Q91MA7
F	184	ASP	-	expression tag	UNP Q91MA7
F	185	ILE	-	expression tag	UNP Q91MA7
F	186	PHE	-	expression tag	UNP Q91MA7
F	187	GLU	-	expression tag	UNP Q91MA7
F	188	ALA	-	expression tag	UNP Q91MA7
F	189	GLN	-	expression tag	UNP Q91MA7
F	190	LYS	-	expression tag	UNP Q91MA7
F	191	ILE	-	expression tag	UNP Q91MA7
F	192	GLU	-	expression tag	UNP Q91MA7
F	193	TRP	-	expression tag	UNP Q91MA7
F	194	HIS	-	expression tag	UNP Q91MA7
F	195	GLU	-	expression tag	UNP Q91MA7
F	196	ARG	-	expression tag	UNP Q91MA7
F	197	LEU	-	expression tag	UNP Q91MA7
F	198	VAL	-	expression tag	UNP Q91MA7
F	199	PRO	-	expression tag	UNP Q91MA7
F	200	ARG	-	expression tag	UNP Q91MA7
F	201	GLY	-	expression tag	UNP Q91MA7
F	202	SER	-	expression tag	UNP Q91MA7
F	203	PRO	-	expression tag	UNP Q91MA7
F	204	GLY	-	expression tag	UNP Q91MA7
F	205	SER	-	expression tag	UNP Q91MA7
F	206	GLY	-	expression tag	UNP Q91MA7
F	207	TYR	-	expression tag	UNP Q91MA7
F	208	ILE	-	expression tag	UNP Q91MA7
F	209	PRO	-	expression tag	UNP Q91MA7
F	210	GLU	-	expression tag	UNP Q91MA7
F	211	ALA	-	expression tag	UNP Q91MA7
F	212	PRO	-	expression tag	UNP Q91MA7
F	213	ARG	-	expression tag	UNP Q91MA7
F	214	ASP	-	expression tag	UNP Q91MA7
F	215	GLY	-	expression tag	UNP Q91MA7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	216	GLN	-	expression tag	UNP Q91MA7
F	217	ALA	-	expression tag	UNP Q91MA7
F	218	TYR	-	expression tag	UNP Q91MA7
F	219	VAL	-	expression tag	UNP Q91MA7
F	220	ARG	-	expression tag	UNP Q91MA7
F	221	LYS	-	expression tag	UNP Q91MA7
F	222	ASP	-	expression tag	UNP Q91MA7
F	223	GLY	-	expression tag	UNP Q91MA7
F	224	GLU	-	expression tag	UNP Q91MA7
F	225	TRP	-	expression tag	UNP Q91MA7
F	226	VAL	-	expression tag	UNP Q91MA7
F	227	LEU	-	expression tag	UNP Q91MA7
F	228	LEU	-	expression tag	UNP Q91MA7
F	229	SER	-	expression tag	UNP Q91MA7
F	230	THR	-	expression tag	UNP Q91MA7
F	231	PHE	-	expression tag	UNP Q91MA7
F	232	LEU	-	expression tag	UNP Q91MA7
F	233	GLY	-	expression tag	UNP Q91MA7
F	234	HIS	-	expression tag	UNP Q91MA7
F	235	HIS	-	expression tag	UNP Q91MA7
F	236	HIS	-	expression tag	UNP Q91MA7
F	237	HIS	-	expression tag	UNP Q91MA7
F	238	HIS	-	expression tag	UNP Q91MA7
F	239	HIS	-	expression tag	UNP Q91MA7

- Molecule 3 is a protein called De novo designed protein H3mb.

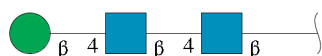
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	G	57	Total	C	N	O	S	0	0	0
			412	267	78	66	1			
3	H	57	Total	C	N	O	S	0	0	0
			375	242	71	61	1			

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



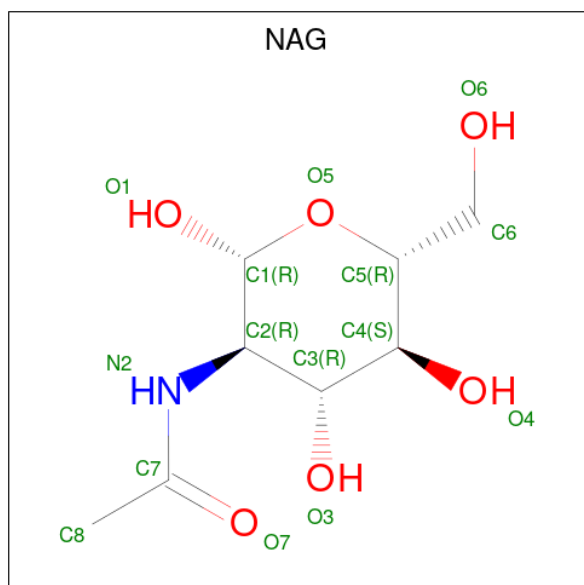
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	J	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	O	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 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				ZeroOcc	AltConf	Trace
5	L	3	Total	C	N	O	0	0	0
			39	22	2	15			
5	N	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	C	1	Total	C	N	O	0	0
			14	8	1	5		
6	C	1	Total	C	N	O	0	0
			14	8	1	5		
6	E	1	Total	C	N	O	0	0
			14	8	1	5		
6	E	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	20	Total	O	0	0
			20	20		
7	B	12	Total	O	0	0
			12	12		
7	C	26	Total	O	0	0
			26	26		
7	D	15	Total	O	0	0
			15	15		
7	E	10	Total	O	0	0
			10	10		
7	F	5	Total	O	0	0
			5	5		
7	G	3	Total	O	0	0
			3	3		
7	H	3	Total	O	0	0
			3	3		

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

Chain J:  50% 50%

MAG1
MAG2

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

Chain K:  100%

MAG1
MAG2

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

Chain M:  100%

MAG1
MAG2

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

Chain O:  100%

MAG1
MAG2

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

Chain L:  67% 33%

MAG1
MAG2
BMA3

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

Chain N:  100%

MAG1
MAG2
BMA3

4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	69.92Å 240.84Å 70.70Å 90.00° 117.30° 90.00°	Depositor
Resolution (Å)	43.24 – 2.75 43.24 – 2.75	Depositor EDS
% Data completeness (in resolution range)	89.0 (43.24-2.75) 88.9 (43.24-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 2.77Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.232 , 0.289 0.249 , 0.302	Depositor DCC
R_{free} test set	2364 reflections (4.41%)	wwPDB-VP
Wilson B-factor (Å ²)	57.3	Xtrriage
Anisotropy	0.725	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 40.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.036 for l,-k,h	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	12887	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.10	0/2523	0.28	0/3439
1	C	0.11	0/2518	0.28	0/3432
1	E	0.09	0/2505	0.28	0/3412
2	B	0.12	0/1446	0.28	0/1943
2	D	0.12	0/1519	0.28	0/2040
2	F	0.12	0/1454	0.26	0/1954
3	G	0.13	0/418	0.24	0/564
3	H	0.14	0/381	0.30	0/520
All	All	0.11	0/12764	0.28	0/17304

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2463	0	2406	17	0
1	C	2461	0	2407	13	0
1	E	2450	0	2395	19	0
2	B	1422	0	1340	14	0
2	D	1495	0	1414	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1427	0	1351	9	0
3	G	412	0	378	4	0
3	H	375	0	297	1	0
4	I	28	0	25	0	0
4	J	28	0	25	1	0
4	K	28	0	25	0	0
4	M	28	0	25	0	0
4	O	28	0	25	0	0
5	L	39	0	34	0	0
5	N	39	0	34	0	0
6	A	14	0	13	0	0
6	C	28	0	26	0	0
6	E	28	0	26	1	0
7	A	20	0	0	2	0
7	B	12	0	0	1	0
7	C	26	0	0	1	0
7	D	15	0	0	1	0
7	E	10	0	0	0	0
7	F	5	0	0	0	0
7	G	3	0	0	0	0
7	H	3	0	0	0	0
All	All	12887	0	12246	74	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 3.

