



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:06 AM UTC

PDB ID : 5BR6 / pdb_00005br6
Title : Crystal structure of hemagglutinin of A/Taiwan/2/2013 (H6N1) in complex with LSTc
Authors : Ni, F.; Kondrashkina, E.; Wang, Q.
Deposited on : 2015-05-29
Resolution : 2.43 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

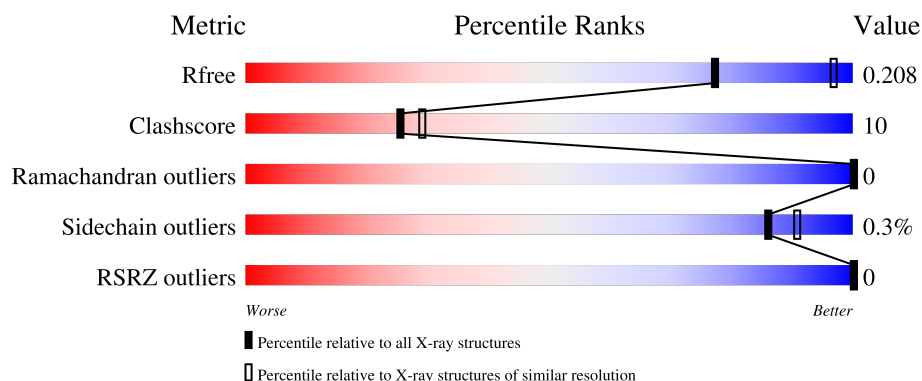
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.43 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.



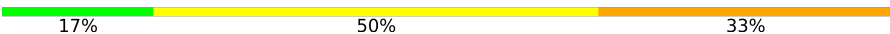
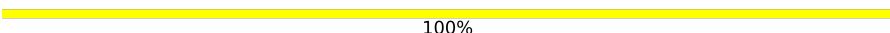
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2340 (2.46-2.42)
Clashscore	190562	2400 (2.46-2.42)
Ramachandran outliers	187476	2379 (2.46-2.42)
Sidechain outliers	187428	2379 (2.46-2.42)
RSRZ outliers	180081	2340 (2.46-2.42)

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	326	 83% 17%
1	C	326	 85% 14% .
2	B	171	 87% 13%
2	D	171	 90% 10%
3	E	3	 33% 67%

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Mol	Chain	Length	Quality of chain
3	G	3	 67% 33%
4	F	6	 17% 50% 33%
4	H	6	 100%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	FUC	F	6	X	-	-	-
4	FUC	H	6	X	-	-	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9064 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.

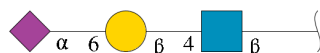
- Molecule 1 is a protein called HEMAGGLUTININ HA1 CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	0	0
			2577	1634	439	491	13			
1	C	326	Total	C	N	O	S	0	0	0
			2577	1634	439	491	13			

- Molecule 2 is a protein called HEMAGGLUTININ HA2 CHAIN.

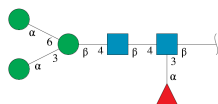
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	171	Total	C	N	O	S	0	0	0
			1381	860	242	272	7			
2	D	171	Total	C	N	O	S	0	0	0
			1381	860	242	272	7			

- Molecule 3 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



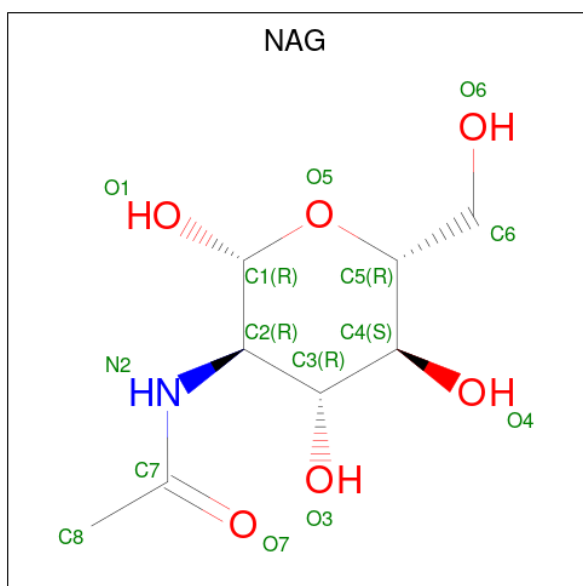
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	3	Total	C	N	O	0	0	0
			45	25	2	18			
3	G	3	Total	C	N	O	0	0	0
			45	25	2	18			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	6	Total	C	N	O	0	0	0
			71	40	2	29			
4	H	6	Total	C	N	O	0	0	0
			71	40	2	29			

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



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

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

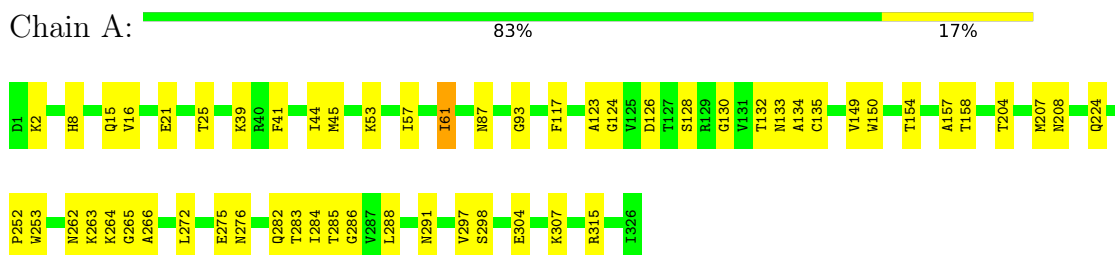
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	227	Total	O	0	0
			227	227		
6	B	164	Total	O	0	0
			164	164		
6	C	234	Total	O	0	0
			234	234		
6	D	179	Total	O	0	0
			179	179		

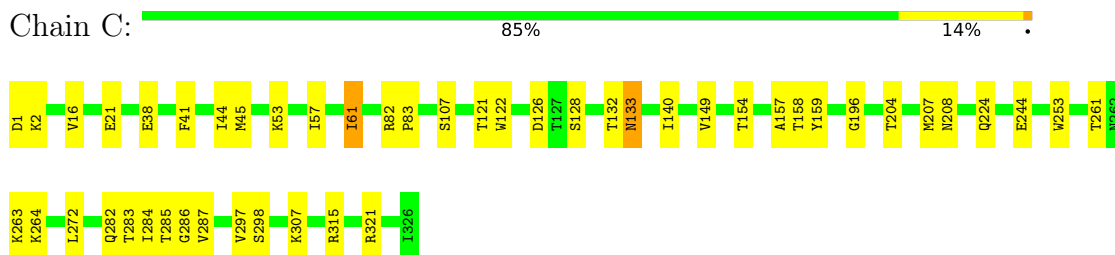
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and 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.

