Full wwPDB X-ray Structure Validation Report (i)

Mar 29, 2021 – 12:12 pm BST

PDB ID	:	6ZZW
Title	:	Structure of the N terminal domain of Bc2L-C lectin (1-131) in complex with Globo H (H-type 3) and CAS No 912569-62-1
Authors	:	Lal, K.; Bermeo, R.; Imberty, A.; Varrot, A.
Deposited on	:	2020-08-05
Resolution	:	1.90 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

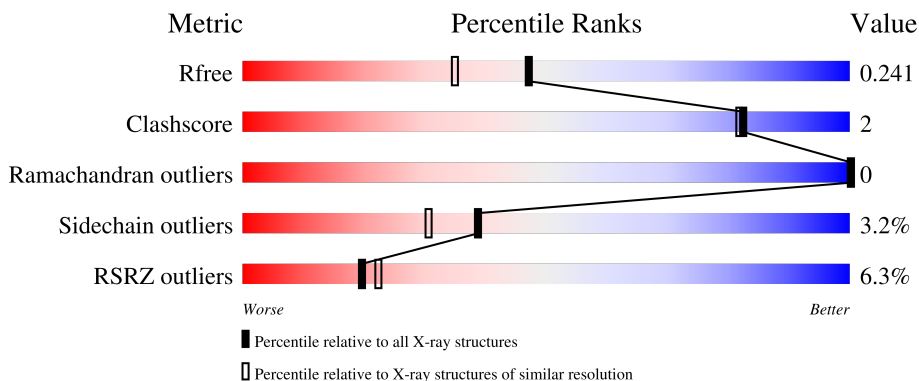|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.18
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.18

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 1.90 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.
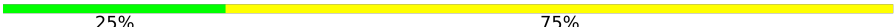
Metric	Percentile Ranks	Value
Rfree		0.241
Clashscore		2
Ramachandran outliers		0
Sidechain outliers		3.2%
RSRZ outliers		6.3%

Worse ◀ ▶ *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	134	5% / 92% / 6% •
1	B	134	8% / 90% / 10% •
1	C	134	5% / 89% / 9% •
2	D	5	100%
2	E	5	20% / 60% / 20%

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Mol	Chain	Length	Quality of chain
3	F	4	

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3296 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 Lectin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	131	Total	C	N	O	S	0	1	0
			962	621	154	183	4			
1	C	131	Total	C	N	O	S	0	0	0
			951	610	154	184	3			
1	B	133	Total	C	N	O	S	0	0	0
			971	625	157	185	4			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP B4EH86
A	-1	HIS	-	expression tag	UNP B4EH86
C	-2	GLY	-	expression tag	UNP B4EH86
C	-1	HIS	-	expression tag	UNP B4EH86
B	-2	GLY	-	expression tag	UNP B4EH86
B	-1	HIS	-	expression tag	UNP B4EH86

- Molecule 2 is an oligosaccharide called alpha-L-fucopyranose-(1-2)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-3)-alpha-D-galactopyranose-(1-4)-beta-D-galactopyranose.
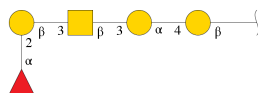
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	5	Total	C	N	O	0	0	0
			58	32	1	25			
2	E	5	Total	C	N	O	0	0	0
			58	32	1	25			

- Molecule 3 is an oligosaccharide called alpha-L-fucopyranose-(1-2)-beta-D-galactopyranose-

(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-3)-alpha-D-galactopyranose.
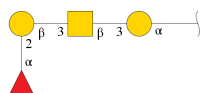
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	4	Total	C	N	O	0	0	0
			47	26	1	20			

- Molecule 4 is [3-(2-methylimidazol-1-yl)phenyl]methanamine (three-letter code: QT5) (formula: $C_{11}H_{13}N_3$) (labeled as "Ligand of Interest" by depositor).
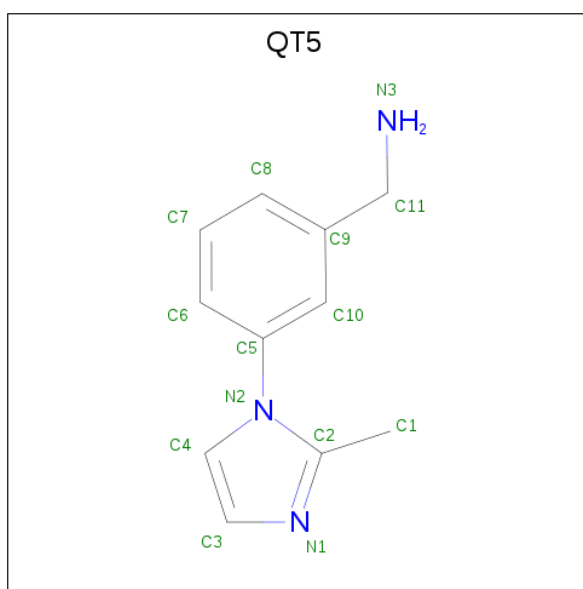
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			14	11	3		
4	C	1	Total	C	N	0	0
			14	11	3		
4	B	1	Total	C	N	0	0
			14	11	3		

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	64	Total 69	O 69	0	5
6	C	66	Total 72	O 72	0	6
6	B	62	Total 65	O 65	0	3

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: Lectin
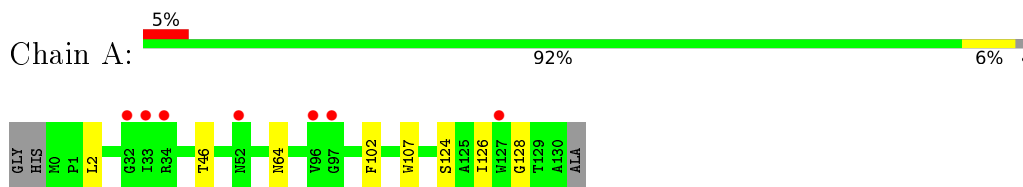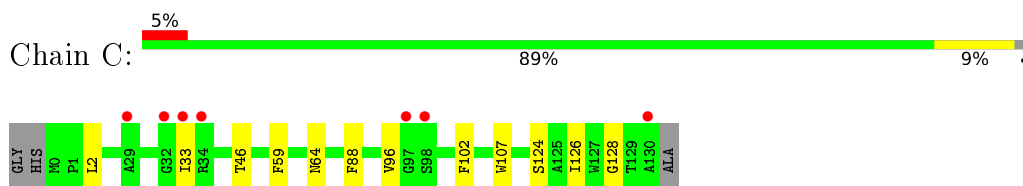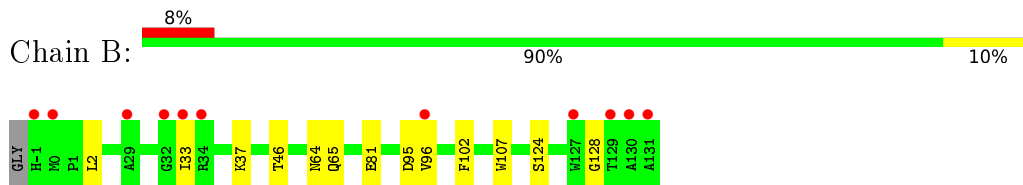
Chain A:

- Molecule 1: Lectin

Chain C:

- Molecule 1: Lectin

Chain B:

- Molecule 2: alpha-L-fucopyranose-(1-2)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-3)-alpha-D-galactopyranose-(1-4)-beta-D-galactopyranose

Chain D:
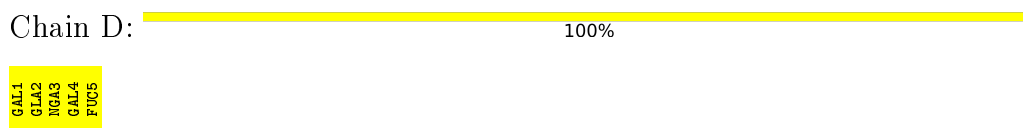
- Molecule 2: alpha-L-fucopyranose-(1-2)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-3)-alpha-D-galactopyranose-(1-4)-beta-D-galactopyranose
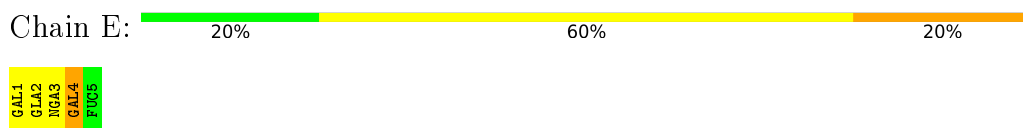
Chain E:

● Molecule 3: alpha-L-fucopyranose-(1-2)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-3)-alpha-D-galactopyranose

Chain F:

	25%	75%

GLA1 NGA2 GAL3 FUC4

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	74.46Å 42.91Å 103.34Å 90.00° 96.10° 90.00°	Depositor
Resolution (Å)	37.13 – 1.90 37.13 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.4 (37.13-1.90) 98.4 (37.13-1.90)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	3.32 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.181 , 0.238 0.190 , 0.241	Depositor DCC
R_{free} test set	1224 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å^2)	18.1	Xtriage
Anisotropy	0.486	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.44 , 60.1	EDS
L-test for twinning[2]	$<|L|> = 0.51$, $<L^2> = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	3296	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.16% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1] Intensities estimated from amplitudes.
[2] Theoretical values of $<|L|>$, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GLA, GAL, NGA, NA, QT5, FUC

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	0.81	0/988	0.86	0/1352
1	B	0.81	1/994 (0.1%)	0.91	0/1360
1	C	0.75	0/972	0.89	0/1331
All	All	0.79	1/2954 (0.0%)	0.89	0/4043

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	81	GLU	CD-OE2	-6.75	1.18	1.25

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	962	0	962	4	0
1	B	971	0	966	6	0
1	C	951	0	946	8	0
2	D	58	0	51	0	0
2	E	58	0	51	1	0
3	F	47	0	42	0	0
4	A	14	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	14	0	0	1	0
4	C	14	0	0	1	0
5	A	1	0	0	0	0
6	A	69	0	0	0	0
6	B	65	0	0	0	0
6	C	72	0	0	2	0
All	All	3296	0	3018	15	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 2.

All (15) 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:2:LEU:HD13	1:C:128:GLY:HA3	1.62	0.81
1:C:2:LEU:HD13	1:B:128:GLY:HA3	1.63	0.79
1:A:128:GLY:HA3	1:B:2:LEU:HD13	1.78	0.65
1:B:64:ASN:HB3	1:B:102:PHE:CE2	2.40	0.56
1:B:33:ILE:HG22	1:B:96:VAL:HG11	1.88	0.56
1:B:37:LYS:HE2	1:B:95:ASP:OD1	2.11	0.51
4:B:201:QT5:C1	2:E:4:GAL:O3	2.59	0.51
1:C:2:LEU:CD1	1:B:128:GLY:HA3	2.39	0.50
1:C:64:ASN:HB3	1:C:102:PHE:CE2	2.47	0.48
1:C:126:ILE:HG12	6:C:310:HOH:O	2.13	0.48
1:A:64:ASN:HB3	1:A:102:PHE:CE2	2.49	0.47
4:C:201:QT5:N1	6:C:305:HOH:O	2.36	0.46
1:C:33:ILE:HG22	1:C:96:VAL:HG11	1.98	0.45
1:A:126:ILE:HD13	1:C:126:ILE:HG21	2.00	0.43
1:C:59:PHE:HB2	1:C:88:PHE:CE2	2.56	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	130/134 (97%)	127 (98%)	3 (2%)	0	100	100
1	B	131/134 (98%)	127 (97%)	4 (3%)	0	100	100
1	C	129/134 (96%)	126 (98%)	3 (2%)	0	100	100
All	All	390/402 (97%)	380 (97%)	10 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2   Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	104/106 (98%)	101 (97%)	3 (3%)	42	35
1	B	103/106 (97%)	99 (96%)	4 (4%)	32	23
1	C	102/106 (96%)	99 (97%)	3 (3%)	42	35
All	All	309/318 (97%)	299 (97%)	10 (3%)	39	30

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	THR
1	A	107	TRP
1	A	124	SER
1	C	46	THR
1	C	107	TRP
1	C	124	SER
1	B	46	THR
1	B	65	GLN
1	B	107	TRP
1	B	124	SER

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)

14 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	D	1	2	12,12,12	0.84	0	17,17,17	2.33	8 (47%)
2	GLA	D	2	2	11,11,12	1.12	1 (9%)	15,15,17	1.75	3 (20%)
2	NGA	D	3	2	14,14,15	0.86	0	17,19,21	1.57	4 (23%)
2	GAL	D	4	2	11,11,12	1.40	1 (9%)	15,15,17	1.05	1 (6%)
2	FUC	D	5	2	10,10,11	1.41	3 (30%)	14,14,16	0.95	1 (7%)
2	GAL	E	1	2	12,12,12	0.71	0	17,17,17	1.80	3 (17%)
2	GLA	E	2	2	11,11,12	0.92	0	15,15,17	2.26	7 (46%)
2	NGA	E	3	2	14,14,15	0.58	0	17,19,21	2.71	5 (29%)
2	GAL	E	4	2	11,11,12	1.26	2 (18%)	15,15,17	1.28	4 (26%)
2	FUC	E	5	2	10,10,11	1.01	0	14,14,16	1.05	0
3	GLA	F	1	3	12,12,12	0.54	0	17,17,17	0.84	0
3	NGA	F	2	3	14,14,15	1.12	1 (7%)	17,19,21	1.96	7 (41%)
3	GAL	F	3	3	11,11,12	1.86	3 (27%)	15,15,17	1.24	1 (6%)
3	FUC	F	4	3	10,10,11	0.91	1 (10%)	14,14,16	1.40	2 (14%)

