



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:33 PM UTC

PDB ID : 4LN6 / pdb_00004ln6
Title : The crystal structure of hemagglutinin from a h7n9 influenza virus (a/shanghai/2/2013)
Authors : Yang, H.; Carney, P.J.; Chang, J.C.; Villanueva, J.M.; Stevens, J.
Deposited on : 2013-07-11
Resolution : 2.12 Å(reported)

This is a Full wwPDB X-ray Structure 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/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

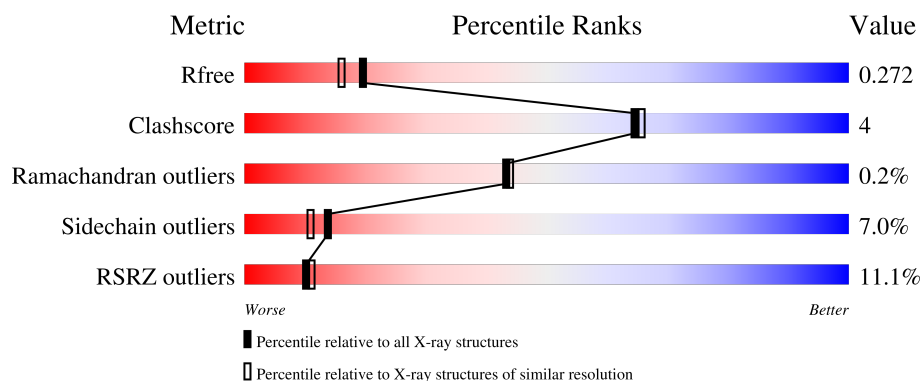
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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	8290 (2.14-2.10)
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)
RSRZ outliers	180081	8294 (2.14-2.10)

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	325	8% 86% 9% ..
1	C	325	9% 85% 10% ..
1	E	325	9% 85% 10% ..
1	G	325	14% 85% 11% ..
1	I	325	10% 86% 9% ..

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	K	325	
2	B	181	
2	D	181	
2	F	181	
2	H	181	
2	J	181	
2	L	181	
3	M	2	
3	Q	2	
4	N	3	
4	P	3	
4	R	3	
4	S	3	
5	O	4	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 23253 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.

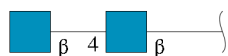
- Molecule 1 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	316	Total	C	N	O	S	1	0	0
			2412	1498	436	463	15			
1	C	316	Total	C	N	O	S	1	0	0
			2412	1498	436	463	15			
1	E	316	Total	C	N	O	S	1	0	0
			2412	1498	436	463	15			
1	G	316	Total	C	N	O	S	1	0	0
			2412	1498	436	463	15			
1	I	316	Total	C	N	O	S	1	0	0
			2412	1498	436	463	15			
1	K	316	Total	C	N	O	S	1	0	0
			2412	1498	436	463	15			

- Molecule 2 is a protein called Hemagglutinin.

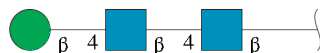
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	167	Total	C	N	O	S	0	0	0
			1360	838	238	277	7			
2	D	167	Total	C	N	O	S	0	0	0
			1360	838	238	277	7			
2	F	167	Total	C	N	O	S	0	0	0
			1360	838	238	277	7			
2	H	169	Total	C	N	O	S	0	0	0
			1375	849	240	279	7			
2	J	169	Total	C	N	O	S	0	0	0
			1375	849	240	279	7			
2	L	169	Total	C	N	O	S	0	0	0
			1375	849	240	279	7			

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



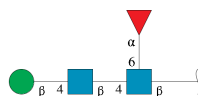
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	Q	2	Total	C	N	O	0	0	0
			28	16	2	10			

- 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				ZeroOcc	AltConf	Trace
4	N	3	Total	C	N	O	0	0	0
			39	22	2	15			
4	P	3	Total	C	N	O	0	0	0
			39	22	2	15			
4	R	3	Total	C	N	O	0	0	0
			39	22	2	15			
4	S	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.

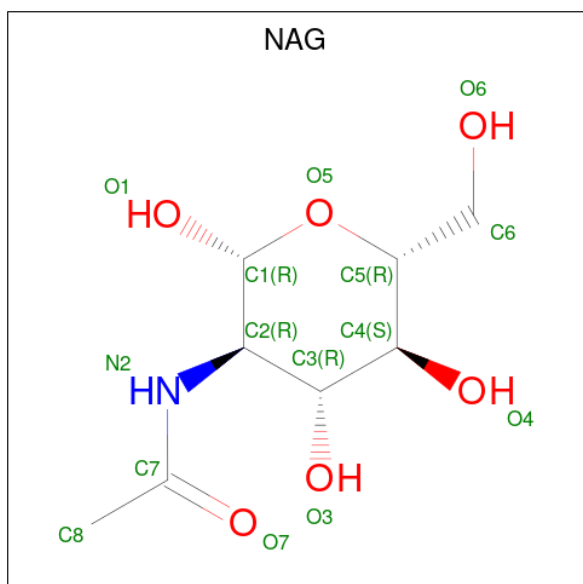


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	O	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Ca	0	0
			1	1		
6	C	1	Total	Ca	0	0
			1	1		
6	E	1	Total	Ca	0	0
			1	1		
6	G	1	Total	Ca	0	0
			1	1		
6	I	1	Total	Ca	0	0
			1	1		
6	K	1	Total	Ca	0	0
			1	1		

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	N	O	0	0
			14	8	1	5		
7	D	1	Total	C	N	O	0	0
			14	8	1	5		
7	F	1	Total	C	N	O	0	0
			14	8	1	5		
7	H	1	Total	C	N	O	0	0
			14	8	1	5		
7	J	1	Total	C	N	O	0	0
			14	8	1	5		

Continued on next page...

Continued from previous page...

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

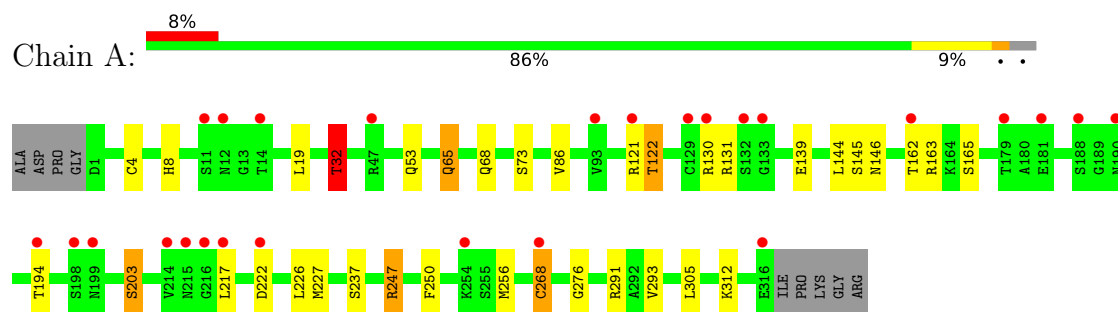
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	32	Total	O	0	0
			32	32		
8	B	12	Total	O	0	0
			12	12		
8	C	32	Total	O	0	0
			32	32		
8	D	12	Total	O	0	0
			12	12		
8	E	24	Total	O	0	0
			24	24		
8	F	15	Total	O	0	0
			15	15		
8	G	24	Total	O	0	0
			24	24		
8	H	15	Total	O	0	0
			15	15		
8	I	16	Total	O	0	0
			16	16		
8	J	14	Total	O	0	0
			14	14		
8	K	18	Total	O	0	0
			18	18		
8	L	11	Total	O	0	0
			11	11		

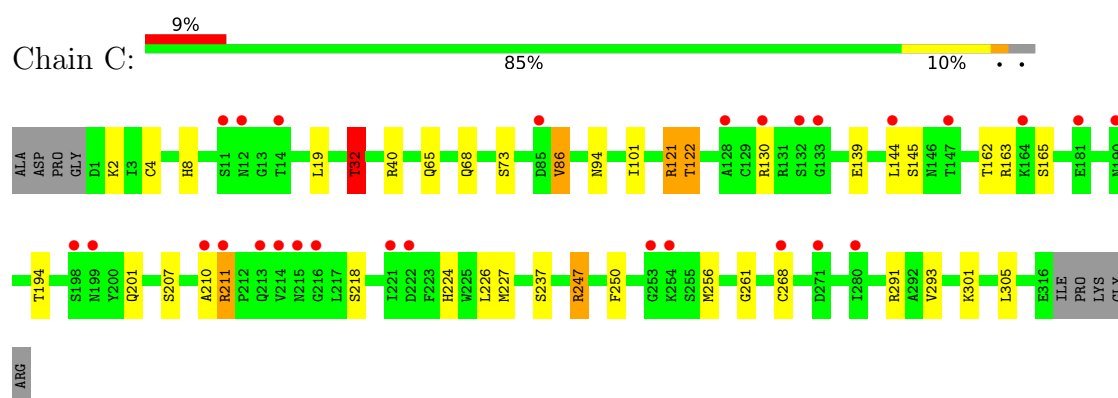
3 Residue-property plots [i](#)

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 electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

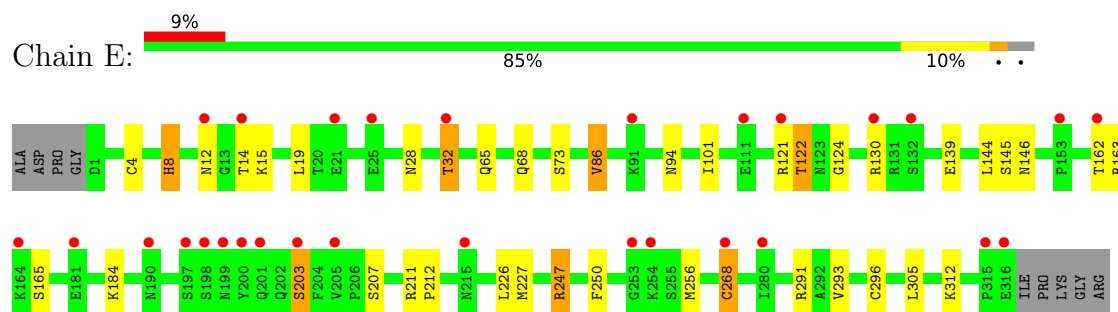
- Molecule 1: Hemagglutinin



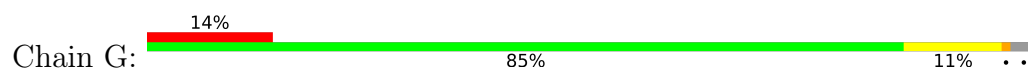
- Molecule 1: Hemagglutinin

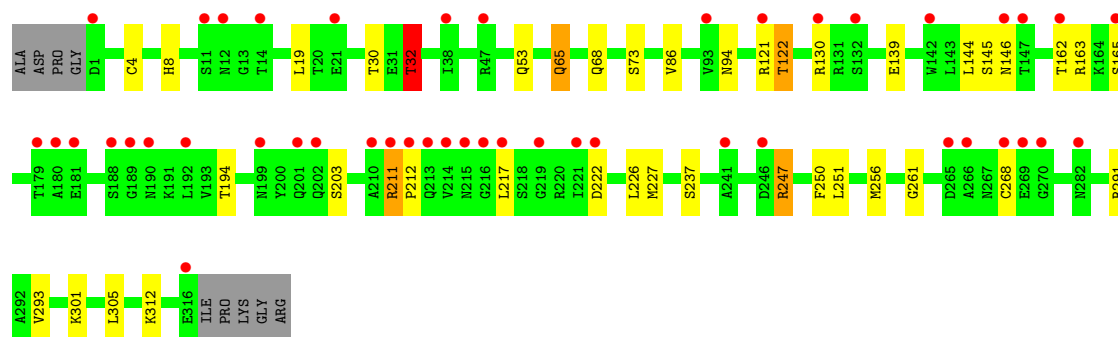


- Molecule 1: Hemagglutinin

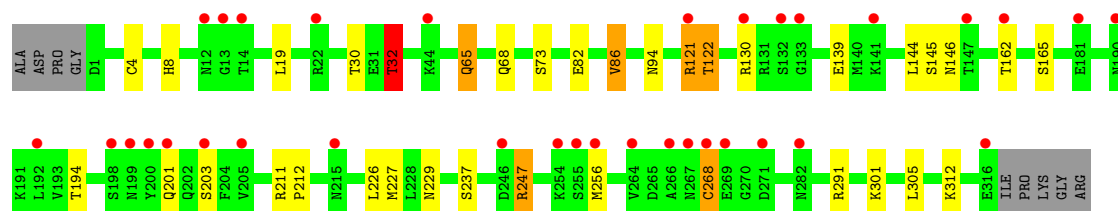
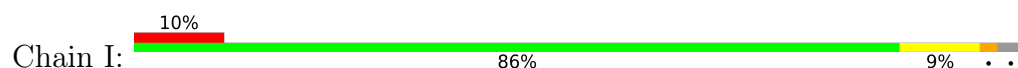


- Molecule 1: Hemagglutinin

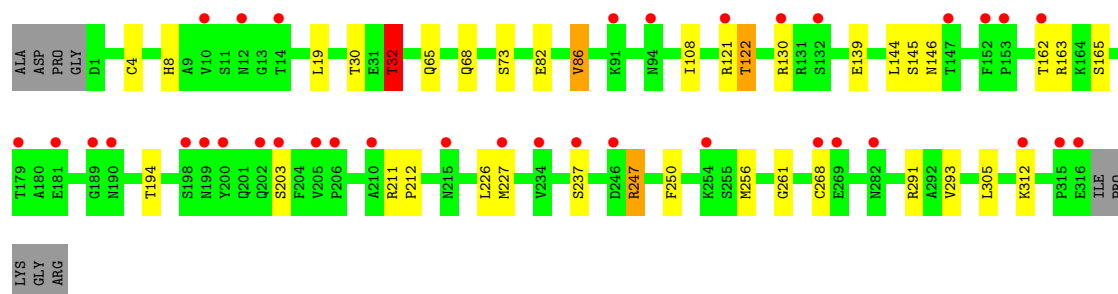
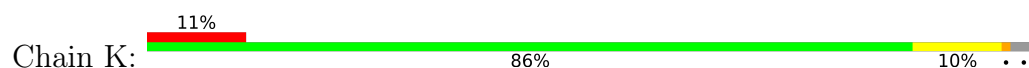




