



Full wwPDB X-ray Structure Validation Report i

Jun 30, 2022 – 04:09 PM EDT

PDB ID : 7MQM
Title : AAC(3)-IIIa in complex with CoA and gentamicin
Authors : Zielinski, M.; Berghuis, A.M.
Deposited on : 2021-05-05
Resolution : 1.60 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 i 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](#) ①) 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	:	2.29
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)	:	2.29

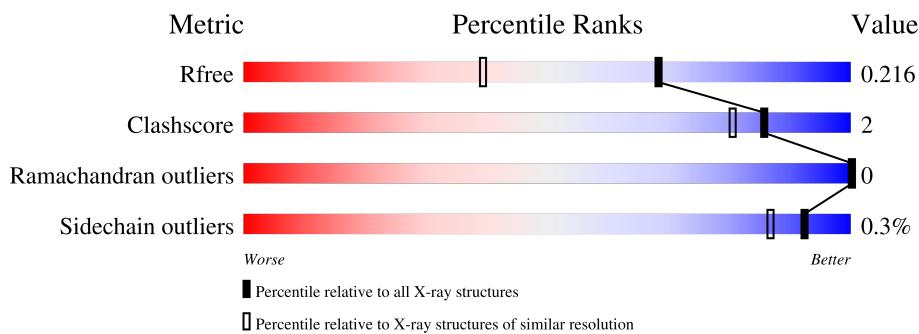
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)

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%

Mol	Chain	Length	Quality of chain
1	A	274	93% • 5%
1	B	274	91% • 5%
1	C	274	90% 5% 5%
1	D	274	91% 5% 5%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 9900 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.

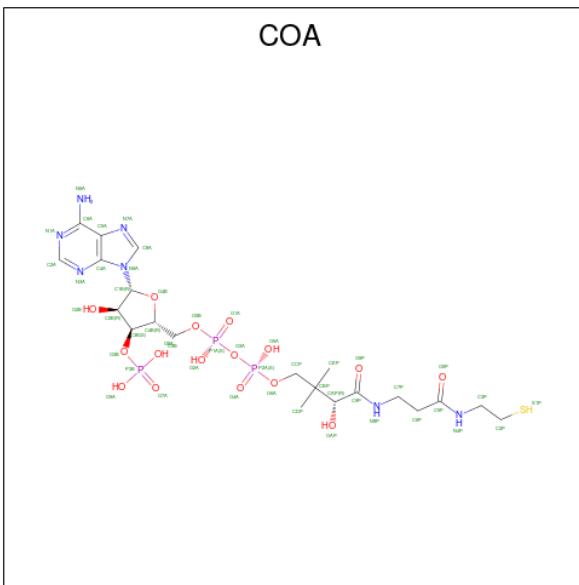
- Molecule 1 is a protein called Aminoglycoside N(3)-acetyltransferase III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	261	Total 2060	C 1314	N 360	O 376	S 10	0	7	0
1	B	261	Total 2059	C 1315	N 359	O 375	S 10	0	7	0
1	C	260	Total 2041	C 1303	N 351	O 376	S 11	0	7	0
1	D	261	Total 2018	C 1289	N 352	O 367	S 10	0	3	0

There are 12 discrepancies between the modelled and reference sequences:

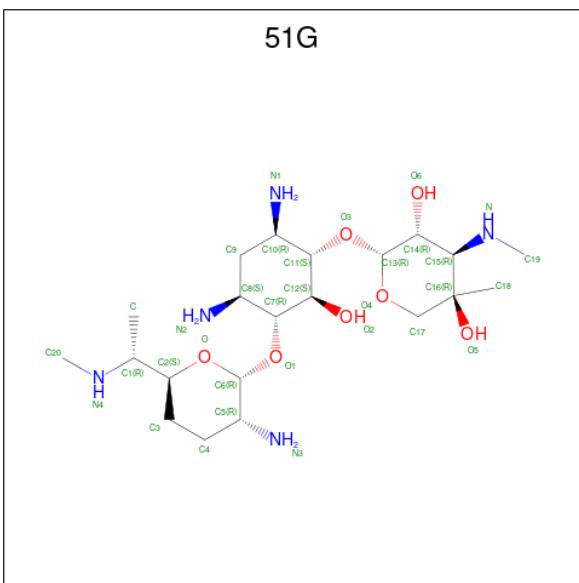
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P29808
A	-1	SER	-	expression tag	UNP P29808
A	0	HIS	-	expression tag	UNP P29808
B	-2	GLY	-	expression tag	UNP P29808
B	-1	SER	-	expression tag	UNP P29808
B	0	HIS	-	expression tag	UNP P29808
C	-2	GLY	-	expression tag	UNP P29808
C	-1	SER	-	expression tag	UNP P29808
C	0	HIS	-	expression tag	UNP P29808
D	-2	GLY	-	expression tag	UNP P29808
D	-1	SER	-	expression tag	UNP P29808
D	0	HIS	-	expression tag	UNP P29808

- Molecule 2 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S) (labeled as "Ligand of Interest" by depositor).



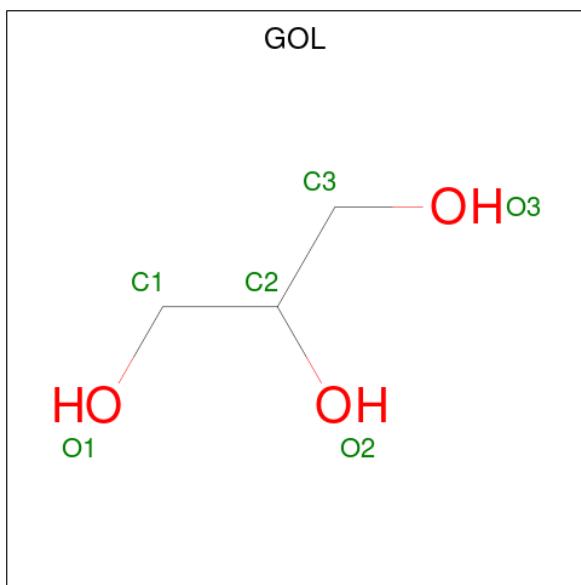
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
2	A	1	48	21	7	16	3	1	0	0
2	B	1	48	21	7	16	3	1	0	0
2	C	1	96	42	14	32	6	2	0	1
2	D	1	48	21	7	16	3	1	0	0

- Molecule 3 is gentamicin C1 (three-letter code: 51G) (formula: C₂₁H₄₃N₅O₇) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C 33	N 21	O 5	0	0
3	B	1	Total	C 66	N 42	O 10	0	1
3	C	1	Total	C 33	N 21	O 5	0	0
3	D	1	Total	C 33	N 21	O 5	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C 6	O 3	0	0
4	B	1	Total	C 6	O 3	0	0

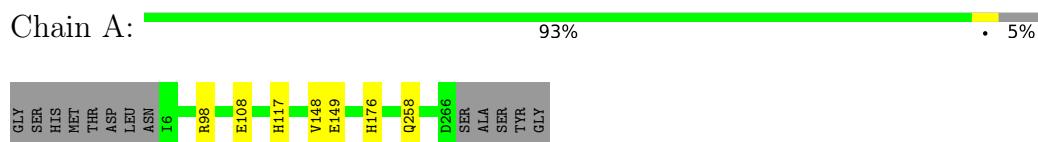
- Molecule 5 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	317	Total	O 317		0	1
5	B	325	Total	O 325		0	0
5	C	334	Total	O 334		0	1
5	D	329	Total	O 329		0	1

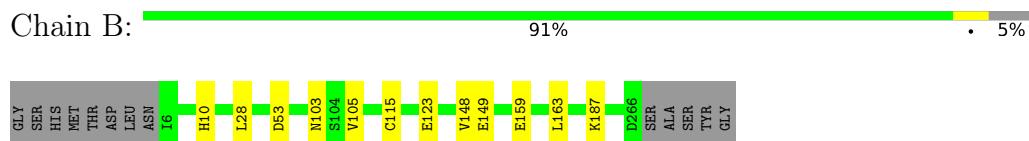
3 Residue-property plots

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

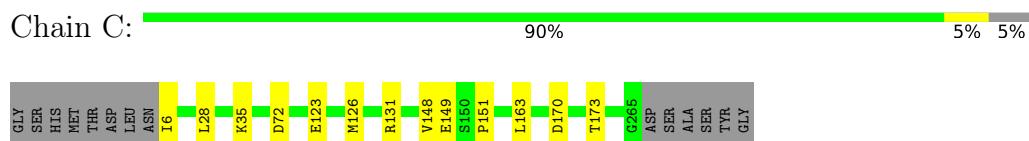
- Molecule 1: Aminoglycoside N(3)-acetyltransferase III



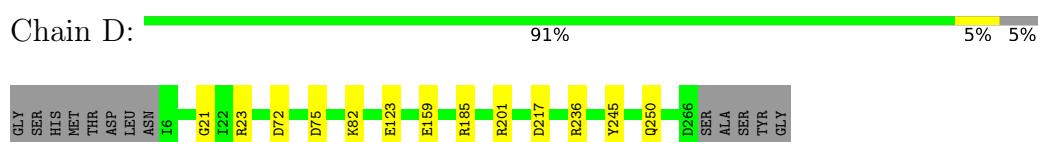
- Molecule 1: Aminoglycoside N(3)-acetyltransferase III



- Molecule 1: Aminoglycoside N(3)-acetyltransferase III



- Molecule 1: Aminoglycoside N(3)-acetyltransferase III



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	130.57 Å 91.06 Å 100.52 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.05 – 1.60 31.05 – 1.39	Depositor EDS
% Data completeness (in resolution range)	99.4 (31.05-1.60) 99.0 (31.05-1.39)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ ¹	2.85 (at 1.39 Å)	Xtriage
Refinement program	PHENIX (1.15.1_3469: ???)	Depositor
R , R_{free}	0.197 , 0.216 0.195 , 0.216	Depositor DCC
R_{free} test set	2458 reflections (1.05%)	wwPDB-VP
Wilson B-factor (Å ²)	2.1	Xtriage
Anisotropy	3.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.4	EDS
L-test for twinning ²	$< L > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	9900	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.32 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.5527e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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: 51G, GOL, CSO, COA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.26	0/2104	0.45	0/2868
1	B	0.27	0/2103	0.45	0/2869
1	C	0.26	0/2085	0.45	0/2845
1	D	0.26	0/2062	0.47	0/2812
All	All	0.26	0/8354	0.46	0/11394

