



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 11, 2023 – 12:54 PM EDT

PDB ID : 7RC9
Title : Crystal structure of human TLR8 ectodomain bound to small molecule antagonist 21
Authors : Critton, D.A.
Deposited on : 2021-07-07
Resolution : 2.76 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

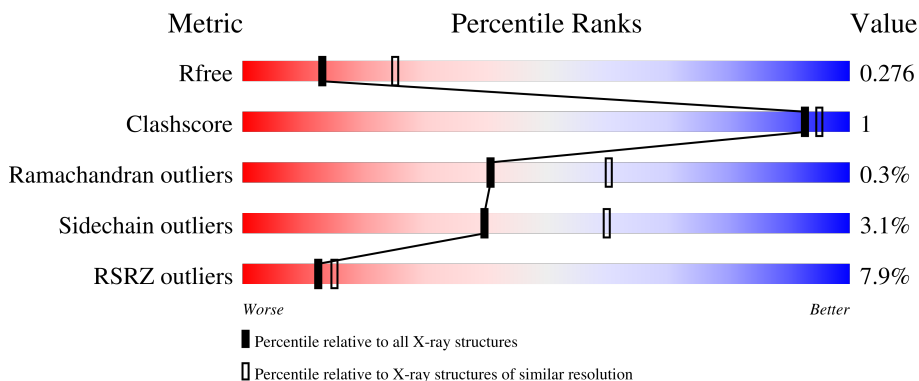
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.76 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	811	
1	B	811	
2	C	3	
2	D	3	
3	E	5	

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Mol	Chain	Length	Quality of chain
3	F	5	
3	H	5	
4	G	4	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NAG	A	903	-	-	-	X
5	NAG	B	901	-	-	-	X
5	NAG	B	903	-	-	-	X
5	NAG	B	904	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 12205 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.

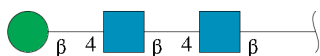
- Molecule 1 is a protein called Toll-like receptor 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	737	5725	3683	956	1067	19	0	2	0
1	B	737	5729	3685	957	1068	19	0	2	0

There are 20 discrepancies between the modelled and reference sequences:

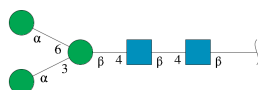
Chain	Residue	Modelled	Actual	Comment	Reference
A	23	ARG	-	expression tag	UNP Q9NR97
A	24	SER	-	expression tag	UNP Q9NR97
A	25	PRO	-	expression tag	UNP Q9NR97
A	26	TRP	-	expression tag	UNP Q9NR97
A	828	GLU	-	expression tag	UNP Q9NR97
A	829	PHE	-	expression tag	UNP Q9NR97
A	830	LEU	-	expression tag	UNP Q9NR97
A	831	VAL	-	expression tag	UNP Q9NR97
A	832	PRO	-	expression tag	UNP Q9NR97
A	833	ARG	-	expression tag	UNP Q9NR97
B	23	ARG	-	expression tag	UNP Q9NR97
B	24	SER	-	expression tag	UNP Q9NR97
B	25	PRO	-	expression tag	UNP Q9NR97
B	26	TRP	-	expression tag	UNP Q9NR97
B	828	GLU	-	expression tag	UNP Q9NR97
B	829	PHE	-	expression tag	UNP Q9NR97
B	830	LEU	-	expression tag	UNP Q9NR97
B	831	VAL	-	expression tag	UNP Q9NR97
B	832	PRO	-	expression tag	UNP Q9NR97
B	833	ARG	-	expression tag	UNP Q9NR97

- Molecule 2 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
			Total	C	N	O			
2	C	3	39	22	2	15	0	0	0
2	D	3	39	22	2	15	0	0	0

- Molecule 3 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-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	E	5	61	34	2	25	0	0	0
3	F	5	61	34	2	25	0	0	0
3	H	5	61	34	2	25	0	0	0

- Molecule 4 is an oligosaccharide called 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.



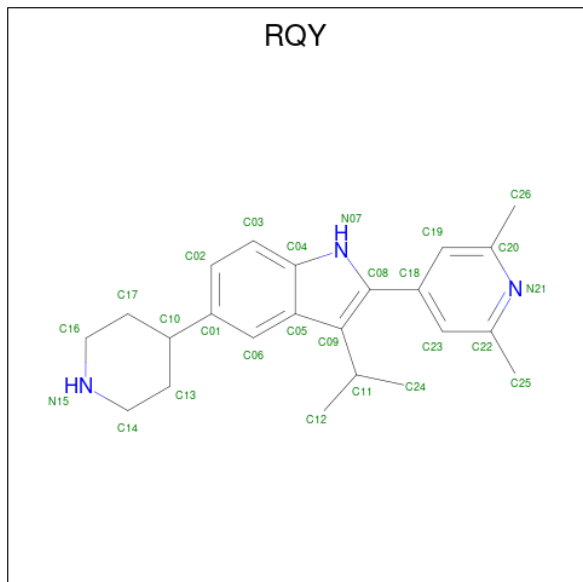
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	G	4	50	28	2	20	0	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 6 is 2-(2,6-dimethylpyridin-4-yl)-5-(piperidin-4-yl)-3-(propan-2-yl)-1H-indole (three-letter code: RQY) (formula: C₂₃H₂₉N₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	N	0	0
			26	23	3		
6	B	1	Total	C	N	0	0
			26	23	3		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	110	Total	O	0	0
			110	110		
7	B	82	Total	O	0	0
			82	82		

CYS
VAL
SER
ASP
VAL
THR
GLU
PHE
LEU
VAL
PRO
ARG

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

Chain C:  100%

MAG1
MAG2
BMA3

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

Chain D:  67% 33%

MAG1
MAG2
BMA3

- Molecule 3: 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

Chain E:  20% 80%

MAG1
MAG2
BMA3
MAN4
MAN5

- Molecule 3: 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

Chain F:  60% 40%

MAG1
MAG2
BMA3
MAN4
MAN5

- Molecule 3: 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

Chain H:  40% 60%

MAG1
MAG2
BMA3
MAN4
MAN5

- Molecule 4: 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 G:  75% 25%

MAG1
MAG2
BMA3
MAY4

4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	160.89Å 83.88Å 153.52Å 90.00° 119.72° 90.00°	Depositor
Resolution (Å)	40.41 – 2.76 40.01 – 2.76	Depositor EDS
% Data completeness (in resolution range)	99.0 (40.41-2.76) 99.5 (40.01-2.76)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.77Å)	Xtrriage
Refinement program	BUSTER 2.11.6	Depositor
R, R_{free}	0.234 , 0.262 0.247 , 0.276	Depositor DCC
R_{free} test set	2331 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	63.7	Xtrriage
Anisotropy	0.633	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.009 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12205	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% 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: RQY, 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	0.39	0/5852	0.59	1/7979 (0.0%)
1	B	0.39	0/5856	0.58	1/7984 (0.0%)
All	All	0.39	0/11708	0.59	2/15963 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	604	ASN	C-N-CA	5.23	134.78	121.70
1	B	604	ASN	C-N-CA	5.22	134.75	121.70

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	5725	0	5496	16	0
1	B	5729	0	5502	19	0
2	C	39	0	34	0	0
2	D	39	0	34	0	0
3	E	61	0	52	0	0
3	F	61	0	52	0	0
3	H	61	0	52	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	G	50	0	43	0	0
5	A	98	0	91	0	0
5	B	98	0	91	0	0
6	A	26	0	0	0	0
6	B	26	0	0	1	0
7	A	110	0	0	0	0
7	B	82	0	0	0	0
All	All	12205	0	11447	35	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 1.