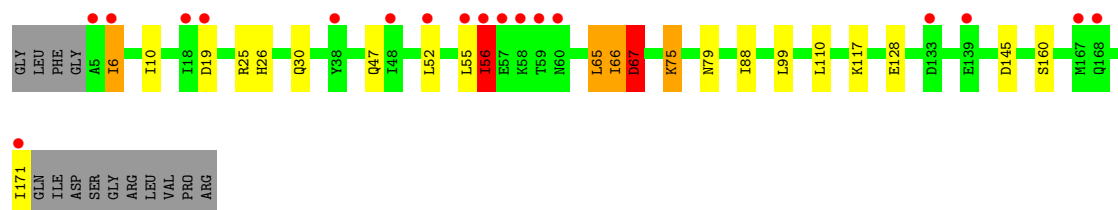
• Molecule 1: Hemagglutinin



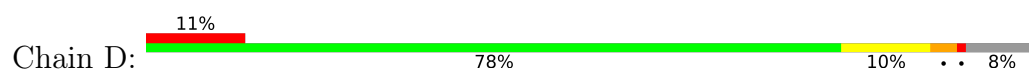
• Molecule 1: Hemagglutinin

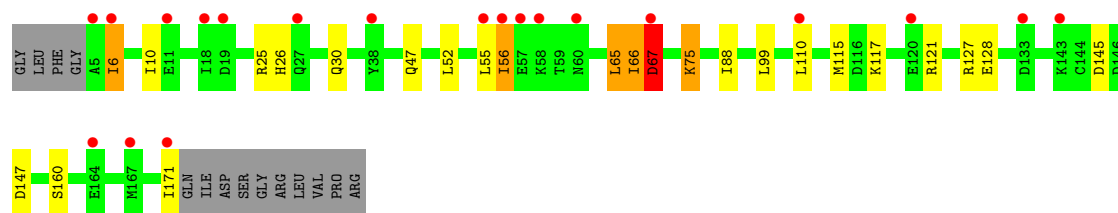


• Molecule 2: Hemagglutinin

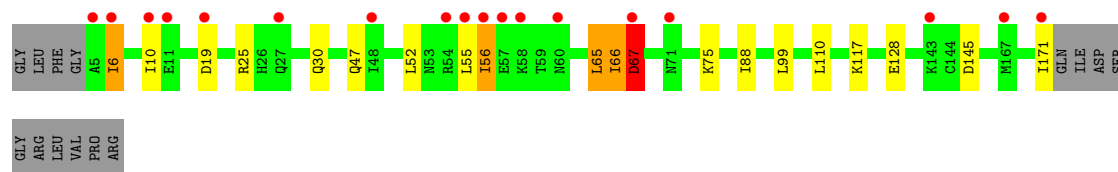
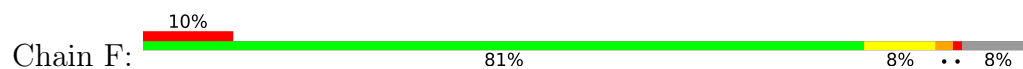


• Molecule 2: Hemagglutinin

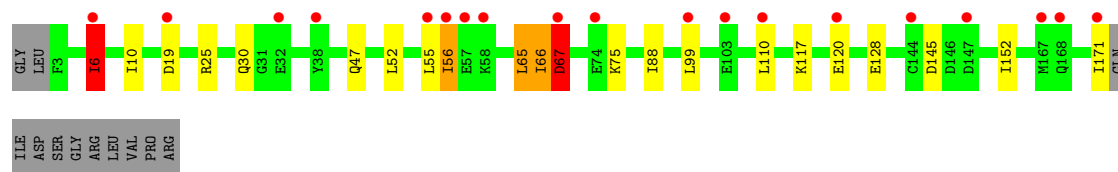
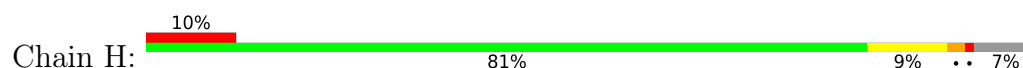




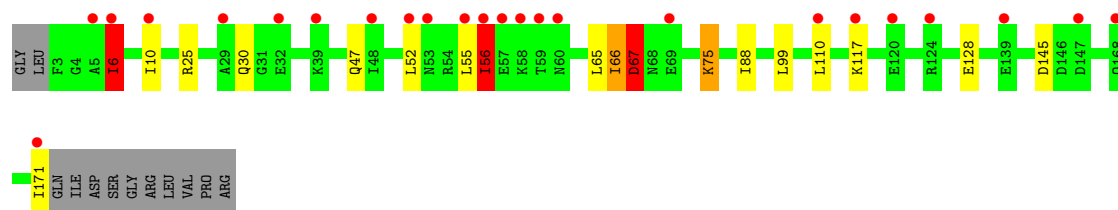
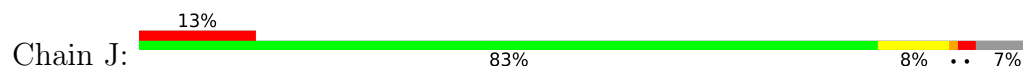
● Molecule 2: Hemagglutinin



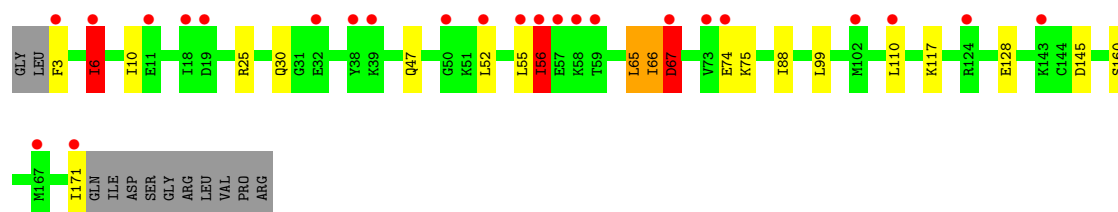
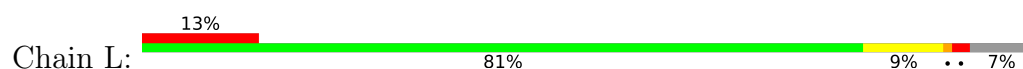
● Molecule 2: Hemagglutinin



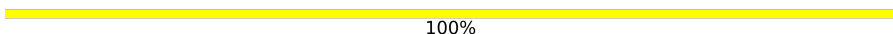
● Molecule 2: Hemagglutinin



● Molecule 2: Hemagglutinin



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

Chain M:  100%

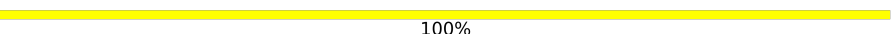
MAG1
MAG2

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

Chain Q:  50% 50%

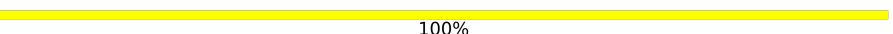
MAG1
MAG2

- Molecule 4: 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
EMA3

- 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:  100%

MAG1
MAG2
EMA3

- 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:  33% 67%

MAG1
MAG2
EMA3

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

Chain S:  67% 33%

MAG1
MAG2
EMA3

- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	154.02Å 152.83Å 155.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.07 – 2.12 49.07 – 2.12	Depositor EDS
% Data completeness (in resolution range)	95.3 (49.07-2.12) 96.3 (49.07-2.12)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.24 (at 2.12Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.238 , 0.259 0.249 , 0.272	Depositor DCC
R_{free} test set	17049 reflections (8.19%)	wwPDB-VP
Wilson B-factor (Å ²)	33.1	Xtriage
Anisotropy	0.316	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 30.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.39$	Xtriage
Estimated twinning fraction	0.000 for l,-k,h 0.000 for -h,-l,-k 0.000 for k,h,-l 0.096 for l,h,k 0.096 for k,l,h	Xtriage
Reported twinning fraction	0.852 for H, K, L 0.063 for L, H, K 0.085 for -K, -L, H	Depositor
Outliers	0 of 201333 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	23253	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.02% 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: BMA, CA, NAG, FUC

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	1.27	3/2458 (0.1%)	1.08	5/3322 (0.2%)
1	C	1.30	3/2458 (0.1%)	1.09	5/3322 (0.2%)
1	E	1.31	6/2458 (0.2%)	1.11	5/3322 (0.2%)
1	G	1.19	3/2458 (0.1%)	1.07	5/3322 (0.2%)
1	I	1.17	2/2458 (0.1%)	1.06	7/3322 (0.2%)
1	K	1.18	2/2458 (0.1%)	1.09	6/3322 (0.2%)
2	B	1.22	3/1383 (0.2%)	1.05	2/1864 (0.1%)
2	D	1.26	4/1383 (0.3%)	1.09	2/1864 (0.1%)
2	F	1.23	1/1383 (0.1%)	1.08	2/1864 (0.1%)
2	H	1.13	1/1399 (0.1%)	1.05	4/1885 (0.2%)
2	J	1.13	1/1399 (0.1%)	1.05	2/1885 (0.1%)
2	L	1.14	3/1399 (0.2%)	1.04	2/1885 (0.1%)
All	All	1.22	32/23094 (0.1%)	1.08	47/31179 (0.2%)

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	268	CYS	CB-SG	-18.17	1.21	1.81
1	I	268	CYS	CB-SG	14.50	2.29	1.81
1	E	268	CYS	CB-SG	12.17	2.21	1.81
1	G	268	CYS	CB-SG	-11.12	1.44	1.81
1	A	268	CYS	CB-SG	-11.03	1.44	1.81
1	A	131	ARG	CA-C	8.58	1.56	1.52
2	B	67	ASP	CB-CG	-7.75	1.32	1.52
1	C	261	GLY	C-O	-7.45	1.19	1.24
2	D	67	ASP	CB-CG	-6.83	1.34	1.52
2	B	160	SER	C-O	-6.82	1.16	1.24
2	F	67	ASP	CB-CG	-6.77	1.35	1.52
1	G	261	GLY	C-O	-6.63	1.19	1.24
2	L	74	GLU	CD-OE1	6.27	1.37	1.25
2	J	67	ASP	CB-CG	-5.95	1.37	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	67	ASP	CB-CG	-5.92	1.37	1.52
2	H	67	ASP	CB-CG	-5.90	1.37	1.52
2	D	121	ARG	CA-C	5.70	1.60	1.52
2	D	160	SER	C-O	-5.66	1.17	1.24
1	K	82	GLU	C-O	-5.64	1.16	1.24
1	I	82	GLU	C-O	-5.61	1.16	1.24
2	D	115	MET	N-CA	5.60	1.53	1.46
1	K	261	GLY	C-O	-5.54	1.20	1.24
1	E	184	LYS	CA-C	5.51	1.60	1.52
2	L	160	SER	C-O	-5.46	1.17	1.24
2	B	79	ASN	C-O	-5.38	1.17	1.24
1	G	251	LEU	C-O	-5.28	1.17	1.23
1	E	15	LYS	C-O	-5.14	1.17	1.23
1	A	276	GLY	C-O	-5.09	1.19	1.24
1	E	124	GLY	CA-C	5.08	1.57	1.52
1	C	2	LYS	CA-C	-5.06	1.46	1.52
1	E	12	ASN	CG-ND2	5.02	1.43	1.33
1	E	296	CYS	CA-C	5.01	1.59	1.52

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	268	CYS	CA-CB-SG	12.74	143.71	114.40
1	E	268	CYS	CA-CB-SG	-7.46	97.25	114.40
1	I	122	THR	N-CA-CB	-6.64	101.38	110.95
1	I	86	VAL	N-CA-CB	-6.48	101.55	112.44
1	K	122	THR	N-CA-CB	-6.48	101.62	110.95
1	I	32	THR	N-CA-CB	-6.46	101.96	110.88
1	K	86	VAL	N-CA-CB	-6.39	101.70	112.44
2	D	127	ARG	CB-CA-C	-6.37	108.57	117.23
1	C	32	THR	N-CA-CB	-6.32	101.36	110.65
1	A	32	THR	N-CA-CB	-6.20	102.33	110.88
1	E	86	VAL	N-CA-CB	-6.19	102.04	112.44
1	C	122	THR	N-CA-CB	-6.15	102.10	110.95
1	C	86	VAL	N-CA-CB	-5.99	102.37	112.44
2	H	6	ILE	N-CA-CB	-5.99	101.62	111.45
1	A	122	THR	N-CA-CB	-5.96	102.37	110.95
2	D	67	ASP	CB-CG-OD1	-5.81	105.03	118.40
1	C	247	ARG	NE-CZ-NH2	-5.74	114.03	119.20
1	G	32	THR	N-CA-CB	-5.73	102.97	110.88
2	L	67	ASP	CB-CG-OD1	-5.70	105.28	118.40
1	E	247	ARG	NE-CZ-NH1	5.67	127.17	121.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	122	THR	N-CA-CB	-5.66	102.81	110.95
2	H	67	ASP	CB-CG-OD1	-5.63	105.44	118.40
1	G	122	THR	N-CA-CB	-5.57	102.93	110.95
2	J	6	ILE	N-CA-CB	-5.54	102.36	111.45
1	K	32	THR	N-CA-CB	-5.53	103.25	110.88
1	G	247	ARG	NE-CZ-NH1	5.53	127.03	121.50
1	A	217	LEU	N-CA-C	5.45	118.28	109.40
2	F	19	ASP	CB-CA-C	-5.45	100.20	110.01
1	C	247	ARG	NE-CZ-NH1	5.40	126.90	121.50
1	K	247	ARG	NE-CZ-NH1	5.34	126.84	121.50
2	L	6	ILE	N-CA-CB	-5.32	102.72	111.45
2	B	19	ASP	CB-CA-C	-5.31	100.44	110.01
2	F	67	ASP	CA-CB-CG	-5.31	107.29	112.60
1	K	247	ARG	NE-CZ-NH2	-5.30	114.43	119.20
2	J	67	ASP	CB-CG-OD1	-5.25	106.33	118.40
2	B	67	ASP	CB-CG-OD1	-5.25	106.33	118.40
2	H	19	ASP	CB-CA-C	-5.24	100.59	110.01
1	I	247	ARG	NE-CZ-NH1	5.20	126.70	121.50
1	A	65	GLN	CB-CA-C	-5.16	99.43	110.32
1	A	247	ARG	NE-CZ-NH2	-5.10	114.61	119.20
1	G	217	LEU	N-CA-C	5.09	117.79	109.59
1	I	65	GLN	CB-CA-C	-5.07	99.62	110.32
1	E	247	ARG	NE-CZ-NH2	-5.05	114.65	119.20
2	H	152	ILE	N-CA-C	-5.03	105.94	110.82
1	I	121	ARG	N-CA-C	-5.03	103.08	110.52
1	I	229	ASN	N-CA-C	5.02	116.82	109.84
1	G	65	GLN	CB-CA-C	-5.02	98.94	110.18

