



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:35 AM UTC

PDB ID : 5MOK / pdb_00005mok
Title : Crystal structure of human IgE-Fc epsilon 3-4
Authors : Dore, K.A.; Davies, A.M.; Drinkwater, N.; Beavil, A.J.; McDonnell, J.M.; Sutton, B.J.
Deposited on : 2016-12-14
Resolution : 2.00 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

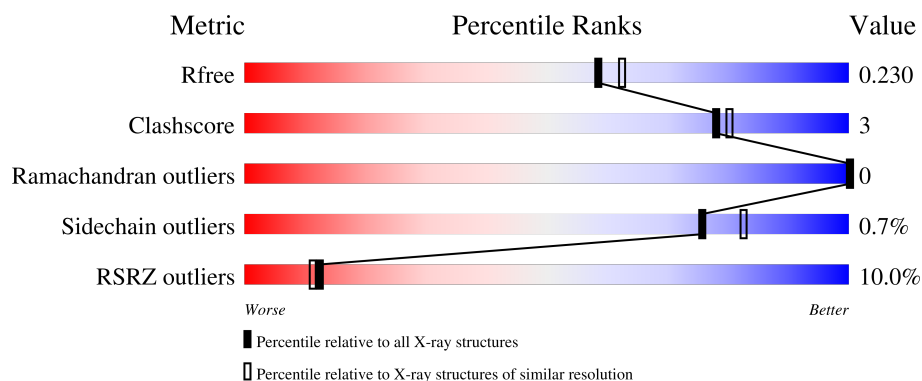
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	223	11% 90% 7%
1	B	223	8% 87% 8%
1	C	223	9% 80% 9% 11%
1	D	223	8% 81% 9% 9%
2	E	4	75% 25%

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Mol	Chain	Length	Quality of chain
3	F	7	 43% 57%
3	H	7	 43% 57%
4	G	4	 50% 25% 25%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7173 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.

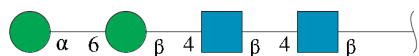
- Molecule 1 is a protein called Ig epsilon chain C region.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	0	3	0
			1601	1007	280	307	7			
1	B	205	Total	C	N	O	S	0	5	0
			1594	1002	285	301	6			
1	C	198	Total	C	N	O	S	0	3	0
			1536	964	272	294	6			
1	D	202	Total	C	N	O	S	0	10	0
			1627	1026	291	304	6			

There are 20 discrepancies between the modelled and reference sequences:

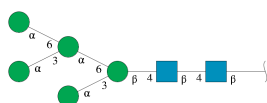
Chain	Residue	Modelled	Actual	Comment	Reference
A	325	ALA	-	expression tag	UNP P01854
A	326	ASP	-	expression tag	UNP P01854
A	327	PRO	-	expression tag	UNP P01854
A	371	GLN	ASN	conflict	UNP P01854
A	383	GLN	ASN	conflict	UNP P01854
B	325	ALA	-	expression tag	UNP P01854
B	326	ASP	-	expression tag	UNP P01854
B	327	PRO	-	expression tag	UNP P01854
B	371	GLN	ASN	conflict	UNP P01854
B	383	GLN	ASN	conflict	UNP P01854
C	325	ALA	-	expression tag	UNP P01854
C	326	ASP	-	expression tag	UNP P01854
C	327	PRO	-	expression tag	UNP P01854
C	371	GLN	ASN	conflict	UNP P01854
C	383	GLN	ASN	conflict	UNP P01854
D	325	ALA	-	expression tag	UNP P01854
D	326	ASP	-	expression tag	UNP P01854
D	327	PRO	-	expression tag	UNP P01854
D	371	GLN	ASN	conflict	UNP P01854
D	383	GLN	ASN	conflict	UNP P01854

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



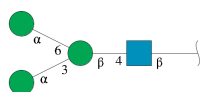
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	4	Total	C	N	O	0	0	0
			50	28	2	20			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	7	Total	C	N	O	0	0	0
			83	46	2	35			
3	H	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[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	G	4	Total	C	N	O	0	0	0
			47	26	1	20			

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	4	2		
5	D	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			4	2	2		
6	C	1	Total	C	O	0	0
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		

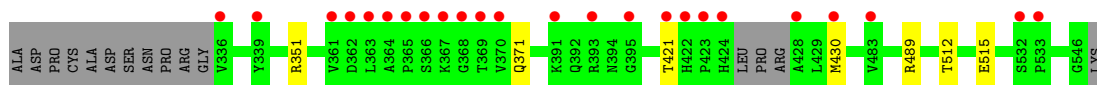
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	132	Total	O	0	0
			132	132		
7	B	141	Total	O	0	0
			141	141		
7	C	133	Total	O	0	0
			133	133		
7	D	113	Total	O	0	0
			113	113		

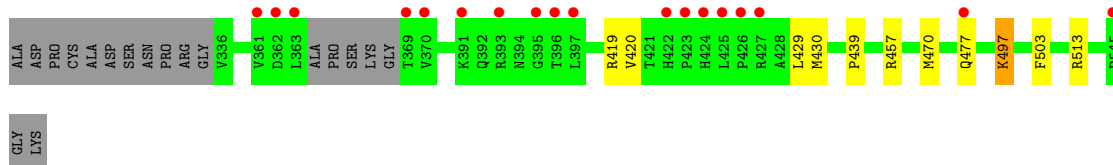
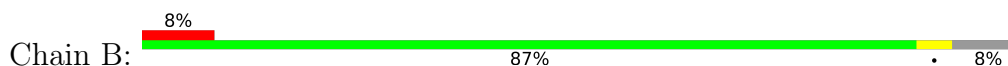
3 Residue-property plots [i](#)

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.