The worst 5 of 35 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:CYS:N	1:B:188:GLU:HA	2.07	0.69
1:A:187:CYS:N	1:A:188:GLU:HA	2.07	0.68
1:B:409:ILE:HD12	1:B:430:ILE:HD11	1.86	0.58
1:A:732:LEU:HD12	1:A:756:LEU:HA	1.84	0.57
1:B:732:LEU:HD12	1:B:756:LEU:HA	1.85	0.57

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	727/811 (90%)	673 (93%)	51 (7%)	3 (0%)	34 53
1	B	727/811 (90%)	671 (92%)	54 (7%)	2 (0%)	41 60
All	All	1454/1622 (90%)	1344 (92%)	105 (7%)	5 (0%)	41 60

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	605	LEU
1	B	605	LEU
1	A	606	GLU
1	A	378	VAL
1	B	378	VAL

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	624/755 (83%)	603 (97%)	21 (3%)	37	58
1	B	625/755 (83%)	608 (97%)	17 (3%)	44	65
All	All	1249/1510 (83%)	1211 (97%)	38 (3%)	40	61

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	420	LEU
1	B	703	LEU
1	B	529	ILE
1	B	605	LEU
1	B	750	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	ASN
1	A	135	ASN
1	B	97	ASN
1	B	135	ASN
1	B	388	GLN

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](#)

25 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	C	1	1,2	14,14,15	0.29	0	17,19,21	0.59	0
2	NAG	C	2	2	14,14,15	0.28	0	17,19,21	0.67	0
2	BMA	C	3	2	11,11,12	0.33	0	15,15,17	0.54	0
2	NAG	D	1	1,2	14,14,15	0.32	0	17,19,21	0.53	0
2	NAG	D	2	2	14,14,15	0.34	0	17,19,21	1.58	2 (11%)
2	BMA	D	3	2	11,11,12	0.37	0	15,15,17	0.42	0
3	NAG	E	1	1,3	14,14,15	0.29	0	17,19,21	0.67	1 (5%)
3	NAG	E	2	3	14,14,15	0.28	0	17,19,21	0.60	1 (5%)
3	BMA	E	3	3	11,11,12	0.29	0	15,15,17	0.56	0
3	MAN	E	4	3	11,11,12	0.37	0	15,15,17	0.82	1 (6%)
3	MAN	E	5	3	11,11,12	0.36	0	15,15,17	0.84	1 (6%)
3	NAG	F	1	1,3	14,14,15	0.30	0	17,19,21	0.60	0
3	NAG	F	2	3	14,14,15	0.32	0	17,19,21	0.58	0
3	BMA	F	3	3	11,11,12	0.32	0	15,15,17	0.65	0
3	MAN	F	4	3	11,11,12	0.42	0	15,15,17	0.87	2 (13%)
3	MAN	F	5	3	11,11,12	0.37	0	15,15,17	0.81	1 (6%)
4	NAG	G	1	1,4	14,14,15	0.29	0	17,19,21	0.58	0
4	NAG	G	2	4	14,14,15	0.29	0	17,19,21	0.57	0
4	BMA	G	3	4	11,11,12	0.40	0	15,15,17	0.77	0
4	MAN	G	4	4	11,11,12	0.39	0	15,15,17	1.01	1 (6%)
3	NAG	H	1	1,3	14,14,15	0.28	0	17,19,21	0.69	1 (5%)
3	NAG	H	2	3	14,14,15	0.27	0	17,19,21	0.56	0
3	BMA	H	3	3	11,11,12	0.29	0	15,15,17	0.57	0
3	MAN	H	4	3	11,11,12	0.37	0	15,15,17	0.89	1 (6%)
3	MAN	H	5	3	11,11,12	0.40	0	15,15,17	1.02	1 (6%)

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

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	NAG	O5-C1-C2	-5.87	102.02	111.29
4	G	4	MAN	C1-O5-C5	3.50	116.94	112.19
3	H	5	MAN	C1-O5-C5	3.32	116.68	112.19
3	H	4	MAN	C1-O5-C5	2.97	116.21	112.19
3	E	5	MAN	C1-O5-C5	2.49	115.57	112.19

There are no chirality outliers.

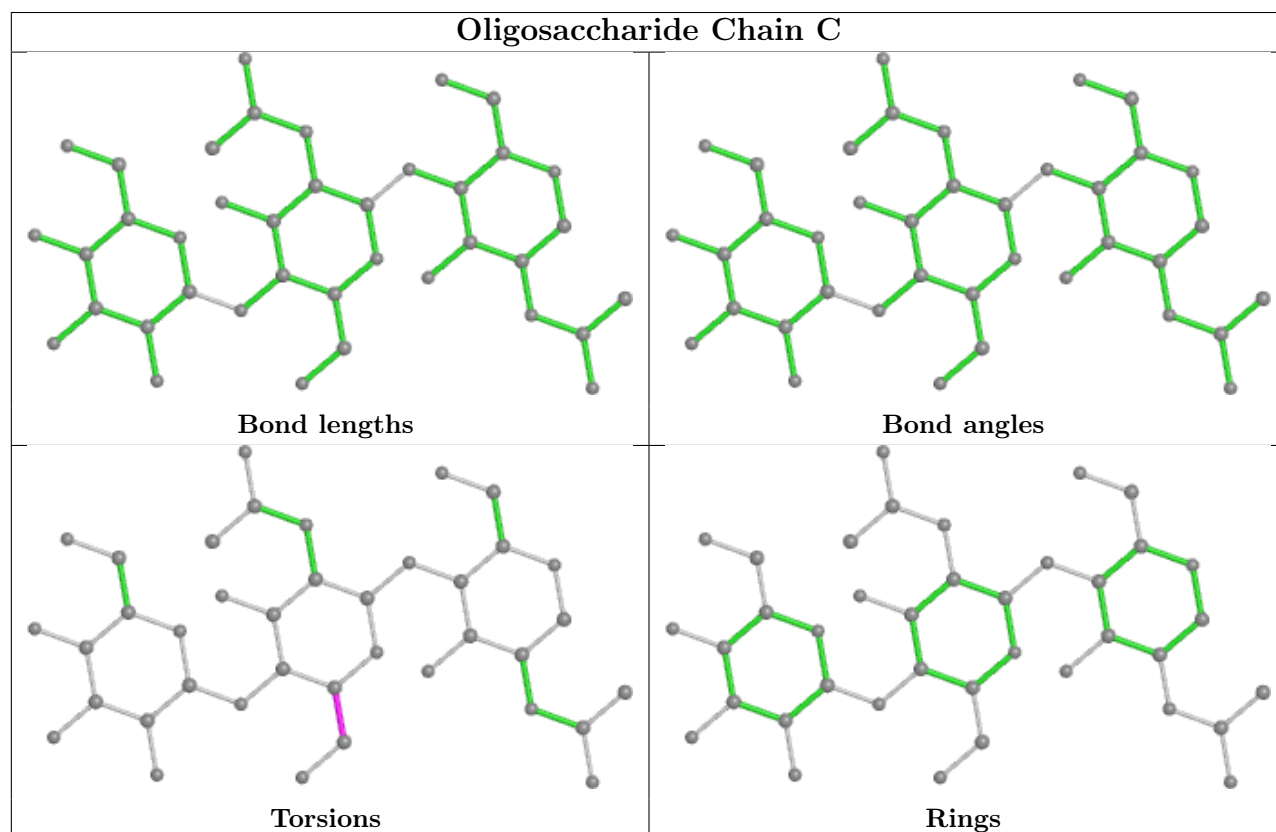
All (1) torsion outliers are listed below:

