wwPDB X-ray Structure Validation Summary Report (i)

Oct 27, 2026 – 12:13 PM EDT

PDB ID	:	9Y5C / pdb_00009y5c
Title	:	Chimeric antibody 2C7 Fab fragment against gonococcal lipooligosaccharide bound to octasaccharide antigen
Authors	:	Beernink, P.T.; Silipo, A.; Rice, P.A.; Ram, S.
Deposited on	:	2025-09-04
Resolution	:	1.60 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 (i)) were used in the production of this report:

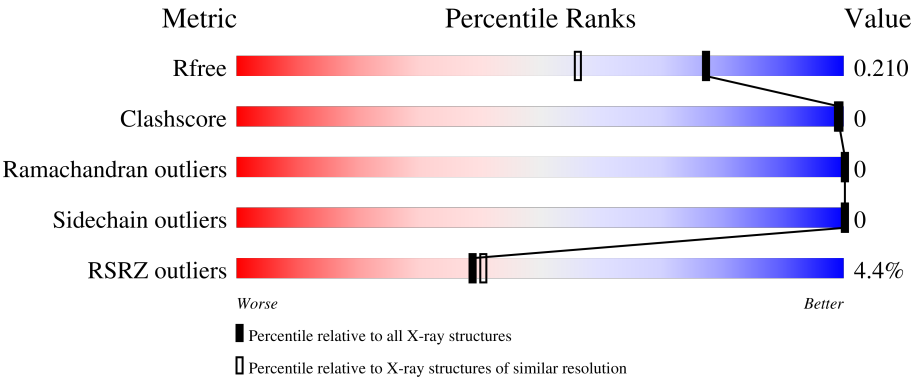
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 1.60 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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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 <=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	221	7% 85% 14%
1	C	221	3% 99%
2	B	215	4% 97%
2	D	215	4% 98%
3	E	8	100%

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Mol	Chain	Length	Quality of chain
3	F	8	100%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 13579 atoms, of which 6203 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.

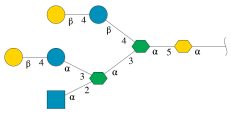
- Molecule 1 is a protein called Fab heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	189	Total	C	H	N	O	S	0	1	0
			2819	925	1356	243	289	6			
1	C	220	Total	C	H	N	O	S	0	0	0
			3250	1050	1582	277	334	7			

- Molecule 2 is a protein called Fab lambda light chain.

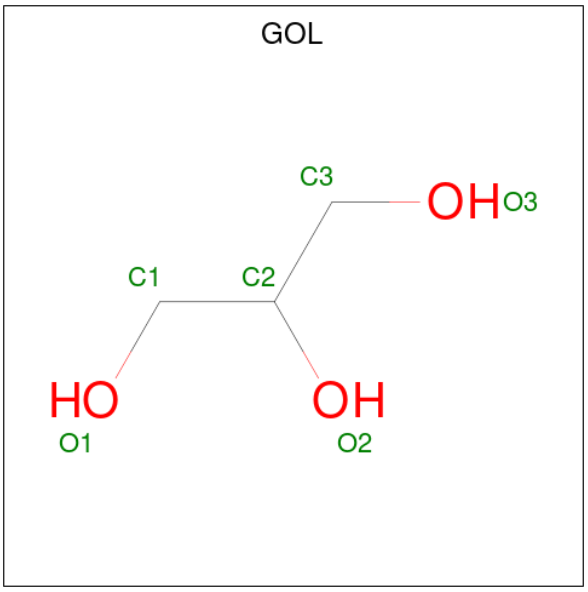
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	211	Total	C	H	N	O	S	0	4	0
			3139	1004	1547	267	316	5			
2	D	213	Total	C	H	N	O	S	0	1	0
			3126	1004	1532	265	320	5			

