



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 7, 2020 – 02:36 am BST

PDB ID : 6IPB  
Title : Crystal Structure of the Cofactor-binding Domain of the Human Phase II Drug Metabolism Enzyme UGT2B15  
Authors : Zhang, L.; Xie, W.; Wang, C.  
Deposited on : 2018-11-02  
Resolution : 1.78 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

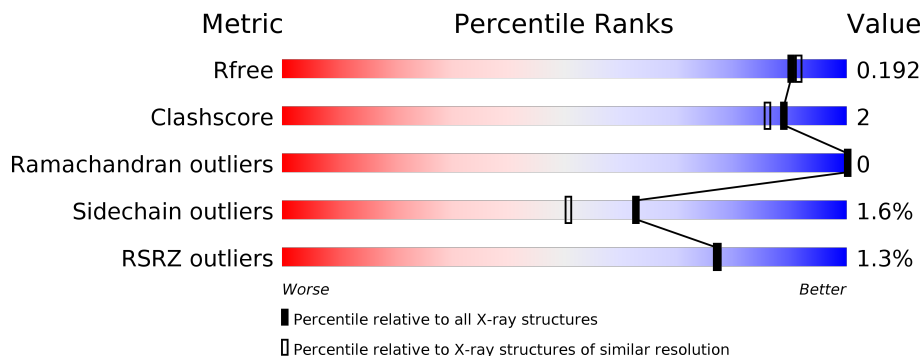
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.78 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	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	191	 84% 5% • 10%
1	B	191	 84% 5% 11%
1	C	191	 82% 7% • 11%
1	D	191	 82% 5% • 12%

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 5899 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 UDP-glucuronosyltransferase 2B15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	171	1294	824	227	233	10	0	0	0
1	B	170	1303	828	229	236	10	0	0	0
1	C	170	1293	823	226	234	10	0	0	0
1	D	169	1290	821	222	237	10	0	0	0

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	261	MET	-	initiating methionine	UNP P54855
A	262	GLY	-	expression tag	UNP P54855
A	263	SER	-	expression tag	UNP P54855
A	264	SER	-	expression tag	UNP P54855
A	265	HIS	-	expression tag	UNP P54855
A	266	HIS	-	expression tag	UNP P54855
A	267	HIS	-	expression tag	UNP P54855
A	268	HIS	-	expression tag	UNP P54855
A	269	HIS	-	expression tag	UNP P54855
A	270	HIS	-	expression tag	UNP P54855
A	271	HIS	-	expression tag	UNP P54855
A	272	HIS	-	expression tag	UNP P54855
A	273	LEU	-	expression tag	UNP P54855
A	274	GLU	-	expression tag	UNP P54855
A	275	VAL	-	expression tag	UNP P54855
A	276	LEU	-	expression tag	UNP P54855
A	277	PHE	-	expression tag	UNP P54855
A	278	GLN	-	expression tag	UNP P54855
A	279	GLY	-	expression tag	UNP P54855
A	280	PRO	-	expression tag	UNP P54855
A	281	HIS	-	expression tag	UNP P54855

