wwPDB X-ray Structure Validation Summary Report (i)

Nov 5, 2026 – 04:09 PM EST

PDB ID	:	11CT / pdb_000011ct
Title	:	Crystal structure of mouse IgG2a-Fc
Authors	:	Guo, M.; Yan, Z.
Deposited on	:	2026-02-17
Resolution	:	3.21 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 (i) 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 (1)) were used in the production of this report:

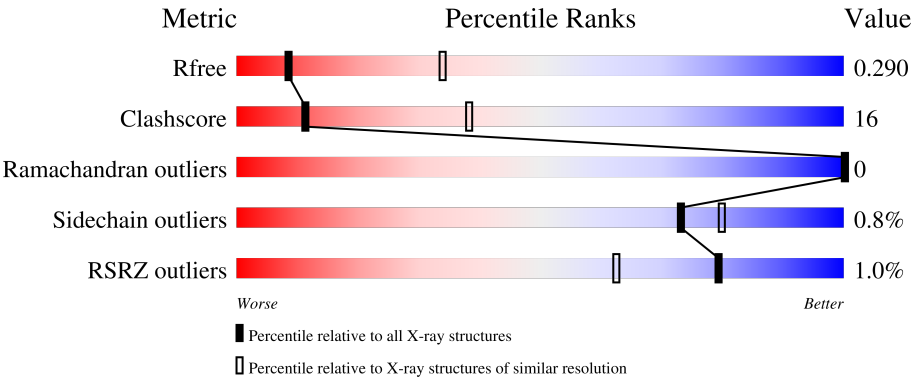
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

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 3.21 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	1768 (3.24-3.20)
Clashscore	190562	1879 (3.24-3.20)
Ramachandran outliers	187476	1844 (3.24-3.20)
Sidechain outliers	187428	1843 (3.24-3.20)
RSRZ outliers	180081	1768 (3.24-3.20)

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 <=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	206	2%, 67%, 32%, ·
1	B	206	64%, 36%
1	C	206	65%, 33%, ·
2	D	9	11%, 78%, 11%
3	E	8	62%, 38%

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Mol	Chain	Length	Quality of chain
4	F	9	

2 Entry composition

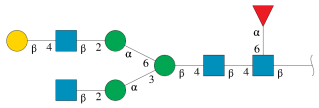
There are 4 unique types of molecules in this entry. The entry contains 5308 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Ig gamma-2A chain C region, A allele.

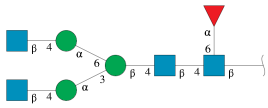
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	206	Total	C	N	O	S	0	0	0
			1663	1054	280	319	10			
1	B	206	Total	C	N	O	S	0	0	0
			1663	1054	280	319	10			
1	C	206	Total	C	N	O	S	0	0	0
			1663	1054	280	319	10			

- Molecule 2 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)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



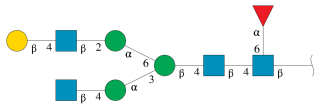
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	9	Total	C	N	O	0	0	0
			110	62	4	44			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	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-(1-4)-alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



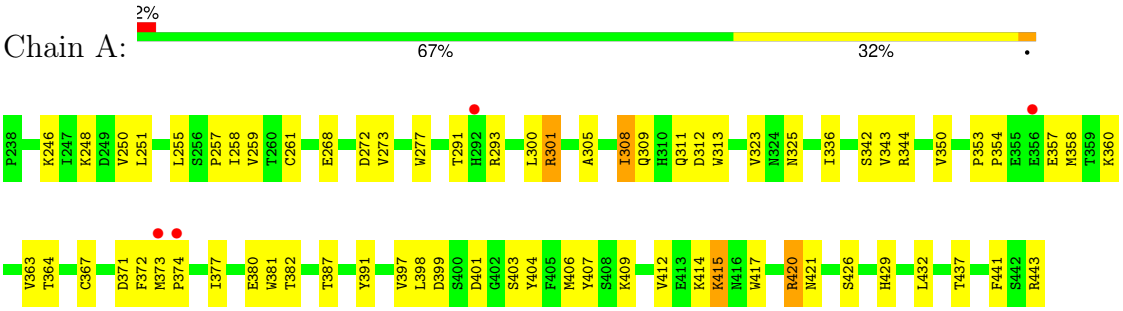
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	9	Total	C	N	O	0	0	0
			110	62	4	44			

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

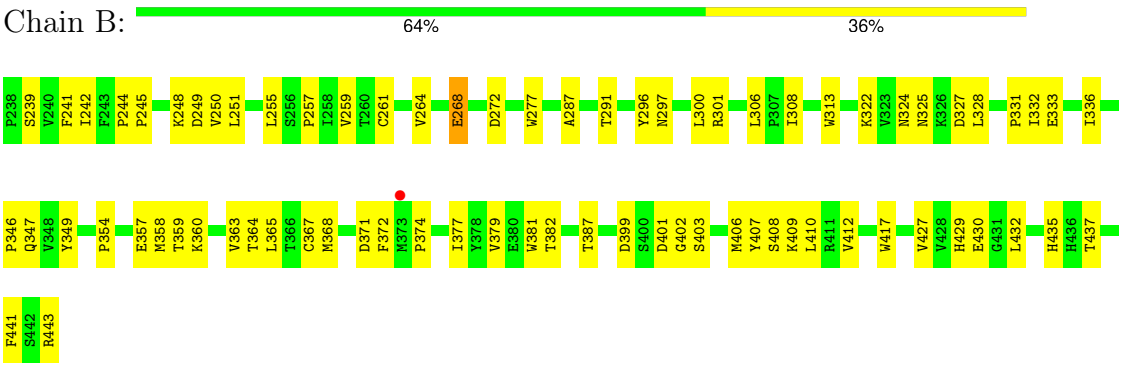
• Molecule 1: Ig gamma-2A chain C region, A allele

