



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 3, 2024 – 05:13 pm GMT

PDB ID : 5J0B
Title : Structure of the immune receptor CD33 in complex with 6'-sialyllactose
Authors : Dodd, R.B.
Deposited on : 2016-03-28
Resolution : 2.48 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

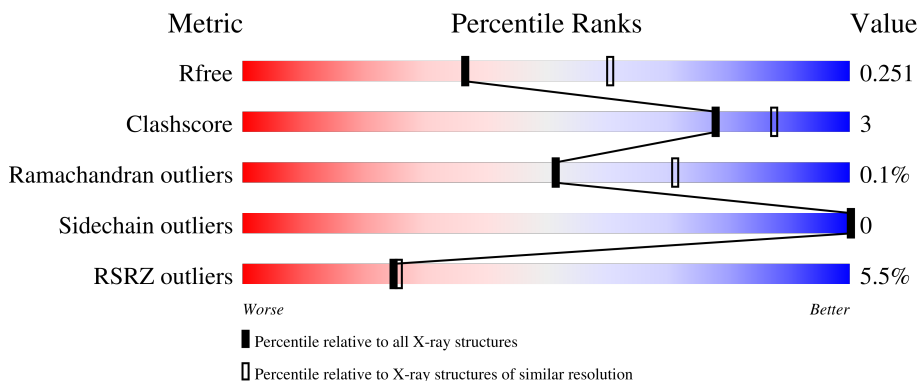
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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}	130704	5857 (2.50-2.46)
Clashscore	141614	6594 (2.50-2.46)
Ramachandran outliers	138981	6469 (2.50-2.46)
Sidechain outliers	138945	6471 (2.50-2.46)
RSRZ outliers	127900	5738 (2.50-2.46)

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	224	
1	B	224	
1	C	224	
1	D	224	
2	E	2	

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Mol	Chain	Length	Quality of chain
2	F	2	 50% 50%
2	G	2	 100%

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 13665 atoms, of which 6724 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 Myeloid cell surface antigen CD33.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	213	3289	1051	1621	296	314	7	0	0	0
1	B	214	3301	1055	1626	297	316	7	0	0	0
1	C	212	3276	1047	1615	295	312	7	0	0	0
1	D	209	3224	1025	1592	291	309	7	0	0	0

There are 52 discrepancies between the modelled and reference sequences:

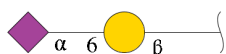
Chain	Residue	Modelled	Actual	Comment	Reference
A	18	GLU	-	expression tag	UNP P20138
A	19	THR	-	expression tag	UNP P20138
A	20	GLY	-	expression tag	UNP P20138
A	69	GLY	ARG	variant	UNP P20138
A	233	GLY	-	expression tag	UNP P20138
A	234	THR	-	expression tag	UNP P20138
A	235	LYS	-	expression tag	UNP P20138
A	236	HIS	-	expression tag	UNP P20138
A	237	HIS	-	expression tag	UNP P20138
A	238	HIS	-	expression tag	UNP P20138
A	239	HIS	-	expression tag	UNP P20138
A	240	HIS	-	expression tag	UNP P20138
A	241	HIS	-	expression tag	UNP P20138
B	18	GLU	-	expression tag	UNP P20138
B	19	THR	-	expression tag	UNP P20138
B	20	GLY	-	expression tag	UNP P20138
B	69	GLY	ARG	variant	UNP P20138
B	233	GLY	-	expression tag	UNP P20138
B	234	THR	-	expression tag	UNP P20138
B	235	LYS	-	expression tag	UNP P20138
B	236	HIS	-	expression tag	UNP P20138

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Chain	Residue	Modelled	Actual	Comment	Reference
B	237	HIS	-	expression tag	UNP P20138
B	238	HIS	-	expression tag	UNP P20138
B	239	HIS	-	expression tag	UNP P20138
B	240	HIS	-	expression tag	UNP P20138
B	241	HIS	-	expression tag	UNP P20138
C	18	GLU	-	expression tag	UNP P20138
C	19	THR	-	expression tag	UNP P20138
C	20	GLY	-	expression tag	UNP P20138
C	69	GLY	ARG	variant	UNP P20138
C	233	GLY	-	expression tag	UNP P20138
C	234	THR	-	expression tag	UNP P20138
C	235	LYS	-	expression tag	UNP P20138
C	236	HIS	-	expression tag	UNP P20138
C	237	HIS	-	expression tag	UNP P20138
C	238	HIS	-	expression tag	UNP P20138
C	239	HIS	-	expression tag	UNP P20138
C	240	HIS	-	expression tag	UNP P20138
C	241	HIS	-	expression tag	UNP P20138
D	18	GLU	-	expression tag	UNP P20138
D	19	THR	-	expression tag	UNP P20138
D	20	GLY	-	expression tag	UNP P20138
D	69	GLY	ARG	variant	UNP P20138
D	233	GLY	-	expression tag	UNP P20138
D	234	THR	-	expression tag	UNP P20138
D	235	LYS	-	expression tag	UNP P20138
D	236	HIS	-	expression tag	UNP P20138
D	237	HIS	-	expression tag	UNP P20138
D	238	HIS	-	expression tag	UNP P20138
D	239	HIS	-	expression tag	UNP P20138
D	240	HIS	-	expression tag	UNP P20138
D	241	HIS	-	expression tag	UNP P20138