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	2060	0	2007	4	0
1	B	2059	0	2001	9	0
1	C	2041	0	1972	11	0
1	D	2018	0	1964	10	0
2	A	48	0	32	0	0
2	B	48	0	32	1	0
2	C	96	0	64	4	0
2	D	48	0	32	1	0
3	A	33	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	66	0	0	1	0
3	C	33	0	0	3	0
3	D	33	0	0	3	0
4	A	6	0	8	0	0
4	B	6	0	8	1	0
5	A	317	0	0	2	0
5	B	325	0	0	3	0
5	C	334	0	0	2	1
5	D	329	0	0	1	1
All	All	9900	0	8120	36	1

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 (36) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:LYS:NZ	5:B:405:HOH:O	2.27	0.68
1:A:176:HIS:NE2	5:A:401:HOH:O	2.27	0.67
1:D:123:GLU:OE2	3:D:302:51G:N1	2.30	0.65
1:A:117:HIS:NE2	5:A:403:HOH:O	2.30	0.65
1:D:201:ARG:HH21	1:D:201:ARG:HG2	1.67	0.59
1:B:123:GLU:OE2	3:B:303[B]:51G:N1	2.35	0.59
1:C:35:LYS:HD2	2:C:301[B]:COA:O4A	2.03	0.58
1:C:35:LYS:HD2	2:C:301[A]:COA:O4A	2.04	0.56
1:C:173:THR:HG1	2:C:301[A]:COA:HS1	1.54	0.55
1:C:123:GLU:OE2	3:C:302:51G:N1	2.39	0.55
1:D:159:GLU:HG2	1:D:250:GLN:NE2	2.20	0.55
1:B:159:GLU:OE2	5:B:402:HOH:O	2.18	0.55
1:B:115:CSO:HA	4:B:302:GOL:H11	1.91	0.53
1:C:148:VAL:HG13	1:C:149[A]:GLU:HG2	1.90	0.53
1:C:6:ILE:N	5:C:407:HOH:O	2.42	0.53
1:C:131:ARG:NH2	5:C:404:HOH:O	2.36	0.52
1:B:103:ASN:OD1	5:B:401:HOH:O	2.18	0.50
1:A:98[B]:ARG:CZ	1:A:108:GLU:OE2	2.62	0.47
1:D:82[B]:LYS:NZ	5:D:1109:HOH:O	2.47	0.47
1:D:72:ASP:OD2	3:D:302:51G:N	2.48	0.47
1:B:105[B]:VAL:HG23	2:B:301:COA:O2A	2.13	0.47
1:B:28:LEU:HD11	1:B:163:LEU:HB2	1.97	0.46
1:D:159:GLU:HG2	1:D:250:GLN:HE22	1.80	0.46
2:D:301:COA:S1P	3:D:302:51G:N2	2.89	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:VAL:HG13	1:B:149:GLU:HG2	1.98	0.45
2:C:301[A]:COA:S1P	3:C:302:51G:N2	2.90	0.45
1:D:75:ASP:OD1	1:D:82[A]:LYS:NZ	2.30	0.45
1:D:236:ARG:HD2	1:D:245:TYR:CE1	2.53	0.44
1:C:126:MET:HG3	1:C:151:PRO:HG2	2.00	0.43
1:A:148:VAL:HG13	1:A:149:GLU:HG2	2.00	0.43
1:C:72:ASP:OD2	3:C:302:51G:N	2.52	0.42
1:B:10:HIS:NE2	1:B:53:ASP:OD2	2.43	0.42
1:D:185:ARG:NH1	1:D:217:ASP:OD2	2.53	0.42
1:C:28[B]:LEU:HD11	1:C:163:LEU:HB2	2.03	0.41
1:C:28[A]:LEU:HD11	1:C:163:LEU:HB2	2.03	0.40
1:D:21:GLY:O	1:D:23:ARG:HG3	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:529:HOH:O	5:D:1173:HOH:O[1_554]	2.18	0.02

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	265/274 (97%)	257 (97%)	8 (3%)	0	100 100
1	B	266/274 (97%)	258 (97%)	8 (3%)	0	100 100
1	C	264/274 (96%)	255 (97%)	9 (3%)	0	100 100
1	D	261/274 (95%)	253 (97%)	8 (3%)	0	100 100
All	All	1056/1096 (96%)	1023 (97%)	33 (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	207/214 (97%)	205 (99%)	2 (1%)	76 61
1	B	205/214 (96%)	205 (100%)	0	100 100
1	C	204/214 (95%)	202 (99%)	2 (1%)	76 61
1	D	201/214 (94%)	201 (100%)	0	100 100
All	All	817/856 (95%)	813 (100%)	4 (0%)	92 80

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	258[A]	GLN
1	A	258[B]	GLN
1	C	170[A]	ASP
1	C	170[B]	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	117	HIS
1	D	250	GLN

5.3.3 RNA [\(i\)](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [\(i\)](#)

4 non-standard protein/DNA/RNA residues 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
1	CSO	A	115	1	3,6,7	0.61	0	0,6,8	-	-
1	CSO	B	115	1	3,6,7	0.54	0	0,6,8	-	-
1	CSO	D	115	1	3,6,7	0.55	0	0,6,8	-	-
1	CSO	C	115	1	3,6,7	0.53	0	0,6,8	-	-

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
1	CSO	A	115	1	-	0/1/5/7	-
1	CSO	B	115	1	-	0/1/5/7	-
1	CSO	D	115	1	-	0/1/5/7	-
1	CSO	C	115	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	115	CSO	1	0

5.5 Carbohydrates [\(i\)](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [\(i\)](#)

12 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$
3	51G	C	302	-	31,35,35	1.13	3 (9%)	33,52,52	1.57	3 (9%)
3	51G	A	302	-	31,35,35	1.42	4 (12%)	33,52,52	1.78	8 (24%)
4	GOL	A	303	-	5,5,5	0.94	0	5,5,5	0.94	0
3	51G	B	303[A]	-	31,35,35	1.04	3 (9%)	33,52,52	1.69	7 (21%)
4	GOL	B	302	-	5,5,5	0.90	0	5,5,5	1.04	0
2	COA	D	301	-	41,50,50	3.80	14 (34%)	52,75,75	2.04	9 (17%)
2	COA	C	301[B]	-	41,50,50	3.85	14 (34%)	52,75,75	1.98	10 (19%)
2	COA	A	301	-	41,50,50	3.84	14 (34%)	52,75,75	1.90	9 (17%)
3	51G	B	303[B]	-	31,35,35	1.08	3 (9%)	33,52,52	1.53	4 (12%)
3	51G	D	302	-	31,35,35	1.23	4 (12%)	33,52,52	1.46	5 (15%)
2	COA	B	301	-	41,50,50	3.85	15 (36%)	52,75,75	1.96	8 (15%)
2	COA	C	301[A]	-	41,50,50	3.93	15 (36%)	52,75,75	2.02	7 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	51G	C	302	-	-	10/15/69/69	0/3/3/3
3	51G	A	302	-	-	7/15/69/69	0/3/3/3
4	GOL	A	303	-	-	2/4/4/4	-
3	51G	B	303[A]	-	-	8/15/69/69	1/3/3/3
4	GOL	B	302	-	-	2/4/4/4	-
2	COA	D	301	-	-	3/44/64/64	0/3/3/3
2	COA	C	301[B]	-	-	3/44/64/64	0/3/3/3
2	COA	A	301	-	-	4/44/64/64	0/3/3/3
3	51G	B	303[B]	-	-	6/15/69/69	0/3/3/3
3	51G	D	302	-	-	6/15/69/69	0/3/3/3
2	COA	B	301	-	-	2/44/64/64	0/3/3/3
2	COA	C	301[A]	-	-	3/44/64/64	0/3/3/3