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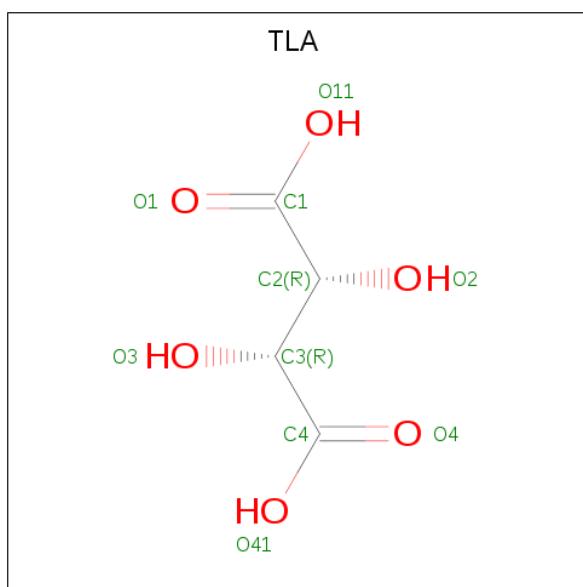
Chain	Residue	Modelled	Actual	Comment	Reference
A	282	MET	-	expression tag	UNP P54855
A	283	MET	-	expression tag	UNP P54855
B	261	MET	-	initiating methionine	UNP P54855
B	262	GLY	-	expression tag	UNP P54855
B	263	SER	-	expression tag	UNP P54855
B	264	SER	-	expression tag	UNP P54855
B	265	HIS	-	expression tag	UNP P54855
B	266	HIS	-	expression tag	UNP P54855
B	267	HIS	-	expression tag	UNP P54855
B	268	HIS	-	expression tag	UNP P54855
B	269	HIS	-	expression tag	UNP P54855
B	270	HIS	-	expression tag	UNP P54855
B	271	HIS	-	expression tag	UNP P54855
B	272	HIS	-	expression tag	UNP P54855
B	273	LEU	-	expression tag	UNP P54855
B	274	GLU	-	expression tag	UNP P54855
B	275	VAL	-	expression tag	UNP P54855
B	276	LEU	-	expression tag	UNP P54855
B	277	PHE	-	expression tag	UNP P54855
B	278	GLN	-	expression tag	UNP P54855
B	279	GLY	-	expression tag	UNP P54855
B	280	PRO	-	expression tag	UNP P54855
B	281	HIS	-	expression tag	UNP P54855
B	282	MET	-	expression tag	UNP P54855
B	283	MET	-	expression tag	UNP P54855
C	261	MET	-	initiating methionine	UNP P54855
C	262	GLY	-	expression tag	UNP P54855
C	263	SER	-	expression tag	UNP P54855
C	264	SER	-	expression tag	UNP P54855
C	265	HIS	-	expression tag	UNP P54855
C	266	HIS	-	expression tag	UNP P54855
C	267	HIS	-	expression tag	UNP P54855
C	268	HIS	-	expression tag	UNP P54855
C	269	HIS	-	expression tag	UNP P54855
C	270	HIS	-	expression tag	UNP P54855
C	271	HIS	-	expression tag	UNP P54855
C	272	HIS	-	expression tag	UNP P54855
C	273	LEU	-	expression tag	UNP P54855
C	274	GLU	-	expression tag	UNP P54855
C	275	VAL	-	expression tag	UNP P54855
C	276	LEU	-	expression tag	UNP P54855
C	277	PHE	-	expression tag	UNP P54855

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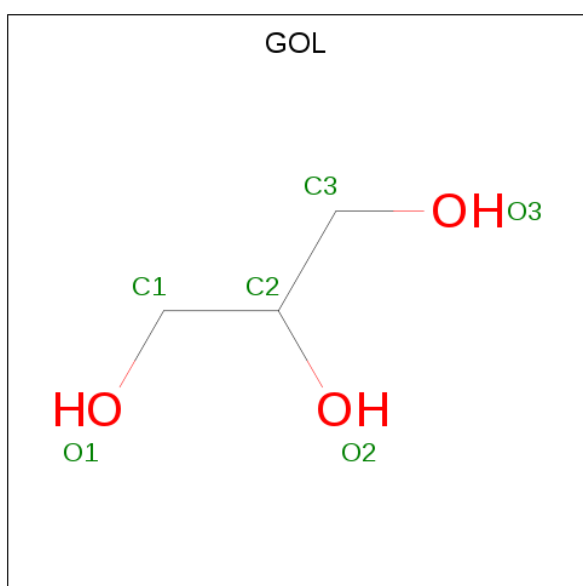
Chain	Residue	Modelled	Actual	Comment	Reference
C	278	GLN	-	expression tag	UNP P54855
C	279	GLY	-	expression tag	UNP P54855
C	280	PRO	-	expression tag	UNP P54855
C	281	HIS	-	expression tag	UNP P54855
C	282	MET	-	expression tag	UNP P54855
C	283	MET	-	expression tag	UNP P54855
D	261	MET	-	initiating methionine	UNP P54855
D	262	GLY	-	expression tag	UNP P54855
D	263	SER	-	expression tag	UNP P54855
D	264	SER	-	expression tag	UNP P54855
D	265	HIS	-	expression tag	UNP P54855
D	266	HIS	-	expression tag	UNP P54855
D	267	HIS	-	expression tag	UNP P54855
D	268	HIS	-	expression tag	UNP P54855
D	269	HIS	-	expression tag	UNP P54855
D	270	HIS	-	expression tag	UNP P54855
D	271	HIS	-	expression tag	UNP P54855
D	272	HIS	-	expression tag	UNP P54855
D	273	LEU	-	expression tag	UNP P54855
D	274	GLU	-	expression tag	UNP P54855
D	275	VAL	-	expression tag	UNP P54855
D	276	LEU	-	expression tag	UNP P54855
D	277	PHE	-	expression tag	UNP P54855
D	278	GLN	-	expression tag	UNP P54855
D	279	GLY	-	expression tag	UNP P54855
D	280	PRO	-	expression tag	UNP P54855
D	281	HIS	-	expression tag	UNP P54855
D	282	MET	-	expression tag	UNP P54855
D	283	MET	-	expression tag	UNP P54855