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	D	1	2	-	2/2/22/22	0/1/1/1
2	GLA	D	2	2	-	2/2/19/22	0/1/1/1
2	NGA	D	3	2	-	2/6/23/26	0/1/1/1
2	GAL	D	4	2	-	2/2/19/22	0/1/1/1
2	FUC	D	5	2	-	-	0/1/1/1
2	GAL	E	1	2	-	2/2/22/22	0/1/1/1
2	GLA	E	2	2	-	0/2/19/22	0/1/1/1
2	NGA	E	3	2	-	0/6/23/26	0/1/1/1
2	GAL	E	4	2	-	0/2/19/22	0/1/1/1
2	FUC	E	5	2	-	-	0/1/1/1
3	GLA	F	1	3	-	0/2/22/22	0/1/1/1
3	NGA	F	2	3	-	2/6/23/26	0/1/1/1
3	GAL	F	3	3	-	0/2/19/22	0/1/1/1
3	FUC	F	4	3	-	-	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	3	GAL	O5-C5	-3.60	1.36	1.43
2	D	4	GAL	O5-C1	-3.57	1.38	1.43
3	F	3	GAL	C2-C3	-3.38	1.47	1.52
3	F	2	NGA	C1-C2	3.33	1.57	1.52
2	D	5	FUC	O5-C1	2.71	1.48	1.43
2	E	4	GAL	O5-C5	-2.70	1.38	1.43
2	D	5	FUC	O4-C4	2.53	1.48	1.43
3	F	3	GAL	O5-C1	-2.50	1.39	1.43
2	D	2	GLA	O2-C2	2.29	1.48	1.43
3	F	4	FUC	O2-C2	-2.24	1.38	1.43
2	D	5	FUC	C4-C3	2.05	1.57	1.52
2	E	4	GAL	O5-C1	-2.03	1.40	1.43

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	3	NGA	C1-O5-C5	-8.89	100.15	112.19
2	D	1	GAL	O4-C4-C3	-4.94	98.93	110.35
2	E	1	GAL	C3-C4-C5	-4.55	102.12	110.24
2	E	2	GLA	C1-O5-C5	-4.54	106.05	112.19
2	D	1	GAL	O4-C4-C5	4.20	119.74	109.30
2	E	3	NGA	O5-C5-C6	4.19	113.78	107.20
3	F	2	NGA	C2-N2-C7	-3.78	117.52	122.90
2	D	2	GLA	O4-C4-C3	3.65	118.78	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	2	GLA	O3-C3-C4	-3.64	101.93	110.35
2	D	3	NGA	O3-C3-C4	-3.33	102.65	110.35
2	D	2	GLA	C2-C3-C4	3.12	116.30	110.89
2	E	2	GLA	C1-C2-C3	3.10	113.48	109.67
2	D	1	GAL	C4-C3-C2	-3.10	105.41	110.82
3	F	2	NGA	O5-C1-C2	-3.08	106.43	111.29
3	F	2	NGA	O3-C3-C4	-3.07	103.25	110.35
2	E	1	GAL	O1-C1-C2	3.02	117.54	109.03
2	D	3	NGA	O3-C3-C2	3.01	115.70	109.47
3	F	4	FUC	C2-C3-C4	-2.99	105.72	110.89
2	D	1	GAL	O1-C1-C2	2.95	117.33	109.03
2	E	1	GAL	O5-C1-C2	-2.65	105.55	110.28
2	D	1	GAL	C3-C4-C5	-2.58	105.63	110.24
2	D	4	GAL	O2-C2-C3	-2.54	105.06	110.14
2	E	3	NGA	O3-C3-C4	-2.52	104.51	110.35
2	E	4	GAL	O3-C3-C2	-2.51	105.19	109.99
3	F	4	FUC	C3-C4-C5	2.50	113.66	109.77
2	E	2	GLA	C3-C4-C5	-2.45	105.87	110.24
2	D	1	GAL	O5-C1-C2	-2.41	105.99	110.28
3	F	3	GAL	O4-C4-C5	2.40	115.25	109.30
2	D	2	GLA	C1-O5-C5	2.37	115.40	112.19
2	E	3	NGA	O3-C3-C2	2.34	114.31	109.47
3	F	2	NGA	C1-O5-C5	2.34	115.36	112.19
2	D	3	NGA	C2-N2-C7	-2.32	119.61	122.90
2	D	1	GAL	O2-C2-C1	2.31	114.52	109.16
2	E	4	GAL	O5-C1-C2	2.18	114.13	110.77
3	F	2	NGA	O5-C5-C6	2.17	110.60	107.20
2	E	2	GLA	O3-C3-C2	2.17	114.14	109.99
2	E	2	GLA	C6-C5-C4	2.16	118.06	113.00
2	D	5	FUC	C2-C3-C4	-2.16	107.16	110.89
2	E	3	NGA	O5-C5-C4	-2.16	105.58	110.83
3	F	2	NGA	C8-C7-N2	2.15	119.73	116.10
3	F	2	NGA	C3-C4-C5	2.14	114.06	110.24
2	D	1	GAL	C6-C5-C4	2.11	117.95	113.00
2	E	4	GAL	O4-C4-C3	2.09	115.18	110.35
2	D	3	NGA	C6-C5-C4	-2.01	108.29	113.00
2	E	4	GAL	O2-C2-C1	-2.01	105.04	109.15
2	E	2	GLA	O5-C1-C2	-2.00	107.68	110.77

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	2	GLA	C4-C5-C6-O6
2	E	1	GAL	O5-C5-C6-O6
2	D	1	GAL	O5-C5-C6-O6
2	E	1	GAL	C4-C5-C6-O6
2	D	2	GLA	O5-C5-C6-O6
2	D	3	NGA	C4-C5-C6-O6
3	F	2	NGA	O5-C5-C6-O6
2	D	4	GAL	C4-C5-C6-O6
2	D	3	NGA	O5-C5-C6-O6
2	D	1	GAL	C4-C5-C6-O6
3	F	2	NGA	C4-C5-C6-O6
2	D	4	GAL	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	4	GAL	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 D