All (89) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301[A]	COA	O4B-C1B	15.88	1.63	1.41
2	C	301[B]	COA	O4B-C1B	15.62	1.62	1.41
2	A	301	COA	O4B-C1B	15.51	1.62	1.41
2	B	301	COA	O4B-C1B	15.49	1.62	1.41
2	D	301	COA	O4B-C1B	15.23	1.62	1.41
2	C	301[A]	COA	C2B-C1B	-12.16	1.35	1.53
2	C	301[B]	COA	C2B-C1B	-12.01	1.35	1.53
2	B	301	COA	C2B-C1B	-11.92	1.35	1.53
2	D	301	COA	C2B-C1B	-11.85	1.35	1.53
2	A	301	COA	C2B-C1B	-11.84	1.35	1.53
2	C	301[A]	COA	C5P-N4P	6.22	1.47	1.33
2	D	301	COA	O4B-C4B	-6.21	1.31	1.45
2	B	301	COA	O4B-C4B	-6.20	1.31	1.45
2	C	301[A]	COA	O4B-C4B	-6.17	1.31	1.45
2	A	301	COA	O4B-C4B	-6.13	1.31	1.45
2	C	301[B]	COA	O4B-C4B	-6.00	1.31	1.45
2	C	301[B]	COA	C5P-N4P	5.97	1.47	1.33
2	B	301	COA	C5P-N4P	5.94	1.46	1.33
2	D	301	COA	C5P-N4P	5.84	1.46	1.33
2	A	301	COA	C5P-N4P	5.80	1.46	1.33
2	C	301[A]	COA	C9P-N8P	5.65	1.46	1.33
2	A	301	COA	C9P-N8P	5.52	1.45	1.33
2	B	301	COA	C9P-N8P	5.44	1.45	1.33
2	C	301[B]	COA	C9P-N8P	5.35	1.45	1.33
2	D	301	COA	C9P-N8P	5.29	1.45	1.33
2	C	301[B]	COA	C2A-N3A	5.20	1.40	1.32
2	A	301	COA	C2A-N3A	5.15	1.40	1.32
2	B	301	COA	C2A-N3A	5.10	1.40	1.32
2	D	301	COA	C2A-N3A	5.09	1.40	1.32
2	C	301[A]	COA	C2A-N3A	4.94	1.40	1.32
2	C	301[B]	COA	P3B-O3B	4.06	1.67	1.59
2	A	301	COA	P3B-O3B	4.02	1.66	1.59
2	B	301	COA	P3B-O3B	3.97	1.66	1.59
2	C	301[A]	COA	C6A-N6A	3.96	1.48	1.34
3	A	302	51G	O4-C17	-3.96	1.38	1.43
2	D	301	COA	P3B-O3B	3.96	1.66	1.59
2	C	301[B]	COA	C6A-N6A	3.94	1.48	1.34
2	A	301	COA	C6A-N6A	3.93	1.48	1.34
2	D	301	COA	C6A-N6A	3.89	1.48	1.34
2	B	301	COA	C6A-N6A	3.81	1.48	1.34
2	C	301[A]	COA	P3B-O3B	3.70	1.66	1.59
3	A	302	51G	O5-C16	-3.26	1.39	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	302	51G	C6-C5	3.04	1.58	1.52
2	C	301[A]	COA	O5P-C5P	-2.80	1.17	1.23
2	B	301	COA	O5P-C5P	-2.77	1.17	1.23
2	D	301	COA	O5P-C5P	-2.76	1.17	1.23
2	C	301[B]	COA	O5P-C5P	-2.74	1.17	1.23
2	C	301[A]	COA	C6P-C5P	2.72	1.56	1.51
2	A	301	COA	O5P-C5P	-2.70	1.17	1.23
3	C	302	51G	O5-C16	-2.67	1.40	1.44
3	A	302	51G	C14-C15	2.60	1.59	1.53
3	B	303[A]	51G	O5-C16	-2.58	1.40	1.44
2	A	301	COA	C6P-C5P	2.58	1.56	1.51
3	B	303[B]	51G	O5-C16	-2.56	1.40	1.44
2	C	301[B]	COA	C6P-C5P	2.54	1.56	1.51
2	B	301	COA	C5A-C4A	-2.51	1.34	1.40
2	C	301[A]	COA	P1A-O5B	2.47	1.69	1.59
2	A	301	COA	C5A-C4A	-2.46	1.34	1.40
2	D	301	COA	C6P-C5P	2.43	1.56	1.51
2	D	301	COA	C5A-C4A	-2.43	1.34	1.40
2	B	301	COA	C6P-C5P	2.42	1.56	1.51
2	C	301[A]	COA	C5A-C4A	-2.38	1.34	1.40
3	D	302	51G	O5-C16	-2.36	1.40	1.44
2	C	301[B]	COA	C5A-C4A	-2.33	1.34	1.40
2	C	301[A]	COA	O3B-C3B	-2.29	1.35	1.44
2	C	301[A]	COA	O9P-C9P	-2.29	1.18	1.23
3	D	302	51G	C1-N4	2.28	1.50	1.48
2	B	301	COA	O3B-C3B	-2.27	1.35	1.44
2	D	301	COA	O3B-C3B	-2.27	1.35	1.44
2	C	301[B]	COA	O3B-C3B	-2.25	1.35	1.44
2	C	301[B]	COA	P1A-O5B	2.24	1.68	1.59
2	A	301	COA	O3B-C3B	-2.23	1.36	1.44
3	B	303[A]	51G	C12-C11	2.22	1.58	1.52
2	D	301	COA	O9P-C9P	-2.22	1.19	1.23
3	B	303[A]	51G	C11-C10	2.22	1.58	1.53
3	C	302	51G	O4-C17	-2.21	1.40	1.43
2	C	301[A]	COA	P2A-O6A	2.19	1.68	1.59
3	B	303[B]	51G	O4-C17	-2.18	1.40	1.43
2	D	301	COA	P1A-O5B	2.16	1.68	1.59
3	B	303[B]	51G	C12-C7	2.15	1.58	1.52
3	C	302	51G	C3-C2	2.15	1.56	1.52
2	B	301	COA	P1A-O5B	2.13	1.67	1.59
3	D	302	51G	O4-C17	-2.12	1.41	1.43
2	A	301	COA	P1A-O5B	2.12	1.67	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	COA	O9P-C9P	-2.11	1.19	1.23
3	A	302	51G	C13-C14	2.08	1.58	1.52
2	B	301	COA	O9P-C9P	-2.08	1.19	1.23
2	B	301	COA	P2A-O6A	2.04	1.67	1.59
2	C	301[B]	COA	O9P-C9P	-2.00	1.19	1.23

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301[A]	COA	C5A-C6A-N6A	8.98	133.99	120.35
2	D	301	COA	C5A-C6A-N6A	8.47	133.23	120.35
2	C	301[B]	COA	C5A-C6A-N6A	8.08	132.63	120.35
2	B	301	COA	C5A-C6A-N6A	8.02	132.54	120.35
2	A	301	COA	C5A-C6A-N6A	7.55	131.83	120.35
2	C	301[A]	COA	N6A-C6A-N1A	-6.30	105.49	118.57
2	D	301	COA	N6A-C6A-N1A	-5.91	106.30	118.57
2	B	301	COA	N6A-C6A-N1A	-5.77	106.60	118.57
2	C	301[B]	COA	N6A-C6A-N1A	-5.70	106.73	118.57
2	C	301[A]	COA	N3A-C2A-N1A	-5.49	120.09	128.68
2	D	301	COA	N3A-C2A-N1A	-5.49	120.10	128.68
2	A	301	COA	N3A-C2A-N1A	-5.47	120.13	128.68
2	B	301	COA	N3A-C2A-N1A	-5.44	120.18	128.68
2	C	301[B]	COA	N3A-C2A-N1A	-5.43	120.19	128.68
2	A	301	COA	N6A-C6A-N1A	-5.28	107.61	118.57
3	A	302	51G	C13-C14-C15	4.72	117.15	109.34
2	D	301	COA	C6P-C7P-N8P	-4.69	102.42	111.90
3	C	302	51G	C17-O4-C13	4.59	118.92	111.53
2	B	301	COA	C6P-C7P-N8P	-4.50	102.81	111.90
3	B	303[B]	51G	C6-O-C2	4.46	122.44	113.69
3	D	302	51G	C17-O4-C13	4.46	118.71	111.53
2	C	301[B]	COA	C6P-C7P-N8P	-4.44	102.94	111.90
3	B	303[A]	51G	C17-O4-C13	4.39	118.61	111.53
3	A	302	51G	C17-O4-C13	4.38	118.59	111.53
3	B	303[B]	51G	C17-O4-C13	4.32	118.49	111.53
3	B	303[A]	51G	O-C2-C3	4.20	114.27	109.84
3	C	302	51G	O-C2-C3	4.15	114.21	109.84
2	A	301	COA	C6P-C7P-N8P	-4.05	103.71	111.90
3	B	303[A]	51G	C6-O-C2	3.87	121.29	113.69
3	C	302	51G	C6-O-C2	3.84	121.22	113.69
2	C	301[A]	COA	C1B-N9A-C4A	-3.54	120.42	126.64
3	D	302	51G	C6-O-C2	3.30	120.17	113.69
3	A	302	51G	C6-O-C2	3.12	119.80	113.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	COA	C1B-N9A-C4A	-3.02	121.34	126.64
3	B	303[B]	51G	O-C2-C3	2.98	112.98	109.84
2	B	301	COA	C1B-N9A-C4A	-2.96	121.45	126.64
3	A	302	51G	O-C2-C3	2.95	112.94	109.84
2	D	301	COA	C1B-N9A-C4A	-2.92	121.50	126.64
3	A	302	51G	O3-C11-C10	2.76	115.77	109.18
3	A	302	51G	C8-C9-C10	2.72	116.77	111.18
2	C	301[B]	COA	C1B-N9A-C4A	-2.72	121.87	126.64
2	C	301[B]	COA	C3B-C2B-C1B	2.71	105.90	99.89
2	B	301	COA	C3B-C2B-C1B	2.68	105.82	99.89
2	C	301[A]	COA	P2A-O3A-P1A	-2.68	123.64	132.83
2	C	301[A]	COA	C3B-C2B-C1B	2.67	105.81	99.89
2	D	301	COA	C3B-C2B-C1B	2.62	105.70	99.89
2	A	301	COA	C3B-C2B-C1B	2.61	105.66	99.89
2	C	301[B]	COA	CDP-CBP-CAP	2.59	113.31	108.82
3	B	303[A]	51G	C7-C12-C11	2.57	114.30	108.96
3	D	302	51G	O-C2-C3	2.50	112.47	109.84
2	A	301	COA	C7P-N8P-C9P	-2.46	118.20	122.59
2	D	301	COA	C3P-N4P-C5P	-2.40	118.37	122.84
3	B	303[B]	51G	O1-C7-C8	-2.39	103.47	109.18
3	B	303[A]	51G	O3-C11-C10	2.36	114.81	109.18
2	C	301[A]	COA	C6P-C7P-N8P	-2.30	107.25	111.90
2	B	301	COA	C7P-N8P-C9P	-2.25	118.58	122.59
2	A	301	COA	P2A-O3A-P1A	-2.24	125.13	132.83
2	C	301[B]	COA	O6A-CCP-CBP	-2.23	106.97	110.55
2	C	301[B]	COA	C7P-N8P-C9P	-2.22	118.64	122.59
3	D	302	51G	O1-C7-C8	-2.21	103.91	109.18
3	A	302	51G	O4-C13-C14	2.18	113.39	110.04
2	B	301	COA	CDP-CBP-CAP	2.18	112.59	108.82
2	D	301	COA	C2P-C3P-N4P	-2.16	107.36	112.31
2	A	301	COA	CDP-CBP-CAP	2.16	112.57	108.82
3	A	302	51G	O3-C13-O4	-2.13	104.34	109.08
2	C	301[B]	COA	P2A-O3A-P1A	-2.11	125.60	132.83
3	B	303[A]	51G	O3-C11-C12	-2.04	101.85	107.28
3	D	302	51G	C7-C12-C11	2.04	113.19	108.96
2	D	301	COA	O6A-CCP-CBP	-2.01	107.31	110.55
3	B	303[A]	51G	C13-O3-C11	2.00	122.92	117.96

There are no chirality outliers.