Chain A:



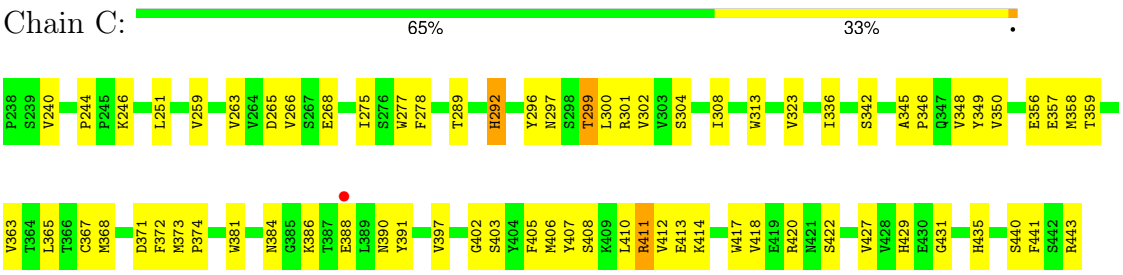
• Molecule 1: Ig gamma-2A chain C region, A allele

Chain B:



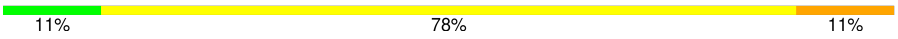
• Molecule 1: Ig gamma-2A chain C region, A allele

Chain C:



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

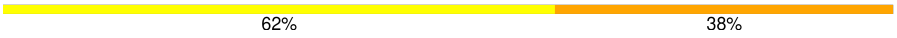
Chain D:





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

Chain E:





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

Chain F:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	135.25Å 98.14Å 61.92Å 90.00° 99.53° 90.00°	Depositor
Resolution (Å)	66.69 – 3.21 66.69 – 3.21	Depositor EDS
% Data completeness (in resolution range)	99.6 (66.69-3.21) 99.5 (66.69-3.21)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.68 (at 3.19Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.239 , 0.290 0.239 , 0.290	Depositor DCC
R_{free} test set	626 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å^2)	81.2	Xtriage
Anisotropy	0.104	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 56.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	5308	wwPDB-VP
Average B, all atoms (Å^2)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.28% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: NAG, BMA, GAL, FUC, MAN

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	0.80	1/1706 (0.1%)	1.25	2/2322 (0.1%)
1	B	0.79	0/1706	1.16	2/2322 (0.1%)
1	C	0.77	0/1706	1.14	2/2322 (0.1%)
All	All	0.79	1/5118 (0.0%)	1.18	6/6966 (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	A	0	2
1	B	0	2
1	C	0	3
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	353	PRO	C-O	-5.04	1.20	1.25

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	268	GLU	N-CA-C	-6.06	104.68	111.28
1	A	291	THR	N-CA-C	-5.45	102.33	110.23
1	A	372	PHE	CA-CB-CG	5.37	119.17	113.80
1	B	402	GLY	N-CA-C	-5.33	107.97	115.32
1	C	402	GLY	N-CA-C	-5.13	108.25	115.32

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	301	ARG	Sidechain
1	A	420	ARG	Sidechain
1	B	301	ARG	Sidechain
1	B	443	ARG	Sidechain
1	C	301	ARG	Sidechain

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	1663	0	1629	52	0
1	B	1663	0	1629	62	0
1	C	1663	0	1629	58	0
2	D	110	0	94	1	0
3	E	99	0	85	3	0
4	F	110	0	94	8	0
All	All	5308	0	5160	170	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 16.

The worst 5 of 170 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:291:THR:CG2	1:C:386:LYS:HB3	1.77	1.15
1:B:291:THR:HG22	1:C:386:LYS:HB3	1.19	1.12
1:B:287:ALA:HB2	1:B:306:LEU:HD12	1.61	0.80
1:A:350:VAL:CG1	1:A:441:PHE:CE1	2.67	0.77
3:E:2:NAG:H4	3:E:8:FUC:H61	1.67	0.76

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	204/206 (99%)	201 (98%)	3 (2%)	0	100	100
1	B	204/206 (99%)	202 (99%)	2 (1%)	0	100	100
1	C	204/206 (99%)	201 (98%)	3 (2%)	0	100	100
All	All	612/618 (99%)	604 (99%)	8 (1%)	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	197/197 (100%)	194 (98%)	3 (2%)	57	74
1	B	197/197 (100%)	197 (100%)	0	100	100
1	C	197/197 (100%)	195 (99%)	2 (1%)	68	78
All	All	591/591 (100%)	586 (99%)	5 (1%)	73	80

