



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 7, 2020 – 04:41 PM BST

PDB ID : 6F1H
Title : C1rC1s complex
Authors : Almitairi, J.O.M.; Venkatraman Girija, U.; Furze, C.M.; Simpson-Gray, X.;
Badakshi, F.; Marshall, J.E.; Mitchell, D.A.; Moody, P.C.E.; Wallis, R.
Deposited on : 2017-11-22
Resolution : 4.50 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

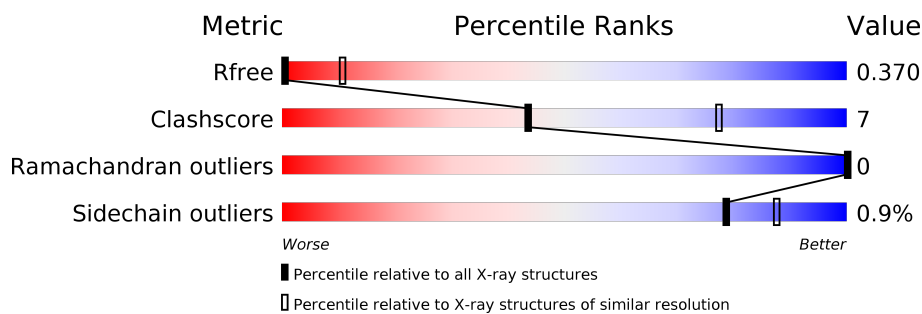
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.50 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	1055 (5.20-3.80)
Clashscore	141614	1123 (5.20-3.80)
Ramachandran outliers	138981	1069 (5.20-3.80)
Sidechain outliers	138945	1050 (5.20-3.80)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	291	84% 16%
1	C	291	78% 19% ..
2	B	276	87% 13%
2	D	276	86% 14%
3	E	7	29% 57% 14%
4	F	7	14% 43% 43%
5	G	3	67% 33%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	H	3	<div><div></div><div>33%</div><div>33%</div><div>33%</div></div>
5	I	3	<div><div></div><div>33%</div><div>67%</div></div>

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 9318 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.

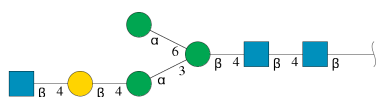
- Molecule 1 is a protein called Complement C1r subcomponent.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	291	Total	C	N	O	S	0	0	0
			2328	1477	382	454	15			
1	C	286	Total	C	N	O	S	0	0	0
			2294	1455	376	448	15			

- Molecule 2 is a protein called Complement C1s subcomponent.

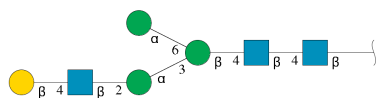
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	275	Total	C	N	O	S	0	0	0
			2178	1381	354	429	14			
2	B	276	Total	C	N	O	S	0	0	0
			2188	1388	355	430	15			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-beta-D-galactopyranose-(1-4)-alpha-D-mannopyranose-(1-3)-[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
3	E	7	Total	C	N	O	0	0	0
			86	48	3	35			

- Molecule 4 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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
4	F	7	Total	C	N	O	0	0	0
			86	48	3	35			

- Molecule 5 is an oligosaccharide called 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
5	G	3	Total	C	N	O	0	0	0
			39	22	2	15			
5	H	3	Total	C	N	O	0	0	0
			39	22	2	15			
5	I	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	3	Total	Ca	0	0
			3	3		
6	A	3	Total	Ca	0	0
			3	3		
6	D	3	Total	Ca	0	0
			3	3		
6	C	3	Total	Ca	0	0
			3	3		

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

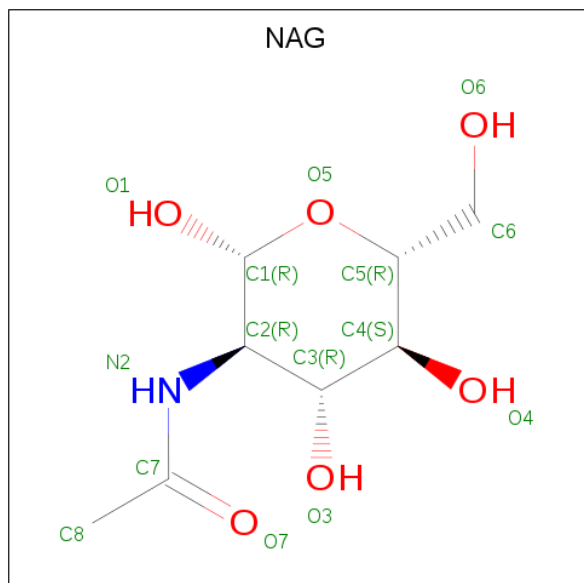
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	2	Total	Na	0	0
			2	2		
7	A	1	Total	Na	0	0
			1	1		

Continued on next page...

Continued from previous page...

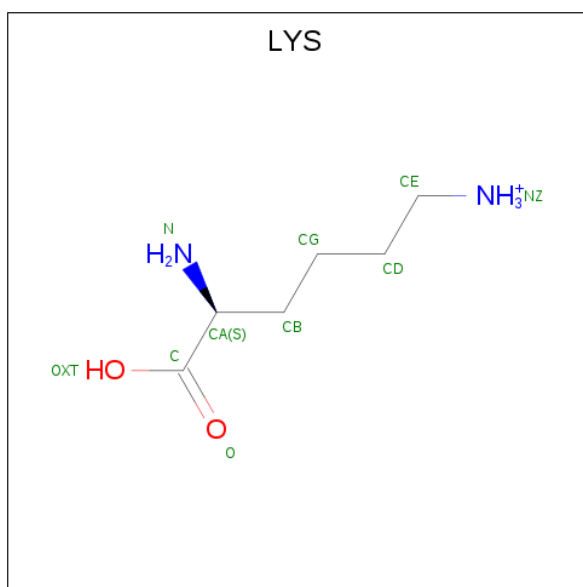
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	2	Total	Na	0	0
			2	2		
7	C	1	Total	Na	0	0
			1	1		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 9 is LYSINE (three-letter code: LYS) (formula: $C_6H_{15}N_2O_2$).

