



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 06:12 AM UTC

PDB ID : 4X4M / pdb_00004x4m
Title : Structure of FcγRI in complex with Fc reveals the importance of glycan recognition for high affinity IgG binding
Authors : Lu, J.; Sun, P.D.
Deposited on : 2014-12-03
Resolution : 3.48 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

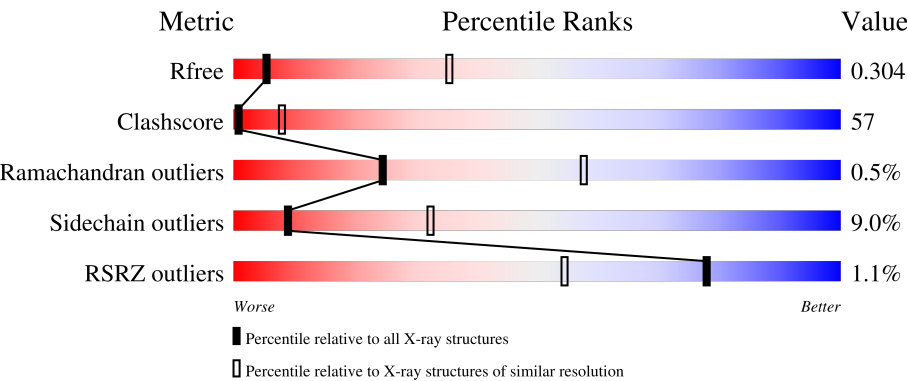
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.48 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	1083 (3.52-3.44)
Clashscore	190562	1139 (3.52-3.44)
Ramachandran outliers	187476	1111 (3.52-3.44)
Sidechain outliers	187428	1112 (3.52-3.44)
RSRZ outliers	180081	1082 (3.52-3.44)

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	219	39%55%5%
1	B	219	35%53%10%.
1	C	219	%42%46%8%.
1	D	219	%34%55%9%.
2	E	275	%27%54%13%6%

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Mol	Chain	Length	Quality of chain
2	F	275	
3	G	8	
3	H	8	
4	I	9	
5	J	6	
6	K	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
3	BMA	G	3	-	-	X	-
3	MAN	G	6	-	-	X	-
3	MAN	H	4	-	-	X	-
3	MAN	H	6	-	-	X	-
4	NAG	I	2	-	-	X	-
4	BMA	I	3	-	-	X	-
4	MAN	I	4	-	-	X	-
4	MAN	I	7	-	-	X	-
5	NAG	J	4	-	-	X	-
7	NAG	D	1001	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 11374 atoms, of which 8 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 Ig gamma-1 chain C region.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	218	Total	C	H	N	O	S	0	0	0
			1737	1101	8	290	331	7			
1	B	216	Total	C	N	O	S		0	0	0
			1716	1093	288	329	6				
1	C	212	Total	C	N	O	S		0	0	0
			1694	1080	284	324	6				
1	D	214	Total	C	N	O	S		0	0	0
			1705	1086	286	327	6				

- Molecule 2 is a protein called High affinity immunoglobulin gamma Fc receptor I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	259	Total	C	N	O	S	0	0	0
			2046	1299	352	386	9			
2	F	258	Total	C	N	O	S	0	0	0
			2038	1293	351	385	9			

There are 48 discrepancies between the modelled and reference sequences:

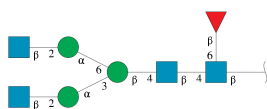
Chain	Residue	Modelled	Actual	Comment	Reference
E	25	LYS	THR	engineered mutation	UNP P12314
E	38	SER	THR	engineered mutation	UNP P12314
E	46	PRO	LEU	engineered mutation	UNP P12314
E	63	ILE	THR	engineered mutation	UNP P12314
E	69	THR	SER	engineered mutation	UNP P12314
E	71	HIS	ARG	engineered mutation	UNP P12314
E	77	GLU	VAL	engineered mutation	UNP P12314
E	78	ASP	ASN	engineered mutation	UNP P12314
E	100	VAL	ILE	engineered mutation	UNP P12314
E	114	LEU	PHE	engineered mutation	UNP P12314
E	160	MET	ILE	engineered mutation	UNP P12314
E	163	SER	ASN	engineered mutation	UNP P12314

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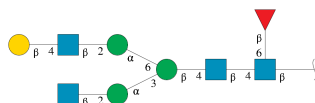
Chain	Residue	Modelled	Actual	Comment	Reference
E	195	THR	ASN	engineered mutation	UNP P12314
E	206	THR	ASN	engineered mutation	UNP P12314
E	207	PRO	LEU	engineered mutation	UNP P12314
E	240	ASP	ASN	engineered mutation	UNP P12314
E	283	HIS	LEU	engineered mutation	UNP P12314
E	285	GLN	LEU	engineered mutation	UNP P12314
E	290	HIS	-	expression tag	UNP P12314
E	291	HIS	-	expression tag	UNP P12314
E	292	HIS	-	expression tag	UNP P12314
E	293	HIS	-	expression tag	UNP P12314
E	294	HIS	-	expression tag	UNP P12314
E	295	HIS	-	expression tag	UNP P12314
F	25	LYS	THR	engineered mutation	UNP P12314
F	38	SER	THR	engineered mutation	UNP P12314
F	46	PRO	LEU	engineered mutation	UNP P12314
F	63	ILE	THR	engineered mutation	UNP P12314
F	69	THR	SER	engineered mutation	UNP P12314
F	71	HIS	ARG	engineered mutation	UNP P12314
F	77	GLU	VAL	engineered mutation	UNP P12314
F	78	ASP	ASN	engineered mutation	UNP P12314
F	100	VAL	ILE	engineered mutation	UNP P12314
F	114	LEU	PHE	engineered mutation	UNP P12314
F	160	MET	ILE	engineered mutation	UNP P12314
F	163	SER	ASN	engineered mutation	UNP P12314
F	195	THR	ASN	engineered mutation	UNP P12314
F	206	THR	ASN	engineered mutation	UNP P12314
F	207	PRO	LEU	engineered mutation	UNP P12314
F	240	ASP	ASN	engineered mutation	UNP P12314
F	283	HIS	LEU	engineered mutation	UNP P12314
F	285	GLN	LEU	engineered mutation	UNP P12314
F	290	HIS	-	expression tag	UNP P12314
F	291	HIS	-	expression tag	UNP P12314
F	292	HIS	-	expression tag	UNP P12314
F	293	HIS	-	expression tag	UNP P12314
F	294	HIS	-	expression tag	UNP P12314
F	295	HIS	-	expression tag	UNP P12314

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



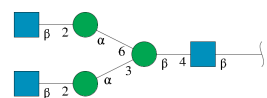
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	8	Total	C	N	O	0	0	0
			99	56	4	39			
3	H	8	Total	C	N	O	0	0	0
			99	56	4	39			

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



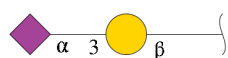
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	I	9	Total	C	N	O	0	0	0
			110	62	4	44			

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	J	6	Total	C	N	O	0	0	0
			75	42	3	30			

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



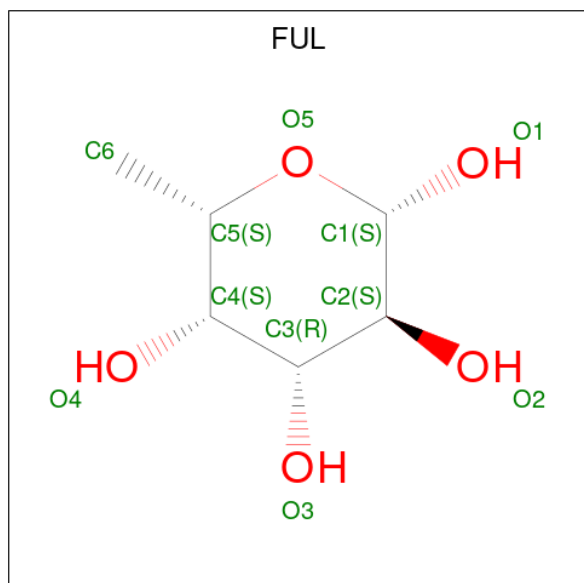
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	K	2	Total	C	N	O	0	0	0
			31	17	1	13			

- 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	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is beta-L-fucopyranose (CCD ID: FUL) (formula: $C_6H_{12}O_5$).