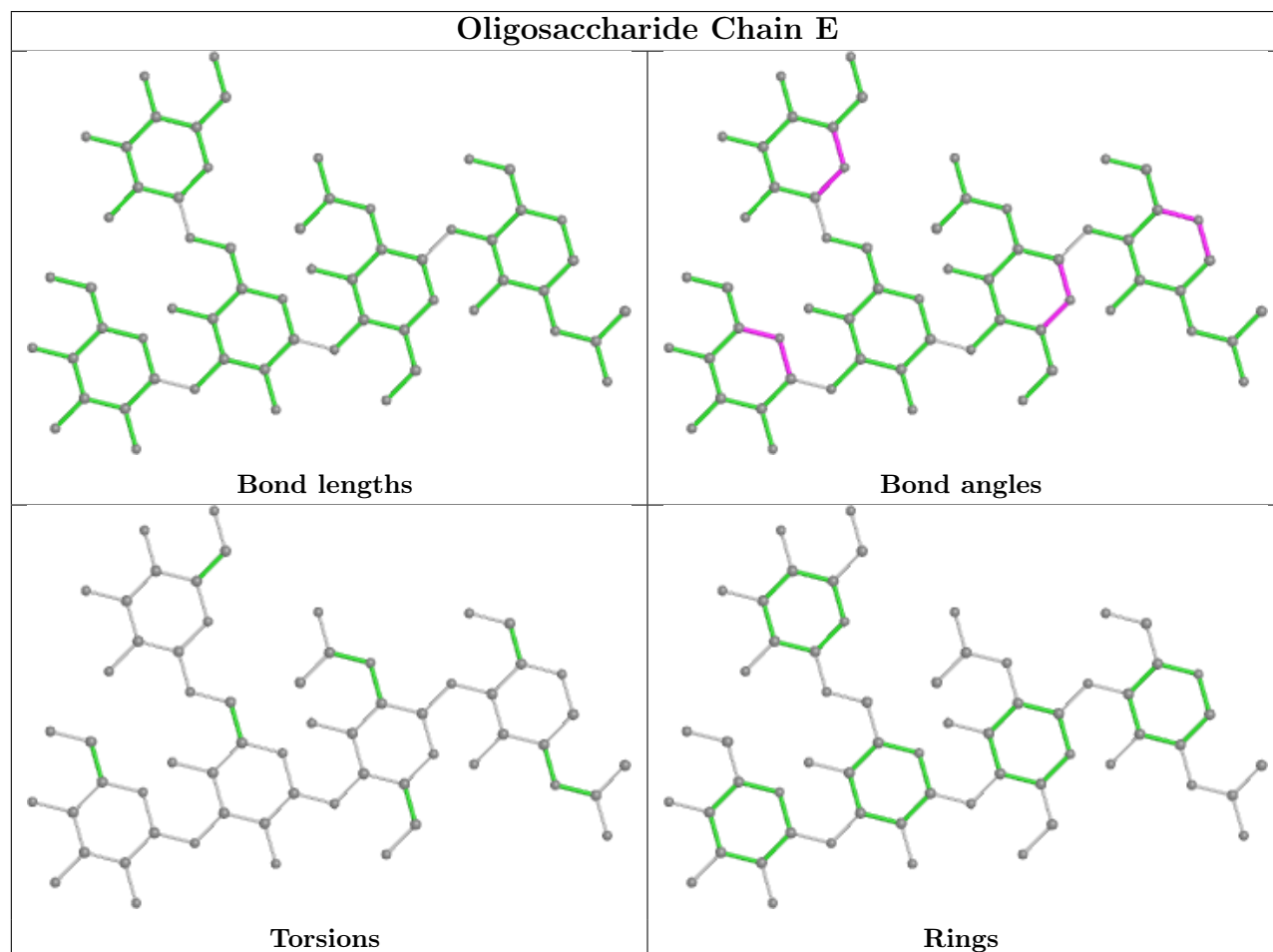
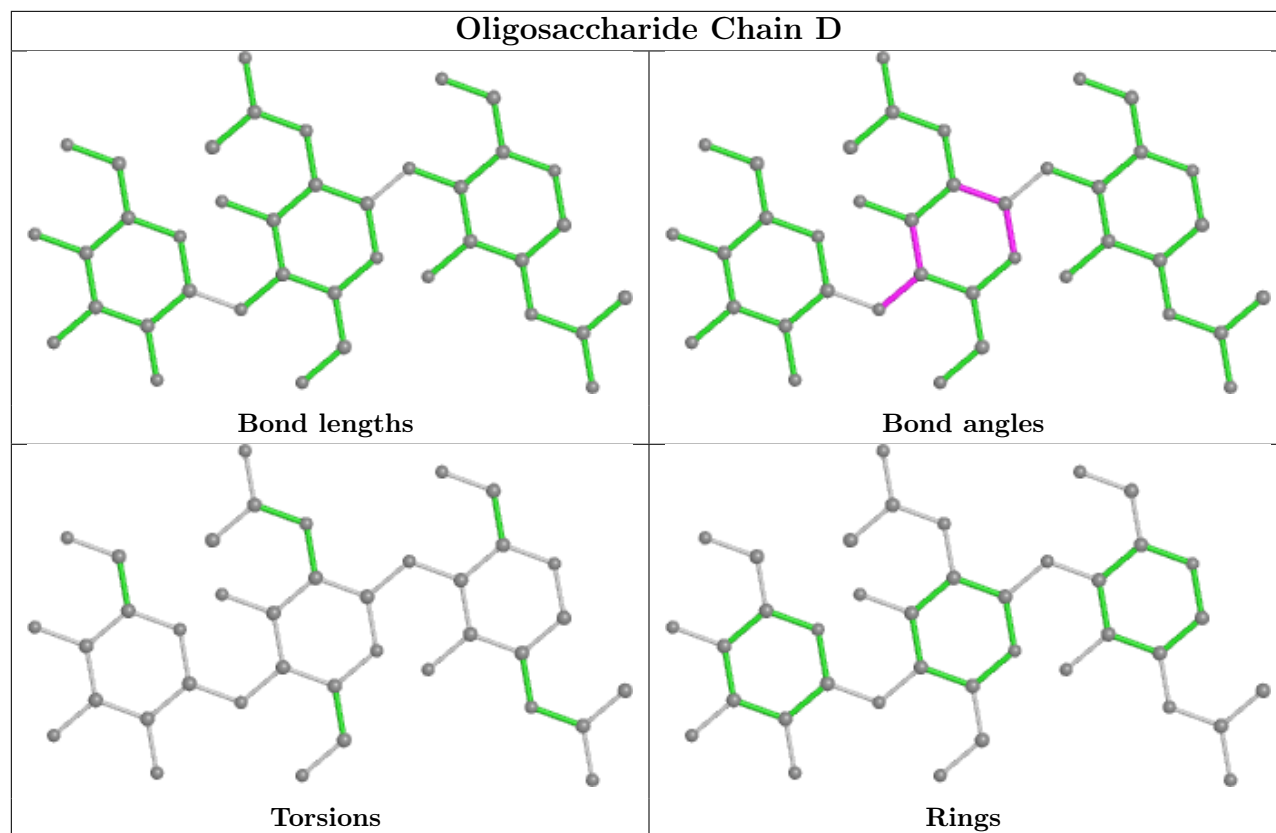
Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C4-C5-C6-O6