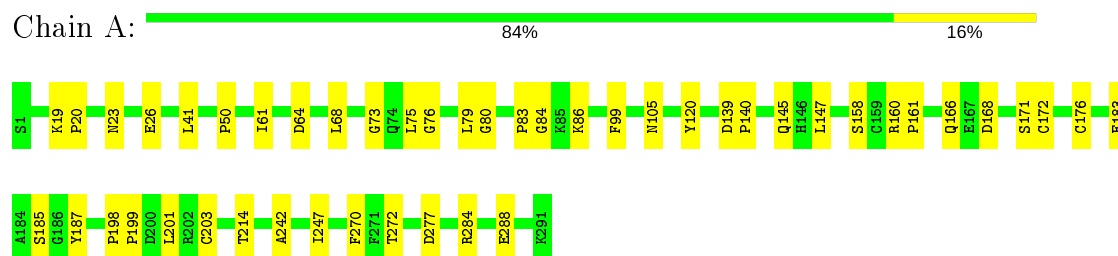


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	C	1	Total	C	N	O	0	0
			9	6	2	1		

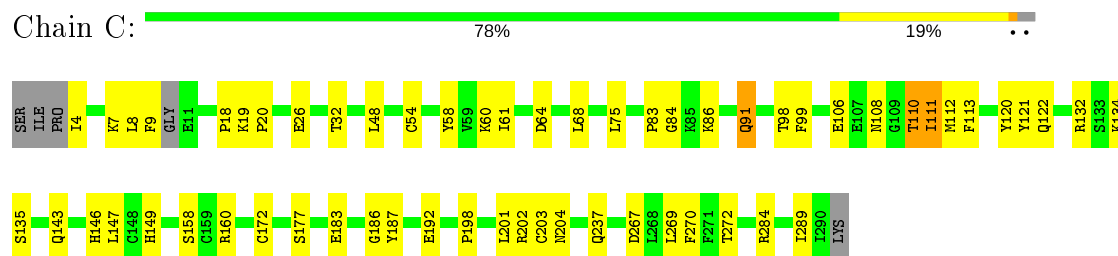
3 Residue-property plots

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. 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. 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.

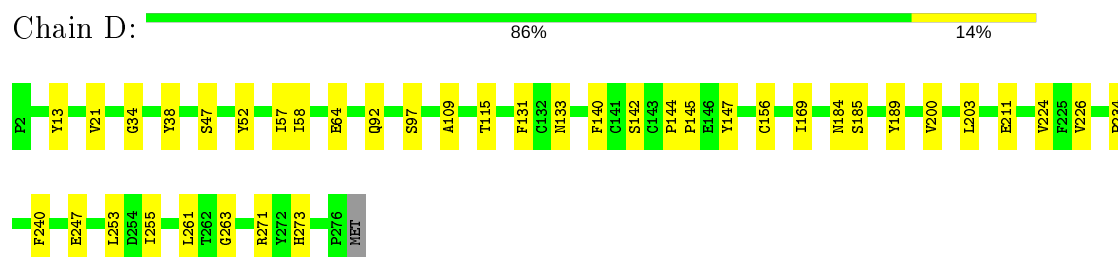
- Molecule 1: Complement C1r subcomponent



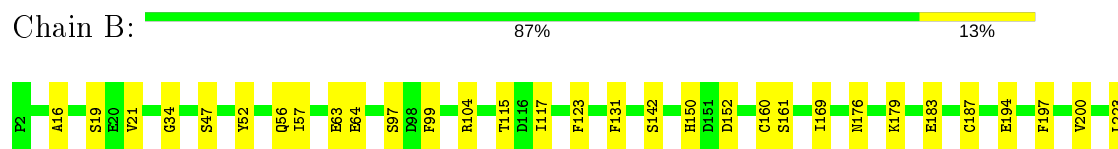
- Molecule 1: Complement C1r subcomponent



- Molecule 2: Complement C1s subcomponent



- Molecule 2: Complement C1s subcomponent

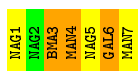




- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-beta-D-galactopyranose-(1-4)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.21Å 88.34Å 197.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.64 – 4.50 80.64 – 4.50	Depositor EDS
% Data completeness (in resolution range)	97.1 (80.64-4.50) 97.4 (80.64-4.50)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 4.47Å)	Xtriage
Refinement program	PHENIX dev_2722	Depositor
R, R_{free}	0.303 , 0.340 0.335 , 0.370	Depositor DCC
R_{free} test set	485 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å ²)	151.5	Xtriage
Anisotropy	0.930	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 167.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.077 for k,h,-l	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	9318	wwPDB-VP
Average B, all atoms (Å ²)	255.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.26% 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, NA, CA, GAL, 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	0.26	0/2393	0.47	0/3243
1	C	0.27	0/2357	0.49	0/3193
2	B	0.26	0/2251	0.47	0/3060
2	D	0.27	0/2241	0.50	0/3047
All	All	0.26	0/9242	0.48	0/12543

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	2328	0	2192	30	0
1	C	2294	0	2149	46	0
2	B	2188	0	2016	20	0
2	D	2178	0	2000	25	0
3	E	86	0	73	1	0
4	F	86	0	73	4	0
5	G	39	0	34	5	0
5	H	39	0	34	2	0
5	I	39	0	32	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	3	0	0	0	0
6	B	3	0	0	0	0
6	C	3	0	0	0	0
6	D	3	0	0	0	0
7	A	1	0	0	0	0
7	B	2	0	0	0	0
7	C	1	0	0	0	0
7	D	2	0	0	0	0
8	A	14	0	13	0	0
9	C	9	0	12	1	0
All	All	9318	0	8628	121	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 7.

