



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 10, 2020 – 01:47 PM BST

PDB ID : 4BSV
Title : Heterodimeric Fc Antibody Azymetric Variant 1
Authors : Suits, M.D.L.; Spreter, T.; Cabrera, E.E.; Dixit, S.B.; Lario, P.I.; Poon, D.K.Y.; D'Angelo, I.E.P.; Boulanger, M.J.
Deposited on : 2013-06-11
Resolution : 1.75 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
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) : 2.13.1

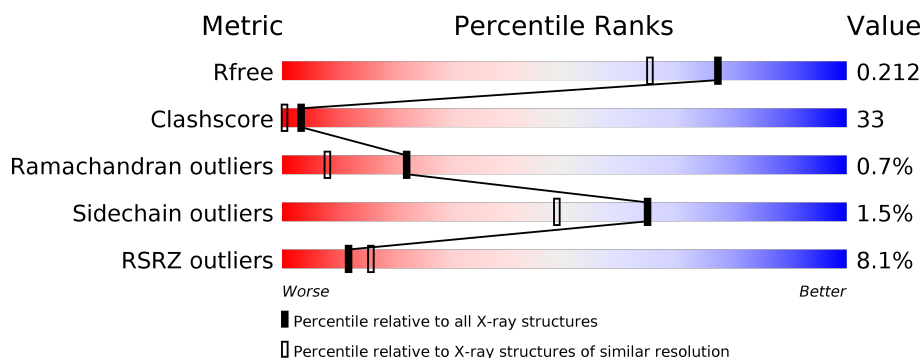
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 on 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	232	<div> <div>11%</div> <div> <div>45%</div> <div>47%</div> <div>7%</div> </div> </div>
2	B	232	<div> <div>4%</div> <div> <div>41%</div> <div>48%</div> <div>7%</div> </div> </div>
3	C	2	<div> <div>50%</div> <div>50%</div> </div>
4	D	5	<div> <div>60%</div> <div>40%</div> </div>
5	E	2	<div> <div>50%</div> <div>50%</div> </div>
6	F	9	<div> <div>11%</div> <div>44%</div> <div>44%</div> </div>

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
4	NAG	D	1[B]	-	-	X	-
6	NAG	F	2[B]	-	-	X	-
7	EDO	A	1456[B]	-	-	X	-
7	EDO	A	1461	-	-	X	-
7	EDO	A	1462	-	-	X	-
7	EDO	B	1455	-	-	X	-
7	EDO	B	1456[A]	-	-	X	-
7	EDO	B	1456[B]	-	-	X	-
7	EDO	B	1458[A]	-	-	X	-
7	EDO	B	1458[B]	-	-	X	-
7	EDO	B	1459	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 7945 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 HETERODIMERIC FC ANTIBODY AZYMETRIC VARIANT 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	210	Total	C	N	O	S	0	210	0
			3350	2135	564	638	13			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	222	GLY	-	expression tag	UNP P01857
A	350	VAL	THR	engineered mutation	UNP P01857
A	351	TYR	LEU	microheterogeneity	UNP P01857
A	366	LEU	THR	microheterogeneity	UNP P01857
A	392	MET	LYS	microheterogeneity	UNP P01857
A	394	TRP	THR	microheterogeneity	UNP P01857
A	405	ALA	PHE	microheterogeneity	UNP P01857
A	407	VAL	TYR	microheterogeneity	UNP P01857

- Molecule 2 is a protein called HETERODIMERIC FC ANTIBODY AZYMETRIC VARIANT 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	210	Total	C	N	O	S	0	210	0
			3350	2135	564	638	13			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	222	GLY	-	expression tag	UNP P01857
B	350	VAL	THR	engineered mutation	UNP P01857
B	351	TYR	LEU	microheterogeneity	UNP P01857
B	366	LEU	THR	microheterogeneity	UNP P01857
B	392	MET	LYS	microheterogeneity	UNP P01857
B	394	THR	TRP	microheterogeneity	UNP P01857

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Chain	Residue	Modelled	Actual	Comment	Reference
B	405	ALA	PHE	microheterogeneity	UNP P01857
B	407	VAL	TYR	microheterogeneity	UNP P01857

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	2	Total	C	N	O	0	2	0
			48	28	2	18			

- 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)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	5	Total	C	N	O	0	5	0
			122	68	4	50			

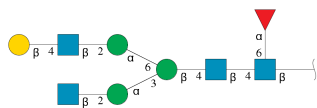
- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	2	Total	C	N	O	0	2	0
			50	28	2	20			

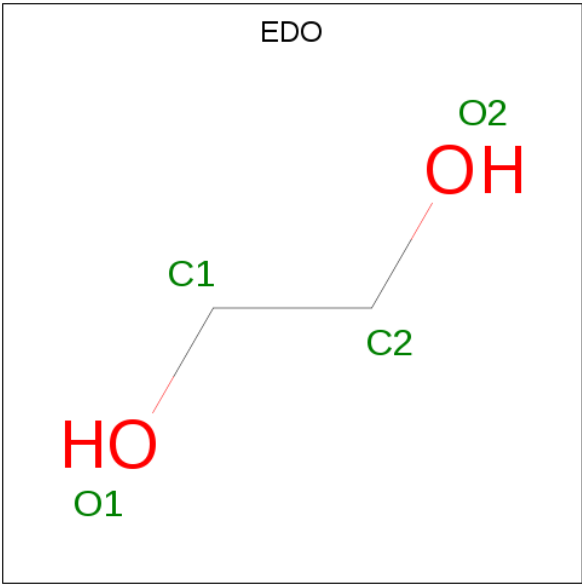
- Molecule 6 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose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

-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
6	F	9	220	124	8	88	0	9	0

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
7	A	1	4	2	2	0	0
7	A	1	8	4	4	0	1
7	A	1	4	2	2	0	0
7	A	1	4	2	2	0	0
7	B	1	4	2	2	0	0
7	B	1	8	4	4	0	1
7	B	1	4	2	2	0	0
7	B	1	8	4	4	0	1

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 8 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	3	Total	I	0	1
			4	4		