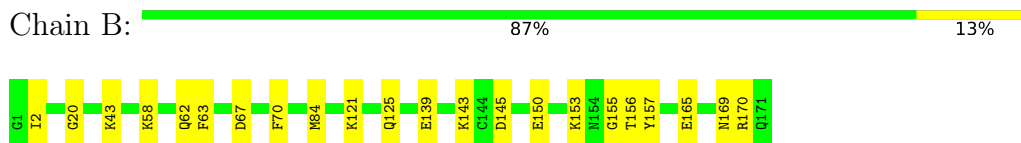
- Molecule 1: HEMAGGLUTININ HA1 CHAIN



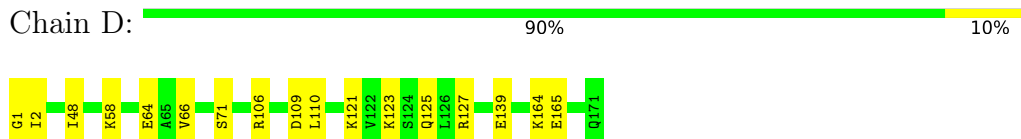
- Molecule 1: HEMAGGLUTININ HA1 CHAIN



- Molecule 2: HEMAGGLUTININ HA2 CHAIN



- Molecule 2: HEMAGGLUTININ HA2 CHAIN



- Molecule 3: N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





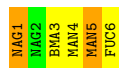
- Molecule 3: N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G: 67% 33%



- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F: 17% 50% 33%



- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H: 100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, α , β , γ	113.67Å 113.67Å 163.16Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	37.68 – 2.43 37.68 – 2.43	Depositor EDS
% Data completeness (in resolution range)	100.0 (37.68-2.43) 100.0 (37.68-2.43)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.42Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.203 , 0.225 (Not available) , 0.208	Depositor DCC
R_{free} test set	4463 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	31.2	Xtriage
Anisotropy	0.390	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 27.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.458 for -h,-k,l 0.044 for h,-h-k,-l 0.045 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9064	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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: MAN, SIA, BMA, FUC, GAL, NAG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.28	0/2638	0.70	2/3589 (0.1%)
1	C	0.31	1/2638 (0.0%)	0.70	3/3589 (0.1%)
2	B	0.26	0/1409	0.65	0/1897
2	D	0.26	0/1409	0.66	1/1897 (0.1%)
All	All	0.28	1/8094 (0.0%)	0.68	6/10972 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	132	THR	C-N	-8.52	1.20	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	53	LYS	CB-CA-C	-5.71	109.46	117.23
1	A	154	THR	N-CA-C	-5.52	103.24	110.53
1	A	53	LYS	CB-CA-C	-5.52	109.73	117.23
1	C	132	THR	CA-C-N	5.35	132.64	121.94
1	C	132	THR	C-N-CA	5.35	132.64	121.94
2	D	127	ARG	CB-CA-C	-5.05	110.77	116.63

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	133	ASN	Mainchain

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	2577	0	2527	57	0
1	C	2577	0	2527	46	0
2	B	1381	0	1294	28	0
2	D	1381	0	1294	19	0
3	E	45	0	38	1	0
3	G	45	0	38	8	0
4	F	71	0	61	2	0
4	H	71	0	61	0	0
5	A	56	0	52	2	0
5	C	56	0	52	2	0
6	A	227	0	0	38	1
6	B	164	0	0	19	3
6	C	234	0	0	28	1
6	D	179	0	0	15	2
All	All	9064	0	7944	155	5

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 10.

