



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:13 AM UTC

PDB ID : 2DU1 / pdb_00002du1
Title : Crystal Structure of basic winged bean lectin in complex with Methyl-alpha-N-acetyl-D galactosamine
Authors : Kulkarni, K.A.; Katiyar, S.; Surolia, A.; Vijayan, M.; Suguna, K.
Deposited on : 2006-07-19
Resolution : 2.60 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

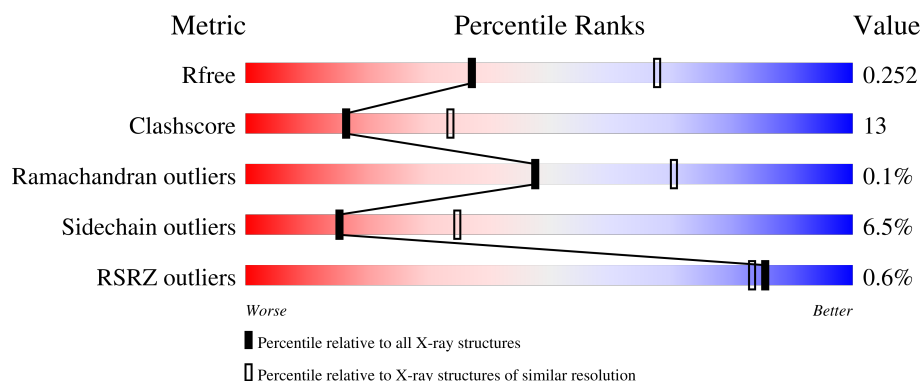
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

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



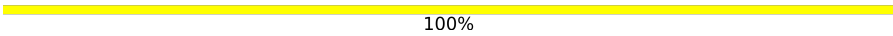
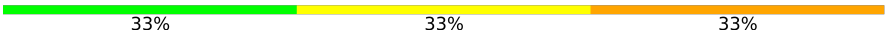
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	241	 71% 24% . .
1	B	241	 74% 20% 5% .
1	C	241	 69% 26% . .
1	D	241	 71% 24% . .
2	E	3	 67% 33%

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Mol	Chain	Length	Quality of chain
2	F	3	
2	G	3	
2	H	3	
3	I	2	

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
2	NAG	G	3	-	-	X	-

2 Entry composition [i](#)

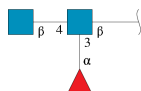
There are 8 unique types of molecules in this entry. The entry contains 7888 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Basic agglutinin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	237	Total	C	N	O	0	0	0
			1829	1178	304	347			
1	B	237	Total	C	N	O	0	0	0
			1820	1172	301	347			
1	C	237	Total	C	N	O	0	0	0
			1823	1173	304	346			
1	D	237	Total	C	N	O	0	0	0
			1829	1178	304	347			

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



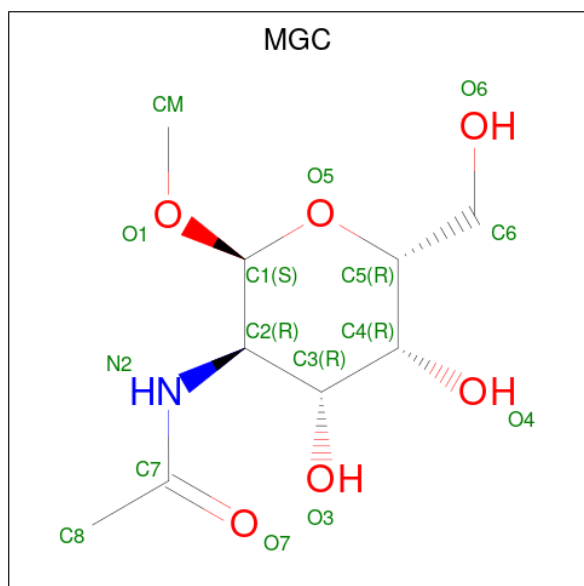
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	3	Total	C	N	O	0	0	0
			38	22	2	14			
2	F	3	Total	C	N	O	0	0	0
			38	22	2	14			
2	G	3	Total	C	N	O	0	0	0
			38	22	2	14			
2	H	3	Total	C	N	O	0	0	0
			38	22	2	14			

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



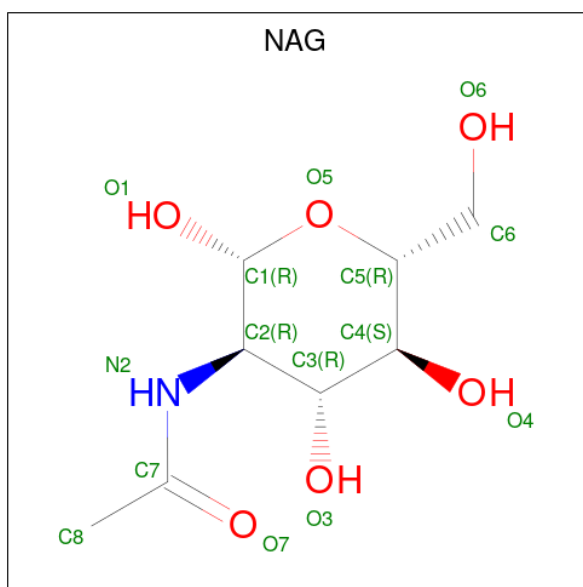
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is methyl 2-acetamido-2-deoxy- α -D-galactopyranoside (CCD ID: MGC) (formula: $C_9H_{17}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			16	9	1	6		
4	B	1	Total	C	N	O	0	0
			16	9	1	6		
4	C	1	Total	C	N	O	0	0
			16	9	1	6		
4	D	1	Total	C	N	O	0	0
			16	9	1	6		

- Molecule 5 is 2-acetamido-2-deoxy- β -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	C	1	Total	C	N	O	0	0
			14	8	1	5		
5	D	1	Total	C	N	O	0	0
			14	8	1	5		

- 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	B	1	Total	Ca	0	0
			1	1		
6	C	1	Total	Ca	0	0
			1	1		
6	D	1	Total	Ca	0	0
			1	1		

- Molecule 7 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Mn	0	0
			1	1		
7	B	1	Total	Mn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	1	Total 1	Mn 1	0	0
7	D	1	Total 1	Mn 1	0	0

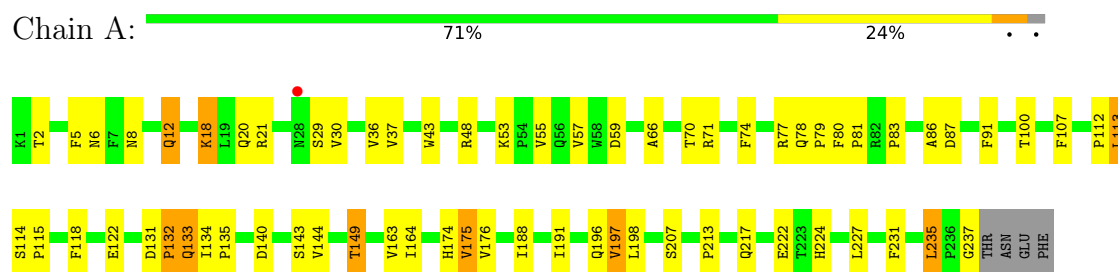
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	88	Total 88	O 88	0	0
8	B	94	Total 94	O 94	0	0
8	C	51	Total 51	O 51	0	0
8	D	60	Total 60	O 60	0	0

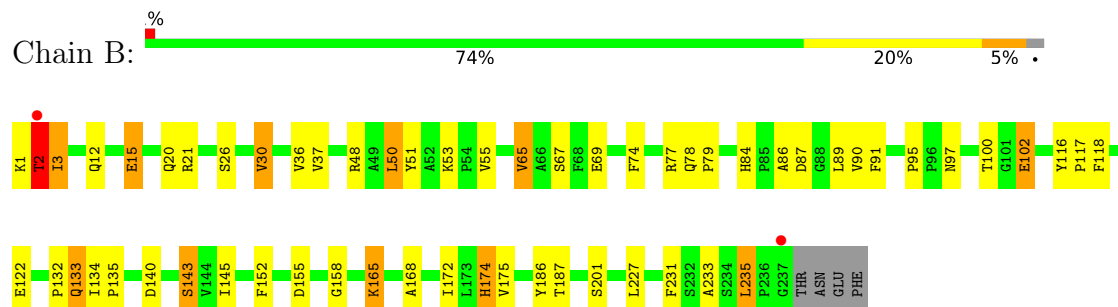
3 Residue-property plots

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.