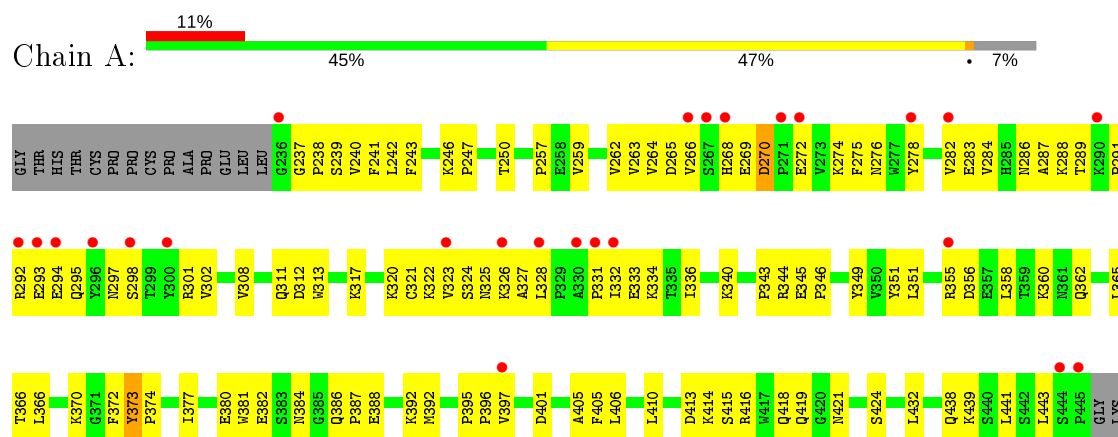
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	342	Total	O	0	0
			342	342		
9	B	411	Total	O	0	0
			411	411		

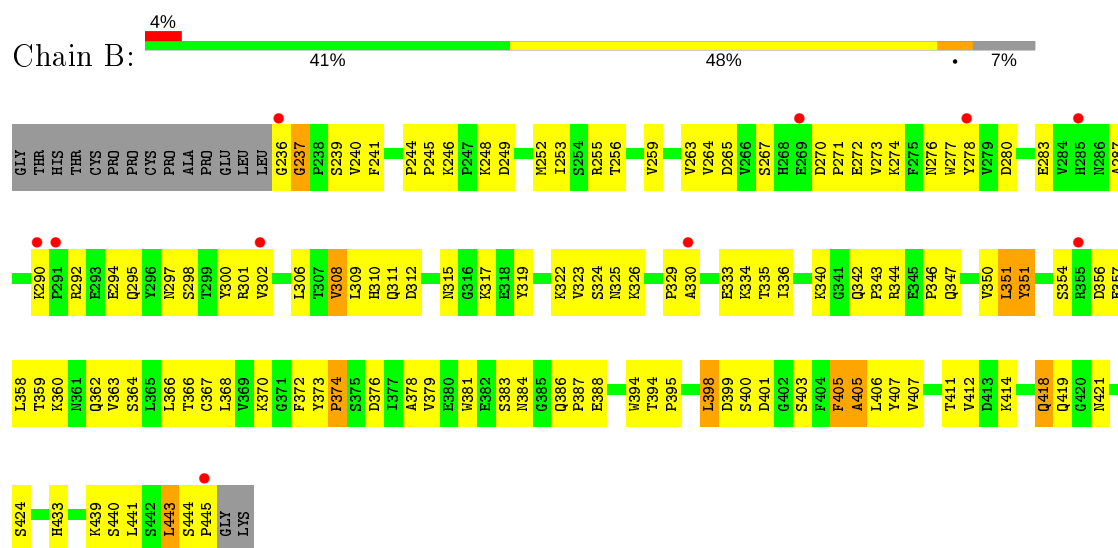
3 Residue-property plots

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: HETERODIMERIC FC ANTIBODY AZYMETRIC VARIANT 2



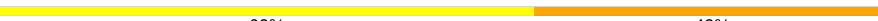
• Molecule 2: HETERODIMERIC FC ANTIBODY AZYMETRIC VARIANT 2



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



- Molecule 4: beta-D-galactopyranose-(1-4)-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 D:  60% 40%


NAG1
MAN1
NAG2
NAG3
NAG4
GAL5

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose

Chain E:  50% 50%


MAN1
NAG2

- Molecule 6: 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 F:  11% 44% 44%


NAG1
NAG2
MAN1
NAG3
NAG4
NAG5
GAL6
MAN7
NAG8
FUC9

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	49.54Å 74.92Å 148.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.38 – 1.75 41.38 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.1 (41.38-1.75) 99.0 (41.38-1.75)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.74 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.178 , 0.208 0.181 , 0.212	Depositor DCC
R_{free} test set	2849 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7945	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.51% 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: BMA, NAG, EDO, GAL, FUC, IOD, 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	0.54	3/3439 (0.1%)	0.60	0/4677
2	B	0.52	0/3439	0.72	5/4677 (0.1%)
All	All	0.53	3/6878 (0.0%)	0.66	5/9354 (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	4
2	B	0	4
All	All	0	8

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	270[A]	ASP	C-N	-11.34	1.12	1.34
1	A	270[B]	ASP	C-N	-11.34	1.12	1.34
1	A	405[B]	PHE	C-N	-8.19	1.15	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	405[B]	ALA	O-C-N	8.36	136.07	122.70
2	B	405[B]	ALA	C-N-CA	-6.84	104.61	121.70
2	B	405[B]	ALA	CA-C-N	-6.76	102.32	117.20
2	B	252[A]	MET	CG-SD-CE	-5.29	91.74	100.20
2	B	252[B]	MET	CG-SD-CE	-5.29	91.74	100.20

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	373[A]	TYR	Mainchain,Peptide
1	A	373[B]	TYR	Mainchain,Peptide
2	B	373[A]	TYR	Mainchain,Peptide
2	B	373[B]	TYR	Mainchain,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	3350	0	3269	198	0
2	B	3350	0	3273	182	0
3	C	48	0	42	2	0
4	D	122	0	104	32	0
5	E	50	0	44	12	0
6	F	220	0	189	31	0
7	A	20	0	27	20	0
7	B	28	0	38	33	0
8	B	4	0	0	0	0
9	A	342	0	0	78	0
9	B	411	0	0	83	0
All	All	7945	0	6986	438	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 33.