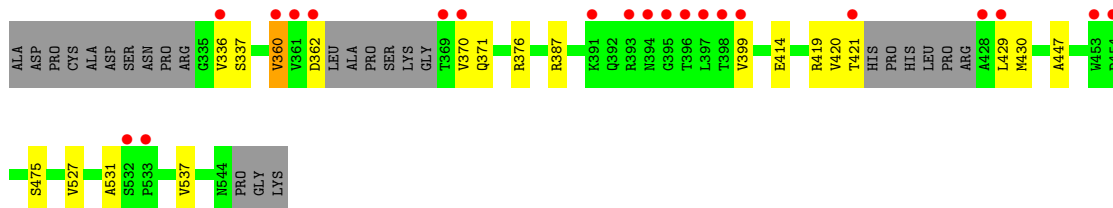
- Molecule 1: Ig epsilon chain C region



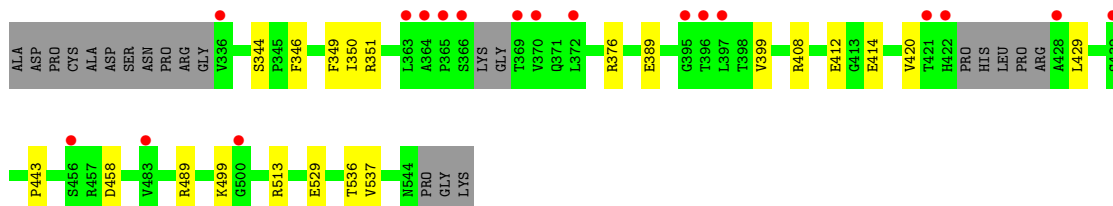
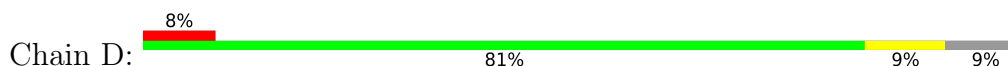
- Molecule 1: Ig epsilon chain C region



- Molecule 1: Ig epsilon chain C region



- Molecule 1: Ig epsilon chain C region



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

Chain E:  75% 25%

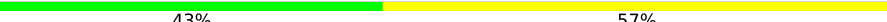


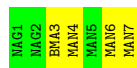
- Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  43% 57%



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

Chain H:  43% 57%



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

Chain G:  50% 25% 25%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.48Å 100.36Å 77.86Å 90.00° 97.35° 90.00°	Depositor
Resolution (Å)	77.22 – 2.00 77.22 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (77.22-2.00) 99.9 (77.22-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.202 , 0.226 0.208 , 0.230	Depositor DCC
R_{free} test set	3444 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	32.9	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 59.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7173	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.08 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.3957e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: EDO, PEG, NAG, MAN, BMA

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	0.14	0/1649	0.37	0/2252
1	B	0.13	0/1648	0.35	0/2253
1	C	0.13	0/1580	0.34	0/2155
1	D	0.13	0/1693	0.35	0/2304
All	All	0.13	0/6570	0.35	0/8964

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	1601	0	1526	6	0
1	B	1594	0	1541	6	0
1	C	1536	0	1466	10	0
1	D	1627	0	1607	13	0
2	E	50	0	43	0	0
3	F	83	0	70	0	0
3	H	83	0	70	0	0
4	G	47	0	40	1	0
5	A	6	0	7	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	7	0	10	1	0
6	A	8	0	12	1	0
6	C	8	0	12	1	0
6	D	4	0	6	1	0
7	A	132	0	0	0	0
7	B	141	0	0	0	0
7	C	133	0	0	0	0
7	D	113	0	0	2	0
All	All	7173	0	6410	36	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 3.

All (36) 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:D:351[B]:ARG:NH1	7:D:701:HOH:O	2.22	0.71
1:C:370:VAL:O	1:C:387:ARG:NH2	2.24	0.68
1:C:371:GLN:HB2	1:C:421:THR:HB	1.80	0.63
1:A:351:ARG:NH1	6:A:606:EDO:O1	2.33	0.62
1:D:408:ARG:NH2	1:D:412:GLU:OE2	2.35	0.59
1:D:489:ARG:HD3	5:D:608:PEG:H32	1.83	0.58
1:D:536[B]:THR:HG21	6:D:609:EDO:H12	1.86	0.56
1:C:420:VAL:HB	1:C:429:LEU:HB2	1.88	0.55
1:B:420:VAL:HB	1:B:429:LEU:HB2	1.89	0.54
1:A:512:THR:HG23	5:A:605:PEG:H21	1.88	0.54
1:D:458:ASP:OD1	1:D:513[A]:ARG:NH1	2.41	0.53
1:C:447:ALA:H	6:C:606:EDO:H12	1.74	0.53
1:D:443:PRO:HG2	1:D:537:VAL:HG11	1.92	0.52
1:B:457:ARG:O	1:B:513:ARG:NH2	2.41	0.51
1:B:497:LYS:HD3	1:B:503:PHE:CE2	2.45	0.51
1:D:346:PHE:HD1	1:D:350[B]:ILE:HD12	1.78	0.47
1:C:419:ARG:HD2	1:C:430:MET:HE2	1.95	0.47
1:D:351[A]:ARG:NH1	7:D:701:HOH:O	2.40	0.47
1:A:515:GLU:HG3	5:A:605:PEG:H41	1.97	0.46
4:G:4:MAN:O6	4:G:4:MAN:O4	2.33	0.45
1:D:389:GLU:HG2	1:D:399:VAL:HG22	2.00	0.44
1:A:430[B]:MET:HE2	1:A:430[B]:MET:HB2	1.75	0.44
1:A:489:ARG:CZ	5:A:605:PEG:H22	2.47	0.44
1:C:360:VAL:HG13	1:C:399:VAL:HB	1.99	0.44
1:D:376[A]:ARG:HD2	1:D:414:GLU:OE2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:531:ALA:HB1	1:C:537:VAL:HG23	2.00	0.43
1:B:419[B]:ARG:NH1	1:B:430:MET:SD	2.92	0.43
1:B:439:PRO:HG2	1:B:470:MET:HE2	2.01	0.43
1:B:497:LYS:HA	1:B:497:LYS:HD2	1.74	0.42
1:D:349:PHE:CZ	1:D:529:GLU:HB3	2.54	0.42
1:C:336:VAL:HG12	1:C:362:ASP:HA	2.00	0.42
1:D:499:LYS:HA	1:D:499:LYS:HD3	1.85	0.42
1:A:371:GLN:HB2	1:A:421:THR:HB	2.02	0.41
1:C:475:SER:HB2	1:C:527:VAL:HB	2.02	0.41
1:D:420:VAL:HB	1:D:429:LEU:HB2	2.02	0.40
1:C:376:ARG:HD2	1:C:414:GLU:OE2	2.22	0.40

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	207/223 (93%)	203 (98%)	4 (2%)	0	100	100
1	B	206/223 (92%)	201 (98%)	5 (2%)	0	100	100
1	C	195/223 (87%)	192 (98%)	3 (2%)	0	100	100
1	D	206/223 (92%)	203 (98%)	3 (2%)	0	100	100
All	All	814/892 (91%)	799 (98%)	15 (2%)	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	171/195 (88%)	171 (100%)	0	100	100
1	B	174/195 (89%)	172 (99%)	2 (1%)	65	73
1	C	165/195 (85%)	163 (99%)	2 (1%)	63	70
1	D	179/195 (92%)	178 (99%)	1 (1%)	78	85
All	All	689/780 (88%)	684 (99%)	5 (1%)	76	82