All (56) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	301	COA	C3B-O3B-P3B-O7A
3	A	302	51G	C10-C11-O3-C13
3	A	302	51G	N4-C1-C2-C3
3	A	302	51G	C-C1-C2-O
3	A	302	51G	N4-C1-C2-O
3	A	302	51G	C2-C1-N4-C20
3	B	303[A]	51G	C14-C15-N-C19
3	B	303[A]	51G	C10-C11-O3-C13
3	B	303[A]	51G	C-C1-C2-C3
3	B	303[A]	51G	N4-C1-C2-C3
3	B	303[A]	51G	C-C1-C2-O
3	B	303[A]	51G	N4-C1-C2-O
3	B	303[B]	51G	C14-C15-N-C19
3	B	303[B]	51G	C2-C1-N4-C20
3	C	302	51G	C14-C15-N-C19
3	C	302	51G	C-C1-C2-C3
3	C	302	51G	N4-C1-C2-C3
3	C	302	51G	C-C1-C2-O
3	C	302	51G	N4-C1-C2-O
3	D	302	51G	C14-C15-N-C19
3	D	302	51G	C2-C1-N4-C20
3	D	302	51G	C-C1-N4-C20
3	B	303[A]	51G	O4-C13-O3-C11
4	A	303	GOL	C1-C2-C3-O3
4	B	302	GOL	C1-C2-C3-O3
4	A	303	GOL	O2-C2-C3-O3
2	A	301	COA	P1A-O3A-P2A-O4A
3	A	302	51G	C-C1-C2-C3
3	C	302	51G	O4-C13-O3-C11
2	A	301	COA	C3B-O3B-P3B-O8A
2	D	301	COA	C3B-O3B-P3B-O9A
2	C	301[A]	COA	P1A-O3A-P2A-O5A
3	B	303[B]	51G	O4-C13-O3-C11
3	C	302	51G	C14-C13-O3-C11
3	D	302	51G	N4-C1-C2-C3
4	B	302	GOL	O2-C2-C3-O3
3	C	302	51G	C2-C1-N4-C20
3	C	302	51G	C5-C6-O1-C7
3	B	303[B]	51G	C14-C13-O3-C11
3	A	302	51G	C-C1-N4-C20
3	B	303[A]	51G	C-C1-N4-C20
3	B	303[B]	51G	C-C1-N4-C20
3	C	302	51G	C-C1-N4-C20

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Mol	Chain	Res	Type	Atoms
2	C	301[B]	COA	C2P-C3P-N4P-C5P
2	C	301[B]	COA	P1A-O3A-P2A-O4A
3	B	303[B]	51G	N4-C1-C2-C3
2	B	301	COA	C2P-C3P-N4P-C5P
2	D	301	COA	C2P-C3P-N4P-C5P
2	A	301	COA	C3B-O3B-P3B-O9A
2	B	301	COA	C3B-O3B-P3B-O8A
2	C	301[A]	COA	C3B-O3B-P3B-O9A
2	C	301[B]	COA	C3B-O3B-P3B-O9A
3	D	302	51G	O4-C13-O3-C11
2	A	301	COA	P1A-O3A-P2A-O5A
2	C	301[A]	COA	P1A-O3A-P2A-O4A
3	D	302	51G	C5-C6-O1-C7

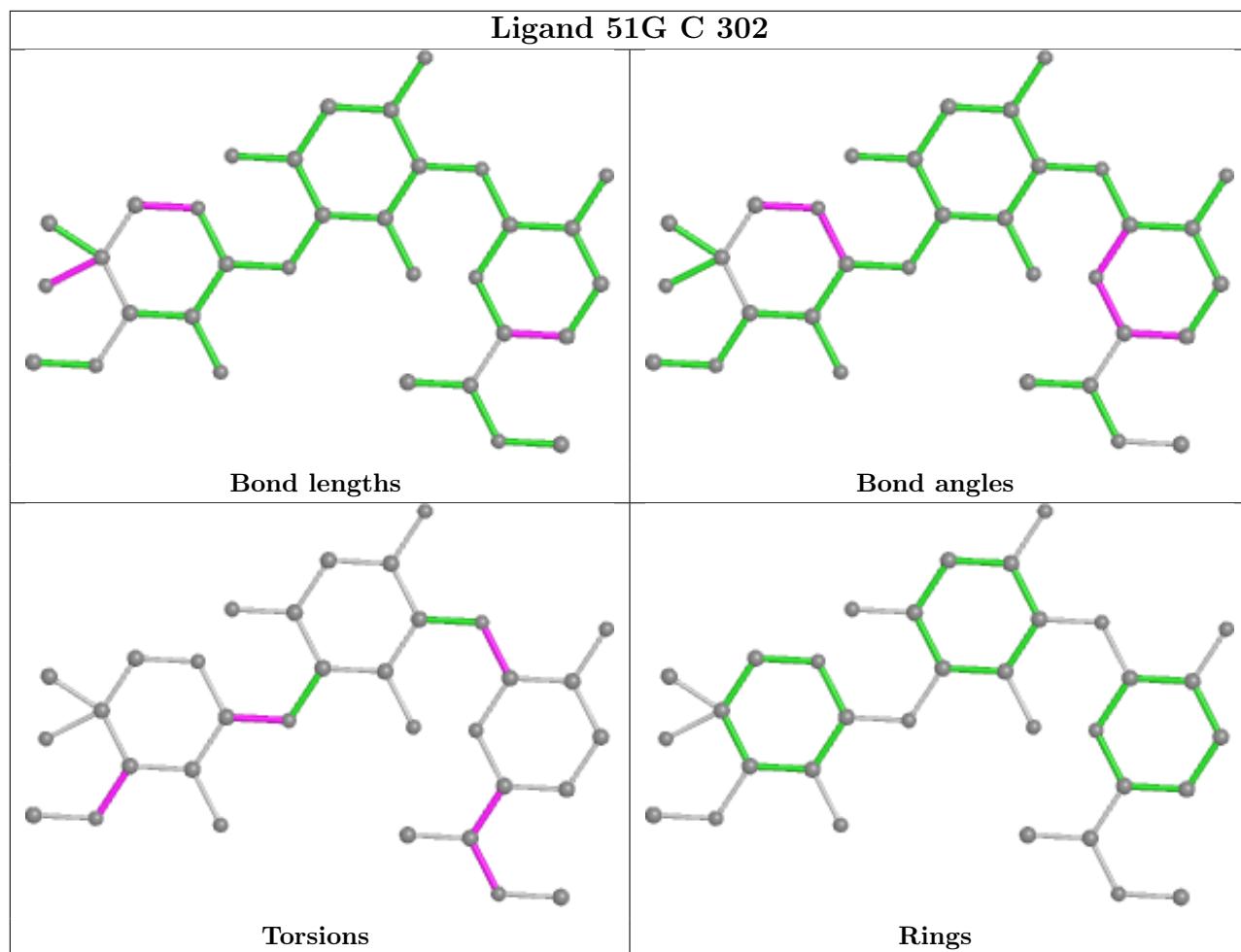
All (1) ring outliers are listed below:

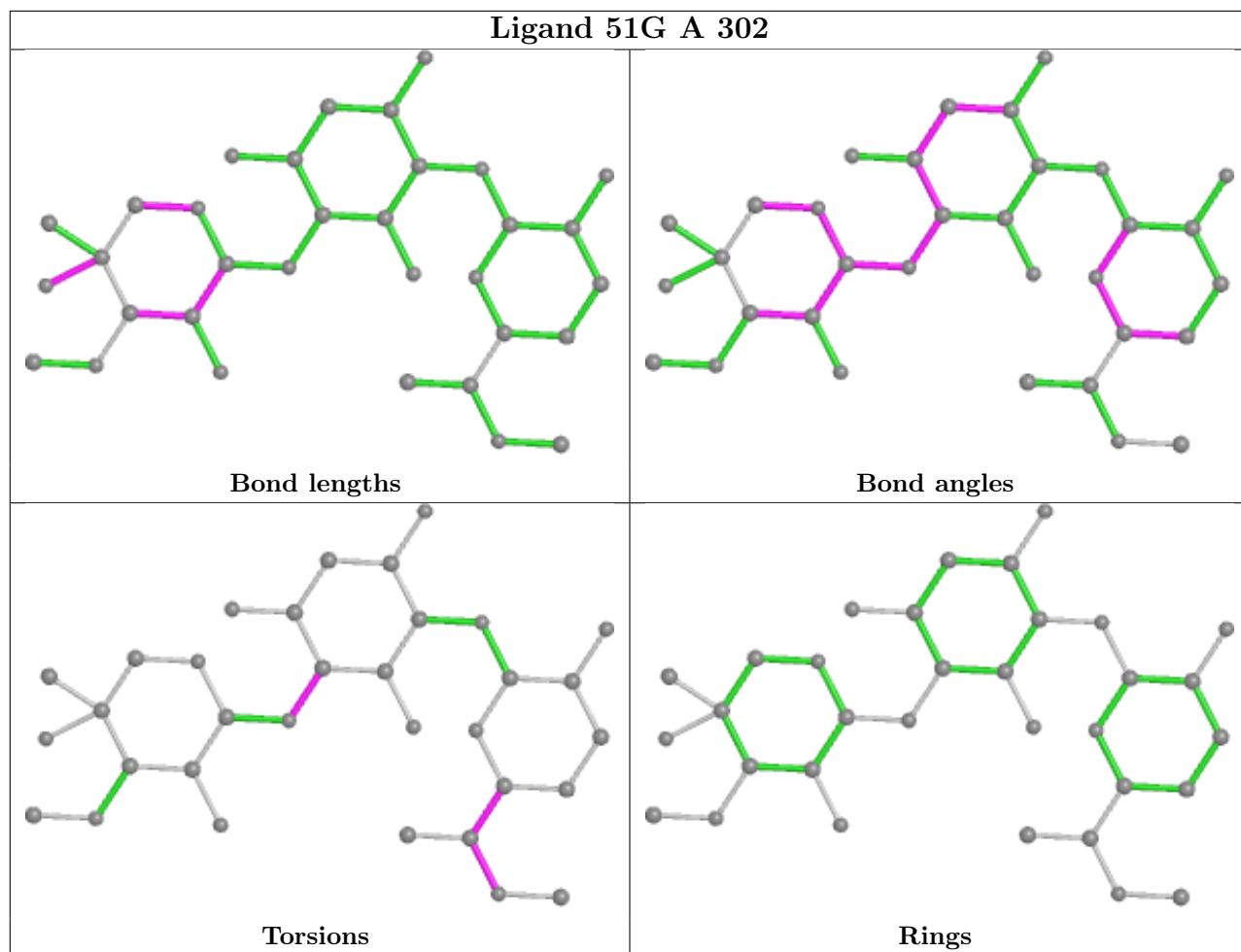
Mol	Chain	Res	Type	Atoms
3	B	303[A]	51G	C13-C14-C15-C16-C17-O4