- Molecule 3 is an oligosaccharide called beta-D-galactopyranose-(1-4)-alpha-D-glucopyranose -(1-3)-[2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-2)]L-glycero-alpha-D-manno-heptopyranose-(1-3)-[beta-D-galactopyranose-(1-4)-beta-D-glucopyranose-(1-4)]L-glycero-alpha-D-manno-heptopyranose-(1-5)-3-deoxy-alpha-D-manno-oct-2-ulopyranosonic acid.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	8	Total	C	H	N	O	0	0	0
			189	54	89	1	45			
3	F	8	Total	C	H	N	O	0	0	0
			189	54	89	1	45			

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C H O 14 3 8 3	0	0

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Na 1 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	206	Total O 206 206	0	0
6	B	193	Total O 193 193	0	0
6	C	233	Total O 233 233	0	0
6	D	220	Total O 220 220	0	0

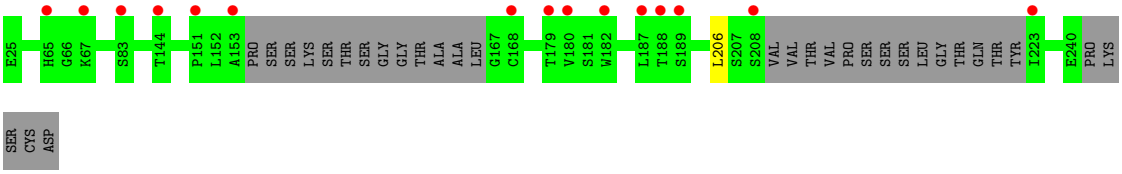
3 Residue-property plots (i)

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: Fab heavy chain

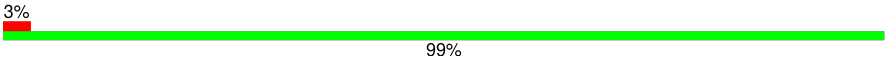
Chain A:

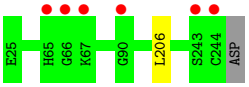




• Molecule 1: Fab heavy chain

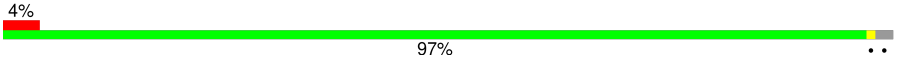
Chain C:

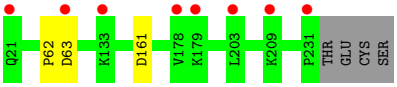




• Molecule 2: Fab lambda light chain

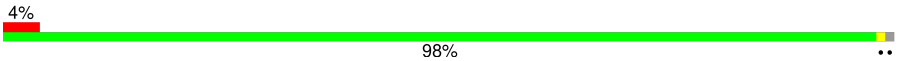
Chain B:

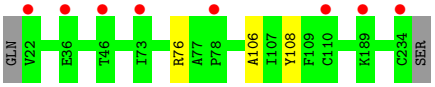




• Molecule 2: Fab lambda light chain

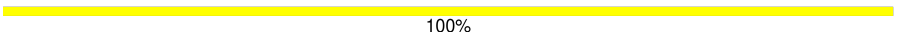
Chain D:





• Molecule 3: beta-D-galactopyranose-(1-4)-alpha-D-glucopyranose-(1-3)-[2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-2)]L-glycero-alpha-D-manno-heptopyranose-(1-3)-[beta-D-galactopyranose-(1-4)-beta-D-glucopyranose-(1-4)]L-glycero-alpha-D-manno-heptopyranose-(1-5)-3-deoxy-alpha-D-manno-oct-2-ulopyranosonic acid

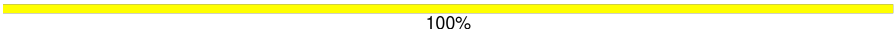
Chain E:





• Molecule 3: beta-D-galactopyranose-(1-4)-alpha-D-glucopyranose-(1-3)-[2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-2)]L-glycero-alpha-D-manno-heptopyranose-(1-3)-[beta-D-galactopyranose-(1-4)-beta-D-glucopyranose-(1-4)]L-glycero-alpha-D-manno-heptopyranose-(1-5)-3-deoxy-alpha-D-manno-oct-2-ulopyranosonic acid