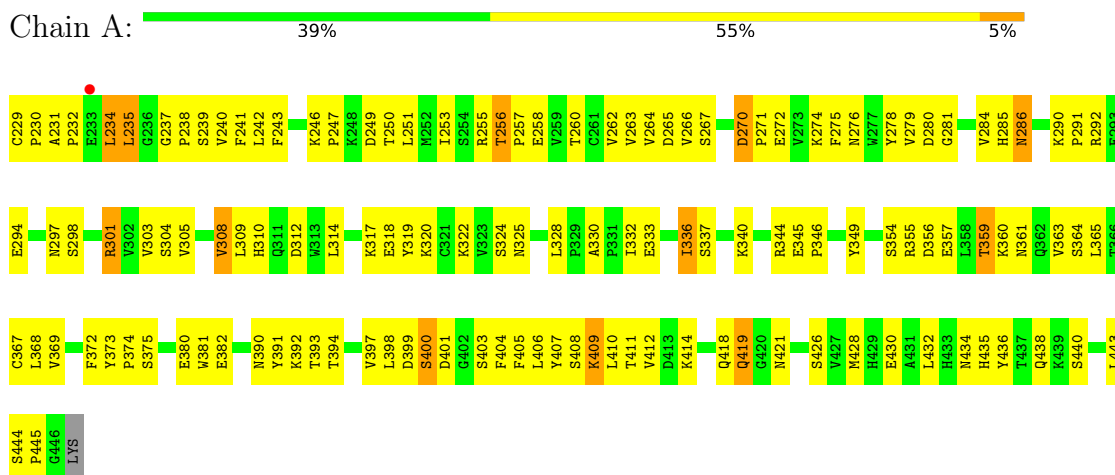


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	D	1	Total	C	O	0	0
			10	6	4		

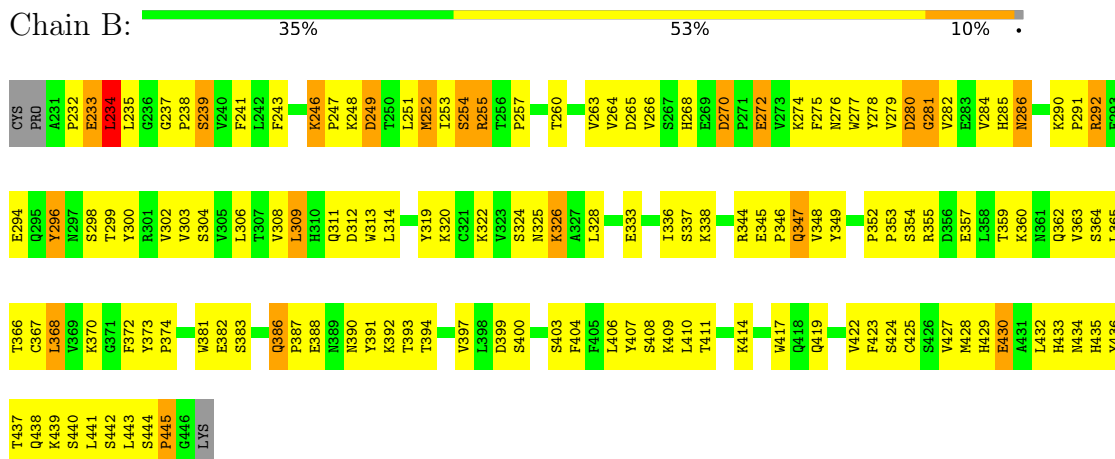
3 Residue-property plots

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: Ig gamma-1 chain C region

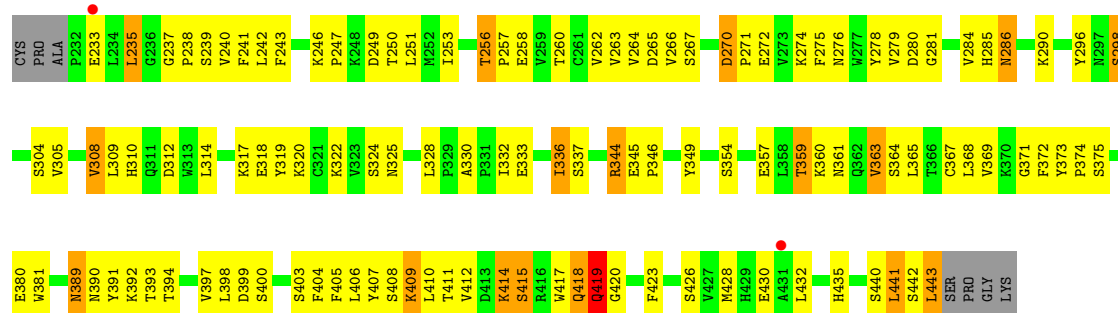


- Molecule 1: Ig gamma-1 chain C region

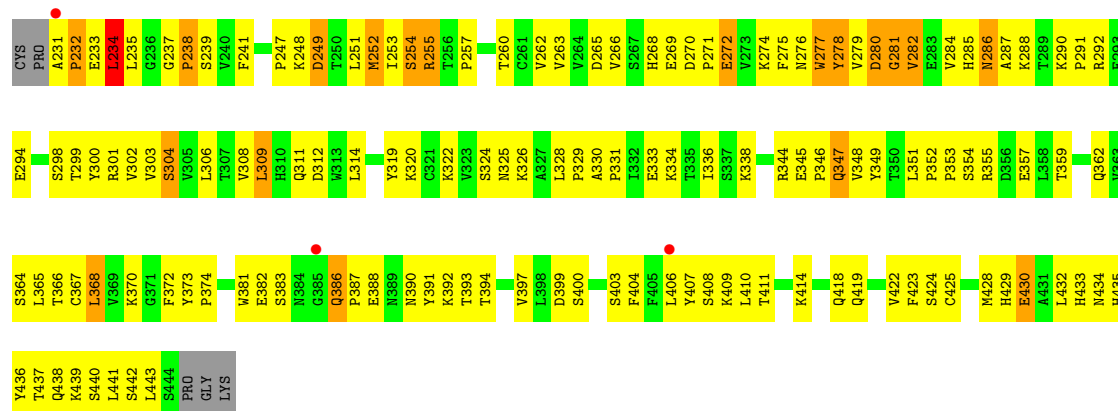


- Molecule 1: Ig gamma-1 chain C region

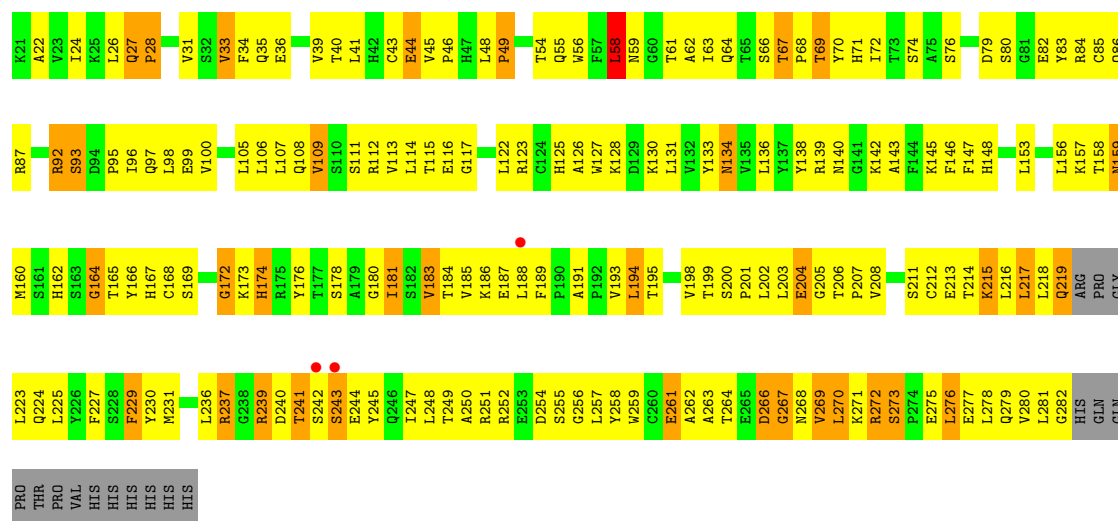




• Molecule 1: Ig gamma-1 chain C region

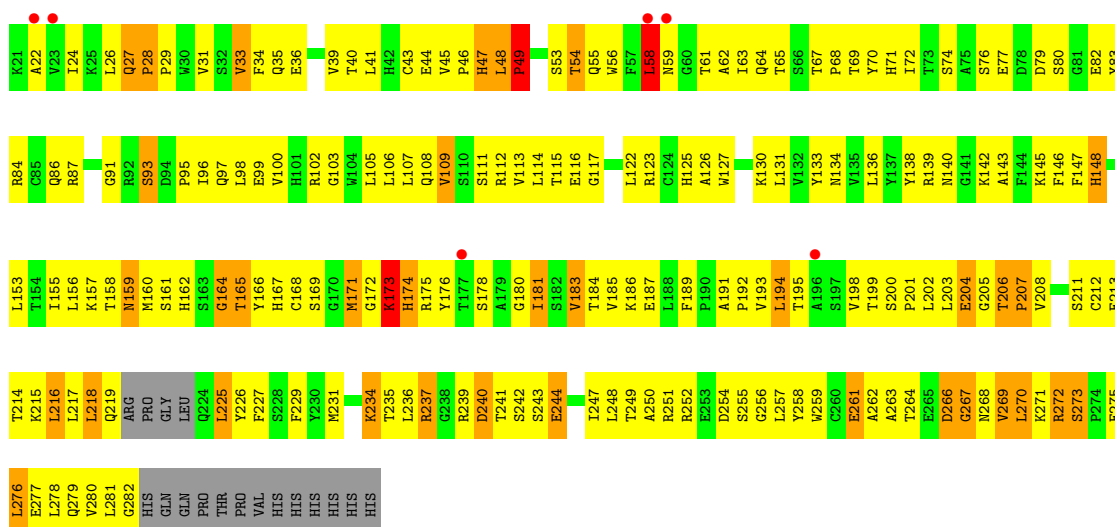


• Molecule 2: High affinity immunoglobulin gamma Fc receptor I



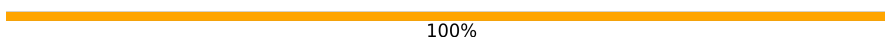
• Molecule 2: High affinity immunoglobulin gamma Fc receptor I