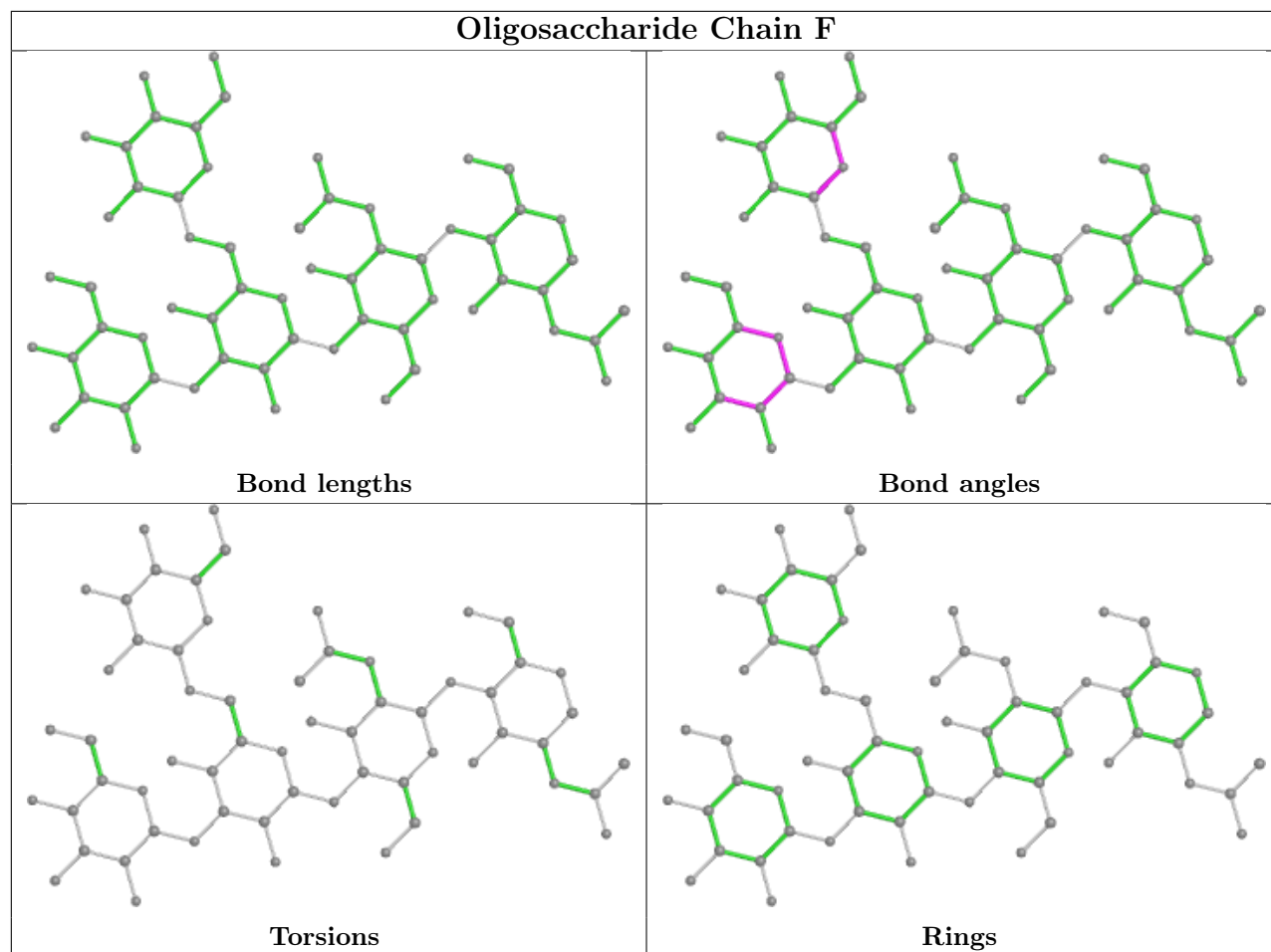
There are no ring outliers.

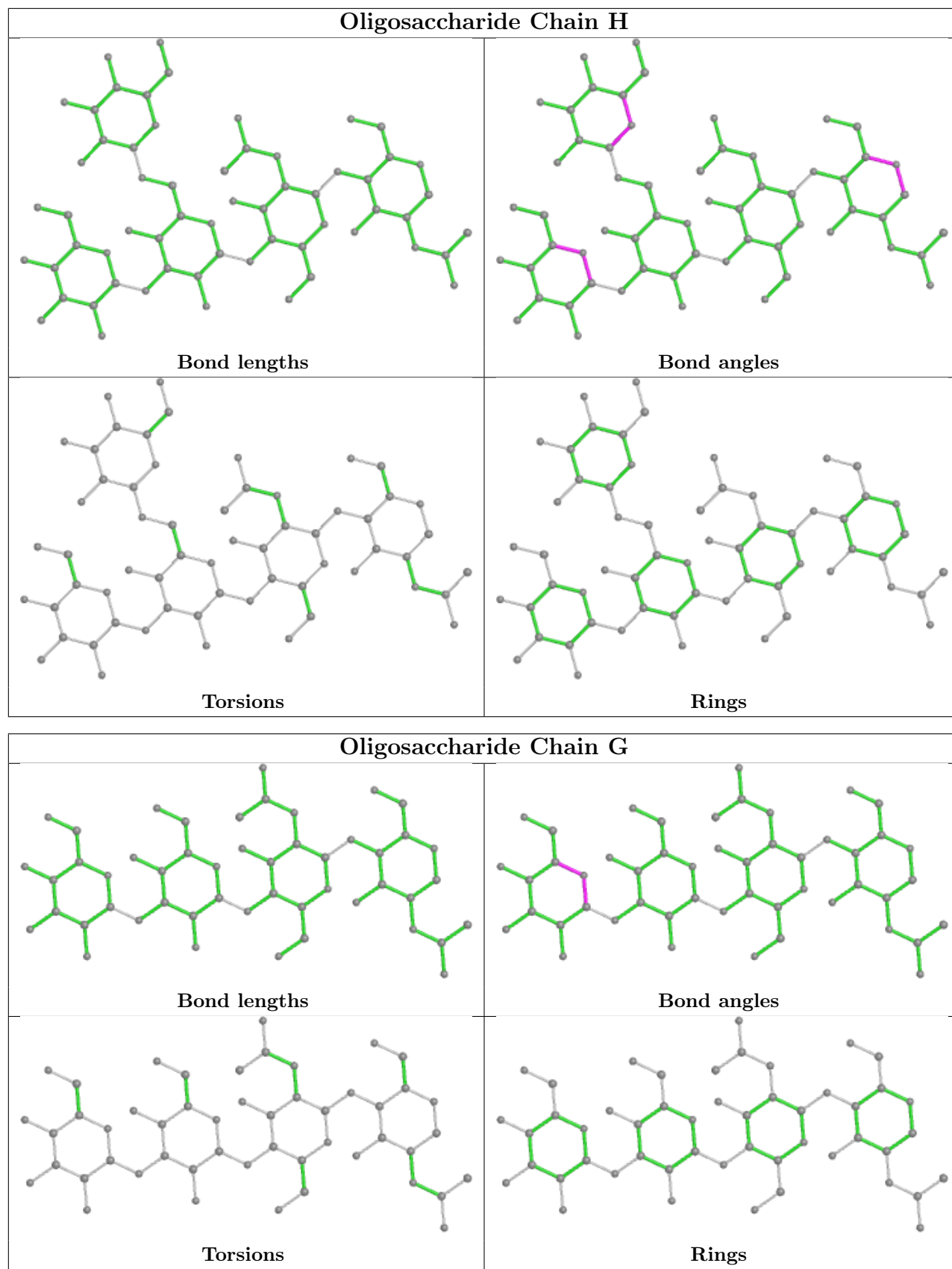
No monomer is involved in short contacts.