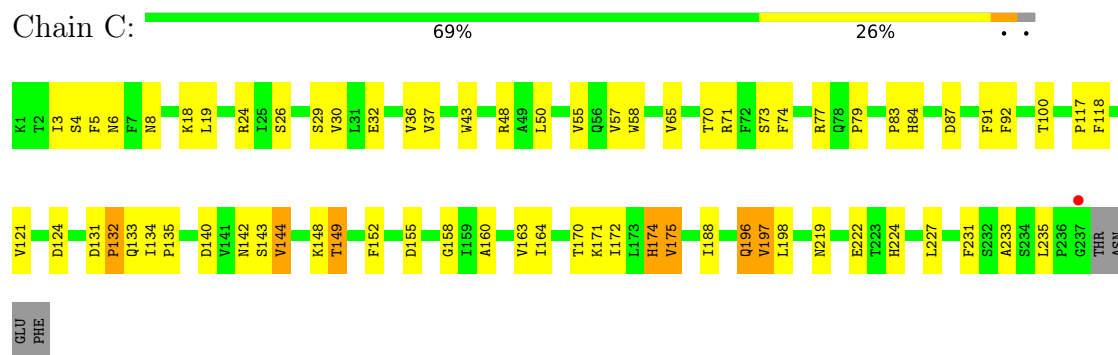
• Molecule 1: Basic agglutinin



• Molecule 1: Basic agglutinin

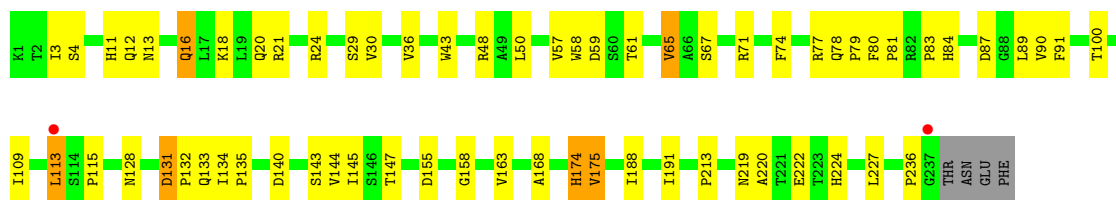


• Molecule 1: Basic agglutinin



• Molecule 1: Basic agglutinin





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

Chain E: 67% 33%



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

Chain F: 33% 67%



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

Chain G: 100%



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

Chain H: 33% 33% 33%



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

Chain I: 100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	157.62Å 90.96Å 73.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.60 30.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	95.8 (30.00-2.60) 95.6 (30.00-2.60)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.06 (at 2.60Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.194 , 0.251 0.203 , 0.252	Depositor DCC
R_{free} test set	1427 reflections (4.49%)	wwPDB-VP
Wilson B-factor (Å ²)	41.2	Xtriage
Anisotropy	0.673	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 54.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7888	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MN, FUC, MGC, NAG, CA

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	0.50	0/1882	0.96	7/2578 (0.3%)
1	B	0.51	0/1873	0.97	9/2567 (0.4%)
1	C	0.45	0/1876	0.96	6/2569 (0.2%)
1	D	0.45	0/1882	0.95	9/2578 (0.3%)
All	All	0.48	0/7513	0.96	31/10292 (0.3%)

There are no bond length outliers.

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	124	ASP	CA-CB-CG	8.81	121.41	112.60
1	B	91	PHE	N-CA-C	-7.20	97.49	109.07
1	D	91	PHE	N-CA-C	-7.20	97.48	109.07
1	C	91	PHE	N-CA-C	-7.08	97.67	109.07
1	A	91	PHE	N-CA-C	-6.53	98.55	109.07
1	B	2	THR	N-CA-C	6.36	118.73	109.07
1	B	78	GLN	CA-C-N	6.00	125.55	119.19
1	B	78	GLN	C-N-CA	6.00	125.55	119.19
1	A	78	GLN	CA-C-N	5.97	125.67	119.05
1	A	78	GLN	C-N-CA	5.97	125.67	119.05
1	A	21	ARG	CB-CA-C	-5.85	109.85	116.63
1	B	3	ILE	N-CA-C	5.79	121.38	109.34
1	B	21	ARG	CB-CA-C	-5.71	109.97	116.54
1	A	132	PRO	N-CA-C	-5.53	101.08	112.47
1	D	132	PRO	N-CA-C	-5.43	101.28	112.47
1	C	132	PRO	N-CA-C	-5.39	101.37	112.47
1	D	131	ASP	N-CA-C	5.37	117.37	110.39
1	D	21	ARG	CB-CA-C	-5.32	110.42	116.54
1	D	29	SER	N-CA-C	5.29	123.87	113.29
1	D	67	SER	N-CA-C	-5.28	101.55	109.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	132	PRO	N-CA-C	-5.28	101.60	112.47
1	A	29	SER	N-CA-C	5.25	124.02	113.31
1	B	51	TYR	N-CA-C	-5.25	102.09	109.96
1	D	78	GLN	CA-C-N	5.18	126.31	119.84
1	D	78	GLN	C-N-CA	5.18	126.31	119.84
1	C	197	VAL	CB-CA-C	-5.17	106.51	111.06
1	C	29	SER	N-CA-C	5.13	123.78	113.31
1	C	131	ASP	N-CA-C	5.12	117.05	110.39
1	B	67	SER	N-CA-C	-5.10	101.84	109.95
1	D	147	THR	N-CA-C	-5.05	105.86	112.23
1	A	131	ASP	N-CA-C	5.04	116.95	110.39