- Molecule 2 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula: C<sub>4</sub>H<sub>6</sub>O<sub>6</sub>) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	C O	0	0
			10	4 6		
2	B	1	Total	C O	0	0
			10	4 6		
2	C	1	Total	C O	0	0
			10	4 6		
2	D	1	Total	C O	0	0
			10	4 6		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>) (labeled as "Ligand of Interest" by author).



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

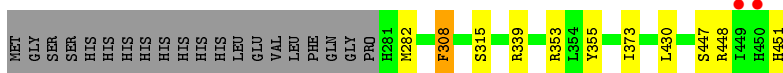
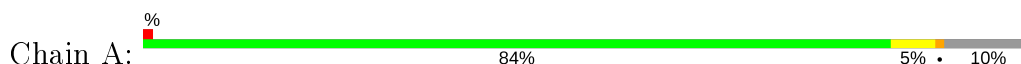
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	169	Total	O	0	0
			169	169		
4	B	153	Total	O	0	0
			153	153		
4	C	162	Total	O	0	0
			162	162		
4	D	171	Total	O	0	0
			171	171		

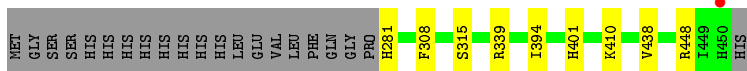
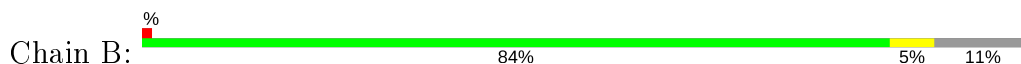
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

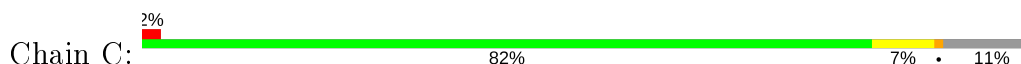
- Molecule 1: UDP-glucuronosyltransferase 2B15



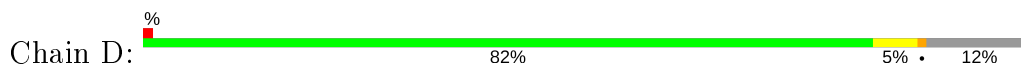
- Molecule 1: UDP-glucuronosyltransferase 2B15



- Molecule 1: UDP-glucuronosyltransferase 2B15



- Molecule 1: UDP-glucuronosyltransferase 2B15





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.07Å 141.82Å 56.88Å 90.00° 115.58° 90.00°	Depositor
Resolution (Å)	70.91 – 1.78 48.25 – 1.78	Depositor EDS
% Data completeness (in resolution range)	99.2 (70.91-1.78) 99.3 (48.25-1.78)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.17 (at 1.77Å)	Xtrriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.146 , 0.180 0.160 , 0.192	Depositor DCC
$R_{free}$ test set	3429 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	22.3	Xtrriage
Anisotropy	0.050	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 49.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.025 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5899	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.11% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: GOL, TLA

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	1.05	1/1321 (0.1%)	1.03	6/1786 (0.3%)
1	B	1.04	0/1332	0.96	1/1801 (0.1%)
1	C	1.05	1/1320 (0.1%)	0.95	2/1784 (0.1%)
1	D	1.09	2/1317 (0.2%)	1.00	4/1780 (0.2%)
All	All	1.06	4/5290 (0.1%)	0.99	13/7151 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	338	TRP	CE3-CZ3	5.89	1.48	1.38
1	C	342	GLY	N-CA	5.44	1.54	1.46
1	D	383	GLU	CD-OE2	5.15	1.31	1.25
1	A	315	SER	CB-OG	5.05	1.48	1.42