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	2412	0	2375	19	0
1	C	2412	0	2375	28	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2412	0	2374	20	0
1	G	2412	0	2375	18	1
1	I	2412	0	2374	13	1
1	K	2412	0	2375	15	0
2	B	1360	0	1262	15	0
2	D	1360	0	1262	17	0
2	F	1360	0	1262	12	0
2	H	1375	0	1274	12	0
2	J	1375	0	1274	15	0
2	L	1375	0	1274	16	0
3	M	28	0	25	0	0
3	Q	28	0	25	1	0
4	N	39	0	34	0	0
4	P	39	0	34	0	0
4	R	39	0	34	1	0
4	S	39	0	34	1	0
5	O	49	0	43	3	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
6	E	1	0	0	0	0
6	G	1	0	0	0	0
6	I	1	0	0	0	0
6	K	1	0	0	0	0
7	B	14	0	13	0	0
7	D	14	0	13	0	0
7	F	14	0	13	0	0
7	H	14	0	13	0	0
7	J	14	0	13	1	0
7	L	14	0	13	0	1
8	A	32	0	0	1	0
8	B	12	0	0	1	0
8	C	32	0	0	5	0
8	D	12	0	0	4	0
8	E	24	0	0	1	0
8	F	15	0	0	0	0
8	G	24	0	0	3	1
8	H	15	0	0	0	0
8	I	16	0	0	0	0
8	J	14	0	0	0	0
8	K	18	0	0	0	0
8	L	11	0	0	3	0
All	All	23253	0	22163	176	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (176) 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:121:ARG:NH1	1:C:145:SER:O	1.77	1.18
1:C:121:ARG:HH11	1:C:121:ARG:HG3	1.15	1.12
1:A:53:GLN:OE1	8:A:501:HOH:O	1.89	0.89
1:A:222:ASP:OD1	1:C:201:GLN:NE2	2.07	0.87
1:A:222:ASP:CG	1:C:201:GLN:NE2	2.34	0.85
1:G:53:GLN:OE1	8:G:501:HOH:O	1.96	0.83
2:F:6:ILE:HD11	2:F:25:ARG:HG2	1.62	0.81
2:L:6:ILE:HD11	2:L:25:ARG:HG2	1.61	0.81
2:B:6:ILE:HD11	2:B:25:ARG:HG2	1.61	0.80
2:D:6:ILE:HD11	2:D:25:ARG:HG2	1.63	0.80
2:J:6:ILE:HD11	2:J:25:ARG:HG2	1.61	0.80
1:K:139:GLU:OE1	1:K:247:ARG:HD3	1.83	0.79
1:A:139:GLU:OE1	1:A:247:ARG:HD3	1.83	0.78
1:G:139:GLU:OE1	1:G:247:ARG:HD3	1.83	0.78
1:I:139:GLU:OE1	1:I:247:ARG:HD3	1.84	0.78
2:H:6:ILE:HD11	2:H:25:ARG:HG2	1.64	0.77
1:C:139:GLU:OE1	1:C:247:ARG:HD3	1.85	0.75
1:E:139:GLU:OE1	1:E:247:ARG:HD3	1.87	0.75
1:C:201:GLN:HB2	8:C:520:HOH:O	1.90	0.71
1:C:121:ARG:HH11	1:C:121:ARG:CG	2.00	0.70
2:L:47:GLN:OE1	2:L:110:LEU:HD11	1.92	0.69
2:D:47:GLN:OE1	2:D:110:LEU:HD11	1.93	0.69
2:F:47:GLN:OE1	2:F:110:LEU:HD11	1.92	0.69
2:B:47:GLN:OE1	2:B:110:LEU:HD11	1.93	0.69
2:J:47:GLN:OE1	2:J:110:LEU:HD11	1.93	0.67
2:D:75:LYS:HD2	1:E:101:ILE:HD11	1.76	0.67
1:A:203:SER:HB2	1:E:207:SER:HB3	1.76	0.67
2:H:47:GLN:OE1	2:H:110:LEU:HD11	1.95	0.66
1:C:224:HIS:HD2	8:C:529:HOH:O	1.80	0.65
2:F:56:ILE:CG2	2:F:56:ILE:O	2.46	0.64
2:J:66:ILE:H	2:J:66:ILE:HD13	1.64	0.63
2:B:56:ILE:CG2	2:B:56:ILE:O	2.47	0.62
2:D:56:ILE:O	2:D:56:ILE:CG2	2.47	0.62
1:A:139:GLU:OE1	1:A:247:ARG:CD	2.48	0.62
1:I:139:GLU:OE1	1:I:247:ARG:CD	2.48	0.62
1:A:121:ARG:HD2	1:A:146:ASN:O	2.00	0.62
5:O:4:FUC:H63	5:O:4:FUC:H2	1.81	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:139:GLU:OE1	1:K:247:ARG:CD	2.48	0.61
1:E:121:ARG:HD2	1:E:146:ASN:O	2.00	0.61
1:G:121:ARG:HD2	1:G:146:ASN:O	2.00	0.61
2:J:56:ILE:CG2	2:J:56:ILE:O	2.48	0.61
2:H:56:ILE:O	2:H:56:ILE:CG2	2.48	0.61
2:L:56:ILE:O	2:L:56:ILE:CG2	2.47	0.61
1:C:121:ARG:NH1	1:C:121:ARG:HG3	1.95	0.60
2:D:26:HIS:HD2	8:D:607:HOH:O	1.84	0.60
1:K:121:ARG:HD3	1:K:145:SER:O	2.02	0.60
1:C:139:GLU:OE1	1:C:247:ARG:CD	2.49	0.60
1:G:121:ARG:HD3	1:G:145:SER:O	2.01	0.60
1:K:291:ARG:HH21	2:L:67:ASP:HB3	1.66	0.60
1:I:121:ARG:HD2	1:I:146:ASN:O	2.02	0.60
1:K:121:ARG:HD2	1:K:146:ASN:O	2.01	0.59
1:G:139:GLU:OE1	1:G:247:ARG:CD	2.49	0.59
1:G:291:ARG:HH21	2:H:67:ASP:HB3	1.66	0.59
1:E:139:GLU:OE1	1:E:247:ARG:CD	2.51	0.59
2:L:67:ASP:HB2	8:L:611:HOH:O	2.03	0.59
2:D:55:LEU:HD22	2:D:99:LEU:HD21	1.85	0.58
1:A:121:ARG:HD3	1:A:145:SER:O	2.03	0.58
2:B:55:LEU:HD22	2:B:99:LEU:HD21	1.85	0.58
2:L:66:ILE:HD13	2:L:66:ILE:H	1.69	0.57
2:B:66:ILE:H	2:B:66:ILE:HD13	1.68	0.57
1:A:222:ASP:OD2	1:C:201:GLN:NE2	2.38	0.57
1:E:121:ARG:HD3	1:E:145:SER:O	2.04	0.57
2:L:55:LEU:HD22	2:L:99:LEU:HD21	1.87	0.57
1:C:211:ARG:HG3	1:C:218:SER:O	2.05	0.56
2:F:66:ILE:H	2:F:66:ILE:HD13	1.71	0.56
2:F:55:LEU:HD22	2:F:99:LEU:HD21	1.87	0.56
1:K:211:ARG:HB2	1:K:212:PRO:CD	2.36	0.56
1:I:4:CYS:SG	2:J:6:ILE:HG23	2.46	0.56
1:I:211:ARG:HB2	1:I:212:PRO:CD	2.36	0.56
2:H:55:LEU:HD22	2:H:99:LEU:HD21	1.87	0.56
2:D:66:ILE:HD13	2:D:66:ILE:H	1.71	0.55
1:I:121:ARG:HD3	1:I:145:SER:O	2.07	0.55
1:E:226:LEU:HD12	1:E:226:LEU:C	2.32	0.54
2:H:66:ILE:HD13	2:H:66:ILE:H	1.73	0.54
2:J:55:LEU:HD22	2:J:99:LEU:HD21	1.89	0.54
1:G:222:ASP:CB	8:G:510:HOH:O	2.56	0.54
1:G:4:CYS:SG	2:H:6:ILE:HG23	2.48	0.53
1:C:291:ARG:HH21	2:D:67:ASP:HB3	1.73	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:291:ARG:HH21	2:J:67:ASP:HB3	1.72	0.53
1:C:4:CYS:SG	2:D:6:ILE:HG23	2.49	0.53
1:G:222:ASP:HB2	8:G:510:HOH:O	2.07	0.53
1:A:291:ARG:HH21	2:B:67:ASP:HB3	1.73	0.53
1:C:207:SER:CB	1:E:203:SER:OG	2.57	0.53
1:E:211:ARG:HB2	1:E:212:PRO:CD	2.39	0.53
1:E:14:THR:HG21	5:O:1:NAG:H82	1.91	0.52
1:G:30:THR:HB	3:Q:1:NAG:H62	1.90	0.52
2:B:75:LYS:HD2	1:C:101:ILE:HD11	1.91	0.51
2:F:56:ILE:O	2:F:56:ILE:HG23	2.10	0.51
1:C:32:THR:HG22	1:C:305:LEU:HB2	1.92	0.51
2:L:47:GLN:CD	2:L:110:LEU:HD11	2.36	0.50
1:K:32:THR:HG22	1:K:305:LEU:HB2	1.94	0.50
1:K:4:CYS:SG	2:L:6:ILE:HG23	2.52	0.50
1:K:226:LEU:C	1:K:226:LEU:HD12	2.37	0.50
1:A:222:ASP:CG	1:C:201:GLN:HE21	2.19	0.50
2:D:66:ILE:HD13	8:D:608:HOH:O	2.12	0.50
2:D:56:ILE:O	2:D:56:ILE:HG23	2.12	0.49
1:A:162:THR:O	1:A:162:THR:HG22	2.12	0.49
1:G:32:THR:HG22	1:G:305:LEU:HB2	1.94	0.49
2:L:66:ILE:HD13	8:L:611:HOH:O	2.11	0.49
1:A:203:SER:HB2	1:E:207:SER:CB	2.41	0.49
2:D:67:ASP:HB2	8:D:608:HOH:O	2.12	0.49
2:J:56:ILE:O	2:J:56:ILE:HG23	2.12	0.49
1:G:211:ARG:HB2	1:G:212:PRO:CD	2.43	0.49
1:G:162:THR:HG22	1:G:162:THR:O	2.13	0.48
1:I:162:THR:O	1:I:162:THR:HG22	2.13	0.48
1:I:32:THR:HG22	1:I:305:LEU:HB2	1.94	0.48
1:G:226:LEU:C	1:G:226:LEU:HD12	2.38	0.48
1:G:293:VAL:HG11	2:H:65:LEU:HD13	1.95	0.48
1:I:211:ARG:HB2	1:I:212:PRO:HD2	1.95	0.48
1:A:32:THR:HG22	1:A:305:LEU:HB2	1.96	0.48
1:E:32:THR:HG22	1:E:305:LEU:HB2	1.95	0.48
2:F:47:GLN:CD	2:F:110:LEU:HD11	2.38	0.48
1:E:162:THR:HG22	1:E:162:THR:O	2.14	0.48
2:B:56:ILE:O	2:B:56:ILE:HG23	2.13	0.47
2:D:47:GLN:CD	2:D:110:LEU:HD11	2.38	0.47
1:K:162:THR:HG22	1:K:162:THR:O	2.13	0.47
2:H:56:ILE:O	2:H:56:ILE:HG23	2.14	0.47
2:J:47:GLN:CD	2:J:110:LEU:HD11	2.40	0.47
1:C:162:THR:HG22	1:C:162:THR:O	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:4:CYS:SG	2:F:6:ILE:HG23	2.55	0.47
1:K:211:ARG:HB2	1:K:212:PRO:HD2	1.96	0.47
2:L:56:ILE:O	2:L:56:ILE:HG23	2.13	0.47
2:B:47:GLN:CD	2:B:110:LEU:HD11	2.39	0.47
1:E:291:ARG:HH21	2:F:67:ASP:HB3	1.80	0.47
1:C:226:LEU:C	1:C:226:LEU:HD12	2.40	0.47
2:D:26:HIS:HE1	8:D:609:HOH:O	1.96	0.47
1:A:226:LEU:HD12	1:A:226:LEU:C	2.39	0.46
1:C:201:GLN:CB	8:C:520:HOH:O	2.57	0.46
2:J:66:ILE:H	2:J:66:ILE:CD1	2.29	0.46
4:R:2:NAG:O3	4:R:3:BMA:H2	2.15	0.46
2:L:47:GLN:OE1	2:L:110:LEU:CD1	2.62	0.46
2:B:26:HIS:HE1	8:B:612:HOH:O	1.99	0.46
2:B:47:GLN:OE1	2:B:110:LEU:CD1	2.62	0.46
1:E:211:ARG:HB2	1:E:212:PRO:HD2	1.96	0.46
1:I:226:LEU:HD12	1:I:226:LEU:C	2.41	0.45
1:K:30:THR:HB	4:S:1:NAG:H62	1.98	0.45
1:E:293:VAL:HG11	2:F:65:LEU:HD13	1.98	0.45
2:F:47:GLN:OE1	2:F:110:LEU:CD1	2.63	0.45
2:H:47:GLN:OE1	2:H:110:LEU:CD1	2.64	0.45
2:D:47:GLN:OE1	2:D:110:LEU:CD1	2.62	0.45
1:A:4:CYS:SG	2:B:6:ILE:HG23	2.58	0.45
2:H:30:GLN:HE22	2:H:145:ASP:HB2	1.82	0.45
2:J:66:ILE:CD1	2:J:66:ILE:N	2.80	0.44
1:A:194:THR:OG1	1:A:237:SER:HB3	2.18	0.44
1:A:293:VAL:HG11	2:B:65:LEU:HD13	1.98	0.44
2:H:47:GLN:CD	2:H:110:LEU:HD11	2.42	0.44
2:J:47:GLN:OE1	2:J:110:LEU:CD1	2.62	0.44
2:B:66:ILE:H	2:B:66:ILE:CD1	2.32	0.43
2:D:30:GLN:HE22	2:D:145:ASP:HB2	1.83	0.43
2:J:30:GLN:HE22	2:J:145:ASP:HB2	1.82	0.43
1:A:163:ARG:HD3	1:A:250:PHE:CZ	2.54	0.43
1:C:210:ALA:C	1:C:211:ARG:HG2	2.41	0.43
1:G:194:THR:OG1	1:G:237:SER:HB3	2.18	0.43
2:L:30:GLN:HE22	2:L:145:ASP:HB2	1.84	0.43
1:E:8:HIS:HE1	8:E:509:HOH:O	2.02	0.43
2:J:6:ILE:CD1	2:J:25:ARG:HG2	2.41	0.42
2:J:75:LYS:HG3	7:J:500:NAG:H81	2.00	0.42
2:L:3:PHE:N	8:L:610:HOH:O	2.51	0.42
2:L:66:ILE:H	2:L:66:ILE:CD1	2.32	0.42
1:C:163:ARG:HD3	1:C:250:PHE:CZ	2.55	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:194:THR:OG1	1:I:237:SER:HB3	2.20	0.42
1:K:194:THR:OG1	1:K:237:SER:HB3	2.19	0.42
1:K:293:VAL:HG11	2:L:65:LEU:HD13	2.02	0.42
1:C:201:GLN:HA	8:C:520:HOH:O	2.20	0.41
1:C:293:VAL:HG11	2:D:65:LEU:HD13	2.01	0.41
1:E:28:ASN:OD1	5:O:1:NAG:H83	2.20	0.41
1:G:163:ARG:HD3	1:G:250:PHE:CZ	2.55	0.41
1:I:301:LYS:HE2	1:I:301:LYS:HB2	1.88	0.41
2:B:30:GLN:HE22	2:B:145:ASP:HB2	1.86	0.41
1:C:40:ARG:NH1	8:C:502:HOH:O	2.52	0.41
1:C:194:THR:OG1	1:C:237:SER:HB3	2.21	0.41
1:E:163:ARG:HD3	1:E:250:PHE:CZ	2.55	0.41
1:K:163:ARG:HD3	1:K:250:PHE:CZ	2.56	0.41
1:C:301:LYS:HE2	1:C:301:LYS:HB2	1.86	0.41
2:F:30:GLN:HE22	2:F:145:ASP:HB2	1.85	0.40
1:G:301:LYS:HE2	1:G:301:LYS:HB2	1.85	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:222:ASP:OD2	1:I:201:GLN:NE2[3_545]	1.66	0.54
7:L:500:NAG:O7	8:G:508:HOH:O[3_555]	2.07	0.13

