



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2024 – 06:00 pm BST

PDB ID : 9FOW
Title : GPR180 N-terminal domain
Authors : Mitrovic, S.A.; Reindl, S.; Nar, H.
Deposited on : 2024-06-12
Resolution : 1.88 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

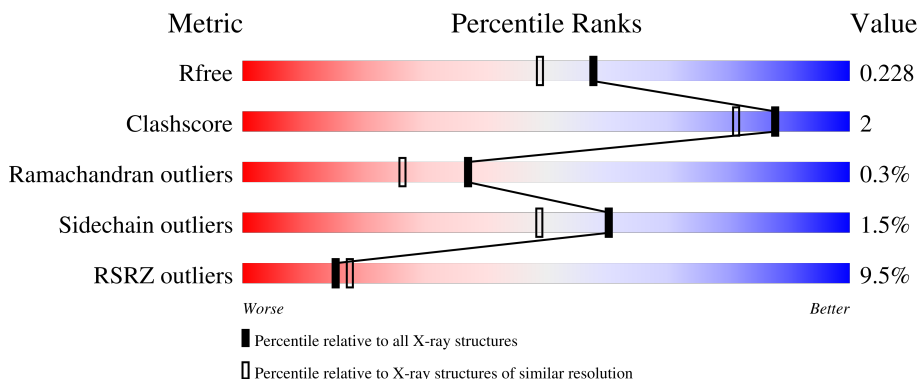
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.88 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}	164625	1090 (1.88-1.88)
Clashscore	180529	1144 (1.88-1.88)
Ramachandran outliers	177936	1135 (1.88-1.88)
Sidechain outliers	177891	1135 (1.88-1.88)
RSRZ outliers	164620	1090 (1.88-1.88)

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	146	 6% 78% 5% 16%
1	B	146	 5% 87% 8%
1	C	146	 14% 88% 9%
2	D	4	 75% 25%
3	E	5	 60% 40%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 6526 atoms, of which 3154 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 Integral membrane protein GPR180.

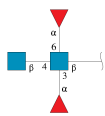
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	123	1927	616	952	171	183	5	0	2	0
1	B	134	2108	679	1037	185	202	5	0	1	0
1	C	133	2070	665	1016	182	202	5	5	1	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	23	ASP	-	expression tag	UNP Q8BPS4
A	163	GLU	-	expression tag	UNP Q8BPS4
A	164	ASN	-	expression tag	UNP Q8BPS4
A	165	LEU	-	expression tag	UNP Q8BPS4
A	166	TYR	-	expression tag	UNP Q8BPS4
A	167	PHE	-	expression tag	UNP Q8BPS4
A	168	GLN	-	expression tag	UNP Q8BPS4
B	23	ASP	-	expression tag	UNP Q8BPS4
B	163	GLU	-	expression tag	UNP Q8BPS4
B	164	ASN	-	expression tag	UNP Q8BPS4
B	165	LEU	-	expression tag	UNP Q8BPS4
B	166	TYR	-	expression tag	UNP Q8BPS4
B	167	PHE	-	expression tag	UNP Q8BPS4
B	168	GLN	-	expression tag	UNP Q8BPS4
C	23	ASP	-	expression tag	UNP Q8BPS4
C	163	GLU	-	expression tag	UNP Q8BPS4
C	164	ASN	-	expression tag	UNP Q8BPS4
C	165	LEU	-	expression tag	UNP Q8BPS4
C	166	TYR	-	expression tag	UNP Q8BPS4
C	167	PHE	-	expression tag	UNP Q8BPS4
C	168	GLN	-	expression tag	UNP Q8BPS4

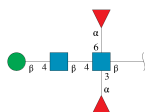
- Molecule 2 is an oligosaccharide called alpha-L-fucopyranose-(1-3)-[2-acetamido-2-deoxy-be

ta-D-glucopyranose-(1-4)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



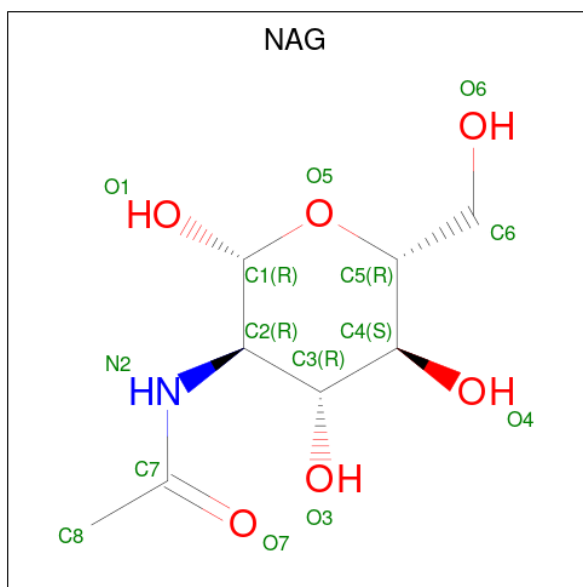
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	D	4	91	28	43	2	18	0	0	0

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



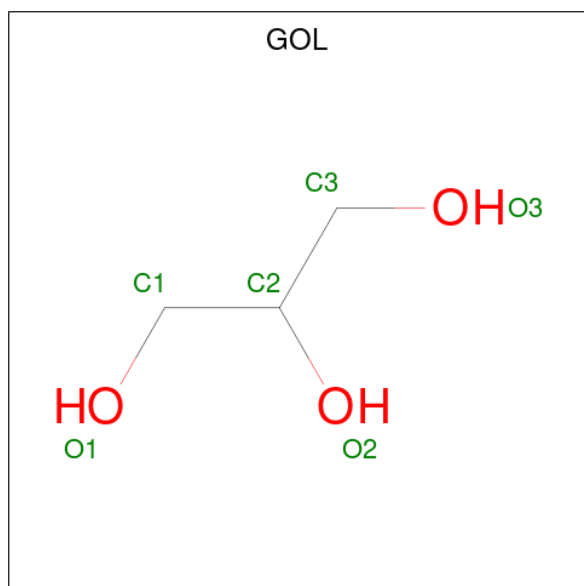
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
3	E	5	111	34	52	2	23	0	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
4	A	1	27	8	13	1	5	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
5	A	1	14	3	8	3	0	0
5	B	1	14	3	8	3	0	0
5	B	1	14	3	8	3	0	0
5	C	1	14	3	8	3	0	0

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			7	2	3	2		
6	B	1	Total	C	H	O	0	0
			7	2	3	2		
6	B	1	Total	C	H	O	0	0
			7	2	3	2		

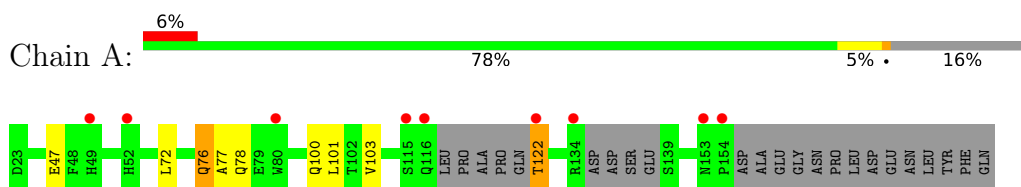
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	39	Total	O	0	0
			39	39		
7	B	37	Total	O	0	0
			37	37		
7	C	39	Total	O	0	0
			39	39		

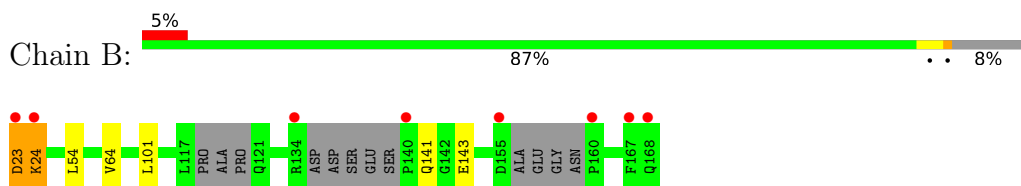
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

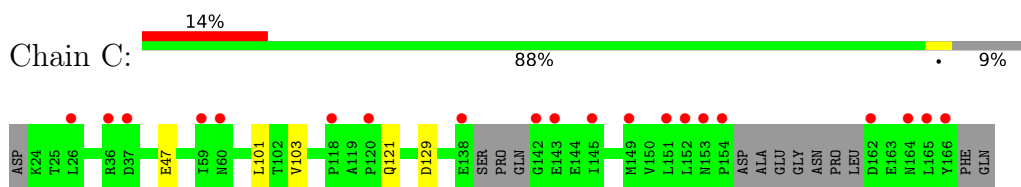
- Molecule 1: Integral membrane protein GPR180



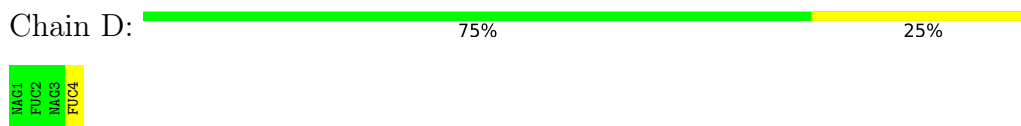
- Molecule 1: Integral membrane protein GPR180



- Molecule 1: Integral membrane protein GPR180



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



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



4 Data and refinement statistics i

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α , β , γ	143.12Å 143.12Å 43.56Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.25 – 1.88 25.25 – 1.88	Depositor EDS
% Data completeness (in resolution range)	90.3 (25.25-1.88) 90.2 (25.25-1.88)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 1.88Å)	Xtrriage
Refinement program	BUSTER 2.11.8	Depositor
R, R_{free}	0.221 , 0.237 0.204 , 0.228	Depositor DCC
R_{free} test set	1816 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	44.4	Xtrriage
Anisotropy	0.021	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 41.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.026 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6526	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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: ACT, FUC, NAG, GOL, 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	0.42	0/1000	0.61	0/1351
1	B	0.43	0/1095	0.64	0/1478
1	C	0.39	0/1078	0.60	0/1459
All	All	0.41	0/3173	0.62	0/4288

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	975	952	952	5	0
1	B	1071	1037	1037	6	0
1	C	1054	1016	1016	4	0
2	D	48	43	43	1	0
3	E	59	52	52	0	0
4	A	14	13	13	0	0
5	A	6	8	8	0	0
5	B	12	16	16	0	0
5	C	6	8	8	1	0
6	A	4	3	3	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	8	6	6	0	0
7	A	39	0	0	0	0
7	B	37	0	0	0	0
7	C	39	0	0	0	0
All	All	3372	3154	3154	12	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 (12) 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:77:ALA:HB3	1:A:122:THR:HG23	1.67	0.75
1:A:76:GLN:H	1:A:100:GLN:HE21	1.57	0.53
1:B:101:LEU:CD1	1:C:103:VAL:HG22	2.39	0.52
1:B:54:LEU:HD22	2:D:4:FUC:H61	1.92	0.52
1:C:129:ASP:O	5:C:201:GOL:H32	2.13	0.49
1:B:23:ASP:O	1:B:24:LYS:HB2	2.13	0.48
1:C:47:GLU:HG3	1:C:121:GLN:O	2.15	0.47
1:B:141:GLN:HB3	1:B:143:GLU:OE2	2.19	0.43
1:B:101:LEU:HD11	1:C:101:LEU:HD11	2.01	0.42
1:A:72:LEU:HB2	1:A:103:VAL:HG12	2.02	0.42
1:A:101:LEU:HD21	1:B:64:VAL:HG21	2.01	0.41
1:A:76:GLN:H	1:A:100:GLN:NE2	2.18	0.41