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



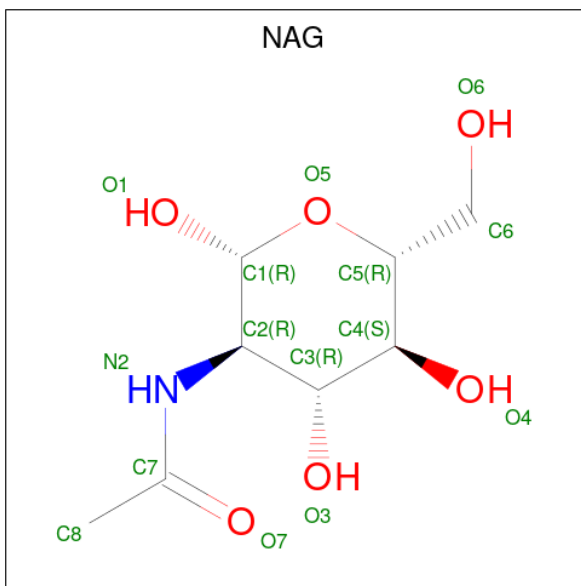
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
			Total	C	H	N				O
2	E	2	60	17	28	1	14	0	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
2	F	2	Total	C	H	N	O	0	0	0
			60	17	28	1	14			
2	G	2	Total	C	H	N	O	0	0	0
			60	17	28	1	14			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



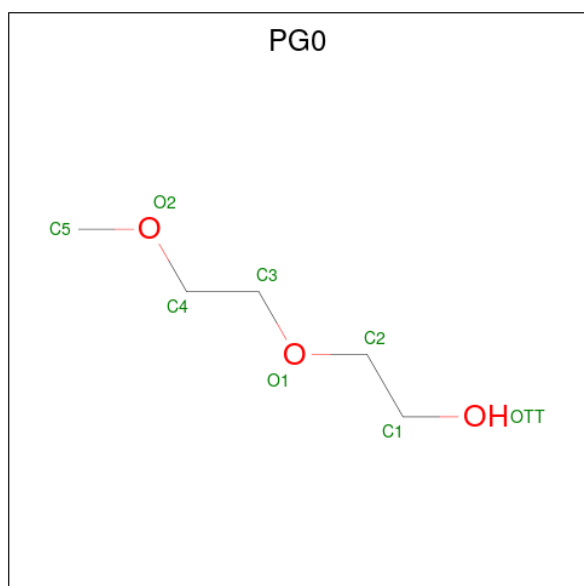
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
3	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	B	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	B	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	B	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
3	C	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	C	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
3	C	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	D	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
3	D	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
3	D	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

- Molecule 4 is 2-(2-METHOXYETHOXY)ETHANOL (three-letter code: PG0) (formula: C₅H₁₂O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	1	Total	C	H	O	0	0
			20	5	12	3		
4	C	1	Total	C	H	O	0	0
			20	5	12	3		

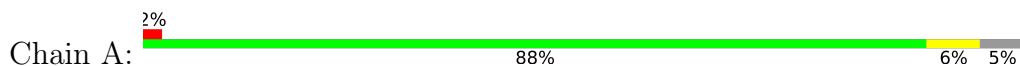
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	6	Total	O	0	0
			6	6		
5	B	10	Total	O	0	0
			10	10		
5	C	5	Total	O	0	0
			5	5		
5	D	4	Total	O	0	0
			4	4		

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.

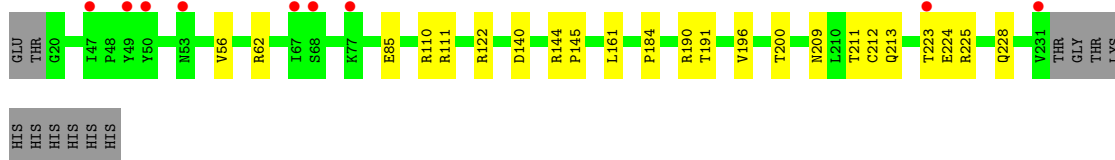
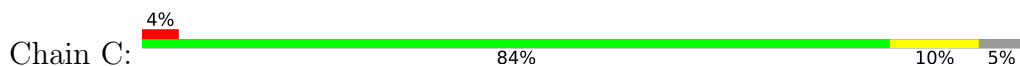
- Molecule 1: Myeloid cell surface antigen CD33



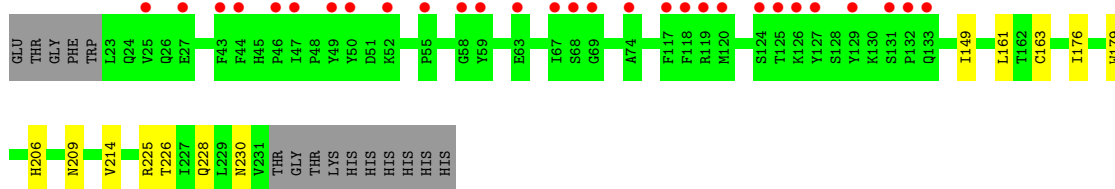
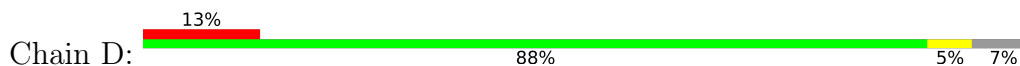
- Molecule 1: Myeloid cell surface antigen CD33



- Molecule 1: Myeloid cell surface antigen CD33



- Molecule 1: Myeloid cell surface antigen CD33



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



GAL1
SIA2

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

Chain F:  50% 50%GAL1
SIA2

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

Chain G:  100%GAL1
SIA2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.49Å 123.68Å 141.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.57 – 2.48 42.57 – 2.48	Depositor EDS
% Data completeness (in resolution range)	97.2 (42.57-2.48) 97.2 (42.57-2.48)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 2.48Å)	Xtrriage
Refinement program	PHENIX (dev_2313: ???)	Depositor
R, R_{free}	0.229 , 0.251 0.230 , 0.251	Depositor DCC
R_{free} test set	1909 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	61.7	Xtrriage
Anisotropy	0.547	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13665	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SIA, PG0, GAL, NAG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.24	0/1713	0.46	0/2336
1	B	0.26	0/1720	0.46	0/2346
1	C	0.26	0/1706	0.47	0/2326
1	D	0.26	0/1674	0.47	0/2282
All	All	0.26	0/6813	0.46	0/9290

There are no bond length outliers.