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	314/325 (97%)	307 (98%)	7 (2%)	0	100	100
1	C	314/325 (97%)	306 (98%)	8 (2%)	0	100	100
1	E	314/325 (97%)	305 (97%)	9 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	314/325 (97%)	305 (97%)	9 (3%)	0	100	100
1	I	314/325 (97%)	305 (97%)	9 (3%)	0	100	100
1	K	314/325 (97%)	305 (97%)	9 (3%)	0	100	100
2	B	165/181 (91%)	160 (97%)	4 (2%)	1 (1%)	21	18
2	D	165/181 (91%)	161 (98%)	3 (2%)	1 (1%)	21	18
2	F	165/181 (91%)	160 (97%)	4 (2%)	1 (1%)	21	18
2	H	167/181 (92%)	163 (98%)	3 (2%)	1 (1%)	21	18
2	J	167/181 (92%)	163 (98%)	3 (2%)	1 (1%)	21	18
2	L	167/181 (92%)	162 (97%)	4 (2%)	1 (1%)	21	18
All	All	2880/3036 (95%)	2802 (97%)	72 (2%)	6 (0%)	43	44

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	56	ILE
2	J	56	ILE
2	L	56	ILE
2	B	56	ILE
2	D	56	ILE
2	F	56	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	265/271 (98%)	249 (94%)	16 (6%)	17	15
1	C	265/271 (98%)	249 (94%)	16 (6%)	17	15
1	E	265/271 (98%)	248 (94%)	17 (6%)	16	13
1	G	265/271 (98%)	248 (94%)	17 (6%)	16	13
1	I	265/271 (98%)	247 (93%)	18 (7%)	14	11
1	K	265/271 (98%)	249 (94%)	16 (6%)	17	15

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	144/155 (93%)	132 (92%)	12 (8%)	10	7
2	D	144/155 (93%)	132 (92%)	12 (8%)	10	7
2	F	144/155 (93%)	133 (92%)	11 (8%)	12	9
2	H	145/155 (94%)	133 (92%)	12 (8%)	10	7
2	J	145/155 (94%)	133 (92%)	12 (8%)	10	7
2	L	145/155 (94%)	133 (92%)	12 (8%)	10	7
All	All	2457/2556 (96%)	2286 (93%)	171 (7%)	14	11

All (171) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	HIS
1	A	19	LEU
1	A	32	THR
1	A	65	GLN
1	A	68	GLN
1	A	73	SER
1	A	86	VAL
1	A	122	THR
1	A	130	ARG
1	A	144	LEU
1	A	165	SER
1	A	203	SER
1	A	227	MET
1	A	256	MET
1	A	268	CYS
1	A	312	LYS
2	B	6	ILE
2	B	10	ILE
2	B	52	LEU
2	B	56	ILE
2	B	65	LEU
2	B	66	ILE
2	B	67	ASP
2	B	75	LYS
2	B	88	ILE
2	B	117	LYS
2	B	128	GLU
2	B	171	ILE
1	C	8	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	19	LEU
1	C	32	THR
1	C	65	GLN
1	C	68	GLN
1	C	73	SER
1	C	86	VAL
1	C	94	ASN
1	C	121	ARG
1	C	122	THR
1	C	130	ARG
1	C	144	LEU
1	C	165	SER
1	C	211	ARG
1	C	227	MET
1	C	256	MET
2	D	6	ILE
2	D	10	ILE
2	D	52	LEU
2	D	65	LEU
2	D	66	ILE
2	D	67	ASP
2	D	75	LYS
2	D	88	ILE
2	D	117	LYS
2	D	128	GLU
2	D	147	ASP
2	D	171	ILE
1	E	8	HIS
1	E	19	LEU
1	E	32	THR
1	E	65	GLN
1	E	68	GLN
1	E	73	SER
1	E	86	VAL
1	E	94	ASN
1	E	122	THR
1	E	130	ARG
1	E	144	LEU
1	E	165	SER
1	E	203	SER
1	E	227	MET
1	E	256	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	268	CYS
1	E	312	LYS
2	F	6	ILE
2	F	10	ILE
2	F	52	LEU
2	F	65	LEU
2	F	66	ILE
2	F	67	ASP
2	F	75	LYS
2	F	88	ILE
2	F	117	LYS
2	F	128	GLU
2	F	171	ILE
1	G	8	HIS
1	G	19	LEU
1	G	32	THR
1	G	65	GLN
1	G	68	GLN
1	G	73	SER
1	G	86	VAL
1	G	94	ASN
1	G	122	THR
1	G	130	ARG
1	G	144	LEU
1	G	165	SER
1	G	203	SER
1	G	211	ARG
1	G	227	MET
1	G	256	MET
1	G	312	LYS
2	H	6	ILE
2	H	10	ILE
2	H	52	LEU
2	H	65	LEU
2	H	66	ILE
2	H	67	ASP
2	H	75	LYS
2	H	88	ILE
2	H	117	LYS
2	H	120	GLU
2	H	128	GLU
2	H	171	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	I	8	HIS
1	I	19	LEU
1	I	30	THR
1	I	32	THR
1	I	65	GLN
1	I	68	GLN
1	I	73	SER
1	I	86	VAL
1	I	94	ASN
1	I	122	THR
1	I	130	ARG
1	I	144	LEU
1	I	165	SER
1	I	203	SER
1	I	227	MET
1	I	256	MET
1	I	268	CYS
1	I	312	LYS
2	J	6	ILE
2	J	10	ILE
2	J	52	LEU
2	J	56	ILE
2	J	65	LEU
2	J	66	ILE
2	J	67	ASP
2	J	75	LYS
2	J	88	ILE
2	J	117	LYS
2	J	128	GLU
2	J	171	ILE
1	K	8	HIS
1	K	19	LEU
1	K	32	THR
1	K	65	GLN
1	K	68	GLN
1	K	73	SER
1	K	86	VAL
1	K	108	ILE
1	K	122	THR
1	K	130	ARG
1	K	144	LEU
1	K	165	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	K	203	SER
1	K	227	MET
1	K	256	MET
1	K	312	LYS
2	L	6	ILE
2	L	10	ILE
2	L	52	LEU
2	L	56	ILE
2	L	65	LEU
2	L	66	ILE
2	L	67	ASP
2	L	75	LYS
2	L	88	ILE
2	L	117	LYS
2	L	128	GLU
2	L	171	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	HIS
1	A	53	GLN
1	A	182	GLN
1	A	202	GLN
2	B	12	ASN
2	B	26	HIS
2	B	30	GLN
1	C	8	HIS
1	C	94	ASN
1	C	182	GLN
1	C	201	GLN
1	C	224	HIS
1	C	287	ASN
2	D	12	ASN
2	D	26	HIS
2	D	30	GLN
1	E	8	HIS
1	E	94	ASN
1	E	154	GLN
1	E	182	GLN
1	E	201	GLN
2	F	30	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	F	42	GLN
1	G	94	ASN
1	G	182	GLN
1	G	224	HIS
2	H	12	ASN
2	H	30	GLN
1	I	8	HIS
1	I	94	ASN
1	I	182	GLN
2	J	12	ASN
2	J	30	GLN
2	J	42	GLN
1	K	8	HIS
1	K	94	ASN
1	K	182	GLN
2	L	12	ASN
2	L	30	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

20 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	$\# Z > 2$
3	NAG	M	1	3,1	14,14,15	0.82	0	17,19,21	1.80	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	M	2	3	14,14,15	0.50	0	17,19,21	1.45	2 (11%)
4	NAG	N	1	1,4	14,14,15	0.85	0	17,19,21	2.36	5 (29%)
4	NAG	N	2	4	14,14,15	0.66	0	17,19,21	1.42	4 (23%)
4	BMA	N	3	4	11,11,12	0.83	0	15,15,17	1.67	3 (20%)
5	NAG	O	1	5,1	14,14,15	2.19	5 (35%)	17,19,21	3.70	9 (52%)
5	NAG	O	2	5	14,14,15	1.03	1 (7%)	17,19,21	1.44	4 (23%)
5	BMA	O	3	5	11,11,12	0.75	0	15,15,17	1.81	4 (26%)
5	FUC	O	4	5	10,10,11	0.85	0	14,14,16	1.47	3 (21%)
4	NAG	P	1	1,4	14,14,15	1.20	1 (7%)	17,19,21	1.10	1 (5%)
4	NAG	P	2	4	14,14,15	0.68	0	17,19,21	1.32	2 (11%)
4	BMA	P	3	4	11,11,12	0.76	0	15,15,17	2.60	3 (20%)
3	NAG	Q	1	3,1	14,14,15	0.61	0	17,19,21	1.84	4 (23%)
3	NAG	Q	2	3	14,14,15	0.62	0	17,19,21	1.48	2 (11%)
4	NAG	R	1	1,4	14,14,15	0.66	0	17,19,21	1.81	2 (11%)
4	NAG	R	2	4	14,14,15	0.69	0	17,19,21	1.10	1 (5%)
4	BMA	R	3	4	11,11,12	0.67	0	15,15,17	2.32	3 (20%)
4	NAG	S	1	1,4	14,14,15	0.99	0	17,19,21	1.63	5 (29%)
4	NAG	S	2	4	14,14,15	0.71	0	17,19,21	1.29	2 (11%)
4	BMA	S	3	4	11,11,12	0.63	0	15,15,17	0.89	1 (6%)

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
3	NAG	M	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	M	2	3	-	2/6/23/26	0/1/1/1
4	NAG	N	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	N	2	4	-	2/6/23/26	0/1/1/1
4	BMA	N	3	4	-	2/2/19/22	0/1/1/1
5	NAG	O	1	5,1	-	1/6/23/26	0/1/1/1
5	NAG	O	2	5	-	0/6/23/26	0/1/1/1
5	BMA	O	3	5	-	2/2/19/22	0/1/1/1
5	FUC	O	4	5	-	-	0/1/1/1
4	NAG	P	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	P	2	4	-	0/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	BMA	P	3	4	-	0/2/19/22	0/1/1/1
3	NAG	Q	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	Q	2	3	-	1/6/23/26	0/1/1/1
4	NAG	R	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	R	2	4	-	2/6/23/26	0/1/1/1
4	BMA	R	3	4	-	1/2/19/22	0/1/1/1
4	NAG	S	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	S	2	4	-	1/6/23/26	0/1/1/1
4	BMA	S	3	4	-	2/2/19/22	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	O	1	NAG	C1-C2	6.20	1.60	1.52
4	P	1	NAG	C1-C2	3.01	1.56	1.52
5	O	2	NAG	C1-C2	2.97	1.56	1.52
5	O	1	NAG	C3-C2	2.48	1.57	1.52
5	O	1	NAG	O5-C1	2.30	1.47	1.43
5	O	1	NAG	O5-C5	2.14	1.47	1.43
5	O	1	NAG	C2-N2	2.01	1.49	1.46

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	O	1	NAG	C1-O5-C5	12.46	128.88	112.19
4	P	3	BMA	C1-O5-C5	8.39	123.43	112.19
4	N	1	NAG	C1-O5-C5	7.38	122.08	112.19
4	R	3	BMA	C1-O5-C5	7.01	121.58	112.19
4	R	1	NAG	C1-C2-N2	-6.08	100.85	110.43
3	Q	1	NAG	C1-C2-N2	5.18	118.60	110.43
5	O	3	BMA	C1-O5-C5	4.34	118.00	112.19
4	N	3	BMA	C1-O5-C5	4.23	117.85	112.19
5	O	3	BMA	C1-C2-C3	3.73	115.07	109.64
3	M	1	NAG	C2-N2-C7	-3.66	117.99	122.90
4	N	1	NAG	O5-C5-C4	3.56	119.48	110.83
4	S	1	NAG	O7-C7-C8	-3.54	115.74	122.05
3	M	2	NAG	O5-C5-C6	3.47	114.42	107.66
3	Q	2	NAG	C4-C3-C2	3.47	116.10	111.02
5	O	1	NAG	O5-C1-C2	-3.40	106.03	111.29
4	R	3	BMA	O5-C5-C4	3.40	119.09	110.83
4	S	1	NAG	C8-C7-N2	3.28	121.56	116.12
4	S	2	NAG	O7-C7-C8	-3.25	116.27	122.05

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	2	NAG	C4-C3-C2	3.19	115.69	111.02
5	O	1	NAG	O7-C7-C8	-3.18	116.40	122.05
4	R	3	BMA	C3-C4-C5	3.14	115.93	110.23
4	P	1	NAG	C1-C2-N2	3.11	115.33	110.43
5	O	1	NAG	O5-C5-C4	2.89	117.87	110.83
3	M	1	NAG	C1-O5-C5	2.87	116.03	112.19
5	O	1	NAG	C2-N2-C7	2.87	126.74	122.90
5	O	4	FUC	C1-O5-C5	2.80	119.57	112.97
5	O	1	NAG	C1-C2-N2	2.78	114.82	110.43
5	O	2	NAG	C3-C4-C5	-2.77	105.21	110.23
5	O	1	NAG	O3-C3-C2	2.75	115.11	109.40
4	P	3	BMA	C3-C4-C5	2.72	115.16	110.23
4	P	2	NAG	O4-C4-C5	2.70	115.96	109.32
5	O	1	NAG	C3-C4-C5	-2.67	105.38	110.23
4	N	3	BMA	C1-C2-C3	2.67	113.54	109.64
4	N	2	NAG	O7-C7-C8	-2.66	117.32	122.05
4	P	3	BMA	O2-C2-C3	2.52	115.37	110.15
5	O	2	NAG	C4-C3-C2	2.50	114.68	111.02
4	N	2	NAG	O5-C5-C6	2.49	112.51	107.66
5	O	4	FUC	O4-C4-C3	2.44	116.13	110.38
4	R	1	NAG	C4-C3-C2	2.44	114.59	111.02
4	N	1	NAG	C4-C3-C2	-2.41	107.48	111.02
3	Q	1	NAG	C1-O5-C5	2.39	115.39	112.19
4	S	3	BMA	O5-C5-C6	2.37	112.28	107.66
3	Q	1	NAG	O7-C7-C8	-2.36	117.85	122.05
4	S	1	NAG	C3-C4-C5	2.35	114.49	110.23
4	P	2	NAG	O5-C5-C4	-2.35	105.11	110.83
3	M	1	NAG	C8-C7-N2	2.33	119.99	116.12
4	N	1	NAG	O5-C1-C2	2.28	114.82	111.29
4	N	2	NAG	C3-C4-C5	-2.28	106.10	110.23
3	Q	1	NAG	O4-C4-C5	2.25	114.87	109.32
5	O	2	NAG	O5-C1-C2	-2.24	107.83	111.29
4	S	1	NAG	O4-C4-C3	-2.22	105.15	110.38
4	N	2	NAG	O4-C4-C5	2.21	114.77	109.32
5	O	2	NAG	O5-C5-C6	2.17	111.88	107.66
4	S	1	NAG	C2-N2-C7	-2.15	120.02	122.90
5	O	1	NAG	O4-C4-C3	2.12	115.37	110.38
3	M	1	NAG	O3-C3-C4	2.11	115.36	110.38
3	Q	2	NAG	C8-C7-N2	2.11	119.61	116.12
4	N	3	BMA	C6-C5-C4	2.09	118.16	113.02
4	N	1	NAG	O6-C6-C5	-2.08	104.27	111.33
4	S	2	NAG	C8-C7-N2	2.06	119.54	116.12