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

Chain G:



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

Chain H:



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

Chain I:



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  33% 67%

MAN1
MAN2
MAN3
MAN4
MAN5
MAN6

- Molecule 6: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose

Chain K:  100%

GAL1
STAG

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	59.92Å 67.99Å 125.03Å 89.86° 112.25° 89.96°	Depositor
Resolution (Å)	40.66 – 3.48 40.66 – 3.48	Depositor EDS
% Data completeness (in resolution range)	89.9 (40.66-3.48) 85.6 (40.66-3.48)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 3.48Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.245 , 0.296 0.260 , 0.304	Depositor DCC
R_{free} test set	1037 reflections (4.45%)	wwPDB-VP
Wilson B-factor (Å ²)	129.1	Xtriage
Anisotropy	0.244	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 640.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.250 for -h,k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11374	wwPDB-VP
Average B, all atoms (Å ²)	182.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.84% 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: BMA, SIA, NAG, MAN, GAL, FUL

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	0.45	0/1778	1.13	14/2425 (0.6%)
1	B	0.44	1/1764 (0.1%)	1.19	16/2405 (0.7%)
1	C	0.44	0/1741	1.08	12/2372 (0.5%)
1	D	0.63	2/1752 (0.1%)	1.21	18/2388 (0.8%)
2	E	0.46	1/2096 (0.0%)	1.33	31/2847 (1.1%)
2	F	0.48	2/2088 (0.1%)	1.29	28/2836 (1.0%)
All	All	0.49	6/11219 (0.1%)	1.21	119/15273 (0.8%)

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	A	0	1
1	B	0	2
1	D	0	1
All	All	0	4

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	234	LEU	C-N	18.56	1.58	1.33
1	D	238	PRO	N-CD	8.43	1.59	1.47
1	B	232	PRO	C-N	-7.35	1.23	1.33
2	F	58	LEU	C-O	-6.34	1.16	1.24
2	E	58	LEU	C-O	-6.29	1.16	1.24

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	243	SER	N-CA-C	14.87	130.85	113.01
2	F	27	GLN	CA-C-N	-11.39	108.65	120.38
2	F	27	GLN	C-N-CA	-11.39	108.65	120.38
2	E	27	GLN	CA-C-N	-11.31	108.73	120.38
2	E	27	GLN	C-N-CA	-11.31	108.73	120.38

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	301	ARG	Sidechain
1	B	233	GLU	Mainchain
1	B	234	LEU	Peptide
1	D	234	LEU	Peptide

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	1729	8	1695	133	0
1	B	1716	0	1683	201	1
1	C	1694	0	1664	134	0
1	D	1705	0	1673	211	1
2	E	2046	0	2013	290	1
2	F	2038	0	2002	302	1
3	G	99	0	85	22	0
3	H	99	0	85	19	0
4	I	110	0	93	25	0
5	J	75	0	64	23	0
6	K	31	0	26	9	0
7	D	14	0	12	13	0
8	D	10	0	10	5	0
All	All	11366	8	11105	1270	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 57.

The worst 5 of 1270 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)
5:J:4:NAG:H4	6:K:1:GAL:C1	1.37	1.50
2:F:45:VAL:HG22	2:F:87:ARG:NH2	1.34	1.36
1:C:417:TRP:HZ3	1:C:423:PHE:CD2	1.43	1.35
2:F:99:GLU:OE2	2:F:112:ARG:NH2	1.64	1.28
2:E:227:PHE:O	2:E:241:THR:CG2	1.80	1.28

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:B:296:TYR:OH	1:D:309:LEU:CD2[1_565]	1.84	0.36
2:E:237:ARG:NH1	2:F:244:GLU:OE1[1_646]	2.19	0.01

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	216/219 (99%)	197 (91%)	18 (8%)	1 (0%)	24	58
1	B	214/219 (98%)	200 (94%)	13 (6%)	1 (0%)	24	58
1	C	210/219 (96%)	197 (94%)	13 (6%)	0	100	100
1	D	212/219 (97%)	200 (94%)	11 (5%)	1 (0%)	24	58
2	E	255/275 (93%)	241 (94%)	12 (5%)	2 (1%)	16	49
2	F	254/275 (92%)	245 (96%)	7 (3%)	2 (1%)	16	49
All	All	1361/1426 (95%)	1280 (94%)	74 (5%)	7 (0%)	24	58

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	445	PRO
1	A	445	PRO
1	D	232	PRO

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Mol	Chain	Res	Type
2	E	49	PRO
2	F	49	PRO

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	201/202 (100%)	191 (95%)	10 (5%)	22	48
1	B	199/202 (98%)	182 (92%)	17 (8%)	10	34
1	C	197/202 (98%)	181 (92%)	16 (8%)	11	35
1	D	198/202 (98%)	183 (92%)	15 (8%)	12	37
2	E	229/244 (94%)	204 (89%)	25 (11%)	6	26
2	F	228/244 (93%)	198 (87%)	30 (13%)	4	20
All	All	1252/1296 (97%)	1139 (91%)	113 (9%)	9	32

5 of 113 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	430	GLU
2	F	266	ASP
2	E	183	VAL
2	F	248	LEU
2	F	181	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	35	GLN
2	F	42	HIS
2	E	42	HIS
2	E	162	HIS
2	F	134	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 ⓘ

33 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	G	1	1,3	14,14,15	1.63	3 (21%)	17,19,21	1.77	4 (23%)
3	NAG	G	2	3	14,14,15	1.59	3 (21%)	17,19,21	1.66	4 (23%)
3	BMA	G	3	3	11,11,12	1.69	2 (18%)	15,15,17	2.27	7 (46%)
3	MAN	G	4	3	11,11,12	1.91	2 (18%)	15,15,17	1.67	3 (20%)
3	NAG	G	5	3	14,14,15	1.61	3 (21%)	17,19,21	1.55	5 (29%)
3	MAN	G	6	3	11,11,12	1.68	3 (27%)	15,15,17	1.04	0
3	NAG	G	7	3	14,14,15	1.54	3 (21%)	17,19,21	1.44	3 (17%)
3	FUL	G	8	3	10,10,11	1.69	2 (20%)	14,14,16	1.04	1 (7%)
3	NAG	H	1	1,3	14,14,15	1.74	4 (28%)	17,19,21	1.88	6 (35%)
3	NAG	H	2	3	14,14,15	1.61	3 (21%)	17,19,21	1.24	2 (11%)
3	BMA	H	3	3	11,11,12	1.61	2 (18%)	15,15,17	2.19	4 (26%)
3	MAN	H	4	3	11,11,12	1.30	1 (9%)	15,15,17	2.28	3 (20%)
3	NAG	H	5	3	14,14,15	1.73	3 (21%)	17,19,21	1.84	4 (23%)
3	MAN	H	6	3	11,11,12	1.69	3 (27%)	15,15,17	1.19	1 (6%)
3	NAG	H	7	3	14,14,15	1.71	3 (21%)	17,19,21	2.12	5 (29%)
3	FUL	H	8	3	10,10,11	1.70	2 (20%)	14,14,16	1.12	2 (14%)
4	NAG	I	1	1,4	14,14,15	1.69	3 (21%)	17,19,21	2.25	8 (47%)
4	NAG	I	2	4	14,14,15	1.65	3 (21%)	17,19,21	1.46	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	BMA	I	3	4	11,11,12	1.78	2 (18%)	15,15,17	1.90	5 (33%)
4	MAN	I	4	4	11,11,12	1.65	2 (18%)	15,15,17	1.06	1 (6%)
4	NAG	I	5	4	14,14,15	1.58	3 (21%)	17,19,21	1.06	1 (5%)
4	GAL	I	6	4	11,11,12	1.46	2 (18%)	15,15,17	1.91	4 (26%)
4	MAN	I	7	4	11,11,12	1.63	3 (27%)	15,15,17	1.16	1 (6%)
4	NAG	I	8	4	14,14,15	1.58	2 (14%)	17,19,21	1.34	1 (5%)
4	FUL	I	9	4	10,10,11	1.86	2 (20%)	14,14,16	0.94	1 (7%)
5	NAG	J	1	5	14,14,15	1.34	2 (14%)	17,19,21	2.05	5 (29%)
5	BMA	J	2	5	11,11,12	0.49	0	15,15,17	1.95	4 (26%)
5	MAN	J	3	5	11,11,12	0.23	0	15,15,17	0.77	0
5	NAG	J	4	5	14,14,15	0.52	0	17,19,21	1.76	2 (11%)
5	MAN	J	5	5	11,11,12	0.43	0	15,15,17	1.72	4 (26%)
5	NAG	J	6	5	14,14,15	0.27	0	17,19,21	0.69	0
6	GAL	K	1	6	11,11,12	1.67	3 (27%)	15,15,17	1.90	4 (26%)
6	SIA	K	2	6	20,20,21	0.55	0	21,28,31	0.91	1 (4%)