All (155) 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)
2:D:66:VAL:HG23	6:D:402:HOH:O	1.24	1.33
1:C:307:LYS:NZ	6:C:501:HOH:O	1.81	1.13
1:A:123:ALA:HA	6:A:501:HOH:O	1.47	1.12
6:C:511:HOH:O	3:G:1:NAG:H81	1.50	1.12
1:A:124:GLY:N	6:A:501:HOH:O	1.83	1.10
1:A:132:THR:HG23	6:A:506:HOH:O	1.53	1.07
1:A:123:ALA:CA	6:A:501:HOH:O	2.00	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:66:VAL:CG2	6:D:402:HOH:O	1.89	1.05
1:C:133:ASN:HD21	3:G:2:GAL:H61	1.21	1.03
1:C:133:ASN:ND2	3:G:2:GAL:H61	1.75	1.01
1:C:196:GLY:O	6:C:502:HOH:O	1.81	0.96
1:A:134:ALA:N	6:A:506:HOH:O	2.00	0.94
1:A:263:LYS:O	6:A:502:HOH:O	1.85	0.94
1:C:121:THR:O	6:C:503:HOH:O	1.84	0.93
1:C:321:ARG:NH2	6:C:507:HOH:O	2.01	0.92
2:D:66:VAL:O	6:D:402:HOH:O	1.87	0.91
1:A:158:THR:N	6:A:507:HOH:O	2.03	0.91
1:A:304:GLU:OE2	6:A:503:HOH:O	1.86	0.91
1:A:275:GLU:O	6:A:504:HOH:O	1.90	0.90
1:C:154:THR:O	6:C:505:HOH:O	1.93	0.87
1:C:283:THR:HG22	1:C:285:THR:H	1.44	0.82
1:A:283:THR:HG22	1:A:285:THR:H	1.45	0.81
2:B:155:GLY:C	6:B:402:HOH:O	2.22	0.81
5:A:402:NAG:O7	6:A:505:HOH:O	1.98	0.80
2:B:43:LYS:NZ	6:B:405:HOH:O	2.14	0.80
2:B:155:GLY:O	6:B:402:HOH:O	1.99	0.80
2:D:66:VAL:C	6:D:402:HOH:O	2.26	0.79
2:D:66:VAL:O	6:D:404:HOH:O	2.01	0.79
2:B:165:GLU:OE2	6:B:403:HOH:O	2.00	0.78
1:C:315:ARG:NH2	6:C:515:HOH:O	2.17	0.77
1:C:21:GLU:OE1	6:C:509:HOH:O	2.03	0.76
1:A:135:CYS:N	6:A:506:HOH:O	2.11	0.76
1:A:291:ASN:OD1	6:A:508:HOH:O	2.04	0.74
1:C:159:TYR:OH	6:C:510:HOH:O	2.04	0.74
1:A:25:THR:O	6:A:509:HOH:O	2.05	0.73
2:B:62:GLN:NE2	6:B:401:HOH:O	1.91	0.73
1:A:45:MET:SD	1:A:263:LYS:NZ	2.61	0.72
2:B:156:THR:CA	6:B:402:HOH:O	2.37	0.71
2:D:164:LYS:NZ	6:D:401:HOH:O	1.84	0.71
6:C:511:HOH:O	3:G:1:NAG:C8	2.19	0.71
2:B:70:PHE:O	6:B:404:HOH:O	2.08	0.71
1:A:132:THR:CG2	6:A:506:HOH:O	2.21	0.71
2:D:165:GLU:OE2	6:D:406:HOH:O	2.10	0.70
1:A:93:GLY:O	6:A:511:HOH:O	2.09	0.70
1:A:224:GLN:OE1	6:A:510:HOH:O	2.08	0.70
1:C:45:MET:N	6:C:506:HOH:O	2.24	0.69
6:C:511:HOH:O	3:G:1:NAG:O7	2.10	0.69
1:C:208:ASN:OD1	6:C:512:HOH:O	2.11	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:511:HOH:O	3:G:1:NAG:C7	2.40	0.68
1:C:21:GLU:OE2	6:C:513:HOH:O	2.13	0.67
1:A:315:ARG:NH1	6:A:517:HOH:O	2.16	0.67
1:A:208:ASN:OD1	6:A:513:HOH:O	2.12	0.66
2:B:165:GLU:CG	6:B:403:HOH:O	2.43	0.66
1:A:21:GLU:OE2	6:A:516:HOH:O	2.14	0.66
1:C:157:ALA:HB1	6:C:522:HOH:O	1.96	0.65
1:C:45:MET:SD	1:C:263:LYS:NZ	2.63	0.65
1:A:134:ALA:CA	6:A:506:HOH:O	2.40	0.63
2:D:1:GLY:N	6:D:410:HOH:O	2.31	0.63
2:B:169:ASN:ND2	6:B:403:HOH:O	2.32	0.62
1:A:45:MET:N	6:A:515:HOH:O	2.31	0.61
2:D:123:LYS:NZ	6:D:405:HOH:O	2.08	0.61
1:C:283:THR:HG23	1:C:298:SER:HB3	1.84	0.60
1:A:266:ALA:N	6:A:522:HOH:O	2.24	0.59
1:A:315:ARG:HD2	6:A:524:HOH:O	2.00	0.59
1:A:262:ASN:N	6:A:534:HOH:O	2.35	0.59
1:A:283:THR:HG23	1:A:298:SER:HB3	1.84	0.59
1:C:158:THR:N	6:C:522:HOH:O	2.37	0.58
2:B:157:TYR:N	6:B:402:HOH:O	2.35	0.58
1:C:158:THR:CG2	6:C:522:HOH:O	2.52	0.58
2:D:109:ASP:OD1	6:D:407:HOH:O	2.17	0.57
1:A:157:ALA:HB1	6:A:507:HOH:O	2.04	0.57
1:C:154:THR:N	6:C:504:HOH:O	1.88	0.56
2:D:64:GLU:N	6:D:403:HOH:O	1.94	0.56
2:B:63:PHE:HZ	2:B:84:MET:HE3	1.71	0.56
1:C:244:GLU:OE2	6:C:516:HOH:O	2.18	0.55
1:A:224:GLN:NE2	6:A:512:HOH:O	2.11	0.54
2:B:156:THR:HA	6:B:402:HOH:O	2.03	0.54
2:D:121:LYS:NZ	6:D:409:HOH:O	2.25	0.54
1:A:315:ARG:NH1	6:A:540:HOH:O	2.41	0.53
1:A:133:ASN:ND2	3:E:2:GAL:H61	2.23	0.53
1:C:158:THR:HG22	6:C:522:HOH:O	2.08	0.53
1:C:283:THR:CG2	1:C:298:SER:HB3	2.39	0.52
1:A:149:VAL:HG23	1:A:253:TRP:HB2	1.91	0.52
1:A:134:ALA:HB3	6:A:506:HOH:O	2.10	0.52
1:A:283:THR:CG2	1:A:298:SER:HB3	2.39	0.52
2:B:145:ASP:HB2	6:B:458:HOH:O	2.10	0.52
2:B:156:THR:N	6:B:402:HOH:O	2.37	0.51
1:C:1:ASP:HB2	6:D:454:HOH:O	2.10	0.51
5:C:401:NAG:O7	5:C:401:NAG:O3	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:2:ILE:HG12	6:B:466:HOH:O	2.11	0.51
1:A:132:THR:C	6:A:506:HOH:O	2.54	0.50
1:C:149:VAL:HG23	1:C:253:TRP:HB2	1.93	0.50
1:C:283:THR:HB	1:C:286:GLY:O	2.12	0.49
2:D:71:SER:O	6:D:408:HOH:O	2.19	0.49
1:A:87:ASN:ND2	6:A:541:HOH:O	2.45	0.49
1:C:224:GLN:OE1	6:C:517:HOH:O	2.20	0.49
1:A:2:LYS:HG2	2:B:139:GLU:HG2	1.94	0.48
1:A:15:GLN:OE1	5:A:402:NAG:H83	2.13	0.48
1:A:283:THR:HB	1:A:286:GLY:O	2.13	0.48
1:C:264:LYS:HD3	6:C:626:HOH:O	2.13	0.48
1:A:126:ASP:OD1	1:A:128:SER:OG	2.32	0.48
2:B:150:GLU:HB3	4:F:1:NAG:O6	2.13	0.47
1:C:2:LYS:HG2	2:D:139:GLU:HG2	1.96	0.47
1:A:16:VAL:HG12	1:A:315:ARG:HG2	1.95	0.47
1:A:265:GLY:HA2	6:A:522:HOH:O	2.12	0.47
1:C:264:LYS:NZ	6:C:528:HOH:O	2.40	0.47
1:A:132:THR:CB	6:A:506:HOH:O	2.53	0.47
1:C:204:THR:HG23	1:C:207:MET:HE2	1.98	0.46
1:C:16:VAL:HG12	1:C:315:ARG:HG2	1.98	0.46
1:C:284:ILE:HG23	1:C:285:THR:HG23	1.98	0.46
1:A:264:LYS:HD3	6:A:640:HOH:O	2.15	0.46
1:C:122:TRP:HA	6:C:503:HOH:O	2.15	0.45
2:D:106:ARG:HD2	6:D:449:HOH:O	2.16	0.45
1:A:204:THR:HG23	1:A:207:MET:HE2	1.97	0.45
1:A:284:ILE:HG23	1:A:285:THR:HG23	1.99	0.45
1:C:315:ARG:NH1	6:C:514:HOH:O	2.14	0.45
1:A:130:GLY:HA3	1:A:150:TRP:HB3	1.97	0.45
1:A:132:THR:OG1	6:A:506:HOH:O	2.20	0.45
2:B:170:ARG:NH1	6:B:409:HOH:O	2.46	0.44
1:C:133:ASN:ND2	3:G:3:SIA:C1	2.80	0.44
1:C:133:ASN:ND2	3:G:3:SIA:O1A	2.49	0.44
1:C:44:ILE:HD11	1:C:282:GLN:HB2	2.00	0.44
1:C:57:ILE:O	1:C:61:ILE:HG13	2.18	0.44
1:A:307:LYS:HG3	6:A:535:HOH:O	2.18	0.44
2:B:67:ASP:HB2	6:B:490:HOH:O	2.18	0.43
2:D:121:LYS:O	2:D:125:GLN:HG3	2.19	0.43
1:A:57:ILE:O	1:A:61:ILE:HG13	2.19	0.43
2:B:165:GLU:HG2	6:B:403:HOH:O	2.12	0.43
1:C:41:PHE:CE2	1:C:272:LEU:HB2	2.54	0.43
1:A:39:LYS:NZ	6:A:548:HOH:O	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:276:ASN:HA	6:A:504:HOH:O	2.18	0.43
1:A:41:PHE:CE2	1:A:272:LEU:HB2	2.53	0.43
1:C:38:GLU:HB2	1:C:287:VAL:HB	2.01	0.43
1:C:126:ASP:OD1	1:C:128:SER:OG	2.37	0.43
2:B:153:LYS:NZ	6:B:422:HOH:O	2.53	0.42
5:C:402:NAG:H81	6:C:705:HOH:O	2.18	0.42
2:D:2:ILE:HD13	2:D:2:ILE:HA	1.90	0.42
2:D:58:LYS:HA	2:D:58:LYS:HD3	1.88	0.42
2:D:48:ILE:HD11	2:D:110:LEU:HD22	2.01	0.42
2:B:84:MET:HE2	2:B:84:MET:HB3	1.96	0.42
2:B:156:THR:C	6:B:402:HOH:O	2.59	0.42
1:C:283:THR:HG21	1:C:297:VAL:HG12	2.01	0.42
1:C:82:ARG:HA	1:C:83:PRO:HD3	1.85	0.42
1:C:107:SER:O	1:C:261:THR:HG22	2.20	0.42
2:B:121:LYS:O	2:B:125:GLN:HG3	2.20	0.42
1:A:288:LEU:HD21	1:A:297:VAL:HG21	2.02	0.41
2:B:58:LYS:HA	2:B:58:LYS:HD3	1.90	0.41
2:B:2:ILE:HD13	2:B:2:ILE:HA	1.91	0.41
1:C:158:THR:HG23	6:C:522:HOH:O	2.19	0.41
4:F:5:MAN:O6	4:F:5:MAN:O4	2.29	0.41
1:A:134:ALA:CB	6:A:506:HOH:O	2.64	0.41
2:B:143:LYS:HA	2:B:143:LYS:HD2	1.91	0.40
1:A:8:HIS:HB2	2:B:20:GLY:O	2.22	0.40
1:A:44:ILE:HD11	1:A:282:GLN:HB2	2.02	0.40
1:A:117:PHE:HB2	1:A:252:PRO:O	2.21	0.40

All (5) 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)
6:B:543:HOH:O	6:B:559:HOH:O[3_675]	1.89	0.31
6:A:614:HOH:O	6:B:442:HOH:O[3_675]	1.95	0.25
6:D:425:HOH:O	6:D:517:HOH:O[3_775]	2.00	0.20
6:C:694:HOH:O	6:D:562:HOH:O[3_775]	2.04	0.16
6:B:538:HOH:O	6:B:561:HOH:O[2_765]	2.06	0.14