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









5.6 Ligand geometry

16 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	NAG	B	904	1	14,14,15	0.32	0	17,19,21	0.75	0
5	NAG	B	901	1	14,14,15	0.29	0	17,19,21	0.50	0
5	NAG	A	903	1	14,14,15	0.31	0	17,19,21	0.61	0
6	RQY	B	908	-	29,29,29	4.64	14 (48%)	33,42,42	1.30	5 (15%)
5	NAG	B	907	1	14,14,15	0.31	0	17,19,21	0.73	1 (5%)
5	NAG	A	902	1	14,14,15	0.29	0	17,19,21	0.56	0
5	NAG	B	903	1	14,14,15	0.31	0	17,19,21	0.63	0
5	NAG	A	907	1	14,14,15	0.30	0	17,19,21	0.74	2 (11%)
5	NAG	B	905	1	14,14,15	0.31	0	17,19,21	0.46	0
5	NAG	B	902	1	14,14,15	0.27	0	17,19,21	0.68	1 (5%)
5	NAG	B	906	1	14,14,15	0.33	0	17,19,21	0.80	1 (5%)
5	NAG	A	901	1	14,14,15	0.29	0	17,19,21	0.54	0
6	RQY	A	908	-	29,29,29	4.64	14 (48%)	33,42,42	1.44	7 (21%)
5	NAG	A	906	1	14,14,15	0.28	0	17,19,21	0.46	0
5	NAG	A	905	1	14,14,15	0.29	0	17,19,21	0.52	0
5	NAG	A	904	1	14,14,15	0.30	0	17,19,21	0.71	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	NAG	B	904	1	-	0/6/23/26	0/1/1/1
5	NAG	B	901	1	-	1/6/23/26	0/1/1/1
5	NAG	A	903	1	-	0/6/23/26	0/1/1/1
6	RQY	B	908	-	-	2/12/20/20	0/4/4/4
5	NAG	B	907	1	-	0/6/23/26	0/1/1/1
5	NAG	A	902	1	-	0/6/23/26	0/1/1/1
5	NAG	B	903	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	907	1	-	0/6/23/26	0/1/1/1
5	NAG	B	905	1	-	0/6/23/26	0/1/1/1
5	NAG	B	902	1	-	0/6/23/26	0/1/1/1
5	NAG	B	906	1	-	0/6/23/26	0/1/1/1
5	NAG	A	901	1	-	1/6/23/26	0/1/1/1
6	RQY	A	908	-	-	3/12/20/20	0/4/4/4
5	NAG	A	906	1	-	1/6/23/26	0/1/1/1
5	NAG	A	905	1	-	0/6/23/26	0/1/1/1
5	NAG	A	904	1	-	0/6/23/26	0/1/1/1

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	908	RQY	C03-C04	9.21	1.57	1.41
6	B	908	RQY	C03-C04	9.21	1.57	1.41
6	A	908	RQY	C06-C05	8.53	1.59	1.42
6	B	908	RQY	C06-C05	8.41	1.58	1.42
6	B	908	RQY	C19-C20	7.69	1.53	1.38

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	908	RQY	C17-C10-C13	2.85	115.51	109.56
6	A	908	RQY	C26-C20-N21	2.75	120.95	116.56
6	B	908	RQY	C25-C22-N21	2.55	120.62	116.56
5	B	906	NAG	C1-O5-C5	2.53	115.63	112.19
6	A	908	RQY	C01-C06-C05	-2.44	120.38	122.00

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

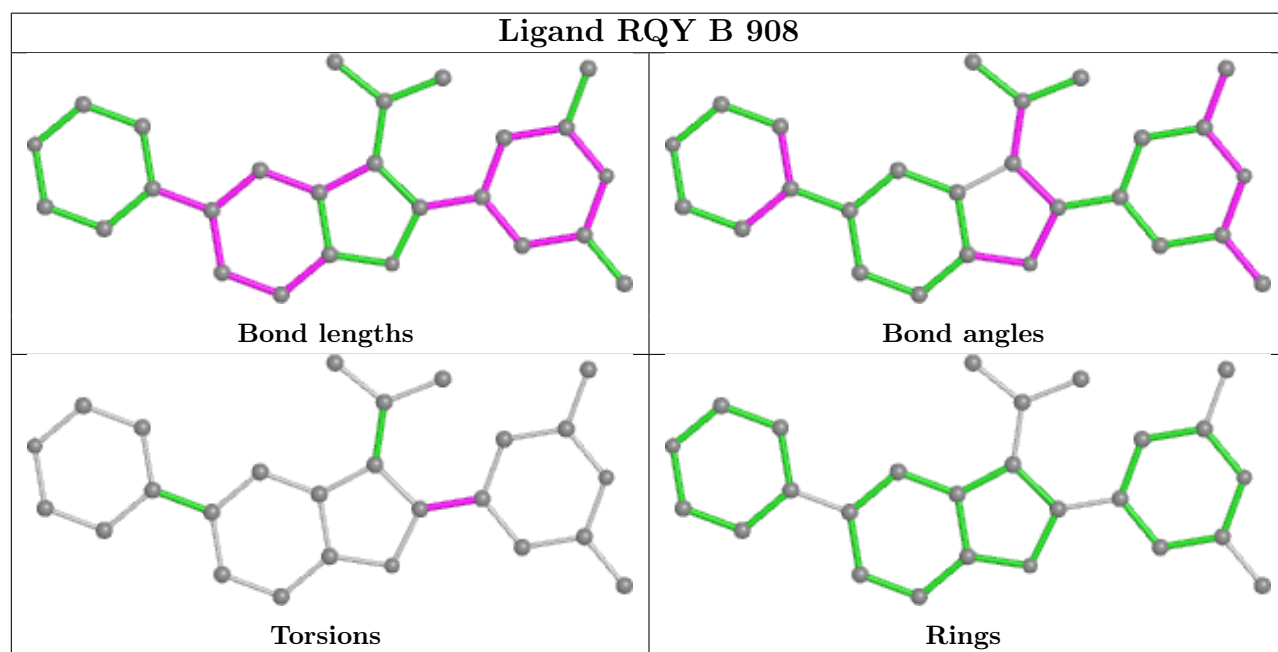
Mol	Chain	Res	Type	Atoms
6	A	908	RQY	N07-C08-C18-C19
6	B	908	RQY	N07-C08-C18-C19
6	A	908	RQY	N07-C08-C18-C23
6	B	908	RQY	N07-C08-C18-C23
5	B	901	NAG	O5-C5-C6-O6

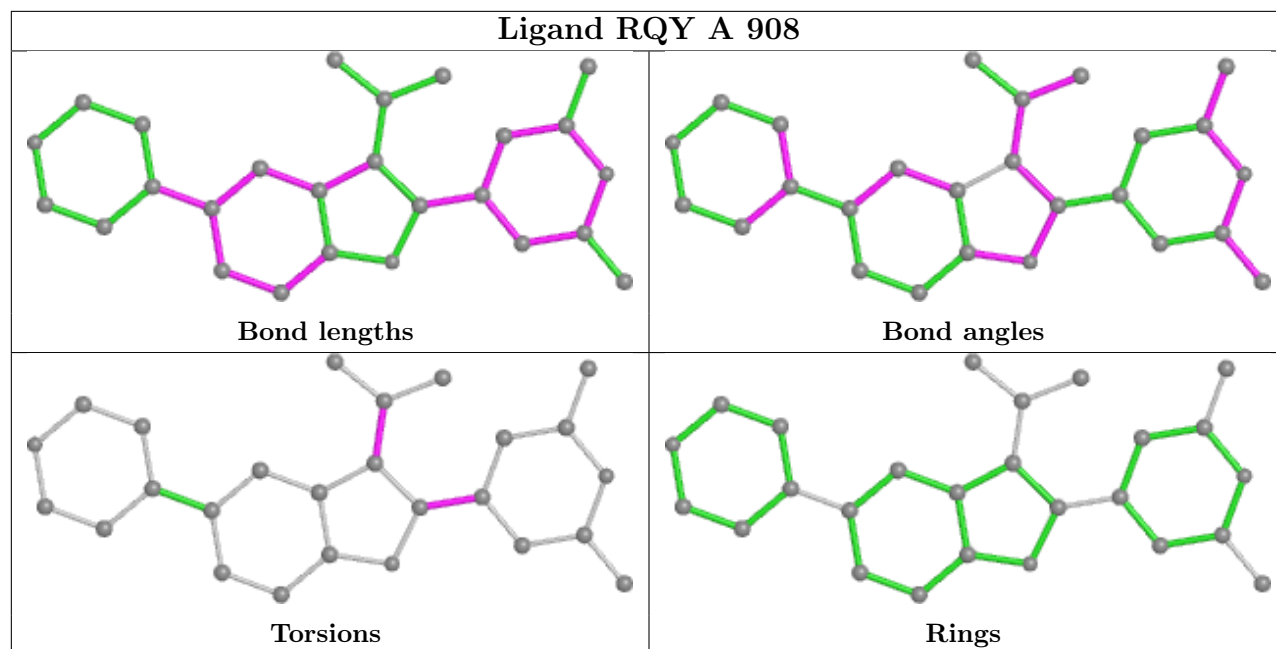
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	908	RQY	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 than 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.