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	G	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	G	2	3	-	3/6/23/26	0/1/1/1
3	BMA	G	3	3	-	1/2/19/22	0/1/1/1
3	MAN	G	4	3	-	2/2/19/22	0/1/1/1
3	NAG	G	5	3	-	6/6/23/26	0/1/1/1
3	MAN	G	6	3	-	2/2/19/22	1/1/1/1
3	NAG	G	7	3	-	3/6/23/26	0/1/1/1
3	FUL	G	8	3	-	-	0/1/1/1
3	NAG	H	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	4/6/23/26	0/1/1/1
3	BMA	H	3	3	-	2/2/19/22	0/1/1/1
3	MAN	H	4	3	-	1/2/19/22	0/1/1/1
3	NAG	H	5	3	-	2/6/23/26	0/1/1/1
3	MAN	H	6	3	-	2/2/19/22	0/1/1/1
3	NAG	H	7	3	-	3/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FUL	H	8	3	-	-	0/1/1/1
4	NAG	I	1	1,4	-	3/6/23/26	0/1/1/1
4	NAG	I	2	4	-	2/6/23/26	0/1/1/1
4	BMA	I	3	4	-	2/2/19/22	0/1/1/1
4	MAN	I	4	4	-	1/2/19/22	1/1/1/1
4	NAG	I	5	4	-	3/6/23/26	0/1/1/1
4	GAL	I	6	4	-	2/2/19/22	0/1/1/1
4	MAN	I	7	4	-	2/2/19/22	0/1/1/1
4	NAG	I	8	4	-	5/6/23/26	0/1/1/1
4	FUL	I	9	4	-	-	0/1/1/1
5	NAG	J	1	5	-	4/6/23/26	0/1/1/1
5	BMA	J	2	5	-	0/2/19/22	0/1/1/1
5	MAN	J	3	5	-	0/2/19/22	0/1/1/1
5	NAG	J	4	5	-	1/6/23/26	0/1/1/1
5	MAN	J	5	5	-	1/2/19/22	0/1/1/1
5	NAG	J	6	5	-	3/6/23/26	0/1/1/1
6	GAL	K	1	6	-	1/2/19/22	0/1/1/1
6	SIA	K	2	6	-	13/18/34/38	0/1/1/1

The worst 5 of 69 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	5	NAG	O5-C1	4.40	1.51	1.43
3	G	4	MAN	O5-C1	4.30	1.50	1.43
3	H	7	NAG	O5-C1	4.14	1.50	1.43
3	H	1	NAG	O5-C1	3.92	1.50	1.43
3	H	6	MAN	O5-C1	3.82	1.50	1.43

The worst 5 of 100 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	3	BMA	C1-C2-C3	6.11	118.54	109.64
3	H	3	BMA	C1-C2-C3	5.92	118.26	109.64
5	J	4	NAG	C1-O5-C5	5.68	119.80	112.19
3	H	4	MAN	C1-C2-C3	5.55	117.72	109.64
5	J	2	BMA	C1-O5-C5	5.25	119.22	112.19

There are no chirality outliers.

5 of 77 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	1	NAG	C3-C2-N2-C7
3	G	5	NAG	C1-C2-N2-C7
5	J	4	NAG	C3-C2-N2-C7
5	J	6	NAG	C8-C7-N2-C2
5	J	6	NAG	O7-C7-N2-C2

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	6	MAN	C1-C2-C3-C4-C5-O5
4	I	4	MAN	C1-C2-C3-C4-C5-O5

31 monomers are involved in 93 short contacts:

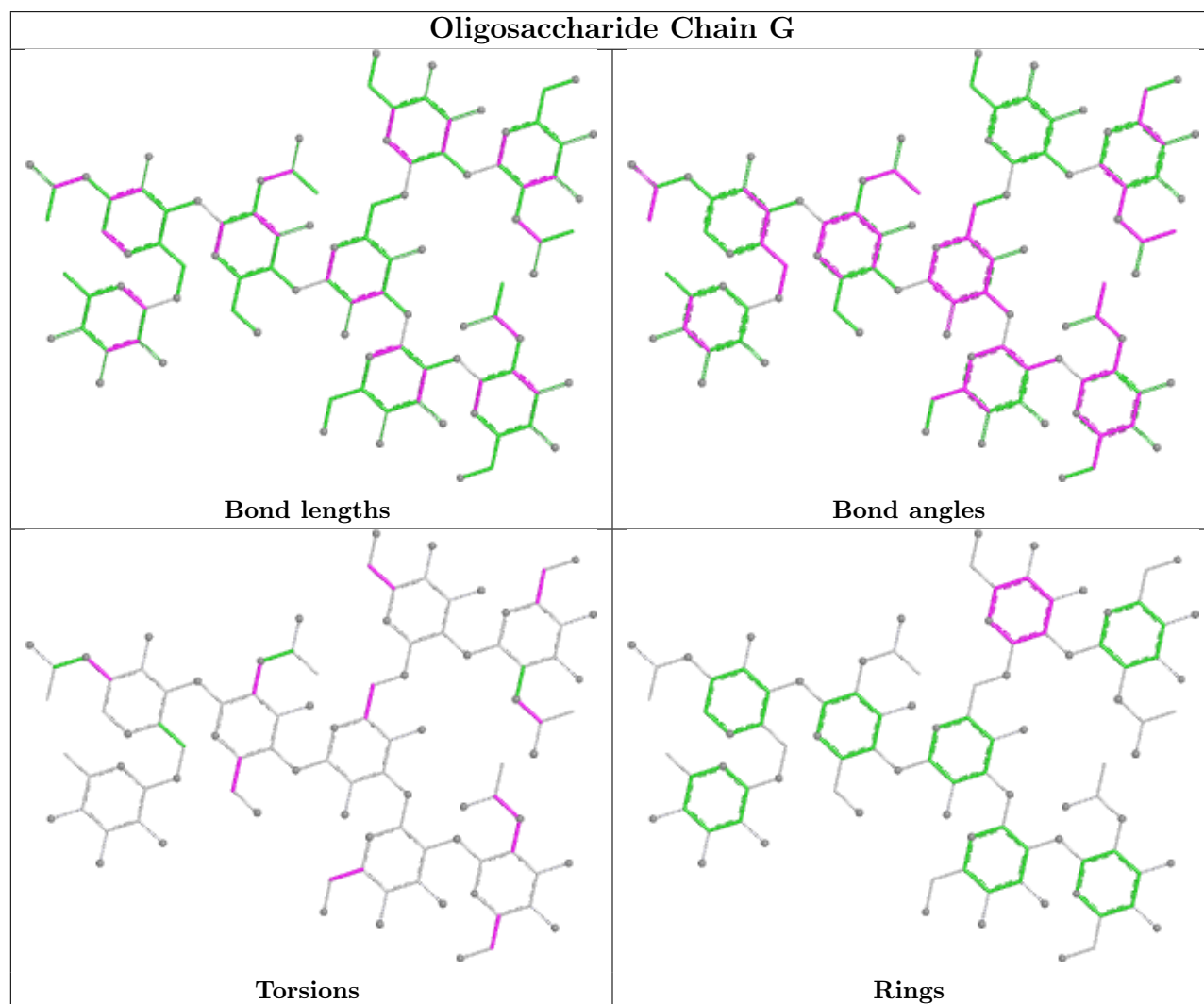
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	8	FUL	2	0
3	G	6	MAN	9	0
3	G	7	NAG	5	0
3	H	6	MAN	6	0
4	I	4	MAN	7	0
4	I	6	GAL	3	0
3	H	8	FUL	2	0
3	G	4	MAN	1	0
5	J	3	MAN	1	0
4	I	3	BMA	7	0
3	G	5	NAG	3	0
6	K	1	GAL	5	0
3	G	3	BMA	7	0
3	H	2	NAG	5	0
6	K	2	SIA	4	0
4	I	2	NAG	7	0
3	G	1	NAG	3	0
3	G	2	NAG	5	0
4	I	5	NAG	4	0
5	J	1	NAG	2	0
3	H	1	NAG	2	0
4	I	1	NAG	3	0
4	I	8	NAG	3	0
5	J	5	MAN	2	0
3	H	7	NAG	2	0
4	I	7	MAN	6	0
5	J	4	NAG	13	0
3	H	4	MAN	7	0