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1829	0	1770	50	0
1	B	1820	0	1750	51	0
1	C	1823	0	1756	49	0
1	D	1829	0	1770	41	0
2	E	38	0	34	0	0
2	F	38	0	34	4	0
2	G	38	0	34	7	0
2	H	38	0	34	3	0
3	I	28	0	25	2	0
4	A	16	0	17	0	0
4	B	16	0	17	0	0
4	C	16	0	17	0	0
4	D	16	0	17	0	0
5	A	14	0	13	0	0
5	C	14	0	13	0	0
5	D	14	0	13	2	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	A	88	0	0	2	0
8	B	94	0	0	2	0
8	C	51	0	0	2	0
8	D	60	0	0	2	0
All	All	7888	0	7314	192	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (192) 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:G:2:FUC:H3	2:G:3:NAG:H82	1.34	1.05
1:D:16:GLN:HA	1:D:16:GLN:HE21	1.28	0.96
1:A:6:ASN:HD21	1:A:8:ASN:HD21	1.16	0.92
1:B:133:GLN:NE2	1:B:134:ILE:H	1.68	0.92
1:B:133:GLN:HE21	1:B:133:GLN:HA	1.34	0.89
1:A:6:ASN:HD21	1:A:8:ASN:ND2	1.77	0.82
1:A:113:LEU:H	1:A:113:LEU:HD23	1.44	0.82
1:D:83:PRO:HG3	5:D:501:NAG:H81	1.63	0.81
1:B:69:GLU:HG3	1:B:165:LYS:HD2	1.64	0.80
2:G:2:FUC:H3	2:G:3:NAG:C8	2.16	0.76
1:B:133:GLN:HE21	1:B:133:GLN:CA	1.98	0.76
2:G:2:FUC:H5	2:G:3:NAG:C1	2.15	0.75
1:C:132:PRO:HG3	1:C:149:THR:HG21	1.68	0.75
2:G:1:NAG:H4	2:G:3:NAG:HN2	1.52	0.75
1:C:140:ASP:HB3	1:C:143:SER:O	1.87	0.74
1:D:59:ASP:OD2	1:D:61:THR:HB	1.86	0.74
1:C:6:ASN:HD21	1:C:8:ASN:ND2	1.86	0.73
1:A:140:ASP:HB3	1:A:143:SER:O	1.88	0.72
1:D:140:ASP:HB3	1:D:143:SER:O	1.91	0.70
1:B:145:ILE:HB	1:C:196:GLN:HE22	1.55	0.70
1:D:65:VAL:HG13	1:D:168:ALA:HB1	1.74	0.70
1:A:197:VAL:HG22	1:A:198:LEU:HG	1.72	0.69
1:D:16:GLN:HA	1:D:16:GLN:NE2	2.06	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:PRO:HG3	1:A:149:THR:HG21	1.74	0.69
1:C:83:PRO:HD3	2:H:1:NAG:H81	1.73	0.68
2:G:2:FUC:C3	2:G:3:NAG:H82	2.20	0.67
1:C:175:VAL:HG22	1:C:188:ILE:HG22	1.76	0.66
1:D:144:VAL:HG22	8:D:4434:HOH:O	1.94	0.66
1:B:65:VAL:HG13	1:B:168:ALA:HB1	1.77	0.66
1:B:133:GLN:HE21	1:B:134:ILE:H	1.41	0.65
1:B:53:LYS:HE3	8:B:2485:HOH:O	1.94	0.65
1:B:140:ASP:HB3	1:B:143:SER:O	1.96	0.65
1:A:83:PRO:HG2	1:A:217:GLN:NE2	2.12	0.64
1:A:176:VAL:HG21	1:B:187:THR:HG21	1.80	0.63
1:A:113:LEU:H	1:A:113:LEU:CD2	2.09	0.63
1:A:176:VAL:HG21	1:B:187:THR:CG2	2.28	0.63
1:B:48:ARG:HD2	1:B:100:THR:OG1	1.98	0.63
3:I:2:NAG:O3	3:I:2:NAG:H83	1.98	0.63
1:C:26:SER:OG	1:C:30:VAL:HG22	1.99	0.63
1:C:6:ASN:HD21	1:C:8:ASN:HD21	1.45	0.62
1:D:90:VAL:HG21	1:D:109:ILE:HD13	1.81	0.62
2:G:1:NAG:H4	2:G:3:NAG:N2	2.12	0.62
2:G:3:NAG:H83	2:G:3:NAG:H3	1.80	0.62
1:C:144:VAL:HG22	8:C:3402:HOH:O	1.99	0.62
1:C:197:VAL:HG23	1:C:198:LEU:HG	1.81	0.62
1:A:71:ARG:HG2	1:A:163:VAL:HG22	1.81	0.61
1:B:133:GLN:HE21	1:B:134:ILE:N	1.98	0.61
1:A:196:GLN:HE22	1:D:145:ILE:HB	1.64	0.61
1:C:117:PRO:HA	1:C:142:ASN:OD1	2.01	0.61
1:D:57:VAL:HG23	1:D:58:TRP:HD1	1.66	0.60
1:C:121:VAL:HG21	1:C:164:ILE:HD13	1.83	0.59
1:D:71:ARG:HG2	1:D:163:VAL:HG22	1.85	0.59
1:C:83:PRO:HD3	2:H:1:NAG:C8	2.32	0.59
1:A:6:ASN:ND2	1:A:8:ASN:ND2	2.49	0.59
1:C:50:LEU:HD11	1:C:92:PHE:HZ	1.68	0.59
1:B:133:GLN:NE2	1:B:133:GLN:HA	2.09	0.58
1:B:133:GLN:NE2	1:B:134:ILE:N	2.45	0.58
1:D:48:ARG:HD2	1:D:100:THR:HG23	1.86	0.58
1:A:36:VAL:O	1:A:36:VAL:HG13	2.04	0.57
1:C:84:HIS:HD2	1:C:84:HIS:O	1.86	0.57
1:B:143:SER:OG	1:C:196:GLN:NE2	2.38	0.57
1:D:20:GLN:OE1	1:D:48:ARG:HD3	2.04	0.57
1:B:2:THR:HB	1:B:233:ALA:O	2.05	0.57
1:C:227:LEU:HD22	1:C:227:LEU:N	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:84:HIS:O	1:B:84:HIS:HD2	1.89	0.56
1:A:18:LYS:HD3	1:A:18:LYS:C	2.31	0.56
1:D:77:ARG:O	1:D:79:PRO:HD3	2.06	0.56
1:B:20:GLN:OE1	1:B:48:ARG:HD3	2.06	0.56
1:C:50:LEU:HD11	1:C:92:PHE:CZ	2.39	0.56
1:A:37:VAL:HG23	1:A:37:VAL:O	2.06	0.56
1:A:196:GLN:NE2	1:D:143:SER:OG	2.39	0.56
1:A:114:SER:N	1:A:115:PRO:HD3	2.22	0.55
1:B:84:HIS:O	1:B:84:HIS:CD2	2.60	0.55
1:A:83:PRO:HG2	1:A:217:GLN:HE21	1.71	0.55
1:C:84:HIS:O	1:C:84:HIS:CD2	2.60	0.54
1:D:128:ASN:HB2	1:D:131:ASP:OD2	2.08	0.54
1:C:4:SER:HA	1:C:231:PHE:O	2.08	0.53
1:D:12:GLN:HG2	1:D:13:ASN:ND2	2.24	0.53
1:C:19:LEU:N	1:C:19:LEU:HD12	2.23	0.52
1:A:113:LEU:HD23	1:A:113:LEU:N	2.21	0.52
1:C:155:ASP:OD2	1:C:158:GLY:HA3	2.09	0.52
2:F:2:FUC:C6	2:F:3:NAG:H2	2.40	0.52
1:A:77:ARG:O	1:A:79:PRO:HD3	2.10	0.52
1:D:155:ASP:OD2	1:D:158:GLY:HA3	2.10	0.52
1:C:36:VAL:HG13	1:C:36:VAL:O	2.10	0.51
1:A:112:PRO:O	1:A:115:PRO:HD3	2.11	0.51
2:F:2:FUC:H62	2:F:3:NAG:H2	1.93	0.51
1:D:43:TRP:CZ3	1:D:213:PRO:HA	2.46	0.51
1:A:48:ARG:HD2	1:A:100:THR:HG23	1.93	0.51
1:B:102:GLU:HA	1:B:102:GLU:OE1	2.10	0.51
1:C:48:ARG:HD2	1:C:100:THR:OG1	2.10	0.51
1:C:24:ARG:HH11	1:C:24:ARG:HB3	1.75	0.51
1:C:50:LEU:HD22	1:C:50:LEU:N	2.26	0.50
1:A:53:LYS:NZ	8:A:1441:HOH:O	2.45	0.50
1:B:133:GLN:NE2	1:B:133:GLN:CA	2.70	0.50
1:B:1:LYS:HA	8:B:2408:HOH:O	2.10	0.50
1:A:176:VAL:CG2	1:B:187:THR:HG21	2.42	0.50
1:A:66:ALA:HB2	1:A:235:LEU:HG	1.94	0.49
1:C:134:ILE:HB	1:C:135:PRO:HA	1.93	0.49
1:B:145:ILE:HB	1:C:196:GLN:NE2	2.23	0.49
1:D:175:VAL:HG13	1:D:188:ILE:HG23	1.94	0.49
1:D:16:GLN:HE21	1:D:16:GLN:CA	2.11	0.48
1:D:134:ILE:HB	1:D:135:PRO:HA	1.96	0.48
2:F:1:NAG:O4	2:F:2:FUC:H5	2.14	0.48
1:A:12:GLN:HE21	1:A:12:GLN:HB2	1.54	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:196:GLN:NE2	1:D:143:SER:CB	2.77	0.47
1:C:77:ARG:O	1:C:79:PRO:HD3	2.15	0.47
1:D:74:PHE:CD1	1:D:74:PHE:C	2.92	0.47
1:A:144:VAL:O	1:A:144:VAL:HG22	2.13	0.47
1:C:152:PHE:C	1:C:152:PHE:CD1	2.92	0.47
1:B:118:PHE:C	1:B:118:PHE:CD1	2.92	0.47
1:C:175:VAL:HG22	1:C:188:ILE:CG2	2.45	0.47
1:A:59:ASP:HB3	1:A:237:GLY:O	2.15	0.46
1:B:155:ASP:OD2	1:B:158:GLY:HA3	2.15	0.46
1:C:3:ILE:HG22	1:C:233:ALA:HB3	1.97	0.46
1:C:71:ARG:HG2	1:C:163:VAL:HG22	1.97	0.46
1:D:24:ARG:HH11	1:D:24:ARG:HG3	1.80	0.46
1:A:48:ARG:HG2	1:A:207:SER:OG	2.15	0.46
1:D:227:LEU:N	1:D:227:LEU:HD22	2.31	0.46
1:C:134:ILE:C	1:C:134:ILE:HD12	2.41	0.46
1:B:134:ILE:HB	1:B:135:PRO:HA	1.96	0.46
1:C:43:TRP:C	1:C:43:TRP:CD1	2.93	0.46
1:C:222:GLU:OE2	1:C:224:HIS:NE2	2.47	0.46
1:D:222:GLU:OE2	1:D:224:HIS:NE2	2.49	0.46
1:A:227:LEU:N	1:A:227:LEU:HD22	2.32	0.45
1:A:175:VAL:HG13	1:A:188:ILE:HG23	1.98	0.45
2:F:2:FUC:H5	2:F:3:NAG:C1	2.47	0.45
1:D:175:VAL:HG13	1:D:188:ILE:CG2	2.46	0.45
1:A:118:PHE:CD1	1:A:118:PHE:C	2.94	0.45
1:B:26:SER:OG	1:B:30:VAL:HG22	2.17	0.45
1:A:20:GLN:OE1	1:A:48:ARG:NH1	2.47	0.45
1:A:107:PHE:HE2	1:A:144:VAL:HG23	1.82	0.45
1:B:15:GLU:O	1:B:15:GLU:OE1	2.35	0.45
1:A:176:VAL:HG21	1:B:187:THR:HG22	1.99	0.44
1:C:144:VAL:O	1:C:144:VAL:HG13	2.17	0.44
1:A:74:PHE:CD1	1:A:74:PHE:C	2.96	0.44
1:B:227:LEU:HD22	1:B:227:LEU:N	2.32	0.44
1:A:222:GLU:OE2	1:A:224:HIS:NE2	2.48	0.44
1:C:74:PHE:C	1:C:74:PHE:CD1	2.96	0.44
1:A:133:GLN:HE21	1:A:133:GLN:HB2	1.58	0.43
1:D:89:LEU:C	1:D:89:LEU:HD12	2.43	0.43
1:A:122:GLU:OE1	1:A:140:ASP:OD2	2.36	0.43
1:A:70:THR:HG22	1:A:164:ILE:HB	1.99	0.43
1:A:134:ILE:HB	1:A:135:PRO:HA	1.99	0.43
1:B:3:ILE:HD11	1:B:231:PHE:HE2	1.84	0.43
1:D:43:TRP:CD1	1:D:43:TRP:C	2.95	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:ALA:HB1	1:B:87:ASP:CG	2.44	0.43
1:A:5:PHE:CZ	1:A:231:PHE:HB3	2.54	0.43
1:C:5:PHE:CZ	1:C:231:PHE:HB3	2.53	0.43
3:I:1:NAG:H62	3:I:2:NAG:C1	2.48	0.43
1:A:86:ALA:HA	1:A:87:ASP:HA	1.77	0.43
1:B:2:THR:OG1	1:B:235:LEU:N	2.44	0.43
1:B:95:PRO:HD3	1:B:117:PRO:O	2.18	0.42
1:C:24:ARG:HD3	8:C:3452:HOH:O	2.19	0.42
1:D:174:HIS:HB2	8:D:4406:HOH:O	2.18	0.42
1:B:37:VAL:O	1:B:37:VAL:HG23	2.20	0.42
1:B:2:THR:HG22	1:B:3:ILE:H	1.84	0.42
1:B:48:ARG:NH2	1:B:116:TYR:OH	2.53	0.42
1:B:74:PHE:C	1:B:74:PHE:CD1	2.97	0.42
1:C:32:GLU:OE2	1:C:36:VAL:HG11	2.20	0.42
1:D:3:ILE:HD12	1:D:4:SER:H	1.84	0.42
1:B:77:ARG:O	1:B:79:PRO:HD3	2.20	0.42
1:B:174:HIS:CD2	1:B:174:HIS:N	2.88	0.42
1:D:113:LEU:C	1:D:115:PRO:HD3	2.45	0.42
1:C:70:THR:HG22	1:C:164:ILE:HB	2.02	0.42
1:C:73:SER:HA	1:C:160:ALA:O	2.19	0.42
1:D:134:ILE:C	1:D:134:ILE:HD12	2.45	0.42
1:C:118:PHE:CD1	1:C:118:PHE:C	2.98	0.42
1:D:219:ASN:HD22	5:D:501:NAG:C7	2.33	0.42
1:B:3:ILE:HD11	1:B:231:PHE:CE2	2.55	0.41
1:B:89:LEU:C	1:B:89:LEU:HD12	2.45	0.41
1:B:97:ASN:N	1:B:97:ASN:ND2	2.69	0.41
1:D:11:HIS:O	1:D:11:HIS:CD2	2.73	0.41
1:D:83:PRO:HD3	1:D:219:ASN:HB2	2.01	0.41
1:A:80:PHE:HA	1:A:81:PRO:HD2	1.91	0.41
1:B:36:VAL:O	1:B:36:VAL:HG13	2.19	0.41
1:A:144:VAL:HG22	8:A:1403:HOH:O	2.20	0.41
1:C:172:ILE:HD11	1:D:191:ILE:HG13	2.03	0.41
1:D:57:VAL:HG23	1:D:58:TRP:CD1	2.50	0.41
1:B:152:PHE:HA	1:B:186:TYR:CE1	2.56	0.41
1:C:57:VAL:HG23	1:C:58:TRP:HD1	1.86	0.41
1:A:43:TRP:CZ3	1:A:213:PRO:HA	2.56	0.41
1:B:50:LEU:N	1:B:50:LEU:HD22	2.36	0.41
1:B:86:ALA:HA	1:B:87:ASP:HA	1.84	0.41
1:B:90:VAL:HG12	1:B:122:GLU:HA	2.03	0.41
1:C:219:ASN:CG	2:H:1:NAG:H82	2.46	0.41
1:C:174:HIS:CD2	1:C:174:HIS:N	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:80:PHE:HA	1:D:81:PRO:HD2	1.96	0.41
1:D:84:HIS:O	1:D:220:ALA:HA	2.22	0.40
1:A:86:ALA:HB1	1:A:87:ASP:CG	2.46	0.40
1:A:191:ILE:HG13	1:B:172:ILE:HD11	2.04	0.40
1:C:170:THR:O	1:C:171:LYS:HB2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	235/241 (98%)	221 (94%)	14 (6%)	0	100	100
1	B	235/241 (98%)	220 (94%)	15 (6%)	0	100	100
1	C	235/241 (98%)	223 (95%)	12 (5%)	0	100	100
1	D	235/241 (98%)	219 (93%)	15 (6%)	1 (0%)	30	51
All	All	940/964 (98%)	883 (94%)	56 (6%)	1 (0%)	48	70