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	308	ILE
1	A	415	LYS
1	A	421	ASN
1	C	292	HIS
1	C	299	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	347	GLN
1	C	362	GLN
1	C	433	HIS
1	C	384	ASN
1	B	290	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

26 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	D	1	1,2	14,14,15	0.71	1 (7%)	17,19,21	0.85	1 (5%)
2	NAG	D	2	2	14,14,15	0.33	0	17,19,21	0.67	1 (5%)
2	BMA	D	3	2	11,11,12	1.67	3 (27%)	15,15,17	1.33	1 (6%)
2	MAN	D	4	2	11,11,12	1.47	1 (9%)	15,15,17	1.85	4 (26%)
2	NAG	D	5	2	14,14,15	0.30	0	17,19,21	0.62	0
2	GAL	D	6	2	11,11,12	2.37	4 (36%)	15,15,17	1.36	2 (13%)
2	MAN	D	7	2	11,11,12	1.25	1 (9%)	15,15,17	1.44	2 (13%)
2	NAG	D	8	2	14,14,15	0.77	1 (7%)	17,19,21	0.97	1 (5%)
2	FUC	D	9	2	10,10,11	2.26	4 (40%)	14,14,16	2.10	6 (42%)
3	NAG	E	1	3,1	14,14,15	0.70	1 (7%)	17,19,21	0.91	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	NAG	E	2	3	14,14,15	1.17	2 (14%)	17,19,21	0.98	1 (5%)
3	BMA	E	3	3	11,11,12	1.72	3 (27%)	15,15,17	2.58	7 (46%)
3	MAN	E	4	3	11,11,12	2.33	4 (36%)	15,15,17	2.17	2 (13%)
3	NAG	E	5	3	14,14,15	0.45	0	17,19,21	0.83	1 (5%)
3	MAN	E	6	3	11,11,12	0.71	0	15,15,17	1.46	2 (13%)
3	NAG	E	7	3	14,14,15	0.35	0	17,19,21	0.97	1 (5%)
3	FUC	E	8	3	10,10,11	1.89	5 (50%)	14,14,16	1.07	2 (14%)
4	NAG	F	1	1,4	14,14,15	2.22	2 (14%)	17,19,21	1.00	1 (5%)
4	NAG	F	2	4	14,14,15	0.95	2 (14%)	17,19,21	1.33	4 (23%)
4	BMA	F	3	4	11,11,12	1.70	3 (27%)	15,15,17	2.21	6 (40%)
4	MAN	F	4	4	11,11,12	1.05	1 (9%)	15,15,17	1.42	3 (20%)
4	NAG	F	5	4	14,14,15	0.45	0	17,19,21	1.17	1 (5%)
4	GAL	F	6	4	11,11,12	2.30	5 (45%)	15,15,17	1.38	3 (20%)
4	MAN	F	7	4	11,11,12	1.61	2 (18%)	15,15,17	2.16	4 (26%)
4	NAG	F	8	4	14,14,15	1.06	2 (14%)	17,19,21	0.83	1 (5%)
4	FUC	F	9	4	10,10,11	2.13	2 (20%)	14,14,16	1.70	3 (21%)

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	D	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	1/6/23/26	0/1/1/1
2	BMA	D	3	2	-	0/2/19/22	0/1/1/1
2	MAN	D	4	2	-	2/2/19/22	0/1/1/1
2	NAG	D	5	2	-	2/6/23/26	0/1/1/1
2	GAL	D	6	2	-	0/2/19/22	0/1/1/1
2	MAN	D	7	2	-	0/2/19/22	0/1/1/1
2	NAG	D	8	2	-	2/6/23/26	0/1/1/1
2	FUC	D	9	2	-	-	0/1/1/1
3	NAG	E	1	3,1	-	1/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	BMA	E	3	3	-	2/2/19/22	0/1/1/1
3	MAN	E	4	3	-	2/2/19/22	0/1/1/1
3	NAG	E	5	3	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	E	6	3	-	1/2/19/22	0/1/1/1
3	NAG	E	7	3	-	4/6/23/26	0/1/1/1
3	FUC	E	8	3	-	-	0/1/1/1
4	NAG	F	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	4/6/23/26	0/1/1/1
4	BMA	F	3	4	-	1/2/19/22	0/1/1/1
4	MAN	F	4	4	-	0/2/19/22	0/1/1/1
4	NAG	F	5	4	-	2/6/23/26	0/1/1/1
4	GAL	F	6	4	-	0/2/19/22	0/1/1/1
4	MAN	F	7	4	-	2/2/19/22	0/1/1/1
4	NAG	F	8	4	-	2/6/23/26	0/1/1/1
4	FUC	F	9	4	-	-	0/1/1/1

The worst 5 of 49 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	1	NAG	O5-C1	-6.69	1.32	1.43
3	E	4	MAN	O5-C1	5.37	1.52	1.43
4	F	9	FUC	C1-C2	4.96	1.64	1.52
4	F	1	NAG	C1-C2	-4.73	1.45	1.52
2	D	6	GAL	C4-C3	4.58	1.64	1.52