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

Mol	Chain	Res	Type
1	B	477	GLN
1	B	497	LYS
1	C	337	SER
1	C	360	VAL
1	D	344	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	481	ASN
1	A	518	GLN
1	B	481	ASN
1	B	518	GLN
1	B	538	GLN
1	C	481	ASN
1	C	518	GLN
1	C	535	GLN
1	D	384	HIS
1	D	535	GLN
1	D	538	GLN

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

22 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	E	1	2,1	14,14,15	0.32	0	17,19,21	0.44	0
2	NAG	E	2	2	14,14,15	0.21	0	17,19,21	0.47	0
2	BMA	E	3	2	11,11,12	0.58	0	15,15,17	0.68	0
2	MAN	E	4	2	11,11,12	0.94	1 (9%)	15,15,17	1.18	2 (13%)
3	NAG	F	1	3,1	14,14,15	0.24	0	17,19,21	0.59	0
3	NAG	F	2	3	14,14,15	0.20	0	17,19,21	0.51	0
3	BMA	F	3	3	11,11,12	0.53	0	15,15,17	0.83	0
3	MAN	F	4	3	11,11,12	0.67	0	15,15,17	0.95	2 (13%)
3	MAN	F	5	3	11,11,12	0.65	0	15,15,17	1.01	2 (13%)
3	MAN	F	6	3	11,11,12	0.63	0	15,15,17	0.93	2 (13%)
3	MAN	F	7	3	11,11,12	0.68	0	15,15,17	1.11	2 (13%)
4	NAG	G	1	4	14,14,15	0.22	0	17,19,21	0.42	0
4	BMA	G	2	4	11,11,12	0.55	0	15,15,17	0.90	0
4	MAN	G	3	4	11,11,12	0.80	0	15,15,17	0.80	1 (6%)
4	MAN	G	4	4	11,11,12	0.84	1 (9%)	15,15,17	1.20	2 (13%)
3	NAG	H	1	3,1	14,14,15	0.22	0	17,19,21	0.41	0
3	NAG	H	2	3	14,14,15	0.32	0	17,19,21	0.51	0
3	BMA	H	3	3	11,11,12	0.57	0	15,15,17	0.87	1 (6%)
3	MAN	H	4	3	11,11,12	0.70	0	15,15,17	1.12	2 (13%)
3	MAN	H	5	3	11,11,12	0.87	0	15,15,17	0.84	0
3	MAN	H	6	3	11,11,12	0.75	0	15,15,17	1.10	2 (13%)
3	MAN	H	7	3	11,11,12	0.60	0	15,15,17	0.89	2 (13%)

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	4	MAN	C1-C2	2.59	1.58	1.52
4	G	4	MAN	C1-C2	2.04	1.57	1.52

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	7	MAN	C1-O5-C5	3.27	116.56	112.19
3	H	4	MAN	C1-O5-C5	2.98	116.18	112.19
2	E	4	MAN	C1-O5-C5	2.92	116.09	112.19
3	H	6	MAN	C1-O5-C5	2.89	116.06	112.19
3	F	5	MAN	C1-O5-C5	2.70	115.80	112.19
3	F	6	MAN	C1-O5-C5	2.37	115.37	112.19
2	E	4	MAN	O2-C2-C3	-2.31	105.37	110.15
4	G	4	MAN	C1-O5-C5	2.29	115.25	112.19
3	H	4	MAN	O2-C2-C3	-2.27	105.45	110.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	4	MAN	C1-O5-C5	2.25	115.21	112.19
3	F	4	MAN	O2-C2-C3	-2.22	105.56	110.15
4	G	4	MAN	C1-C2-C3	2.20	112.84	109.64
3	H	6	MAN	O2-C2-C3	-2.17	105.65	110.15
3	H	7	MAN	C1-O5-C5	2.15	115.07	112.19
3	F	7	MAN	O2-C2-C3	-2.10	105.81	110.15
3	H	7	MAN	O2-C2-C3	-2.09	105.83	110.15
3	F	5	MAN	O2-C2-C3	-2.07	105.86	110.15
3	F	6	MAN	O2-C2-C3	-2.07	105.87	110.15
3	H	3	BMA	O2-C2-C3	-2.03	105.94	110.15
4	G	3	MAN	O2-C2-C3	-2.01	105.98	110.15

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	2	NAG	O5-C5-C6-O6
2	E	4	MAN	O5-C5-C6-O6
4	G	1	NAG	O5-C5-C6-O6
3	F	7	MAN	O5-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6
4	G	1	NAG	C4-C5-C6-O6
2	E	4	MAN	C4-C5-C6-O6
3	H	1	NAG	C8-C7-N2-C2
3	H	1	NAG	O7-C7-N2-C2
4	G	1	NAG	C8-C7-N2-C2
4	G	1	NAG	O7-C7-N2-C2
4	G	4	MAN	O5-C5-C6-O6
3	F	7	MAN	C4-C5-C6-O6
3	F	6	MAN	O5-C5-C6-O6
3	F	3	BMA	C4-C5-C6-O6
2	E	3	BMA	C4-C5-C6-O6
2	E	3	BMA	O5-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6
3	H	5	MAN	O5-C5-C6-O6
3	H	7	MAN	O5-C5-C6-O6
3	H	2	NAG	O5-C5-C6-O6
3	F	6	MAN	C4-C5-C6-O6
2	E	1	NAG	C4-C5-C6-O6
3	F	3	BMA	O5-C5-C6-O6
2	E	1	NAG	O5-C5-C6-O6
3	F	1	NAG	C3-C2-N2-C7