There are no bond angle outliers.

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	1668	1621	1622	11	1
1	B	1675	1626	1629	4	0
1	C	1661	1615	1615	18	0
1	D	1632	1592	1593	9	0
2	E	32	28	28	0	0
2	F	32	28	28	0	0
2	G	32	28	28	0	0
3	A	42	41	39	1	0
3	B	42	41	39	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	42	40	39	0	1
3	D	42	40	39	0	0
4	C	16	24	24	0	0
5	A	6	0	0	0	0
5	B	10	0	0	0	0
5	C	5	0	0	0	0
5	D	4	0	0	0	0
All	All	6941	6724	6723	40	1

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 3.

All (40) 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:110:ARG:NH2	1:B:140:ASP:OD1	2.04	0.90
1:C:110:ARG:NH2	1:C:140:ASP:OD1	2.15	0.79
1:A:110:ARG:NH2	1:A:140:ASP:OD1	2.16	0.77
1:C:144:ARG:NE	1:C:224:GLU:O	2.27	0.66
1:C:62:ARG:NH2	1:C:111:ARG:O	2.31	0.64
1:A:33:GLU:OE1	1:A:110:ARG:NH1	2.33	0.61
1:D:149:ILE:HG12	1:D:161:LEU:CD2	2.32	0.59
1:D:206:HIS:ND1	1:D:230:ASN:O	2.35	0.59
1:C:144:ARG:NH2	1:C:224:GLU:HG3	2.20	0.56
1:C:209:ASN:OD1	1:C:228:GLN:NE2	2.38	0.56
1:A:62:ARG:NH2	1:A:111:ARG:O	2.40	0.55
1:C:145:PRO:HD2	1:C:224:GLU:O	2.08	0.53
1:C:211:THR:HA	1:C:225:ARG:O	2.10	0.51
1:D:225:ARG:NH1	1:D:226:THR:O	2.45	0.49
1:C:212:CYS:O	1:C:225:ARG:N	2.43	0.48
1:A:190:ARG:NH1	1:D:176:ILE:CG2	2.76	0.48
1:C:144:ARG:HD2	1:C:223:THR:HB	1.96	0.48
1:C:144:ARG:HH21	1:C:224:GLU:C	2.17	0.48
1:C:85:GLU:OE2	1:C:111:ARG:CZ	2.62	0.46
1:A:190:ARG:NE	1:A:191:THR:O	2.47	0.46
1:C:190:ARG:NE	1:C:191:THR:O	2.47	0.46
1:D:163:CYS:HB2	1:D:179:TRP:CH2	2.52	0.45
1:C:144:ARG:HH21	1:C:224:GLU:HG3	1.81	0.45
1:B:176:ILE:O	1:B:214:VAL:HA	2.16	0.44
1:C:212:CYS:O	1:C:224:GLU:HA	2.18	0.44
1:A:190:ARG:NH1	1:D:176:ILE:HG22	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:161:LEU:O	1:C:196:VAL:HA	2.18	0.43
1:D:209:ASN:OD1	1:D:228:GLN:NE2	2.50	0.43
1:B:143:HIS:HB3	1:B:167:TRP:CE2	2.54	0.43
1:C:184:PRO:HG2	1:C:200:THR:O	2.19	0.43
1:B:163:CYS:HB2	1:B:179:TRP:CH2	2.54	0.43
1:D:149:ILE:HG12	1:D:161:LEU:HD22	2.02	0.42
1:C:56:VAL:HG22	1:C:122:ARG:HD2	2.01	0.42
1:C:213:GLN:HA	1:C:224:GLU:HA	2.02	0.42
1:A:63:GLU:C	1:A:65:ALA:H	2.23	0.41
1:A:209:ASN:ND2	3:A:303:NAG:O7	2.53	0.41
1:A:63:GLU:HG2	1:A:64:GLY:H	1.85	0.41
1:A:161:LEU:HD12	1:A:197:LEU:HD23	2.01	0.41
1:D:176:ILE:O	1:D:214:VAL:HA	2.21	0.40
1:A:161:LEU:O	1:A:196:VAL:HA	2.21	0.40

All (1) 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:A:49:TYR:OH	3:C:302:NAG:O6[2_554]	2.10	0.10

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	211/224 (94%)	202 (96%)	8 (4%)	1 (0%)	29	46
1	B	212/224 (95%)	206 (97%)	6 (3%)	0	100	100
1	C	210/224 (94%)	204 (97%)	6 (3%)	0	100	100
1	D	207/224 (92%)	202 (98%)	5 (2%)	0	100	100
All	All	840/896 (94%)	814 (97%)	25 (3%)	1 (0%)	51	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	64	GLY

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	189/199 (95%)	189 (100%)	0	100	100
1	B	190/199 (96%)	190 (100%)	0	100	100
1	C	188/199 (94%)	188 (100%)	0	100	100
1	D	186/199 (94%)	186 (100%)	0	100	100
All	All	753/796 (95%)	753 (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. There are no such sidechains identified.