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	129.52Å 71.65Å 116.60Å 90.00° 114.98° 90.00°	Depositor
Resolution (Å)	64.07 – 1.60 64.07 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (64.07-1.60) 99.9 (64.07-1.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.20 (at 1.40Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.193 , 0.210 0.192 , 0.210	Depositor DCC
R_{free} test set	1987 reflections (1.26%)	wwPDB-VP
Wilson B-factor (Å^2)	30.6	Xtriage
Anisotropy	0.167	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 40.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	13579	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.66% 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: NA, KDO, NDG, GOL, GMH, GLC, GAL, BGC

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	0.55	0/1502	0.67	0/2039
1	C	0.59	0/1710	0.67	0/2328
2	B	0.54	0/1649	0.69	1/2256 (0.0%)
2	D	0.66	1/1636 (0.1%)	0.76	1/2240 (0.0%)
All	All	0.59	1/6497 (0.0%)	0.70	2/8863 (0.0%)

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
2	D	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	108	TYR	C-O	-5.11	1.18	1.24

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	161	ASP	CA-CB-CG	5.29	117.89	112.60
2	D	106	ALA	CA-C-O	-5.04	115.75	121.25

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	76	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	1463	1356	1408	1	0
1	C	1668	1582	1616	1	0
2	B	1592	1547	1552	1	0
2	D	1594	1532	1552	0	0
3	E	100	89	77	0	0
3	F	100	89	78	0	0
4	A	6	8	8	0	0
5	B	1	0	0	0	0
6	A	206	0	0	0	0
6	B	193	0	0	0	0
6	C	233	0	0	0	0
6	D	220	0	0	0	0
All	All	7376	6203	6291	3	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 0.

All (3) 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:B:62:PRO:O	2:B:63:ASP:HB2	2.07	0.54
1:C:206:LEU:HD12	1:C:206:LEU:C	2.43	0.44
1:A:206:LEU:C	1:A:206:LEU:HD12	2.43	0.43

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	184/221 (83%)	181 (98%)	3 (2%)	0	100	100
1	C	218/221 (99%)	213 (98%)	5 (2%)	0	100	100
2	B	213/215 (99%)	205 (96%)	8 (4%)	0	100	100
2	D	212/215 (99%)	202 (95%)	10 (5%)	0	100	100
All	All	827/872 (95%)	801 (97%)	26 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	167/193 (86%)	167 (100%)	0	100	100
1	C	192/193 (100%)	192 (100%)	0	100	100
2	B	178/178 (100%)	178 (100%)	0	100	100
2	D	177/178 (99%)	177 (100%)	0	100	100
All	All	714/742 (96%)	714 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	75	ASN
1	C	220	GLN
1	C	57	ASN
2	B	101	GLN
1	C	199	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)