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	O	3	BMA	O5-C5-C6	2.05	111.65	107.66
4	R	2	NAG	C4-C3-C2	2.04	114.01	111.02
5	O	3	BMA	O2-C2-C1	2.03	113.88	109.22
5	O	4	FUC	O5-C5-C6	2.03	111.81	107.40
3	M	1	NAG	O5-C5-C6	2.02	111.60	107.66

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	N	2	NAG	O5-C5-C6-O6
4	S	3	BMA	O5-C5-C6-O6
5	O	3	BMA	O5-C5-C6-O6
4	N	3	BMA	C4-C5-C6-O6
4	N	2	NAG	C4-C5-C6-O6
3	M	2	NAG	O5-C5-C6-O6
4	R	2	NAG	O5-C5-C6-O6
4	N	3	BMA	O5-C5-C6-O6
4	N	1	NAG	C4-C5-C6-O6
4	R	2	NAG	C4-C5-C6-O6
4	N	1	NAG	O5-C5-C6-O6
5	O	3	BMA	C4-C5-C6-O6
3	M	2	NAG	C4-C5-C6-O6
4	S	3	BMA	C4-C5-C6-O6
4	R	3	BMA	C4-C5-C6-O6
5	O	1	NAG	C3-C2-N2-C7
4	S	2	NAG	C4-C5-C6-O6
3	Q	2	NAG	C1-C2-N2-C7

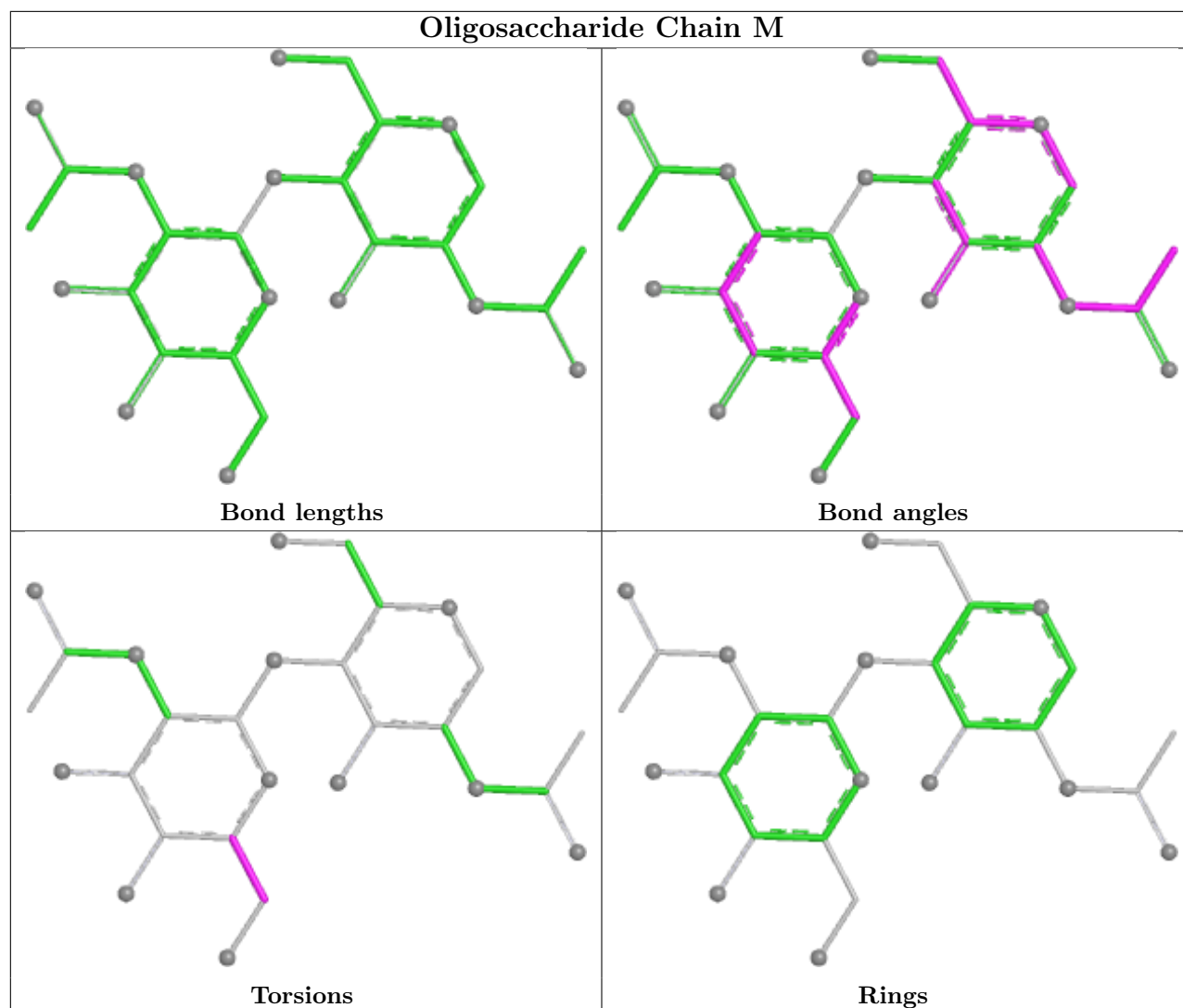
There are no ring outliers.

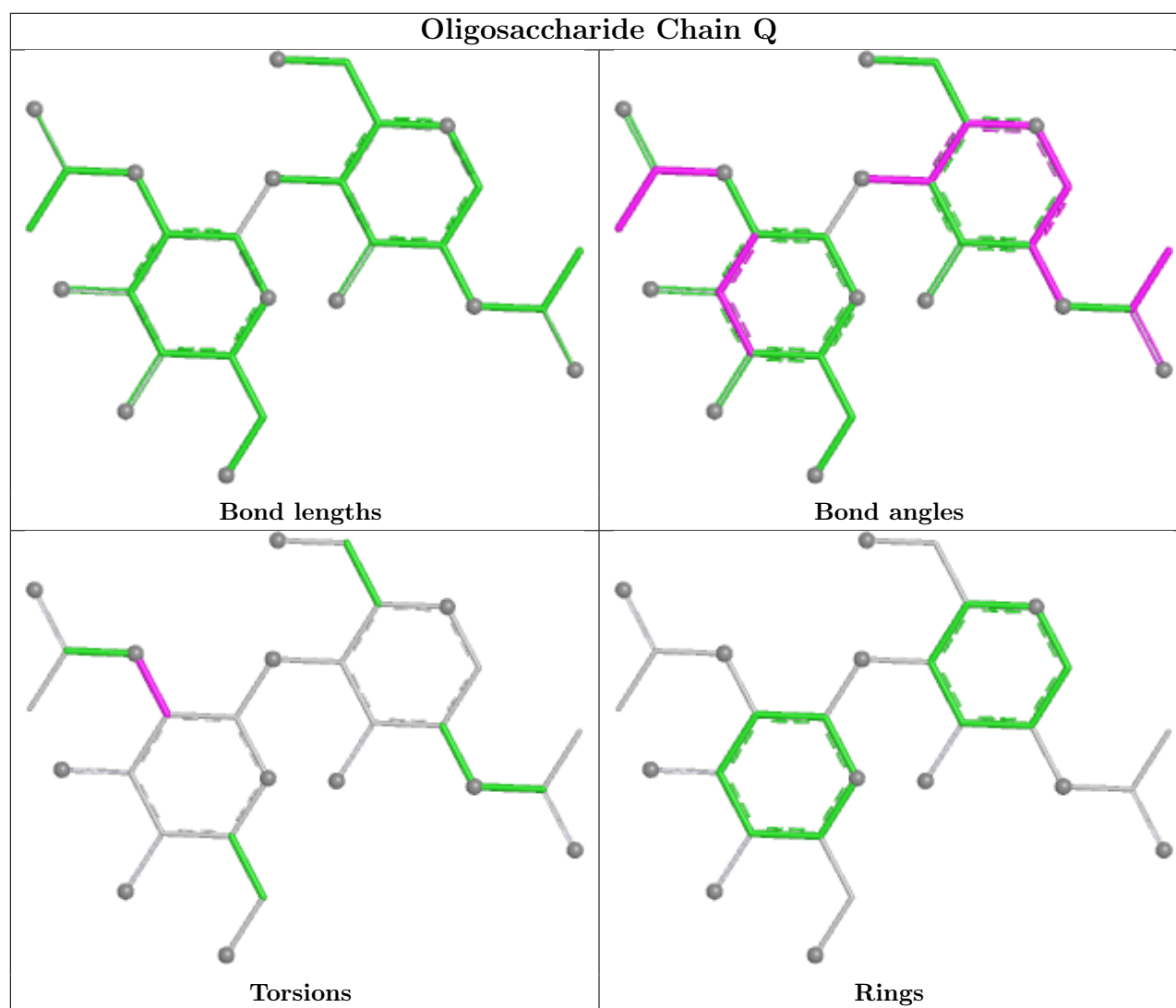
6 monomers are involved in 6 short contacts:

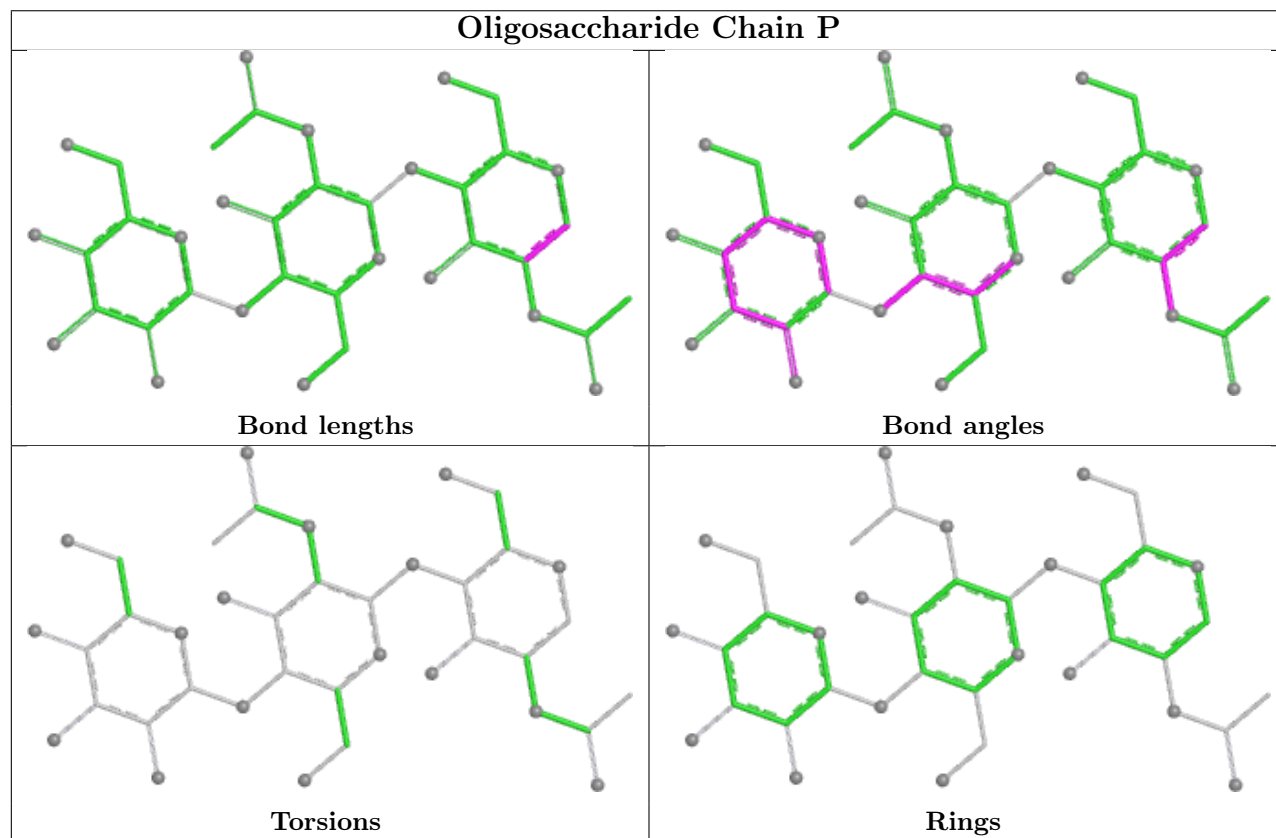
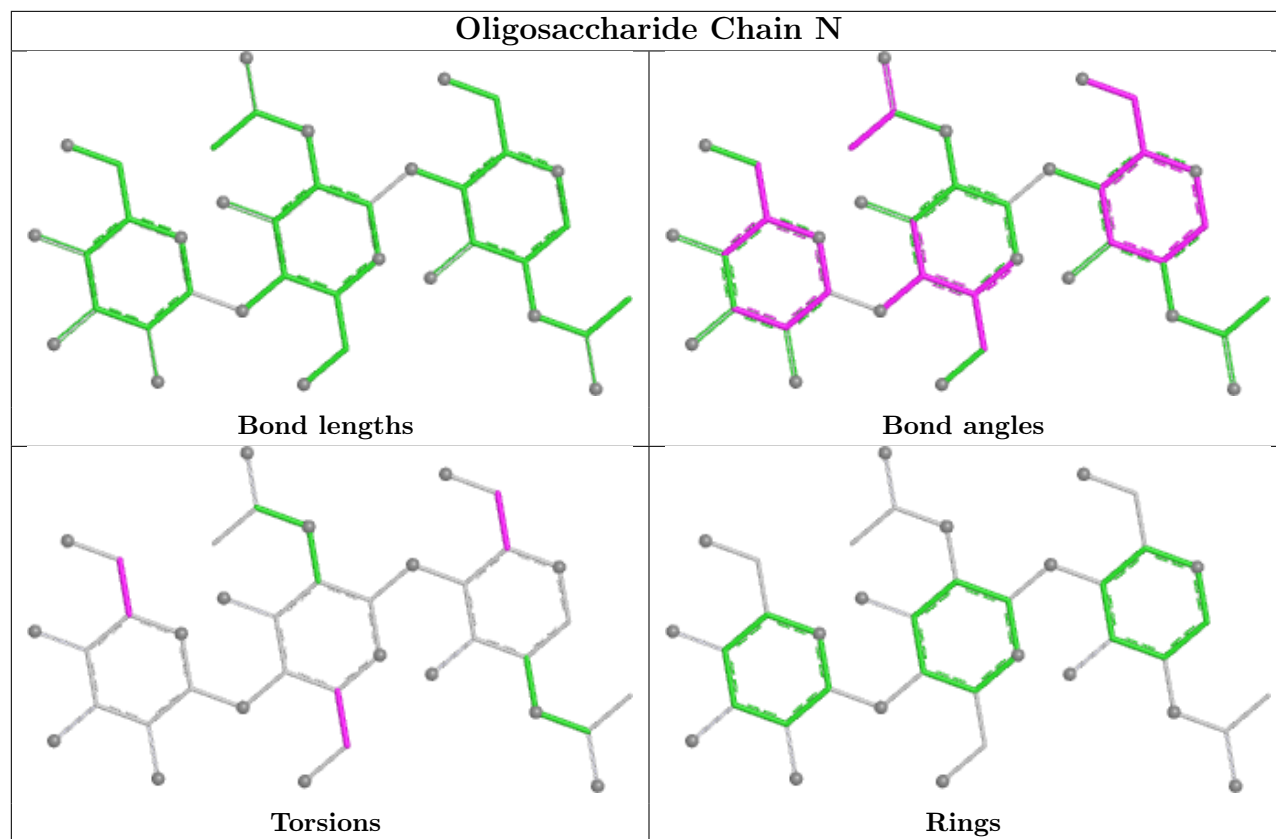
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	O	4	FUC	1	0
3	Q	1	NAG	1	0
4	S	1	NAG	1	0
4	R	3	BMA	1	0
4	R	2	NAG	1	0
5	O	1	NAG	2	0