The worst 5 of 74 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:E:150:ARG:HH12	6:E:401:NAG:H81	1.57	0.70
1:A:167:THR:HG22	1:A:244:VAL:HG22	1.79	0.64
1:E:102:VAL:HG22	1:E:232:ILE:HB	1.82	0.62
2:B:82:LYS:NZ	7:B:301:HOH:O	2.33	0.62
1:C:97:CYS:SG	1:C:98:TYR:N	2.73	0.61

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 X-ray entries followed by that with respect to entries of similar resolution.

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	320/323 (99%)	308 (96%)	11 (3%)	1 (0%)	36	56
1	C	318/323 (98%)	307 (96%)	10 (3%)	1 (0%)	36	56
1	E	318/323 (98%)	305 (96%)	12 (4%)	1 (0%)	36	56
2	B	175/239 (73%)	167 (95%)	8 (5%)	0	100	100
2	D	186/239 (78%)	174 (94%)	12 (6%)	0	100	100
2	F	175/239 (73%)	165 (94%)	10 (6%)	0	100	100
3	G	55/77 (71%)	50 (91%)	5 (9%)	0	100	100
3	H	55/77 (71%)	50 (91%)	5 (9%)	0	100	100
All	All	1602/1840 (87%)	1526 (95%)	73 (5%)	3 (0%)	43	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	ILE
1	C	62	ILE
1	E	62	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 X-ray entries followed by that with respect to entries of similar resolution.

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	280/283 (99%)	278 (99%)	2 (1%)	76	86
1	C	280/283 (99%)	279 (100%)	1 (0%)	84	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	279/283 (99%)	274 (98%)	5 (2%)	51	71
2	B	149/199 (75%)	148 (99%)	1 (1%)	76	86
2	D	157/199 (79%)	154 (98%)	3 (2%)	50	70
2	F	151/199 (76%)	148 (98%)	3 (2%)	48	69
3	G	32/70 (46%)	31 (97%)	1 (3%)	35	59
3	H	22/70 (31%)	19 (86%)	3 (14%)	3	6
All	All	1350/1586 (85%)	1331 (99%)	19 (1%)	59	75

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	160	ASP
3	H	12	ARG
3	H	42	ASP
3	H	9	TRP
1	E	34	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	188	ASN
1	C	188	ASN
3	H	3	HIS
3	H	38	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

16 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	I	1	4,1	14,14,15	0.31	0	17,19,21	0.41	0
4	NAG	I	2	4	14,14,15	0.20	0	17,19,21	0.40	0
4	NAG	J	1	4,1	14,14,15	0.23	0	17,19,21	0.43	0
4	NAG	J	2	4	14,14,15	0.21	0	17,19,21	0.49	0
4	NAG	K	1	2,4	14,14,15	0.31	0	17,19,21	0.59	0
4	NAG	K	2	4	14,14,15	0.33	0	17,19,21	0.42	0
5	NAG	L	1	5,1	14,14,15	0.23	0	17,19,21	0.52	0
5	NAG	L	2	5	14,14,15	0.28	0	17,19,21	0.69	0
5	BMA	L	3	5	11,11,12	0.46	0	15,15,17	0.85	1 (6%)
4	NAG	M	1	4,1	14,14,15	0.24	0	17,19,21	0.40	0
4	NAG	M	2	4	14,14,15	0.21	0	17,19,21	0.46	0
5	NAG	N	1	5,1	14,14,15	0.34	0	17,19,21	0.43	0
5	NAG	N	2	5	14,14,15	0.25	0	17,19,21	0.41	0
5	BMA	N	3	5	11,11,12	0.61	0	15,15,17	0.69	0
4	NAG	O	1	4,1	14,14,15	0.23	0	17,19,21	0.43	0
4	NAG	O	2	4	14,14,15	0.24	0	17,19,21	0.45	0

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

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

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	3	BMA	C1-O5-C5	2.13	115.04	112.19

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

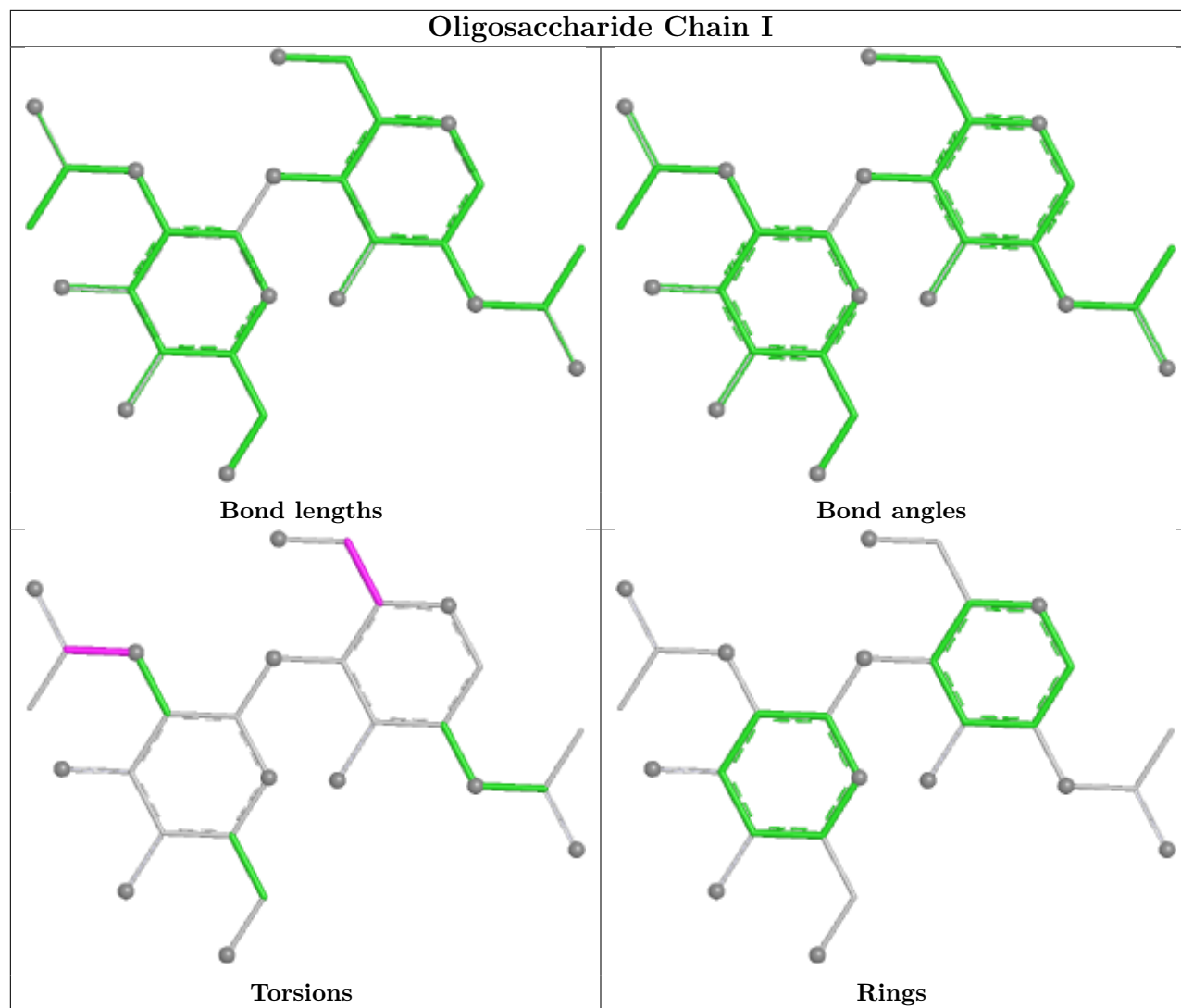
Mol	Chain	Res	Type	Atoms
4	O	2	NAG	O5-C5-C6-O6
4	K	1	NAG	O5-C5-C6-O6
4	K	1	NAG	C4-C5-C6-O6
4	I	1	NAG	O5-C5-C6-O6
4	I	2	NAG	C8-C7-N2-C2