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	324/326 (99%)	315 (97%)	9 (3%)	0	100	100
1	C	324/326 (99%)	313 (97%)	11 (3%)	0	100	100
2	B	169/171 (99%)	166 (98%)	3 (2%)	0	100	100
2	D	169/171 (99%)	166 (98%)	3 (2%)	0	100	100
All	All	986/994 (99%)	960 (97%)	26 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	287/287 (100%)	286 (100%)	1 (0%)	86	91
1	C	287/287 (100%)	285 (99%)	2 (1%)	76	83
2	B	146/146 (100%)	146 (100%)	0	100	100
2	D	146/146 (100%)	146 (100%)	0	100	100
All	All	866/866 (100%)	863 (100%)	3 (0%)	86	91

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	ILE
1	C	61	ILE
1	C	140	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	87	ASN
1	A	133	ASN
1	C	15	GLN
1	C	133	ASN
2	D	50	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

18 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	E	1	3	14,14,15	0.21	0	17,19,21	0.43	0
3	GAL	E	2	3	11,11,12	0.67	0	15,15,17	0.93	0
3	SIA	E	3	3	20,20,21	1.18	2 (10%)	21,28,31	1.69	4 (19%)
4	NAG	F	1	4,2	14,14,15	0.83	1 (7%)	17,19,21	0.93	1 (5%)
4	NAG	F	2	4	14,14,15	0.29	0	17,19,21	0.44	0
4	BMA	F	3	4	11,11,12	0.94	0	15,15,17	1.34	3 (20%)
4	MAN	F	4	4	11,11,12	0.85	1 (9%)	15,15,17	1.28	2 (13%)
4	MAN	F	5	4	11,11,12	1.09	2 (18%)	15,15,17	1.48	4 (26%)
4	FUC	F	6	4	10,10,11	0.62	0	14,14,16	1.07	1 (7%)
3	NAG	G	1	3	14,14,15	0.22	0	17,19,21	0.41	0
3	GAL	G	2	3	11,11,12	0.67	0	15,15,17	0.90	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SIA	G	3	3	20,20,21	1.19	2 (10%)	21,28,31	1.72	4 (19%)
4	NAG	H	1	4,2	14,14,15	0.30	0	17,19,21	0.85	1 (5%)
4	NAG	H	2	4	14,14,15	0.31	0	17,19,21	0.63	1 (5%)
4	BMA	H	3	4	11,11,12	0.95	0	15,15,17	1.22	2 (13%)
4	MAN	H	4	4	11,11,12	0.76	0	15,15,17	0.99	2 (13%)
4	MAN	H	5	4	11,11,12	0.76	0	15,15,17	1.26	2 (13%)
4	FUC	H	6	4	10,10,11	0.70	0	14,14,16	1.36	2 (14%)

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	E	1	3	-	0/6/23/26	0/1/1/1
3	GAL	E	2	3	-	2/2/19/22	0/1/1/1
3	SIA	E	3	3	-	2/18/34/38	0/1/1/1
4	NAG	F	1	4,2	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
4	BMA	F	3	4	-	2/2/19/22	0/1/1/1
4	MAN	F	4	4	-	0/2/19/22	1/1/1/1
4	MAN	F	5	4	-	1/2/19/22	0/1/1/1
4	FUC	F	6	4	1/1/4/5	-	0/1/1/1
3	NAG	G	1	3	-	0/6/23/26	0/1/1/1
3	GAL	G	2	3	-	2/2/19/22	0/1/1/1
3	SIA	G	3	3	-	2/18/34/38	0/1/1/1
4	NAG	H	1	4,2	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	1/6/23/26	0/1/1/1
4	BMA	H	3	4	-	2/2/19/22	0/1/1/1
4	MAN	H	4	4	-	1/2/19/22	1/1/1/1
4	MAN	H	5	4	-	1/2/19/22	1/1/1/1
4	FUC	H	6	4	1/1/4/5	-	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	1	NAG	O5-C1	-2.90	1.38	1.43
3	E	3	SIA	C10-N5	2.83	1.43	1.34
3	G	3	SIA	C10-N5	2.81	1.43	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	5	MAN	C1-C2	2.61	1.58	1.52
3	G	3	SIA	O6-C6	-2.26	1.40	1.44
4	F	5	MAN	C2-C3	2.20	1.55	1.52
3	E	3	SIA	O6-C6	-2.19	1.40	1.44
4	F	4	MAN	O5-C5	2.02	1.47	1.43

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	3	SIA	O6-C2-C1	4.13	115.51	107.72
3	E	3	SIA	O6-C2-C1	4.12	115.49	107.72
4	H	5	MAN	C1-O5-C5	3.82	117.30	112.19
4	F	4	MAN	C1-O5-C5	3.52	116.90	112.19
3	G	3	SIA	O1B-C1-C2	3.40	121.55	112.71
3	E	3	SIA	O1B-C1-C2	3.37	121.48	112.71
4	H	6	FUC	C1-O5-C5	3.30	120.74	112.97
3	G	3	SIA	O6-C2-C3	-3.26	106.17	110.56
3	E	3	SIA	O6-C2-C3	-3.13	106.34	110.56
4	F	5	MAN	C1-C2-C3	3.11	114.17	109.64
4	H	3	BMA	C1-O5-C5	2.71	115.82	112.19
4	F	5	MAN	C1-O5-C5	2.59	115.65	112.19
4	H	4	MAN	C1-O5-C5	2.58	115.65	112.19
4	F	3	BMA	O3-C3-C2	2.54	115.23	110.05
4	H	1	NAG	O3-C3-C4	2.47	116.20	110.38
4	F	6	FUC	C1-O5-C5	2.46	118.77	112.97
4	H	3	BMA	O3-C3-C2	2.36	114.87	110.05
4	F	1	NAG	C3-C4-C5	2.27	114.35	110.23
4	F	3	BMA	O3-C3-C4	2.25	115.69	110.38
4	H	5	MAN	O2-C2-C3	-2.23	105.54	110.15
4	F	4	MAN	O2-C2-C3	-2.22	105.55	110.15
4	H	4	MAN	O2-C2-C3	-2.21	105.58	110.15
4	H	2	NAG	C1-O5-C5	2.19	115.12	112.19
3	G	3	SIA	O1B-C1-O1A	-2.12	119.26	124.08
4	F	3	BMA	C1-O5-C5	2.09	114.99	112.19
4	F	5	MAN	O5-C1-C2	2.08	115.74	110.79
3	E	3	SIA	O1B-C1-O1A	-2.06	119.41	124.08
4	H	6	FUC	C1-C2-C3	2.02	112.59	109.64
4	F	5	MAN	O2-C2-C3	-2.01	106.00	110.15

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	F	6	FUC	C1
4	H	6	FUC	C1

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	3	BMA	O5-C5-C6-O6
4	F	2	NAG	O5-C5-C6-O6
4	F	3	BMA	O5-C5-C6-O6
4	H	3	BMA	C4-C5-C6-O6
4	F	5	MAN	O5-C5-C6-O6
4	F	3	BMA	C4-C5-C6-O6
3	E	3	SIA	C11-C10-N5-C5
3	E	3	SIA	O10-C10-N5-C5
3	G	3	SIA	C11-C10-N5-C5
3	G	3	SIA	O10-C10-N5-C5
4	F	2	NAG	C4-C5-C6-O6
3	E	2	GAL	C4-C5-C6-O6
4	H	5	MAN	O5-C5-C6-O6
4	H	4	MAN	O5-C5-C6-O6
4	H	2	NAG	O5-C5-C6-O6
3	G	2	GAL	C4-C5-C6-O6
3	E	2	GAL	O5-C5-C6-O6
3	G	2	GAL	O5-C5-C6-O6

All (3) ring outliers are listed below:

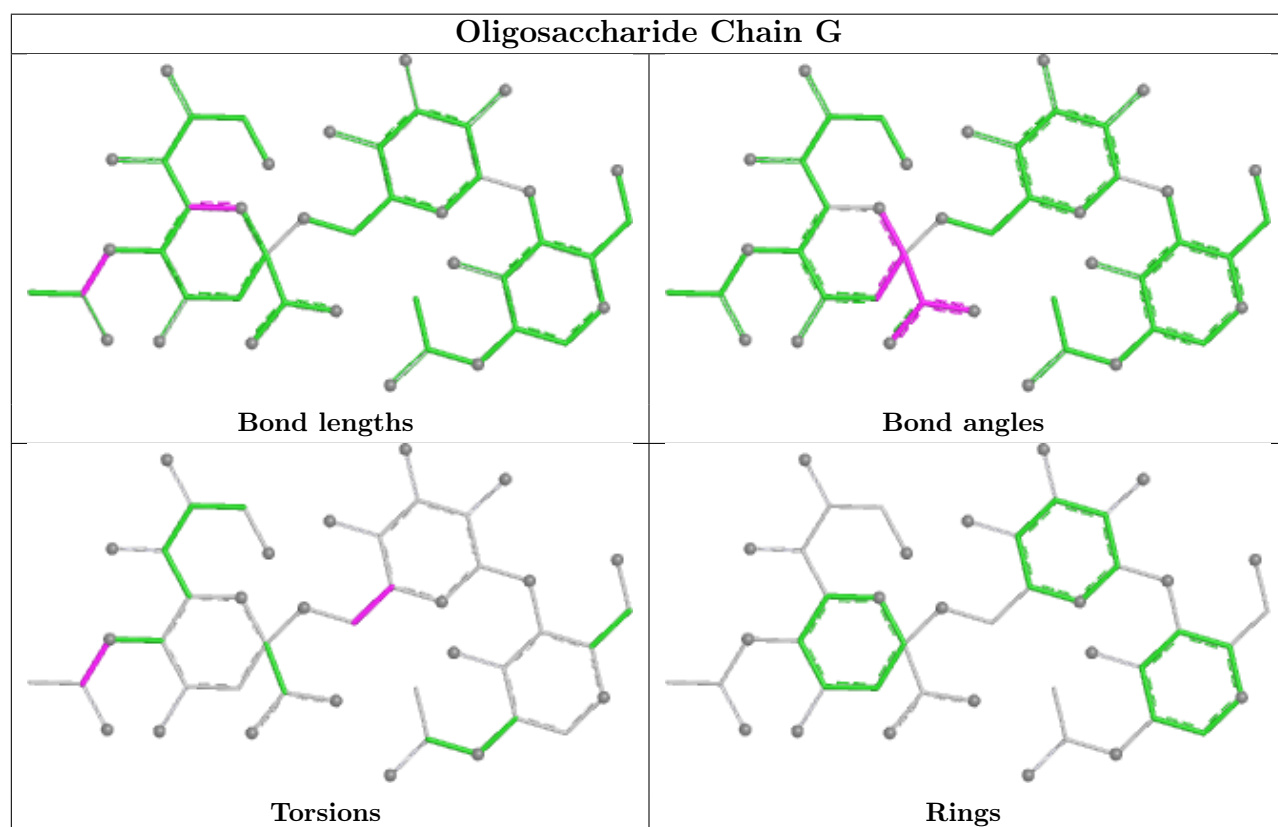
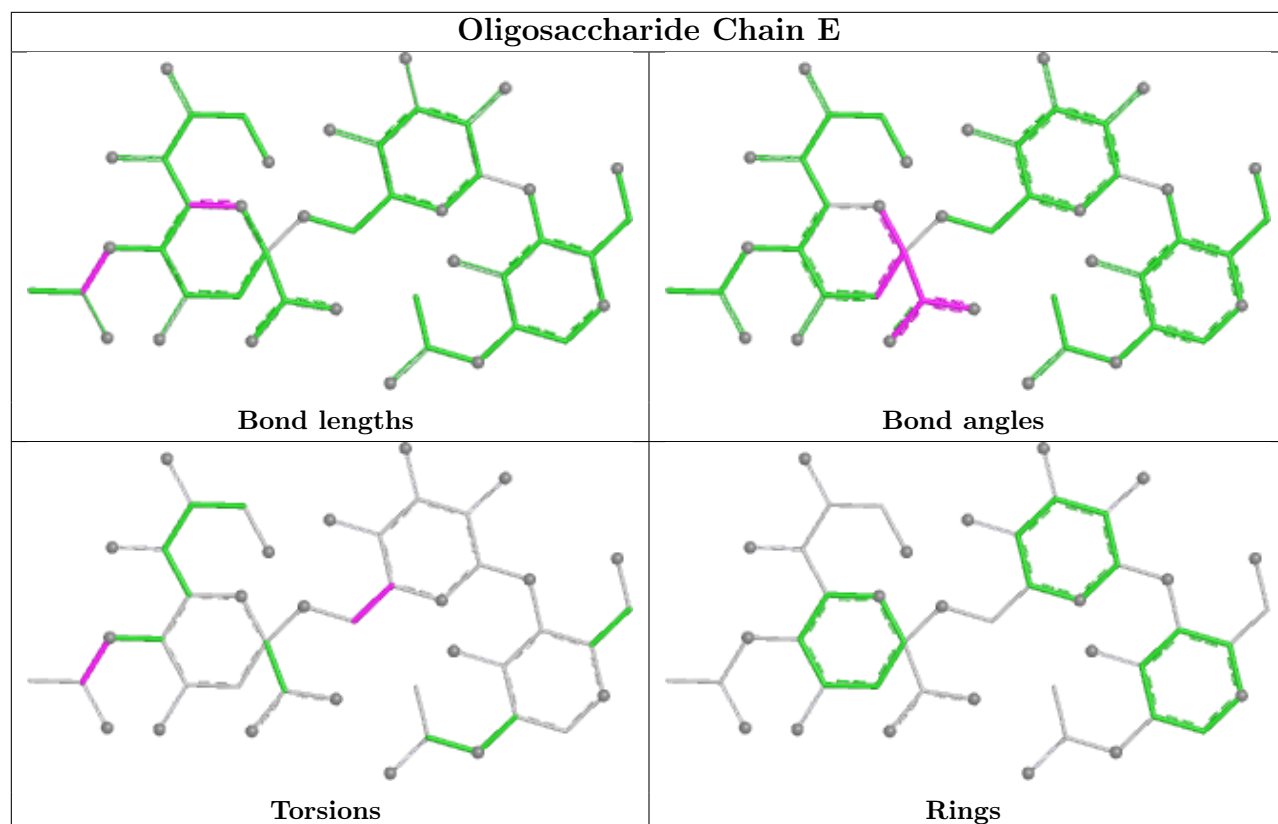
Mol	Chain	Res	Type	Atoms
4	F	4	MAN	C1-C2-C3-C4-C5-O5
4	H	4	MAN	C1-C2-C3-C4-C5-O5
4	H	5	MAN	C1-C2-C3-C4-C5-O5