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](#)

6 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	GAL	E	1	2	12,12,12	0.42	0	17,17,17	0.77	0
2	SIA	E	2	2	20,20,21	0.34	0	24,28,31	0.54	0
2	GAL	F	1	2	12,12,12	0.36	0	17,17,17	0.77	0
2	SIA	F	2	2	20,20,21	0.95	2 (10%)	24,28,31	1.12	2 (8%)
2	GAL	G	1	2	12,12,12	0.40	0	17,17,17	0.74	0
2	SIA	G	2	2	20,20,21	0.36	0	24,28,31	0.55	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
2	GAL	E	1	2	-	0/2/22/22	0/1/1/1
2	SIA	E	2	2	-	2/18/34/38	0/1/1/1
2	GAL	F	1	2	-	0/2/22/22	0/1/1/1
2	SIA	F	2	2	-	3/18/34/38	0/1/1/1
2	GAL	G	1	2	-	0/2/22/22	0/1/1/1
2	SIA	G	2	2	-	3/18/34/38	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	2	SIA	O1A-C1	2.92	1.31	1.22
2	F	2	SIA	O1B-C1	-2.62	1.22	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	2	SIA	O1A-C1-C2	-3.50	114.31	122.57
2	F	2	SIA	O1B-C1-C2	3.37	122.66	113.03