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(Å ²)	Q<0.9
1	A	737/811 (90%)	0.24	26 (3%) 44 52	45, 78, 122, 165	0
1	B	737/811 (90%)	0.68	90 (12%) 4 4	53, 101, 149, 182	0
All	All	1474/1622 (90%)	0.46	116 (7%) 12 15	45, 87, 140, 182	0

The worst 5 of 116 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	65	VAL	9.1
1	B	603	TYR	8.2
1	B	236	TYR	6.3
1	B	89	LEU	6.1
1	B	121	PHE	5.7

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	0.67	0.31	119,123,124,126	0
3	MAN	F	5	11/12	0.69	0.20	123,126,132,133	0
3	MAN	F	4	11/12	0.70	0.16	115,118,121,122	0
4	BMA	G	3	11/12	0.72	0.24	102,106,110,115	0
2	BMA	D	3	11/12	0.77	0.33	92,95,97,97	0

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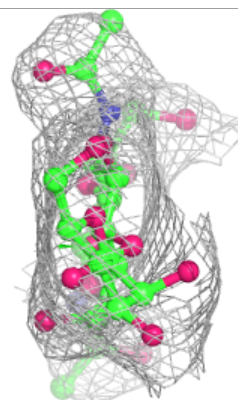
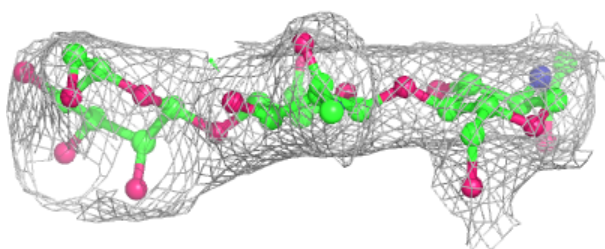
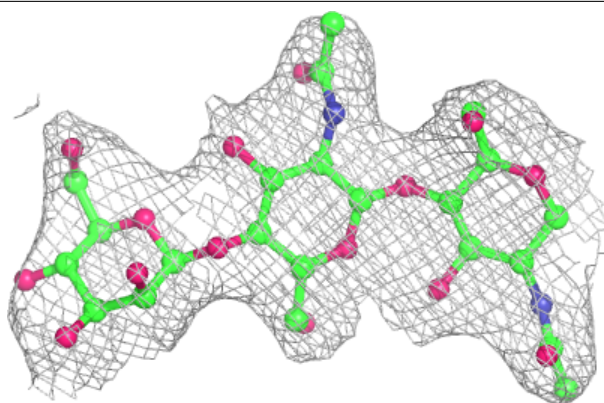
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	BMA	F	3	11/12	0.79	0.15	110,116,122,123	0
3	MAN	E	5	11/12	0.81	0.15	98,100,104,106	0
4	NAG	G	2	14/15	0.81	0.16	81,85,90,97	0
3	MAN	H	5	11/12	0.85	0.24	117,120,123,125	0
3	BMA	H	3	11/12	0.85	0.22	97,105,109,113	0
3	MAN	E	4	11/12	0.86	0.12	92,97,98,100	0
3	MAN	H	4	11/12	0.89	0.24	109,112,117,119	0
3	BMA	E	3	11/12	0.90	0.14	81,88,92,95	0
2	NAG	D	2	14/15	0.90	0.21	73,79,84,87	0
2	BMA	C	3	11/12	0.90	0.16	78,80,84,85	0
4	NAG	G	1	14/15	0.92	0.17	63,67,69,74	0
3	NAG	H	1	14/15	0.93	0.16	64,67,73,74	0
3	NAG	F	2	14/15	0.94	0.19	93,97,100,103	0
3	NAG	H	2	14/15	0.95	0.19	73,78,84,90	0
2	NAG	D	1	14/15	0.96	0.16	52,55,59,66	0
3	NAG	E	2	14/15	0.96	0.14	60,66,69,75	0
2	NAG	C	2	14/15	0.96	0.19	63,67,69,73	0
3	NAG	E	1	14/15	0.97	0.15	49,53,57,58	0
3	NAG	F	1	14/15	0.97	0.22	81,85,91,91	0
2	NAG	C	1	14/15	0.97	0.20	51,56,59,60	0

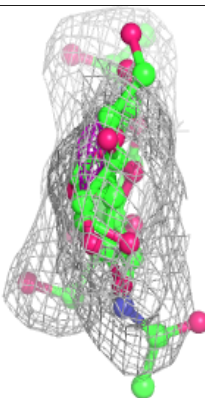
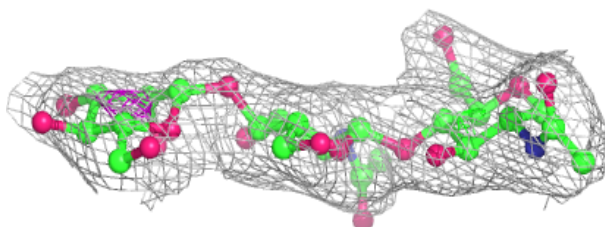
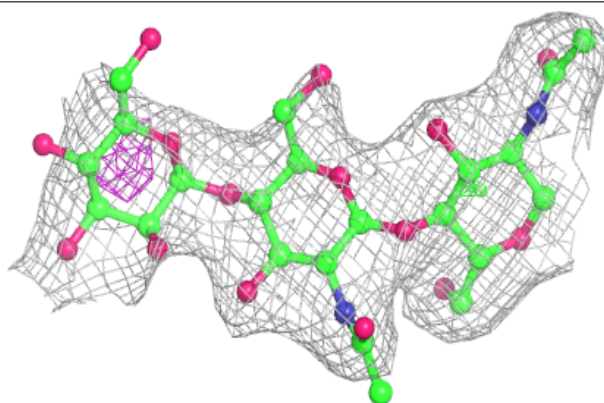
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

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

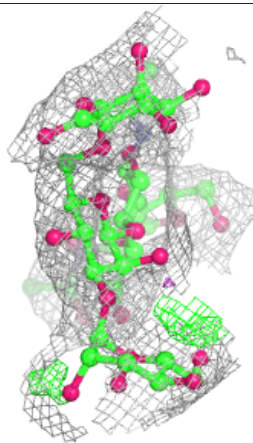
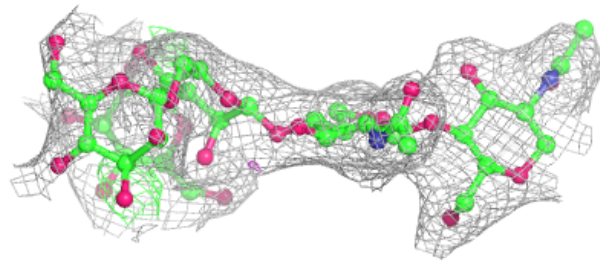
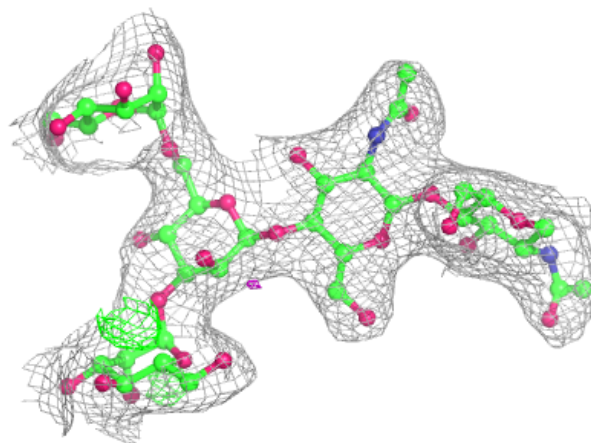
**Electron density around Chain D:**