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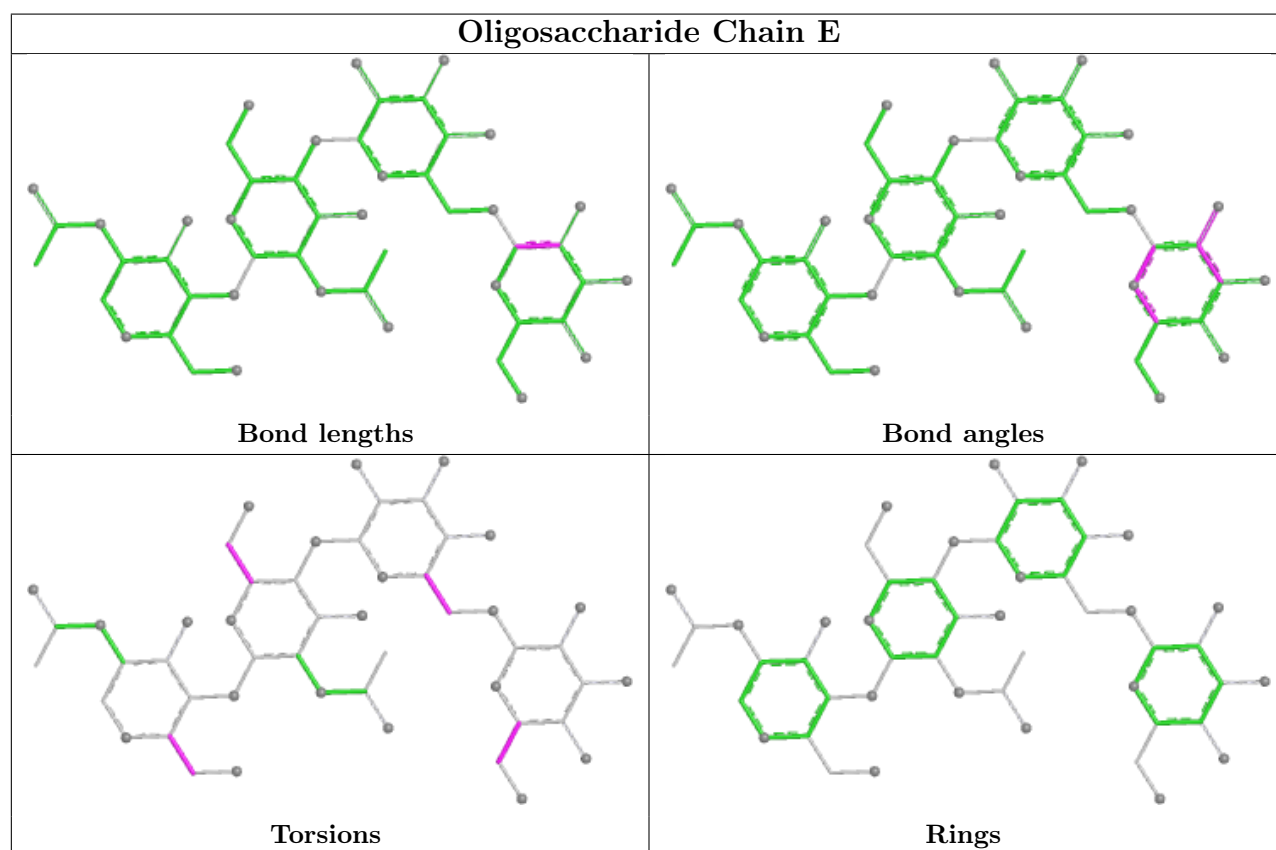
Mol	Chain	Res	Type	Atoms
3	F	1	NAG	C1-C2-N2-C7

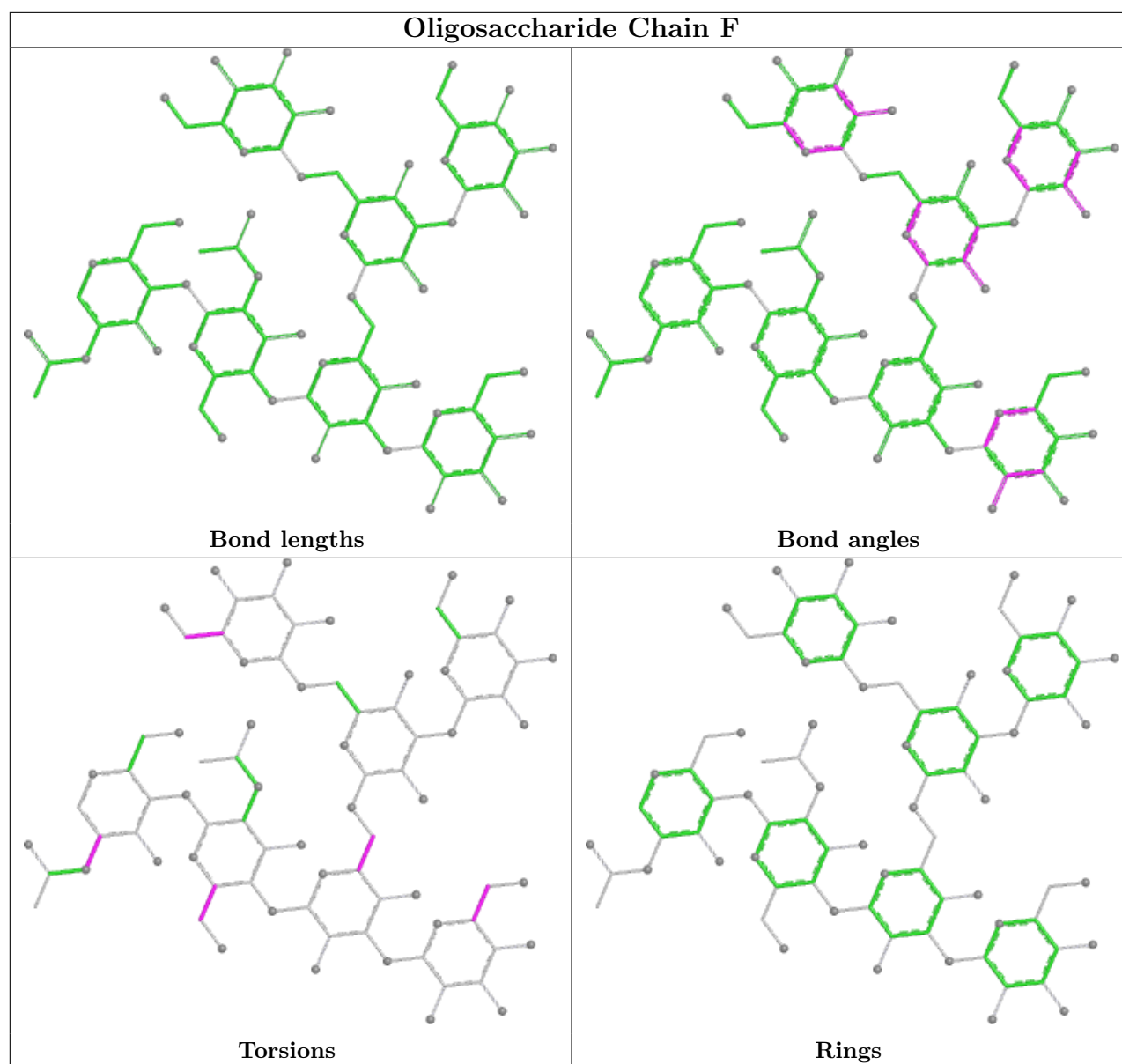
There are no ring outliers.