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	2	SIA	O8-C8-C9-O9

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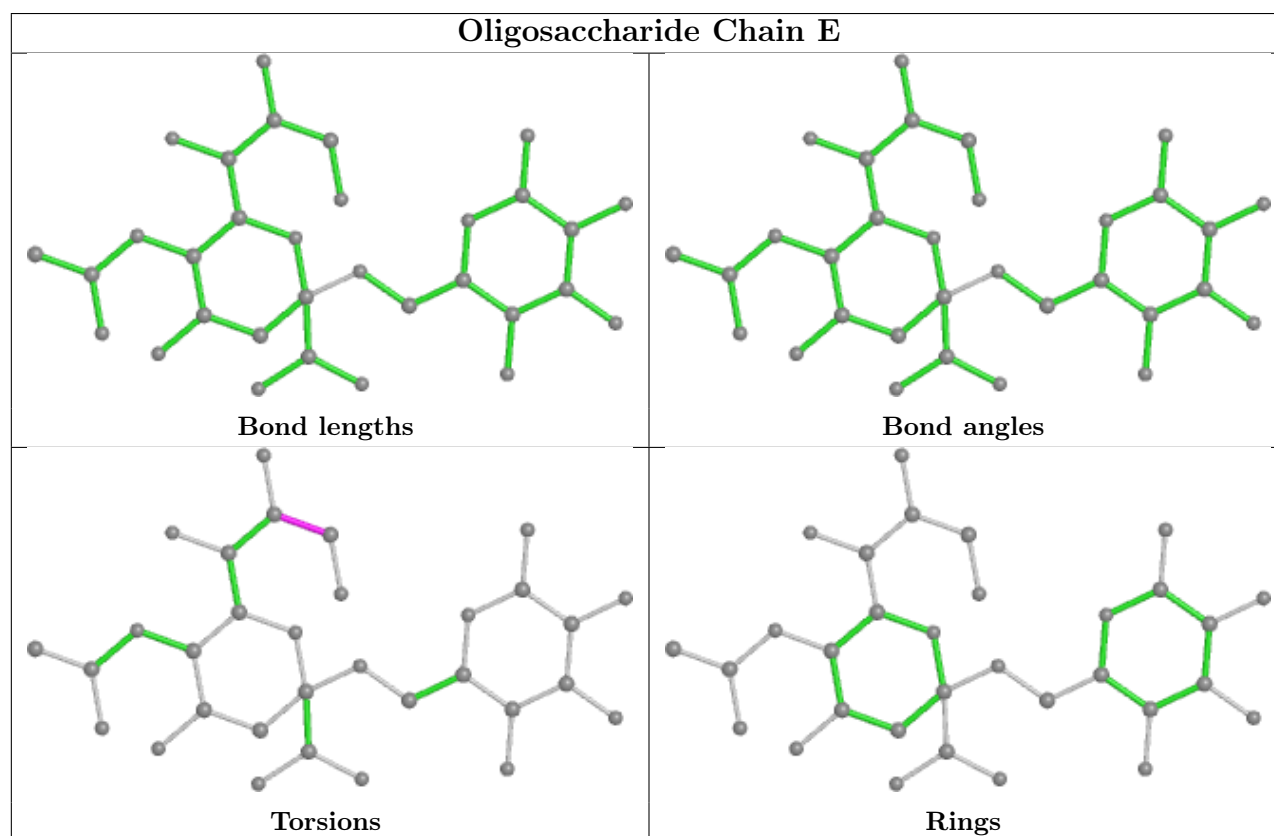
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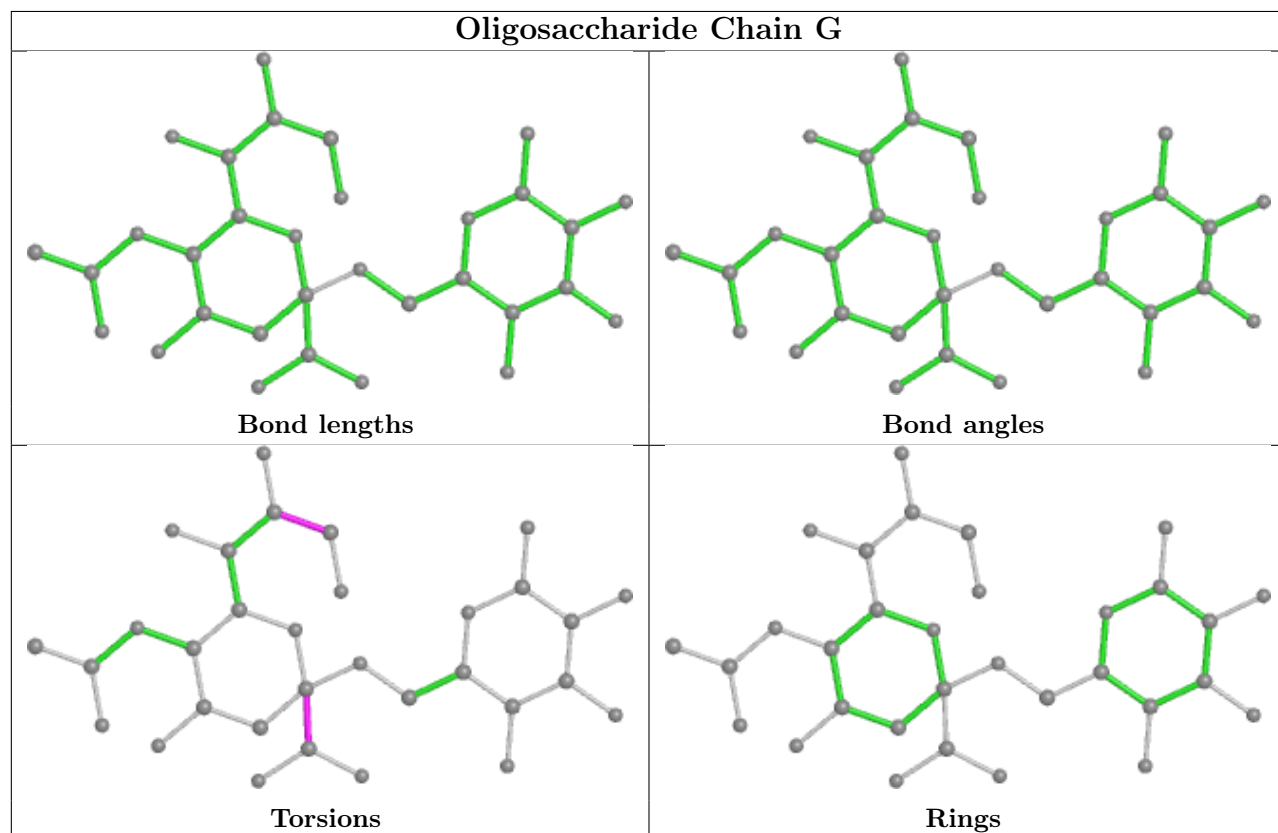
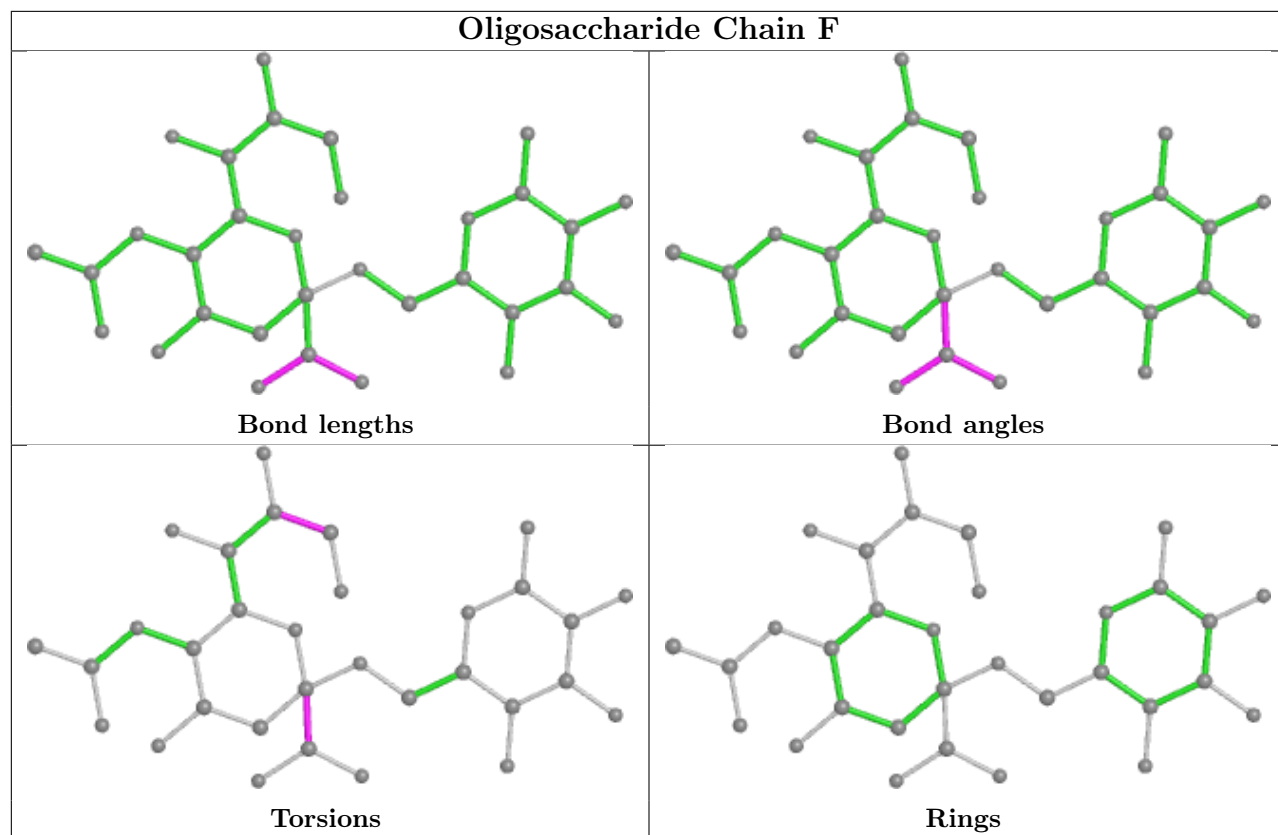
Mol	Chain	Res	Type	Atoms
2	F	2	SIA	O8-C8-C9-O9
2	G	2	SIA	O8-C8-C9-O9
2	E	2	SIA	C7-C8-C9-O9
2	F	2	SIA	C7-C8-C9-O9
2	G	2	SIA	C7-C8-C9-O9
2	F	2	SIA	O1A-C1-C2-O6
2	G	2	SIA	O1A-C1-C2-O6

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.