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	4	MAN	C1-O5-C5	7.25	121.91	112.19
4	F	7	MAN	C1-O5-C5	6.03	120.27	112.19
4	F	3	BMA	C1-O5-C5	-5.02	105.45	112.19
2	D	7	MAN	C1-O5-C5	4.83	118.66	112.19
3	E	3	BMA	O2-C2-C3	-4.73	100.35	110.15

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

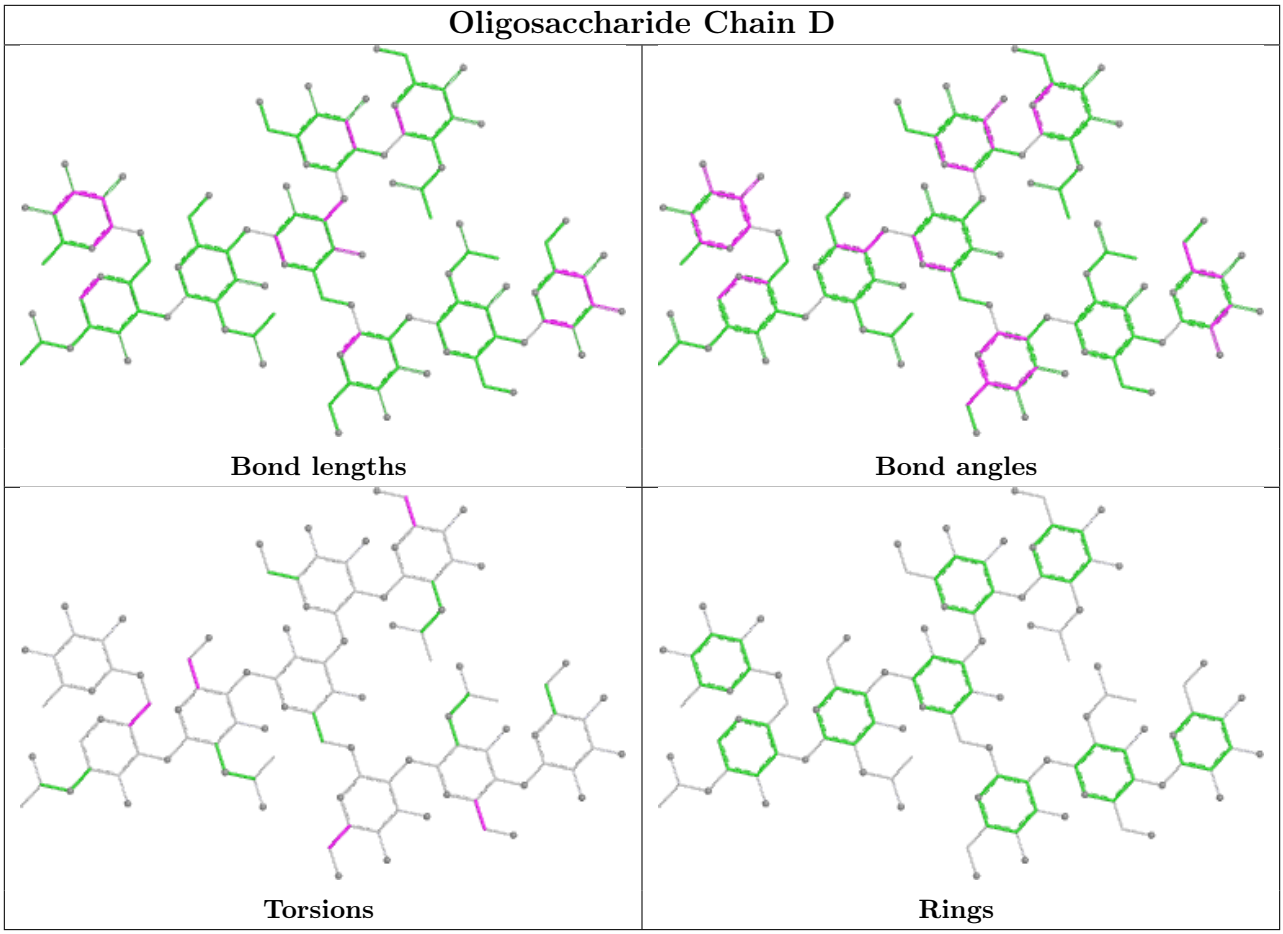
Mol	Chain	Res	Type	Atoms
4	F	2	NAG	C1-C2-N2-C7
2	D	1	NAG	C4-C5-C6-O6
2	D	1	NAG	O5-C5-C6-O6
2	D	4	MAN	O5-C5-C6-O6
3	E	7	NAG	O5-C5-C6-O6

There are no ring outliers.