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	236	PRO

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	202/210 (96%)	189 (94%)	13 (6%)	16	35
1	B	200/210 (95%)	185 (92%)	15 (8%)	12	28
1	C	200/210 (95%)	187 (94%)	13 (6%)	15	35
1	D	202/210 (96%)	191 (95%)	11 (5%)	20	42
All	All	804/840 (96%)	752 (94%)	52 (6%)	15	35

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	12	GLN
1	A	18	LYS
1	A	30	VAL
1	A	55	VAL
1	A	57	VAL
1	A	113	LEU
1	A	133	GLN
1	A	149	THR
1	A	174	HIS
1	A	175	VAL
1	A	197	VAL
1	A	235	LEU
1	B	2	THR
1	B	12	GLN
1	B	15	GLU
1	B	30	VAL
1	B	50	LEU
1	B	55	VAL
1	B	65	VAL
1	B	102	GLU
1	B	133	GLN
1	B	143	SER
1	B	165	LYS
1	B	174	HIS
1	B	175	VAL
1	B	201	SER
1	B	235	LEU
1	C	18	LYS
1	C	37	VAL
1	C	55	VAL
1	C	65	VAL
1	C	87	ASP

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Mol	Chain	Res	Type
1	C	133	GLN
1	C	144	VAL
1	C	148	LYS
1	C	149	THR
1	C	174	HIS
1	C	175	VAL
1	C	196	GLN
1	C	235	LEU
1	D	16	GLN
1	D	18	LYS
1	D	30	VAL
1	D	36	VAL
1	D	50	LEU
1	D	65	VAL
1	D	87	ASP
1	D	113	LEU
1	D	133	GLN
1	D	174	HIS
1	D	175	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	9	GLN
1	A	12	GLN
1	A	13	ASN
1	A	16	GLN
1	A	38	ASN
1	A	78	GLN
1	A	133	GLN
1	A	196	GLN
1	A	203	ASN
1	B	6	ASN
1	B	9	GLN
1	B	12	GLN
1	B	38	ASN
1	B	64	ASN
1	B	78	GLN
1	B	84	HIS
1	B	97	ASN
1	B	111	ASN

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Mol	Chain	Res	Type
1	B	133	GLN
1	B	203	ASN
1	C	8	ASN
1	C	12	GLN
1	C	16	GLN
1	C	38	ASN
1	C	64	ASN
1	C	78	GLN
1	C	84	HIS
1	C	196	GLN
1	D	11	HIS
1	D	13	ASN
1	D	16	GLN
1	D	38	ASN
1	D	64	ASN
1	D	78	GLN
1	D	133	GLN
1	D	196	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 ⓘ

14 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	E	1	1,2	14,14,15	0.54	0	17,19,21	0.71	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FUC	E	2	2	10,10,11	0.62	0	14,14,16	0.39	0
2	NAG	E	3	2	14,14,15	0.53	0	17,19,21	0.70	1 (5%)
2	NAG	F	1	1,2	14,14,15	0.54	0	17,19,21	0.76	1 (5%)
2	FUC	F	2	2	10,10,11	0.67	0	14,14,16	0.40	0
2	NAG	F	3	2	14,14,15	0.65	0	17,19,21	0.75	1 (5%)
2	NAG	G	1	1,2	14,14,15	0.69	0	17,19,21	0.69	0
2	FUC	G	2	2	10,10,11	0.60	0	14,14,16	0.32	0
2	NAG	G	3	2	14,14,15	0.70	0	17,19,21	0.77	0
2	NAG	H	1	1,2	14,14,15	0.60	0	17,19,21	0.78	1 (5%)
2	FUC	H	2	2	10,10,11	0.59	0	14,14,16	0.27	0
2	NAG	H	3	2	14,14,15	0.65	0	17,19,21	0.68	1 (5%)
3	NAG	I	1	3,1	14,14,15	0.71	0	17,19,21	0.78	1 (5%)
3	NAG	I	2	3	14,14,15	0.62	0	17,19,21	0.67	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
2	NAG	E	1	1,2	-	0/6/23/26	0/1/1/1
2	FUC	E	2	2	-	-	0/1/1/1
2	NAG	E	3	2	-	2/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	0/6/23/26	0/1/1/1
2	FUC	F	2	2	-	-	0/1/1/1
2	NAG	F	3	2	-	4/6/23/26	0/1/1/1
2	NAG	G	1	1,2	-	0/6/23/26	0/1/1/1
2	FUC	G	2	2	-	-	0/1/1/1
2	NAG	G	3	2	-	5/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	2/6/23/26	0/1/1/1
2	FUC	H	2	2	-	-	0/1/1/1
2	NAG	H	3	2	-	5/6/23/26	0/1/1/1
3	NAG	I	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	I	2	3	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	1	NAG	C2-N2-C7	-2.29	119.83	122.90
2	F	1	NAG	C2-N2-C7	-2.27	119.86	122.90
2	E	3	NAG	C2-N2-C7	-2.21	119.94	122.90
2	H	3	NAG	C2-N2-C7	-2.11	120.07	122.90
2	H	1	NAG	C2-N2-C7	-2.08	120.12	122.90
2	F	3	NAG	C2-N2-C7	-2.07	120.12	122.90
3	I	2	NAG	C2-N2-C7	-2.04	120.17	122.90

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	3	NAG	C8-C7-N2-C2
2	E	3	NAG	O7-C7-N2-C2
2	F	3	NAG	C8-C7-N2-C2
2	F	3	NAG	O7-C7-N2-C2
2	G	3	NAG	C3-C2-N2-C7
2	G	3	NAG	C8-C7-N2-C2
2	G	3	NAG	O7-C7-N2-C2
2	H	1	NAG	C8-C7-N2-C2
2	H	1	NAG	O7-C7-N2-C2
3	I	2	NAG	C8-C7-N2-C2
3	I	2	NAG	O7-C7-N2-C2
3	I	1	NAG	C8-C7-N2-C2
3	I	1	NAG	O7-C7-N2-C2
2	G	3	NAG	O5-C5-C6-O6
3	I	2	NAG	O5-C5-C6-O6
2	G	3	NAG	C4-C5-C6-O6
3	I	2	NAG	C4-C5-C6-O6
2	F	3	NAG	O5-C5-C6-O6
2	H	3	NAG	C8-C7-N2-C2
2	H	3	NAG	C4-C5-C6-O6
2	F	3	NAG	C4-C5-C6-O6
2	H	3	NAG	O7-C7-N2-C2
2	H	3	NAG	O5-C5-C6-O6
2	H	3	NAG	C1-C2-N2-C7

There are no ring outliers.