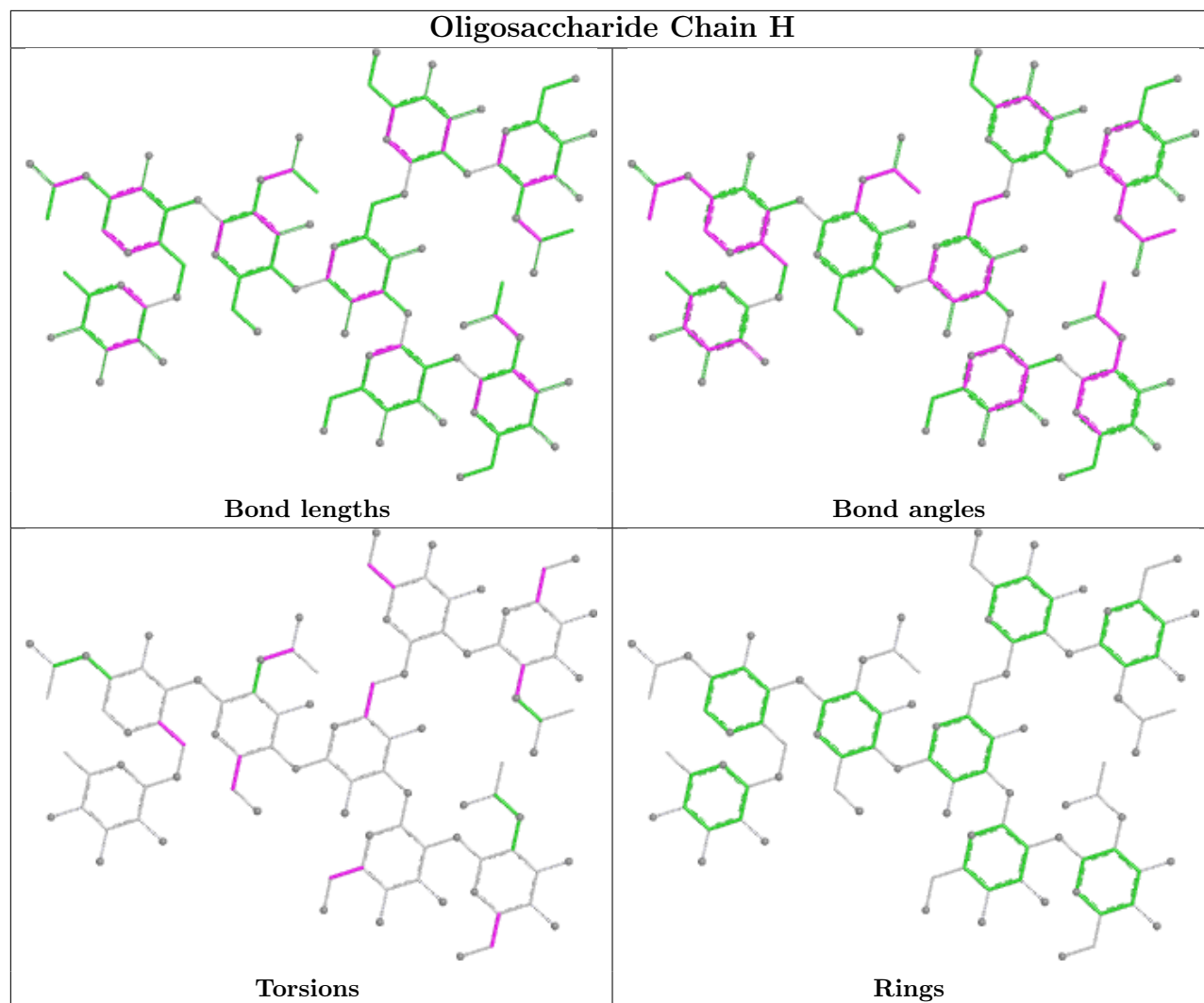
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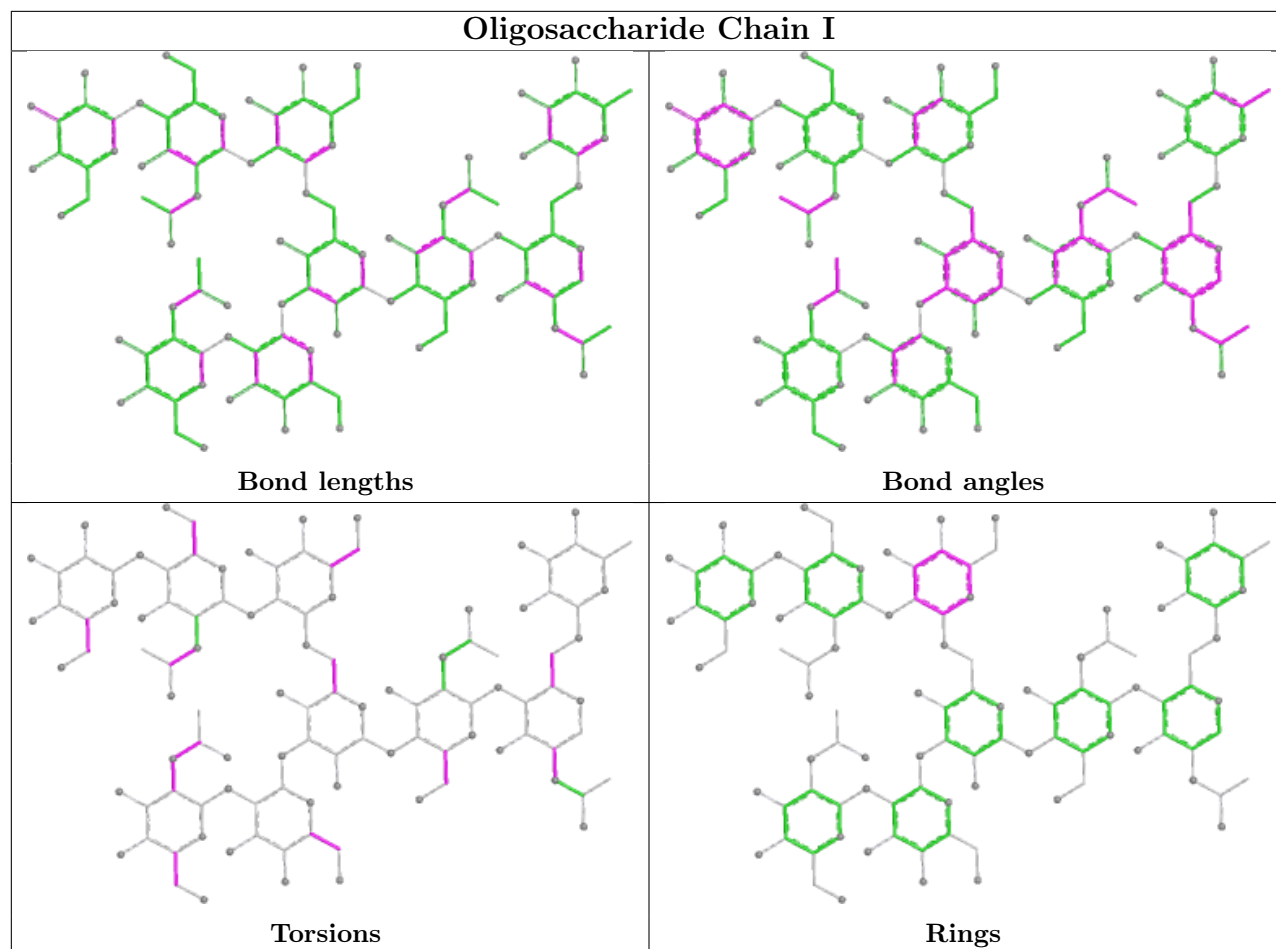
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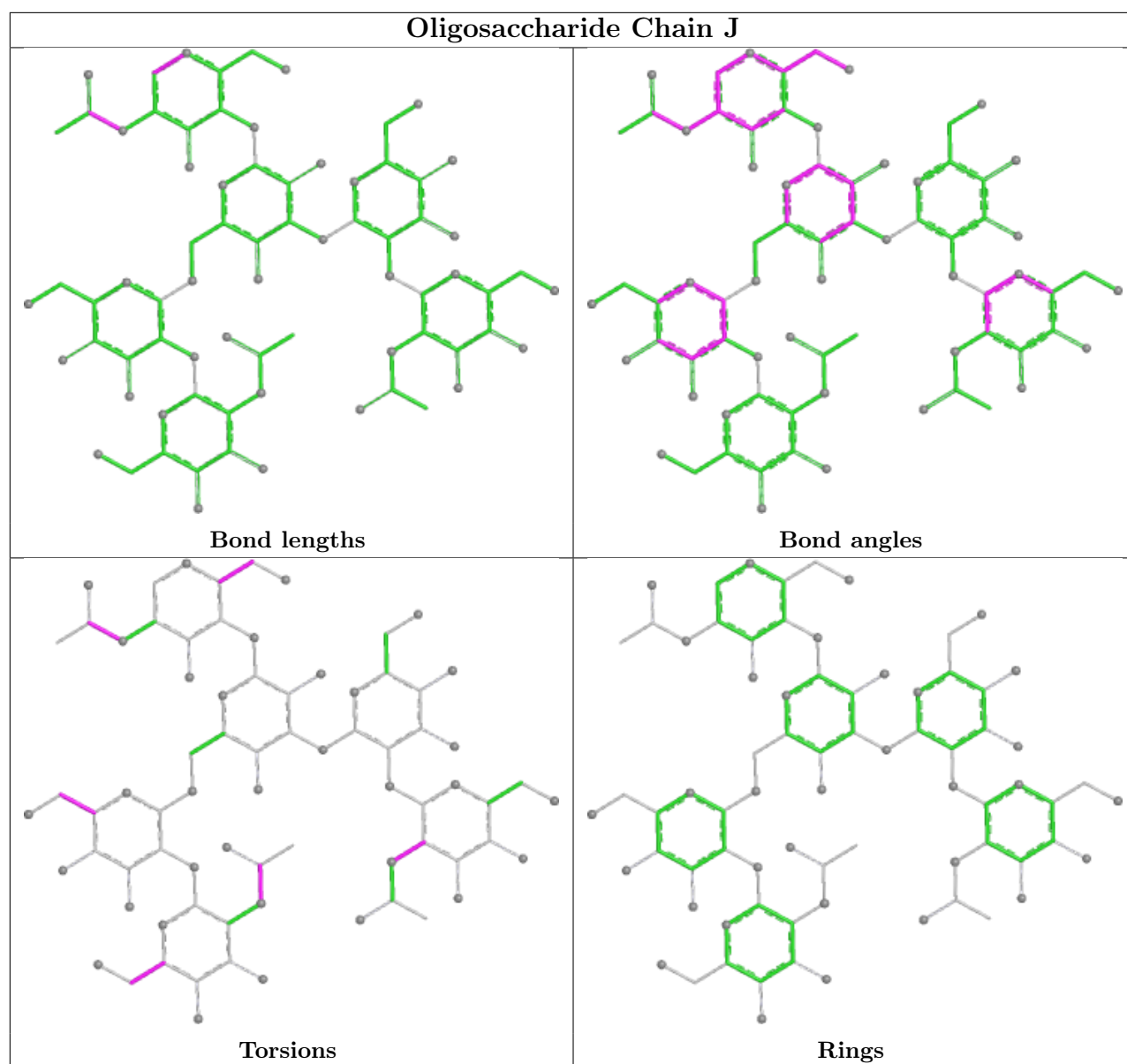
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	J	2	BMA	2	0
3	H	5	NAG	5	0
5	J	6	NAG	6	0