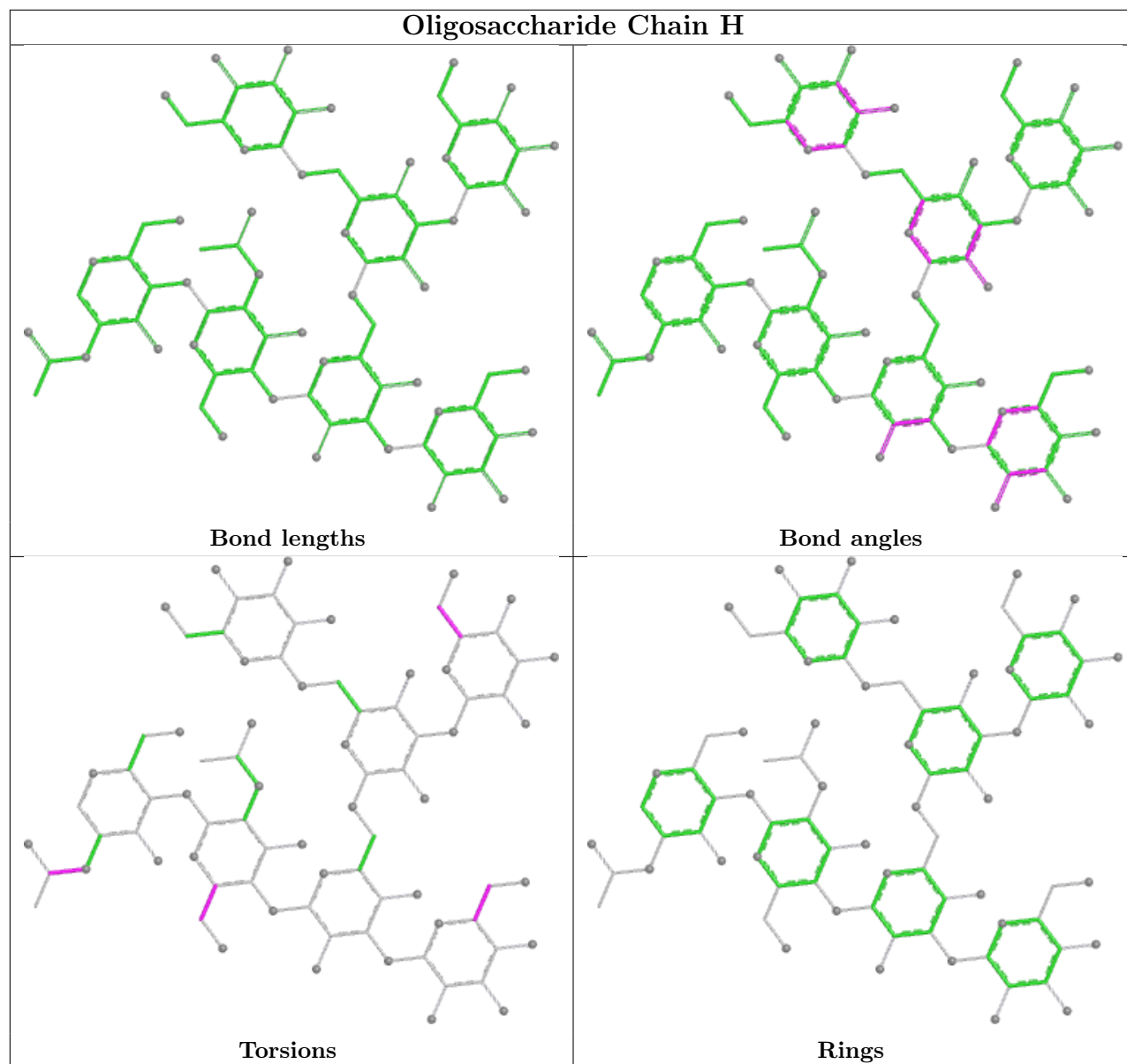
1 monomer is involved in 1 short contact:

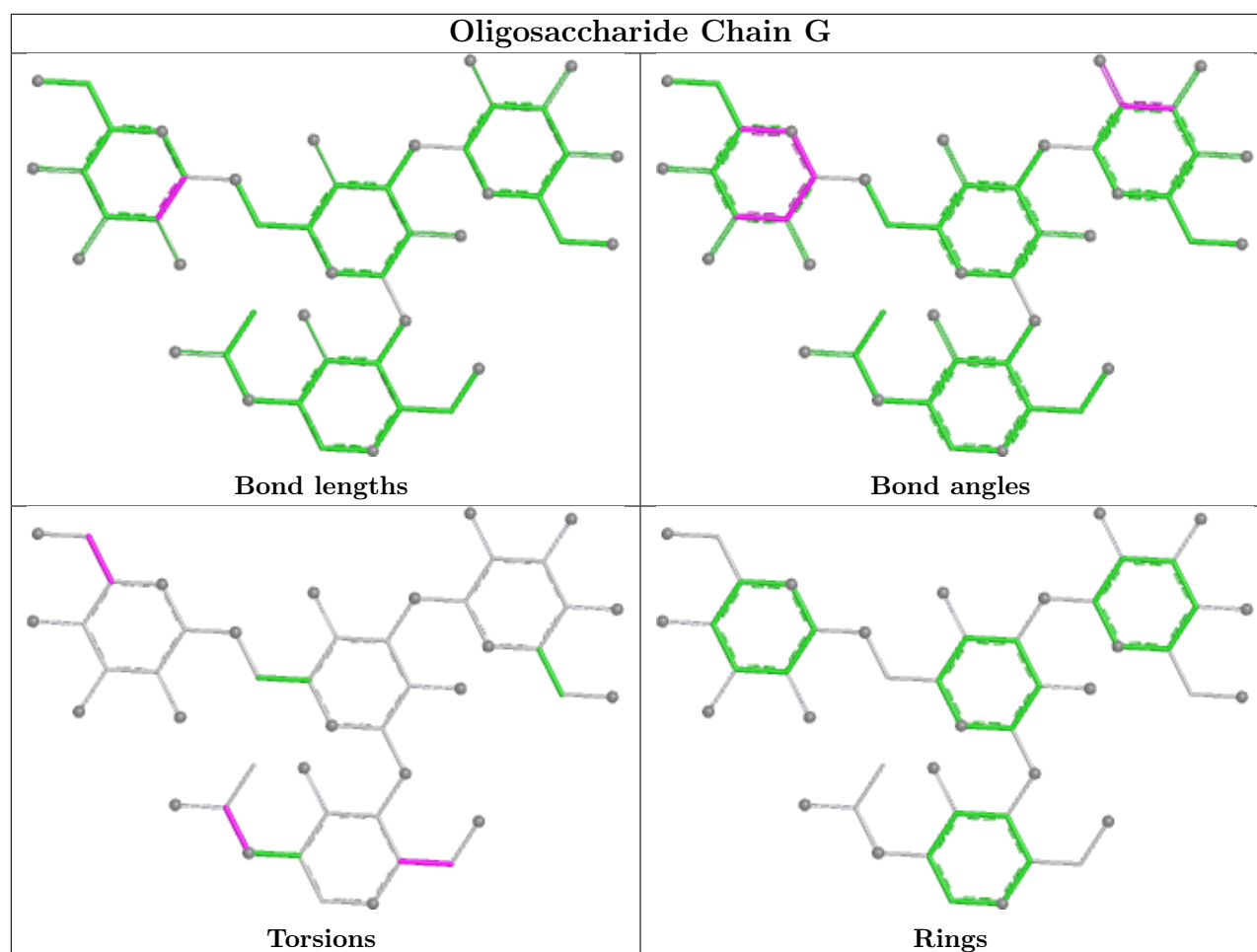
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	4	MAN	1	0