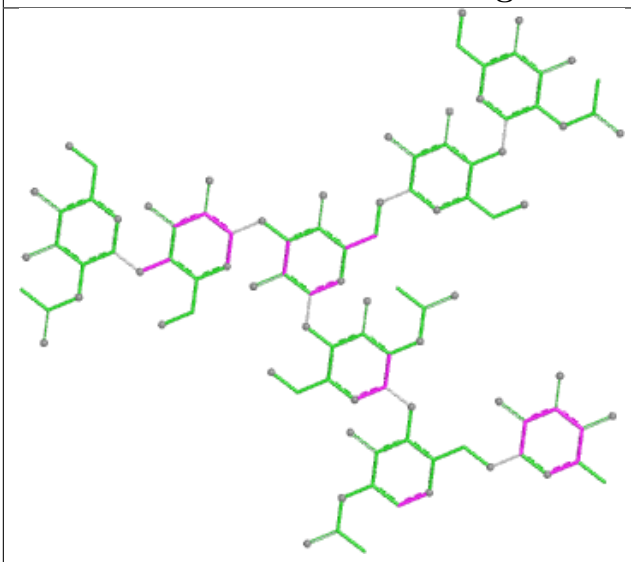
11 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	1	NAG	3	0
4	F	9	FUC	3	0
3	E	8	FUC	1	0
4	F	2	NAG	2	0
4	F	6	GAL	1	0
3	E	3	BMA	2	0
2	D	6	GAL	1	0
4	F	3	BMA	1	0
3	E	2	NAG	1	0
4	F	7	MAN	2	0
4	F	8	NAG	1	0

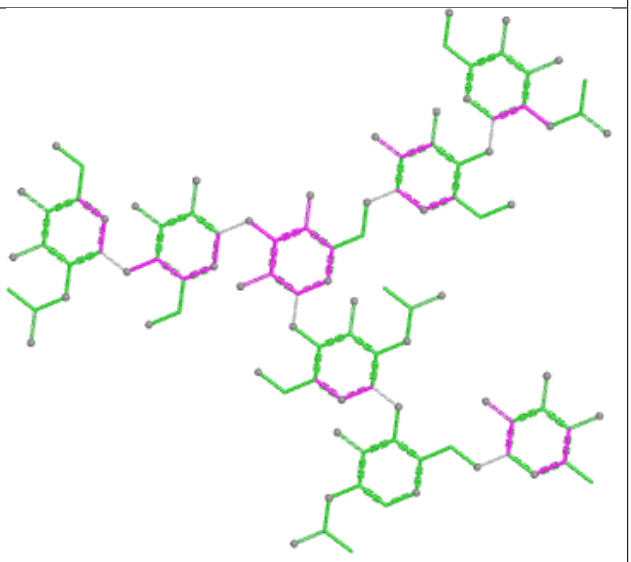
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