Bond lengths

Bond angles

Torsions

Rings

Oligosaccharide Chain F

Bond lengths — Bond angles — Torsions — Rings

Oligosaccharide Chain E

Bond lengths — Bond angles — Torsions — Rings
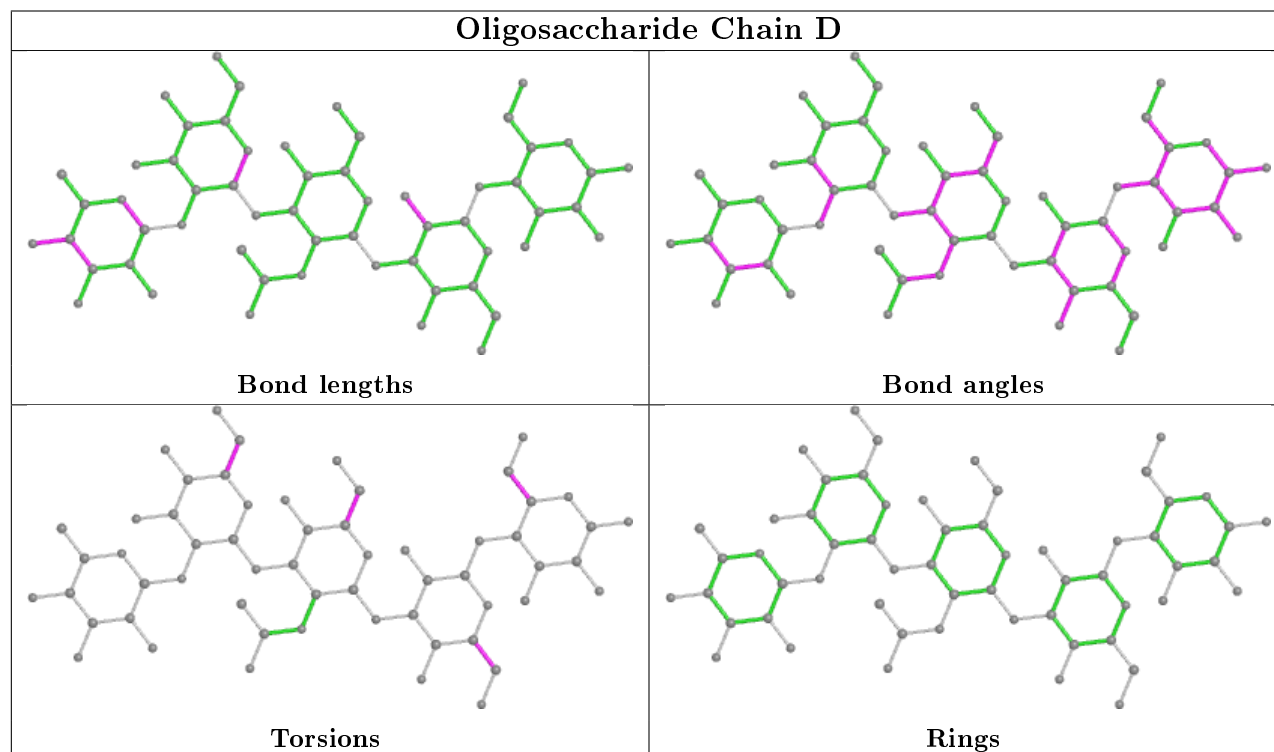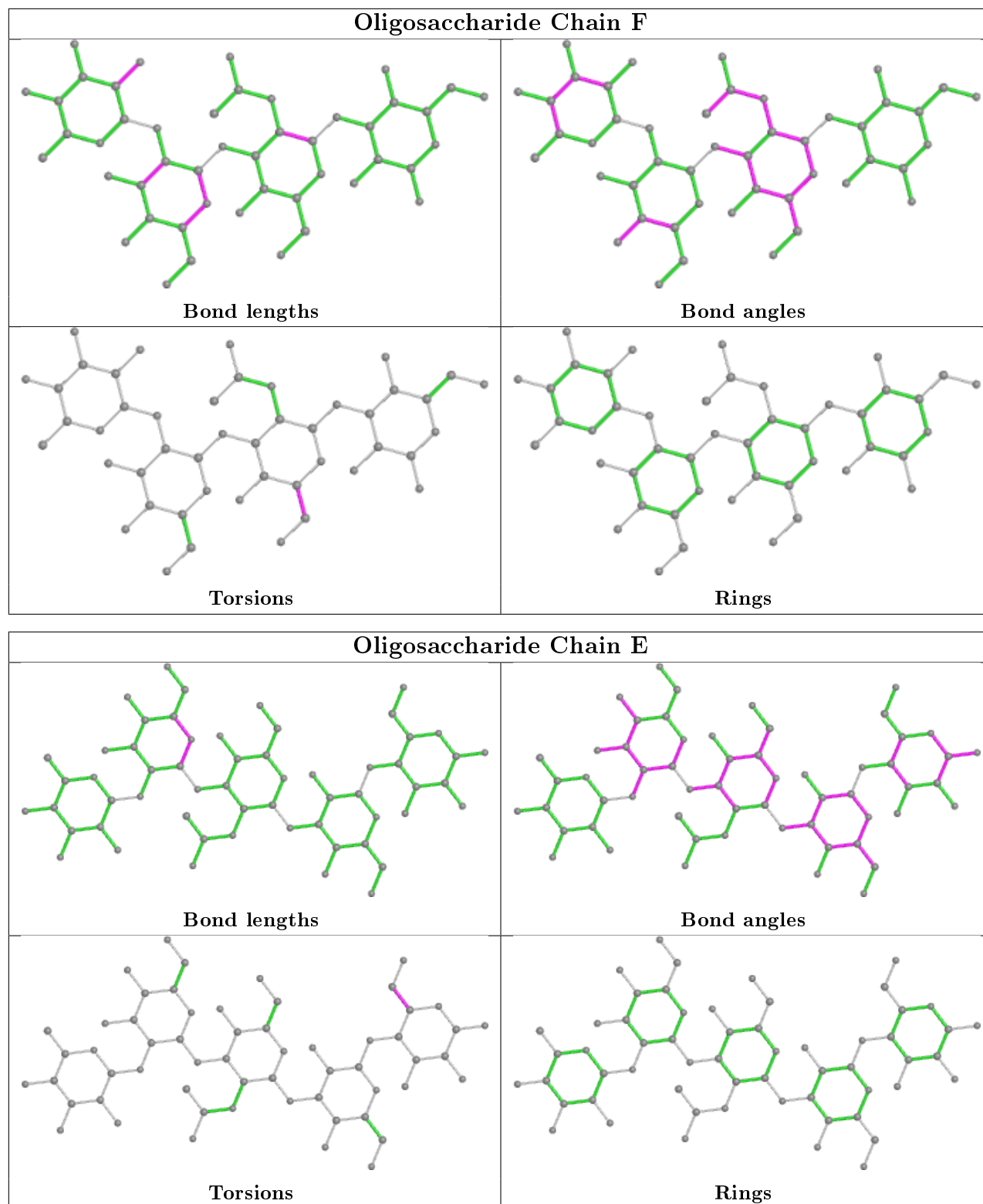
5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul

statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
4	QT5	B	201	-	15,15,15	0.90	1 (6%)	14,20,20	1.00	1 (7%)
4	QT5	C	201	-	15,15,15	0.66	1 (6%)	14,20,20	0.84	1 (7%)
4	QT5	A	201	-	15,15,15	0.68	0	14,20,20	0.85	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	QT5	B	201	-	-	0/6/6/6	0/2/2/2
4	QT5	C	201	-	-	0/6/6/6	0/2/2/2
4	QT5	A	201	-	-	0/6/6/6	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	201	QT5	C2-N2	2.92	1.41	1.37
4	C	201	QT5	C2-N2	2.11	1.40	1.37

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	201	QT5	C4-N2-C5	2.49	126.90	124.18
4	C	201	QT5	C4-N2-C5	2.07	126.44	124.18