The worst 5 of 121 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:145:GLN:NE2	1:A:172:CYS:SG	2.54	0.81
1:C:26:GLU:HA	1:C:99:PHE:O	1.87	0.75
1:C:106:GLU:HG3	1:C:112:MET:HB2	1.71	0.71
1:C:203:CYS:HB2	1:C:270:PHE:HB3	1.73	0.70
2:D:184:ASN:OD1	2:D:261:LEU:HA	1.94	0.67

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	289/291 (99%)	258 (89%)	31 (11%)	0	100	100
1	C	282/291 (97%)	253 (90%)	29 (10%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	274/276 (99%)	265 (97%)	9 (3%)	0	100	100
2	D	273/276 (99%)	262 (96%)	11 (4%)	0	100	100
All	All	1118/1134 (99%)	1038 (93%)	80 (7%)	0	100	100

There are no Ramachandran outliers to report.

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	261/261 (100%)	260 (100%)	1 (0%)	91	94
1	C	257/261 (98%)	252 (98%)	5 (2%)	57	75
2	B	242/242 (100%)	240 (99%)	2 (1%)	81	89
2	D	240/242 (99%)	239 (100%)	1 (0%)	91	94
All	All	1000/1006 (99%)	991 (99%)	9 (1%)	78	87

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	111	ILE
2	B	200	VAL
2	D	156	CYS
1	C	108	ASN
1	C	237	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	ASN

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 ⓘ

23 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	E	1	1,3	14,14,15	0.18	0	17,19,21	0.39	0
3	NAG	E	2	3	14,14,15	0.60	1 (7%)	17,19,21	0.79	0
3	BMA	E	3	3	11,11,12	1.21	1 (9%)	15,15,17	1.30	2 (13%)
3	MAN	E	4	3	11,11,12	0.94	1 (9%)	15,15,17	1.35	2 (13%)
3	GAL	E	5	3	11,11,12	1.07	1 (9%)	15,15,17	1.69	5 (33%)
3	NAG	E	6	3	14,14,15	0.56	0	17,19,21	0.44	0
3	MAN	E	7	3	11,11,12	0.90	1 (9%)	15,15,17	1.33	2 (13%)
4	NAG	F	1	4	14,14,15	0.33	0	17,19,21	0.71	0
4	NAG	F	2	4	14,14,15	0.42	0	17,19,21	0.55	0
4	BMA	F	3	4	11,11,12	1.24	1 (9%)	15,15,17	0.84	0
4	MAN	F	4	4	11,11,12	1.15	2 (18%)	15,15,17	1.26	2 (13%)
4	NAG	F	5	4	14,14,15	0.33	0	17,19,21	0.50	0
4	GAL	F	6	4	11,11,12	0.76	0	15,15,17	1.19	1 (6%)
4	MAN	F	7	4	11,11,12	0.80	0	15,15,17	1.26	2 (13%)
5	NAG	G	1	1,5	14,14,15	0.23	0	17,19,21	0.63	0
5	NAG	G	2	5	14,14,15	0.29	0	17,19,21	0.44	0
5	BMA	G	3	5	11,11,12	0.90	0	15,15,17	1.57	1 (6%)
5	NAG	H	1	2,5	14,14,15	0.46	0	17,19,21	0.92	2 (11%)
5	NAG	H	2	5	14,14,15	0.33	0	17,19,21	0.58	0
5	BMA	H	3	5	11,11,12	0.96	0	15,15,17	0.94	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	I	1	2,5	14,14,15	0.66	0	17,19,21	1.04	1 (5%)
5	NAG	I	2	5	14,14,15	0.42	0	17,19,21	1.24	1 (5%)
5	BMA	I	3	5	11,11,12	1.33	1 (9%)	15,15,17	1.69	3 (20%)

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

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	3	BMA	C2-C3	2.91	1.56	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	4	MAN	C1-C2	2.68	1.58	1.52
3	E	3	BMA	O3-C3	2.66	1.49	1.43
4	F	3	BMA	C2-C3	2.48	1.56	1.52
3	E	5	GAL	C4-C3	2.38	1.58	1.52

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	2	NAG	C1-O5-C5	4.60	118.42	112.19
5	G	3	BMA	C1-O5-C5	4.57	118.39	112.19
5	I	3	BMA	C1-C2-C3	4.22	114.86	109.67
3	E	5	GAL	C1-O5-C5	3.96	117.56	112.19
5	I	1	NAG	C1-O5-C5	3.84	117.40	112.19

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	4	MAN	C4-C5-C6-O6
4	F	4	MAN	C4-C5-C6-O6
3	E	4	MAN	O5-C5-C6-O6
4	F	4	MAN	O5-C5-C6-O6
5	I	1	NAG	O5-C5-C6-O6

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	4	MAN	C1-C2-C3-C4-C5-O5
4	F	7	MAN	C1-C2-C3-C4-C5-O5

13 monomers are involved in 14 short contacts:

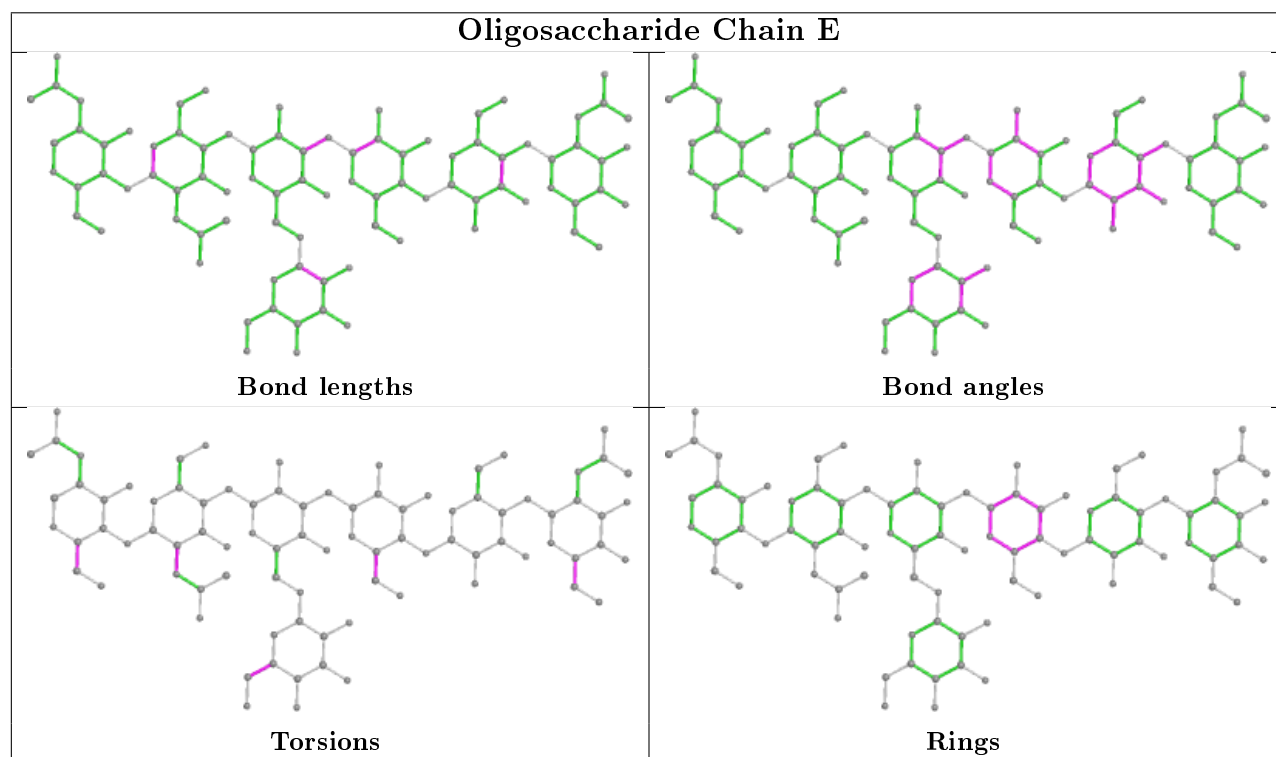
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	I	1	NAG	2	0
5	H	2	NAG	1	0
4	F	5	NAG	1	0
5	G	1	NAG	4	0
4	F	4	MAN	2	0