5.6 Ligand geometry

14 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
3	NAG	A	302	1	14,14,15	0.15	0	17,19,21	0.52	0
3	NAG	B	303	1	14,14,15	0.30	0	17,19,21	0.45	0
3	NAG	C	301	1	14,14,15	0.21	0	17,19,21	0.38	0
3	NAG	D	303	1	14,14,15	0.29	0	17,19,21	0.56	0
3	NAG	A	301	1	14,14,15	0.26	0	17,19,21	0.34	0
3	NAG	C	302	1	14,14,15	0.23	0	17,19,21	0.44	0
4	PG0	C	307	-	7,7,7	0.48	0	6,6,6	0.19	0
3	NAG	D	301	1	14,14,15	0.28	0	17,19,21	0.47	0
4	PG0	C	306	-	7,7,7	0.48	0	6,6,6	0.22	0
3	NAG	C	303	1	14,14,15	0.25	0	17,19,21	0.40	0
3	NAG	D	302	1	14,14,15	0.22	0	17,19,21	0.51	0
3	NAG	B	302	1	14,14,15	0.29	0	17,19,21	0.37	0
3	NAG	A	303	1	14,14,15	0.27	0	17,19,21	0.42	0
3	NAG	B	301	1	14,14,15	0.39	0	17,19,21	0.37	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
3	NAG	A	302	1	-	0/6/23/26	0/1/1/1
3	NAG	B	303	1	-	0/6/23/26	0/1/1/1
3	NAG	C	301	1	-	2/6/23/26	0/1/1/1
3	NAG	D	303	1	-	0/6/23/26	0/1/1/1
3	NAG	A	301	1	-	0/6/23/26	0/1/1/1
3	NAG	C	302	1	-	1/6/23/26	0/1/1/1
4	PG0	C	307	-	-	0/5/5/5	-
3	NAG	D	301	1	-	2/6/23/26	0/1/1/1
4	PG0	C	306	-	-	2/5/5/5	-
3	NAG	C	303	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	D	302	1	-	0/6/23/26	0/1/1/1
3	NAG	B	302	1	-	1/6/23/26	0/1/1/1
3	NAG	A	303	1	-	0/6/23/26	0/1/1/1
3	NAG	B	301	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	301	NAG	O5-C5-C6-O6
3	B	301	NAG	O5-C5-C6-O6
3	C	301	NAG	C4-C5-C6-O6
3	B	301	NAG	C4-C5-C6-O6
3	D	301	NAG	O5-C5-C6-O6
4	C	306	PG0	OTT-C1-C2-O1
3	B	302	NAG	O5-C5-C6-O6
3	D	301	NAG	C4-C5-C6-O6
4	C	306	PG0	O1-C3-C4-O2
3	C	302	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	302	NAG	0	1
3	A	303	NAG	1	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

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, 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	213/224 (95%)	0.36	4 (1%) 66 68	47, 66, 102, 130	0
1	B	214/224 (95%)	0.54	5 (2%) 60 62	47, 71, 106, 145	0
1	C	212/224 (94%)	0.53	9 (4%) 36 38	43, 75, 119, 132	0
1	D	209/224 (93%)	0.84	29 (13%) 2 2	48, 82, 138, 168	0
All	All	848/896 (94%)	0.57	47 (5%) 25 26	43, 72, 123, 168	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	68	SER	5.7
1	D	69	GLY	5.2
1	D	67	ILE	5.0
1	B	69	GLY	4.7
1	D	49	TYR	4.6
1	D	120	MET	3.9
1	C	49	TYR	3.9
1	B	68	SER	3.7
1	D	125	THR	3.7
1	D	25	VAL	3.6
1	B	67	ILE	3.5
1	D	46	PRO	3.5
1	D	44	PHE	3.5
1	C	67	ILE	3.4
1	D	47	ILE	3.3
1	D	50	TYR	3.2
1	D	117	PHE	3.2
1	C	53	ASN	3.1
1	D	118	PHE	2.9
1	D	132	PRO	2.9
1	D	129	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	47	ILE	2.7
1	D	43	PHE	2.7
1	D	133	GLN	2.7
1	D	124	SER	2.6
1	D	63	GLU	2.6
1	D	52	LYS	2.5
1	D	55	PRO	2.4
1	A	67	ILE	2.4
1	A	199	ILE	2.3
1	C	68	SER	2.3
1	C	223	THR	2.3
1	D	119	ARG	2.3
1	A	81	GLU	2.3
1	D	59	TYR	2.3
1	D	58	GLY	2.2
1	D	127	TYR	2.2
1	B	221	VAL	2.2
1	D	131	SER	2.1
1	D	74	ALA	2.1
1	C	231	VAL	2.1
1	A	45	HIS	2.1
1	D	27	GLU	2.1
1	C	77	LYS	2.1
1	C	50	TYR	2.0
1	B	223	THR	2.0
1	D	126	LYS	2.0

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.