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

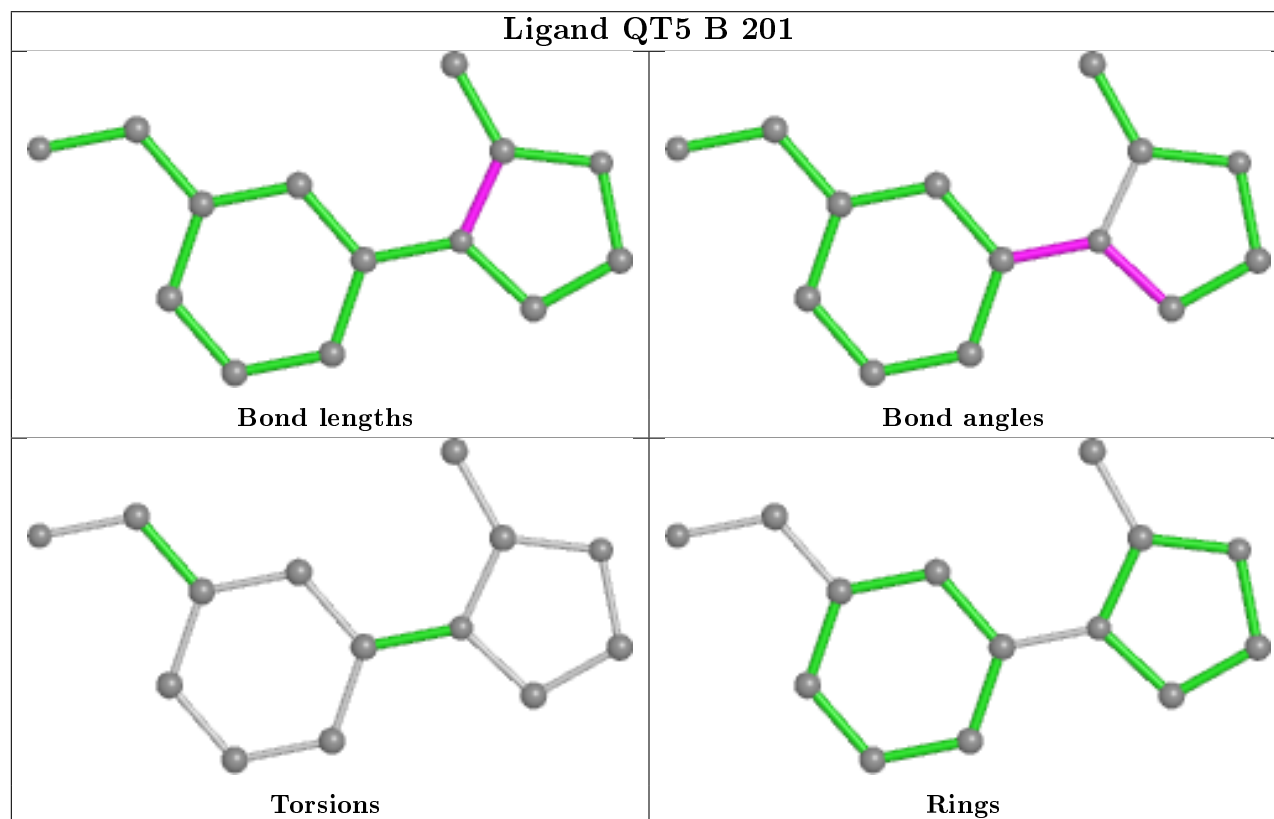2 monomers are involved in 2 short contacts:

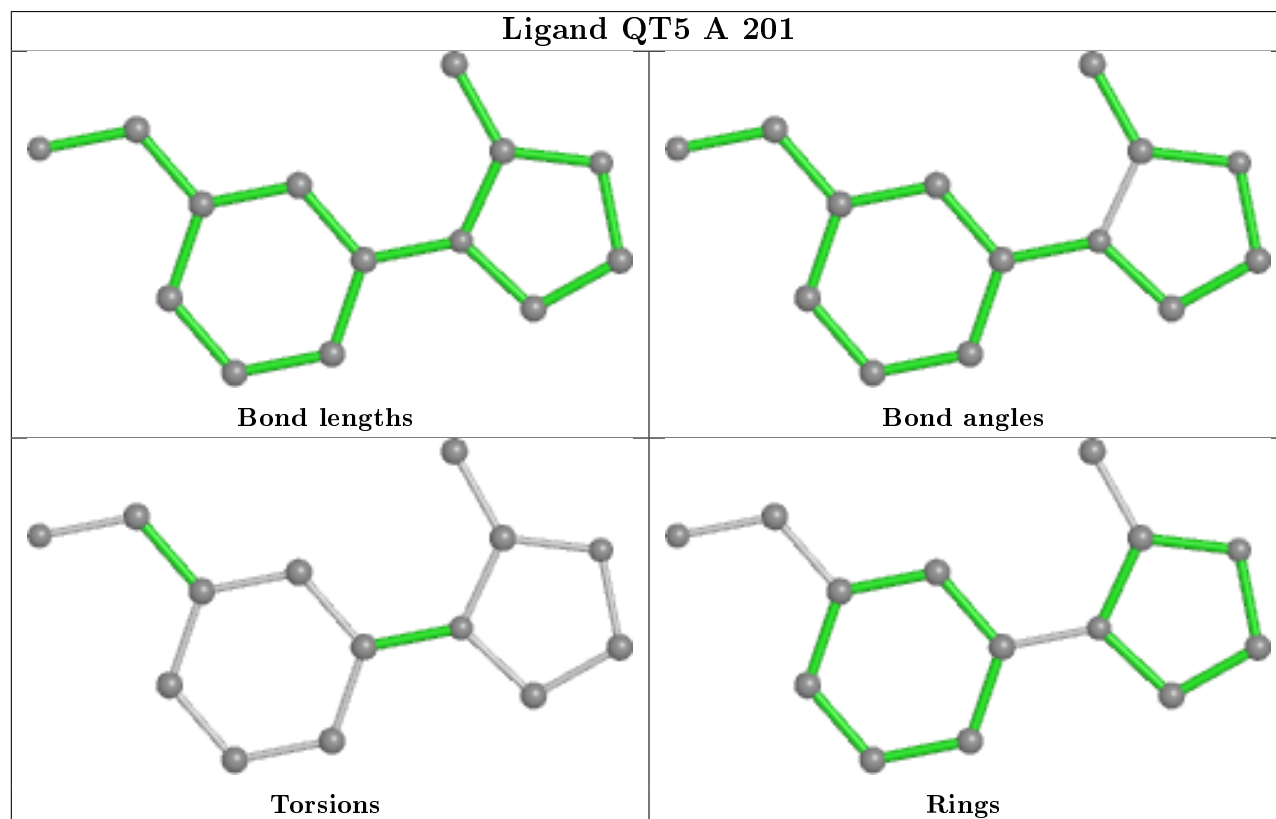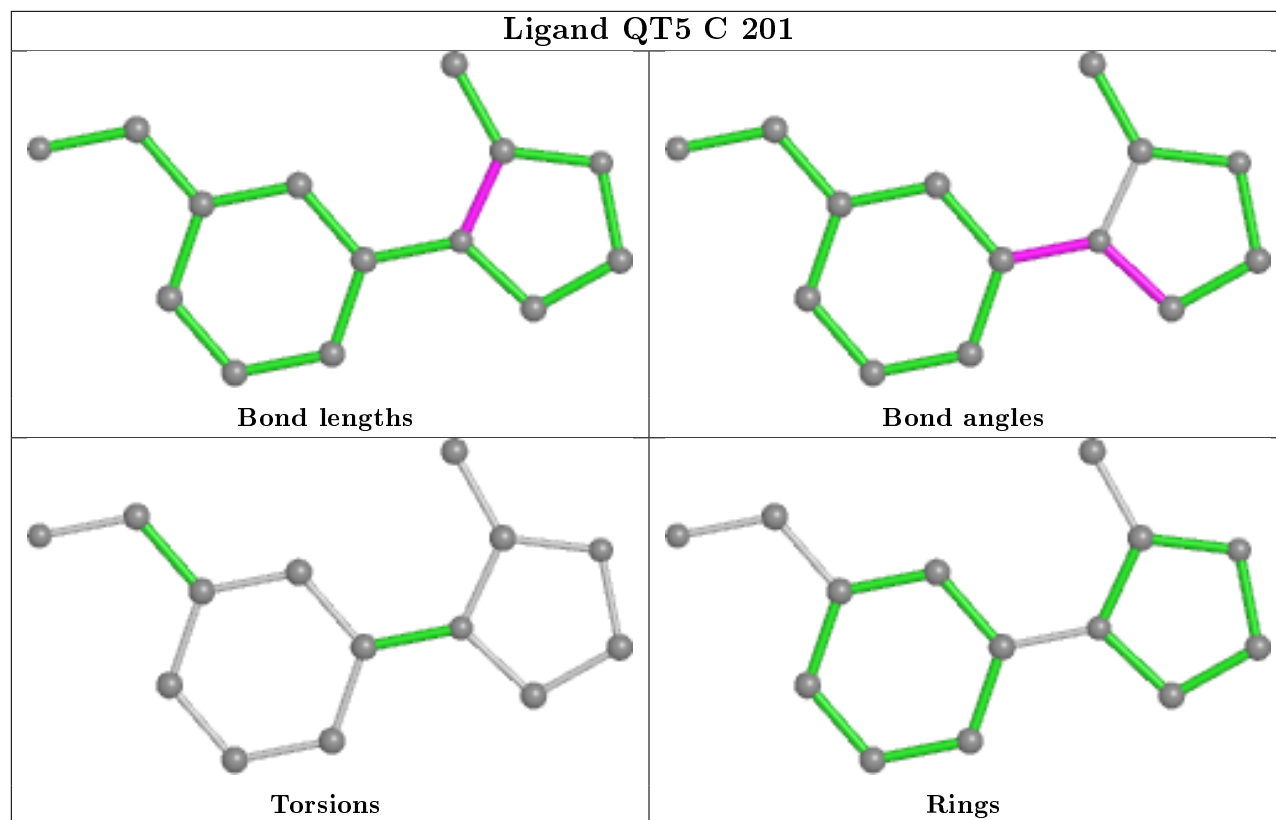| Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	201	QT5	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	201	QT5	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand QT5 B 201