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	119/146 (82%)	118 (99%)	1 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	127/146 (87%)	126 (99%)	0	1 (1%)	16	6
1	C	128/146 (88%)	127 (99%)	1 (1%)	0	100	100
All	All	374/438 (85%)	371 (99%)	2 (0%)	1 (0%)	37	26

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	24	LYS

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	106/124 (86%)	102 (96%)	4 (4%)	28	12
1	B	116/124 (94%)	115 (99%)	1 (1%)	75	69
1	C	114/124 (92%)	114 (100%)	0	100	100
All	All	336/372 (90%)	331 (98%)	5 (2%)	60	49

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

Mol	Chain	Res	Type
1	A	47	GLU
1	A	76	GLN
1	A	78	GLN
1	A	122	THR
1	B	23	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	GLN
1	B	45	HIS
1	C	100	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](#)

9 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	D	1	1,2	14,14,15	0.30	0	17,19,21	0.74	0
2	FUC	D	2	2	10,10,11	0.34	0	14,14,16	0.45	0
2	NAG	D	3	2	14,14,15	0.26	0	17,19,21	0.42	0
2	FUC	D	4	2	10,10,11	0.36	0	14,14,16	0.57	0
3	NAG	E	1	1,3	14,14,15	0.32	0	17,19,21	0.61	0
3	NAG	E	2	3	14,14,15	0.31	0	17,19,21	0.92	1 (5%)
3	BMA	E	3	3	11,11,12	0.68	0	15,15,17	1.45	1 (6%)
3	FUC	E	4	3	10,10,11	0.34	0	14,14,16	0.51	0
3	FUC	E	5	3	10,10,11	0.38	0	14,14,16	0.62	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
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	FUC	D	2	2	-	-	0/1/1/1
2	NAG	D	3	2	-	0/6/23/26	0/1/1/1
2	FUC	D	4	2	-	-	0/1/1/1
3	NAG	E	1	1,3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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	FUC	E	4	3	-	-	0/1/1/1
3	FUC	E	5	3	-	-	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	3	BMA	C1-O5-C5	4.90	118.83	112.19
3	E	2	NAG	C2-N2-C7	3.15	127.39	122.90

There are no chirality outliers.

All (2) torsion outliers are listed below:

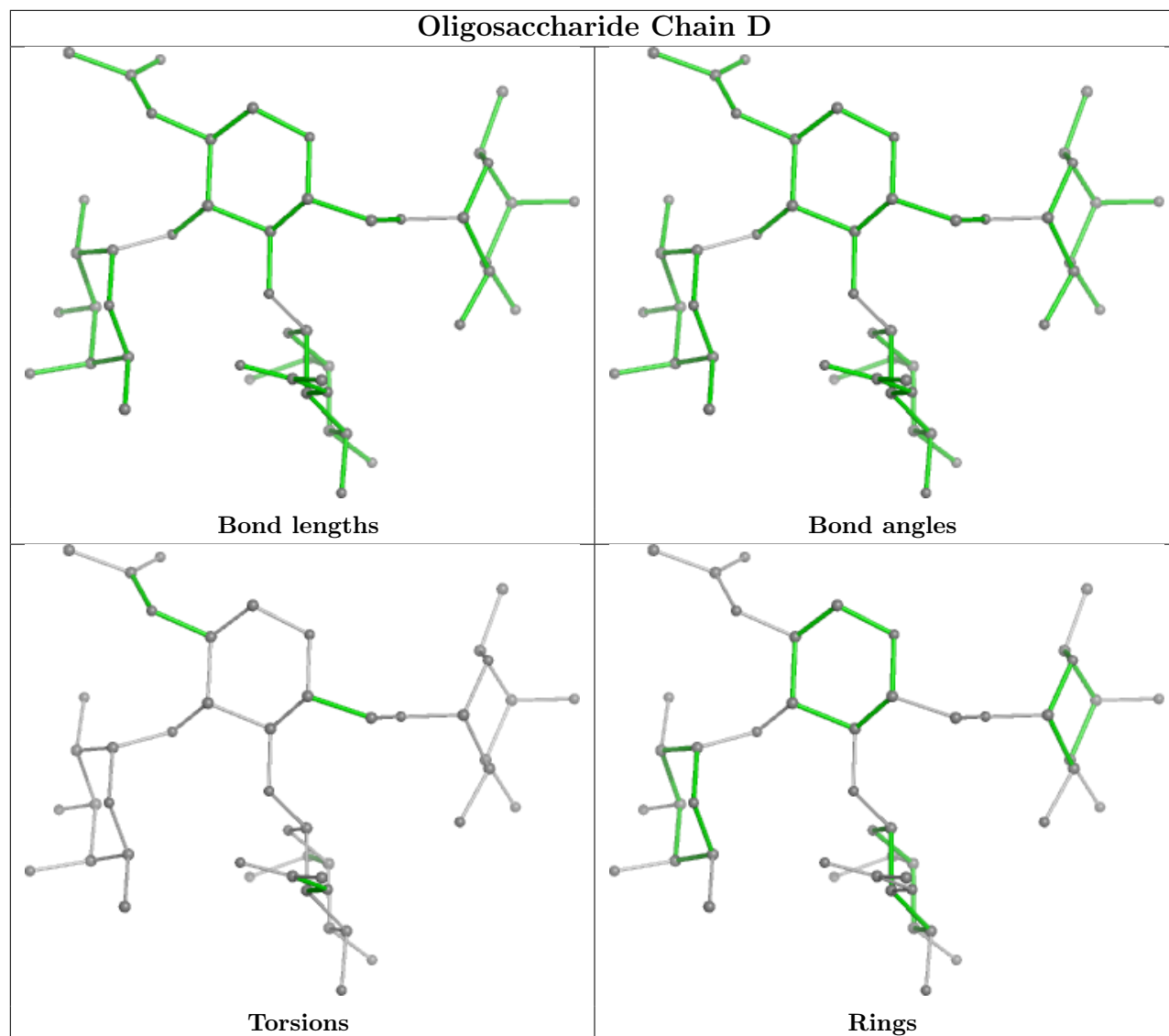
Mol	Chain	Res	Type	Atoms
3	E	2	NAG	C8-C7-N2-C2
3	E	2	NAG	O7-C7-N2-C2

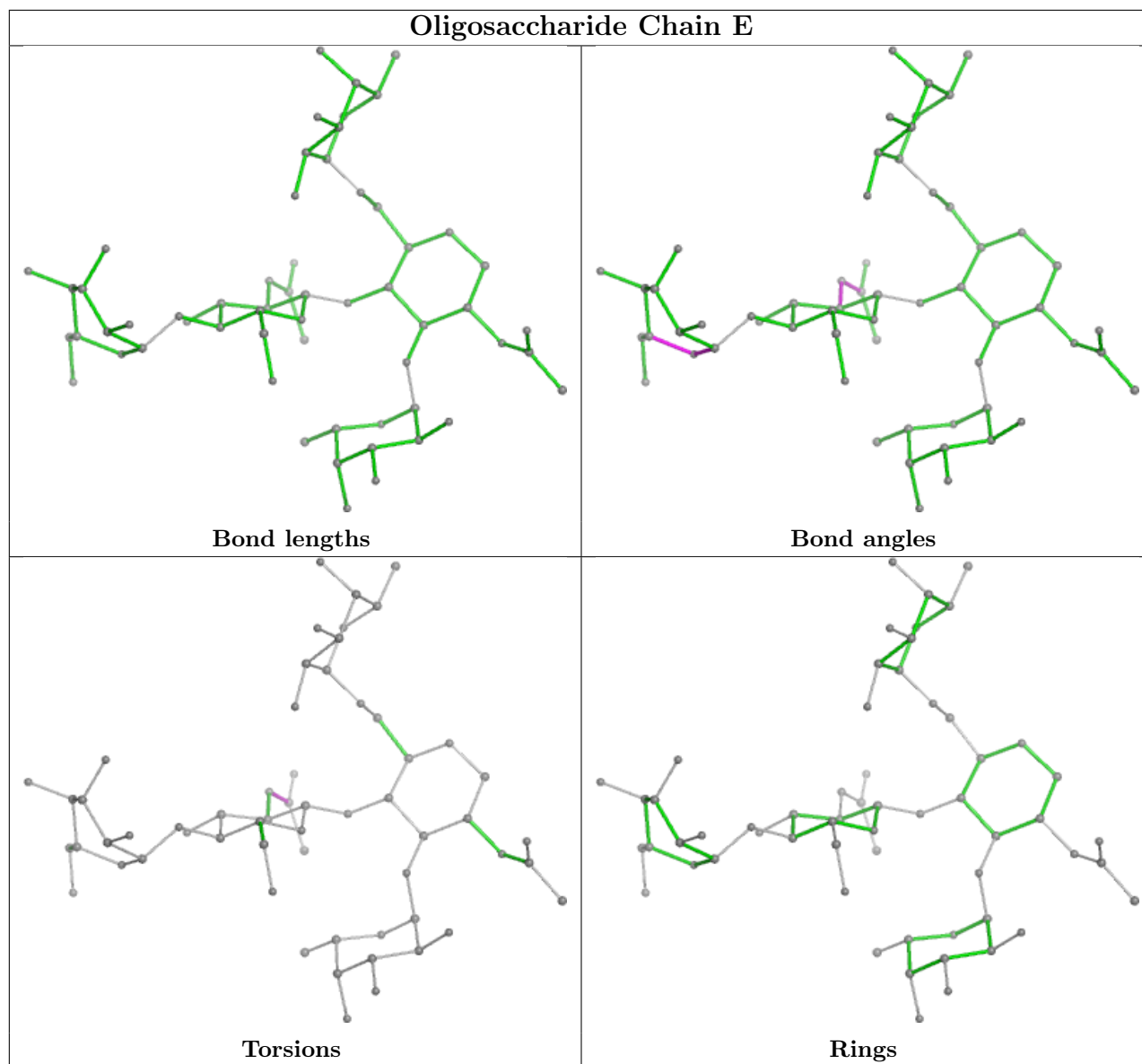
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	4	FUC	1	0

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





5.6 Ligand geometry [i](#)

8 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	GOL	A	202	-	5,5,5	0.08	0	5,5,5	0.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	GOL	B	201	-	5,5,5	0.11	0	5,5,5	0.22	0
5	GOL	B	203	-	5,5,5	0.09	0	5,5,5	0.25	0
6	ACT	A	203	-	3,3,3	0.55	0	3,3,3	1.74	2 (66%)
4	NAG	A	201	1	14,14,15	0.27	0	17,19,21	0.53	0
6	ACT	B	204	-	3,3,3	1.14	0	3,3,3	1.57	1 (33%)
5	GOL	C	201	-	5,5,5	0.16	0	5,5,5	0.25	0
6	ACT	B	202	-	3,3,3	1.11	0	3,3,3	1.55	1 (33%)

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	GOL	A	202	-	-	0/4/4/4	-
5	GOL	B	201	-	-	0/4/4/4	-
5	GOL	B	203	-	-	3/4/4/4	-
4	NAG	A	201	1	-	0/6/23/26	0/1/1/1
5	GOL	C	201	-	-	2/4/4/4	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	203	ACT	OXT-C-O	2.22	130.24	122.05
6	B	204	ACT	OXT-C-O	2.09	129.76	122.05
6	B	202	ACT	OXT-C-O	2.05	129.61	122.05
6	A	203	ACT	O-C-CH3	-2.04	114.37	122.33

There are no chirality outliers.