9 monomers are involved in 16 short contacts:

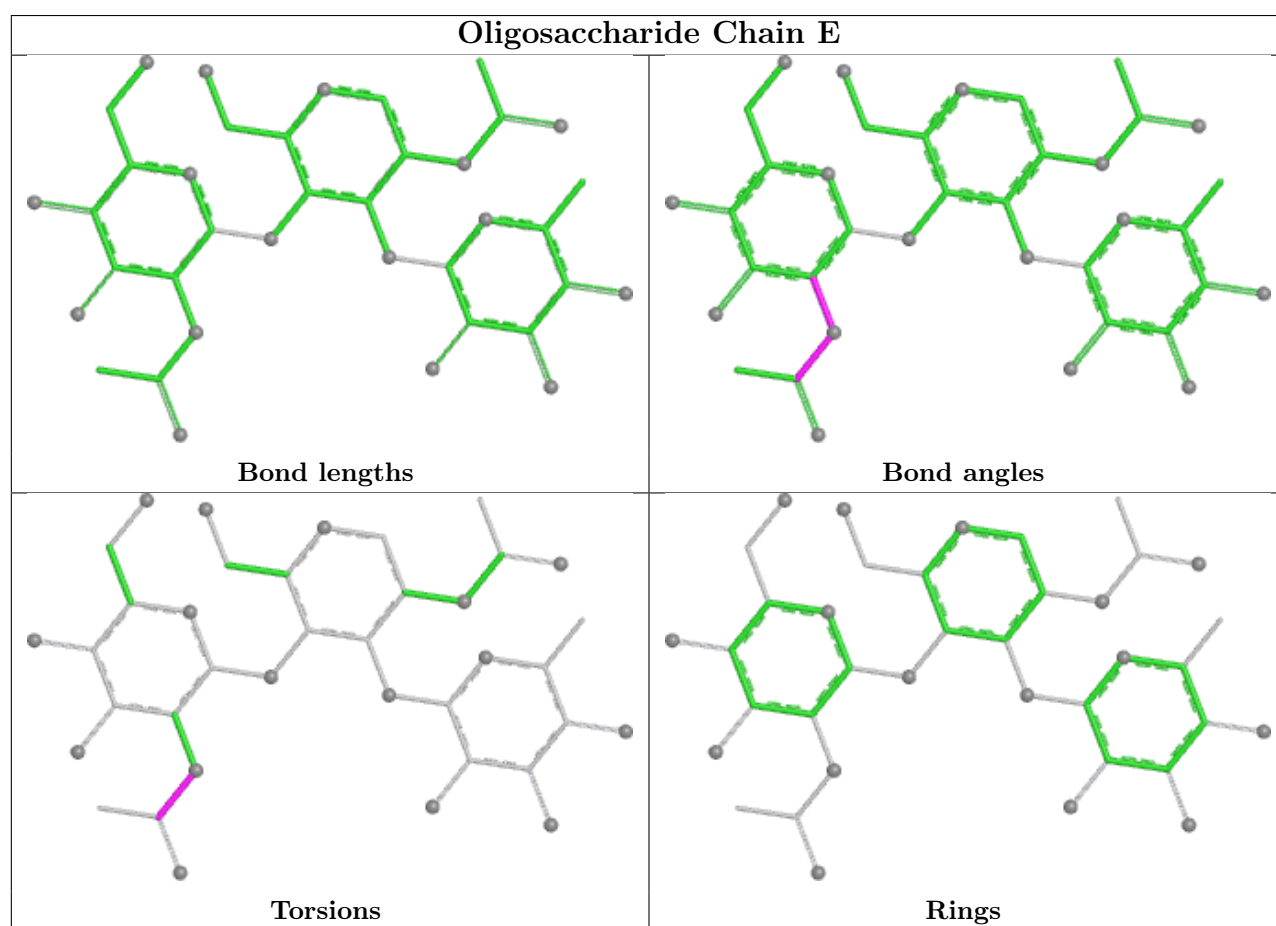
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	2	FUC	4	0

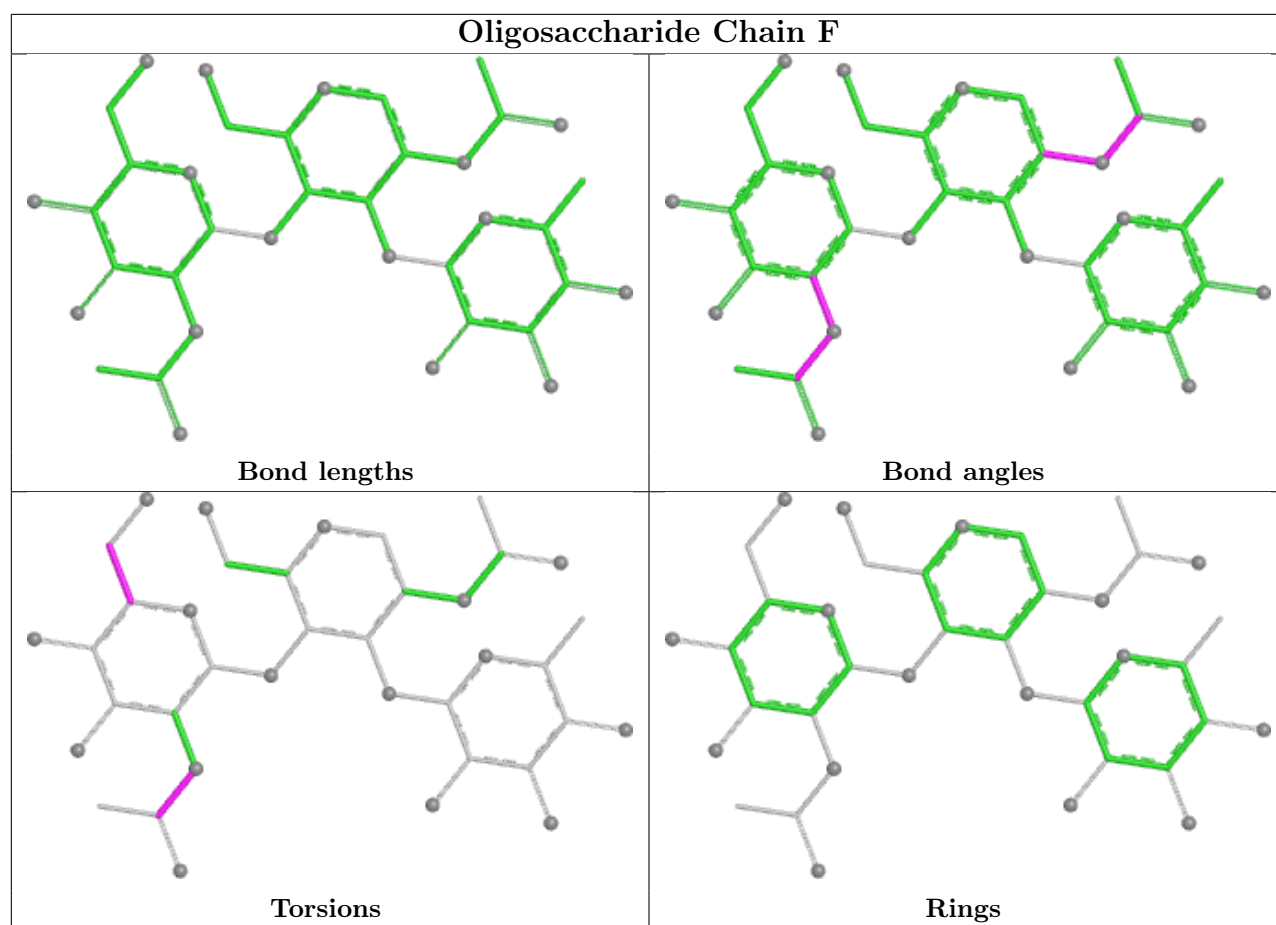
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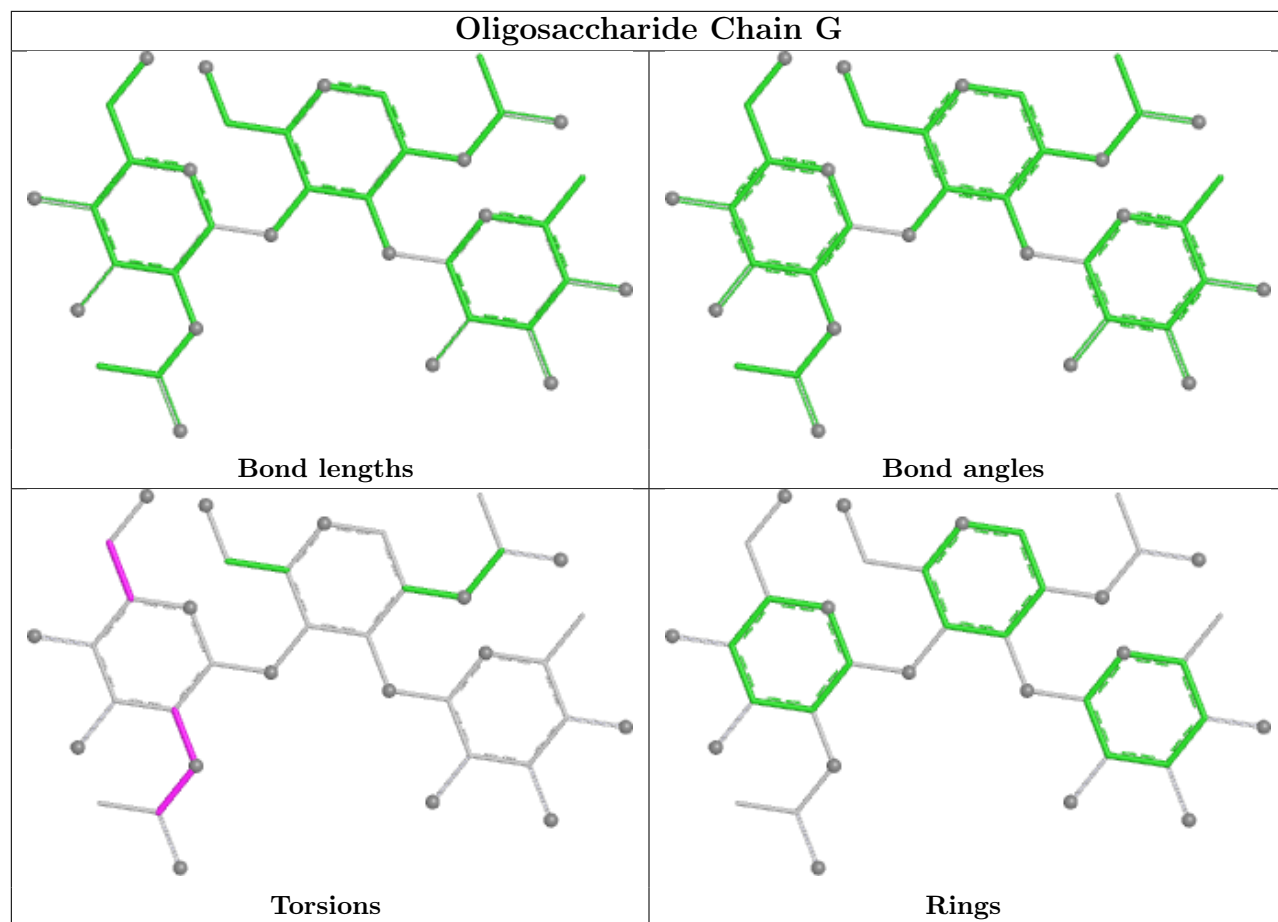
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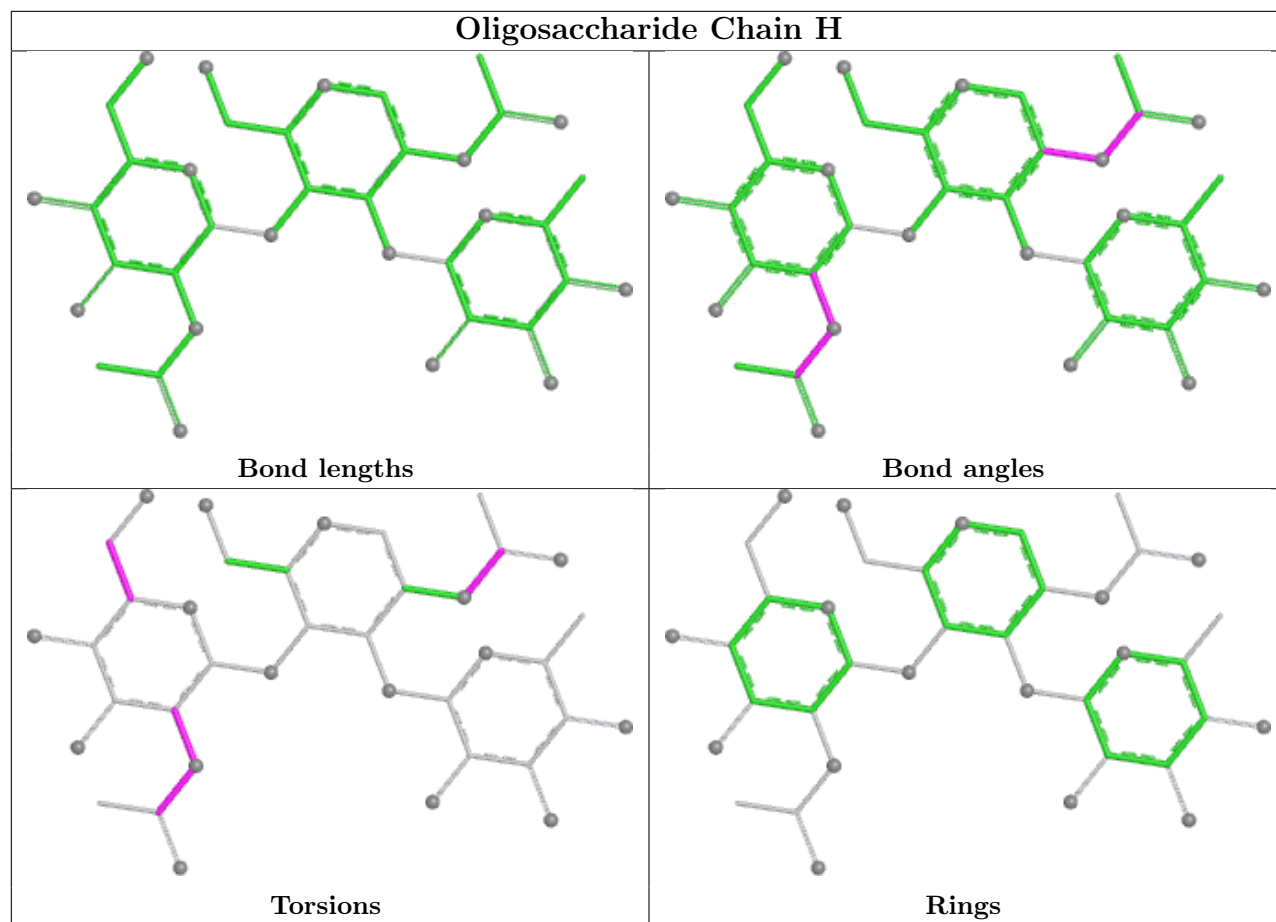
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	3	NAG	7	0
3	I	2	NAG	2	0
2	F	1	NAG	1	0
2	G	1	NAG	2	0
2	G	2	FUC	4	0
3	I	1	NAG	1	0
2	F	3	NAG	3	0
2	H	1	NAG	3	0