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









5.6 Ligand geometry [i](#)

7 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	$\# Z > 2$
5	PEG	A	605	-	5,5,6	0.87	0	4,4,5	0.24	0
6	EDO	A	606	-	3,3,3	0.42	0	2,2,2	0.43	0
6	EDO	C	606	-	3,3,3	0.40	0	2,2,2	0.39	0
5	PEG	D	608	-	6,6,6	0.85	0	5,5,5	0.24	0
6	EDO	A	607	-	3,3,3	0.44	0	2,2,2	0.35	0
6	EDO	C	605	-	3,3,3	0.46	0	2,2,2	0.24	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	D	609	-	3,3,3	0.43	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
5	PEG	A	605	-	-	3/3/3/4	-
6	EDO	A	606	-	-	0/1/1/1	-
6	EDO	C	606	-	-	1/1/1/1	-
5	PEG	D	608	-	-	2/4/4/4	-
6	EDO	A	607	-	-	0/1/1/1	-
6	EDO	C	605	-	-	0/1/1/1	-
6	EDO	D	609	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	605	PEG	C1-C2-O2-C3
5	A	605	PEG	O2-C3-C4-O4
5	A	605	PEG	C4-C3-O2-C2
5	D	608	PEG	C1-C2-O2-C3
5	D	608	PEG	O2-C3-C4-O4
6	C	606	EDO	O1-C1-C2-O2

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	605	PEG	3	0
6	A	606	EDO	1	0
6	C	606	EDO	1	0
5	D	608	PEG	1	0
6	D	609	EDO	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	208/223 (93%)	0.58	24 (11%) 9 8	19, 40, 90, 143	3 (1%)
1	B	205/223 (91%)	0.35	18 (8%) 15 14	18, 37, 91, 121	5 (2%)
1	C	198/223 (88%)	0.41	21 (10%) 11 10	20, 37, 92, 118	3 (1%)
1	D	202/223 (90%)	0.47	18 (8%) 15 14	18, 39, 85, 123	10 (4%)
All	All	813/892 (91%)	0.45	81 (9%) 12 11	18, 38, 92, 143	21 (2%)

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	397	LEU	5.3
1	D	422	HIS	5.2
1	C	398	THR	5.2
1	D	370	VAL	4.6
1	A	363	LEU	4.5
1	D	363	LEU	4.5
1	D	397	LEU	4.5
1	B	363	LEU	4.5
1	A	361	VAL	4.3
1	C	361	VAL	4.3
1	A	366	SER	4.3
1	D	366	SER	4.1
1	A	428	ALA	4.0
1	D	396	THR	3.9
1	B	545	PRO	3.8
1	A	422	HIS	3.7
1	C	428	ALA	3.7
1	A	364	ALA	3.6
1	D	369	THR	3.5
1	A	365	PRO	3.5
1	C	370	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	368	GLY	3.5
1	B	424	HIS	3.5
1	C	396	THR	3.5
1	A	423	PRO	3.4
1	D	365	PRO	3.4
1	A	336	VAL	3.4
1	C	362	ASP	3.3
1	B	425	LEU	3.3
1	D	421	THR	3.2
1	C	454	PRO	3.2
1	A	393	ARG	3.2
1	D	395	GLY	3.2
1	C	453	TRP	3.1
1	D	364	ALA	3.1
1	A	424	HIS	3.1
1	A	370	VAL	3.1
1	A	421	THR	3.0
1	A	369	THR	3.0
1	B	369	THR	3.0
1	C	369	THR	2.8
1	A	533	PRO	2.8
1	B	422	HIS	2.8
1	B	426	PRO	2.8
1	D	336	VAL	2.8
1	B	397	LEU	2.8
1	C	360	VAL	2.8
1	D	483	VAL	2.8
1	A	532	SER	2.7
1	C	533	PRO	2.7
1	B	423	PRO	2.6
1	B	395	GLY	2.6
1	D	428	ALA	2.6
1	C	399	VAL	2.5
1	C	421	THR	2.5
1	C	391	LYS	2.4
1	C	429	LEU	2.4
1	A	483	VAL	2.4
1	A	367	LYS	2.4
1	C	393	ARG	2.4
1	A	430[A]	MET	2.3
1	B	370	VAL	2.3
1	D	432	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	427	ARG	2.3
1	A	391	LYS	2.3
1	C	336	VAL	2.3
1	C	394	ASN	2.3
1	A	362	ASP	2.3
1	C	532	SER	2.2
1	B	362	ASP	2.2
1	B	393	ARG	2.2
1	B	391	LYS	2.2
1	C	395	GLY	2.2
1	D	500	GLY	2.2
1	D	372	LEU	2.2
1	B	361	VAL	2.1
1	A	395	GLY	2.1
1	D	456	SER	2.1
1	B	477	GLN	2.1
1	B	396	THR	2.1
1	A	339	TYR	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.