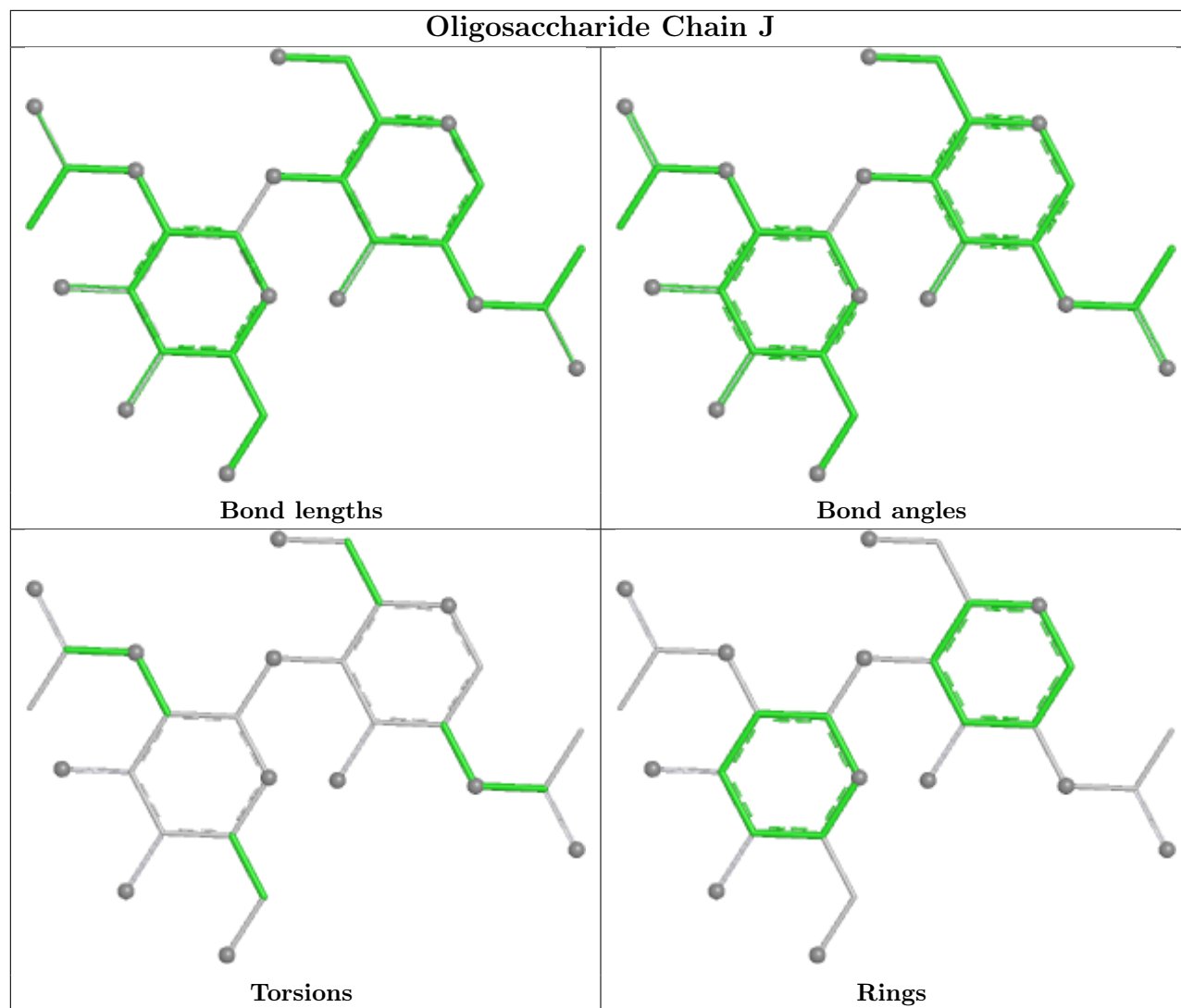
There are no ring outliers.

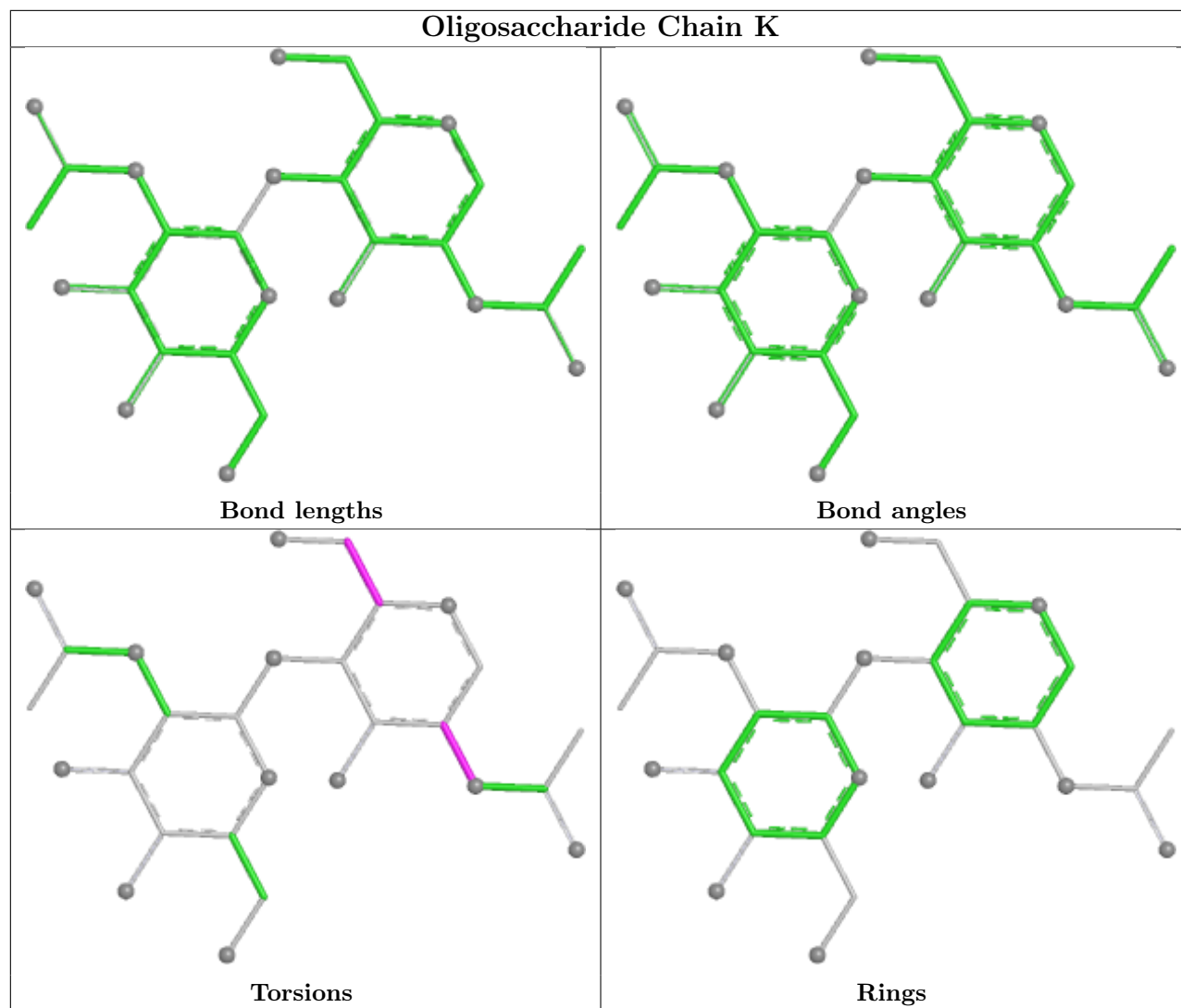
1 monomer is involved in 1 short contact:

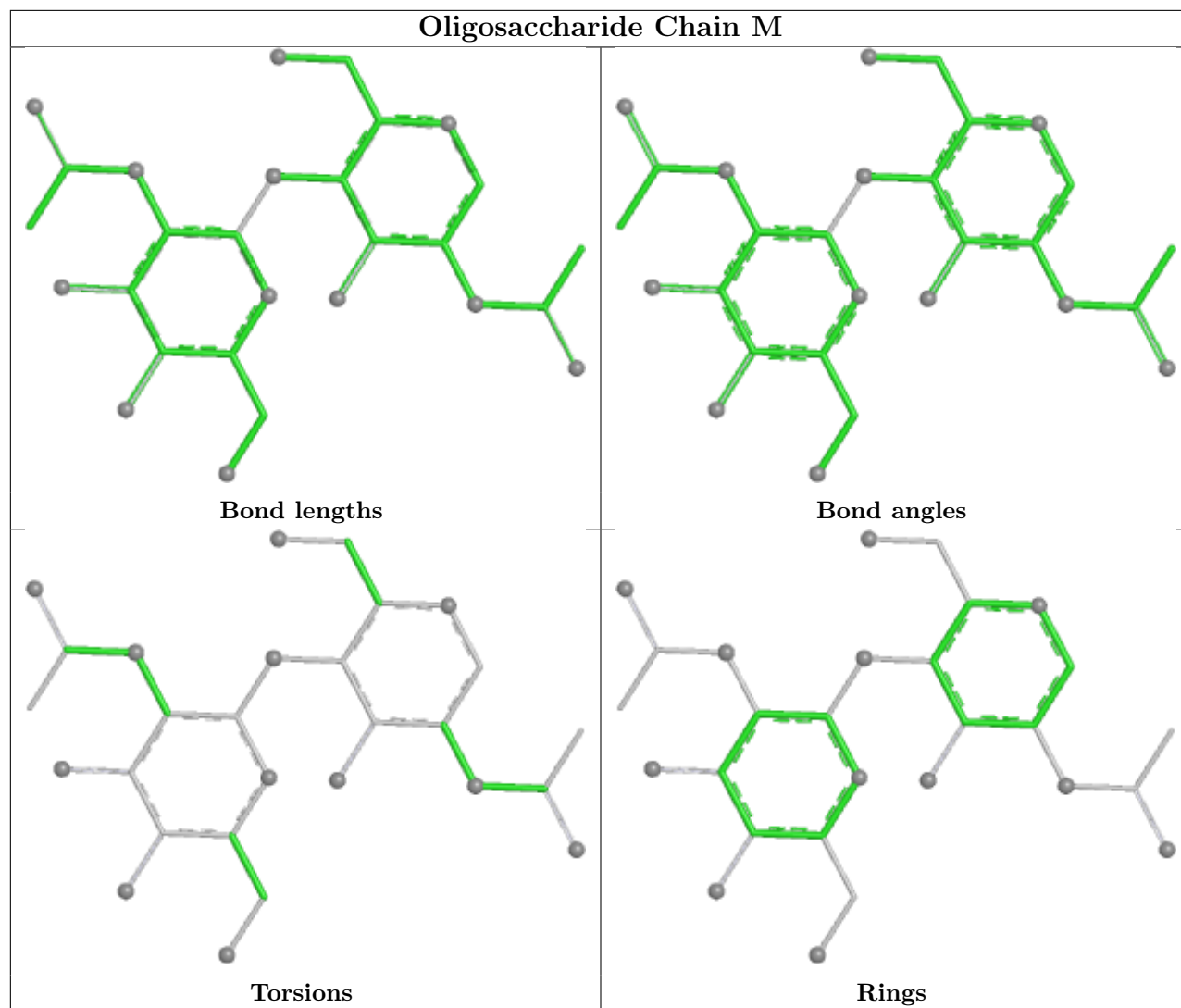
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	J	1	NAG	1	0