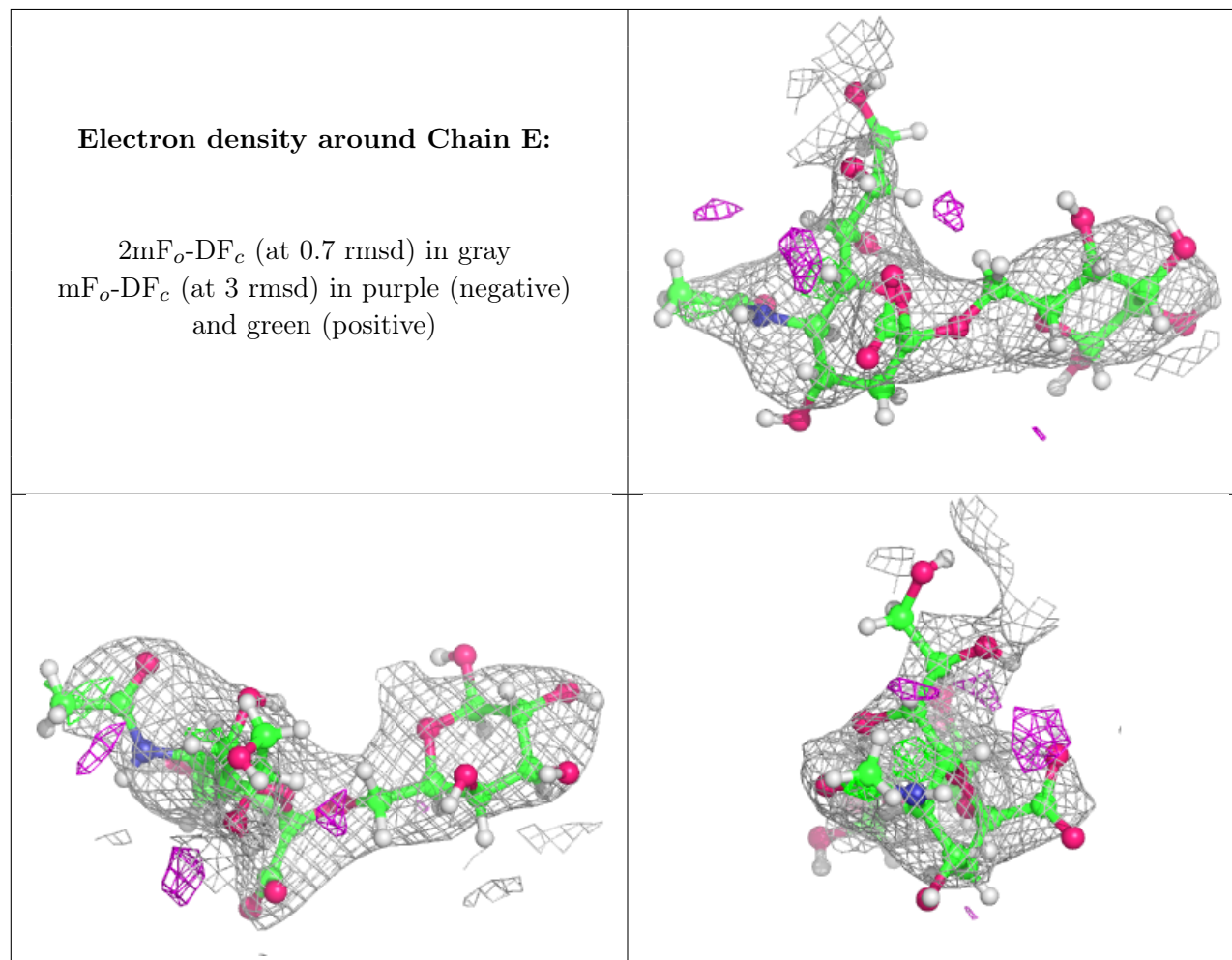
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GAL	G	1	12/12	0.81	0.28	148,157,186,193	0
2	SIA	E	2	20/21	0.83	0.28	176,193,220,223	0

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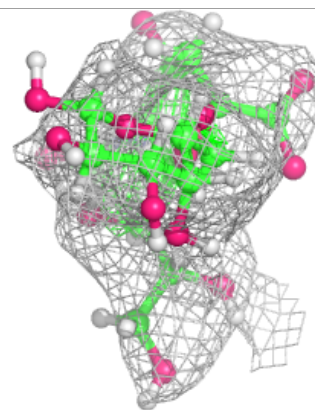
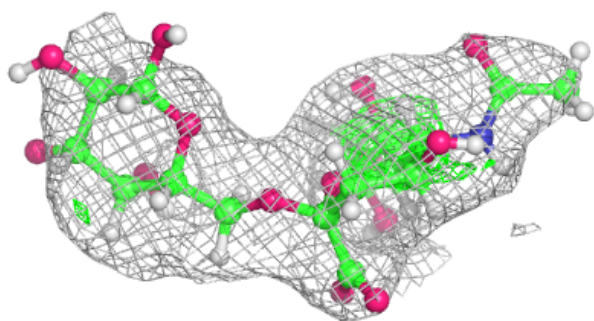
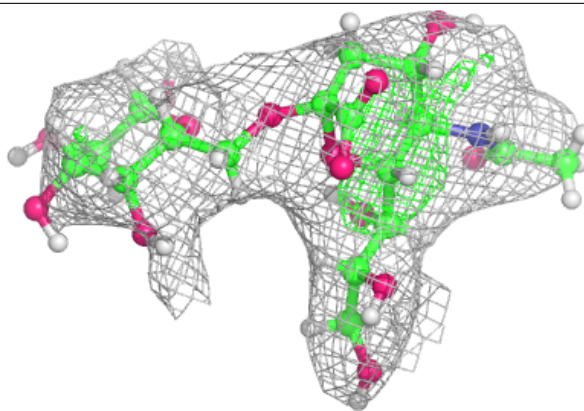
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	GAL	E	1	12/12	0.85	0.26	168,180,212,216	0
2	GAL	F	1	12/12	0.86	0.16	146,167,196,209	0
2	SIA	G	2	20/21	0.86	0.26	141,147,176,177	0
2	SIA	F	2	20/21	0.90	0.20	128,152,164,167	0