The worst 5 of 438 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:A:397[A]:VAL:CG1	9:A:4123:HOH:O	1.64	1.34
7:B:1458[A]:EDO:C2	9:B:2153:HOH:O	1.78	1.31
6:F:8[B]:NAG:O3	6:F:8[B]:NAG:H82	1.24	1.30
5:E:2[A]:NAG:H82	5:E:2[A]:NAG:O3	1.16	1.28
2:B:297[B]:ASN:HD21	6:F:1[B]:NAG:C1	1.50	1.24

There are no symmetry-related clashes.

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	404/232 (174%)	390 (96%)	12 (3%)	2 (0%)	29	12
2	B	404/232 (174%)	386 (96%)	14 (4%)	4 (1%)	15	4
All	All	808/464 (174%)	776 (96%)	26 (3%)	6 (1%)	22	8

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	374[A]	PRO
1	A	374[B]	PRO
2	B	374[A]	PRO
2	B	374[B]	PRO
2	B	237[A]	GLY

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	389/213 (183%)	387 (100%)	2 (0%)	88	83
2	B	389/213 (183%)	380 (98%)	9 (2%)	50	28
All	All	778/426 (183%)	767 (99%)	11 (1%)	65	52

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	351[A]	LEU
2	B	398[A]	LEU
2	B	418[B]	GLN
2	B	308[B]	VAL
2	B	418[A]	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

36 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	C	1[A]	1,3	14,14,15	0.62	0	17,19,21	1.09	2 (11%)
3	NAG	C	1[B]	1,3	14,14,15	0.74	0	17,19,21	0.95	0
3	FUC	C	2[A]	3	10,10,11	0.73	0	14,14,16	1.74	5 (35%)
3	FUC	C	2[B]	3	10,10,11	0.74	0	14,14,16	1.81	6 (42%)
4	NAG	D	1[A]	4	14,14,15	0.66	0	17,19,21	0.94	0
4	NAG	D	1[B]	4	14,14,15	0.73	0	17,19,21	1.88	4 (23%)
4	BMA	D	2[A]	4	11,11,12	0.34	0	15,15,17	1.25	0
4	BMA	D	2[B]	4	11,11,12	0.88	0	15,15,17	0.95	0
4	MAN	D	3[A]	4	11,11,12	0.68	0	15,15,17	1.29	2 (13%)
4	MAN	D	3[B]	4	11,11,12	0.71	0	15,15,17	1.01	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	D	4[A]	4	14,14,15	0.71	0	17,19,21	0.82	0
4	NAG	D	4[B]	4	14,14,15	0.74	0	17,19,21	0.72	0
4	GAL	D	5[A]	4	11,11,12	0.63	0	15,15,17	0.56	0
4	GAL	D	5[B]	4	11,11,12	0.60	0	15,15,17	1.51	1 (6%)
5	MAN	E	1[A]	5	11,11,12	0.72	0	15,15,17	0.79	0
5	MAN	E	1[B]	5	11,11,12	0.59	0	15,15,17	1.86	3 (20%)
5	NAG	E	2[A]	5	14,14,15	0.53	0	17,19,21	0.85	0
5	NAG	E	2[B]	5	14,14,15	0.53	0	17,19,21	0.84	0
6	NAG	F	1[A]	2,6	14,14,15	0.68	0	17,19,21	0.97	0
6	NAG	F	1[B]	6	14,14,15	0.38	0	17,19,21	0.82	0
6	NAG	F	2[A]	6	14,14,15	0.74	0	17,19,21	1.00	1 (5%)
6	NAG	F	2[B]	6	14,14,15	0.58	0	17,19,21	0.86	0
6	BMA	F	3[A]	6	11,11,12	0.63	0	15,15,17	1.23	1 (6%)
6	BMA	F	3[B]	6	11,11,12	0.39	0	15,15,17	1.13	1 (6%)
6	MAN	F	4[A]	6	11,11,12	0.70	0	15,15,17	1.14	1 (6%)
6	MAN	F	4[B]	6	11,11,12	0.67	0	15,15,17	1.28	3 (20%)
6	NAG	F	5[A]	6	14,14,15	0.62	0	17,19,21	1.45	2 (11%)
6	NAG	F	5[B]	6	14,14,15	0.55	0	17,19,21	1.11	2 (11%)
6	GAL	F	6[A]	6	11,11,12	0.52	0	15,15,17	1.38	4 (26%)
6	GAL	F	6[B]	6	11,11,12	0.52	0	15,15,17	1.48	3 (20%)
6	MAN	F	7[A]	6	11,11,12	0.68	0	15,15,17	0.66	0
6	MAN	F	7[B]	6	11,11,12	0.68	0	15,15,17	0.71	0
6	NAG	F	8[A]	6	14,14,15	0.55	0	17,19,21	0.66	0
6	NAG	F	8[B]	6	14,14,15	0.55	0	17,19,21	0.69	0
6	FUC	F	9[A]	6	10,10,11	0.43	0	14,14,16	0.95	1 (7%)
6	FUC	F	9[B]	-	10,10,11	0.57	0	14,14,16	0.80	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	C	1[A]	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	1[B]	1,3	-	0/6/23/26	0/1/1/1
3	FUC	C	2[A]	3	-	-	0/1/1/1
3	FUC	C	2[B]	3	-	-	0/1/1/1
4	NAG	D	1[A]	4	-	2/6/23/26	0/1/1/1
4	NAG	D	1[B]	4	-	2/6/23/26	0/1/1/1

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

There are no bond length outliers.