Bond lengths

Bond angles

Torsions

Rings

Ligand QT5 C 201

Bond lengths

Bond angles

Torsions

Rings

Ligand QT5 A 201

Bond lengths

Bond angles

Torsions

Rings

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 (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(Å²)	Q<0.9
1	A	131/134 (97%)	0.30	7 (5%)	26	29	11, 18, 43, 56	0
1	B	133/134 (99%)	0.38	11 (8%)	11	13	10, 18, 45, 51	0
1	C	131/134 (97%)	0.29	7 (5%)	26	29	11, 18, 43, 49	1 (0%)
All	All	395/402 (98%)	0.32	25 (6%)	20	22	10, 18, 45, 56	1 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	29	ALA	4.3
1	B	29	ALA	3.7
1	C	130	ALA	3.4
1	B	131	ALA	3.3
1	B	96	VAL	3.3
1	C	32	GLY	3.1
1	A	32	GLY	3.0
1	B	0	MET	2.9
1	C	34	ARG	2.9
1	B	34	ARG	2.9
1	B	130	ALA	2.8
1	B	-1	HIS	2.6
1	B	127	TRP	2.5
1	A	34	ARG	2.4
1	B	33	ILE	2.4
1	B	32	GLY	2.3
1	A	52	ASN	2.3
1	A	97	GLY	2.2
1	A	96	VAL	2.2
1	C	33	ILE	2.2
1	A	33	ILE	2.1
1	C	97	GLY	2.1
1	B	129	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	127	TRP	2.0
1	C	98	SER	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.
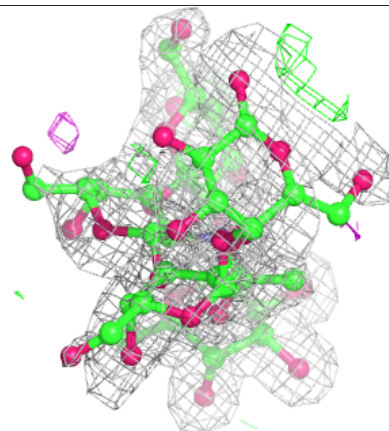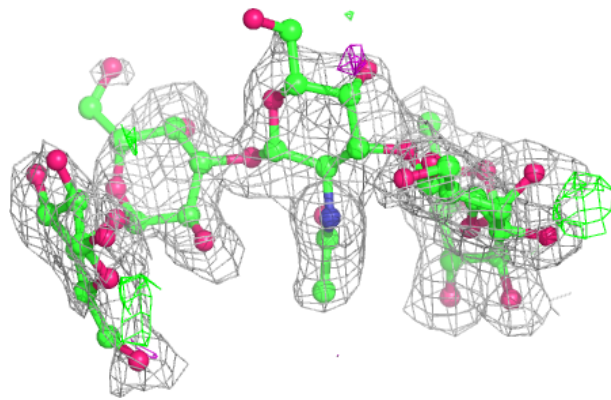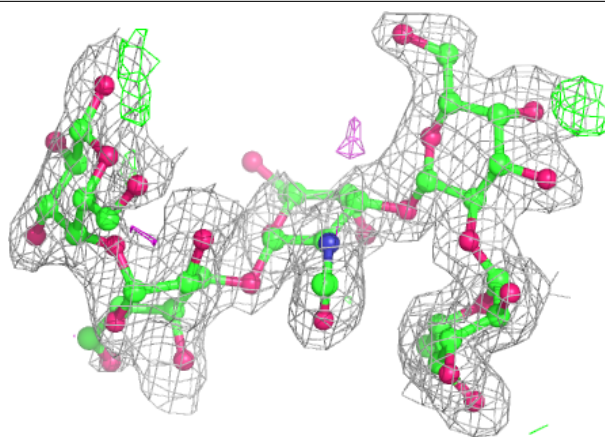
6.3 Carbohydrates (i)