16 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	KDO	E	1	3	16,16,16	1.21	2 (12%)	17,24,24	0.87	0
3	GMH	E	2	3	13,13,14	2.18	8 (61%)	16,18,20	1.03	1 (6%)
3	GMH	E	3	3	13,13,14	1.85	4 (30%)	16,18,20	1.92	3 (18%)
3	GLC	E	4	3	11,11,12	1.63	3 (27%)	15,15,17	0.96	0
3	GAL	E	5	3	11,11,12	1.84	3 (27%)	15,15,17	1.10	1 (6%)
3	NDG	E	6	3	14,14,15	1.31	1 (7%)	17,19,21	1.14	2 (11%)
3	BGC	E	7	3	11,11,12	1.24	0	15,15,17	1.46	4 (26%)
3	GAL	E	8	3	11,11,12	1.95	3 (27%)	15,15,17	0.92	1 (6%)
3	KDO	F	1	3	16,16,16	1.26	2 (12%)	17,24,24	1.11	2 (11%)
3	GMH	F	2	3	13,13,14	2.24	7 (53%)	16,18,20	1.15	1 (6%)
3	GMH	F	3	3	13,13,14	2.14	5 (38%)	16,18,20	2.12	2 (12%)
3	GLC	F	4	3	11,11,12	1.66	2 (18%)	15,15,17	1.28	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	GAL	F	5	3	11,11,12	1.87	3 (27%)	15,15,17	0.86	0
3	NDG	F	6	3	14,14,15	1.24	1 (7%)	17,19,21	1.34	2 (11%)
3	BGC	F	7	3	11,11,12	1.48	3 (27%)	15,15,17	1.54	5 (33%)
3	GAL	F	8	3	11,11,12	1.93	3 (27%)	15,15,17	0.93	1 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	KDO	E	1	3	-	5/12/30/30	0/1/1/1
3	GMH	E	2	3	-	2/6/23/26	0/1/1/1
3	GMH	E	3	3	-	5/6/23/26	0/1/1/1
3	GLC	E	4	3	-	0/2/19/22	0/1/1/1
3	GAL	E	5	3	-	0/2/19/22	0/1/1/1
3	NDG	E	6	3	-	0/6/23/26	0/1/1/1
3	BGC	E	7	3	-	0/2/19/22	0/1/1/1
3	GAL	E	8	3	-	1/2/19/22	0/1/1/1
3	KDO	F	1	3	-	8/12/30/30	0/1/1/1
3	GMH	F	2	3	-	0/6/23/26	0/1/1/1
3	GMH	F	3	3	-	5/6/23/26	0/1/1/1
3	GLC	F	4	3	-	0/2/19/22	0/1/1/1
3	GAL	F	5	3	-	0/2/19/22	0/1/1/1
3	NDG	F	6	3	-	0/6/23/26	0/1/1/1
3	BGC	F	7	3	-	0/2/19/22	0/1/1/1
3	GAL	F	8	3	-	1/2/19/22	0/1/1/1

The worst 5 of 50 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	3	GMH	C6-C5	4.53	1.62	1.52
3	F	4	GLC	C2-C3	4.29	1.59	1.52
3	F	2	GMH	C6-C5	4.11	1.61	1.52
3	F	8	GAL	O2-C2	-3.89	1.35	1.43
3	E	8	GAL	O2-C2	-3.81	1.35	1.43

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	F	3	GMH	C1-O5-C5	6.68	122.42	111.48
3	E	3	GMH	C1-O5-C5	5.53	120.54	111.48
3	F	2	GMH	C1-O5-C5	3.70	117.55	111.48
3	E	2	GMH	C1-O5-C5	3.59	117.36	111.48
3	F	3	GMH	C7-C6-C5	3.57	119.17	112.05

There are no chirality outliers.

5 of 27 torsion outliers are listed below:

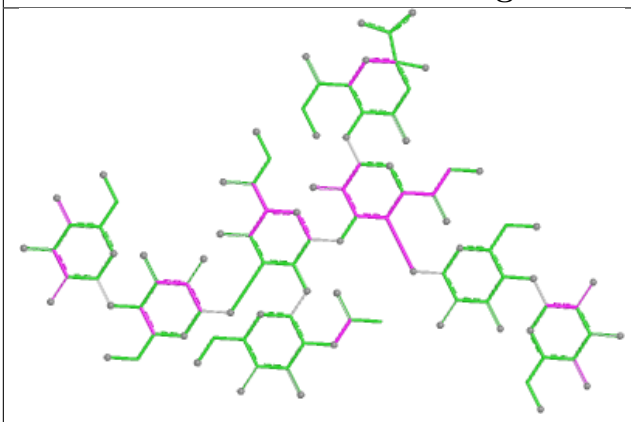
Mol	Chain	Res	Type	Atoms
3	E	1	KDO	C5-C6-C7-O7
3	E	1	KDO	O6-C6-C7-C8
3	E	1	KDO	C6-C7-C8-O8
3	E	1	KDO	O7-C7-C8-O8
3	E	3	GMH	C4-C5-C6-C7

There are no ring outliers.