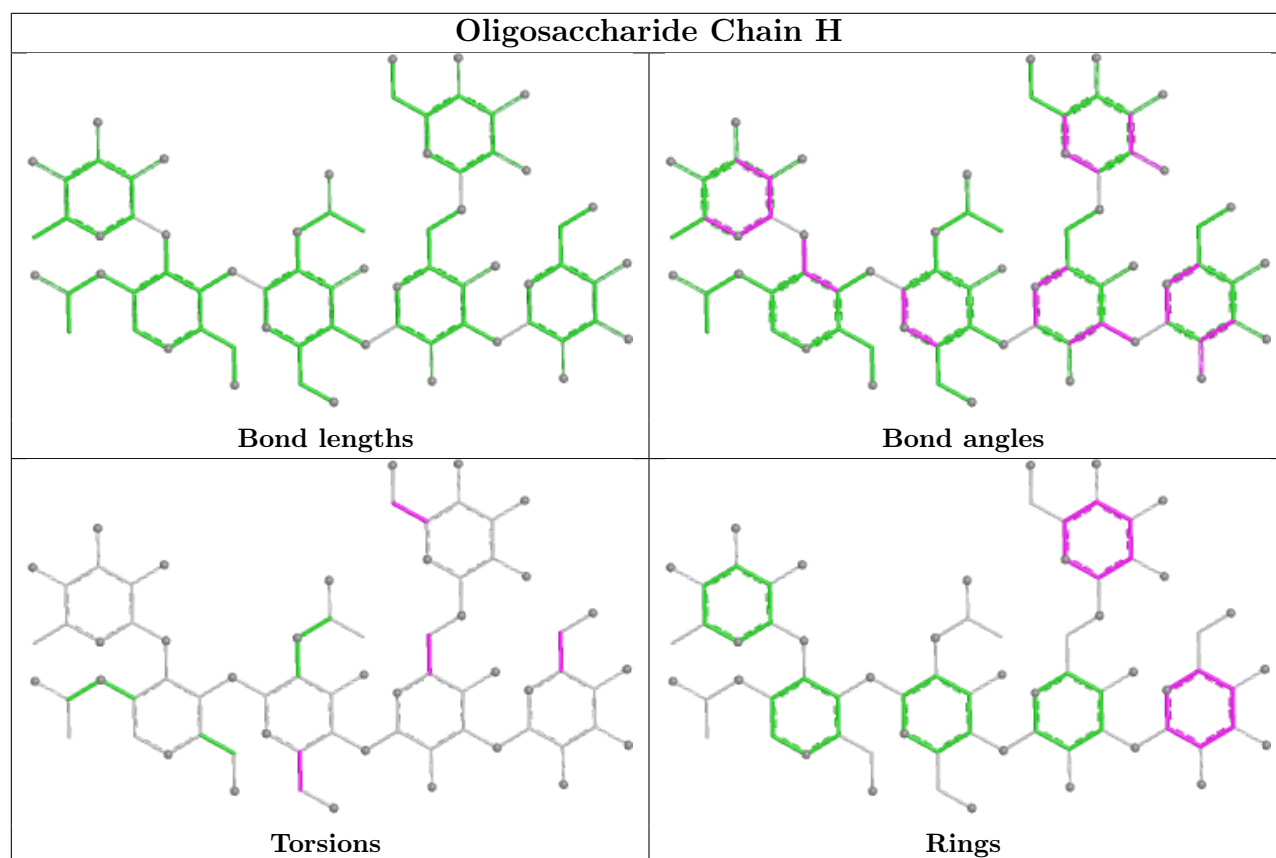
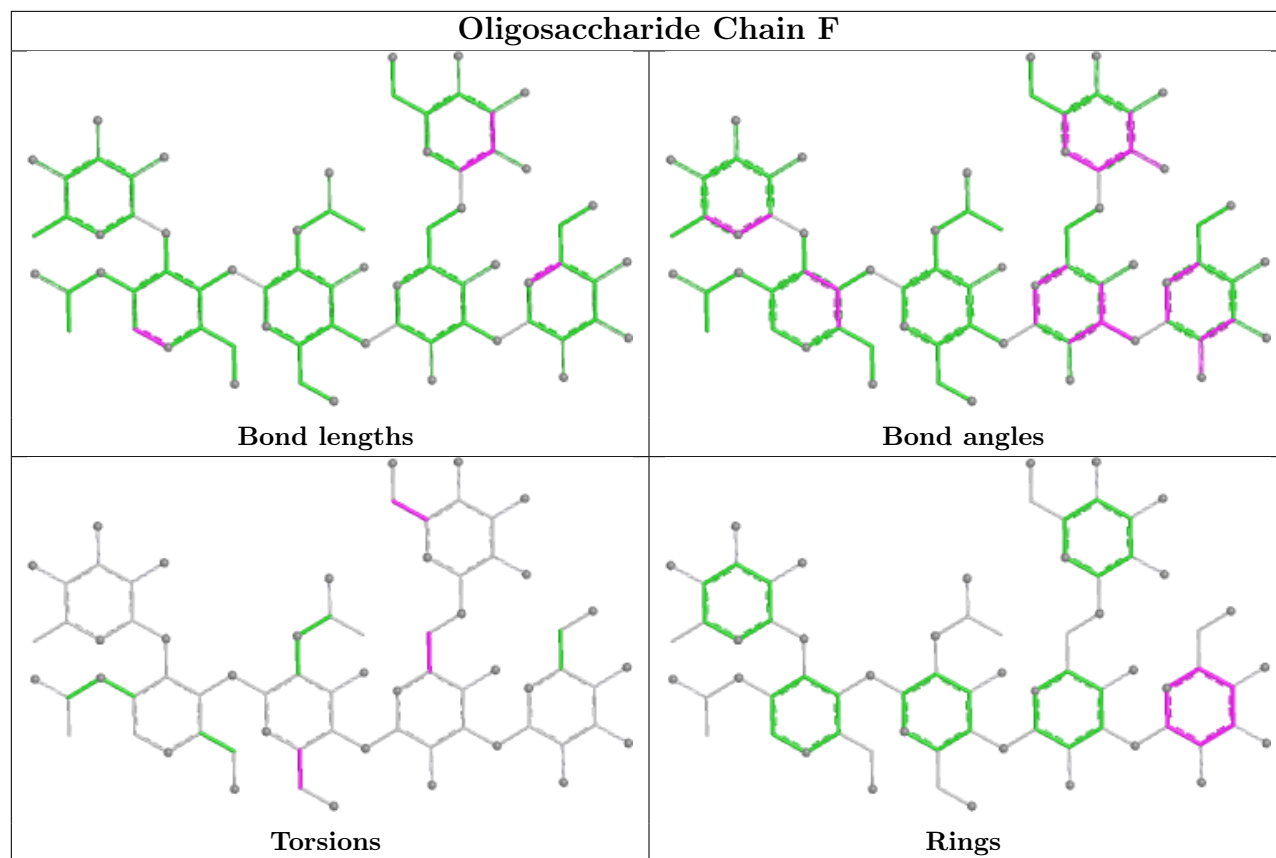
6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	5	MAN	1	0
3	G	2	GAL	2	0
3	G	3	SIA	2	0
4	F	1	NAG	1	0
3	G	1	NAG	4	0
3	E	2	GAL	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

8 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	C	401	1	14,14,15	0.89	1 (7%)	17,19,21	1.12	1 (5%)
5	NAG	C	403	1	14,14,15	1.14	1 (7%)	17,19,21	1.32	2 (11%)
5	NAG	A	401	1	14,14,15	0.91	2 (14%)	17,19,21	1.27	1 (5%)
5	NAG	A	404	1	14,14,15	0.20	0	17,19,21	0.43	0
5	NAG	C	404	1	14,14,15	0.23	0	17,19,21	0.43	0
5	NAG	C	402	1	14,14,15	0.70	1 (7%)	17,19,21	0.73	1 (5%)
5	NAG	A	402	1	14,14,15	0.50	0	17,19,21	0.64	0
5	NAG	A	403	1	14,14,15	0.21	0	17,19,21	0.92	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	C	401	1	-	4/6/23/26	0/1/1/1
5	NAG	C	403	1	-	1/6/23/26	0/1/1/1
5	NAG	A	401	1	-	0/6/23/26	0/1/1/1
5	NAG	A	404	1	-	2/6/23/26	0/1/1/1
5	NAG	C	404	1	-	2/6/23/26	0/1/1/1
5	NAG	C	402	1	-	2/6/23/26	0/1/1/1
5	NAG	A	402	1	-	4/6/23/26	0/1/1/1
5	NAG	A	403	1	-	2/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	403	NAG	C1-C2	3.72	1.57	1.52
5	C	401	NAG	O5-C1	2.67	1.48	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	401	NAG	O5-C1	2.46	1.47	1.43
5	C	402	NAG	O5-C1	-2.33	1.39	1.43
5	A	401	NAG	C1-C2	2.28	1.55	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	401	NAG	C1-O5-C5	4.95	118.81	112.19
5	C	403	NAG	C1-O5-C5	4.35	118.01	112.19
5	C	401	NAG	C1-O5-C5	4.05	117.61	112.19
5	A	403	NAG	C1-O5-C5	3.43	116.78	112.19
5	C	403	NAG	C4-C3-C2	2.66	114.92	111.02
5	C	402	NAG	C3-C4-C5	2.19	114.20	110.23