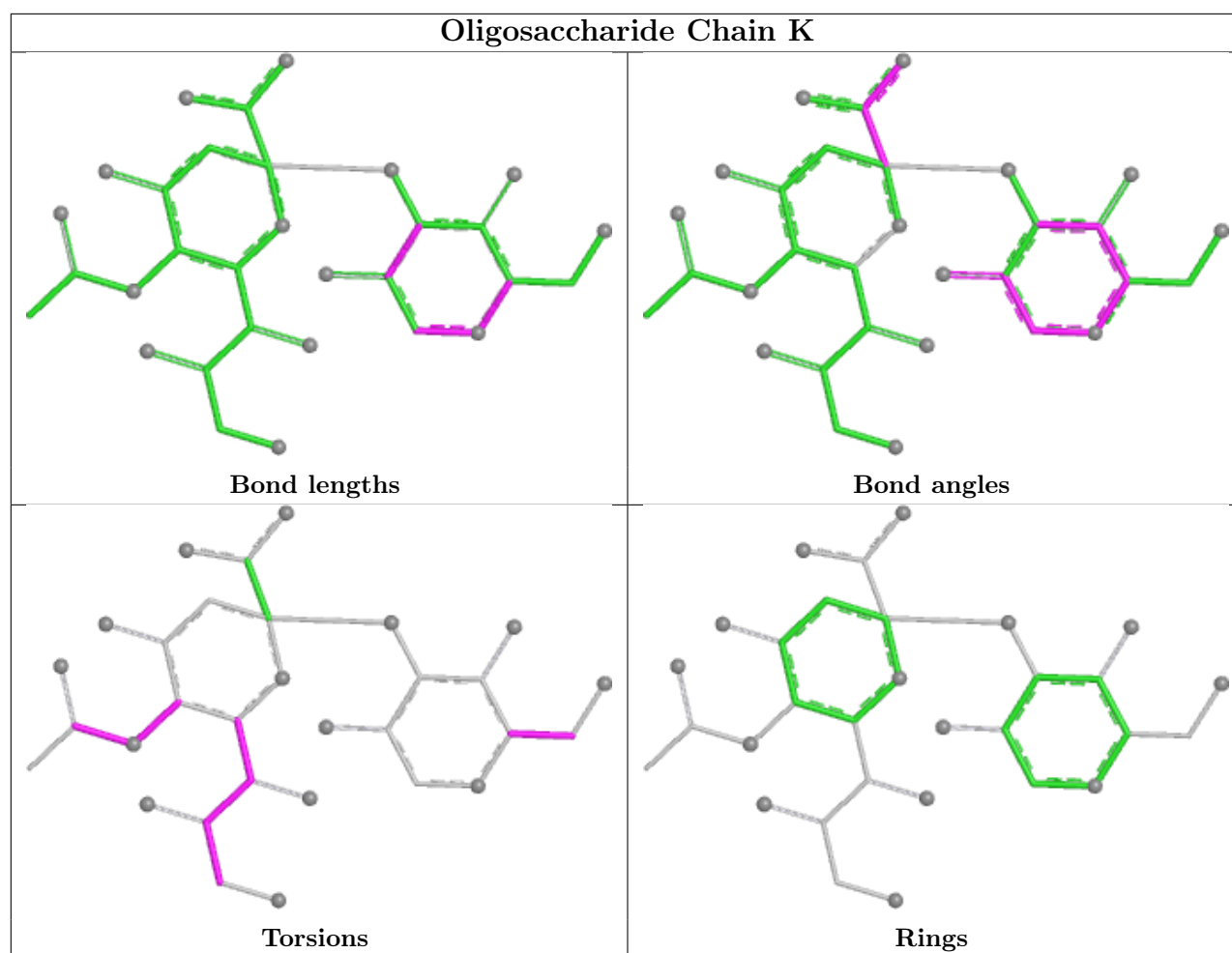
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

2 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	$\# Z > 2$
7	NAG	D	1001	1	14,14,15	1.61	3 (21%)	17,19,21	1.99	6 (35%)
8	FUL	D	1008	-	10,10,11	1.72	2 (20%)	14,14,16	1.10	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
7	NAG	D	1001	1	-	2/6/23/26	0/1/1/1
8	FUL	D	1008	-	-	-	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	D	1008	FUL	O5-C1	3.77	1.50	1.43
7	D	1001	NAG	O5-C1	3.46	1.49	1.43
8	D	1008	FUL	C2-C3	-2.97	1.47	1.52
7	D	1001	NAG	C7-N2	2.93	1.43	1.34
7	D	1001	NAG	C3-C2	-2.56	1.47	1.52

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	D	1001	NAG	C2-N2-C7	-3.70	117.94	122.90
7	D	1001	NAG	C8-C7-N2	3.35	121.68	116.12
7	D	1001	NAG	C1-O5-C5	3.06	116.29	112.19
7	D	1001	NAG	C3-C4-C5	2.95	115.59	110.23
7	D	1001	NAG	O5-C5-C4	2.68	117.34	110.83