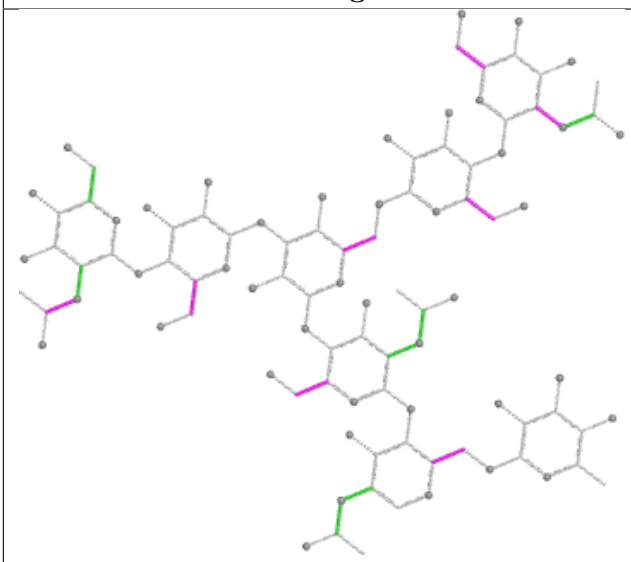
Oligosaccharide Chain E



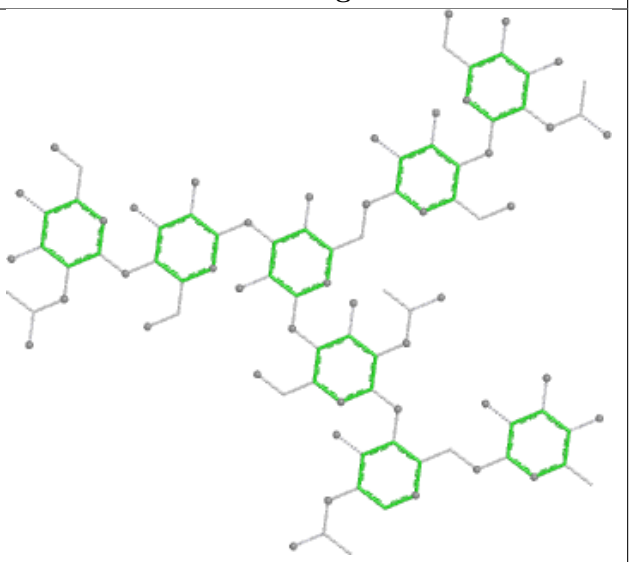
Bond lengths



Bond angles

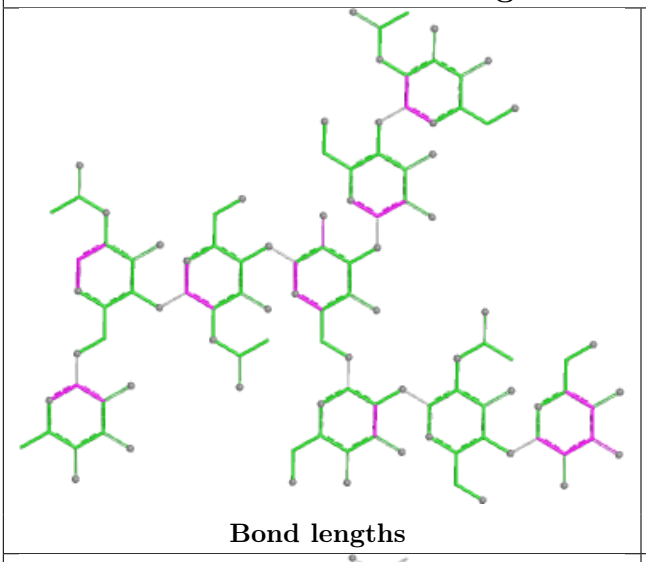


Torsions

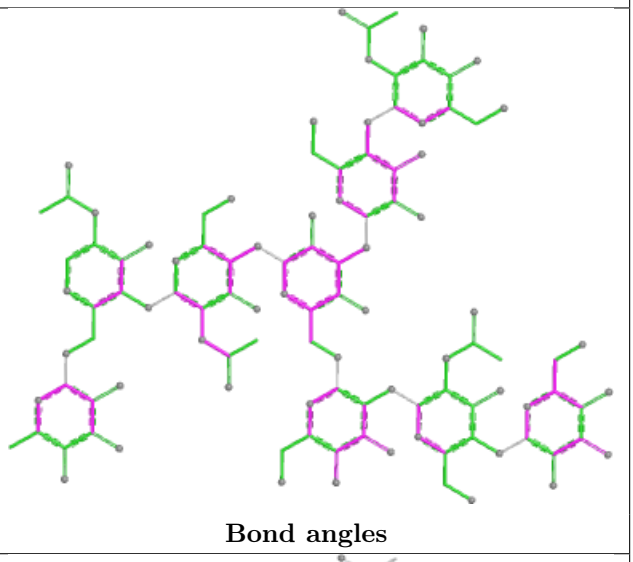


Rings

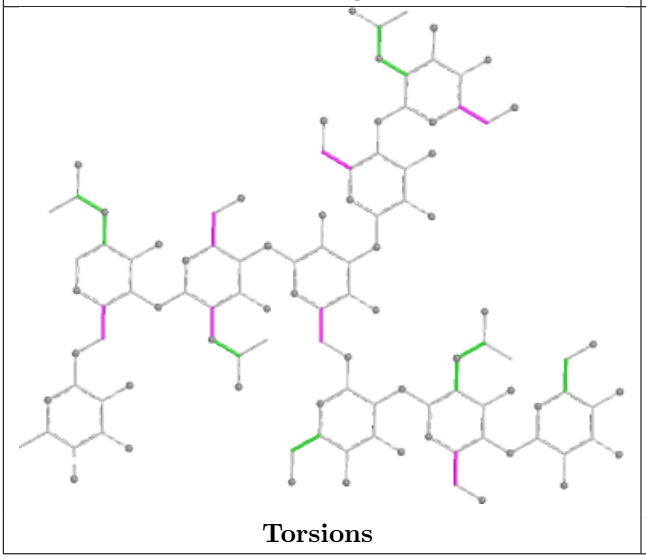
Oligosaccharide Chain F



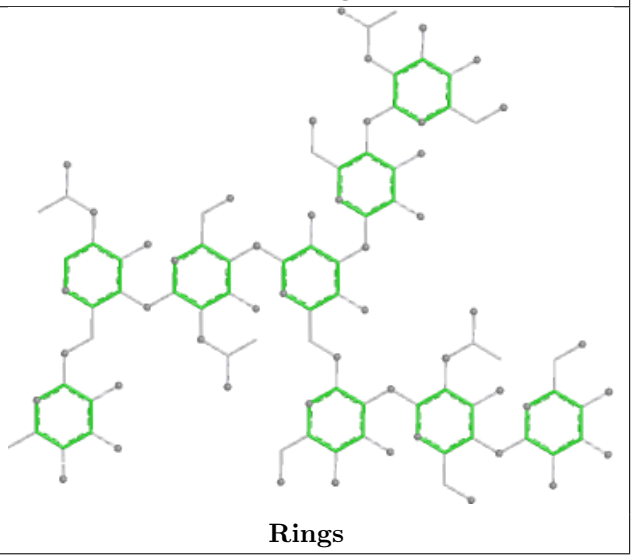
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	206/206 (100%)	0.27	4 (1%)	66	46	44, 65, 103, 119	0
1	B	206/206 (100%)	0.16	1 (0%)	87	76	30, 70, 113, 125	0
1	C	206/206 (100%)	0.16	1 (0%)	87	76	46, 69, 112, 137	0
All	All	618/618 (100%)	0.20	6 (0%)	79	62	30, 68, 111, 137	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	292	HIS	2.9
1	A	374	PRO	2.6
1	C	388	GLU	2.3
1	B	373	MET	2.2
1	A	373	MET	2.1

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

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

6.3 Carbohydrates

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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	FUC	E	8	10/11	0.54	0.13	114,118,124,127	0
4	NAG	F	1	14/15	0.59	0.13	108,125,131,136	0
3	MAN	E	4	11/12	0.64	0.16	92,98,115,122	0