4	F	1	NAG	1	0
4	F	6	GAL	1	0
5	I	2	NAG	1	0

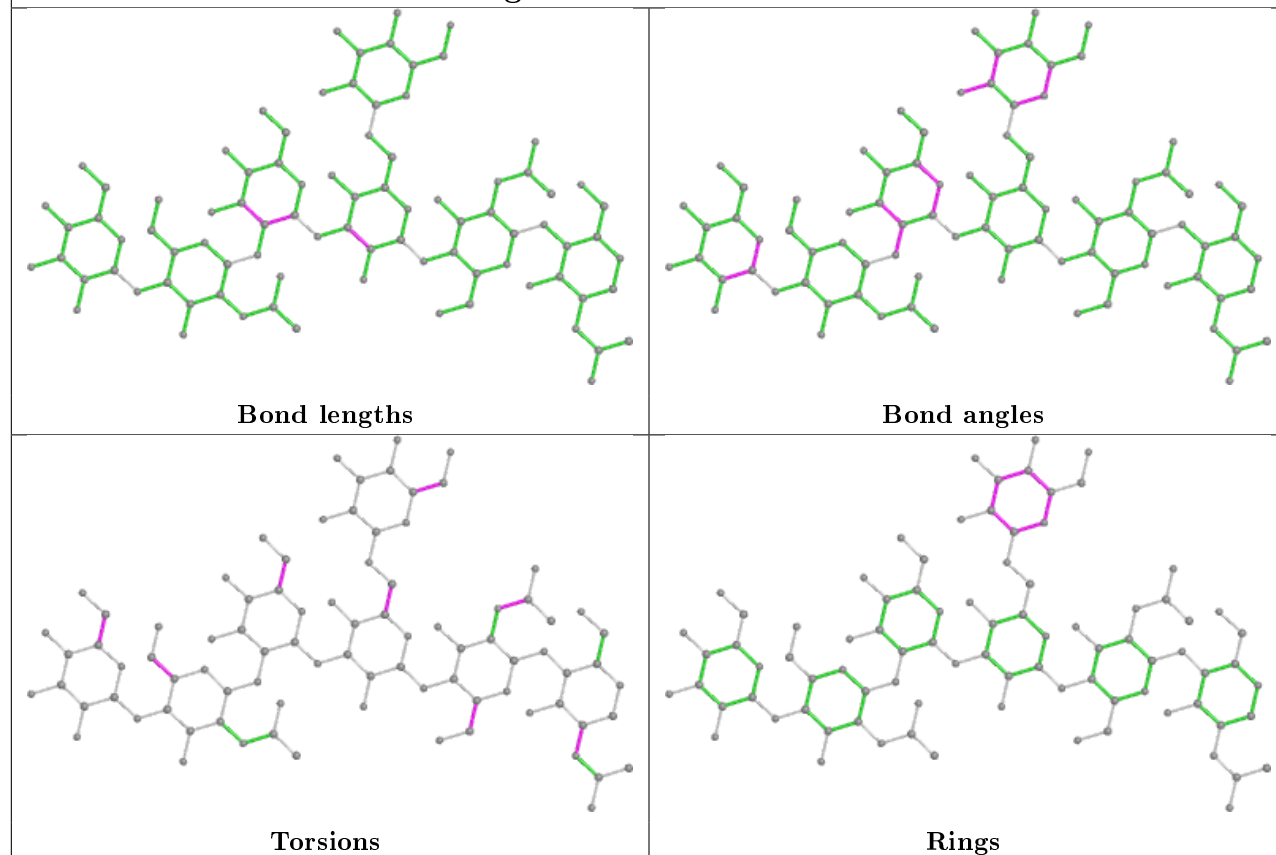
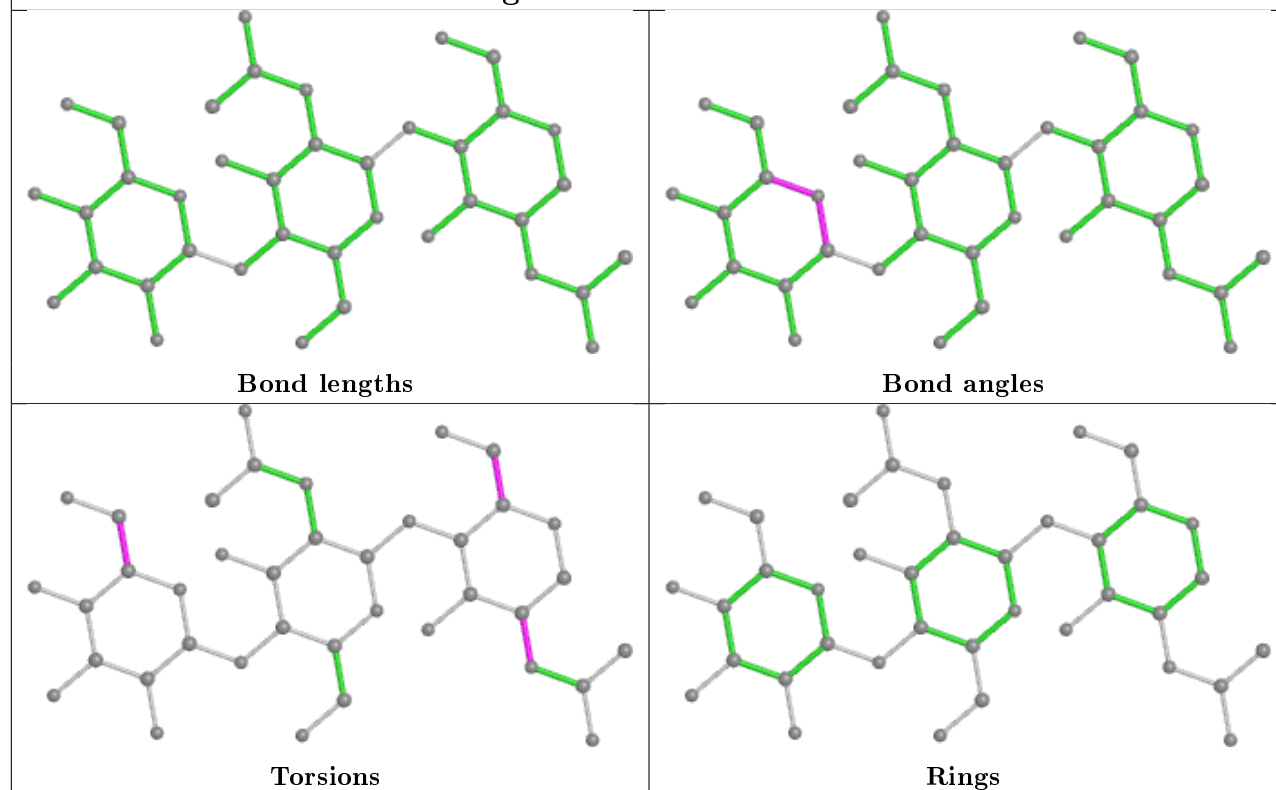
Continued on next page...