All (5) torsion outliers are listed below:

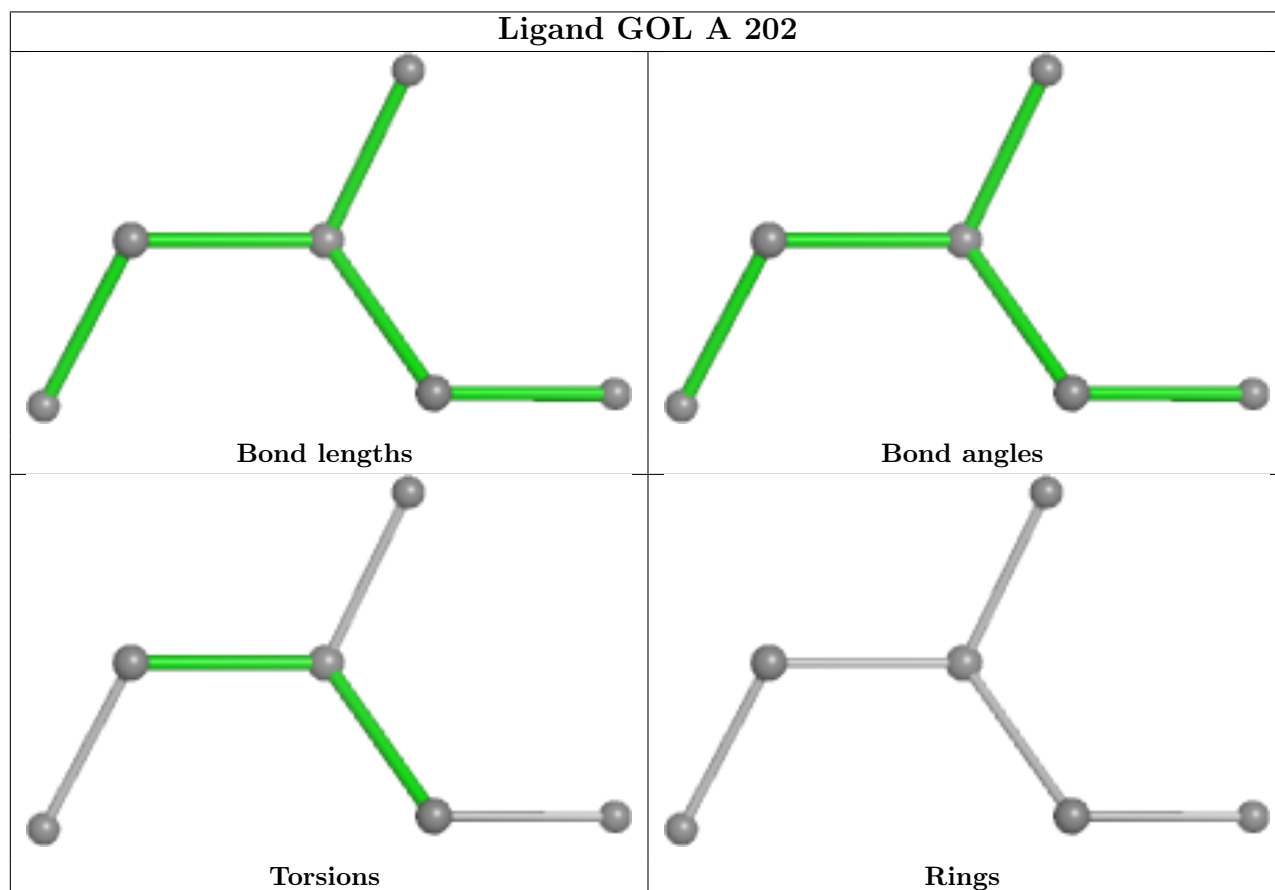
Mol	Chain	Res	Type	Atoms
5	C	201	GOL	C1-C2-C3-O3
5	C	201	GOL	O2-C2-C3-O3
5	B	203	GOL	O1-C1-C2-O2
5	B	203	GOL	C1-C2-C3-O3
5	B	203	GOL	O1-C1-C2-C3

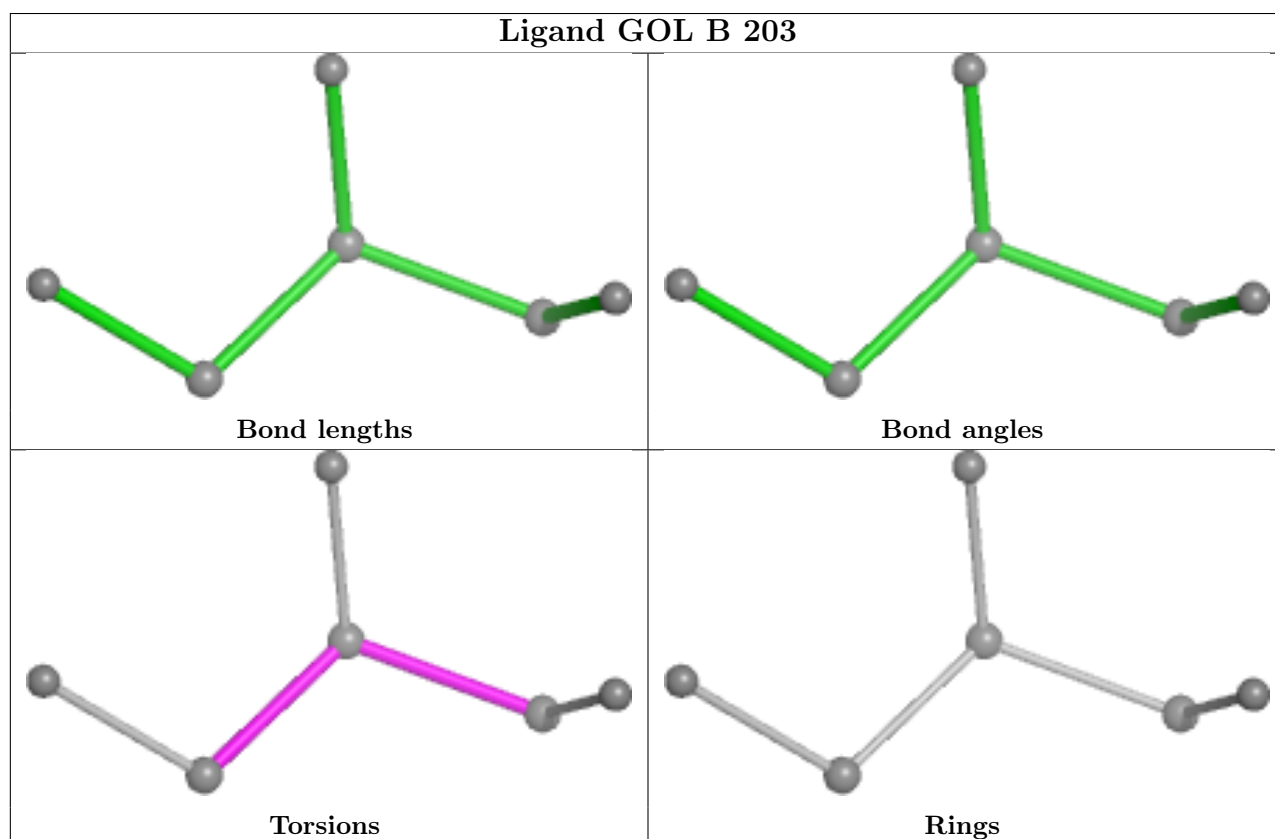
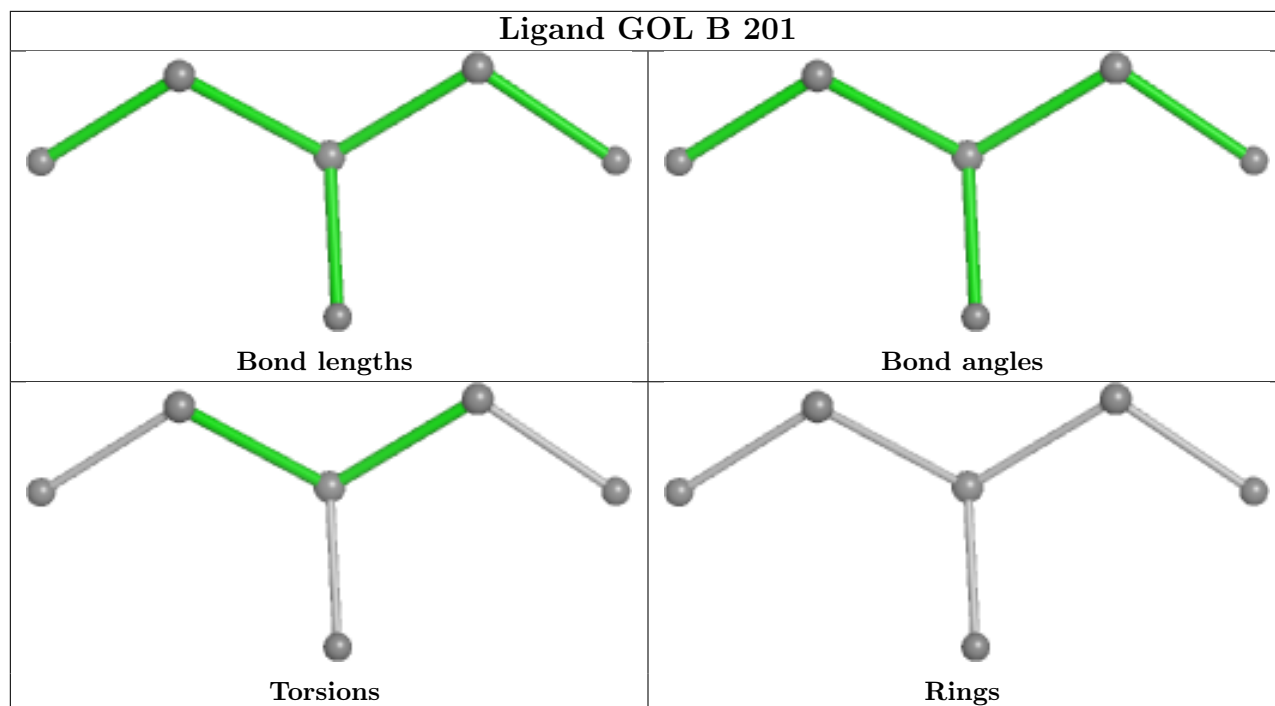
There are no ring outliers.