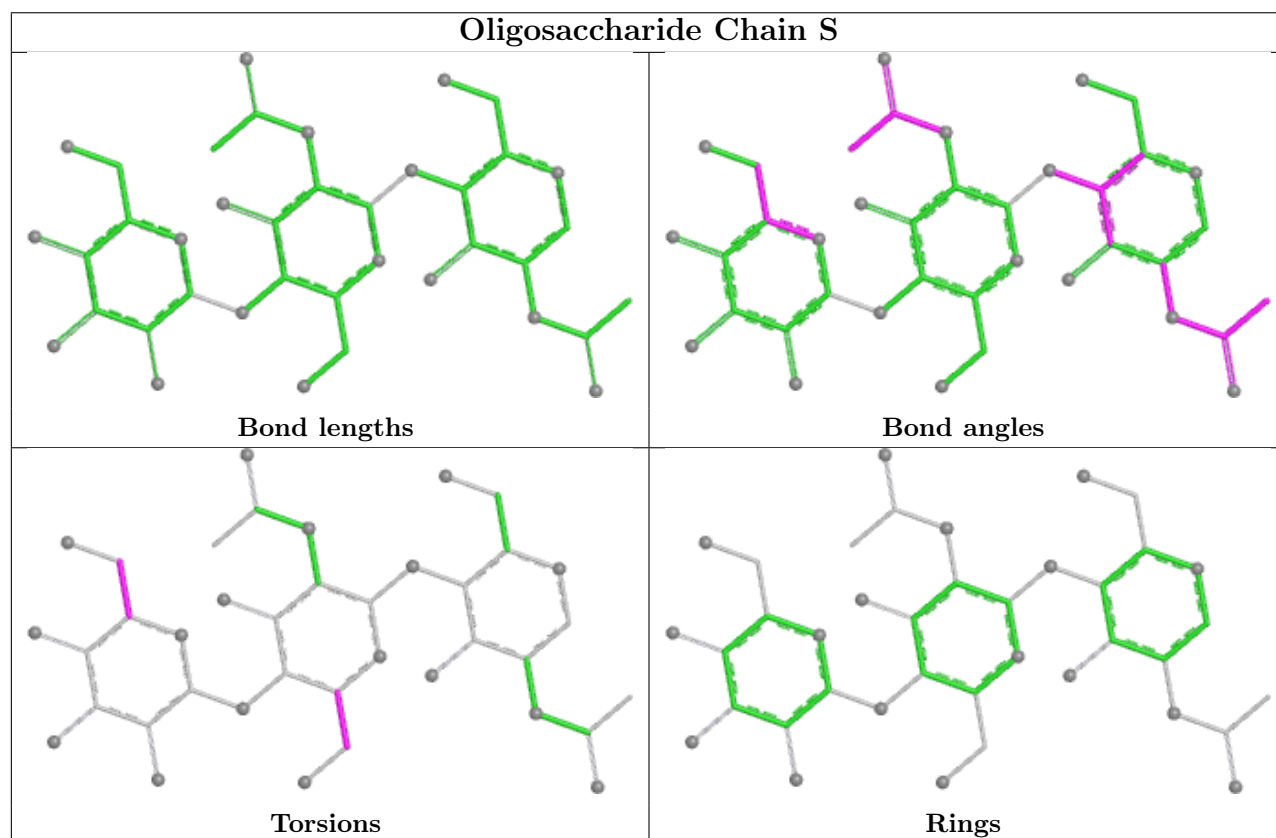
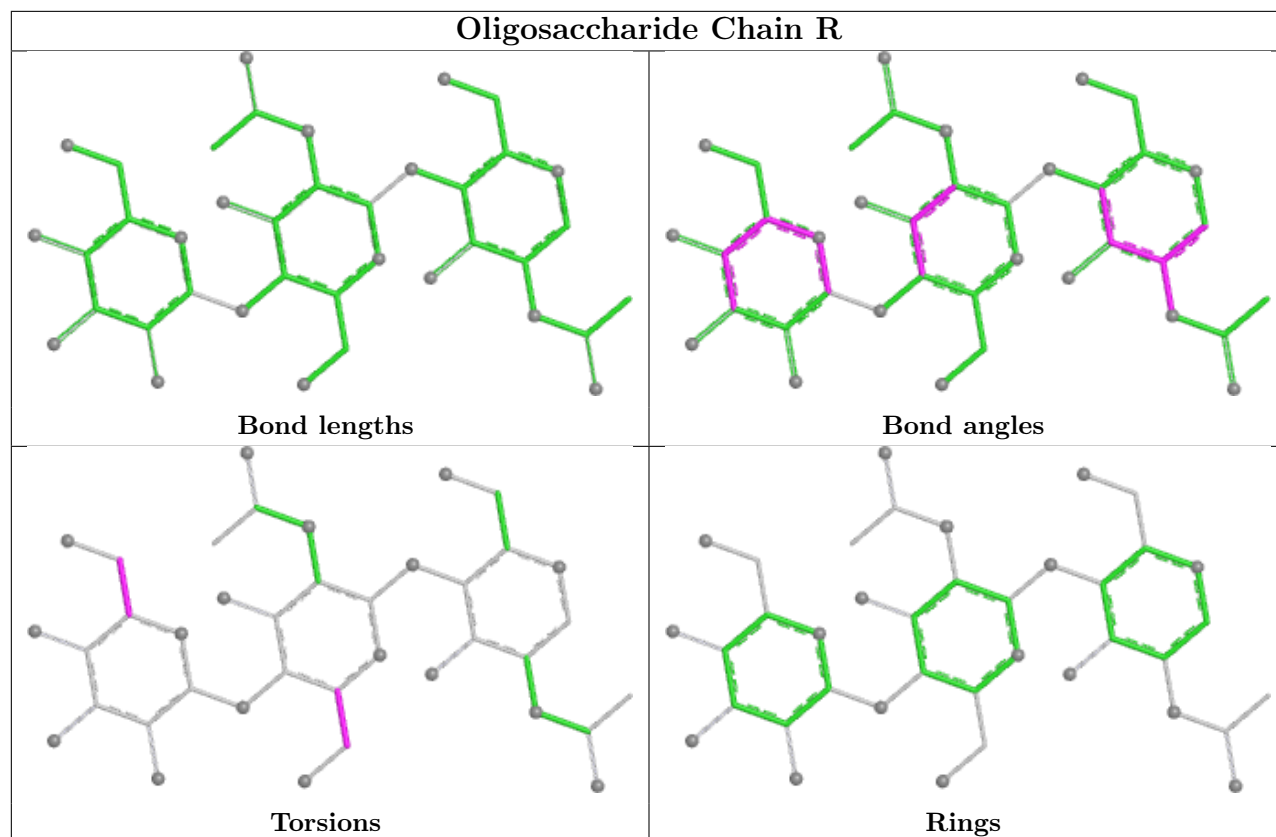
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

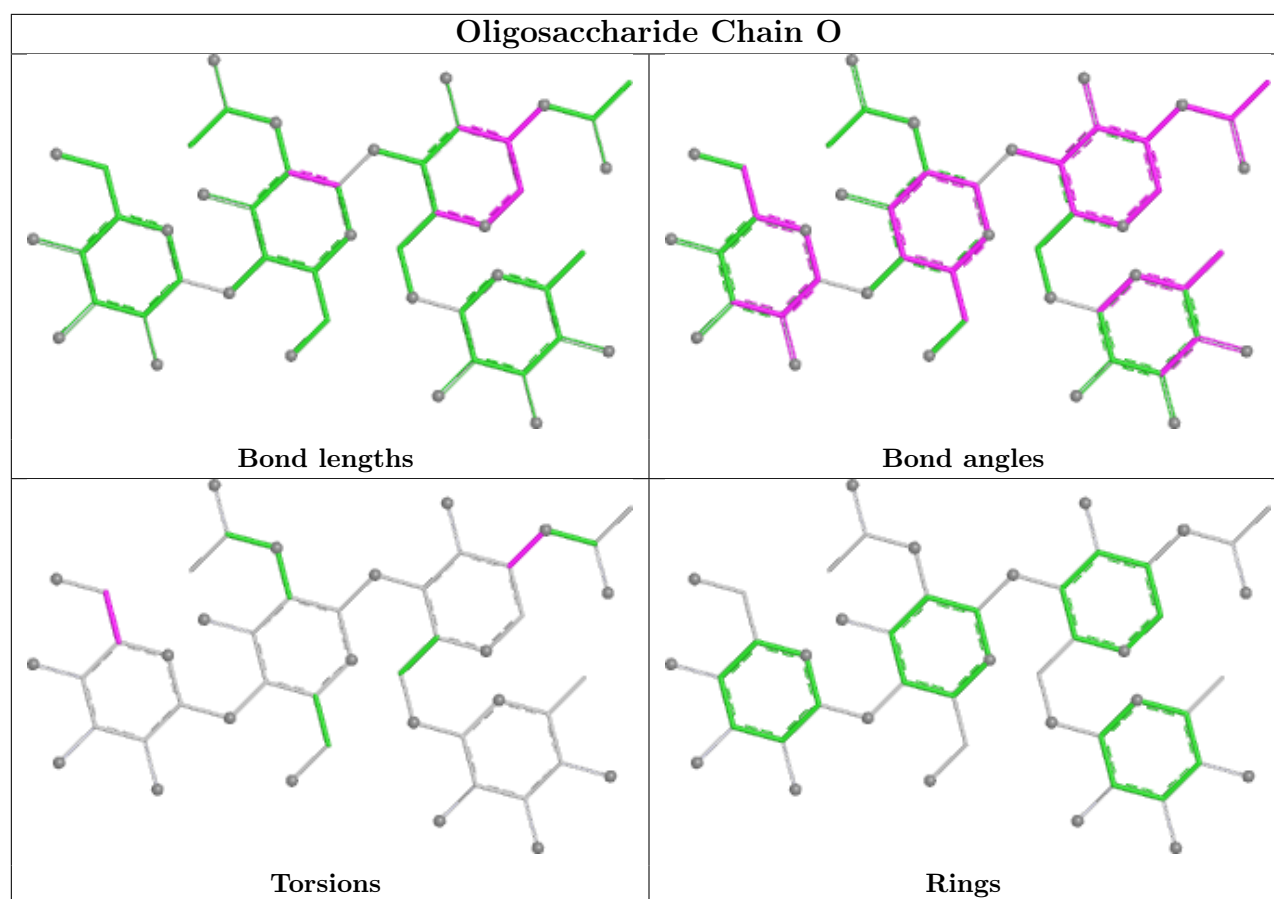
bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
7	NAG	D	500	2	14,14,15	0.95	1 (7%)	17,19,21	1.50	2 (11%)
7	NAG	L	500	2	14,14,15	0.79	0	17,19,21	2.66	7 (41%)
7	NAG	F	500	2	14,14,15	0.90	0	17,19,21	2.26	6 (35%)
7	NAG	B	500	2	14,14,15	0.63	0	17,19,21	2.49	8 (47%)
7	NAG	J	500	2	14,14,15	0.91	1 (7%)	17,19,21	1.99	3 (17%)
7	NAG	H	500	2	14,14,15	1.07	1 (7%)	17,19,21	2.45	7 (41%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	D	500	2	-	1/6/23/26	0/1/1/1
7	NAG	L	500	2	-	0/6/23/26	0/1/1/1
7	NAG	F	500	2	-	0/6/23/26	0/1/1/1
7	NAG	B	500	2	-	0/6/23/26	0/1/1/1
7	NAG	J	500	2	-	0/6/23/26	0/1/1/1
7	NAG	H	500	2	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	J	500	NAG	C1-C2	2.73	1.56	1.52
7	D	500	NAG	O5-C1	2.38	1.47	1.43
7	H	500	NAG	O5-C1	2.15	1.47	1.43

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L	500	NAG	C1-O5-C5	7.45	122.17	112.19
7	B	500	NAG	C1-O5-C5	6.55	120.97	112.19
7	J	500	NAG	C1-O5-C5	6.47	120.85	112.19
7	H	500	NAG	C1-O5-C5	6.37	120.72	112.19
7	F	500	NAG	C1-O5-C5	4.49	118.20	112.19
7	H	500	NAG	O7-C7-N2	4.38	129.72	121.98
7	F	500	NAG	C8-C7-N2	-3.99	109.50	116.12
7	B	500	NAG	C1-C2-N2	3.94	116.64	110.43
7	H	500	NAG	C2-N2-C7	3.72	127.89	122.90
7	F	500	NAG	O5-C1-C2	-3.61	105.71	111.29
7	L	500	NAG	O3-C3-C2	3.54	116.75	109.40
7	B	500	NAG	O6-C6-C5	-3.44	99.63	111.33
7	D	500	NAG	O6-C6-C5	-3.34	99.95	111.33
7	L	500	NAG	O7-C7-N2	3.29	127.80	121.98
7	L	500	NAG	O7-C7-C8	-3.09	116.55	122.05
7	L	500	NAG	C3-C4-C5	-3.00	104.79	110.23
7	F	500	NAG	C1-C2-N2	-2.89	105.87	110.43
7	B	500	NAG	C2-N2-C7	2.70	126.52	122.90
7	H	500	NAG	O7-C7-C8	-2.60	117.42	122.05
7	H	500	NAG	O4-C4-C5	2.55	115.61	109.32
7	B	500	NAG	O7-C7-C8	-2.49	117.61	122.05

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L	500	NAG	C1-C2-N2	2.43	114.26	110.43
7	H	500	NAG	O5-C5-C4	2.37	116.59	110.83
7	F	500	NAG	O7-C7-N2	2.36	126.15	121.98
7	D	500	NAG	O5-C1-C2	-2.28	107.76	111.29
7	J	500	NAG	O5-C1-C2	-2.25	107.81	111.29
7	J	500	NAG	C8-C7-N2	-2.19	112.49	116.12
7	B	500	NAG	O5-C5-C4	2.18	116.13	110.83
7	B	500	NAG	O7-C7-N2	2.17	125.81	121.98
7	B	500	NAG	C3-C4-C5	-2.16	106.31	110.23
7	F	500	NAG	O6-C6-C5	-2.12	104.10	111.33
7	L	500	NAG	O5-C1-C2	-2.02	108.17	111.29
7	H	500	NAG	C8-C7-N2	-2.01	112.79	116.12

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	D	500	NAG	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	L	500	NAG	0	1
7	J	500	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