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	D	1001	NAG	O5-C5-C6-O6
7	D	1001	NAG	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	1001	NAG	13	0
8	D	1008	FUL	5	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	218/219 (99%)	-0.94	1 (0%) 87 69	92, 144, 214, 385	0
1	B	216/219 (98%)	-0.88	0 100 100	86, 150, 207, 283	0
1	C	212/219 (96%)	-0.97	2 (0%) 81 58	70, 141, 203, 463	0
1	D	214/219 (97%)	-0.71	3 (1%) 73 49	85, 163, 225, 273	0
2	E	259/275 (94%)	-0.76	3 (1%) 76 53	100, 218, 411, 457	0
2	F	258/275 (93%)	-0.76	6 (2%) 61 37	123, 222, 330, 393	0
All	All	1377/1426 (96%)	-0.83	15 (1%) 78 54	70, 167, 316, 463	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	23	VAL	4.1
1	A	233	GLU	3.1
1	C	431	ALA	2.7
2	F	58	LEU	2.7
2	E	242	SER	2.6

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

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

6.3 Carbohydrates [i](#)

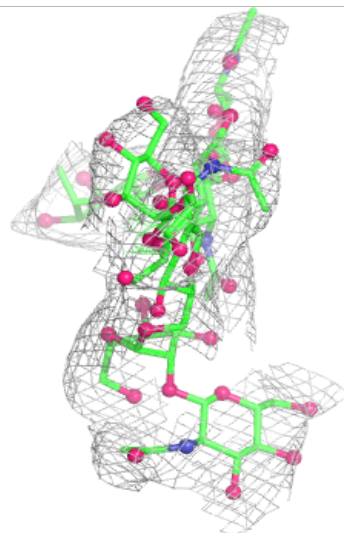
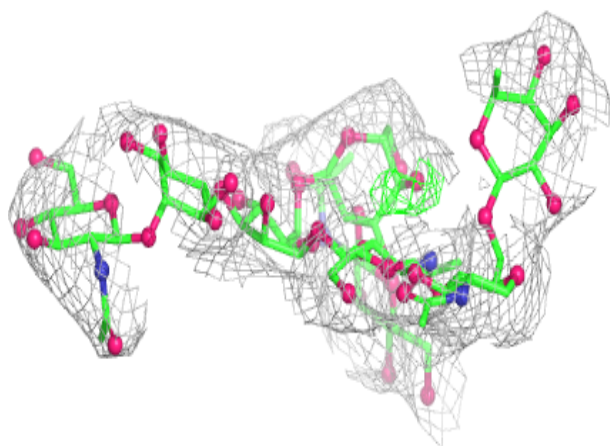
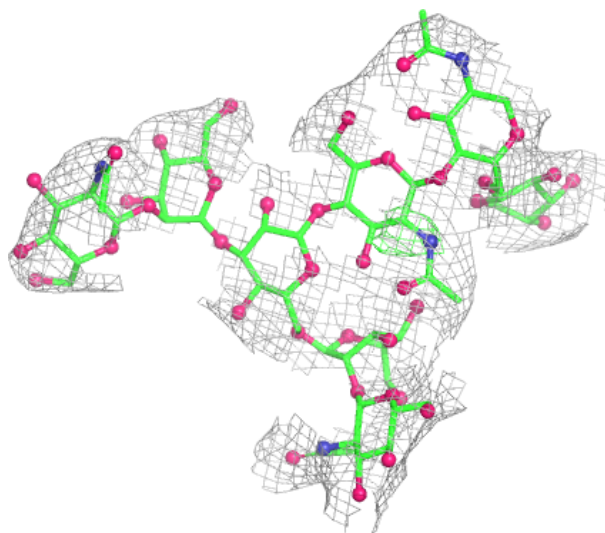
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	FUL	I	9	10/11	0.94	0.05	109,133,138,140	0
6	GAL	K	1	11/12	0.94	0.07	278,291,310,321	0
3	FUL	G	8	10/11	0.96	0.06	128,140,150,154	0
4	NAG	I	5	14/15	0.96	0.05	74,130,156,170	0
3	NAG	H	7	14/15	0.97	0.04	107,118,130,146	0
3	NAG	G	7	14/15	0.97	0.04	70,118,125,126	0
4	NAG	I	8	14/15	0.97	0.06	120,164,176,200	0
3	NAG	H	1	14/15	0.97	0.06	145,188,210,222	0
5	MAN	J	3	11/12	0.97	0.06	205,225,259,266	0
5	NAG	J	4	14/15	0.97	0.09	175,258,267,270	0
3	NAG	H	5	14/15	0.97	0.05	170,189,206,207	0
4	NAG	I	2	14/15	0.98	0.05	93,112,126,126	0
4	MAN	I	4	11/12	0.98	0.04	108,118,133,144	0
3	MAN	G	6	11/12	0.98	0.04	85,104,131,135	0
4	MAN	I	7	11/12	0.98	0.03	156,164,181,186	0
3	NAG	H	2	14/15	0.98	0.06	112,133,150,155	0
3	MAN	H	4	11/12	0.98	0.05	113,158,179,187	0
5	NAG	J	1	14/15	0.98	0.12	185,201,221,225	0
5	BMA	J	2	11/12	0.98	0.04	148,167,183,184	0
3	MAN	G	4	11/12	0.98	0.05	96,112,146,152	0
3	MAN	H	6	11/12	0.98	0.04	88,100,113,114	0
5	MAN	J	5	11/12	0.98	0.05	88,100,113,114	0
5	NAG	J	6	14/15	0.98	0.05	107,118,130,146	0
3	NAG	G	5	14/15	0.98	0.06	135,171,216,235	0
6	SIA	K	2	20/21	0.98	0.04	225,279,306,311	0
3	BMA	H	3	11/12	0.99	0.03	110,131,137,146	0
3	BMA	G	3	11/12	0.99	0.03	92,95,108,116	0
4	GAL	I	6	11/12	0.99	0.07	178,191,201,214	0
3	FUL	H	8	10/11	0.99	0.06	189,205,221,221	0
4	NAG	I	1	14/15	0.99	0.06	127,140,193,194	0
3	NAG	G	2	14/15	0.99	0.05	78,105,119,125	0
4	BMA	I	3	11/12	0.99	0.03	103,120,149,152	0
3	NAG	G	1	14/15	1.00	0.03	116,130,142,155	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.

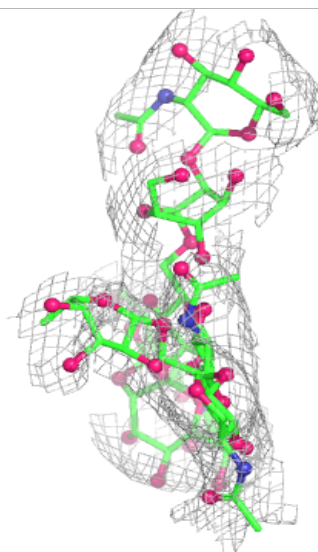
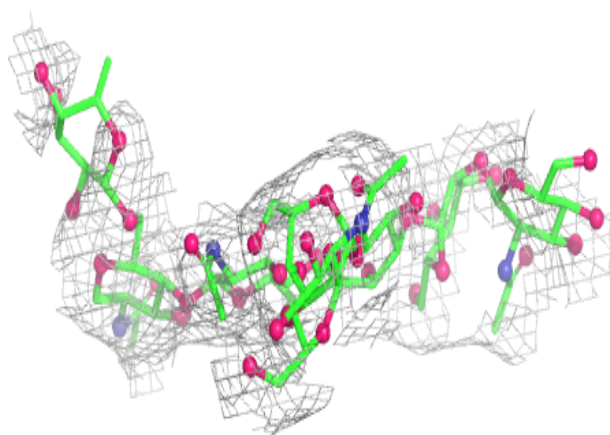
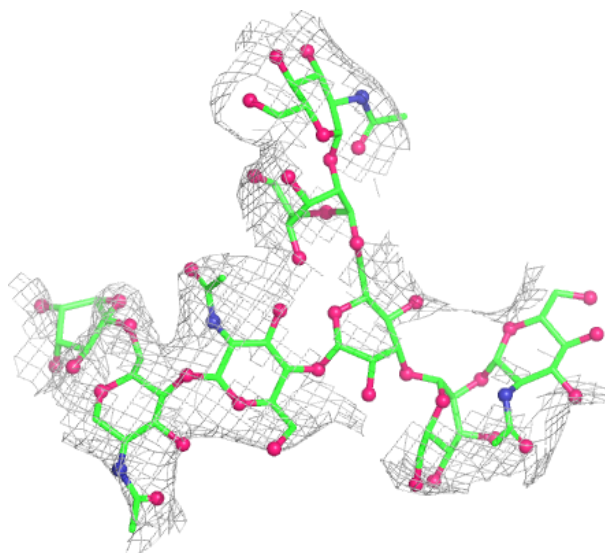
Electron density around Chain G:

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



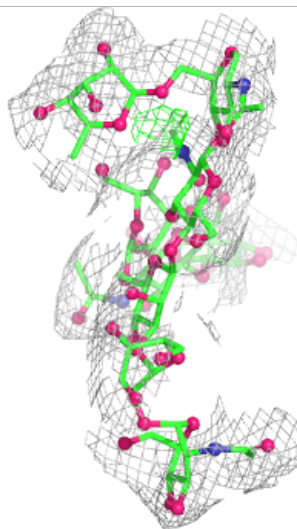
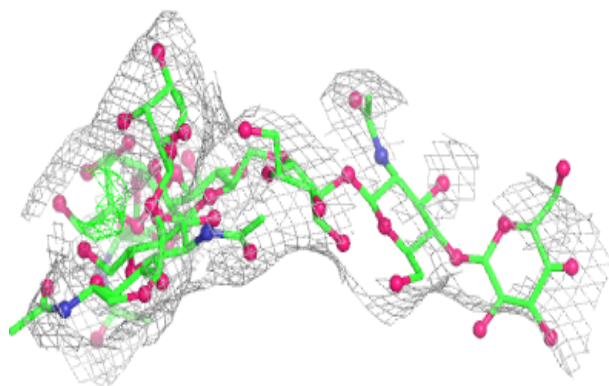
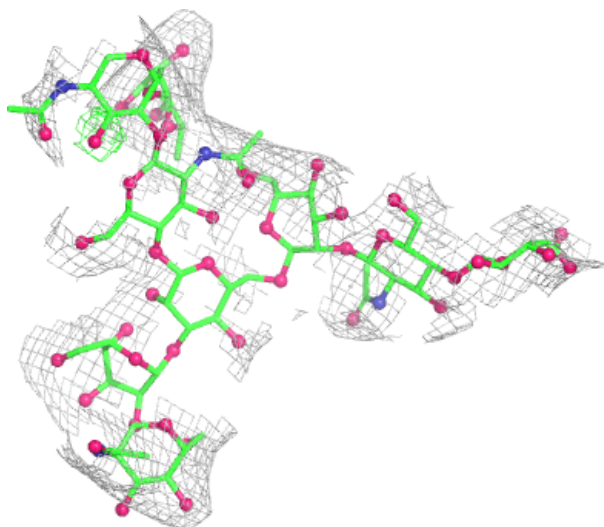
Electron density around Chain H:

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



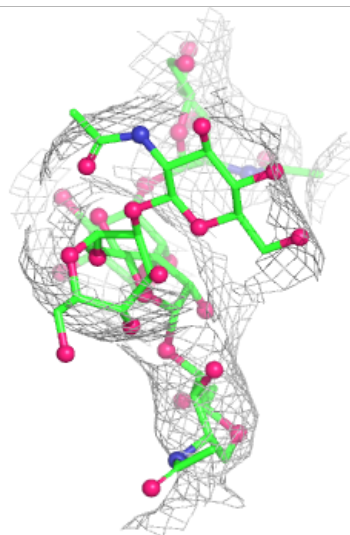
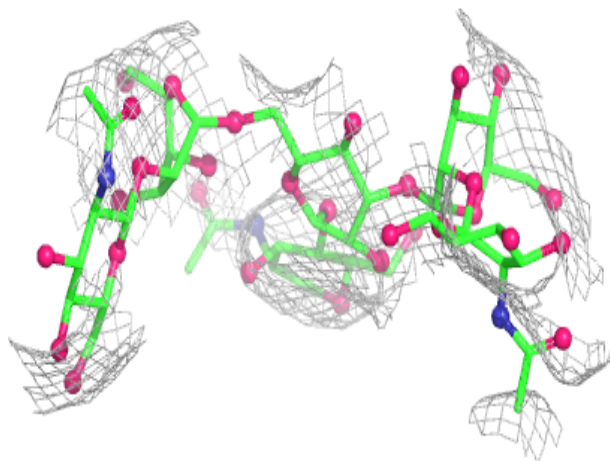
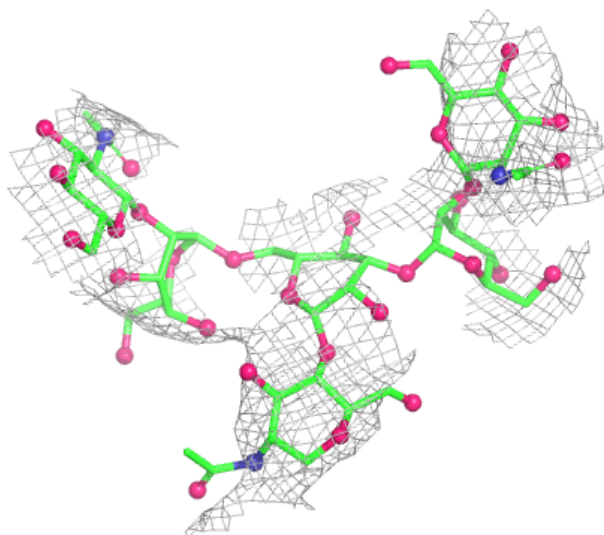
Electron density around Chain I:

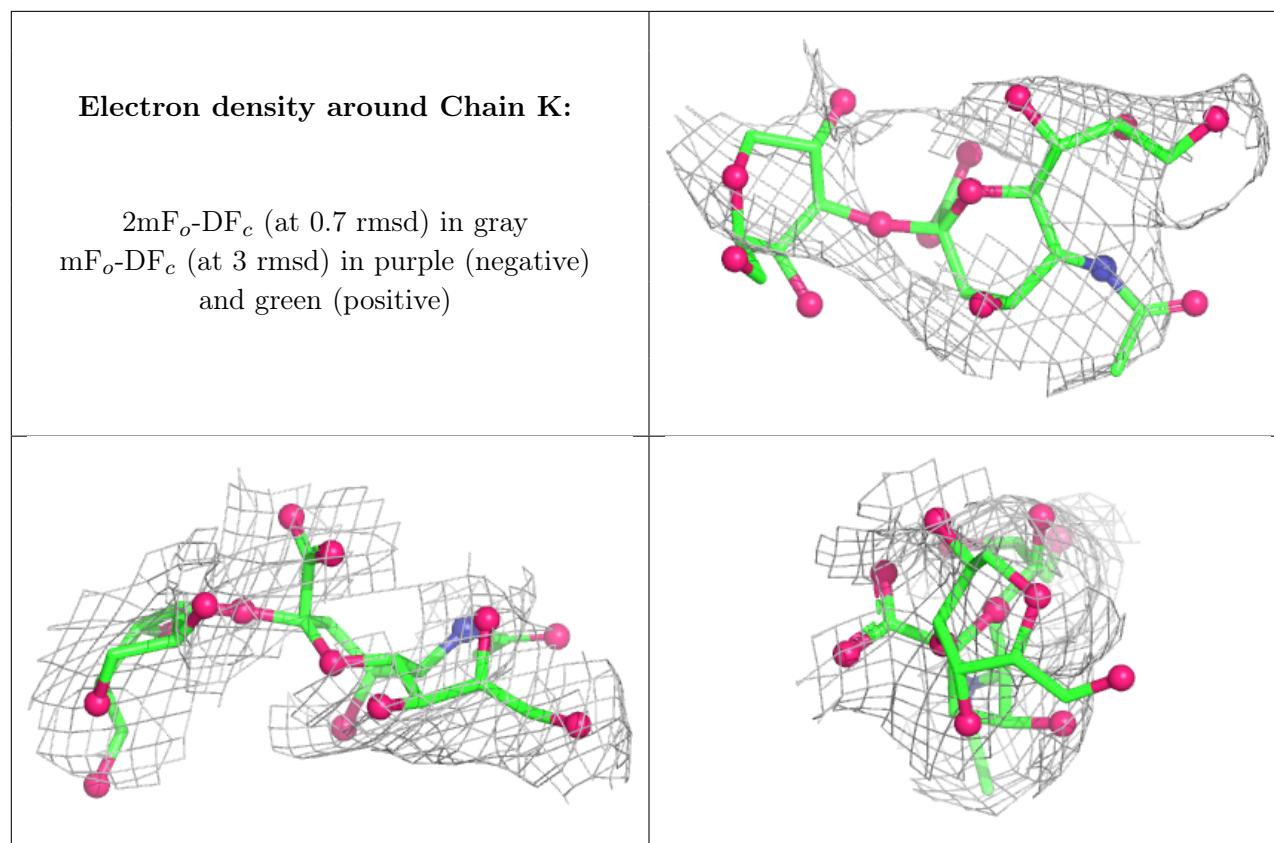
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain J:

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





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
8	FUL	D	1008	10/11	0.96	0.07	189,205,221,221	0
7	NAG	D	1001	14/15	0.98	0.04	184,214,227,227	0

6.5 Other polymers [i](#)

There are no such residues in this entry.