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1[B]	NAG	C1-O5-C5	-5.45	104.80	112.19
5	E	1[B]	MAN	C1-O5-C5	4.92	118.86	112.19
4	D	5[B]	GAL	C3-C4-C5	-4.24	102.68	110.24
6	F	5[A]	NAG	O5-C1-C2	-3.96	105.03	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	1[B]	MAN	O5-C1-C2	3.44	116.08	110.77

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

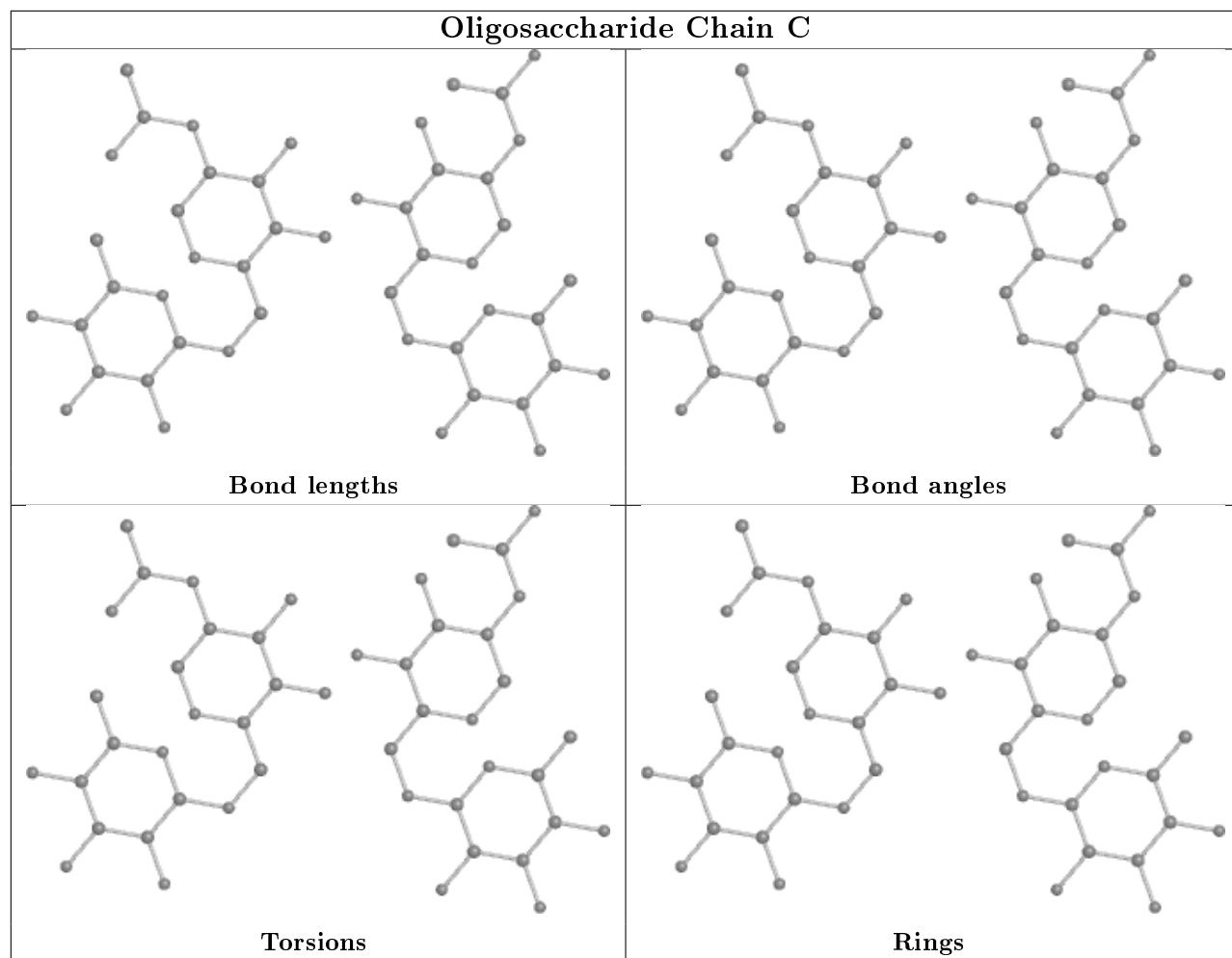
Mol	Chain	Res	Type	Atoms
5	E	2[B]	NAG	O5-C5-C6-O6
6	F	8[A]	NAG	C4-C5-C6-O6
6	F	8[B]	NAG	C4-C5-C6-O6
5	E	2[A]	NAG	O5-C5-C6-O6
6	F	8[B]	NAG	O5-C5-C6-O6

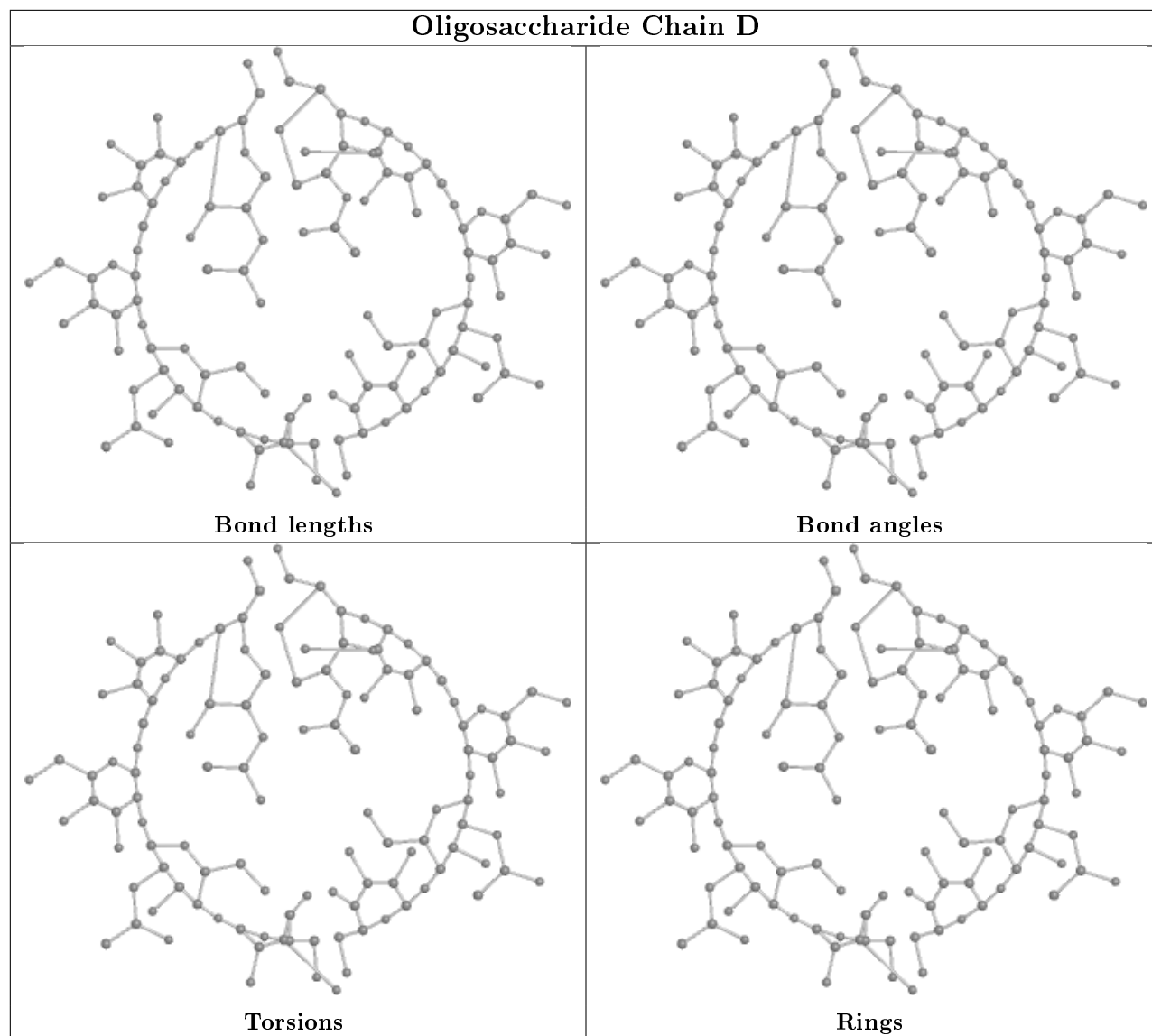
There are no ring outliers.