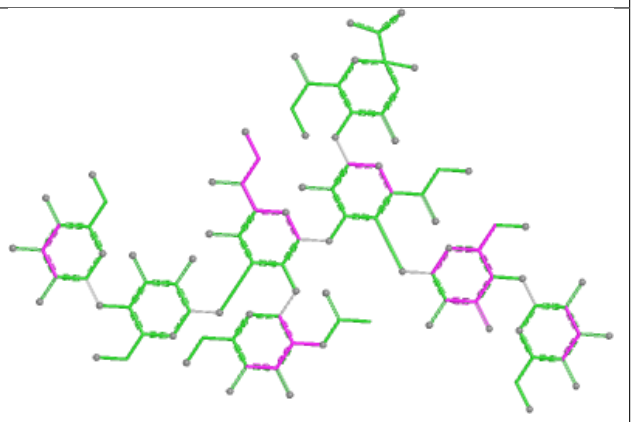
No monomer is involved in short contacts.

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

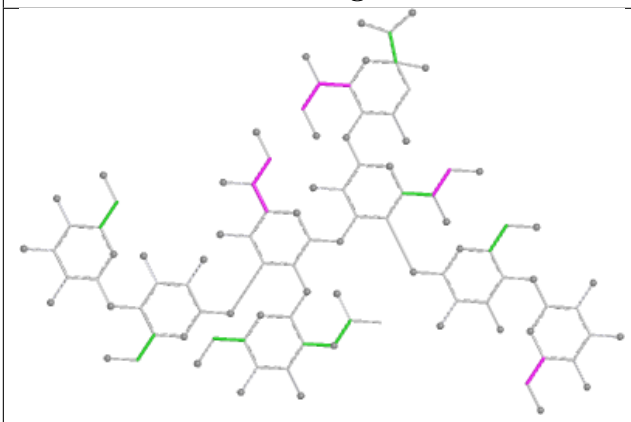
Oligosaccharide Chain E



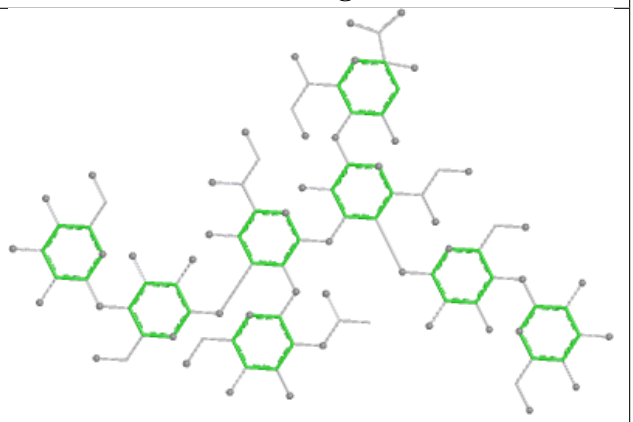
Bond lengths



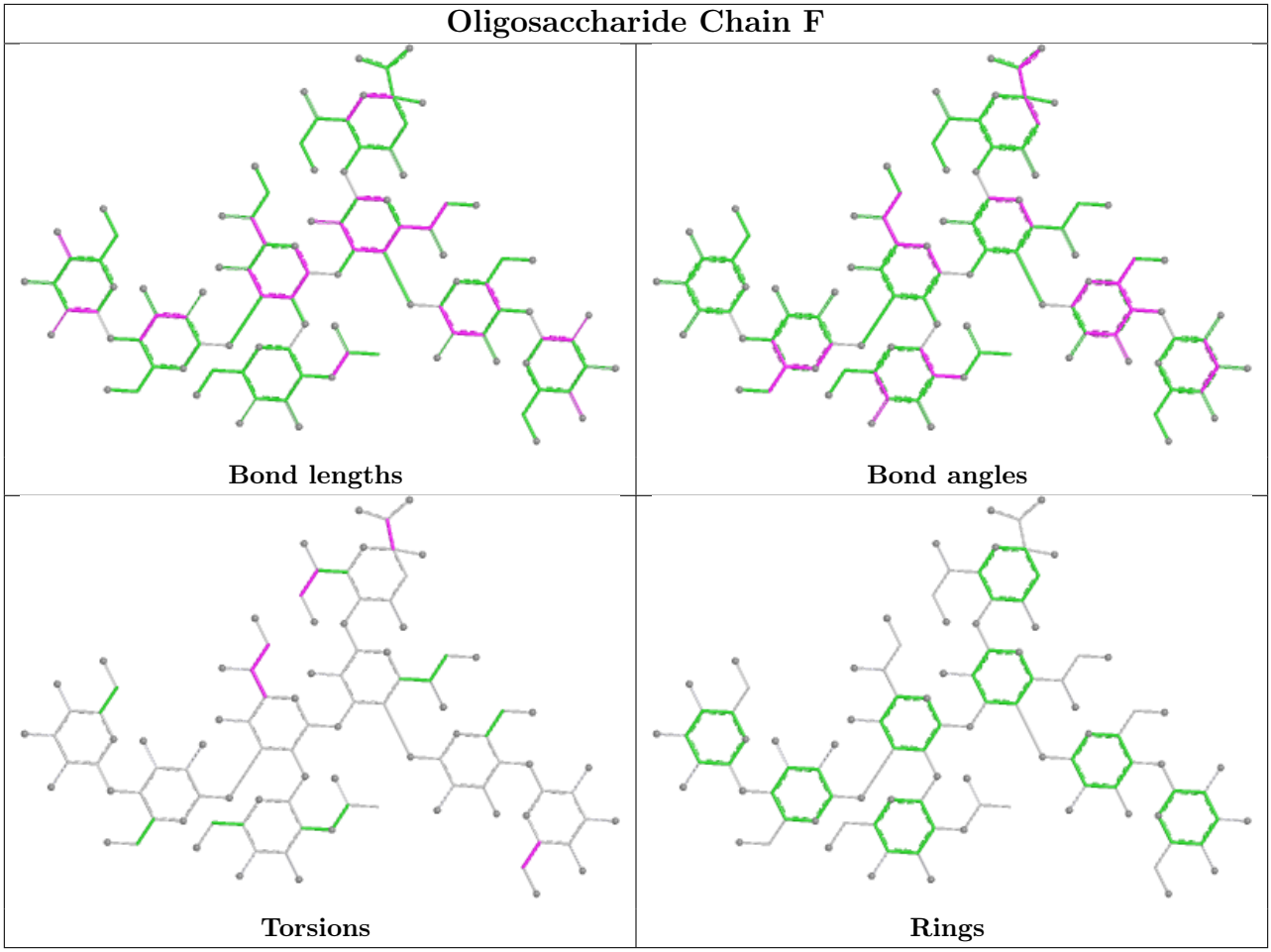
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	GOL	A	301	-	5,5,5	0.34	0	5,5,5	0.44	0

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	GOL	A	301	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	189/221 (85%)	0.50	15 (7%)	18	19	20, 36, 60, 78	1 (0%)
1	C	220/221 (99%)	0.15	6 (2%)	56	59	23, 32, 54, 80	0
2	B	211/215 (98%)	0.44	8 (3%)	44	46	15, 36, 54, 73	3 (1%)
2	D	213/215 (99%)	0.37	8 (3%)	44	46	20, 34, 53, 67	1 (0%)
All	All	833/872 (95%)	0.36	37 (4%)	39	40	15, 34, 56, 80	5 (0%)

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	78	PRO	5.2
1	C	244	CYS	5.1
1	C	65	HIS	4.3
1	A	65	HIS	4.1
2	D	234	CYS	3.3

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	KDO	F	1	16/16	0.62	0.16	71,85,103,111	0
3	KDO	E	1	16/16	0.66	0.19	62,87,107,113	0