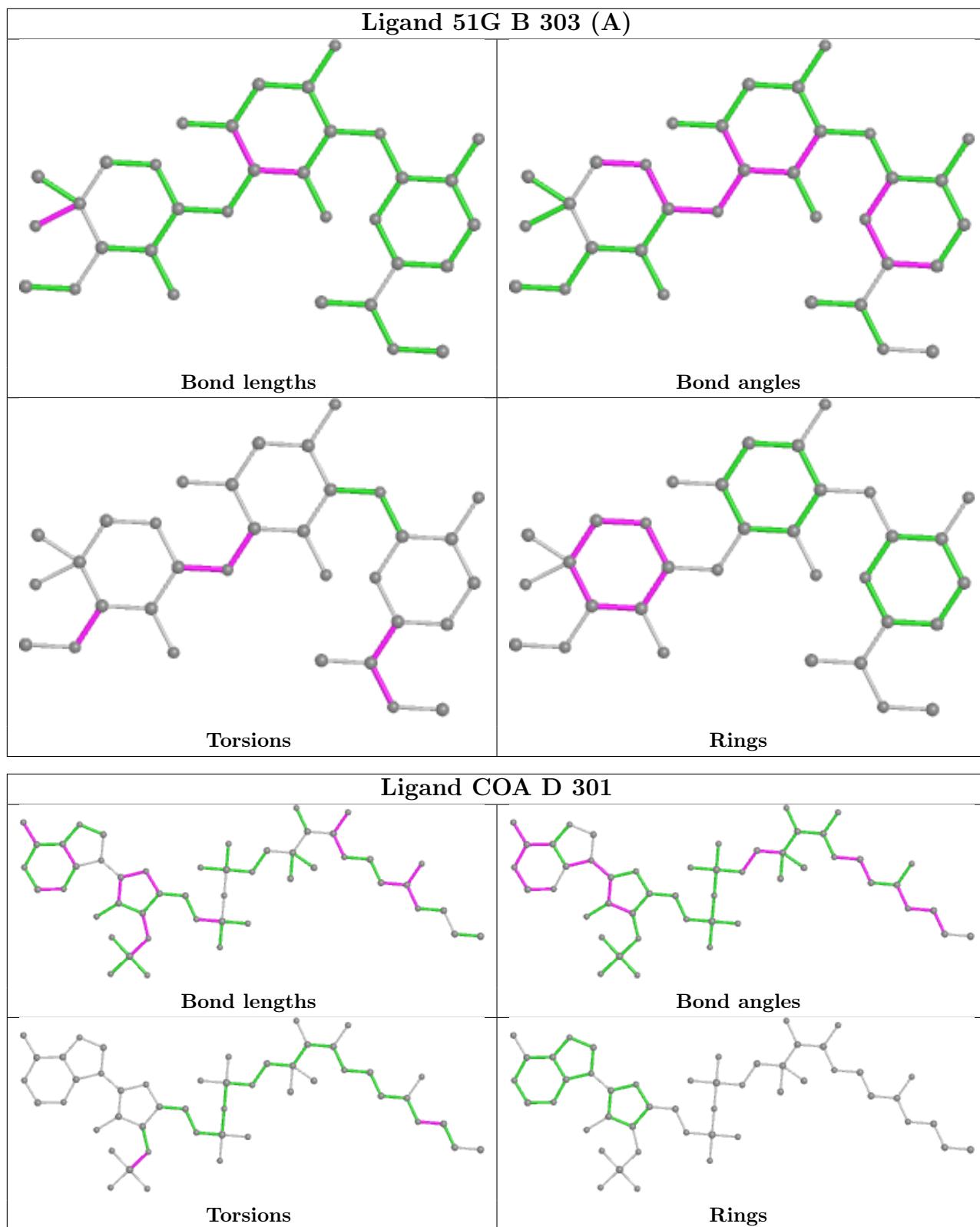
8 monomers are involved in 12 short contacts:

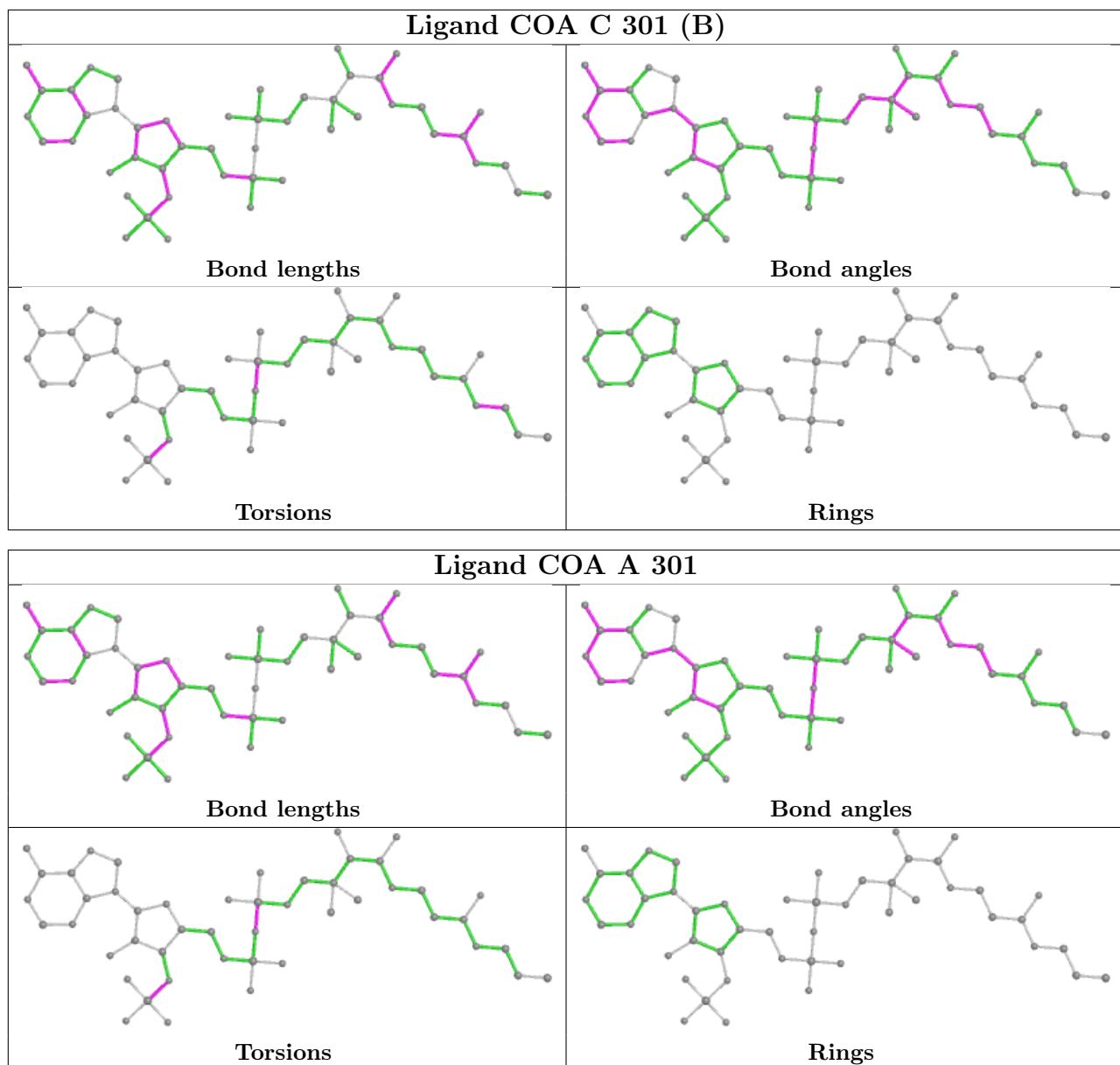
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	302	51G	3	0
4	B	302	GOL	1	0
2	D	301	COA	1	0
2	C	301[B]	COA	1	0
3	B	303[B]	51G	1	0
3	D	302	51G	3	0
2	B	301	COA	1	0
2	C	301[A]	COA	3	0