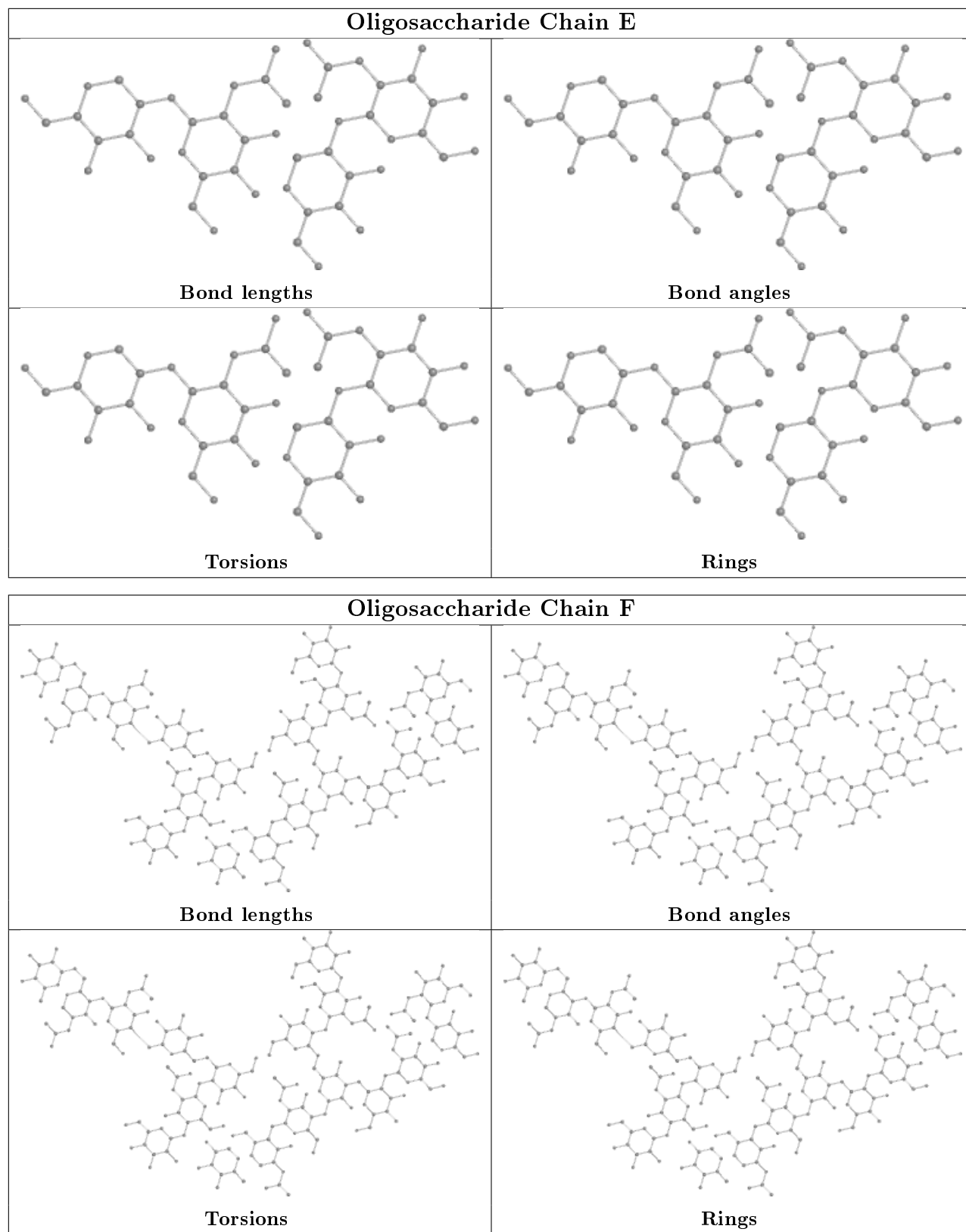
21 monomers are involved in 68 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	F	6[B]	GAL	1	0
4	D	5[A]	GAL	2	0
6	F	9[B]	FUC	2	0
3	C	1[B]	NAG	2	0
4	D	5[B]	GAL	3	0
6	F	1[B]	NAG	5	0
6	F	2[B]	NAG	11	0
6	F	2[A]	NAG	5	0
4	D	4[B]	NAG	5	0
5	E	2[A]	NAG	5	0
4	D	4[A]	NAG	2	0
4	D	1[B]	NAG	7	0
4	D	1[A]	NAG	6	0
6	F	8[A]	NAG	3	0
6	F	8[B]	NAG	3	0
4	D	2[B]	BMA	4	0
5	E	1[A]	MAN	4	0
5	E	1[B]	MAN	4	0
4	D	2[A]	BMA	3	0
6	F	9[A]	FUC	1	0
6	F	3[B]	BMA	3	0