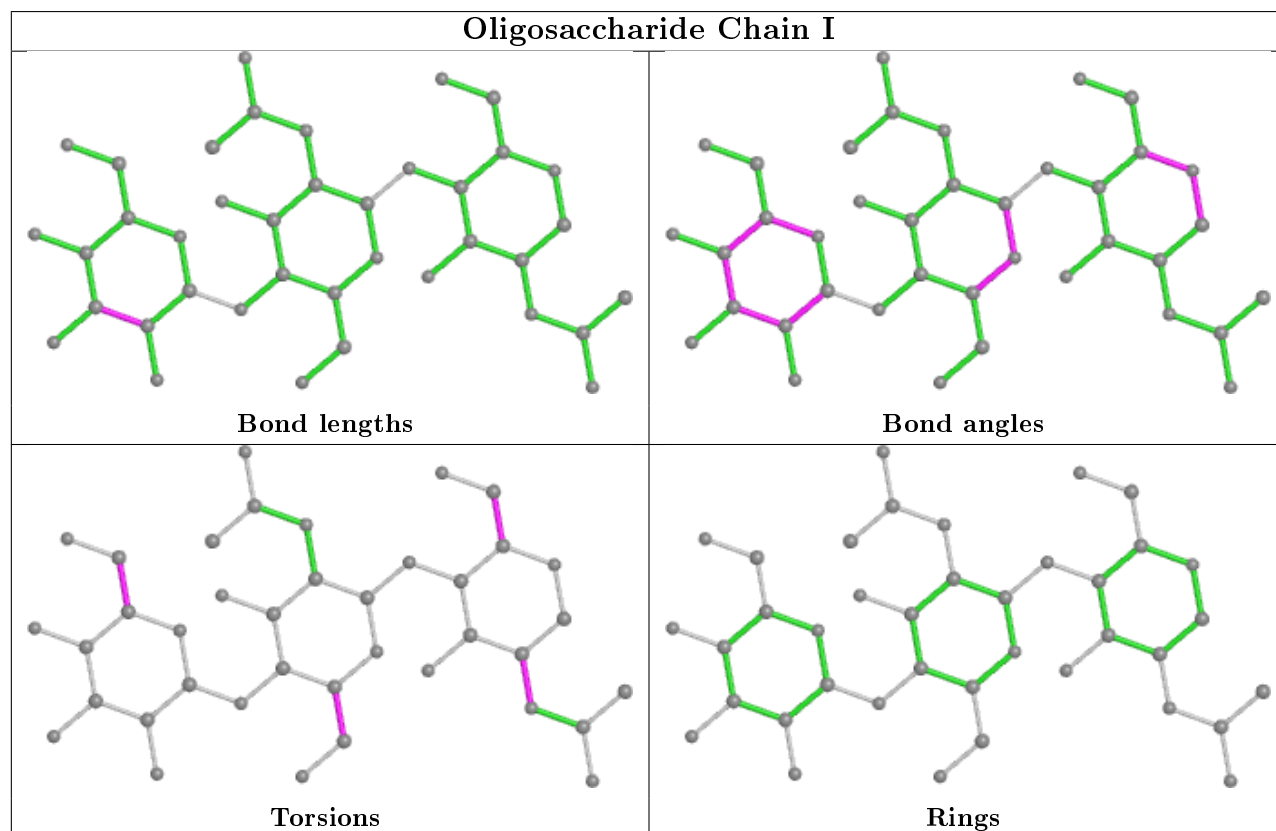
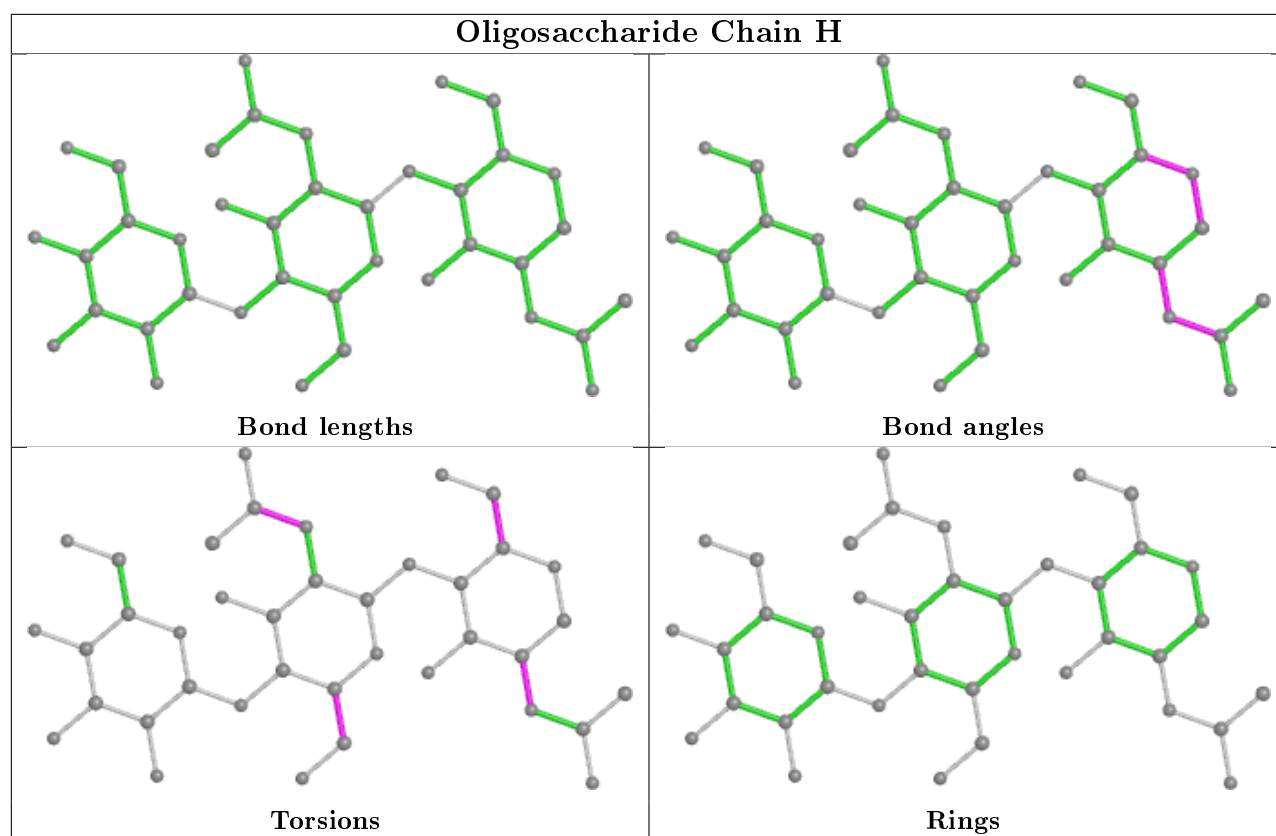
Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	G	2	NAG	2	0
5	G	3	BMA	1	0
5	H	1	NAG	1	0
4	F	3	BMA	1	0
3	E	2	NAG	1	0