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



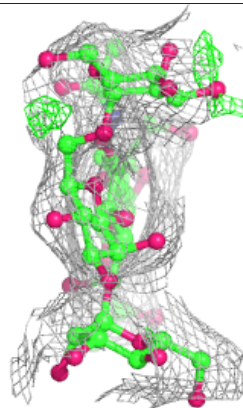
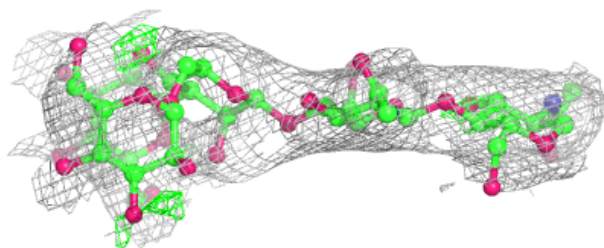
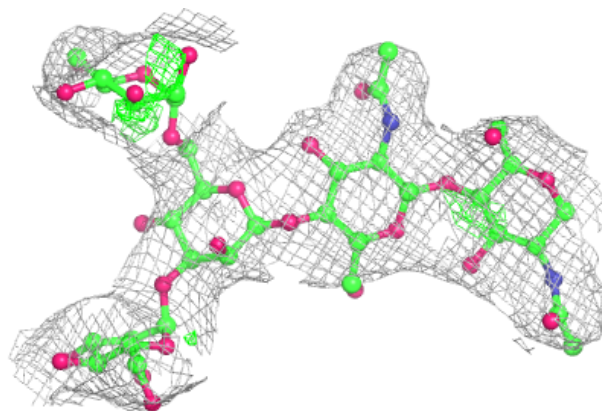
Electron density around Chain E:

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

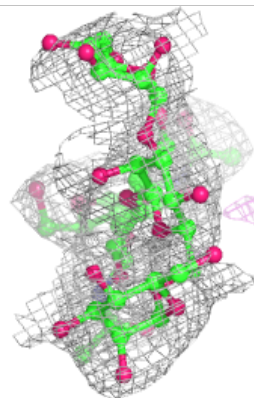
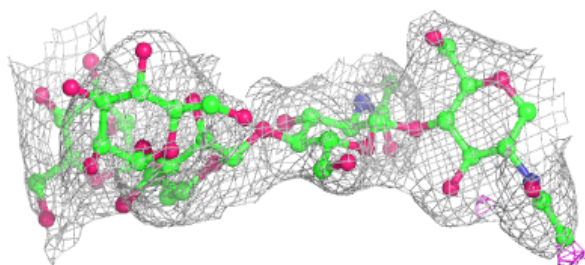
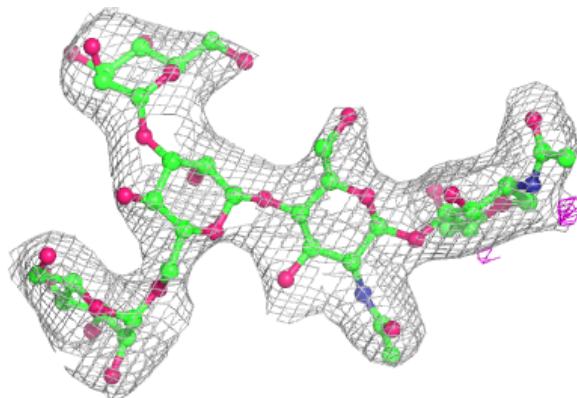


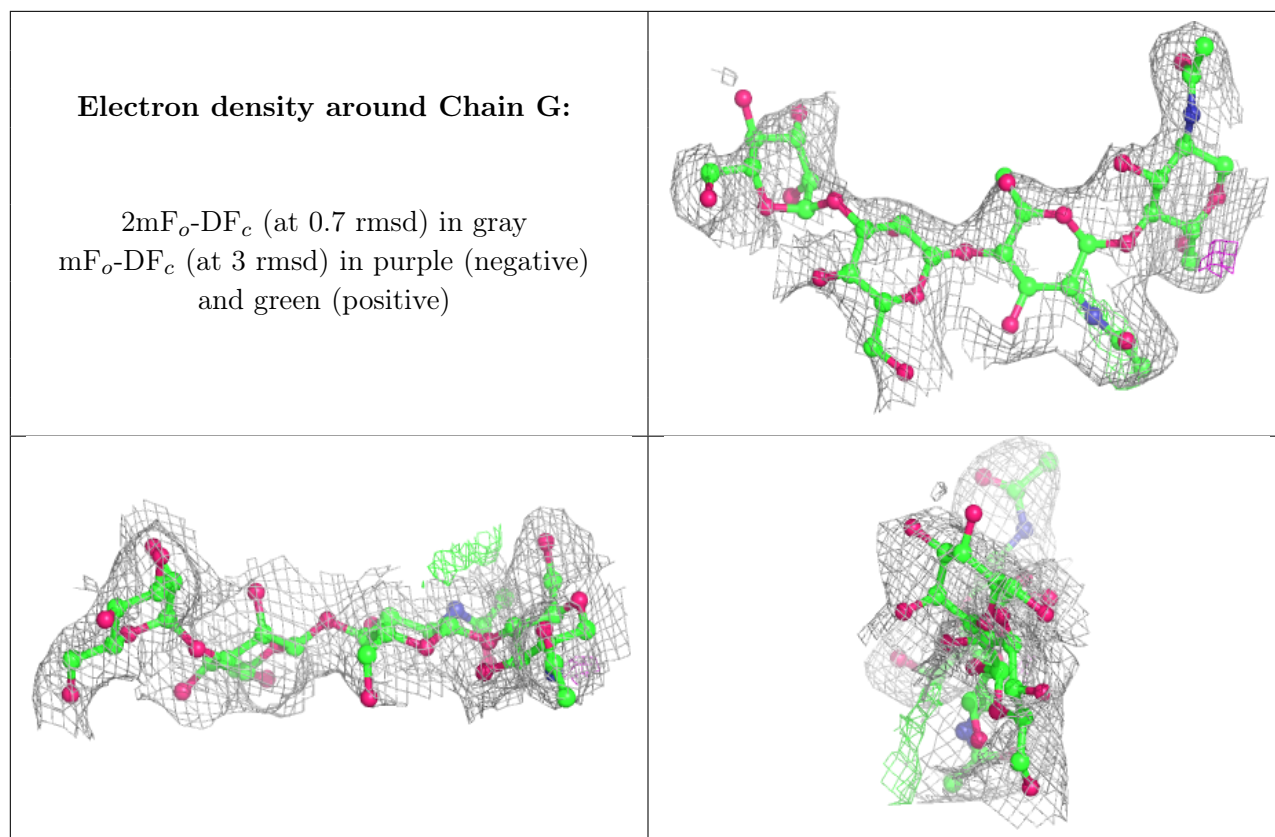
Electron density around Chain F:

$2mF_o-DF_c$ (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.