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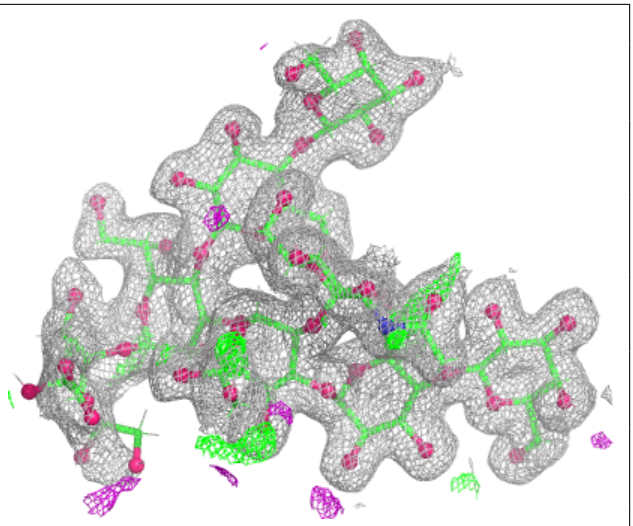
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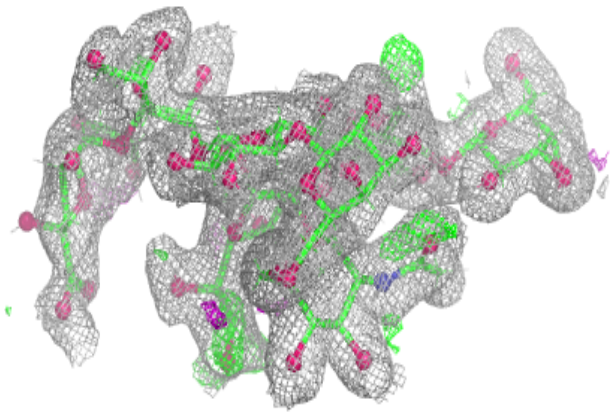
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	GMH	F	2	13/14	0.87	0.11	41,57,68,69	0
3	GMH	F	3	13/14	0.87	0.12	33,44,59,71	0
3	BGC	F	7	11/12	0.89	0.11	41,50,59,67	0
3	GAL	F	8	11/12	0.89	0.09	42,52,65,65	0
3	GAL	E	8	11/12	0.90	0.11	41,51,65,70	0
3	GMH	E	2	13/14	0.90	0.09	37,58,72,87	0
3	GLC	F	4	11/12	0.91	0.10	28,34,45,54	0
3	BGC	E	7	11/12	0.92	0.08	36,47,56,57	0
3	GMH	E	3	13/14	0.92	0.10	28,38,56,67	0
3	NDG	E	6	14/15	0.94	0.09	24,31,40,42	0
3	NDG	F	6	14/15	0.94	0.08	24,35,45,46	0
3	GLC	E	4	11/12	0.95	0.08	23,29,40,48	0
3	GAL	F	5	11/12	0.97	0.06	25,31,38,39	0
3	GAL	E	5	11/12	0.98	0.05	19,23,28,30	0

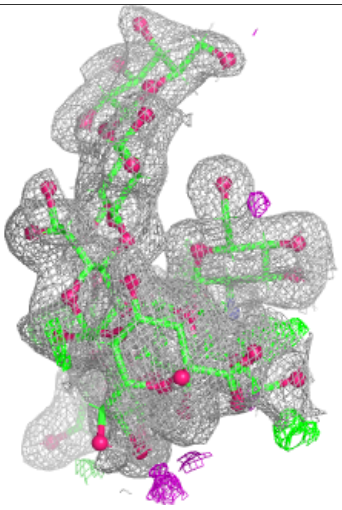
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain E:

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

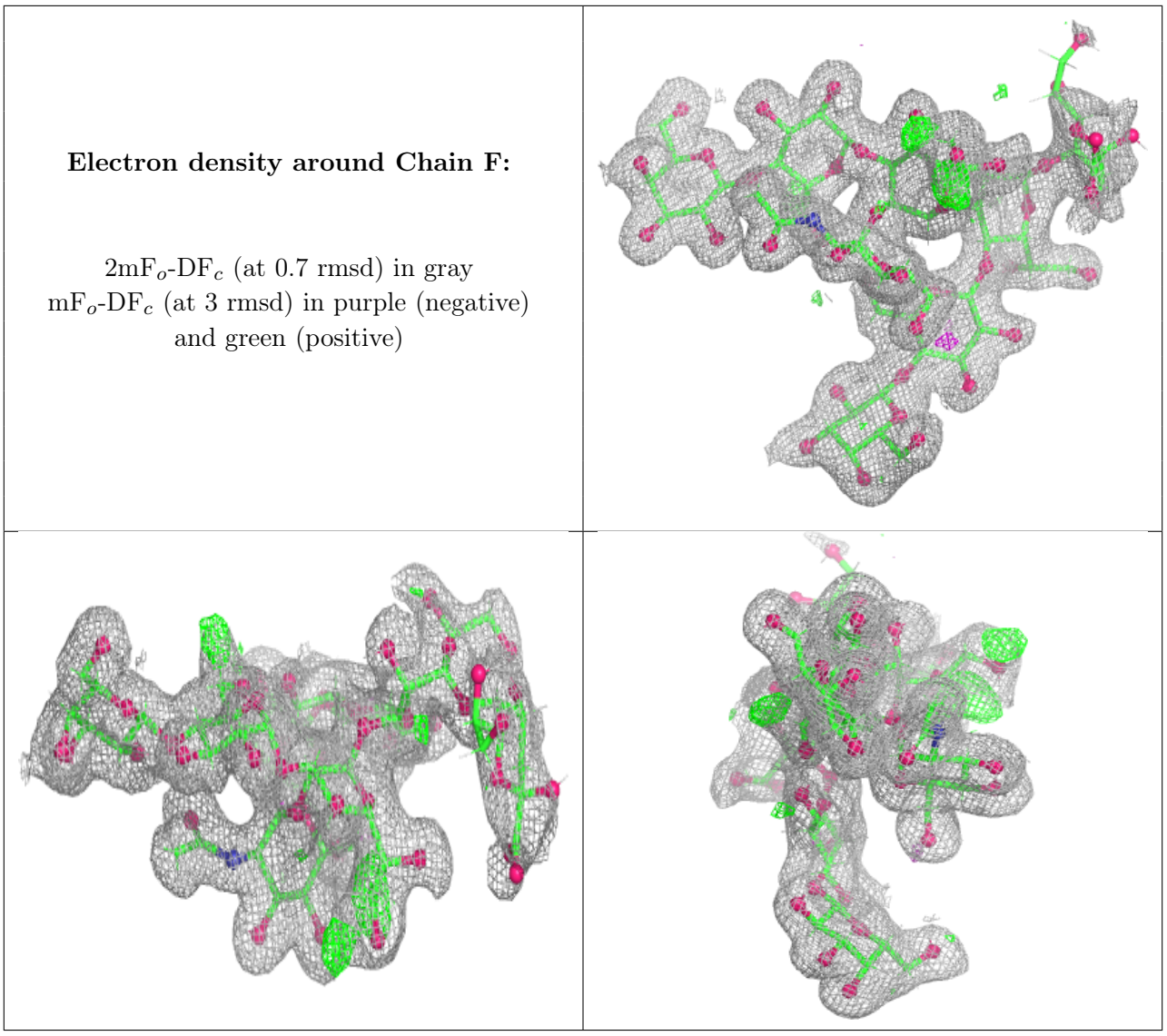






Electron density around Chain F:

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



6.4 Ligands

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
4	GOL	A	301	6/6	0.87	0.10	41,51,62,65	0
5	NA	B	301	1/1	0.97	0.07	36,36,36,36	0

6.5 Other polymers

There are no such residues in this entry.