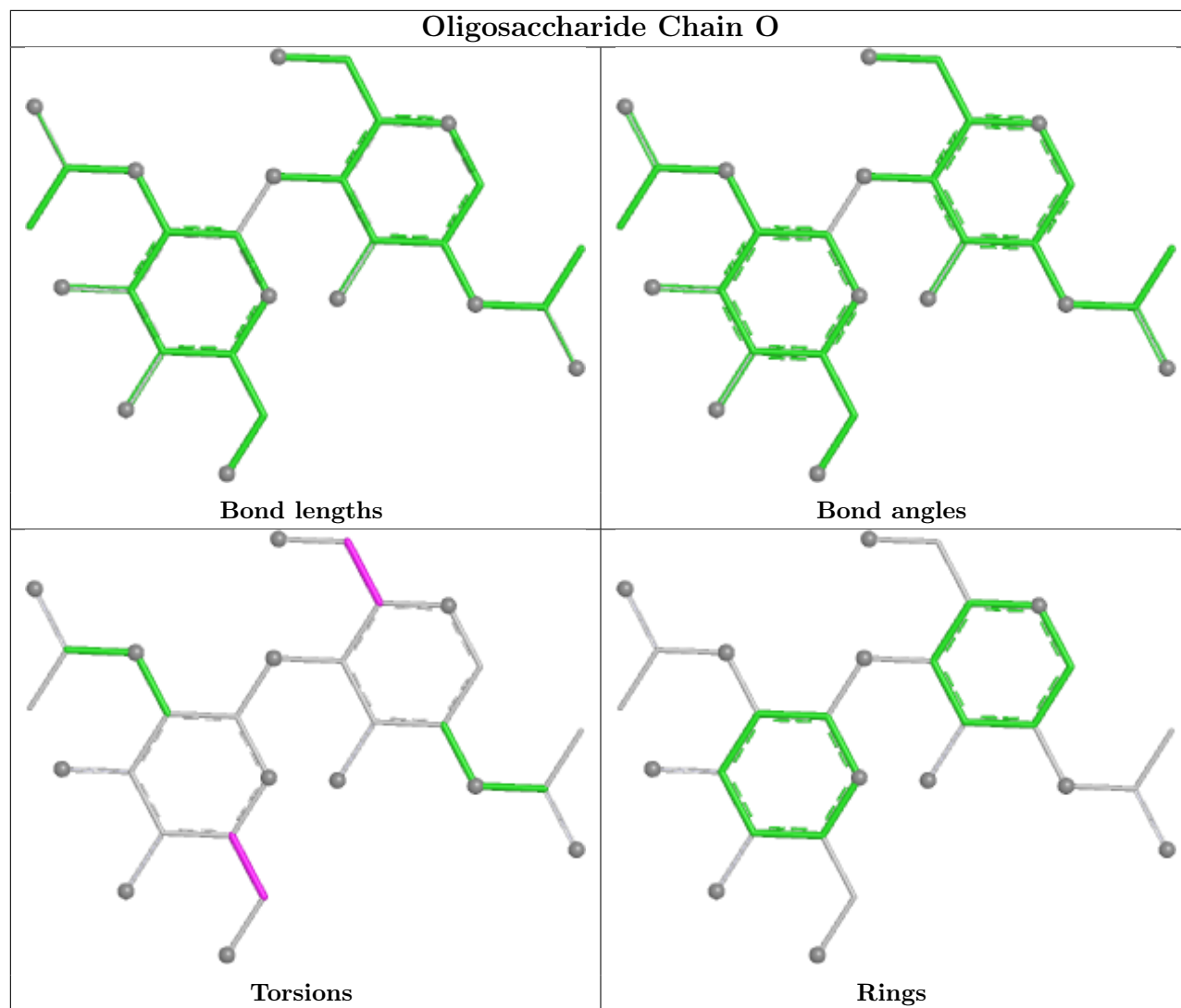
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

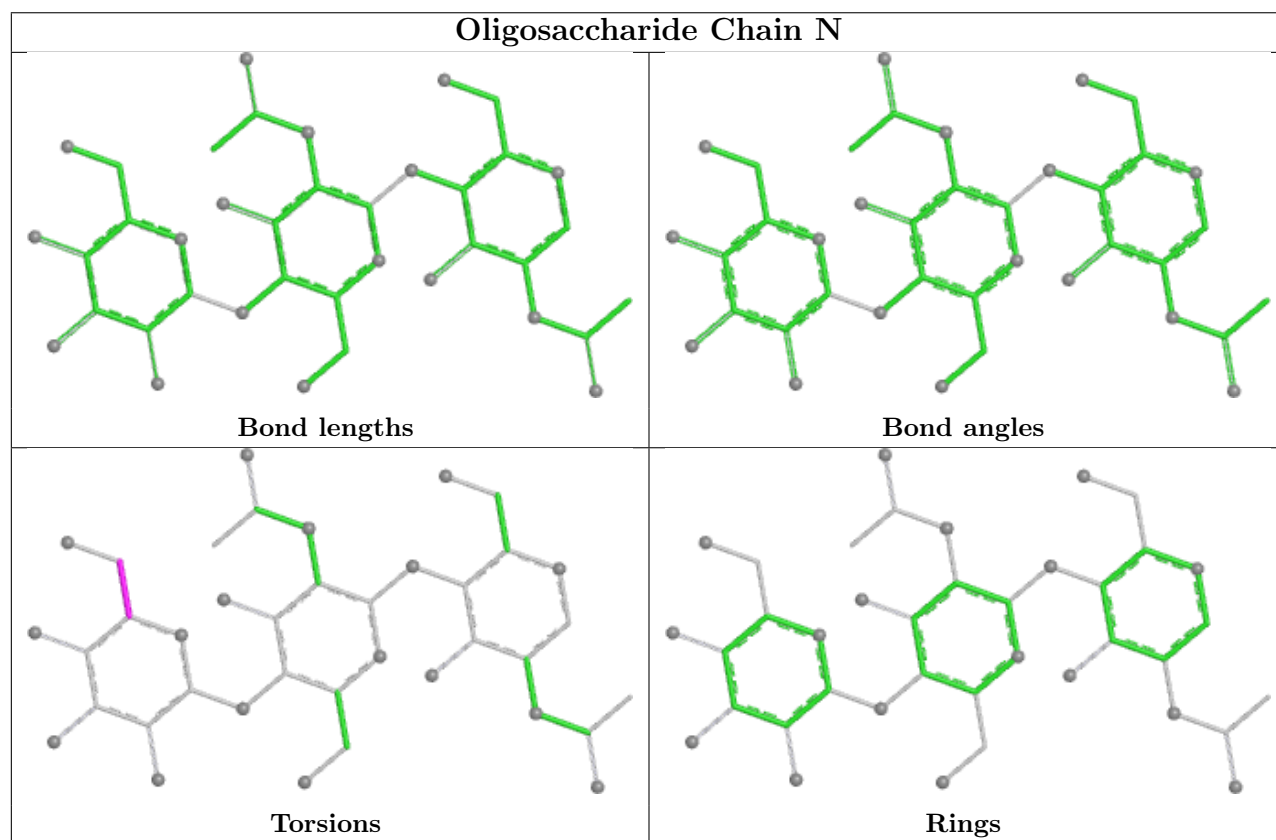
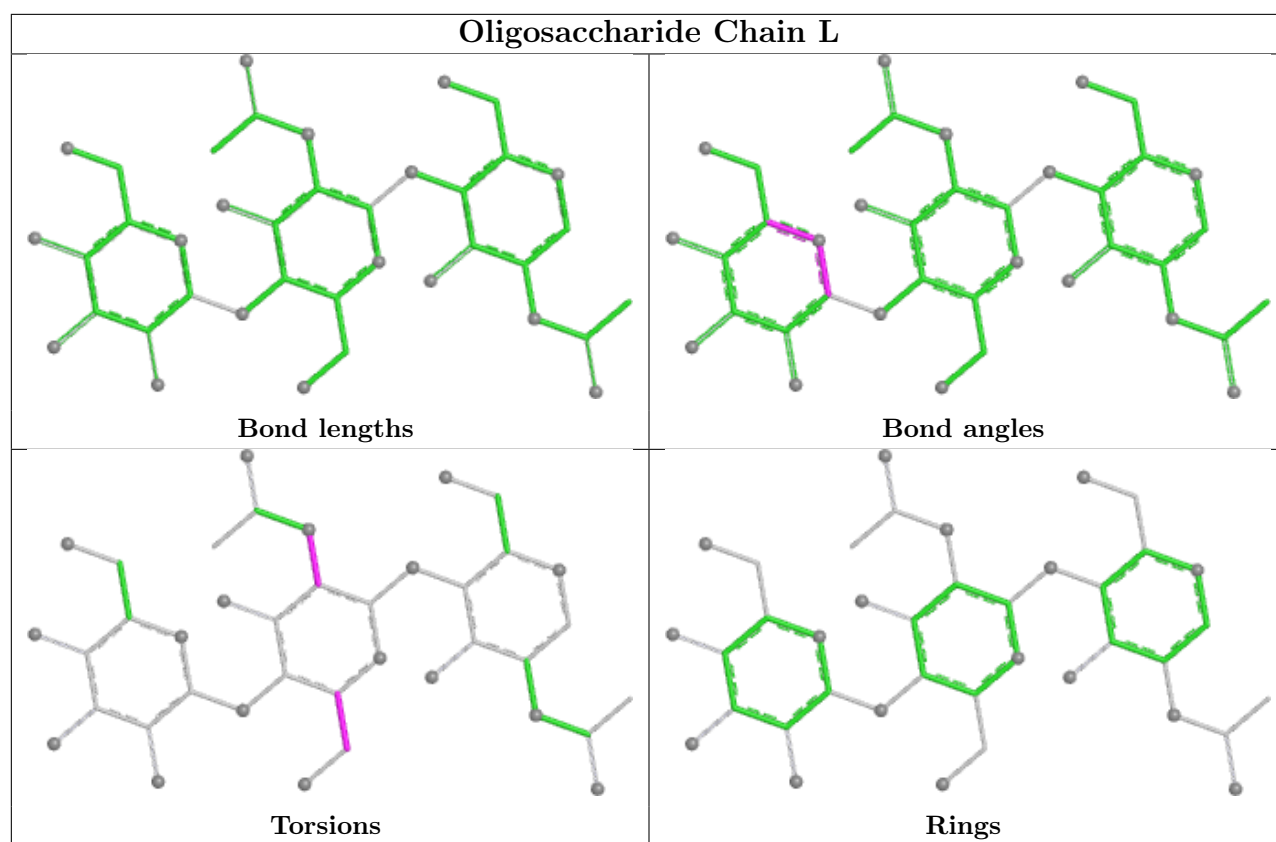