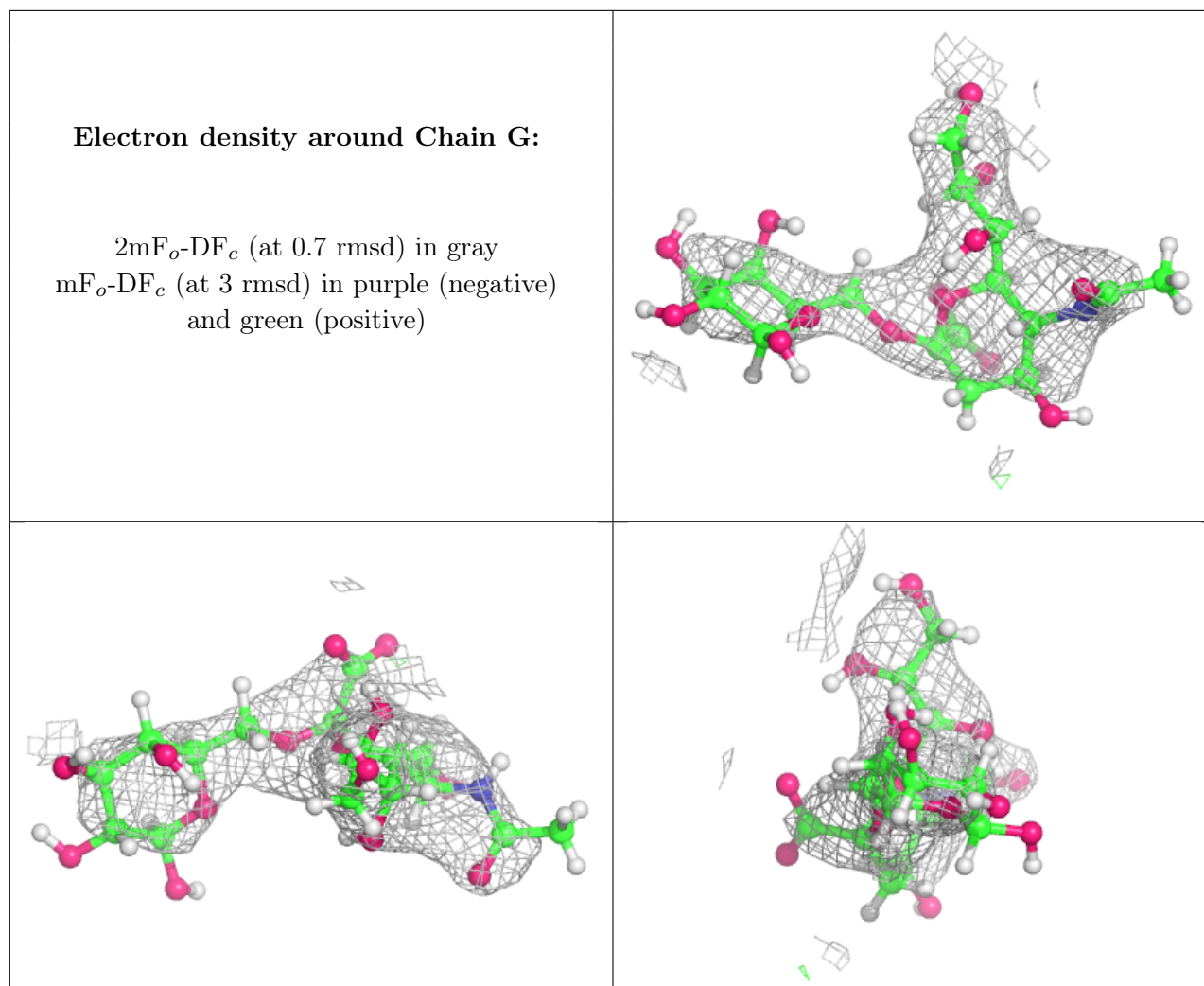
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



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)





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
3	NAG	A	303	14/15	0.70	0.31	157,171,205,205	0
3	NAG	C	302	14/15	0.73	0.30	137,146,175,177	0
3	NAG	B	302	14/15	0.79	0.25	116,131,157,157	0
3	NAG	B	303	14/15	0.81	0.17	115,139,170,171	0
4	PG0	C	307	8/8	0.81	0.20	76,92,99,100	0
3	NAG	C	303	14/15	0.82	0.23	118,132,158,158	0
4	PG0	C	306	8/8	0.88	0.27	98,118,122,123	0
3	NAG	D	301	14/15	0.89	0.16	106,114,136,136	0
3	NAG	D	302	14/15	0.91	0.16	68,76,91,92	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAG	B	301	14/15	0.92	0.16	69,83,92,99	0
3	NAG	A	302	14/15	0.93	0.13	65,74,89,89	0
3	NAG	C	301	14/15	0.93	0.10	60,73,86,86	0
3	NAG	D	303	14/15	0.94	0.19	88,108,144,144	0
3	NAG	A	301	14/15	0.95	0.17	56,68,105,105	0

6.5 Other polymers [i](#)

There are no such residues in this entry.