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







5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 4 are monoatomic - leaving 12 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	$\# Z > 2$
7	EDO	B	1457	-	3,3,3	0.48	0	2,2,2	0.33	0
7	EDO	A	1456[A]	-	3,3,3	0.48	0	2,2,2	0.31	0
7	EDO	A	1456[B]	-	3,3,3	0.49	0	2,2,2	0.34	0
7	EDO	A	1462	-	3,3,3	0.48	0	2,2,2	0.33	0
7	EDO	B	1456[A]	-	3,3,3	0.51	0	2,2,2	0.62	0
7	EDO	B	1458[A]	-	3,3,3	0.62	0	2,2,2	0.10	0
7	EDO	B	1459	-	3,3,3	0.49	0	2,2,2	0.30	0
7	EDO	B	1456[B]	-	3,3,3	0.51	0	2,2,2	0.31	0
7	EDO	B	1455	-	3,3,3	0.50	0	2,2,2	0.35	0
7	EDO	A	1455	-	3,3,3	0.45	0	2,2,2	0.40	0
7	EDO	A	1461	-	3,3,3	0.50	0	2,2,2	0.19	0
7	EDO	B	1458[B]	-	3,3,3	0.57	0	2,2,2	0.36	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
7	EDO	B	1457	-	-	1/1/1/1	-
7	EDO	A	1456[A]	-	-	1/1/1/1	-
7	EDO	A	1456[B]	-	-	1/1/1/1	-
7	EDO	A	1462	-	-	1/1/1/1	-
7	EDO	B	1456[A]	-	-	0/1/1/1	-
7	EDO	B	1458[A]	-	-	1/1/1/1	-
7	EDO	B	1459	-	-	1/1/1/1	-
7	EDO	B	1456[B]	-	-	1/1/1/1	-
7	EDO	B	1455	-	-	1/1/1/1	-
7	EDO	A	1455	-	-	1/1/1/1	-
7	EDO	A	1461	-	-	1/1/1/1	-
7	EDO	B	1458[B]	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	1456[B]	EDO	O1-C1-C2-O2
7	A	1461	EDO	O1-C1-C2-O2
7	A	1462	EDO	O1-C1-C2-O2
7	B	1458[A]	EDO	O1-C1-C2-O2
7	B	1459	EDO	O1-C1-C2-O2

There are no ring outliers.

12 monomers are involved in 52 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	1457	EDO	1	0
7	A	1456[A]	EDO	3	0
7	A	1456[B]	EDO	5	0
7	A	1462	EDO	4	0
7	B	1456[A]	EDO	4	0
7	B	1458[A]	EDO	5	0
7	B	1459	EDO	4	0
7	B	1456[B]	EDO	10	0
7	B	1455	EDO	5	0
7	A	1455	EDO	3	0
7	A	1461	EDO	5	0
7	B	1458[B]	EDO	4	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	270[A]:ASP	C	271[A]:PRO	N	1.12

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	216/232 (93%)	0.76	25 (11%) 4 6	14, 23, 43, 60	12 (5%)
2	B	216/232 (93%)	0.55	10 (4%) 32 38	12, 21, 34, 43	12 (5%)
All	All	432/464 (93%)	0.65	35 (8%) 12 16	12, 22, 38, 60	24 (5%)

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	300[A]	TYR	6.2
1	A	296[A]	TYR	5.6
1	A	445[A]	PRO	4.5
1	A	444[A]	SER	4.2
2	B	236[A]	GLY	3.6

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(Å ²)	Q<0.9
6	NAG	F	8[A]	14/15	0.67	0.23	109,111,113,113	14
6	NAG	F	8[B]	14/15	0.67	0.23	112,116,119,120	14
5	NAG	E	2[A]	14/15	0.70	0.21	100,104,106,106	14
5	NAG	E	2[B]	14/15	0.70	0.21	111,116,118,119	14
3	FUC	C	2[B]	10/11	0.76	0.22	38,42,43,44	10