5.6 Ligand geometry

5 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	402	1	14,14,15	0.37	0	17,19,21	0.57	0
6	NAG	A	401	1	14,14,15	0.20	0	17,19,21	0.42	0
6	NAG	C	401	1	14,14,15	0.25	0	17,19,21	0.40	0
6	NAG	E	402	1	14,14,15	0.25	0	17,19,21	0.51	0
6	NAG	E	401	1	14,14,15	0.31	0	17,19,21	0.68	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	C	402	1	-	2/6/23/26	0/1/1/1
6	NAG	A	401	1	-	1/6/23/26	0/1/1/1
6	NAG	C	401	1	-	1/6/23/26	0/1/1/1
6	NAG	E	402	1	-	2/6/23/26	0/1/1/1
6	NAG	E	401	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	E	402	NAG	C8-C7-N2-C2
6	E	402	NAG	O7-C7-N2-C2
6	C	402	NAG	O5-C5-C6-O6
6	C	401	NAG	O5-C5-C6-O6
6	A	401	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	E	401	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	316/323 (97%)	1.04	43 (13%) 7 5	21, 59, 96, 113	6 (1%)
1	C	316/323 (97%)	0.96	28 (8%) 15 15	28, 61, 90, 105	4 (1%)
1	E	317/323 (98%)	1.00	35 (11%) 10 9	33, 70, 101, 119	3 (0%)
2	B	172/239 (71%)	0.87	13 (7%) 20 19	24, 57, 80, 95	5 (2%)
2	D	185/239 (77%)	0.87	13 (7%) 22 22	24, 62, 85, 97	3 (1%)
2	F	171/239 (71%)	1.00	17 (9%) 13 12	24, 64, 97, 108	6 (3%)
3	G	57/77 (74%)	0.90	4 (7%) 22 22	48, 61, 84, 102	0
3	H	57/77 (74%)	1.49	12 (21%) 2 2	57, 77, 99, 116	0
All	All	1591/1840 (86%)	0.98	165 (10%) 11 11	21, 63, 96, 119	27 (1%)

The worst 5 of 165 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	198	ALA	4.9
2	B	56	ILE	4.8
1	A	199	SER	4.7
2	F	149	ILE	4.7
1	A	163	VAL	4.6

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

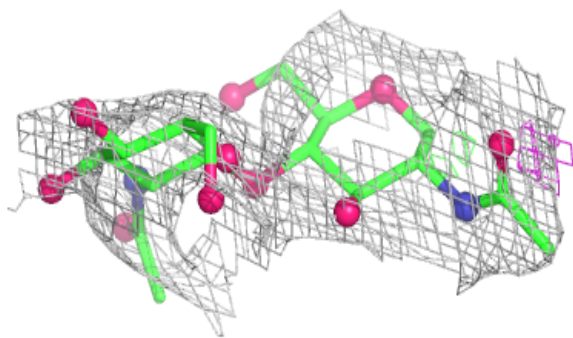
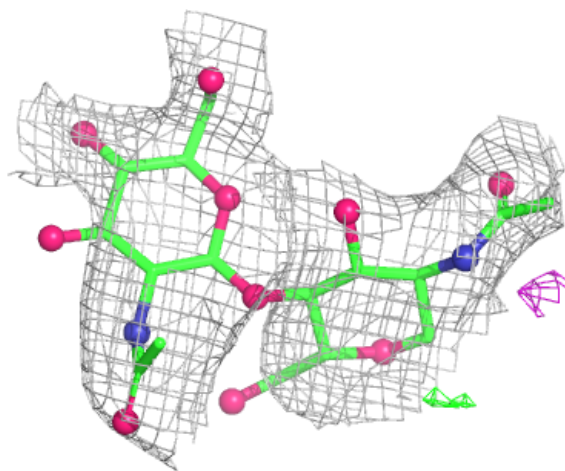
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	L	2	14/15	0.32	0.14	87,118,124,124	0
5	BMA	L	3	11/12	0.33	0.17	109,119,129,129	0
5	BMA	N	3	11/12	0.47	0.13	110,114,131,131	0
4	NAG	J	2	14/15	0.57	0.15	76,110,119,122	0
4	NAG	K	2	14/15	0.60	0.15	89,104,122,122	0
5	NAG	L	1	14/15	0.63	0.15	52,88,99,108	0
4	NAG	I	2	14/15	0.65	0.16	91,109,128,129	0
5	NAG	N	2	14/15	0.69	0.14	73,112,120,122	0
4	NAG	K	1	14/15	0.72	0.14	76,101,112,116	0
4	NAG	O	1	14/15	0.74	0.15	77,97,107,110	0
4	NAG	O	2	14/15	0.75	0.18	103,113,131,131	0
4	NAG	I	1	14/15	0.76	0.14	68,86,125,131	0
4	NAG	M	1	14/15	0.77	0.14	60,68,84,102	0
5	NAG	N	1	14/15	0.77	0.14	41,69,85,95	0
4	NAG	M	2	14/15	0.78	0.12	67,90,105,118	0
4	NAG	J	1	14/15	0.88	0.10	51,78,97,104	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