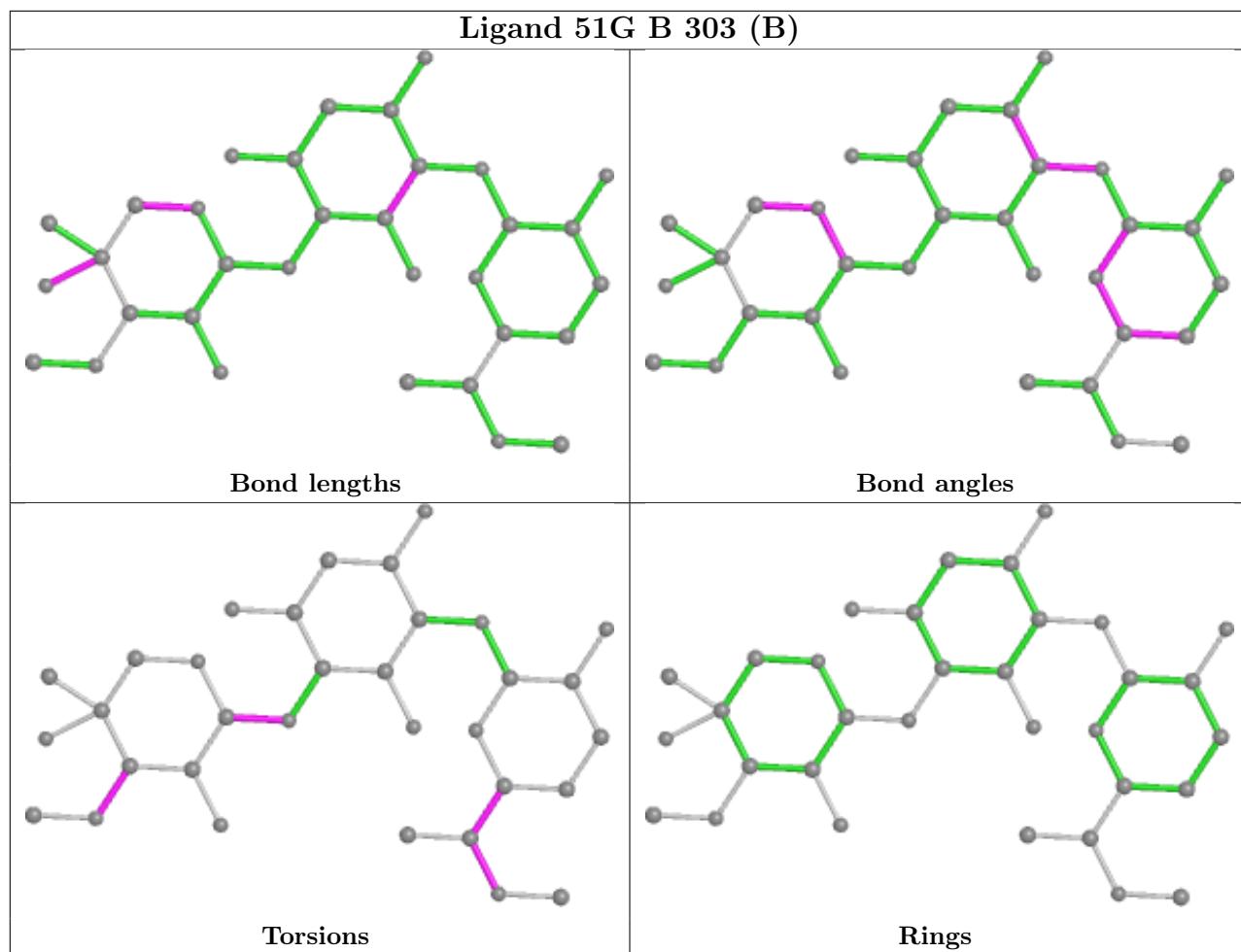
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

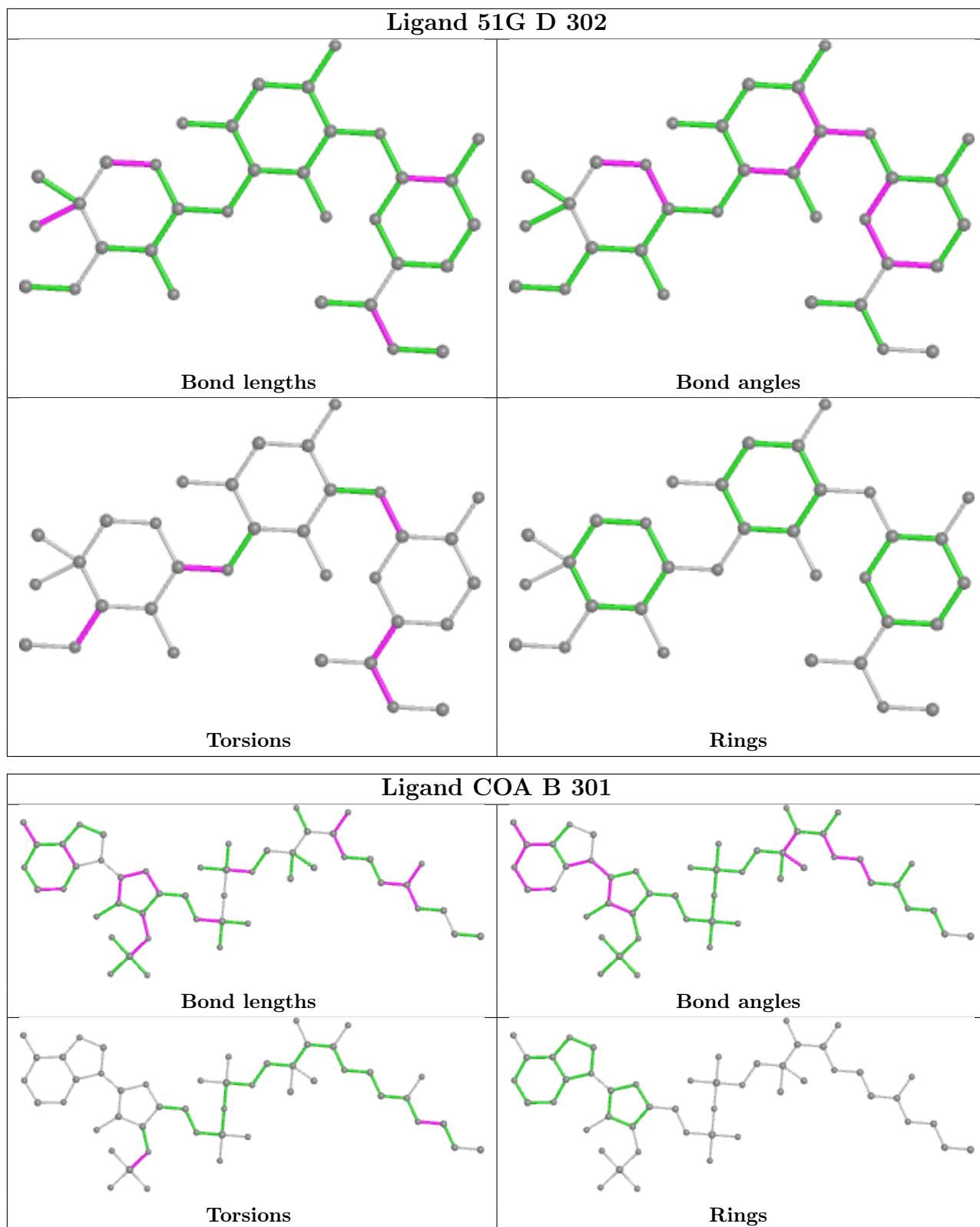


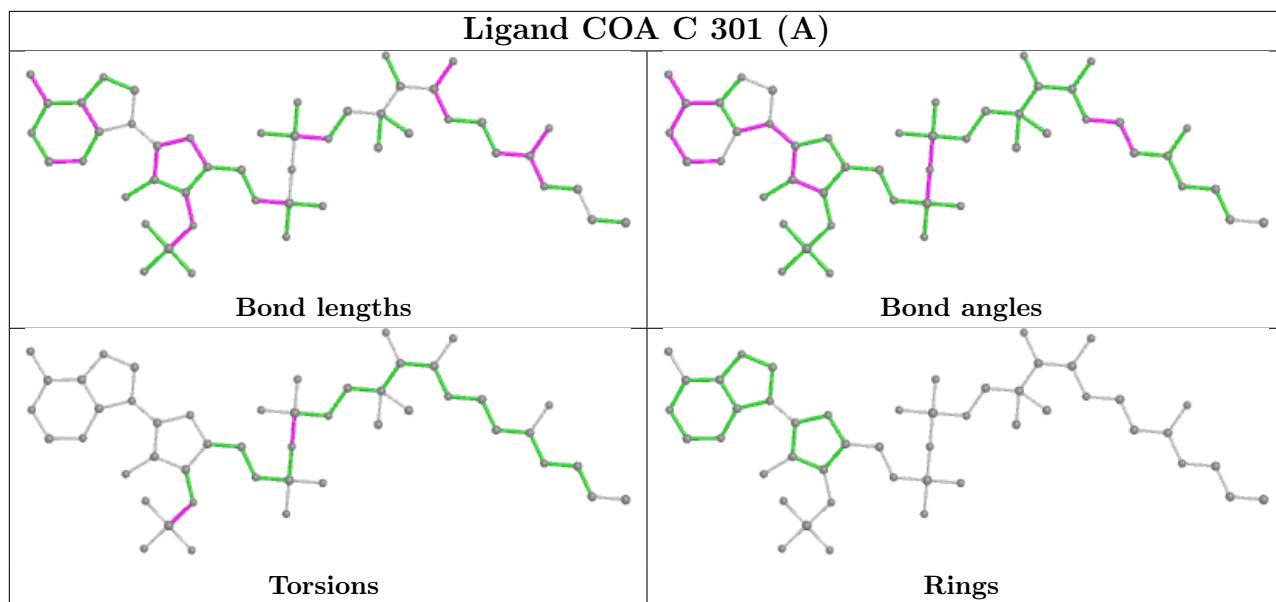












5.7 Other polymers [\(i\)](#)

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 [\(i\)](#)