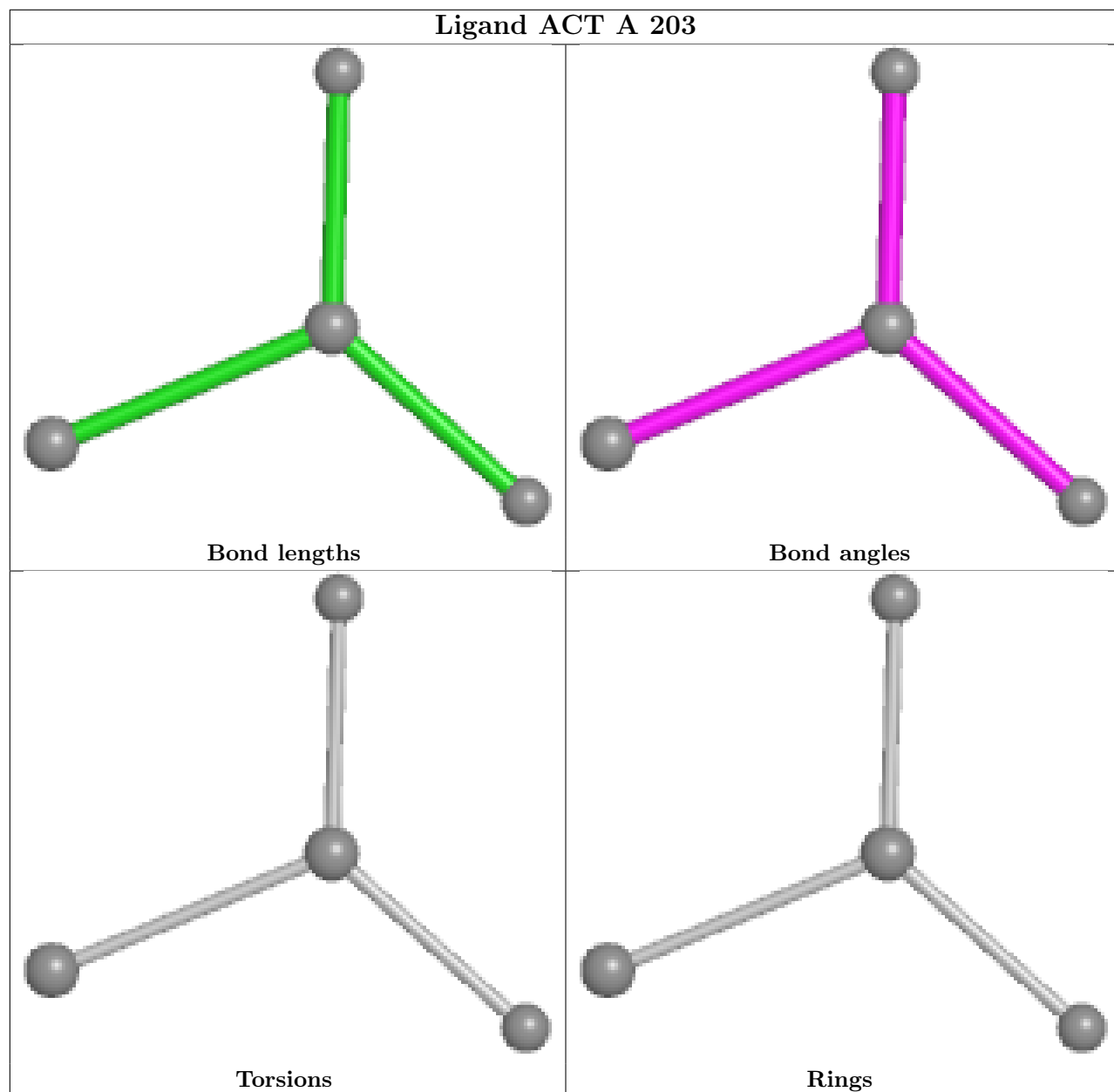
1 monomer is involved in 1 short contact:

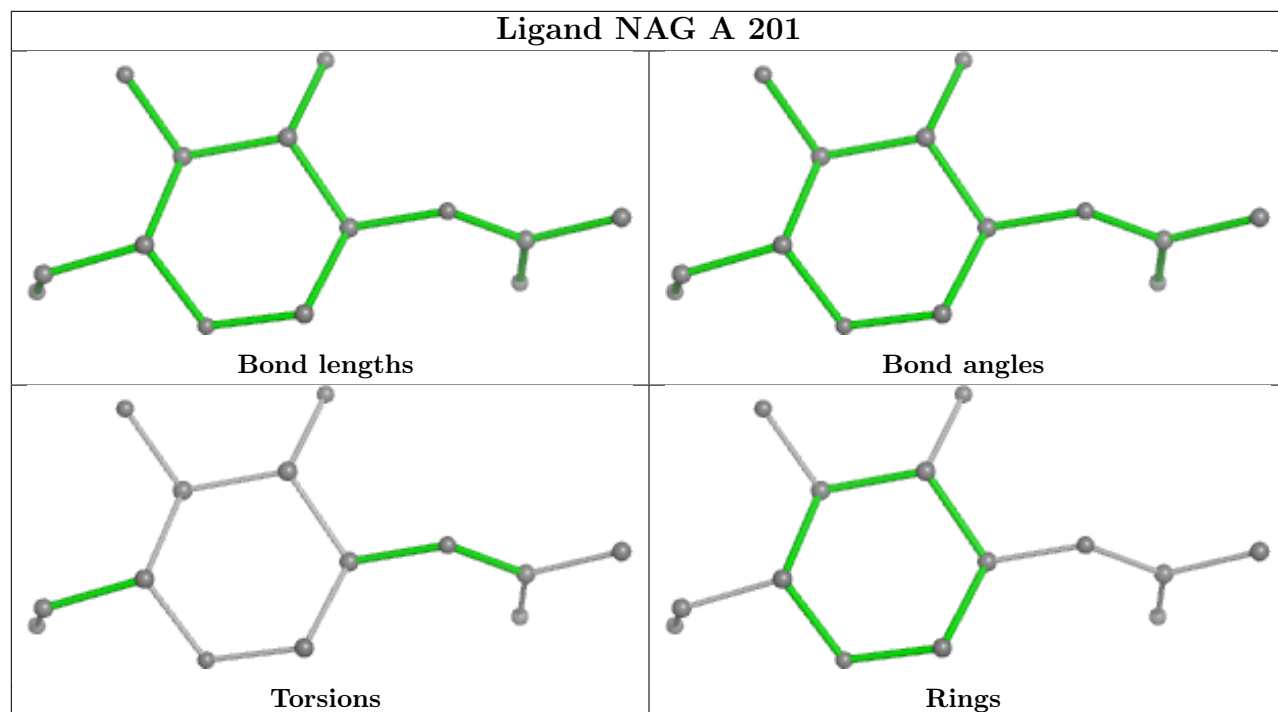
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	201	GOL	1	0

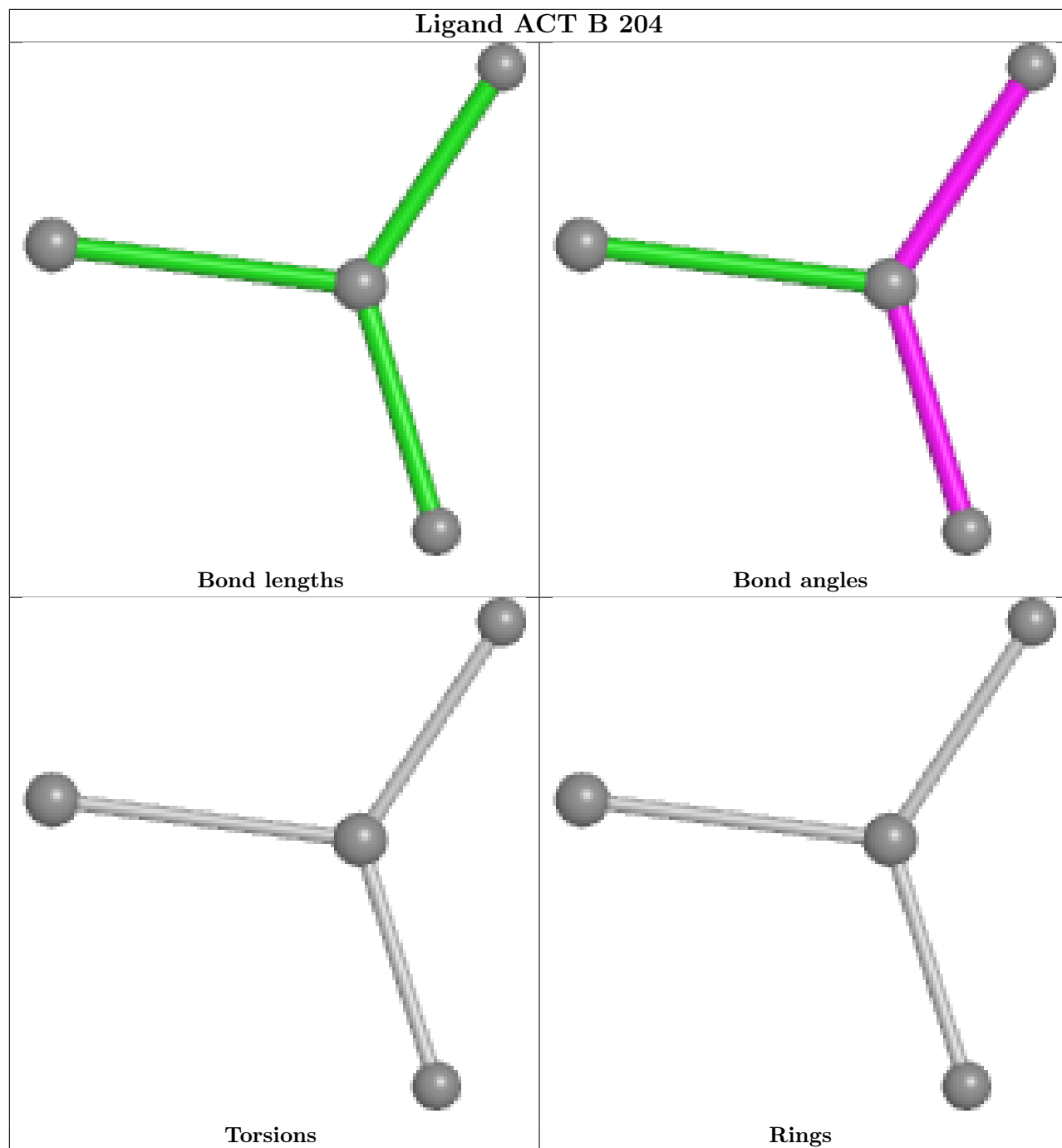
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