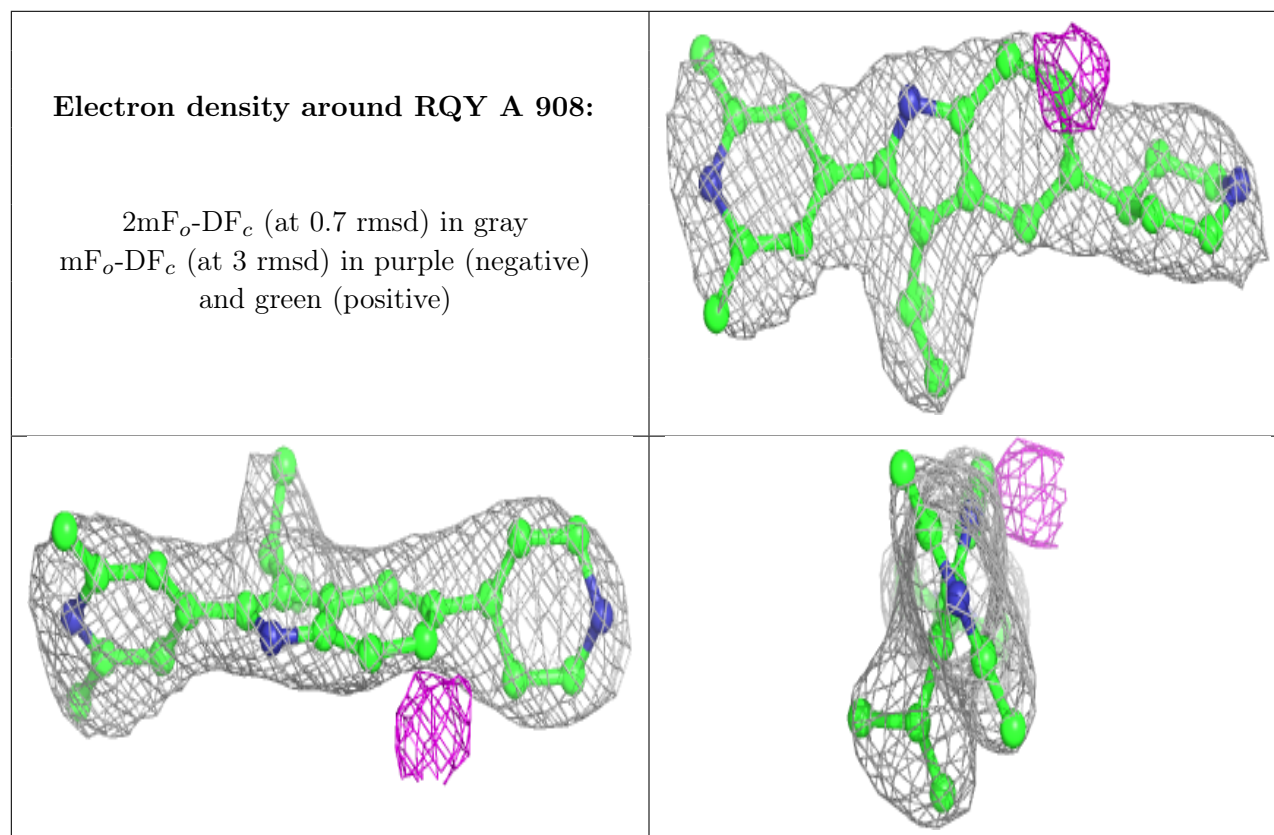
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	B	904	14/15	0.42	0.47	147,152,158,158	0
5	NAG	B	901	14/15	0.63	0.42	181,186,196,197	0
5	NAG	A	903	14/15	0.63	0.52	120,124,128,129	0
5	NAG	B	907	14/15	0.63	0.30	141,144,149,152	0
5	NAG	A	904	14/15	0.68	0.36	126,132,139,141	0
5	NAG	B	903	14/15	0.68	0.40	142,148,154,158	0
5	NAG	B	906	14/15	0.71	0.30	132,137,141,142	0
5	NAG	B	902	14/15	0.72	0.35	159,164,170,174	0
5	NAG	B	905	14/15	0.77	0.28	99,102,106,109	0
5	NAG	A	905	14/15	0.79	0.32	112,113,121,121	0
5	NAG	A	906	14/15	0.82	0.27	103,119,127,132	0
5	NAG	A	901	14/15	0.83	0.15	125,129,138,139	0
5	NAG	A	902	14/15	0.84	0.26	120,123,129,130	0
5	NAG	A	907	14/15	0.90	0.16	101,107,112,115	0

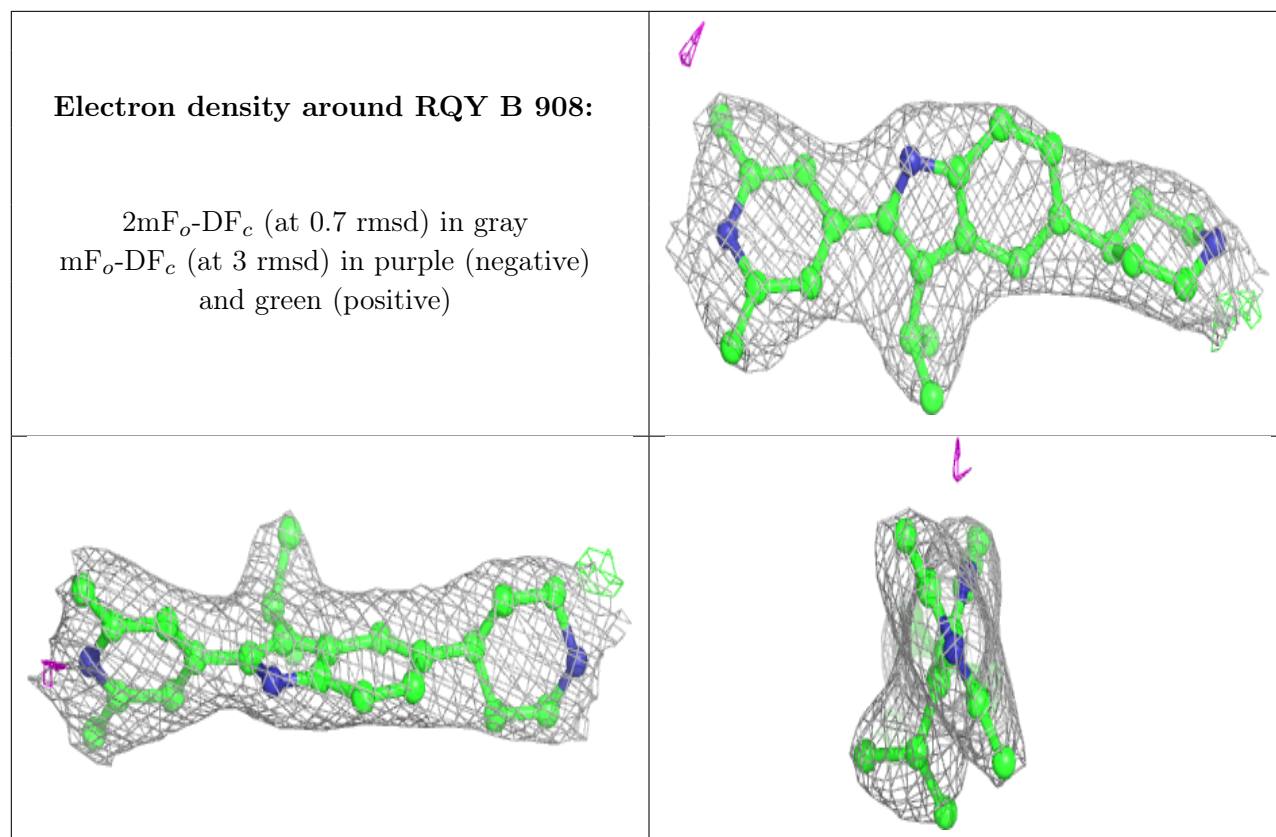
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	RQY	A	908	26/26	0.94	0.22	46,50,55,56	0
6	RQY	B	908	26/26	0.95	0.22	43,51,58,59	0

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.





6.5 Other polymers [i](#)

There are no such residues in this entry.