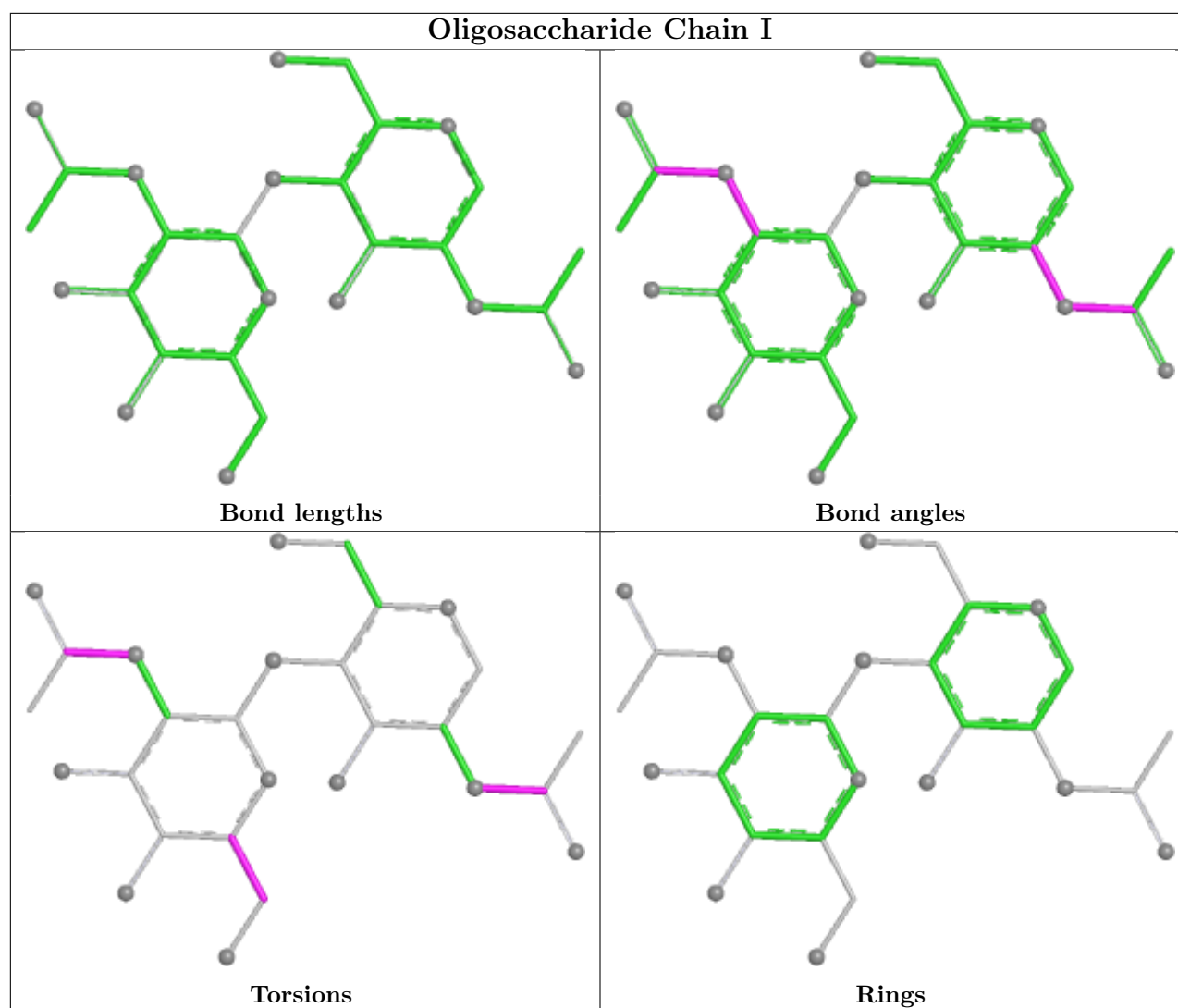
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 8 are monoatomic - leaving 7 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	$\# Z > 2$
4	MGC	C	3401	-	16,16,16	1.14	2 (12%)	22,22,22	0.89	1 (4%)
5	NAG	C	601	1	14,14,15	0.69	0	17,19,21	0.87	1 (5%)
5	NAG	D	501	1	14,14,15	0.65	0	17,19,21	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MGC	A	1401	-	16,16,16	1.28	2 (12%)	22,22,22	0.94	1 (4%)
4	MGC	B	2401	-	16,16,16	1.12	2 (12%)	22,22,22	0.94	1 (4%)
4	MGC	D	4401	-	16,16,16	1.21	2 (12%)	22,22,22	0.94	1 (4%)
5	NAG	A	601	1	14,14,15	0.66	0	17,19,21	0.79	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
4	MGC	C	3401	-	-	0/8/28/28	0/1/1/1
5	NAG	C	601	1	-	4/6/23/26	0/1/1/1
5	NAG	D	501	1	-	2/6/23/26	0/1/1/1
4	MGC	A	1401	-	-	0/8/28/28	0/1/1/1
4	MGC	B	2401	-	-	0/8/28/28	0/1/1/1
4	MGC	D	4401	-	-	0/8/28/28	0/1/1/1
5	NAG	A	601	1	-	4/6/23/26	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1401	MGC	O1-C1	2.98	1.45	1.40
4	A	1401	MGC	O5-C1	2.69	1.48	1.41
4	D	4401	MGC	O5-C1	2.50	1.48	1.41
4	D	4401	MGC	O1-C1	2.49	1.44	1.40
4	B	2401	MGC	O5-C1	2.47	1.48	1.41
4	C	3401	MGC	O5-C1	2.36	1.47	1.41
4	C	3401	MGC	O1-C1	2.33	1.44	1.40
4	B	2401	MGC	O1-C1	2.17	1.43	1.40