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	404	NAG	C4-C5-C6-O6
5	C	401	NAG	C4-C5-C6-O6
5	C	402	NAG	O5-C5-C6-O6
5	A	402	NAG	O5-C5-C6-O6
5	A	403	NAG	O5-C5-C6-O6
5	A	404	NAG	O5-C5-C6-O6
5	C	401	NAG	O5-C5-C6-O6
5	A	402	NAG	C4-C5-C6-O6
5	A	404	NAG	C4-C5-C6-O6
5	C	404	NAG	O5-C5-C6-O6
5	A	402	NAG	C8-C7-N2-C2
5	A	402	NAG	O7-C7-N2-C2
5	A	403	NAG	C4-C5-C6-O6
5	C	402	NAG	C4-C5-C6-O6
5	C	403	NAG	O5-C5-C6-O6
5	C	401	NAG	C3-C2-N2-C7
5	C	401	NAG	C1-C2-N2-C7

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	401	NAG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	402	NAG	1	0
5	A	402	NAG	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 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	326/326 (100%)	-1.37	0 100 100	17, 39, 64, 104	0
1	C	326/326 (100%)	-1.39	0 100 100	17, 39, 63, 99	0
2	B	171/171 (100%)	-1.52	0 100 100	15, 26, 47, 77	0
2	D	171/171 (100%)	-1.55	0 100 100	14, 27, 46, 74	0
All	All	994/994 (100%)	-1.43	0 100 100	14, 33, 61, 104	0

There are no RSRZ outliers to report.

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.

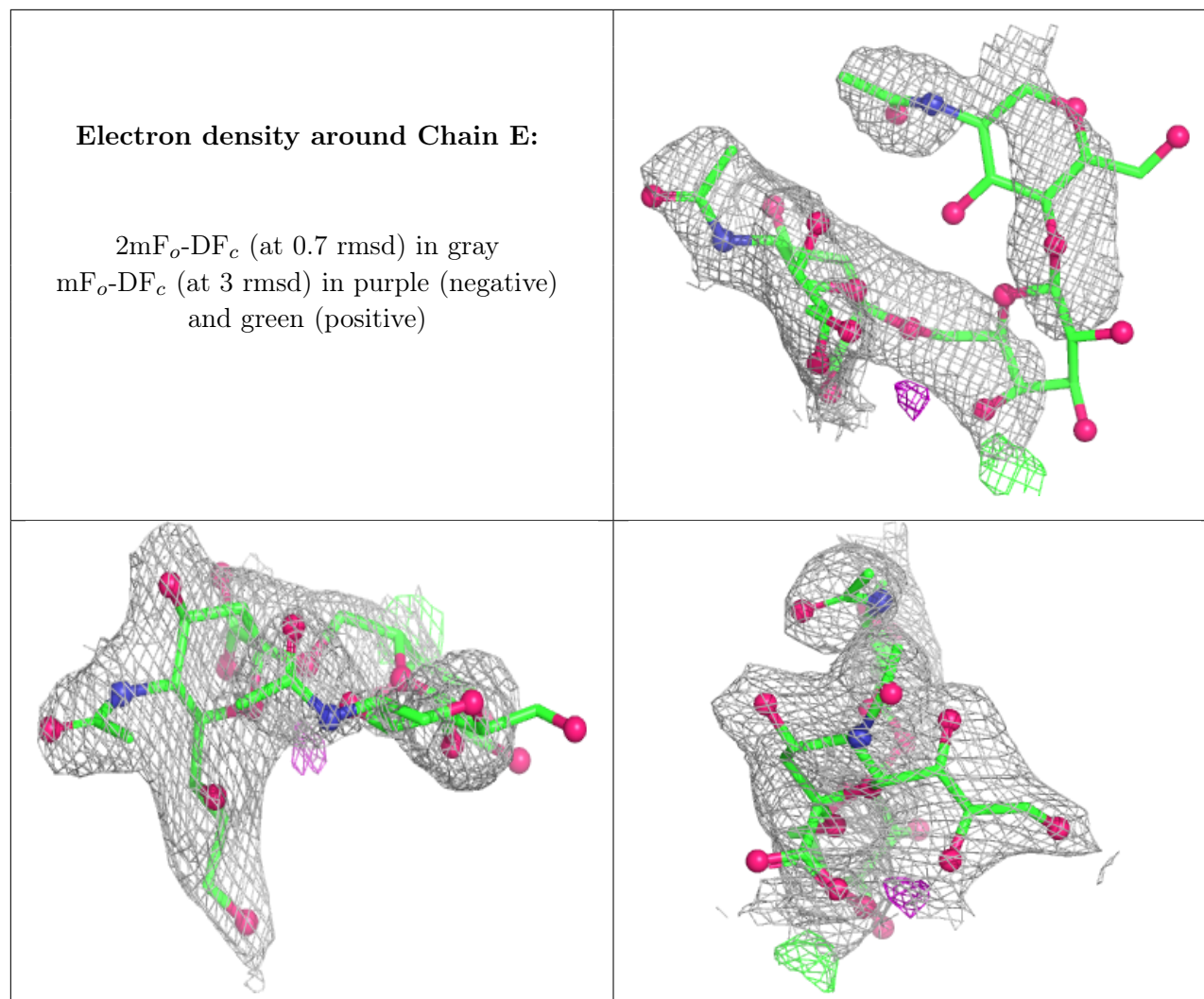
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GAL	G	2	11/12	0.96	0.08	68,92,101,101	0
4	MAN	F	4	11/12	0.96	0.07	53,54,54,54	0
4	MAN	H	5	11/12	0.96	0.07	51,51,52,52	0
4	FUC	H	6	10/11	0.96	0.07	45,45,46,47	0
4	FUC	F	6	10/11	0.97	0.06	44,45,45,46	0
3	GAL	E	2	11/12	0.97	0.08	67,91,100,102	0
3	NAG	G	1	14/15	0.97	0.09	75,100,111,112	0
4	MAN	F	5	11/12	0.98	0.07	52,53,54,54	0
4	NAG	F	1	14/15	0.98	0.05	37,41,44,45	0

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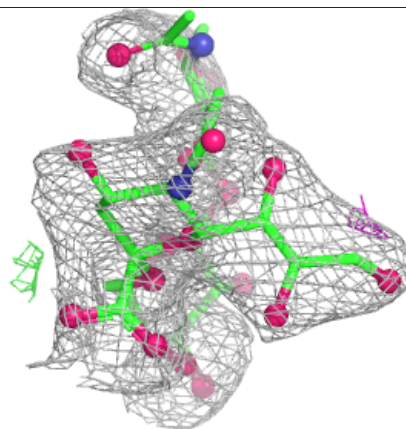
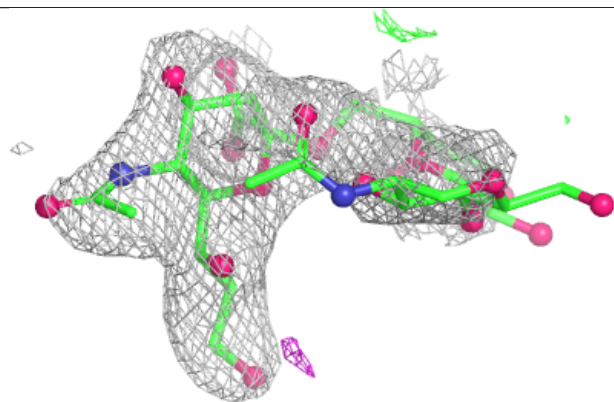
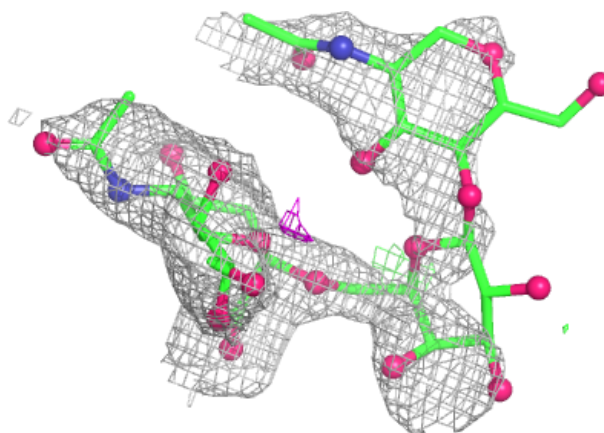
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	H	1	14/15	0.98	0.05	40,42,44,45	0
4	BMA	H	3	11/12	0.98	0.06	51,51,52,52	0
4	MAN	H	4	11/12	0.98	0.06	51,52,52,52	0
4	BMA	F	3	11/12	0.98	0.06	52,53,54,54	0
3	NAG	E	1	14/15	0.98	0.08	74,101,108,111	0
4	NAG	F	2	14/15	0.99	0.05	46,49,51,52	0
3	SIA	G	3	20/21	0.99	0.05	50,59,70,71	0
3	SIA	E	3	20/21	0.99	0.04	51,60,71,73	0
4	NAG	H	2	14/15	0.99	0.04	46,47,50,53	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.