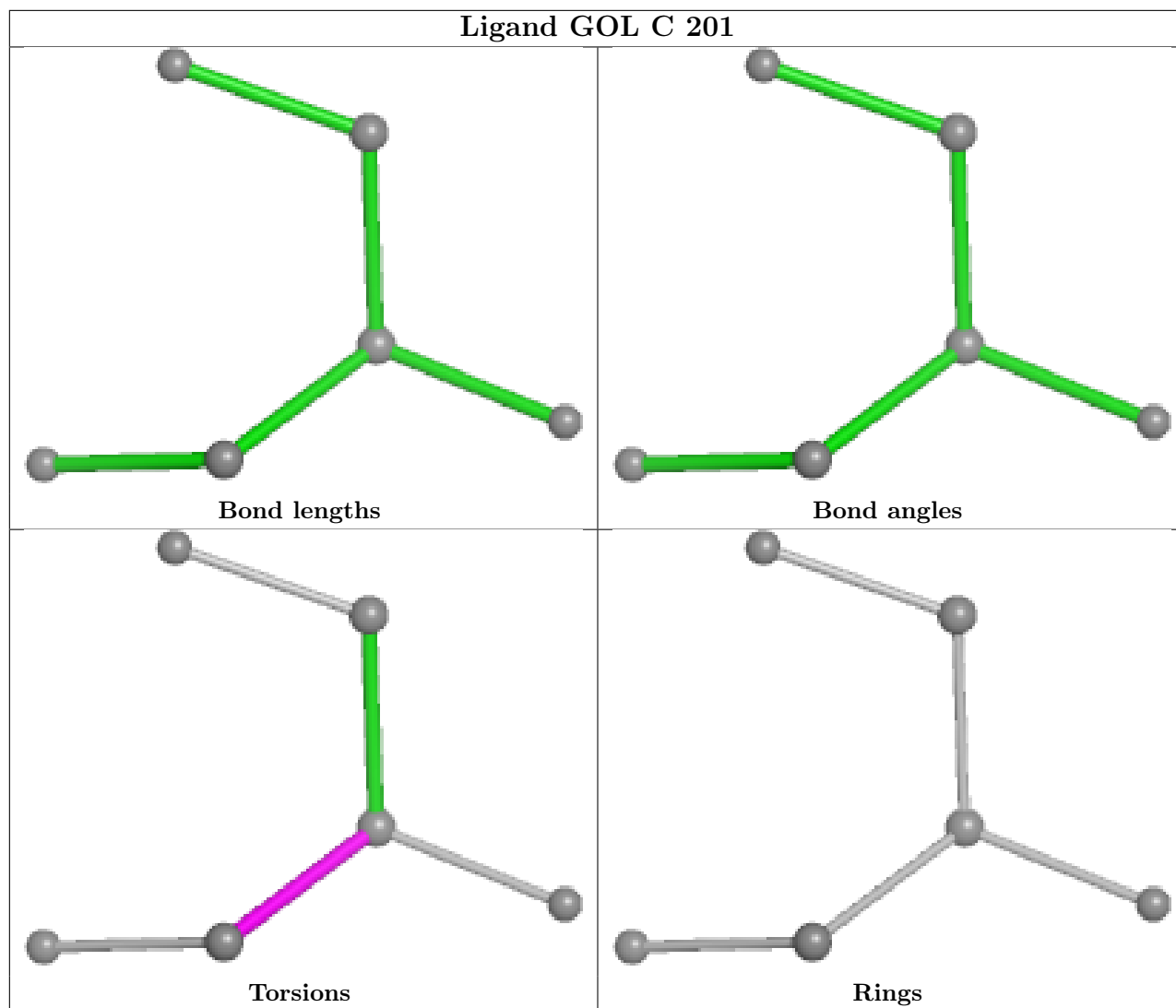


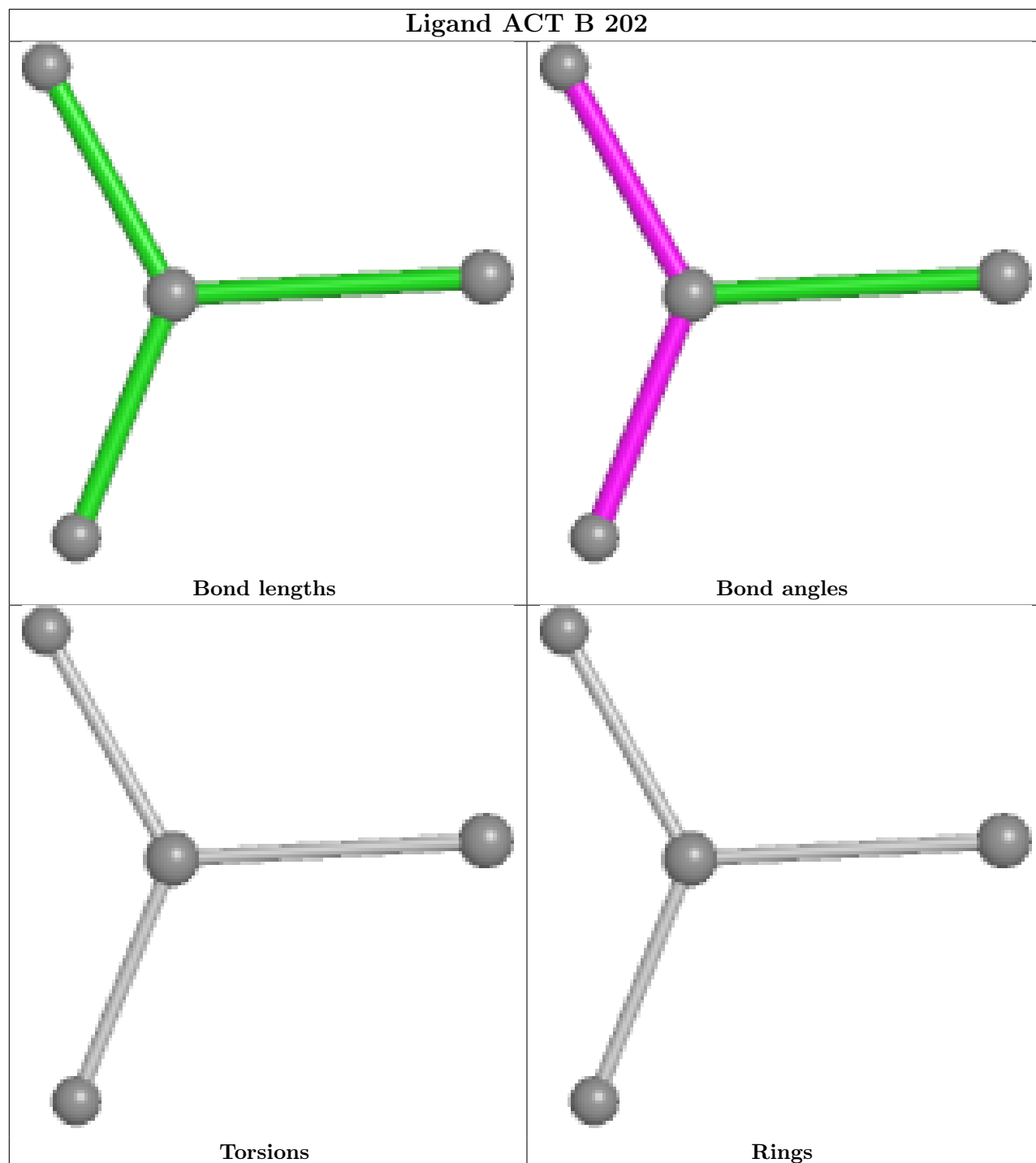












5.7 Other polymers [i](#)

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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	123/146 (84%)	0.51	9 (7%) 22 24	21, 48, 67, 77	3 (2%)
1	B	134/146 (91%)	0.28	8 (5%) 29 29	25, 45, 62, 75	1 (0%)
1	C	133/146 (91%)	0.85	20 (15%) 6 7	34, 55, 85, 98	4 (3%)
All	All	390/438 (89%)	0.55	37 (9%) 15 18	21, 49, 75, 98	8 (2%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	49	HIS	13.4
1	C	166	TYR	7.0
1	A	154	PRO	5.1
1	C	118	PRO	5.0
1	C	154	PRO	4.7
1	C	142	GLY	3.5
1	C	26	LEU	3.5
1	A	115	SER	3.3
1	C	165	LEU	3.1
1	C	149	MET	3.1
1	A	122	THR	3.0
1	B	24	LYS	2.8
1	C	152	LEU	2.8
1	A	153	ASN	2.8
1	C	120	PRO	2.8
1	A	134	ARG	2.8
1	B	155	ASP	2.8
1	C	162	ASP	2.7
1	A	116	GLN	2.7
1	C	138	GLU	2.7
1	B	140	PRO	2.7
1	B	167	PHE	2.6
1	C	164	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	143	GLU	2.6
1	C	145	ILE	2.6
1	B	168	GLN	2.6
1	B	23	ASP	2.5
1	A	80	TRP	2.5
1	C	60	ASN	2.3
1	C	37	ASP	2.3
1	B	160	PRO	2.3
1	C	36	ARG	2.3
1	C	153	ASN	2.3
1	C	151	LEU	2.3
1	C	59	ILE	2.1
1	A	52	HIS	2.0
1	B	134	ARG	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](#)