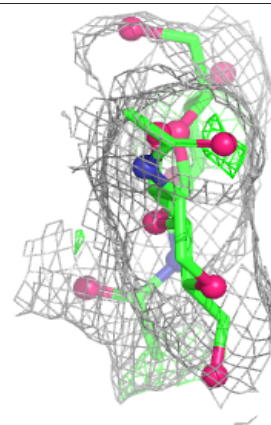
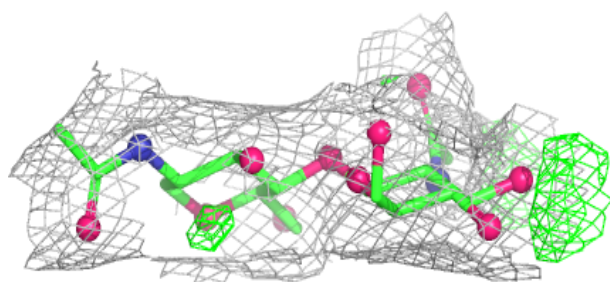
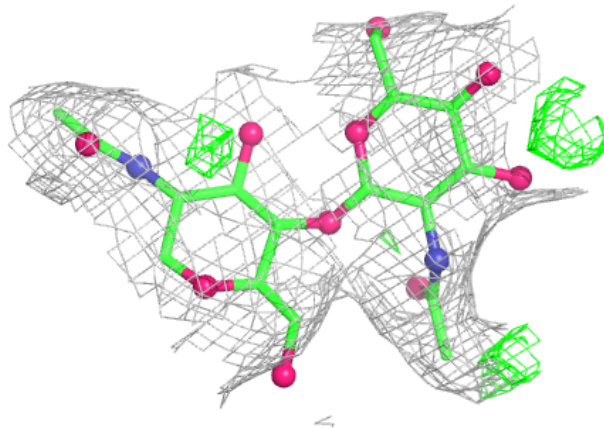
Electron density around Chain I:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



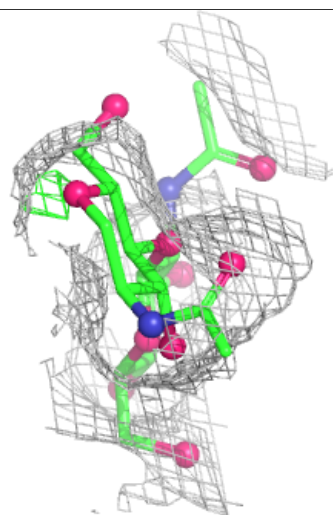
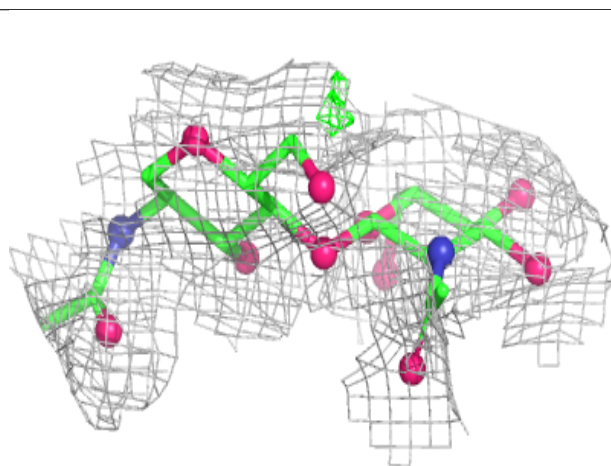
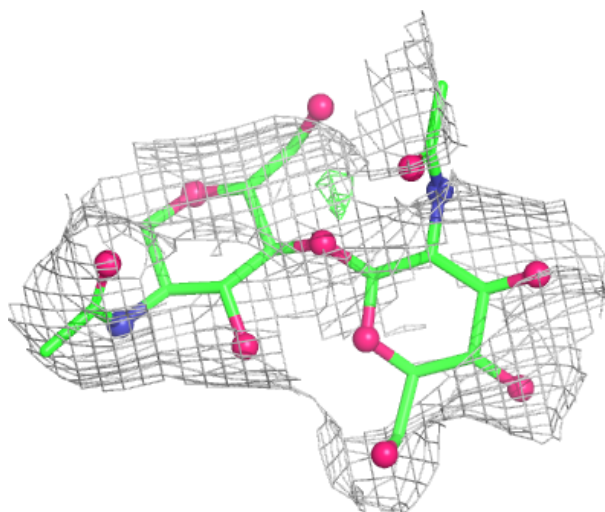
Electron density around Chain J:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



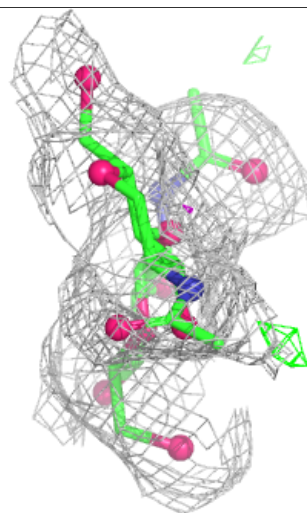
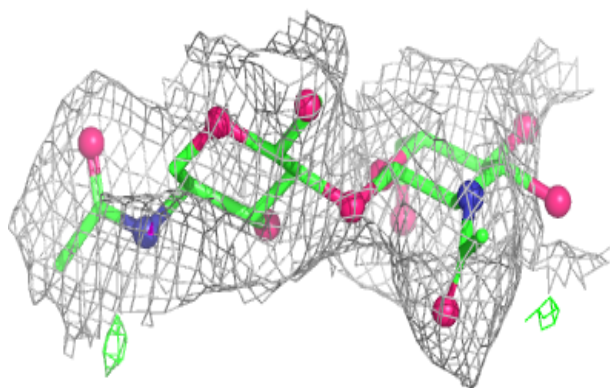
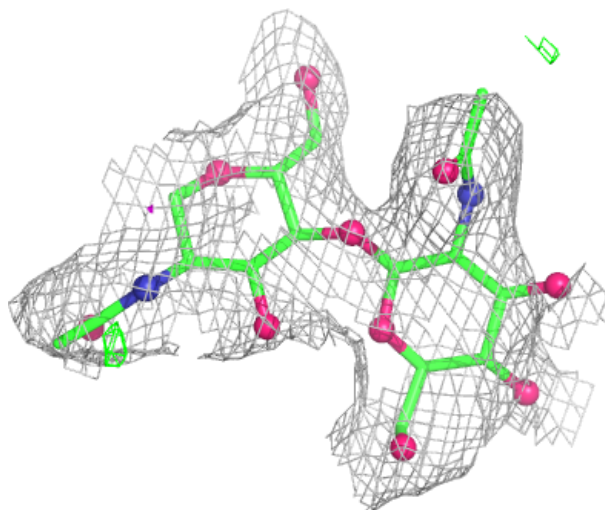
Electron density around Chain K:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