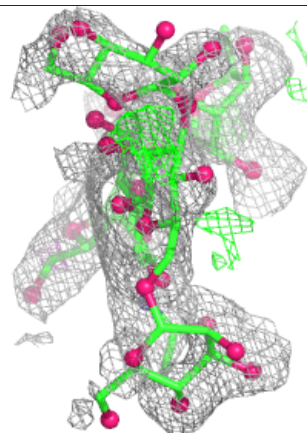
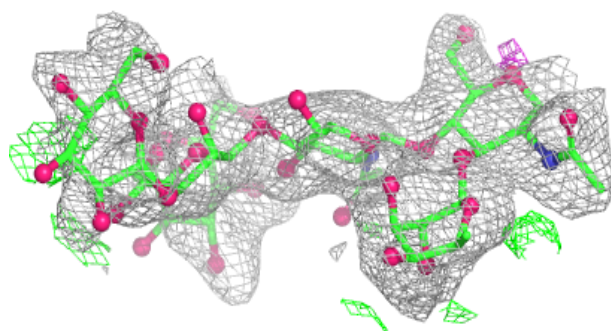
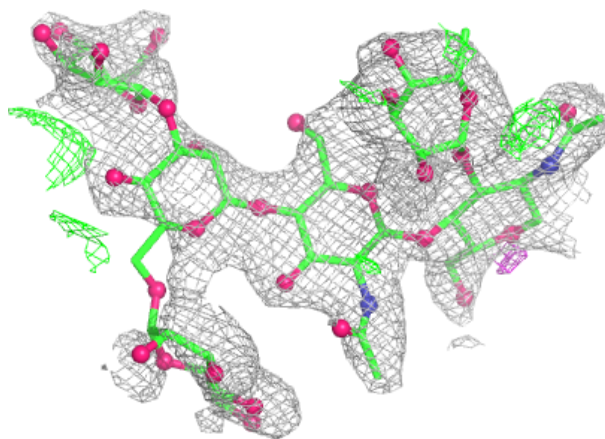
Electron density around Chain G:

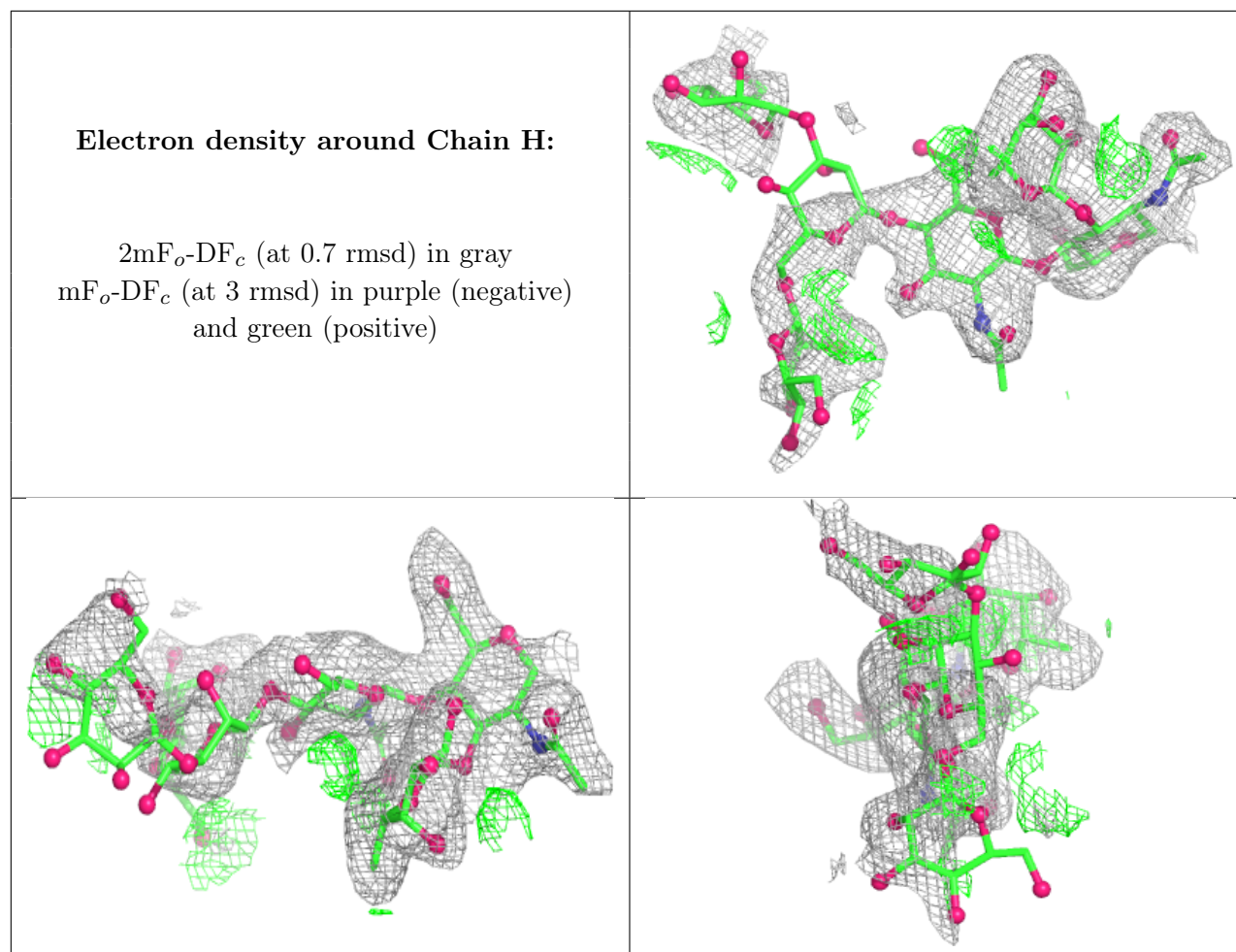
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain F:

$2mF_o - DF_c$ (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
5	NAG	A	401	14/15	0.93	0.07	40,45,45,45	0
5	NAG	A	402	14/15	0.96	0.07	47,48,48,51	0
5	NAG	A	404	14/15	0.96	0.07	50,52,52,53	0
5	NAG	A	403	14/15	0.97	0.06	50,54,56,57	0
5	NAG	C	401	14/15	0.97	0.06	39,42,43,43	0
5	NAG	C	404	14/15	0.97	0.06	47,51,51,51	0
5	NAG	C	403	14/15	0.98	0.05	51,54,57,57	0
5	NAG	C	402	14/15	0.98	0.05	46,47,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.