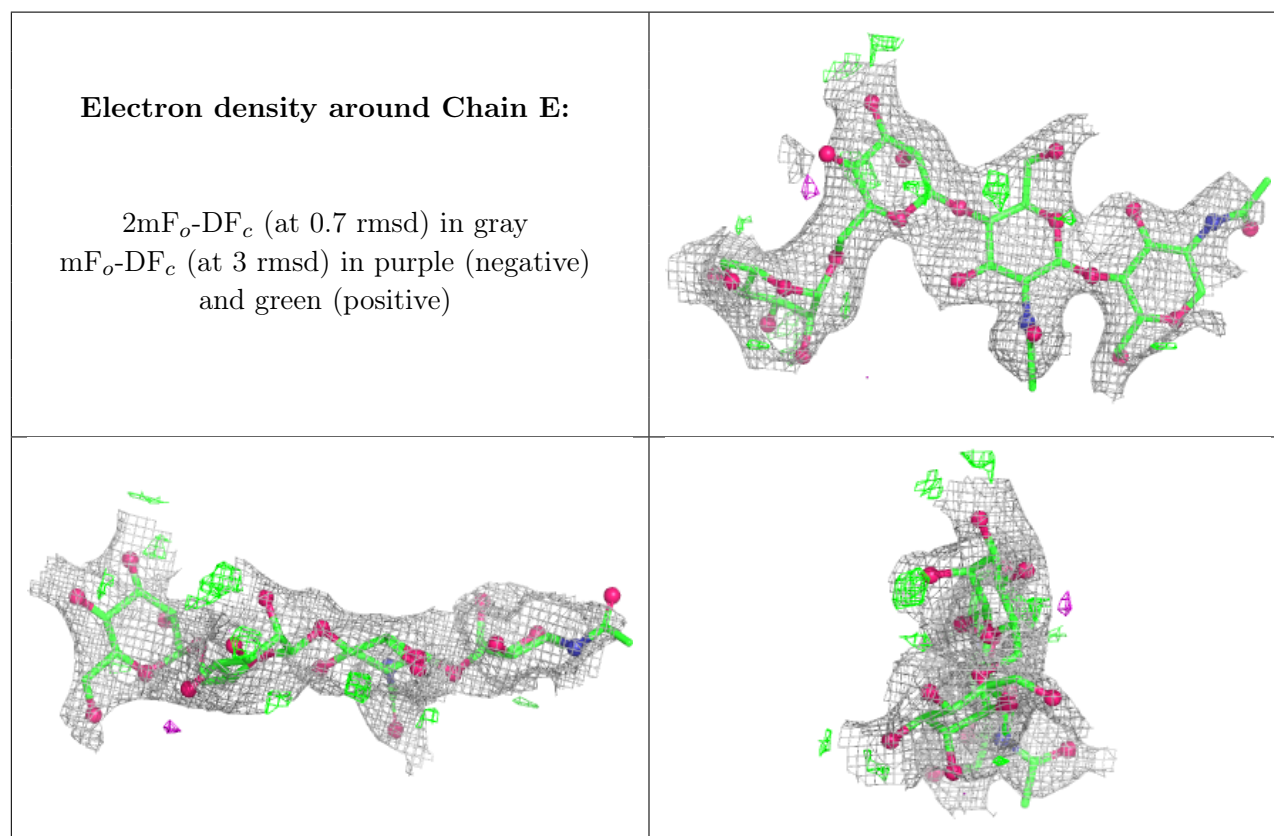
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MAN	G	4	11/12	0.54	0.23	77,89,94,100	0
3	NAG	H	1	14/15	0.59	0.17	75,80,85,87	0
3	MAN	F	6	11/12	0.60	0.17	103,106,108,108	0
4	NAG	G	1	14/15	0.64	0.17	76,81,83,83	0
4	MAN	G	3	11/12	0.65	0.14	90,91,91,91	0
3	MAN	F	7	11/12	0.68	0.13	77,83,84,85	0
2	BMA	E	3	11/12	0.68	0.16	77,80,82,84	0
2	MAN	E	4	11/12	0.68	0.17	82,84,85,85	0
3	NAG	F	1	14/15	0.68	0.16	69,78,83,84	0
2	NAG	E	1	14/15	0.68	0.16	79,86,96,97	0

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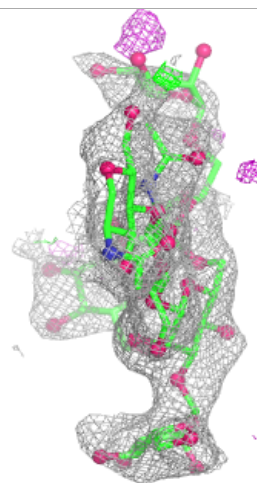
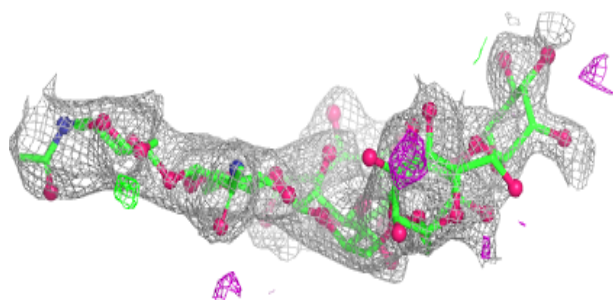
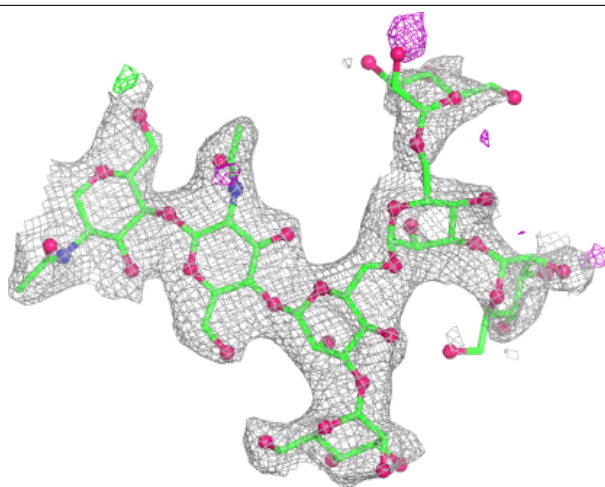
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MAN	F	5	11/12	0.69	0.19	86,89,93,93	0
3	MAN	H	7	11/12	0.71	0.15	77,81,82,83	0
3	MAN	F	4	11/12	0.76	0.14	80,83,93,98	0
4	BMA	G	2	11/12	0.76	0.15	86,88,90,90	0
3	MAN	H	5	11/12	0.81	0.14	56,62,65,68	0
3	MAN	H	4	11/12	0.81	0.13	48,51,54,54	0
3	BMA	H	3	11/12	0.83	0.13	51,55,62,70	0
3	NAG	H	2	14/15	0.83	0.15	54,69,73,75	0
3	NAG	F	2	14/15	0.84	0.13	60,62,65,66	0
2	NAG	E	2	14/15	0.85	0.13	70,78,82,82	0
3	MAN	H	6	11/12	0.88	0.12	38,45,50,50	0
3	BMA	F	3	11/12	0.93	0.10	61,69,74,77	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.