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	D	1	12/12	0.69	0.26	42,52,57,60	0
2	GLA	D	2	11/12	0.75	0.25	40,47,52,54	0
3	GLA	F	1	12/12	0.78	0.26	40,46,50,56	0
2	GAL	E	1	12/12	0.79	0.22	39,44,52,60	0
2	GLA	E	2	11/12	0.86	0.20	32,35,44,48	0
2	NGA	E	3	14/15	0.87	0.18	23,32,44,48	0
2	NGA	D	3	14/15	0.90	0.20	20,32,46,53	0
3	NGA	F	2	14/15	0.90	0.19	21,29,39,46	0
2	GAL	E	4	11/12	0.91	0.14	19,26,34,36	0
3	GAL	F	3	11/12	0.93	0.12	18,24,26,27	0
2	GAL	D	4	11/12	0.94	0.11	19,24,29,37	0
2	FUC	E	5	10/11	0.95	0.08	13,17,17,18	0
2	FUC	D	5	10/11	0.95	0.09	14,16,19,19	0
3	FUC	F	4	10/11	0.96	0.08	14,16,18,18	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.
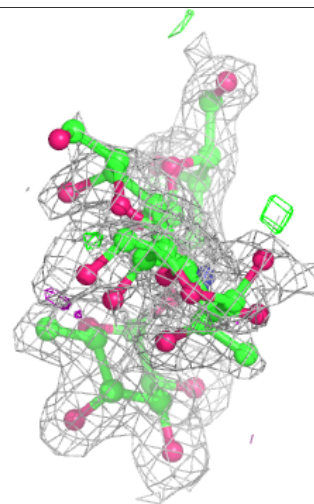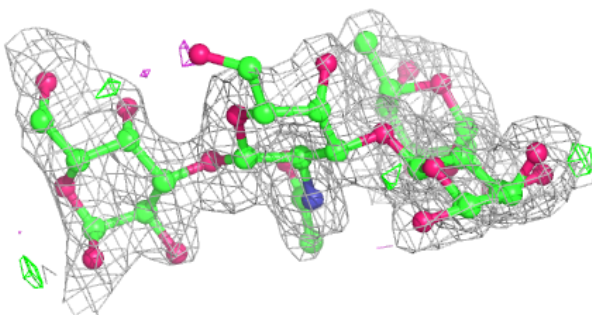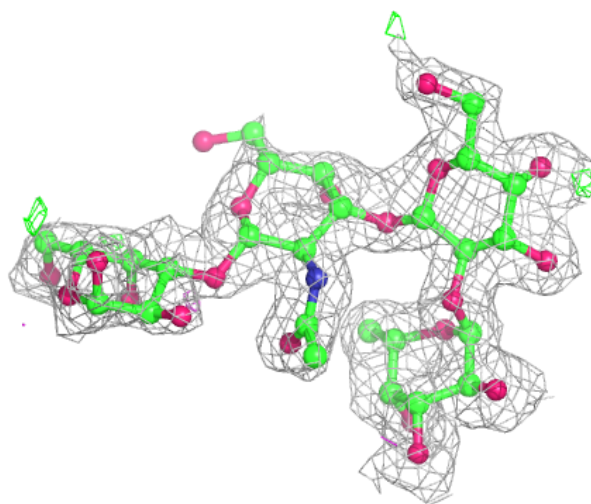
Electron density around Chain D:

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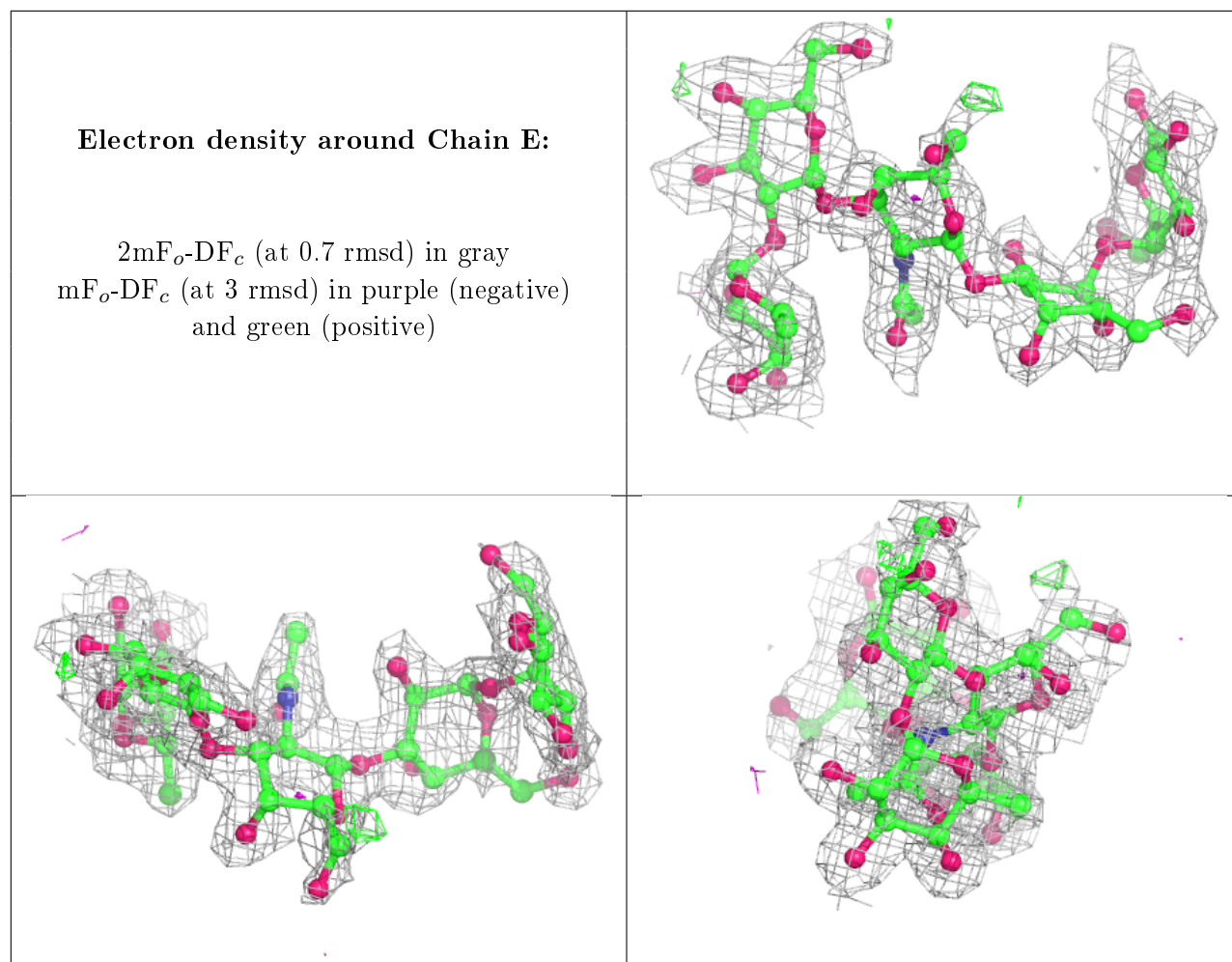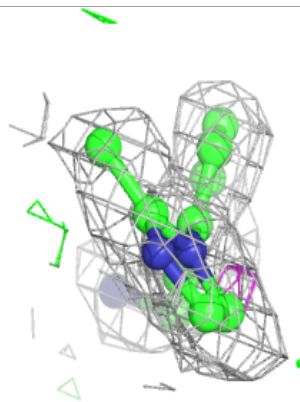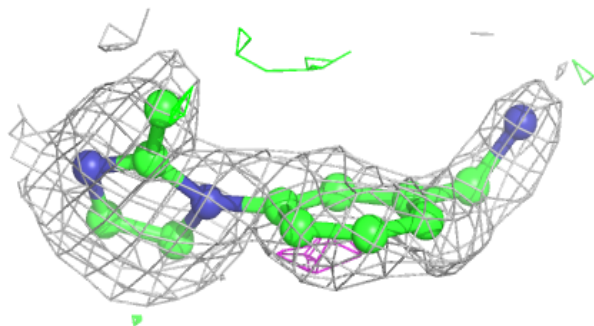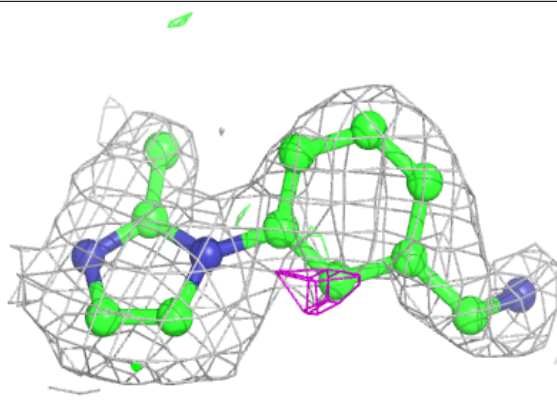$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around Chain F:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around Chain E:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (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.