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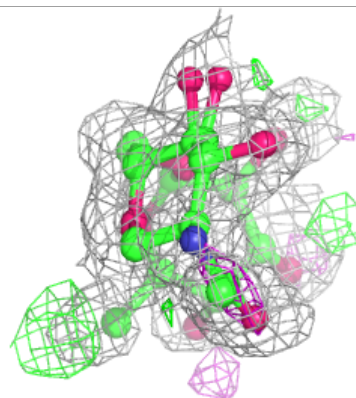
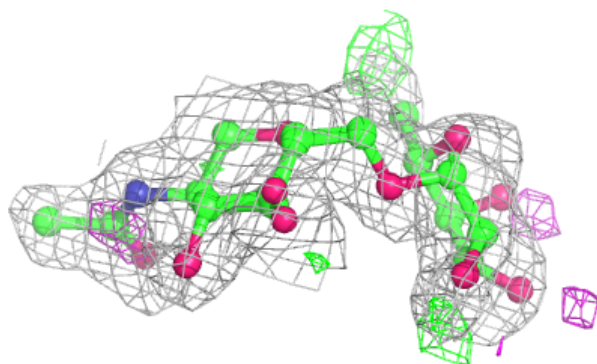
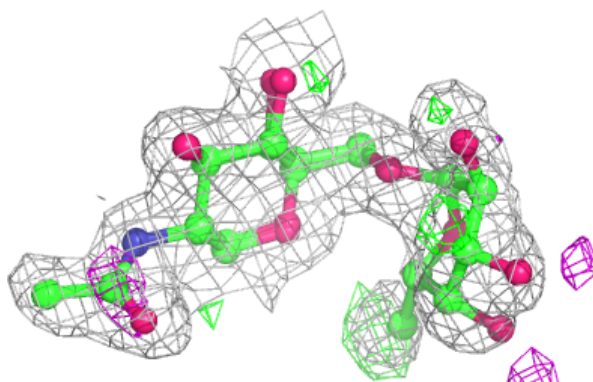
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	FUC	C	2[A]	10/11	0.76	0.22	65,68,71,72	10
4	GAL	D	5[A]	11/12	0.78	0.26	92,100,103,104	11
4	GAL	D	5[B]	11/12	0.78	0.26	23,25,26,26	11
6	GAL	F	6[A]	11/12	0.80	0.21	230,236,238,239	11
6	GAL	F	6[B]	11/12	0.80	0.21	22,26,29,29	11
6	MAN	F	7[A]	11/12	0.84	0.13	106,109,111,115	11
6	MAN	F	7[B]	11/12	0.84	0.13	40,42,45,46	11
5	MAN	E	1[A]	11/12	0.85	0.12	34,35,36,37	11
5	MAN	E	1[B]	11/12	0.85	0.12	133,135,137,138	11
6	FUC	F	9[B]	10/11	0.87	0.18	25,26,26,27	10
6	FUC	F	9[A]	10/11	0.87	0.18	52,54,56,58	10
3	NAG	C	1[A]	14/15	0.89	0.13	24,27,29,30	14
3	NAG	C	1[B]	14/15	0.89	0.13	27,29,30,30	14
4	NAG	D	4[B]	14/15	0.90	0.11	39,41,43,44	14
4	NAG	D	4[A]	14/15	0.90	0.11	22,23,26,27	14
6	MAN	F	4[B]	11/12	0.91	0.14	29,29,31,32	11
6	MAN	F	4[A]	11/12	0.91	0.14	29,31,33,35	11
6	BMA	F	3[A]	11/12	0.91	0.11	41,43,43,45	11
6	BMA	F	3[B]	11/12	0.91	0.11	22,26,27,28	11
4	NAG	D	1[B]	14/15	0.92	0.13	23,25,30,31	14
4	NAG	D	1[A]	14/15	0.92	0.13	25,26,29,30	14
6	NAG	F	1[B]	14/15	0.93	0.10	29,30,37,37	14
4	BMA	D	2[A]	11/12	0.93	0.10	20,21,22,24	11
4	BMA	D	2[B]	11/12	0.93	0.10	33,35,37,38	11
6	NAG	F	1[A]	14/15	0.93	0.10	32,34,37,37	14
6	NAG	F	2[B]	14/15	0.94	0.10	30,33,35,38	14
6	NAG	F	5[A]	14/15	0.94	0.14	34,38,43,43	14
6	NAG	F	5[B]	14/15	0.94	0.14	20,22,29,31	14
6	NAG	F	2[A]	14/15	0.94	0.10	24,27,28,29	14
4	MAN	D	3[B]	11/12	0.96	0.10	33,34,38,40	11
4	MAN	D	3[A]	11/12	0.96	0.10	20,21,25,25	11

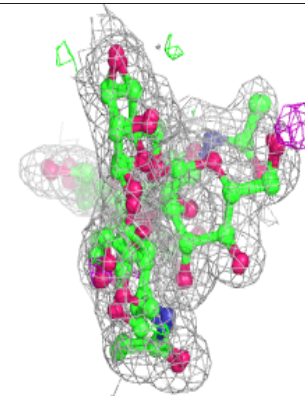
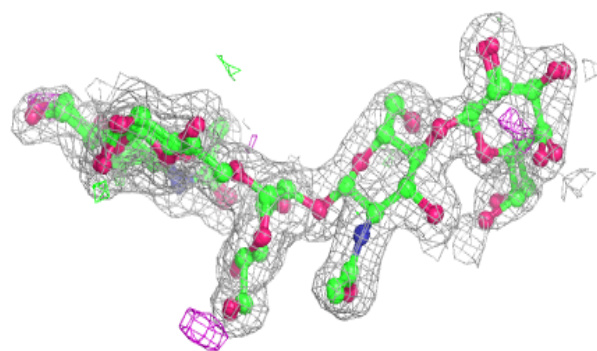
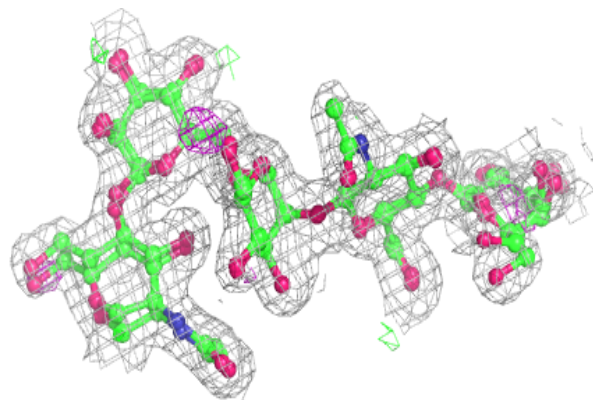
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

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

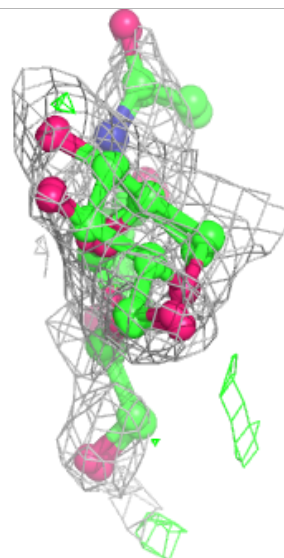
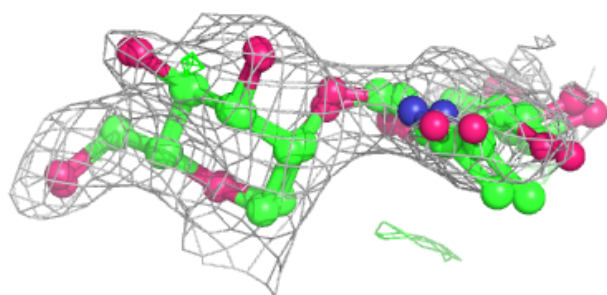
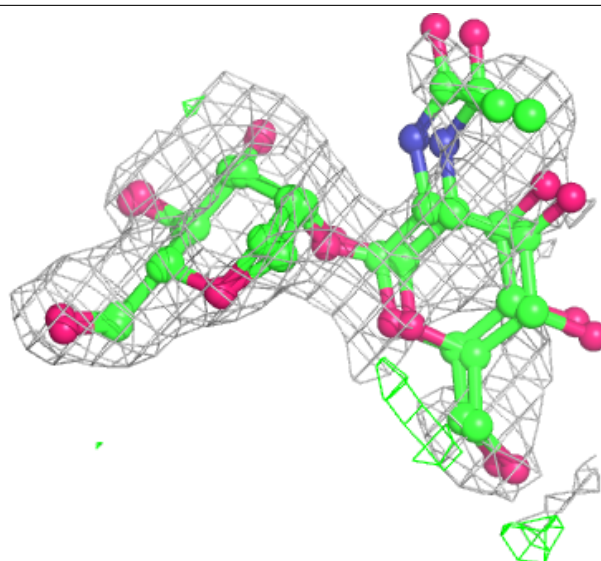
**Electron density around Chain D:**