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



Oligosaccharide Chain F**Oligosaccharide Chain G**



5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 18 are monoatomic - leaving 2 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$
8	NAG	A	305	1	14,14,15	0.47	0	17,19,21	0.75	1 (5%)

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
8	NAG	A	305	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	305	NAG	C1-O5-C5	2.70	115.85	112.19

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

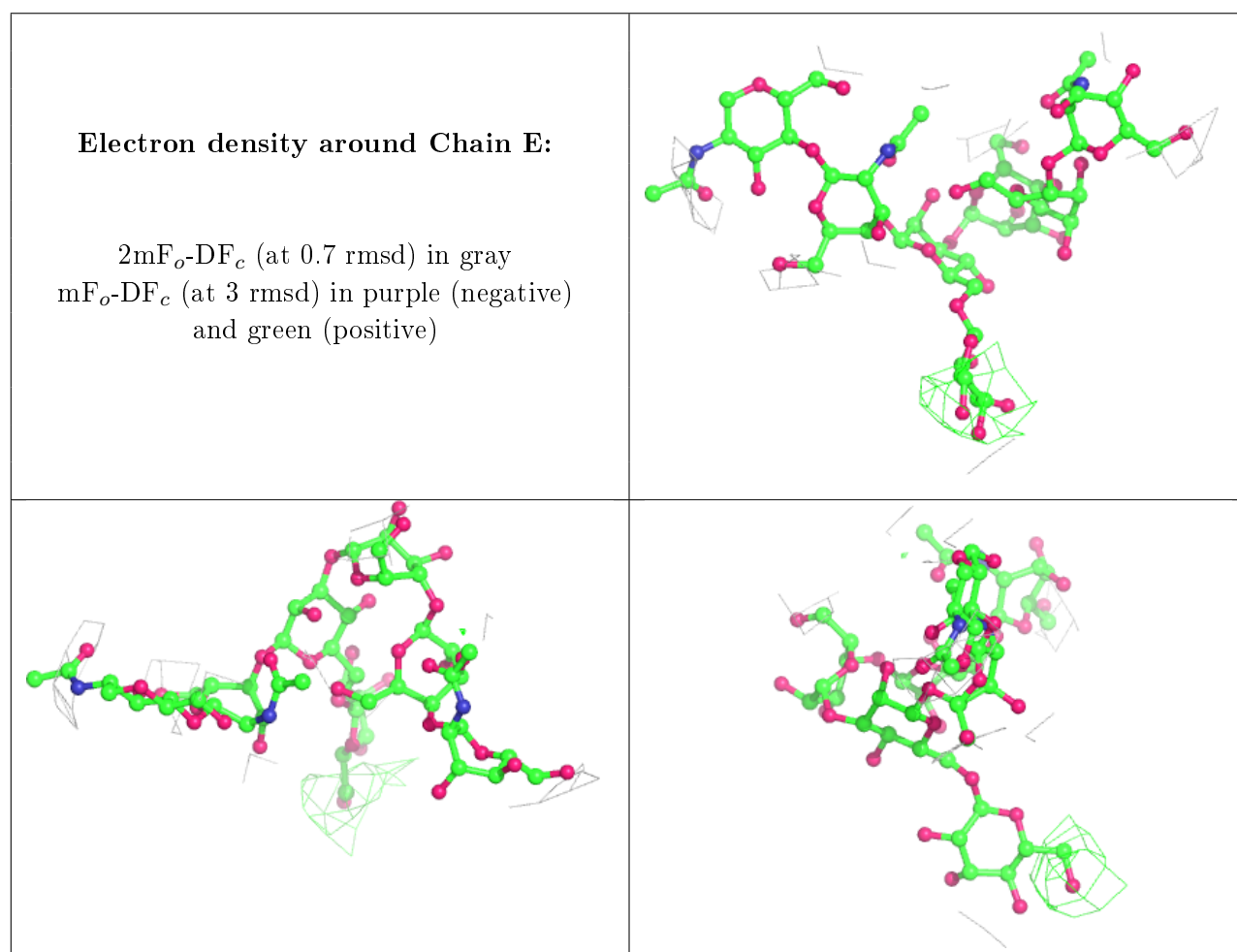
6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

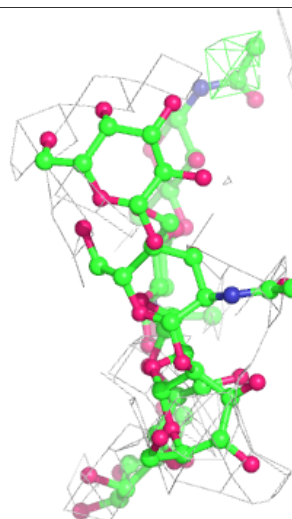
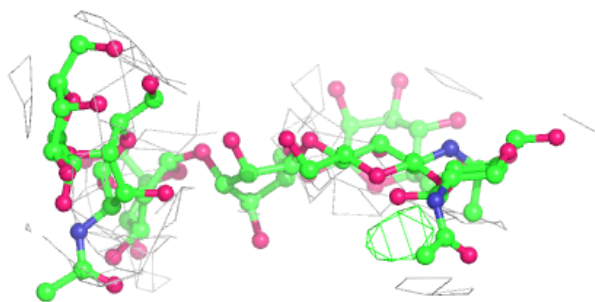
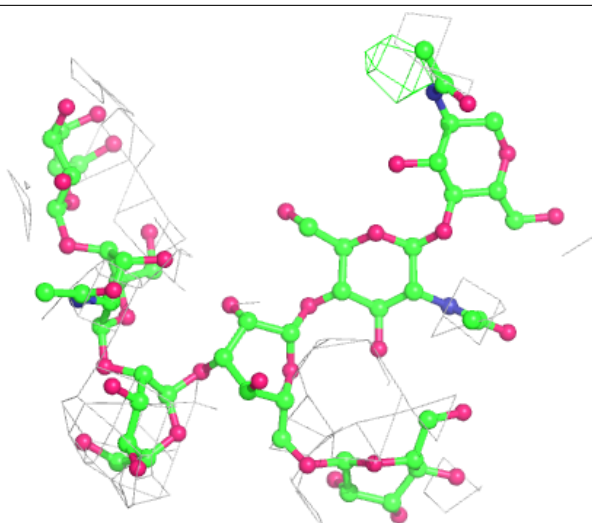
Unable to reproduce the depositors R factor - this section is therefore empty.

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.



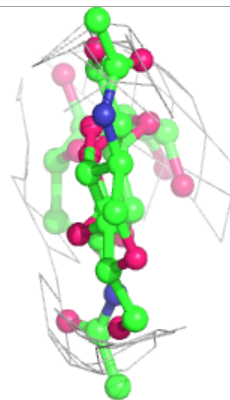
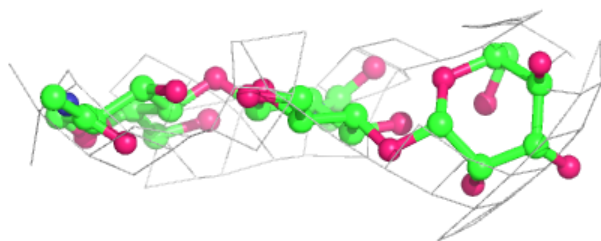
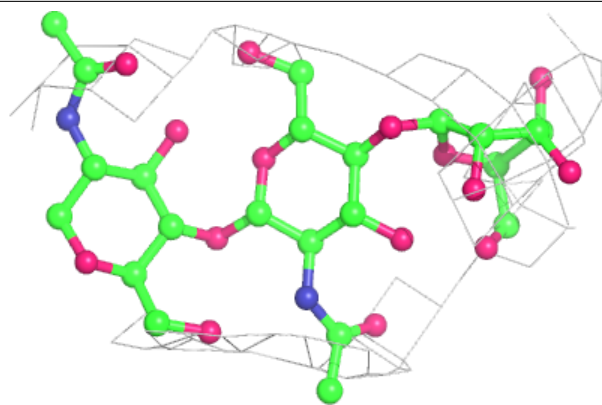
Electron density around Chain F:

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



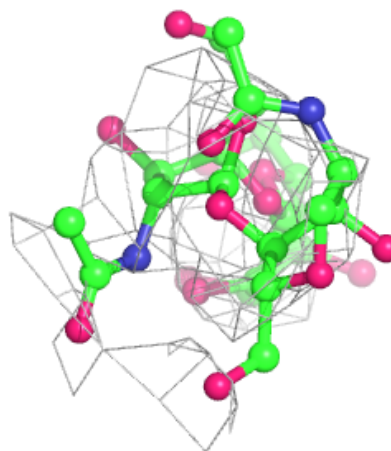
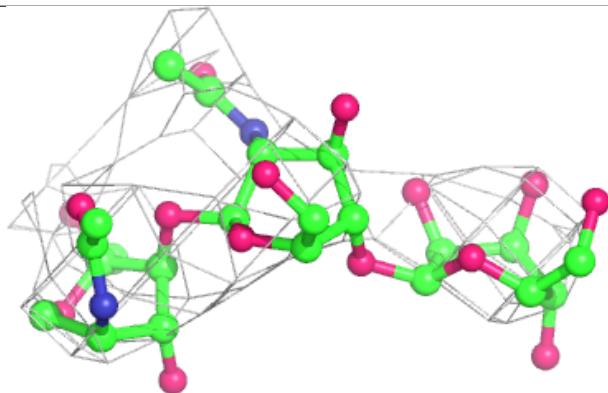
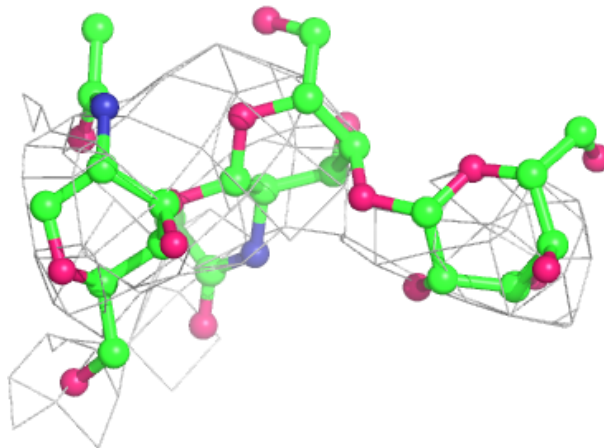
Electron density around Chain G:

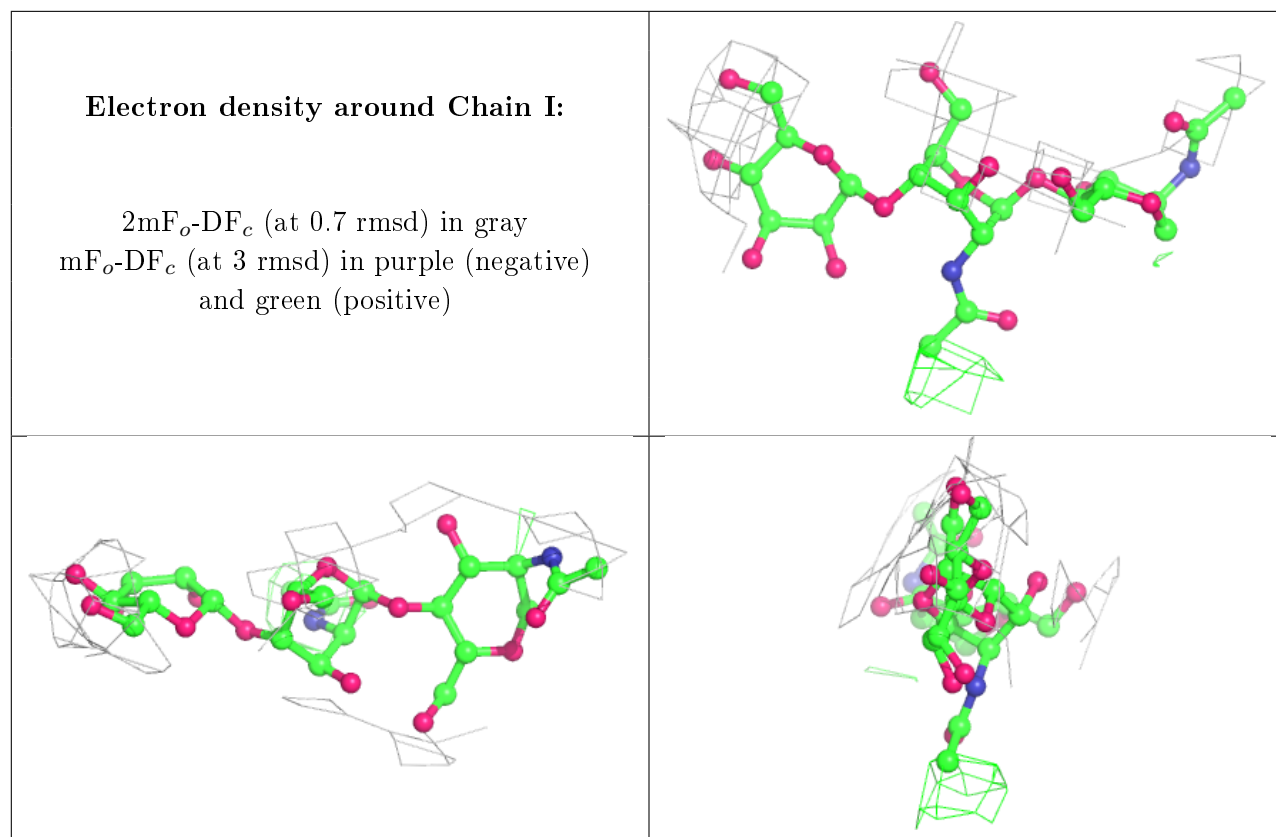
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.