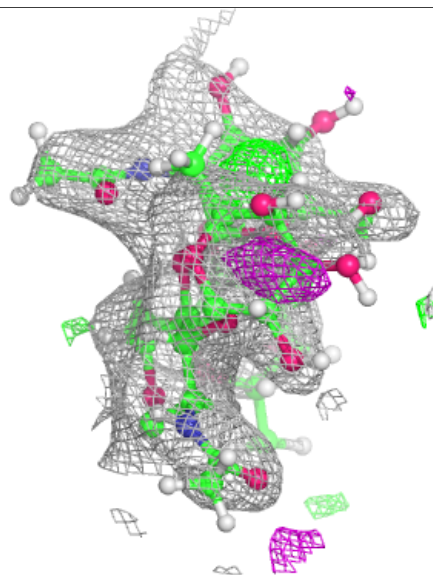
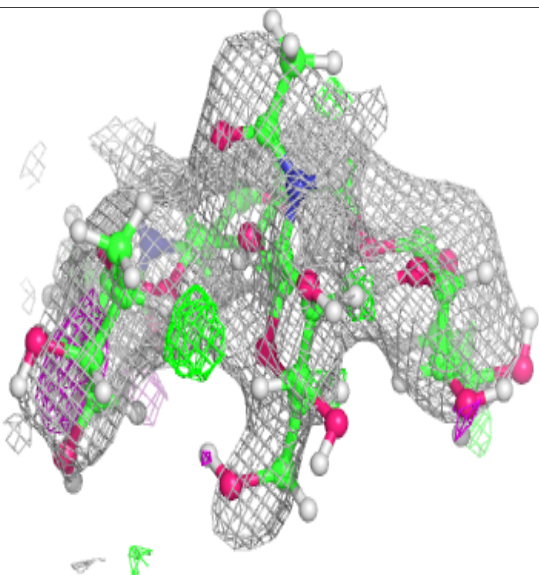
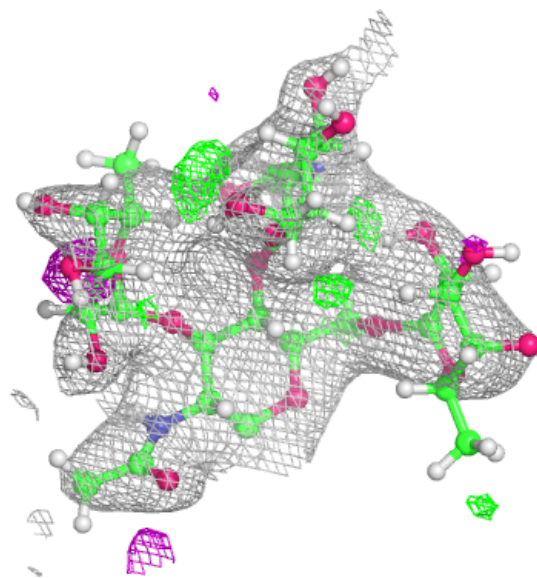
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

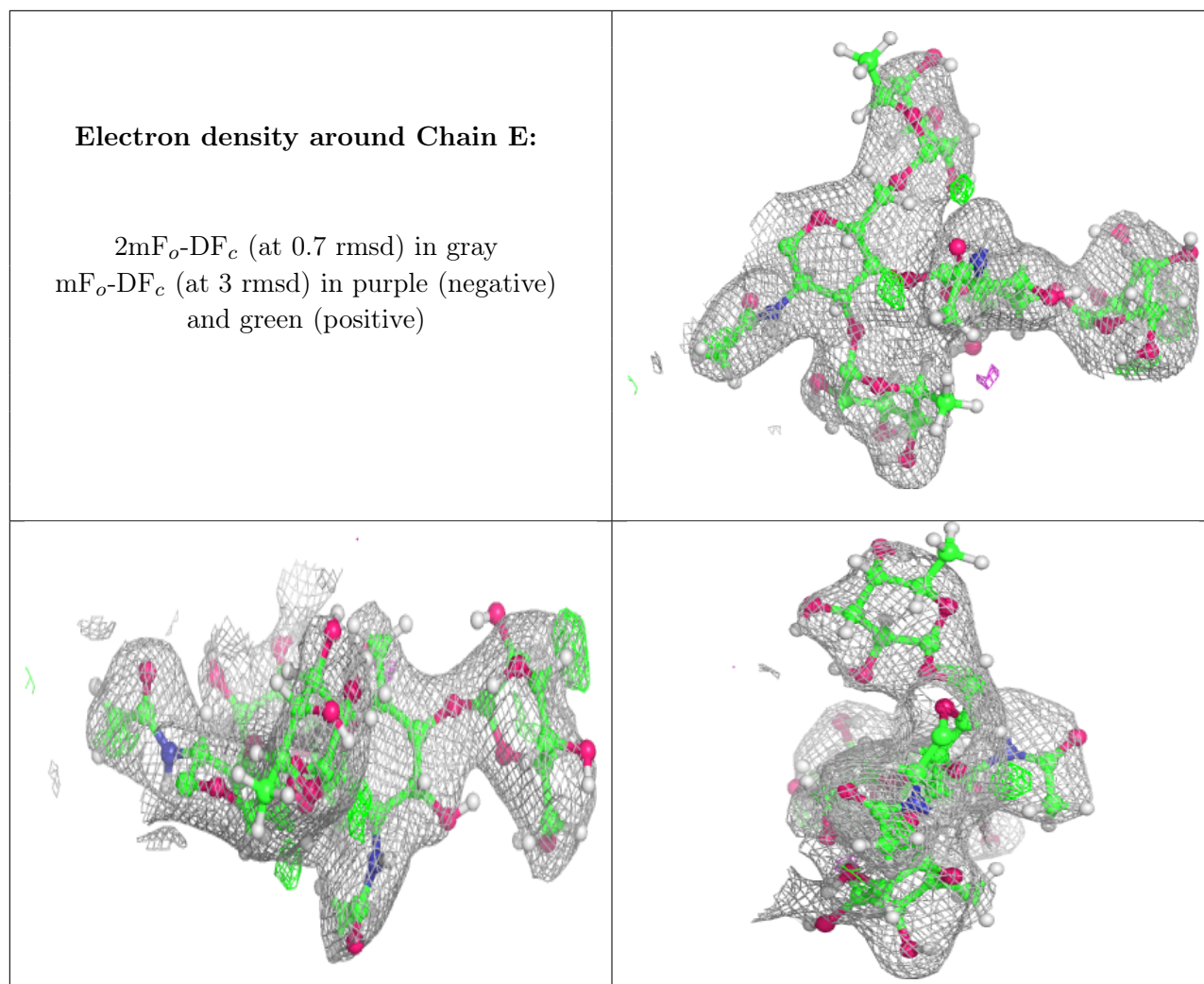
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	BMA	E	3	11/12	0.32	0.16	88,90,91,92	0
2	FUC	D	2	10/11	0.58	0.17	74,75,76,76	0
2	NAG	D	3	14/15	0.59	0.16	78,80,80,81	0
2	FUC	D	4	10/11	0.67	0.17	79,81,81,81	0
3	NAG	E	2	14/15	0.70	0.12	80,83,84,86	0
3	FUC	E	4	10/11	0.84	0.11	73,74,74,74	0
3	FUC	E	5	10/11	0.84	0.16	77,79,79,79	0
2	NAG	D	1	14/15	0.85	0.11	63,69,74,76	0
3	NAG	E	1	14/15	0.87	0.10	65,70,74,77	0

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

Electron density around Chain D:

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



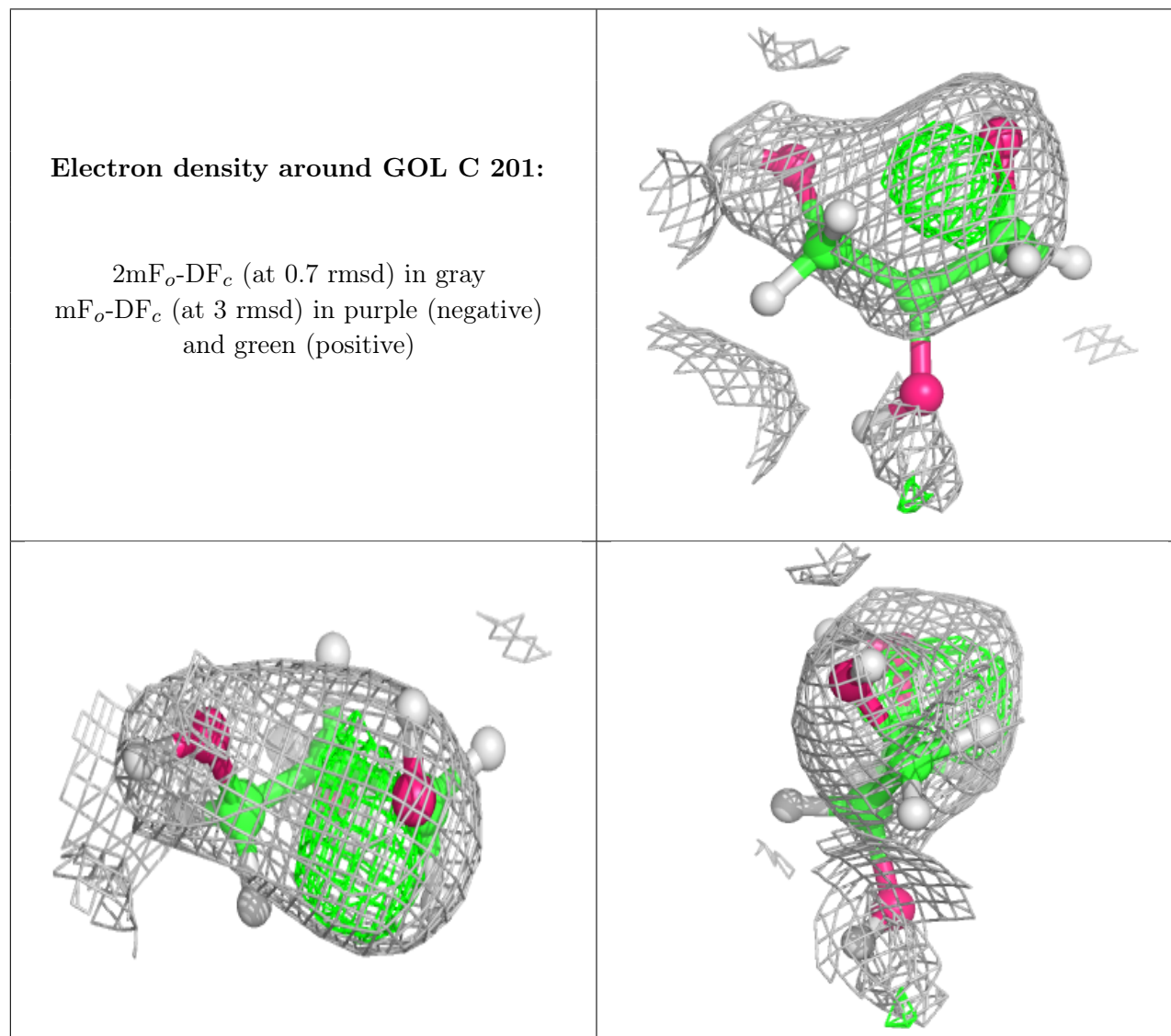


6.4 Ligands [i](#)

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.