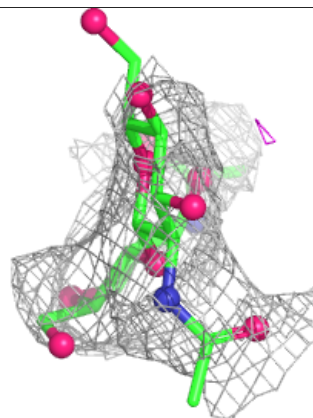
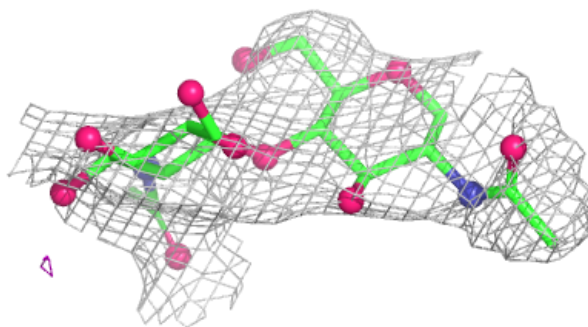
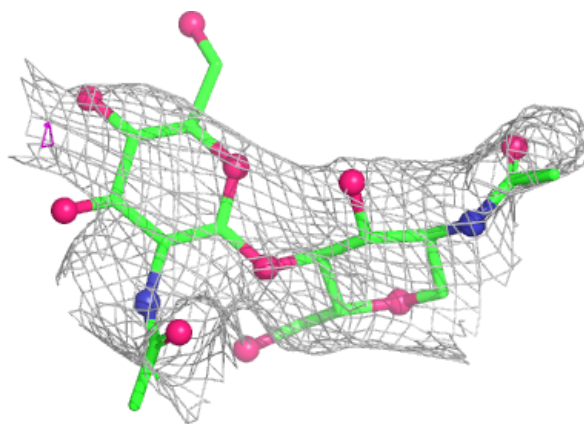
Electron density around Chain M:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



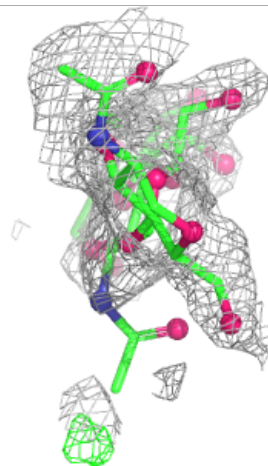
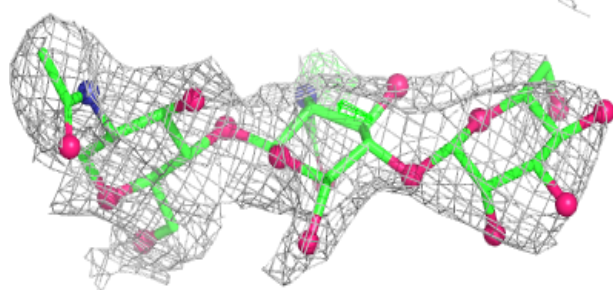
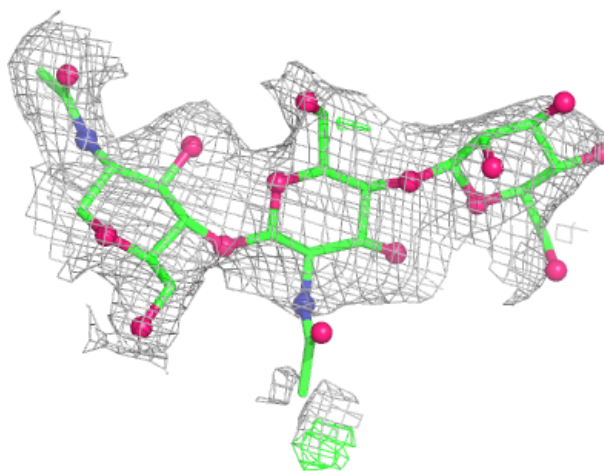
Electron density around Chain O:

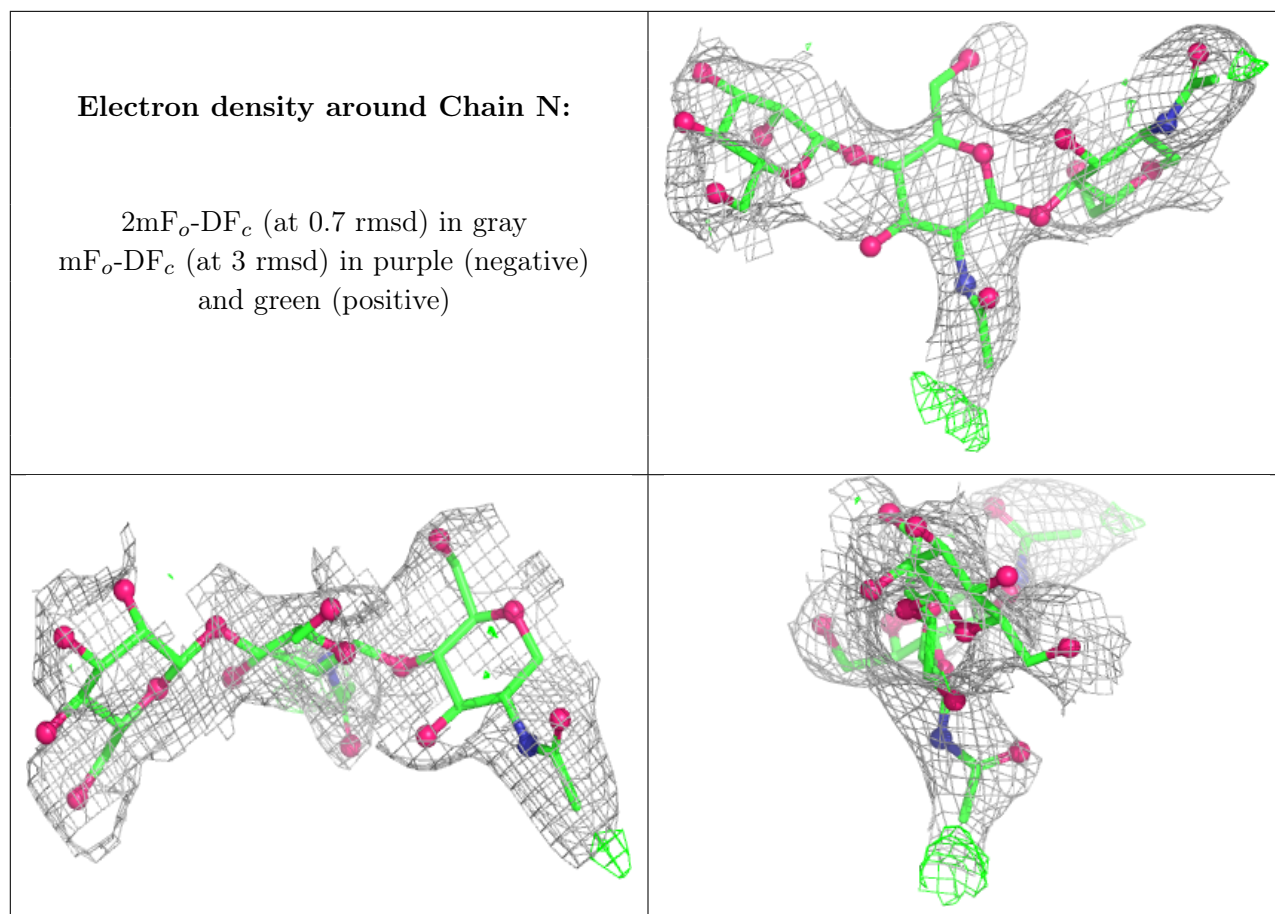
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain L:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	NAG	E	402	14/15	0.54	0.19	84,110,121,131	0
6	NAG	E	401	14/15	0.64	0.14	64,86,96,96	0
6	NAG	C	402	14/15	0.65	0.14	77,86,101,101	0
6	NAG	A	401	14/15	0.66	0.16	77,105,116,121	0
6	NAG	C	401	14/15	0.75	0.13	84,95,104,107	0

6.5 Other polymers [i](#)

There are no such residues in this entry.