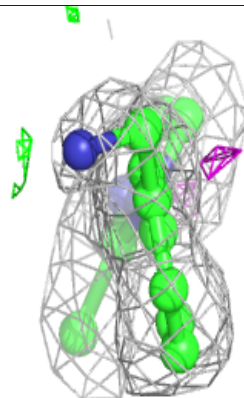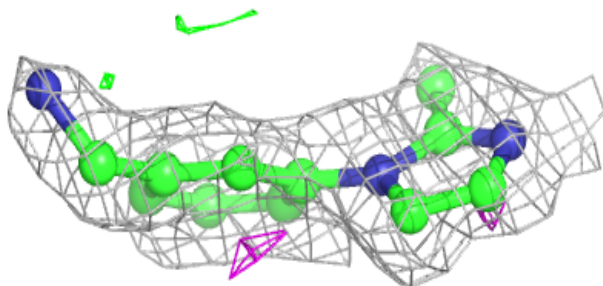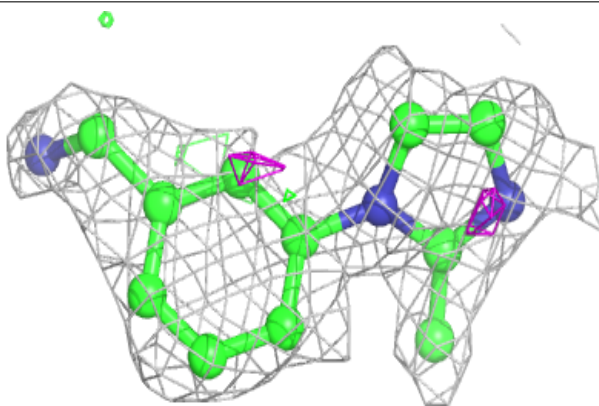| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	QT5	B	201	14/14	0.81	0.20	31,39,44,45	0
4	QT5	C	201	14/14	0.85	0.16	32,35,38,39	0
4	QT5	A	201	14/14	0.85	0.18	25,32,37,37	0
5	NA	A	202	1/1	0.99	0.04	16,16,16,16	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.
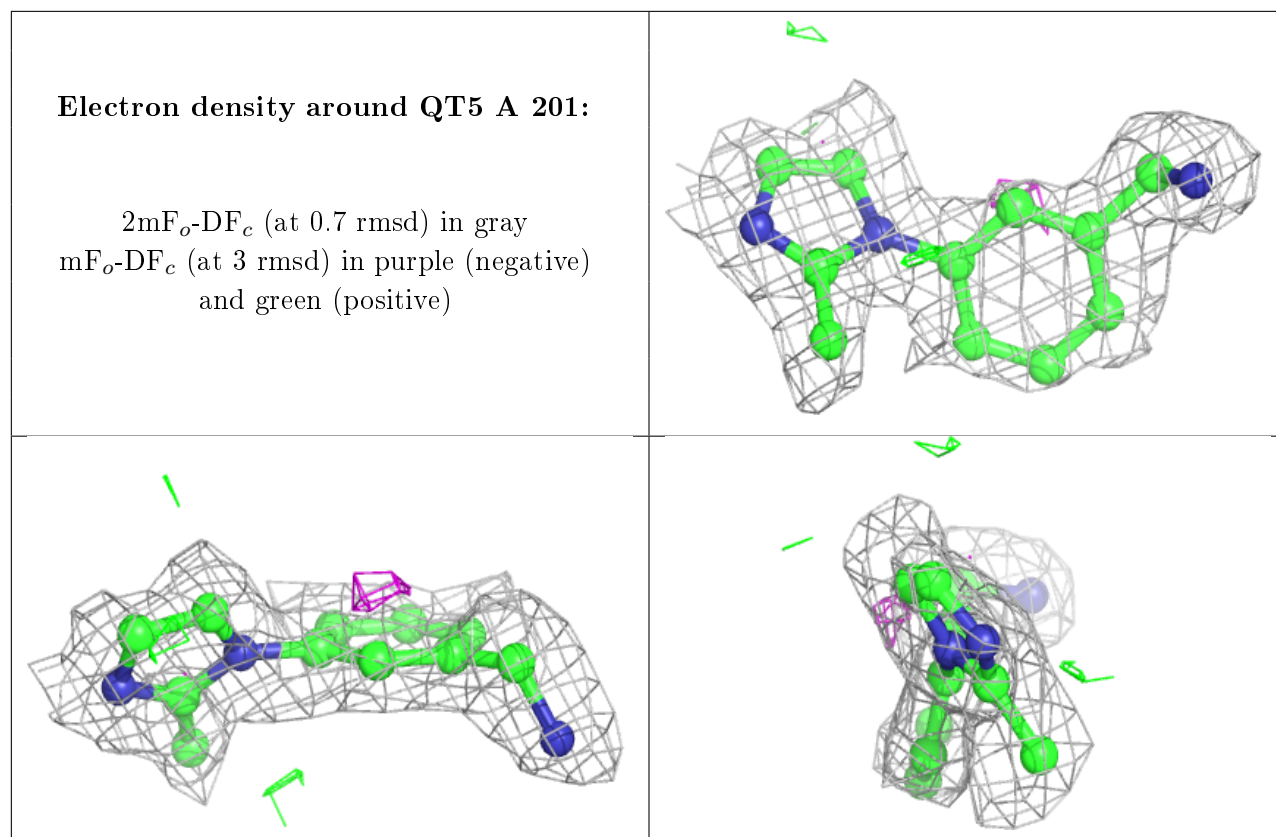
Electron density around QT5 B 201:

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

Electron density around QT5 C 201:

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

Electron density around QT5 A 201:

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

6.5 Other polymers (i)

There are no such residues in this entry.