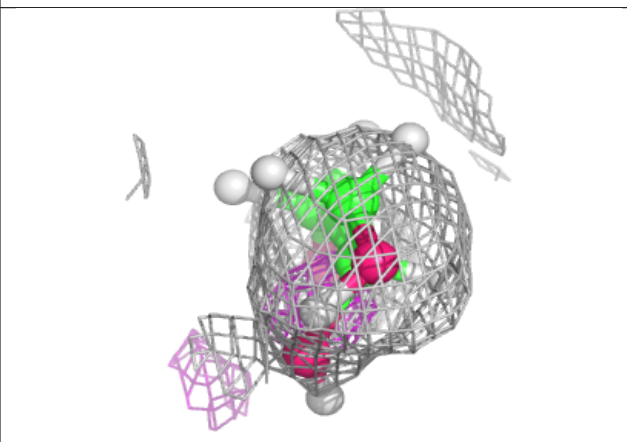
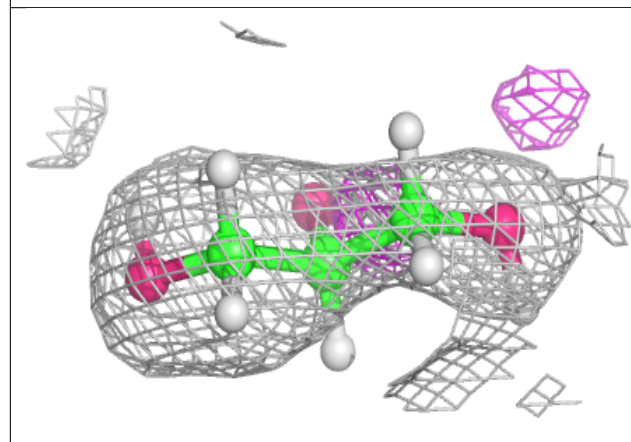
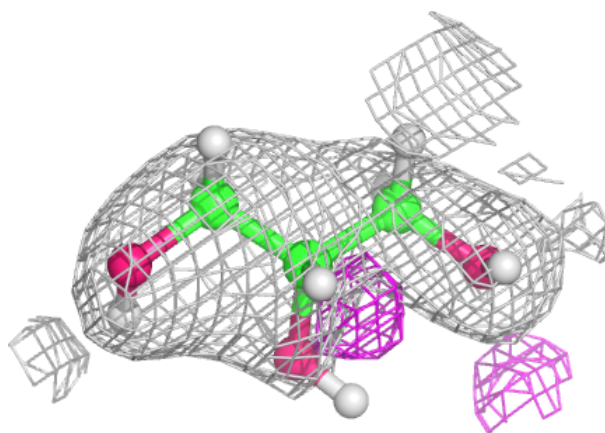
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	GOL	C	201	6/6	0.77	0.24	78,78,78,78	0
5	GOL	B	201	6/6	0.79	0.17	55,58,59,59	0
5	GOL	B	203	6/6	0.81	0.14	71,73,73,73	0
5	GOL	A	202	6/6	0.81	0.21	79,79,80,80	0
6	ACT	B	202	4/4	0.83	0.18	62,63,63,63	0
4	NAG	A	201	14/15	0.84	0.12	71,73,74,74	0
6	ACT	B	204	4/4	0.86	0.16	64,64,64,64	0
6	ACT	A	203	4/4	0.94	0.10	51,52,52,54	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.

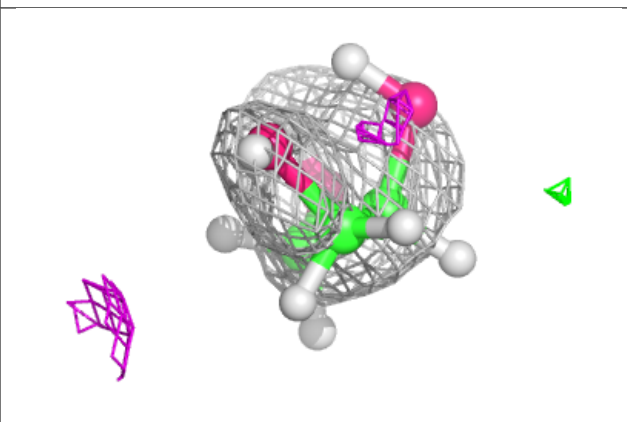
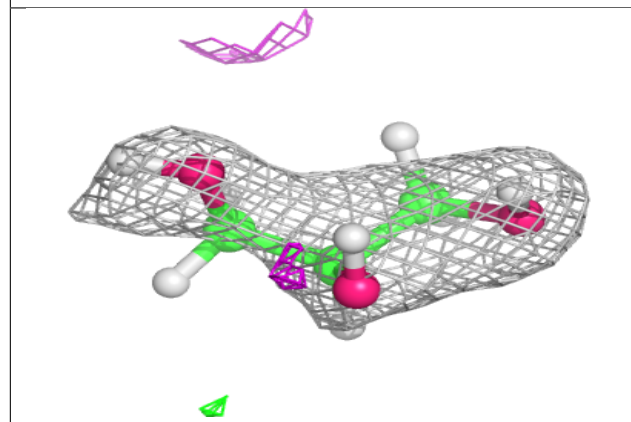
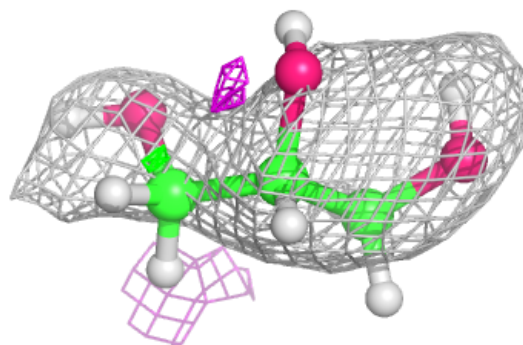


Electron density around GOL B 201:

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

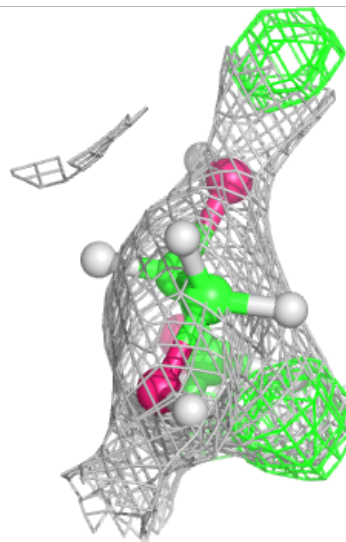
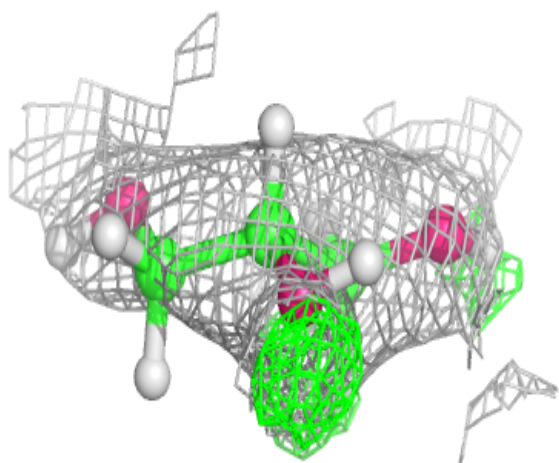
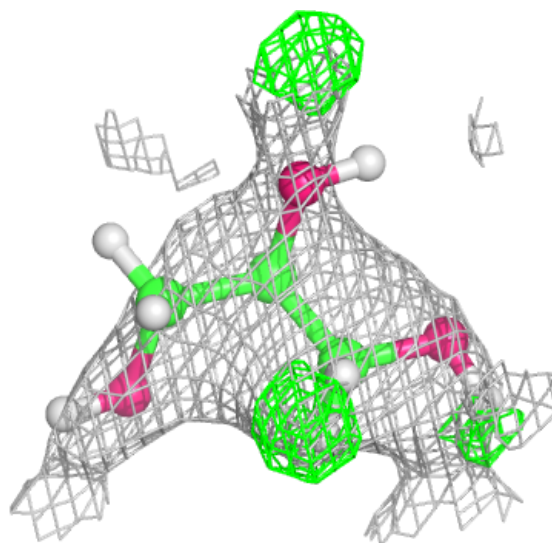
**Electron density around GOL B 203:**

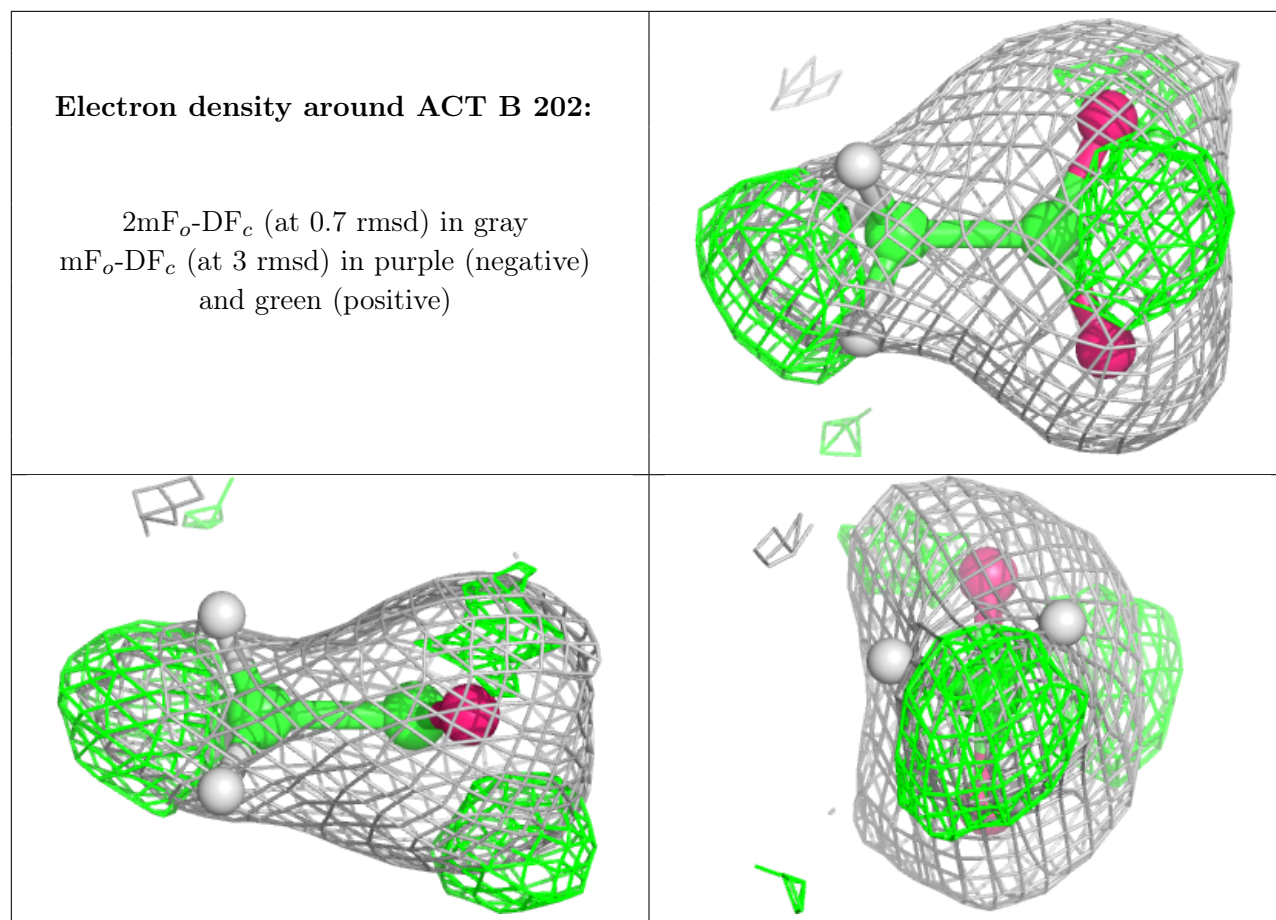
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around GOL A 202:

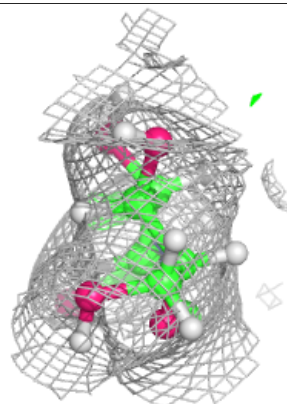
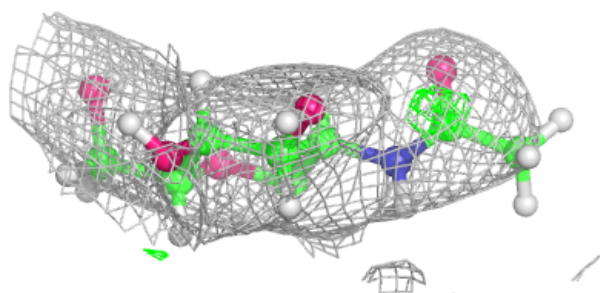
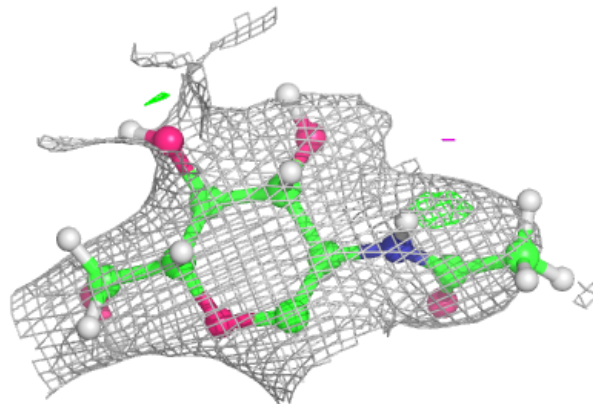
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

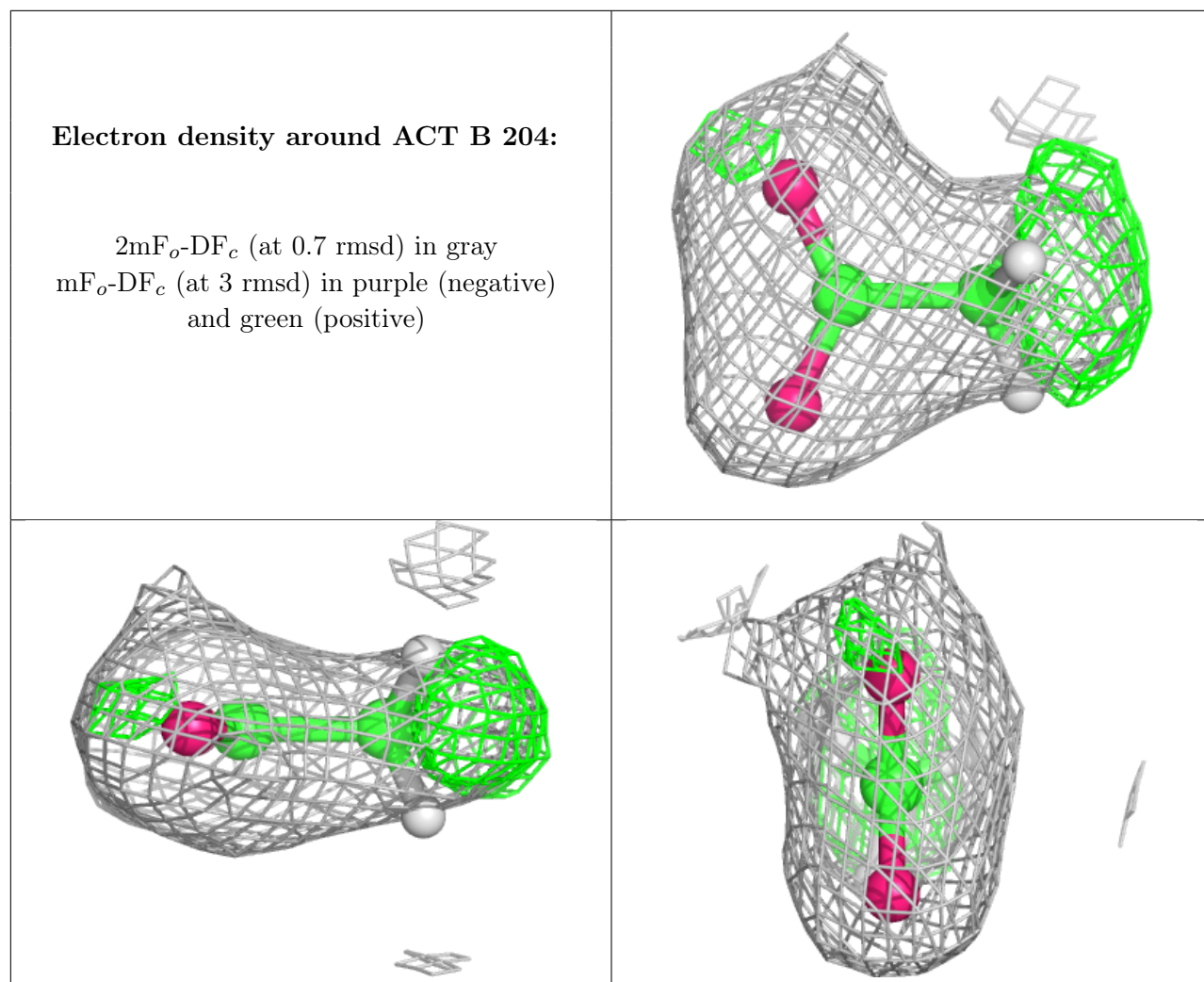


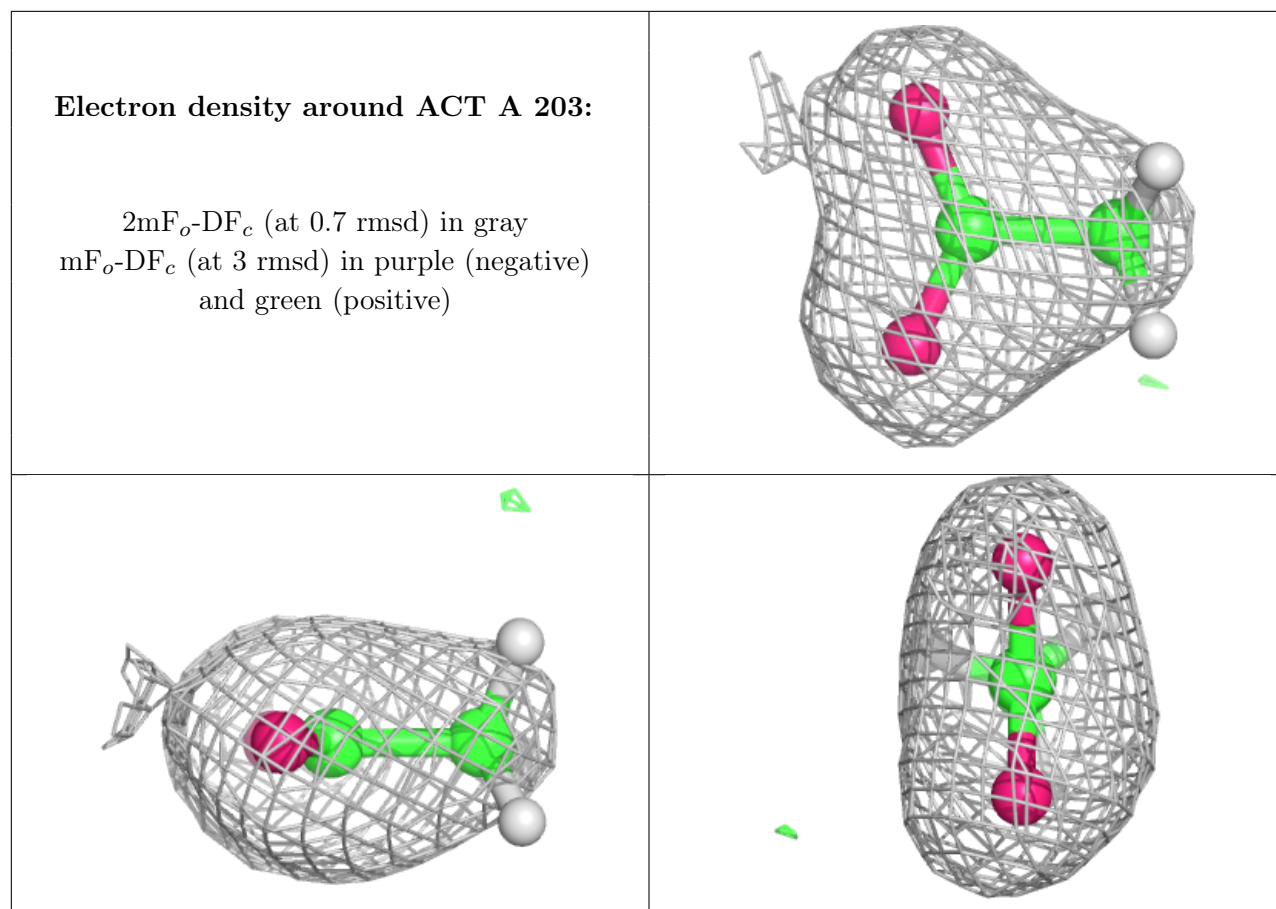


Electron density around NAG A 201:

$2mF_o-DF_c$ (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.