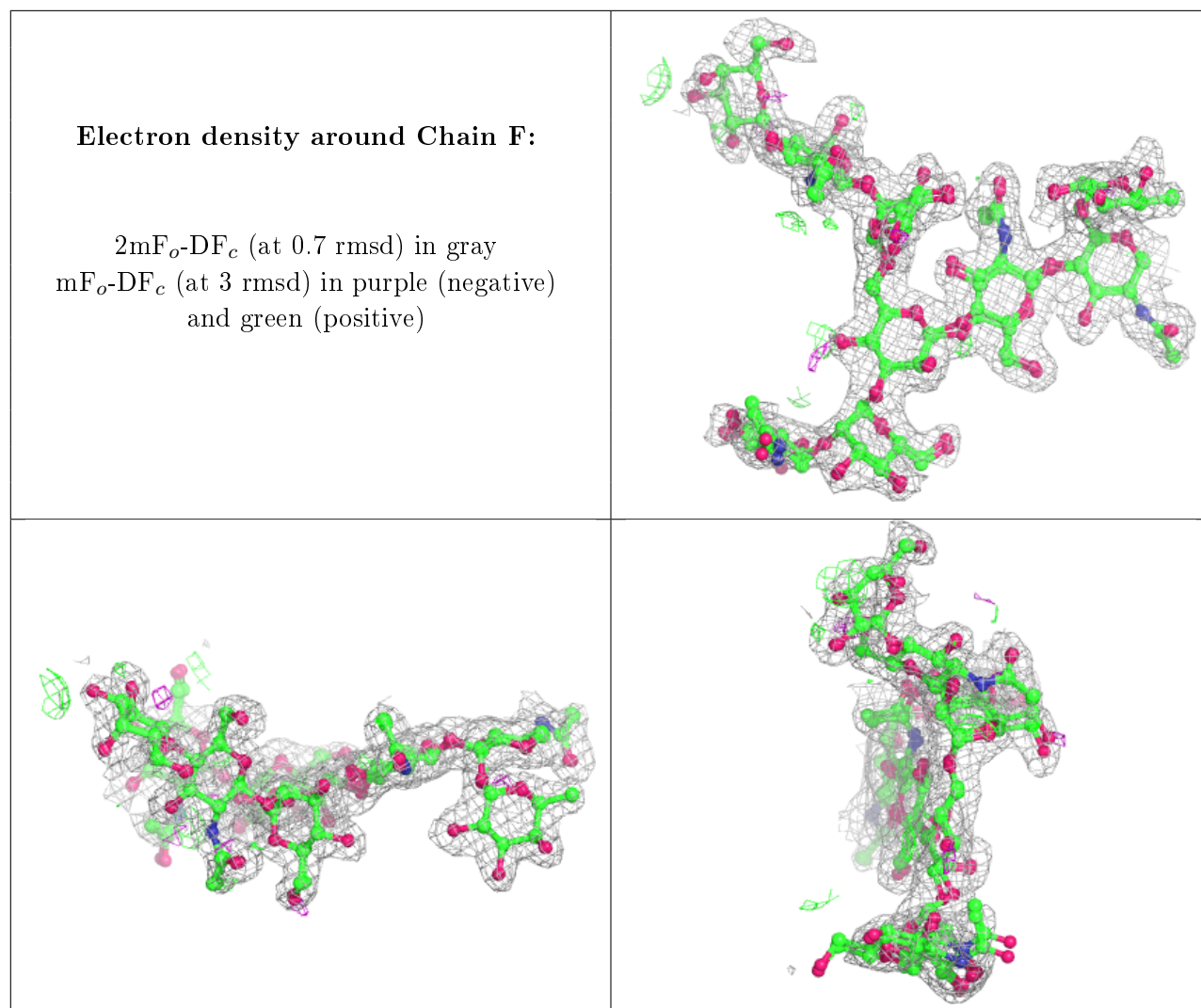
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





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, 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
7	EDO	B	1455	4/4	0.66	0.32	33,35,37,37	4
7	EDO	A	1462	4/4	0.88	0.11	34,34,35,37	4
7	EDO	A	1456[A]	4/4	0.89	0.20	32,34,34,35	4
7	EDO	B	1458[A]	4/4	0.89	0.22	21,23,26,27	4
7	EDO	A	1456[B]	4/4	0.89	0.20	28,30,31,31	4
7	EDO	B	1458[B]	4/4	0.89	0.22	27,29,31,35	4
7	EDO	B	1456[B]	4/4	0.93	0.15	23,24,26,29	4
7	EDO	B	1456[A]	4/4	0.93	0.15	21,21,22,22	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	EDO	A	1461	4/4	0.93	0.22	54,55,55,55	4
7	EDO	B	1459	4/4	0.93	0.20	31,34,34,34	4
7	EDO	B	1457	4/4	0.94	0.17	41,43,44,47	4
7	EDO	A	1455	4/4	0.94	0.22	25,26,28,32	4
8	IOD	B	1460	1/1	1.00	0.13	18,18,18,18	1
8	IOD	B	1462[A]	1/1	1.00	0.06	23,23,23,23	1
8	IOD	B	1461	1/1	1.00	0.13	17,17,17,17	1
8	IOD	B	1462[B]	1/1	1.00	0.06	23,23,23,23	1

6.5 Other polymers [i](#)

There are no such residues in this entry.