6.1 Protein, DNA and RNA chains

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	316/325 (97%)	0.75	26 (8%)	17 19	23, 33, 55, 76	1 (0%)
1	C	316/325 (97%)	0.85	28 (8%)	15 16	24, 34, 53, 74	1 (0%)
1	E	316/325 (97%)	0.81	29 (9%)	14 15	24, 33, 52, 81	1 (0%)
1	G	316/325 (97%)	1.01	46 (14%)	6 6	25, 37, 57, 81	1 (0%)
1	I	316/325 (97%)	0.96	34 (10%)	11 12	25, 35, 54, 79	1 (0%)
1	K	316/325 (97%)	0.98	36 (11%)	10 10	26, 36, 55, 81	1 (0%)
2	B	167/181 (92%)	0.93	18 (10%)	11 12	21, 35, 58, 102	0
2	D	167/181 (92%)	0.91	20 (11%)	9 9	22, 36, 54, 103	0
2	F	167/181 (92%)	0.95	18 (10%)	11 12	22, 36, 53, 90	0
2	H	169/181 (93%)	1.05	19 (11%)	10 11	25, 39, 60, 98	0
2	J	169/181 (93%)	1.05	24 (14%)	6 7	23, 38, 57, 100	0
2	L	169/181 (93%)	1.02	24 (14%)	6 7	24, 38, 56, 94	0
All	All	2904/3036 (95%)	0.92	322 (11%)	10 11	21, 36, 56, 103	6 (0%)

All (322) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	56	ILE	6.9
1	C	12	ASN	6.6
2	F	171	ILE	6.5
2	D	58	LYS	6.3
2	L	171	ILE	6.0
2	D	5	ALA	5.8
2	F	5	ALA	5.7
1	G	222	ASP	5.7
2	J	171	ILE	5.6
2	B	58	LYS	5.6
1	G	221	ILE	5.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	I	199	ASN	5.4
2	B	171	ILE	5.4
2	H	6	ILE	5.4
1	G	211	ARG	5.3
1	I	201	GLN	5.2
2	H	171	ILE	5.1
1	E	12	ASN	5.1
1	C	215	ASN	5.0
2	D	171	ILE	5.0
2	H	56	ILE	5.0
2	B	56	ILE	5.0
2	L	56	ILE	5.0
1	E	201	GLN	4.9
2	H	58	LYS	4.9
2	F	58	LYS	4.8
2	J	58	LYS	4.8
2	B	5	ALA	4.7
1	A	222	ASP	4.7
2	D	56	ILE	4.5
1	E	215	ASN	4.5
1	I	215	ASN	4.5
2	L	58	LYS	4.5
1	G	181	GLU	4.4
2	F	6	ILE	4.4
2	F	57	GLU	4.2
1	C	222	ASP	4.2
1	K	199	ASN	4.2
1	A	216	GLY	4.2
1	K	181	GLU	4.2
1	I	198	SER	4.2
1	I	121	ARG	4.1
1	K	268	CYS	4.0
2	B	57	GLU	4.0
1	E	121	ARG	4.0
1	A	268	CYS	4.0
2	J	6	ILE	3.9
1	G	246	ASP	3.9
1	A	12	ASN	3.9
1	I	267	ASN	3.9
1	A	14	THR	3.9
1	G	212	PRO	3.9
1	C	181	GLU	3.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	E	199	ASN	3.8
1	G	215	ASN	3.8
1	G	147	THR	3.8
1	I	181	GLU	3.8
2	B	6	ILE	3.7
1	G	199	ASN	3.7
1	A	190	ASN	3.7
2	D	6	ILE	3.7
2	F	67	ASP	3.7
1	E	132	SER	3.6
1	K	215	ASN	3.6
2	D	57	GLU	3.6
2	J	56	ILE	3.6
1	C	199	ASN	3.6
2	J	57	GLU	3.6
1	K	202	GLN	3.5
1	G	268	CYS	3.5
1	I	268	CYS	3.5
1	G	12	ASN	3.5
2	J	55	LEU	3.5
1	E	181	GLU	3.5
2	B	59	THR	3.5
1	I	14	THR	3.4
2	H	55	LEU	3.4
1	A	316	GLU	3.4
2	H	57	GLU	3.4
1	C	190	ASN	3.4
2	L	6	ILE	3.4
2	L	57	GLU	3.4
1	A	199	ASN	3.4
1	C	198	SER	3.4
1	I	246	ASP	3.4
1	C	268	CYS	3.3
1	E	316	GLU	3.3
1	E	254	LYS	3.3
1	I	13	GLY	3.2
2	L	39	LYS	3.2
2	L	167	MET	3.1
1	K	12	ASN	3.1
1	E	14	THR	3.1
1	G	14	THR	3.1
1	G	219	GLY	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	215	ASN	3.1
1	C	211	ARG	3.1
1	C	11	SER	3.1
1	G	132	SER	3.1
1	C	210	ALA	3.1
2	B	55	LEU	3.1
1	G	93	VAL	3.0
1	C	214	VAL	3.0
2	L	74	GLU	3.0
2	J	39	LYS	3.0
1	G	130	ARG	3.0
2	J	120	GLU	3.0
1	I	147	THR	3.0
1	A	132	SER	2.9
1	E	315	PRO	2.9
2	F	55	LEU	2.9
2	J	52	LEU	2.9
1	G	162	THR	2.9
1	A	11	SER	2.9
1	K	234	VAL	2.9
1	K	14	THR	2.9
1	K	203	SER	2.9
1	A	121	ARG	2.8
2	J	110	LEU	2.8
1	K	147	THR	2.8
1	K	179	THR	2.8
1	C	216	GLY	2.8
1	I	316	GLU	2.8
1	I	205	VAL	2.8
1	G	47	ARG	2.8
2	B	19	ASP	2.8
2	D	120	GLU	2.8
2	J	69	GLU	2.8
1	A	129	CYS	2.8
1	A	254	LYS	2.8
1	I	12	ASN	2.8
2	F	60	ASN	2.8
1	I	203	SER	2.8
1	K	132	SER	2.8
1	G	269	GLU	2.8
1	K	316	GLU	2.8
1	C	164	LYS	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	179	THR	2.8
1	I	254	LYS	2.8
2	J	48	ILE	2.8
1	E	130	ARG	2.7
1	I	130	ARG	2.7
1	G	202	GLN	2.7
2	B	60	ASN	2.7
1	A	194	THR	2.7
1	E	162	THR	2.7
2	H	168	GLN	2.7
1	E	198	SER	2.7
2	B	167	MET	2.7
1	G	216	GLY	2.7
1	A	179	THR	2.7
2	F	19	ASP	2.7
1	G	192	LEU	2.6
2	D	167	MET	2.6
1	K	190	ASN	2.6
2	H	110	LEU	2.6
1	K	200	TYR	2.6
1	K	246	ASP	2.6
1	C	280	ILE	2.6
1	C	130	ARG	2.6
1	K	189	GLY	2.6
1	A	181	GLU	2.6
2	F	167	MET	2.6
1	G	210	ALA	2.6
1	C	14	THR	2.6
2	L	52	LEU	2.6
2	D	67	ASP	2.6
1	A	47	ARG	2.6
1	K	130	ARG	2.6
1	G	38	ILE	2.6
2	L	59	THR	2.6
1	C	144	LEU	2.6
1	C	221	ILE	2.6
2	B	168	GLN	2.6
2	D	27	GLN	2.6
1	G	316	GLU	2.6
2	F	11	GLU	2.6
1	C	133	GLY	2.6
1	I	282	ASN	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	254	LYS	2.6
2	J	59	THR	2.6
1	G	142	TRP	2.6
1	E	21	GLU	2.5
1	I	44	LYS	2.5
1	A	130	ARG	2.5
1	I	162	THR	2.5
2	B	52	LEU	2.5
1	I	256	MET	2.5
2	D	18	ILE	2.5
1	G	265	ASP	2.5
2	D	19	ASP	2.5
1	C	147	THR	2.5
1	K	254	LYS	2.5
2	J	10	ILE	2.5
2	L	11	GLU	2.5
1	G	266	ALA	2.5
2	H	167	MET	2.5
2	J	60	ASN	2.5
2	H	74	GLU	2.4
2	J	147	ASP	2.4
1	C	128	ALA	2.4
1	K	121	ARG	2.4
1	E	253	GLY	2.4
1	E	280	ILE	2.4
1	I	271	ASP	2.4
2	H	147	ASP	2.4
2	L	19	ASP	2.4
1	E	268	CYS	2.4
1	C	132	SER	2.4
1	K	237	SER	2.4
1	G	121	ARG	2.4
1	A	93	VAL	2.4
1	G	214	VAL	2.4
1	K	205	VAL	2.4
1	E	32	THR	2.4
1	G	217	LEU	2.4
1	I	269	GLU	2.4
2	D	11	GLU	2.4
2	H	103	GLU	2.4
1	E	190	ASN	2.4
1	G	189	GLY	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	H	67	ASP	2.4
1	I	141	LYS	2.4
2	J	124	ARG	2.4
1	E	200	TYR	2.3
2	B	38	TYR	2.3
1	K	210	ALA	2.3
2	H	19	ASP	2.3
1	E	164	LYS	2.3
1	K	91	LYS	2.3
1	G	165	SER	2.3
1	K	269	GLU	2.3
1	I	266	ALA	2.3
2	F	71	ASN	2.3
2	L	110	LEU	2.3
2	D	133	ASP	2.3
2	L	124	ARG	2.3
2	L	102	MET	2.3
1	E	197	SER	2.3
2	L	18	ILE	2.3
1	E	205	VAL	2.3
1	I	264	VAL	2.3
2	J	139	GLU	2.3
1	K	315	PRO	2.3
1	G	188	SER	2.3
2	B	139	GLU	2.3
2	L	3	PHE	2.3
2	B	18	ILE	2.3
1	K	10	VAL	2.3
1	K	153	PRO	2.3
1	G	146	ASN	2.3
2	H	32	GLU	2.2
1	A	162	THR	2.2
1	A	214	VAL	2.2
1	K	206	PRO	2.2
1	I	22	ARG	2.2
2	D	60	ASN	2.2
1	K	312	LYS	2.2
1	A	133	GLY	2.2
2	J	29	ALA	2.2
1	A	217	LEU	2.2
1	G	201	GLN	2.2
1	A	198	SER	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	I	132	SER	2.2
2	F	54	ARG	2.2
1	E	153	PRO	2.2
2	J	168	GLN	2.2
1	I	200	TYR	2.2
1	A	188	SER	2.2
2	J	53	ASN	2.2
1	C	85	ASP	2.2
1	G	1	ASP	2.2
2	F	10	ILE	2.2
1	E	111	GLU	2.2
2	D	164	GLU	2.2
2	L	50	GLY	2.2
2	D	110	LEU	2.2
1	E	203	SER	2.2
1	G	11	SER	2.2
2	H	38	TYR	2.2
1	I	190	ASN	2.2
1	K	94	ASN	2.2
1	K	282	ASN	2.2
2	L	73	VAL	2.1
1	I	133	GLY	2.1
1	G	241	ALA	2.1
1	I	192	LEU	2.1
1	I	255	SER	2.1
1	K	198	SER	2.1
2	L	143	LYS	2.1
1	G	190	ASN	2.1
2	L	38	TYR	2.1
1	G	21	GLU	2.1
2	B	48	ILE	2.1
1	C	253	GLY	2.1
2	H	99	LEU	2.1
2	H	144	CYS	2.1
2	H	120	GLU	2.1
2	J	32	GLU	2.1
2	D	38	TYR	2.1
2	F	27	GLN	2.1
1	K	152	PHE	2.1
2	F	143	LYS	2.1
1	E	25	GLU	2.1
1	G	282	ASN	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	213	GLN	2.1
1	K	162	THR	2.1
1	G	180	ALA	2.1
2	J	5	ALA	2.1
1	K	227	MET	2.0
2	L	32	GLU	2.0
2	D	55	LEU	2.0
1	G	213	GLN	2.0
2	L	67	ASP	2.0
2	D	143	LYS	2.0
1	G	270	GLY	2.0
2	F	48	ILE	2.0
2	L	55	LEU	2.0
1	C	271	ASP	2.0
2	B	133	ASP	2.0
1	E	91	LYS	2.0
2	J	117	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

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.

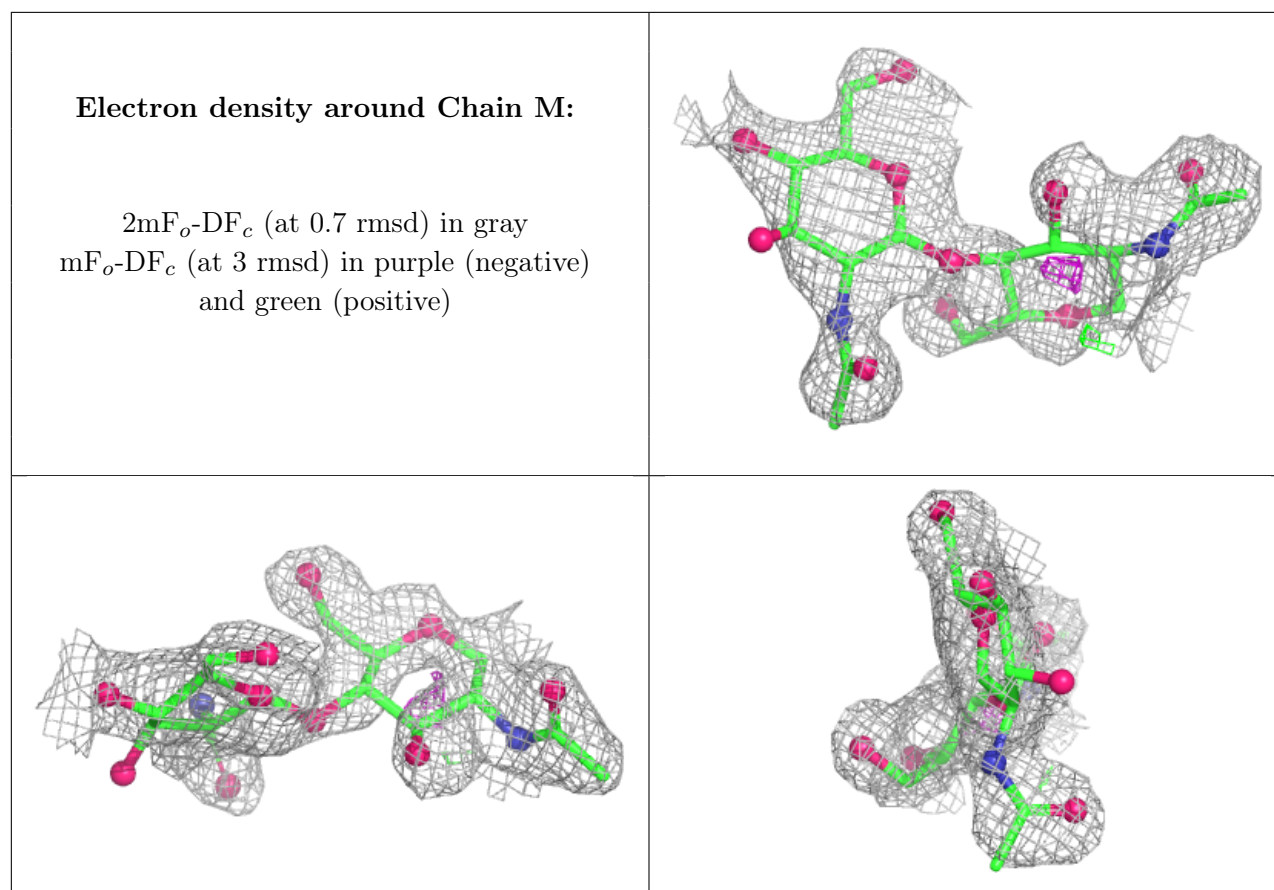
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	BMA	O	3	11/12	0.20	0.18	103,109,112,115	0
4	BMA	P	3	11/12	0.34	0.21	76,87,96,99	0
4	BMA	R	3	11/12	0.36	0.16	87,99,102,103	0
4	BMA	N	3	11/12	0.38	0.18	84,95,97,100	0
4	BMA	S	3	11/12	0.40	0.18	92,100,109,112	0
5	NAG	O	2	14/15	0.43	0.19	70,91,94,98	0
5	FUC	O	4	10/11	0.48	0.24	76,86,91,92	0
5	NAG	O	1	14/15	0.56	0.23	69,82,89,90	0
4	NAG	P	2	14/15	0.58	0.17	63,76,85,90	0
3	NAG	Q	2	14/15	0.62	0.15	62,85,91,92	0
3	NAG	M	1	14/15	0.66	0.17	50,67,76,77	0

Continued on next page...