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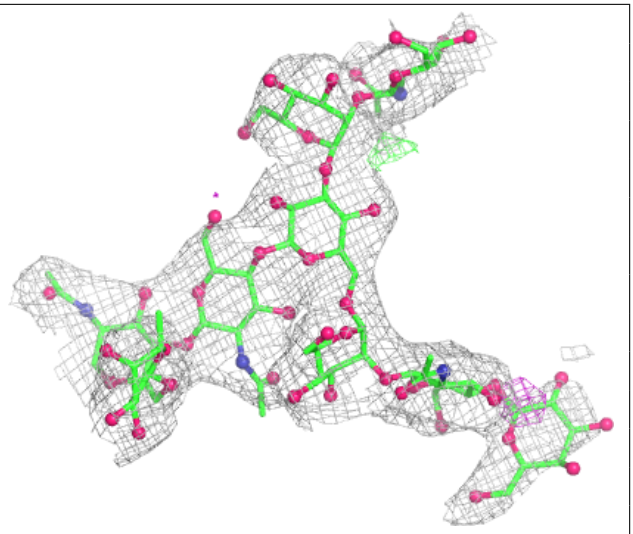
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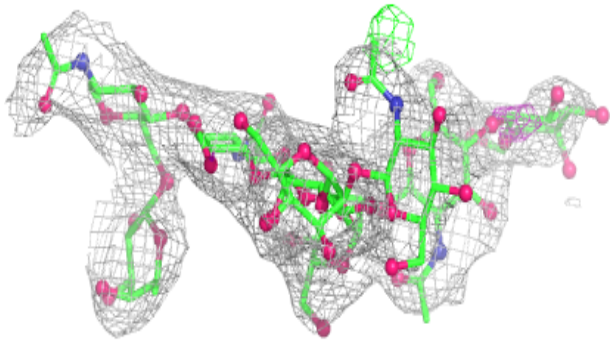
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	NAG	E	7	14/15	0.65	0.13	93,108,117,120	0
4	FUC	F	9	10/11	0.67	0.11	103,112,121,123	0
2	FUC	D	9	10/11	0.68	0.12	88,90,93,98	0
2	NAG	D	8	14/15	0.70	0.11	73,100,115,119	0
3	NAG	E	5	14/15	0.71	0.19	97,105,119,121	0
3	MAN	E	6	11/12	0.72	0.11	101,102,108,111	0
4	MAN	F	7	11/12	0.73	0.10	87,95,102,106	0
4	NAG	F	2	14/15	0.76	0.13	83,94,119,119	0
4	NAG	F	8	14/15	0.77	0.12	83,103,108,108	0
4	MAN	F	4	11/12	0.77	0.10	81,84,92,93	0
2	GAL	D	6	11/12	0.82	0.17	67,79,87,88	0
3	BMA	E	3	11/12	0.82	0.13	86,97,103,105	0
4	GAL	F	6	11/12	0.82	0.12	68,82,89,91	0
3	NAG	E	1	14/15	0.83	0.15	117,122,132,132	0
3	NAG	E	2	14/15	0.85	0.12	84,107,120,125	0
2	NAG	D	1	14/15	0.87	0.09	64,77,89,94	0
4	NAG	F	5	14/15	0.87	0.09	80,91,107,109	0
4	BMA	F	3	11/12	0.88	0.09	82,88,95,97	0
2	MAN	D	7	11/12	0.89	0.07	75,86,93,95	0
2	NAG	D	5	14/15	0.91	0.09	58,70,78,82	0
2	MAN	D	4	11/12	0.91	0.08	64,69,79,84	0
2	NAG	D	2	14/15	0.92	0.09	63,69,77,79	0
2	BMA	D	3	11/12	0.96	0.07	56,65,71,73	0

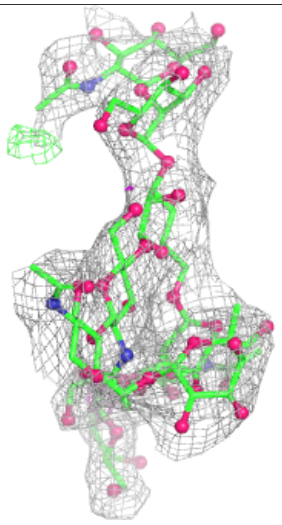
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain D:

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

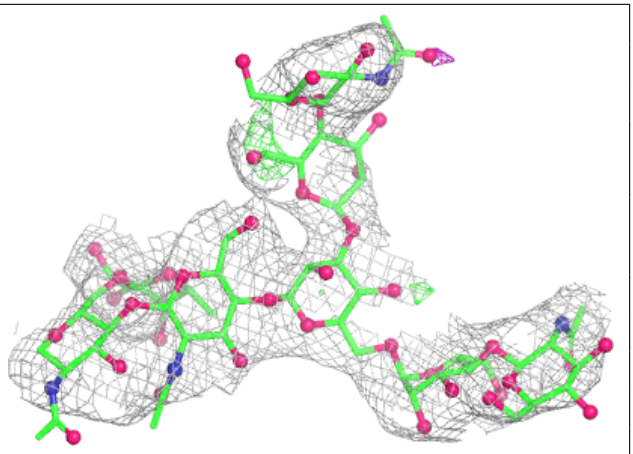


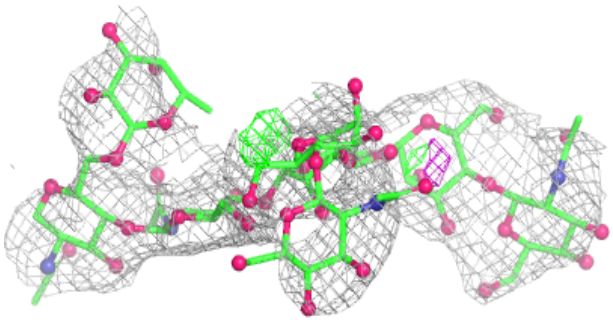


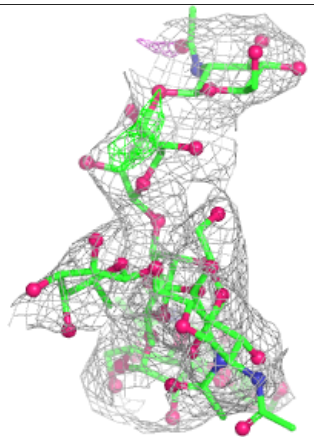


Electron density around Chain E:

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

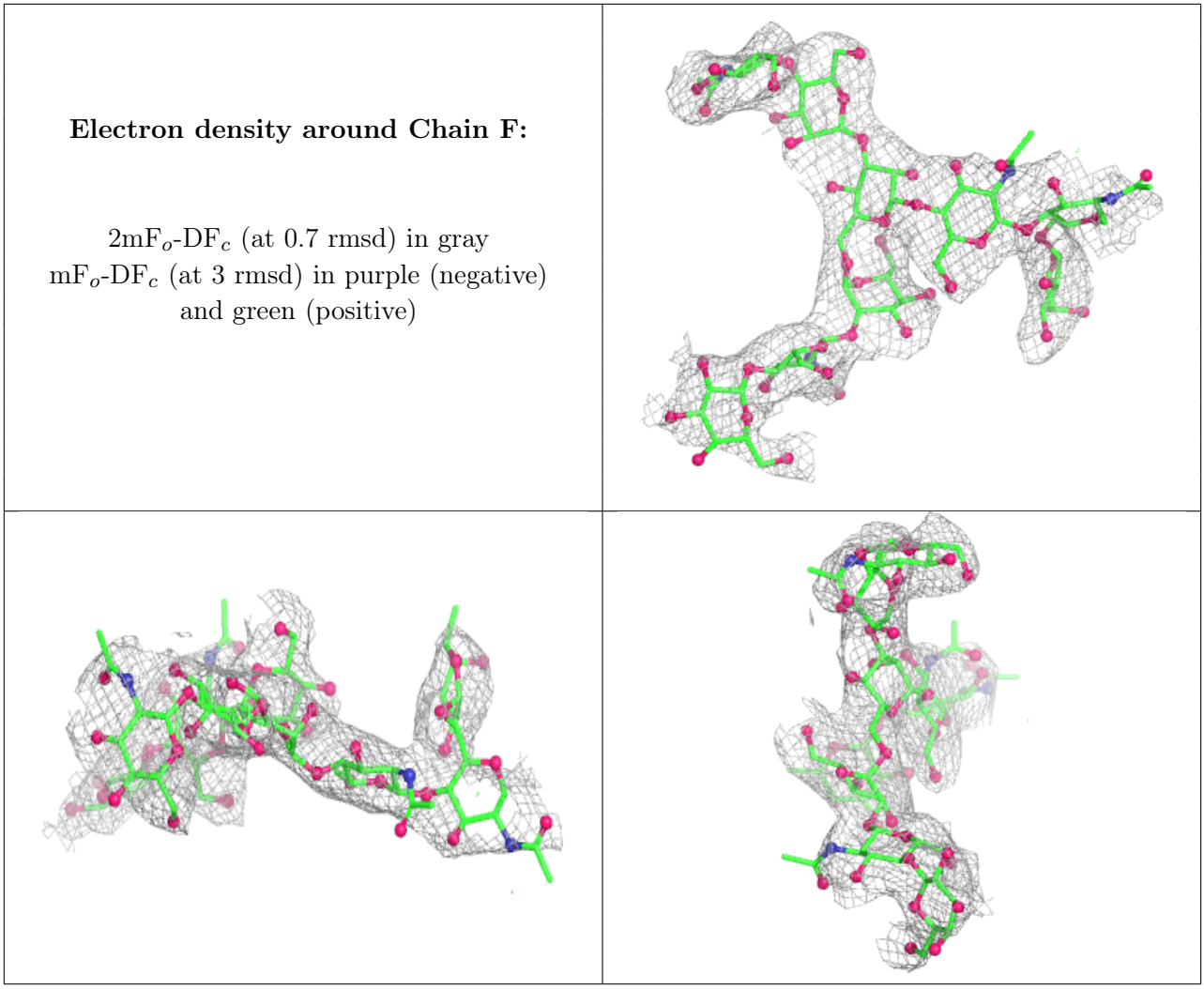






Electron density around Chain F:

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



6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.