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1401	MGC	CM-O1-C1	3.02	117.84	113.26
4	D	4401	MGC	CM-O1-C1	2.89	117.65	113.26
4	C	3401	MGC	CM-O1-C1	2.62	117.24	113.26
4	B	2401	MGC	CM-O1-C1	2.60	117.21	113.26
5	A	601	NAG	C2-N2-C7	-2.19	119.97	122.90
5	C	601	NAG	C2-N2-C7	-2.16	120.01	122.90

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	601	NAG	C8-C7-N2-C2
5	C	601	NAG	O7-C7-N2-C2
5	D	501	NAG	C8-C7-N2-C2
5	D	501	NAG	O7-C7-N2-C2
5	C	601	NAG	O5-C5-C6-O6
5	A	601	NAG	O5-C5-C6-O6
5	C	601	NAG	C4-C5-C6-O6
5	A	601	NAG	C4-C5-C6-O6
5	A	601	NAG	C8-C7-N2-C2
5	A	601	NAG	O7-C7-N2-C2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	501	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	237/241 (98%)	-0.30	1 (0%) 88 86	23, 35, 55, 69	0
1	B	237/241 (98%)	-0.27	2 (0%) 82 80	22, 36, 60, 74	0
1	C	237/241 (98%)	-0.23	1 (0%) 88 86	28, 39, 63, 78	0
1	D	237/241 (98%)	-0.19	2 (0%) 82 80	26, 40, 65, 86	0
All	All	948/964 (98%)	-0.25	6 (0%) 85 83	22, 38, 62, 86	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	237	GLY	4.8
1	B	237	GLY	4.4
1	D	237	GLY	3.6
1	B	2	THR	2.9
1	A	28	ASN	2.4
1	D	113	LEU	2.2

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.

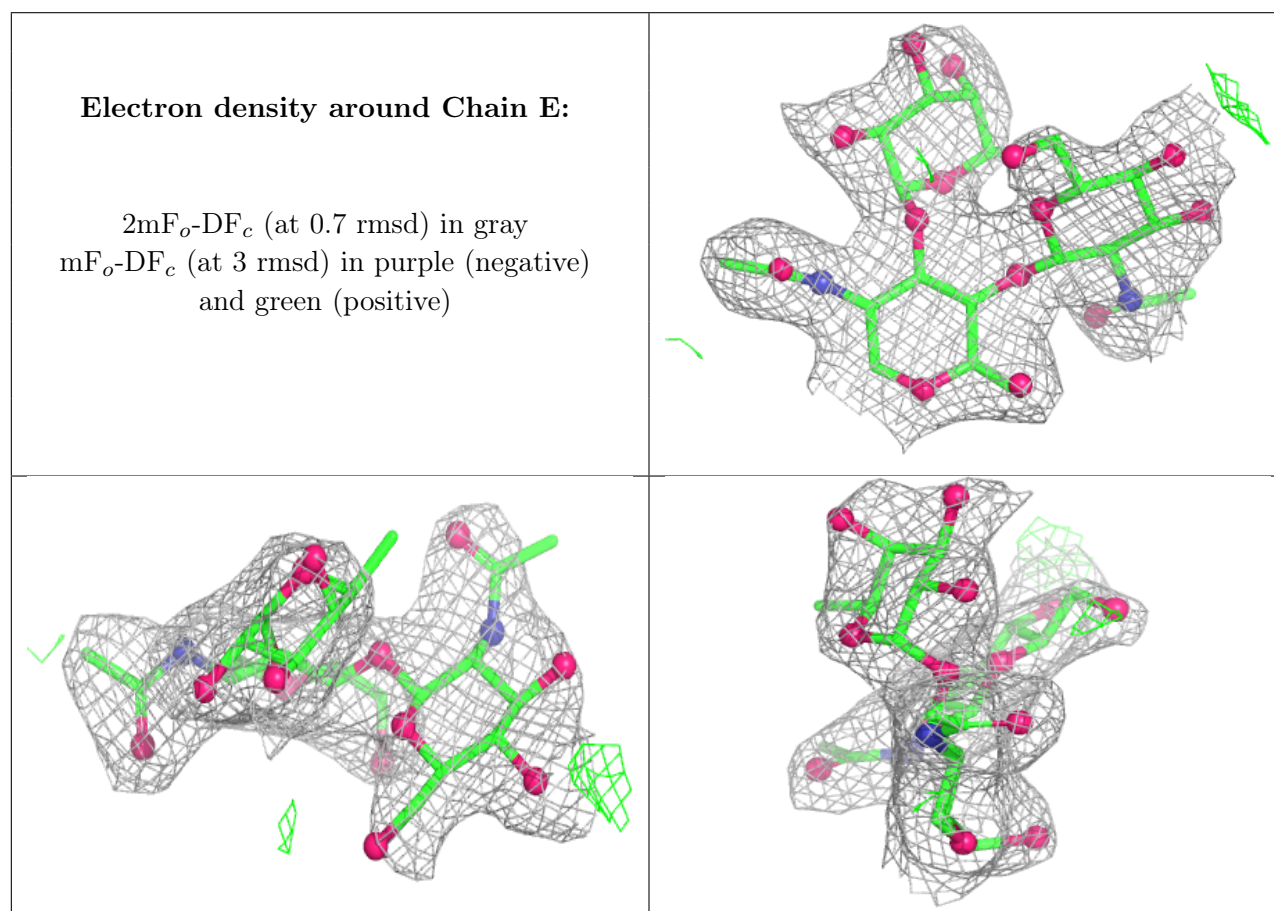
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	I	2	14/15	0.66	0.12	83,87,87,88	0

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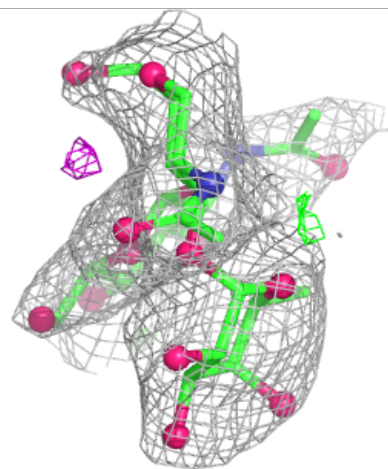
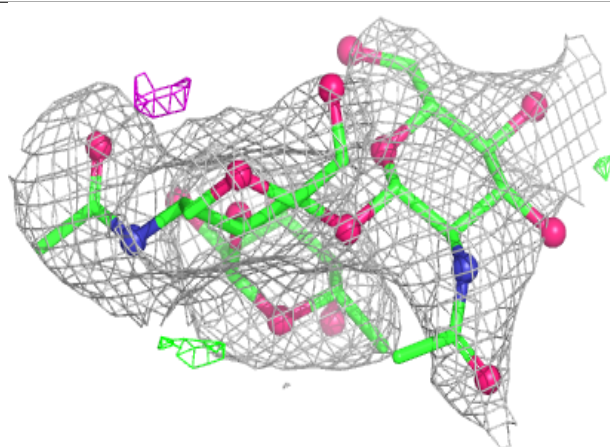
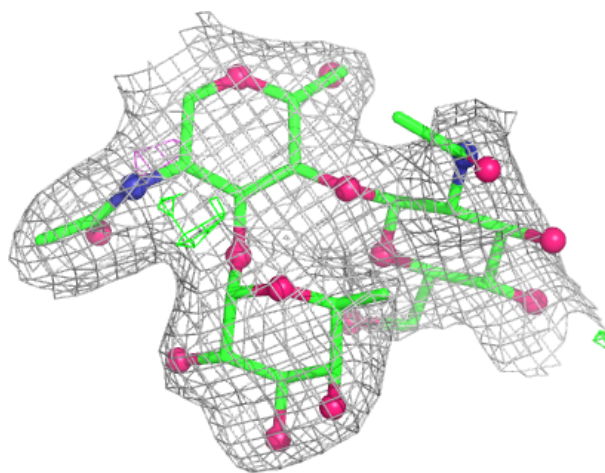
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	F	3	14/15	0.73	0.11	72,75,80,81	0
2	FUC	H	2	10/11	0.78	0.12	71,72,73,75	0
2	NAG	H	3	14/15	0.80	0.12	62,64,67,70	0
2	NAG	G	3	14/15	0.81	0.12	72,74,77,79	0
2	NAG	G	1	14/15	0.81	0.12	51,60,67,69	0
3	NAG	I	1	14/15	0.82	0.14	66,70,74,78	0
2	FUC	F	2	10/11	0.82	0.09	69,70,72,72	0
2	FUC	G	2	10/11	0.86	0.09	64,65,67,67	0
2	NAG	E	3	14/15	0.86	0.09	61,63,66,67	0
2	FUC	E	2	10/11	0.88	0.10	59,62,62,63	0
2	NAG	E	1	14/15	0.91	0.07	48,51,57,58	0
2	NAG	H	1	14/15	0.92	0.07	57,62,64,67	0
2	NAG	F	1	14/15	0.93	0.07	54,58,66,68	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.