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

6.2 Non-standard residues in protein, DNA, RNA chains [\(i\)](#)

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

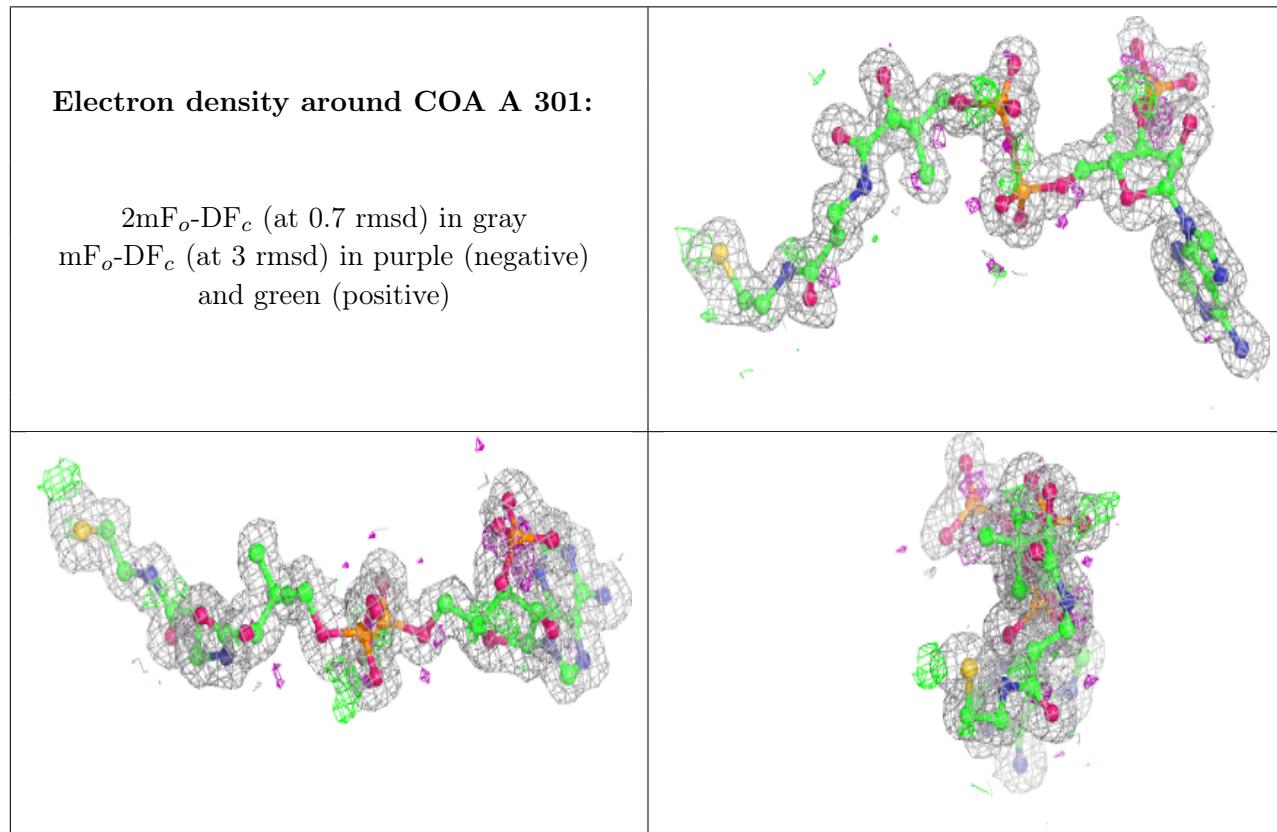
6.3 Carbohydrates [\(i\)](#)

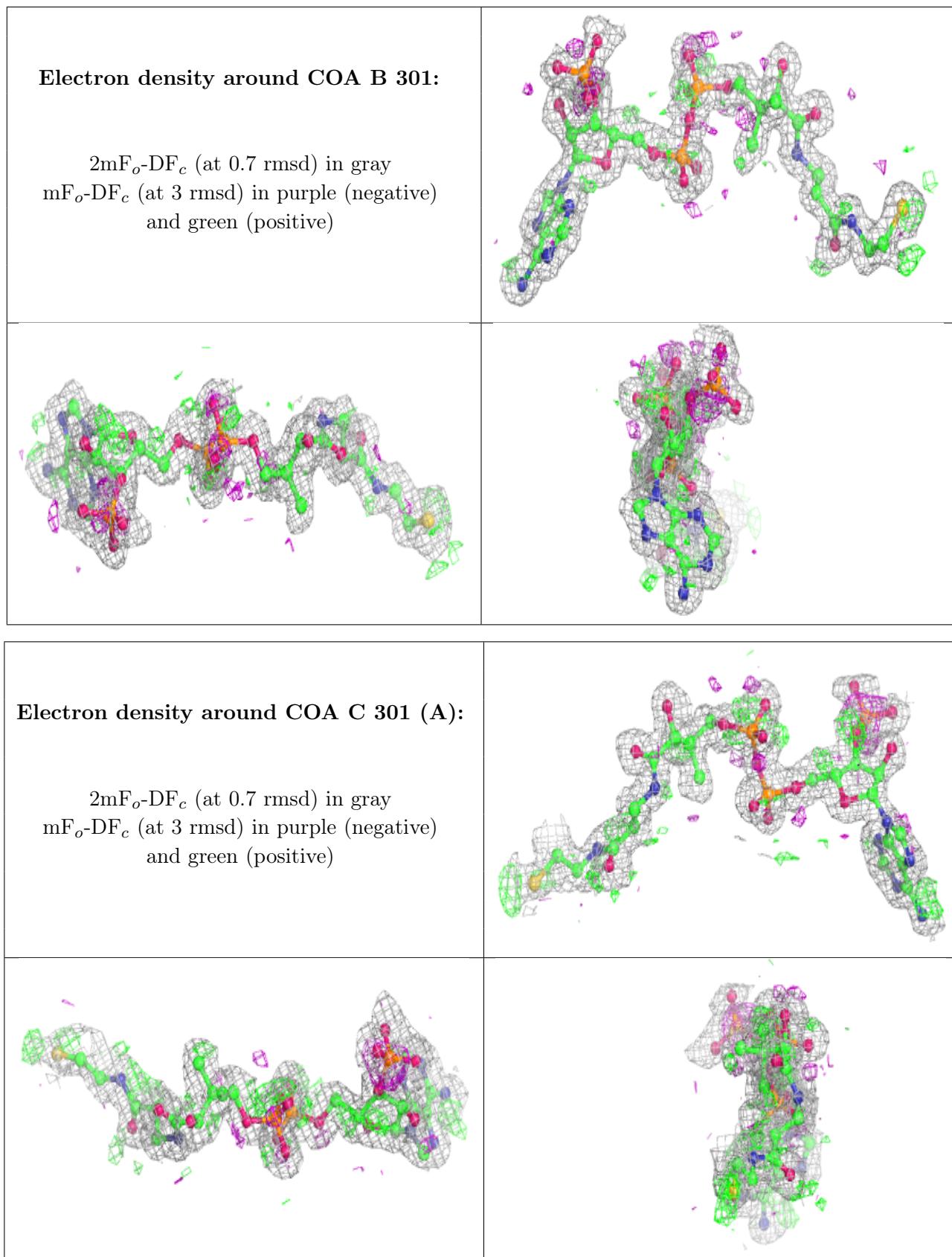
Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [\(i\)](#)

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

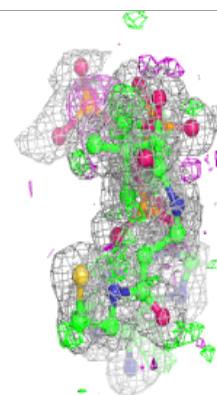
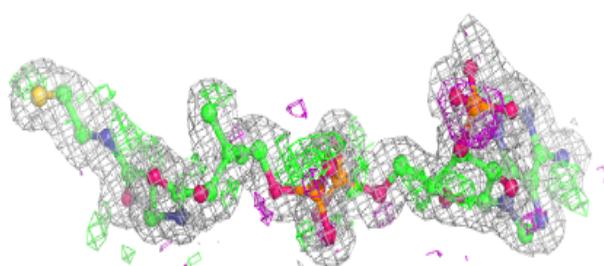
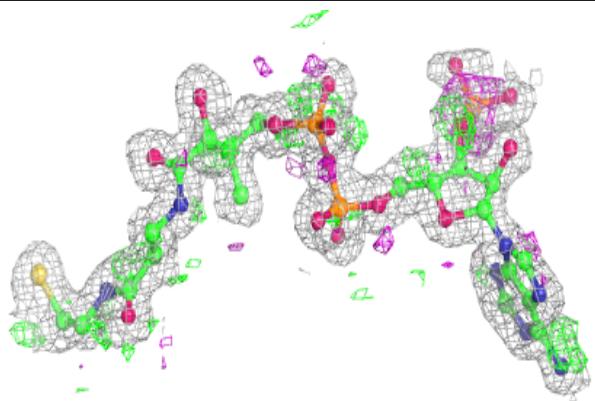
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



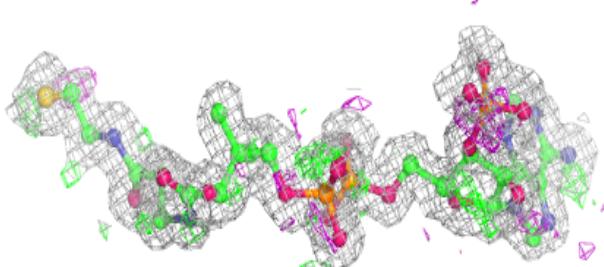
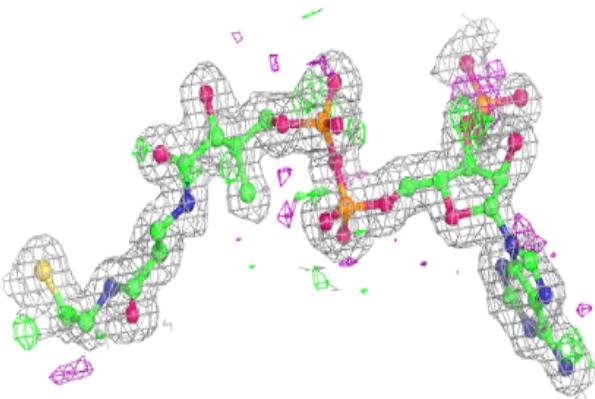