Continued from previous page...

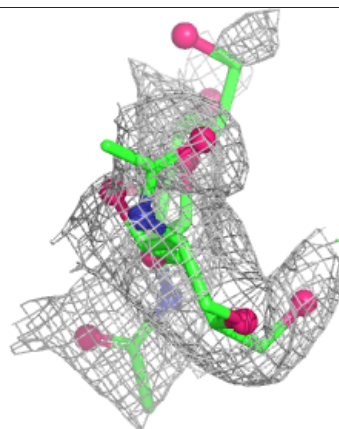
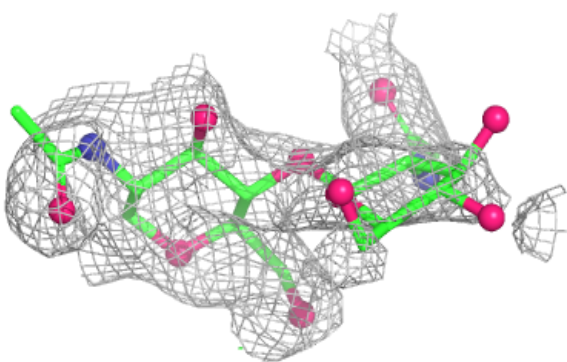
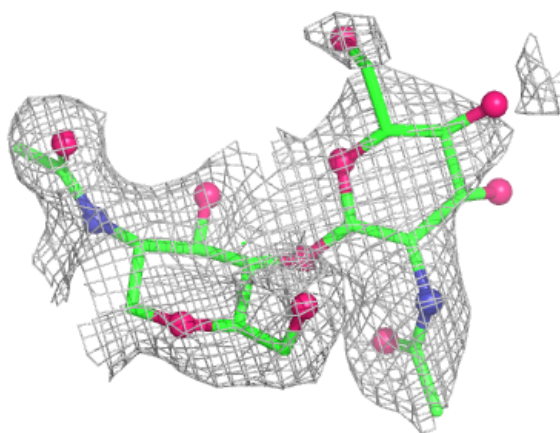
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	N	1	14/15	0.68	0.17	41,66,73,73	0
4	NAG	P	1	14/15	0.70	0.17	45,57,62,71	0
4	NAG	S	2	14/15	0.71	0.16	56,70,84,97	0
4	NAG	R	2	14/15	0.72	0.15	58,71,88,96	0
4	NAG	N	2	14/15	0.72	0.16	69,79,84,90	0
3	NAG	Q	1	14/15	0.73	0.15	46,61,68,74	0
3	NAG	M	2	14/15	0.77	0.13	61,76,84,89	0
4	NAG	S	1	14/15	0.78	0.13	44,49,52,58	0
4	NAG	R	1	14/15	0.84	0.12	49,60,64,65	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.

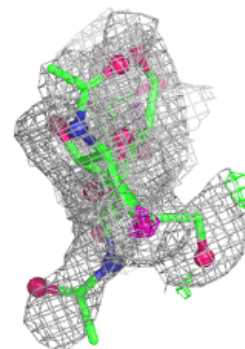
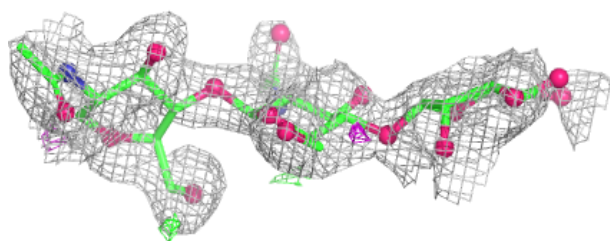
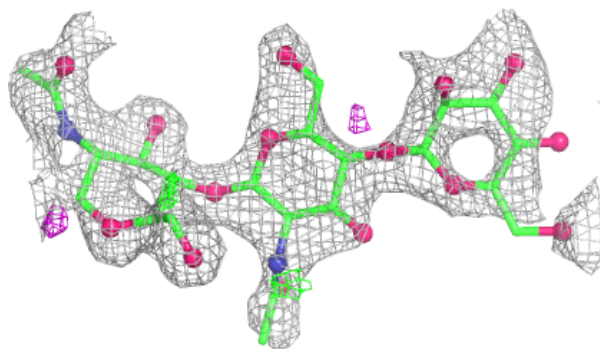


Electron density around Chain Q:

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

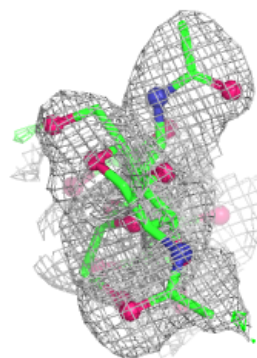
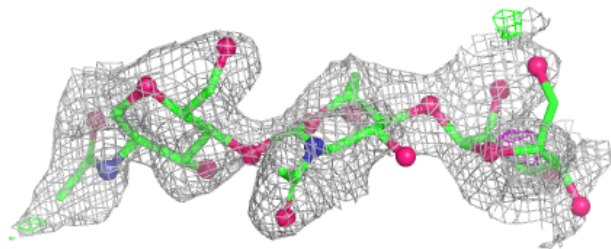
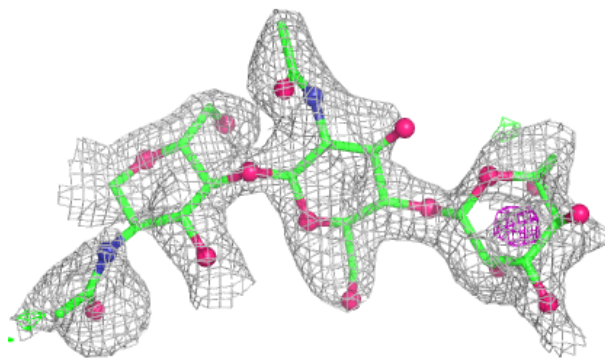
**Electron density around Chain N:**

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

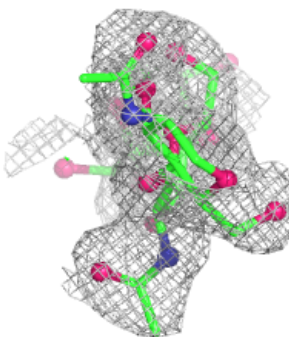
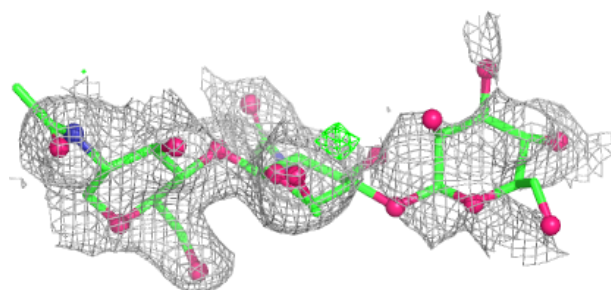
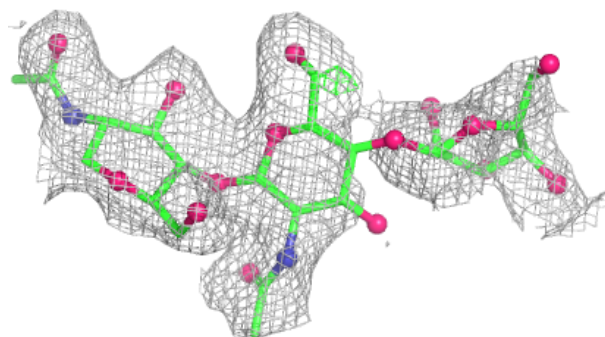


Electron density around Chain P:

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

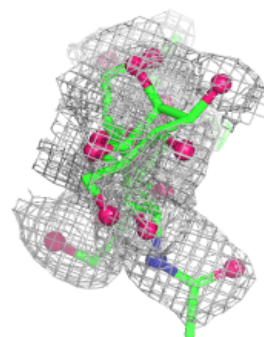
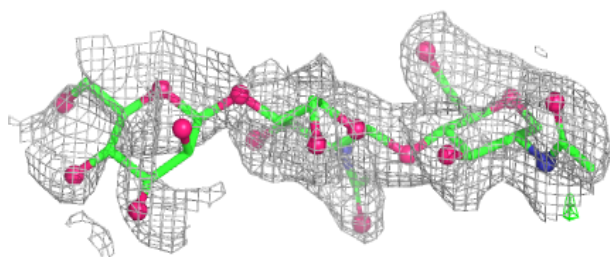
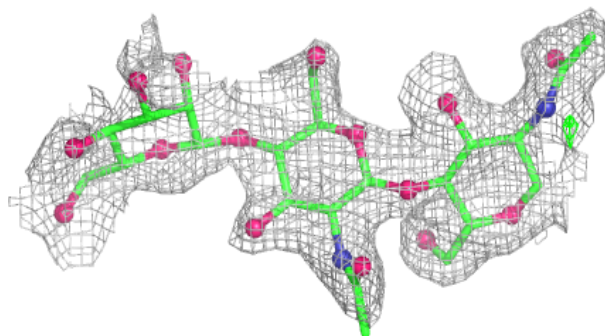
**Electron density around Chain R:**

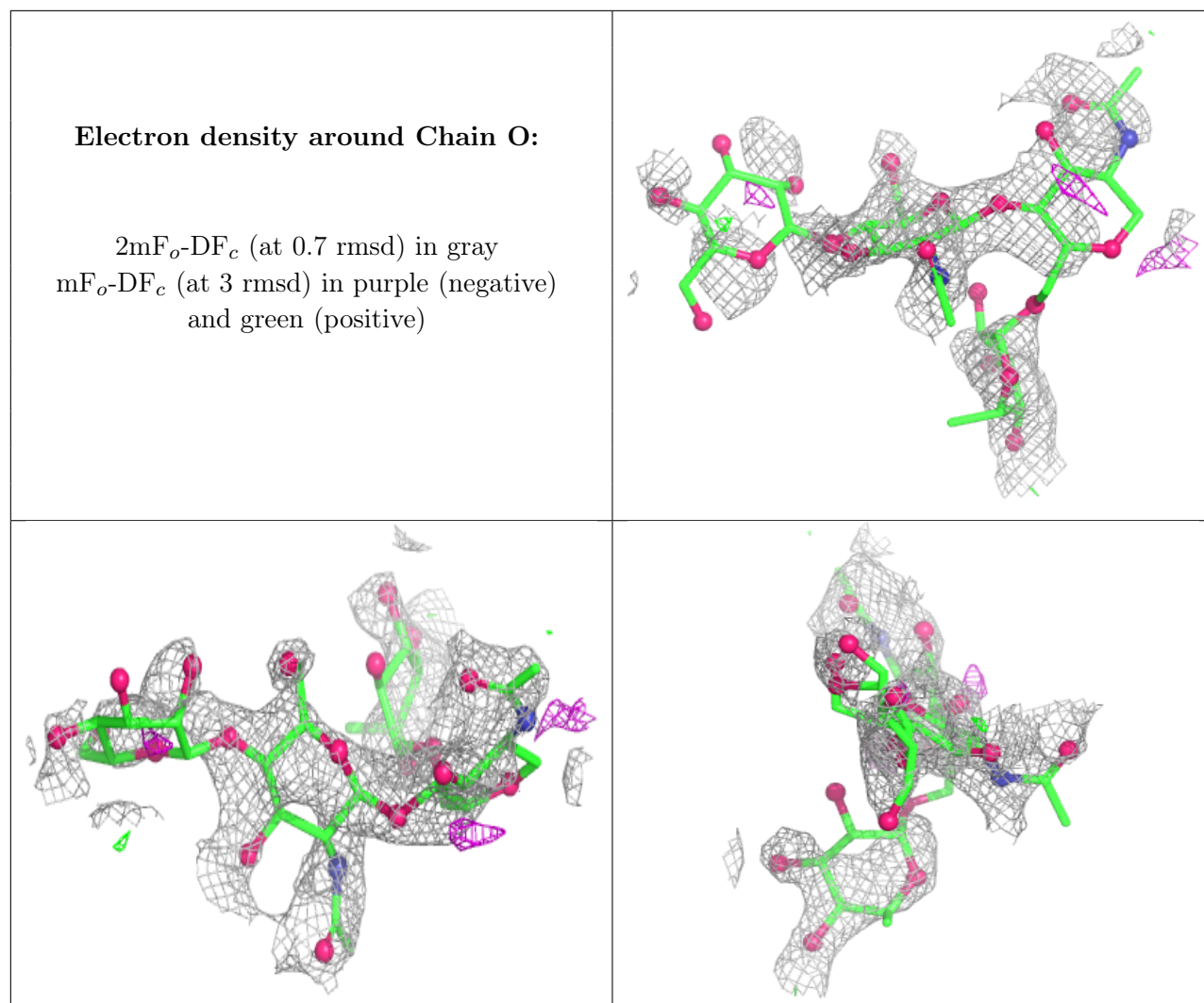
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain S:

$2mF_o-DF_c$ (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($\text{\AA}^2$)	Q<0.9
7	NAG	J	500	14/15	0.72	0.14	44,54,59,62	0
7	NAG	D	500	14/15	0.77	0.14	44,51,56,59	0
7	NAG	F	500	14/15	0.80	0.13	43,49,54,57	0
7	NAG	B	500	14/15	0.80	0.13	39,46,51,55	0
7	NAG	L	500	14/15	0.82	0.13	45,50,55,55	0
7	NAG	H	500	14/15	0.83	0.12	41,46,53,56	0
6	CA	C	404	1/1	0.86	0.09	46,46,46,46	0
6	CA	K	404	1/1	0.87	0.09	44,44,44,44	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	CA	A	403	1/1	0.88	0.09	42,42,42,42	0
6	CA	E	408	1/1	0.92	0.08	41,41,41,41	0
6	CA	G	403	1/1	0.94	0.06	35,35,35,35	0
6	CA	I	404	1/1	0.95	0.06	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.