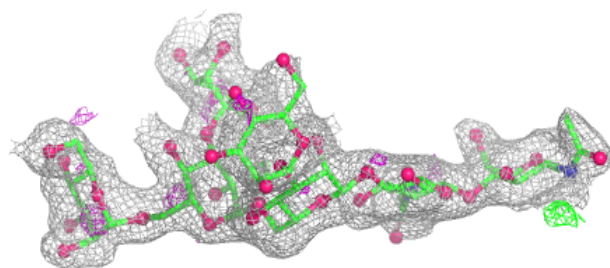
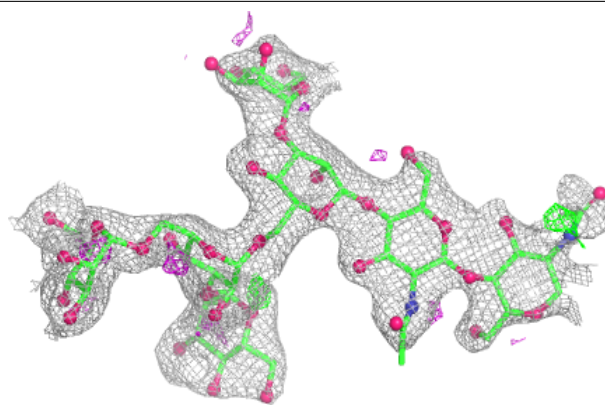
Electron density around Chain F:

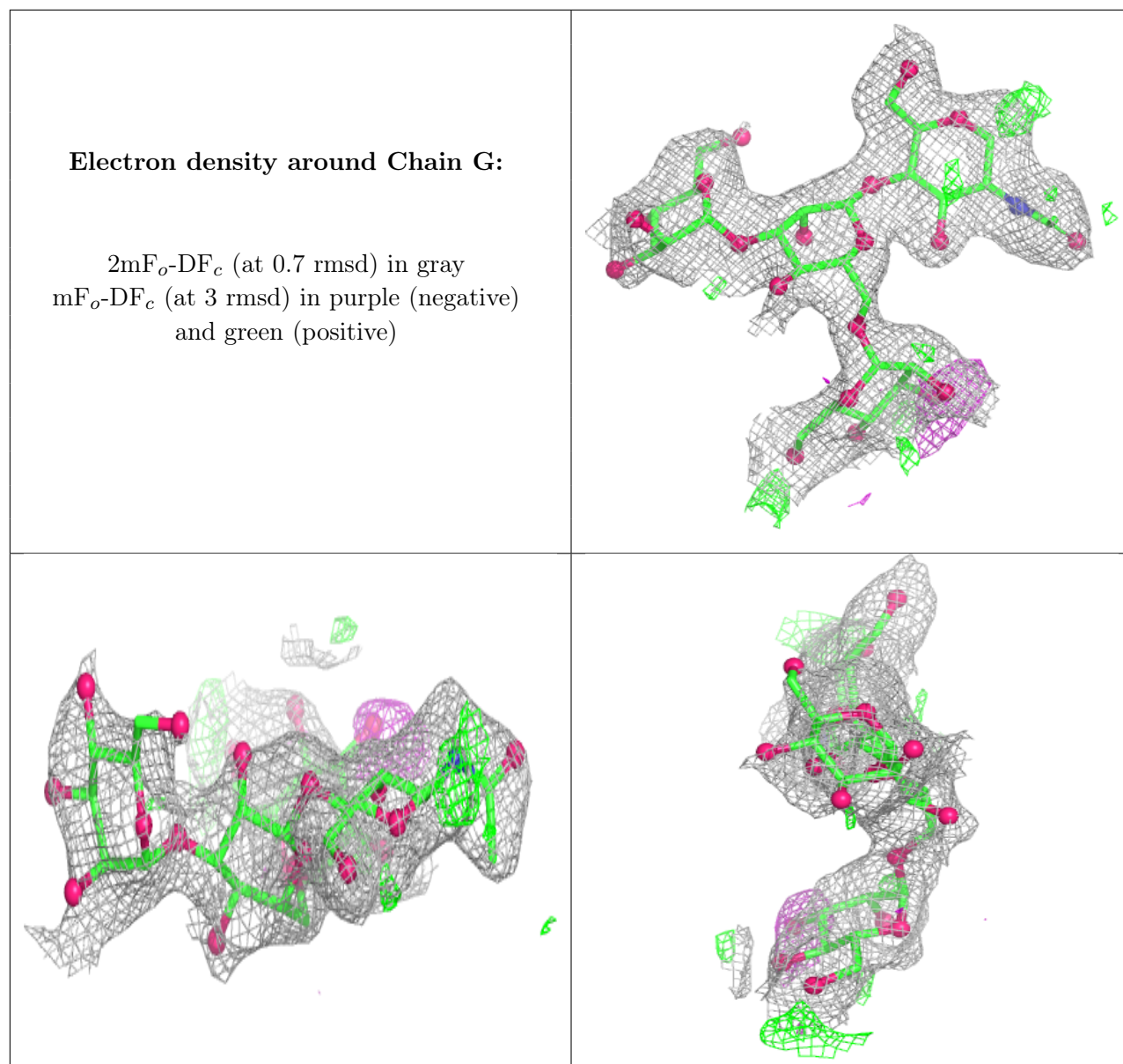
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain H:

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





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
5	PEG	D	608	7/7	0.74	0.17	60,61,63,64	0
6	EDO	A	607	4/4	0.75	0.17	55,57,58,59	0
6	EDO	D	609	4/4	0.76	0.20	68,69,69,70	0
6	EDO	A	606	4/4	0.78	0.17	58,59,59,60	0
5	PEG	A	605	6/7	0.80	0.17	51,57,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	EDO	C	605	4/4	0.84	0.17	36,38,40,42	0
6	EDO	C	606	4/4	0.89	0.25	49,49,49,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.