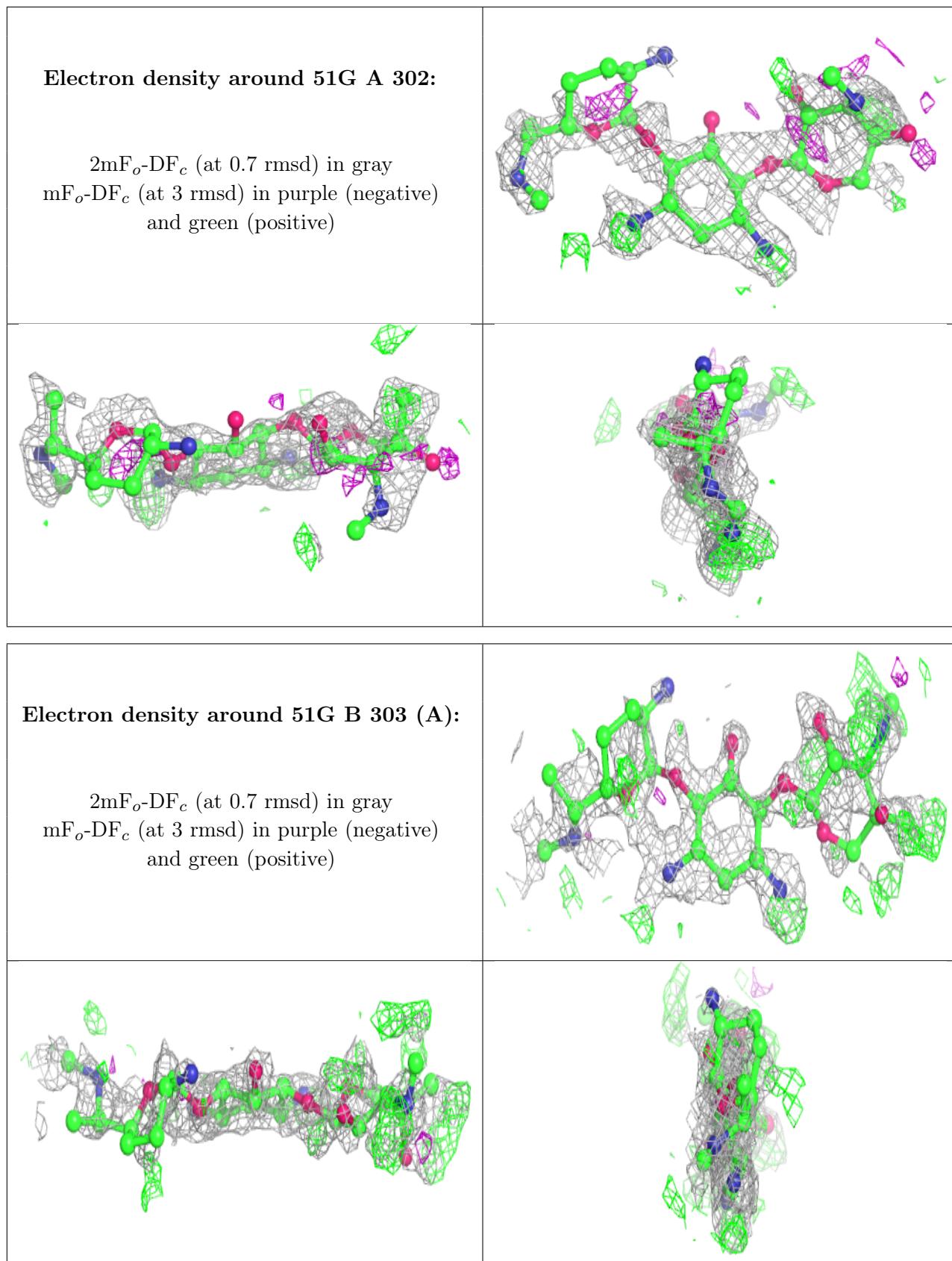
Electron density around COA C 301 (B):

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 COA D 301:**

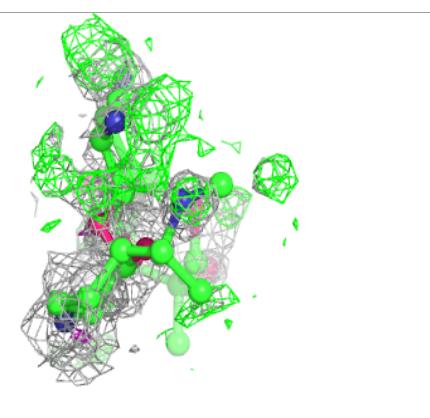
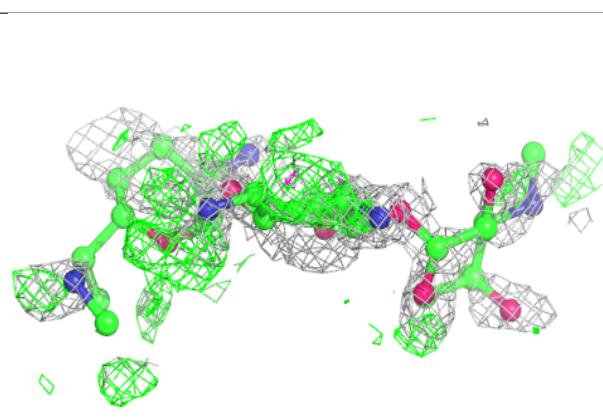
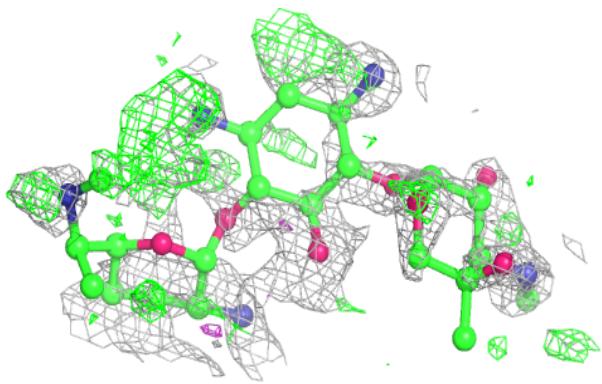
2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



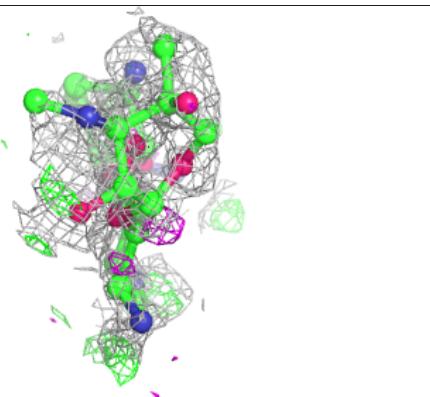
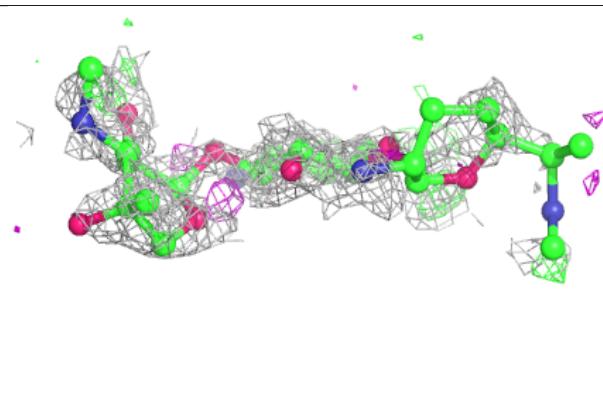
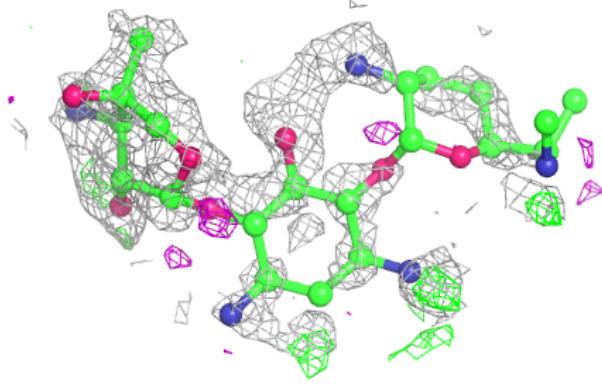


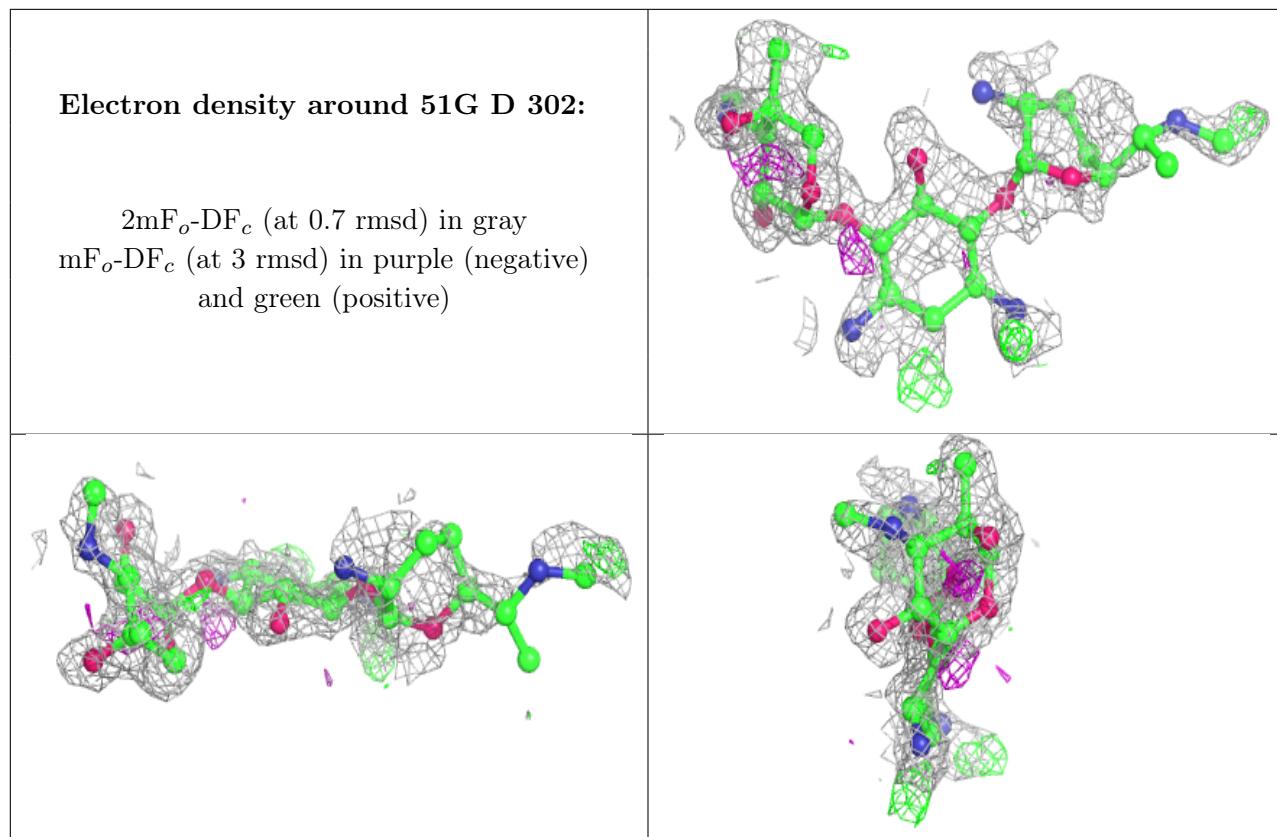
Electron density around 51G B 303 (B):

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 51G C 302:**

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 [\(i\)](#)

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