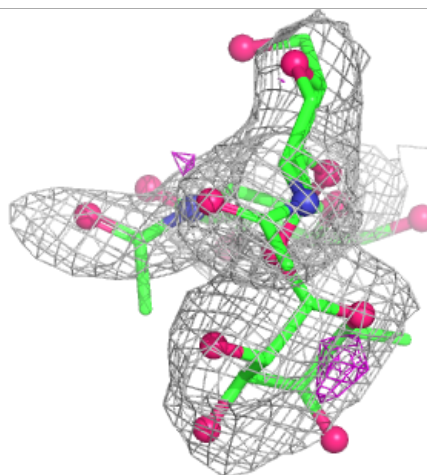
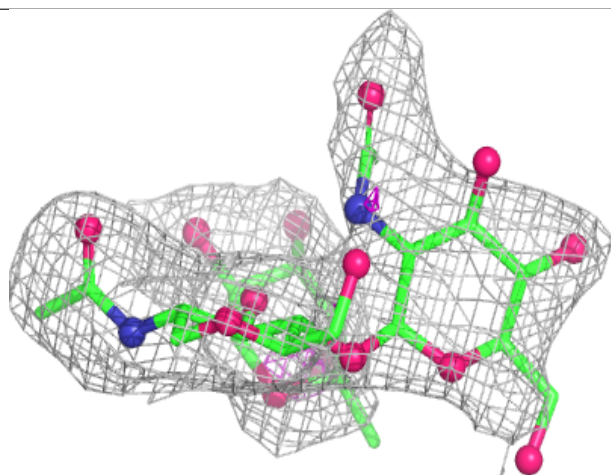
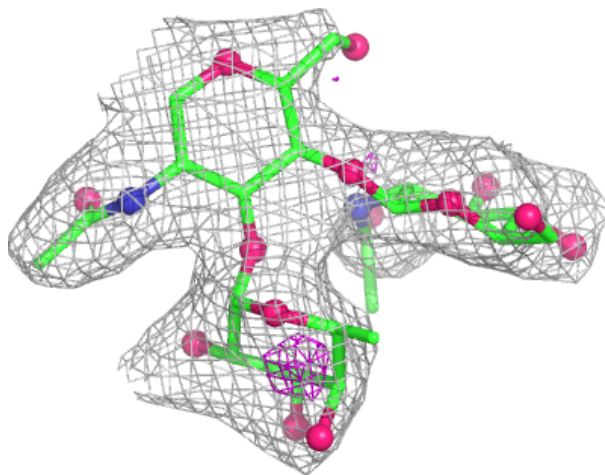
Electron density around Chain F:

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



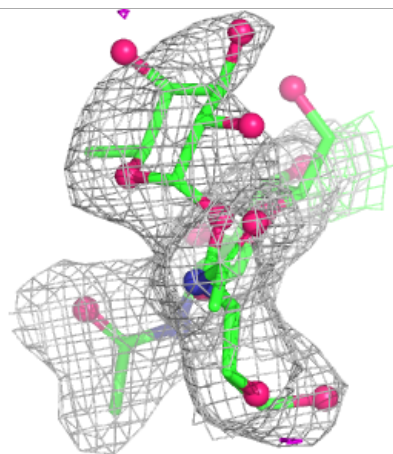
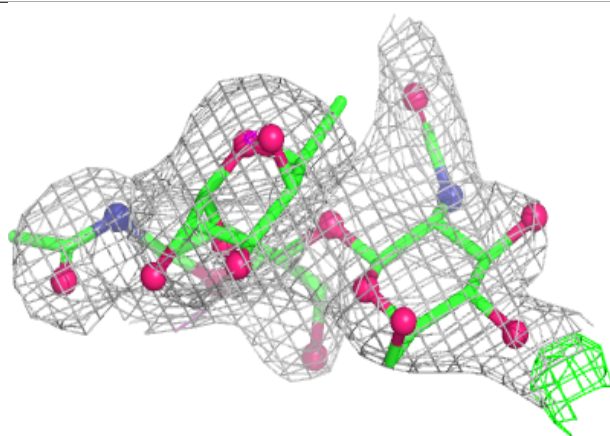
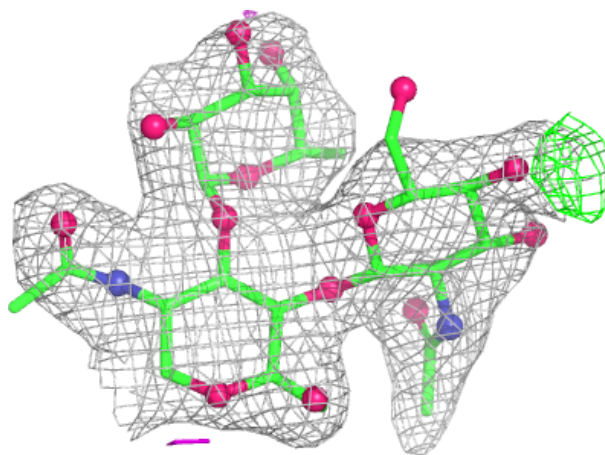
Electron density around Chain G:

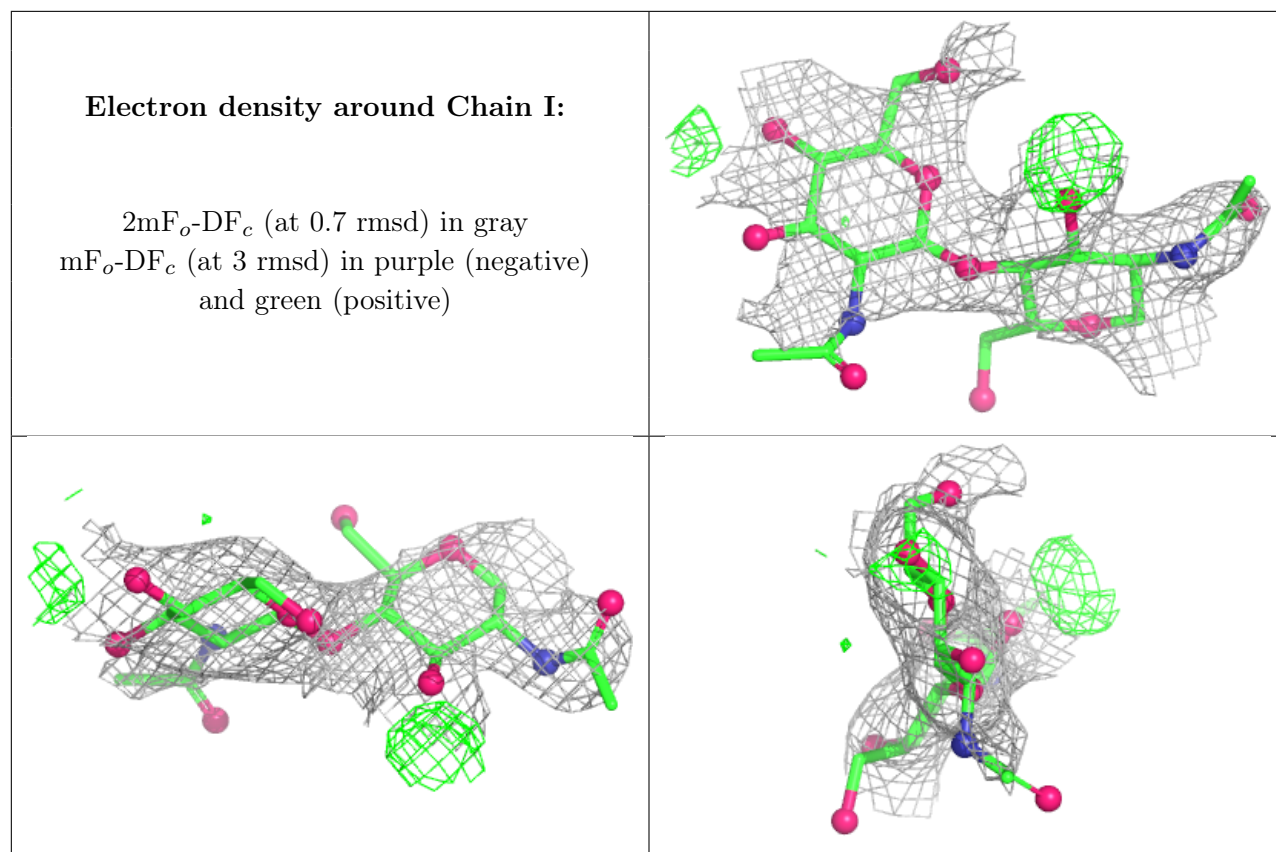
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain H:

$2mF_o-DF_c$ (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
5	NAG	D	501	14/15	0.66	0.12	76,78,80,81	0
5	NAG	C	601	14/15	0.79	0.10	57,59,62,62	0
5	NAG	A	601	14/15	0.80	0.09	52,56,58,58	0
4	MGC	C	3401	16/16	0.92	0.08	51,54,56,57	0
7	MN	C	3300	1/1	0.92	0.08	50,50,50,50	0
4	MGC	D	4401	16/16	0.93	0.08	45,48,50,51	0
4	MGC	A	1401	16/16	0.94	0.07	40,41,43,44	0
6	CA	D	4303	1/1	0.95	0.05	36,36,36,36	0
4	MGC	B	2401	16/16	0.96	0.06	33,37,39,40	0
6	CA	B	2303	1/1	0.96	0.03	32,32,32,32	0
6	CA	C	3303	1/1	0.97	0.05	41,41,41,41	0
6	CA	A	1303	1/1	0.98	0.03	33,33,33,33	0
7	MN	B	2300	1/1	0.99	0.04	34,34,34,34	0
7	MN	A	1300	1/1	0.99	0.03	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	MN	D	4300	1/1	0.99	0.05	40,40,40,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.