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	308	PHE	CB-CG-CD1	7.32	125.92	120.80
1	D	308	PHE	CB-CG-CD1	6.24	125.17	120.80
1	C	419	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	A	353	ARG	NE-CZ-NH2	-5.69	117.46	120.30
1	B	448	ARG	NE-CZ-NH2	-5.65	117.47	120.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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	1294	0	1305	2	0
1	B	1303	0	1310	5	0
1	C	1293	0	1307	7	0
1	D	1290	0	1302	6	0
2	A	10	0	4	0	0
2	B	10	0	4	0	0
2	C	10	0	4	1	0
2	D	10	0	4	0	0
3	A	6	0	8	0	0
3	D	18	0	24	0	0
4	A	169	0	0	0	0
4	B	153	0	0	4	0
4	C	162	0	0	0	0
4	D	171	0	0	2	0
All	All	5899	0	5272	20	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.

The worst 5 of 20 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:D:315:SER:HB2	4:D:614:HOH:O	1.92	0.69
1:C:446:LEU:O	1:C:449:ILE:HB	1.99	0.63
1:A:447:SER:O	1:A:451:HIS:N	2.34	0.60
1:A:373:ILE:HD11	1:A:430:LEU:HD21	1.87	0.57
1:B:401:HIS:HD2	4:B:725:HOH:O	1.88	0.56

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	169/191 (88%)	167 (99%)	2 (1%)	0	100	100
1	B	168/191 (88%)	167 (99%)	1 (1%)	0	100	100
1	C	168/191 (88%)	165 (98%)	3 (2%)	0	100	100
1	D	167/191 (87%)	167 (100%)	0	0	100	100
All	All	672/764 (88%)	666 (99%)	6 (1%)	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	138/164 (84%)	136 (99%)	2 (1%)	67	56
1	B	141/164 (86%)	138 (98%)	3 (2%)	53	38
1	C	139/164 (85%)	137 (99%)	2 (1%)	67	56
1	D	140/164 (85%)	138 (99%)	2 (1%)	67	56
All	All	558/656 (85%)	549 (98%)	9 (2%)	62	51

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

Mol	Chain	Res	Type
1	B	339	ARG
1	D	339	ARG
1	C	339	ARG

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Mol	Chain	Res	Type
1	B	281	HIS
1	C	308	PHE

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

Mol	Chain	Res	Type
1	B	401	HIS
1	B	450	HIS
1	C	316	ASN

### 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](#)

There are no carbohydrates in this entry.

### 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	$\# Z  > 2$
3	GOL	A	502	-	5,5,5	0.79	0	5,5,5	0.40	0
2	TLA	B	501	-	3,9,9	0.95	0	6,12,12	1.60	1 (16%)
3	GOL	D	503	-	5,5,5	0.67	0	5,5,5	0.70	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GOL	D	504	-	5,5,5	0.75	0	5,5,5	0.83	0
3	GOL	D	502	-	5,5,5	0.44	0	5,5,5	0.22	0
2	TLA	C	501	-	3,9,9	1.32	0	6,12,12	0.72	0
2	TLA	A	501	-	3,9,9	1.07	0	6,12,12	1.41	1 (16%)
2	TLA	D	501	-	3,9,9	0.57	0	6,12,12	1.31	1 (16%)

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	GOL	A	502	-	-	0/4/4/4	-
2	TLA	B	501	-	-	0/4/12/12	-
3	GOL	D	503	-	-	0/4/4/4	-
3	GOL	D	504	-	-	2/4/4/4	-
3	GOL	D	502	-	-	0/4/4/4	-
2	TLA	C	501	-	-	0/4/12/12	-
2	TLA	A	501	-	-	0/4/12/12	-
2	TLA	D	501	-	-	0/4/12/12	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	TLA	C1-C2-C3	-3.37	105.85	113.11
2	A	501	TLA	O3-C3-C4	-2.41	105.30	111.10
2	D	501	TLA	O3-C3-C4	-2.16	105.91	111.10

There are no chirality outliers.

All (2) torsion outliers are listed below:

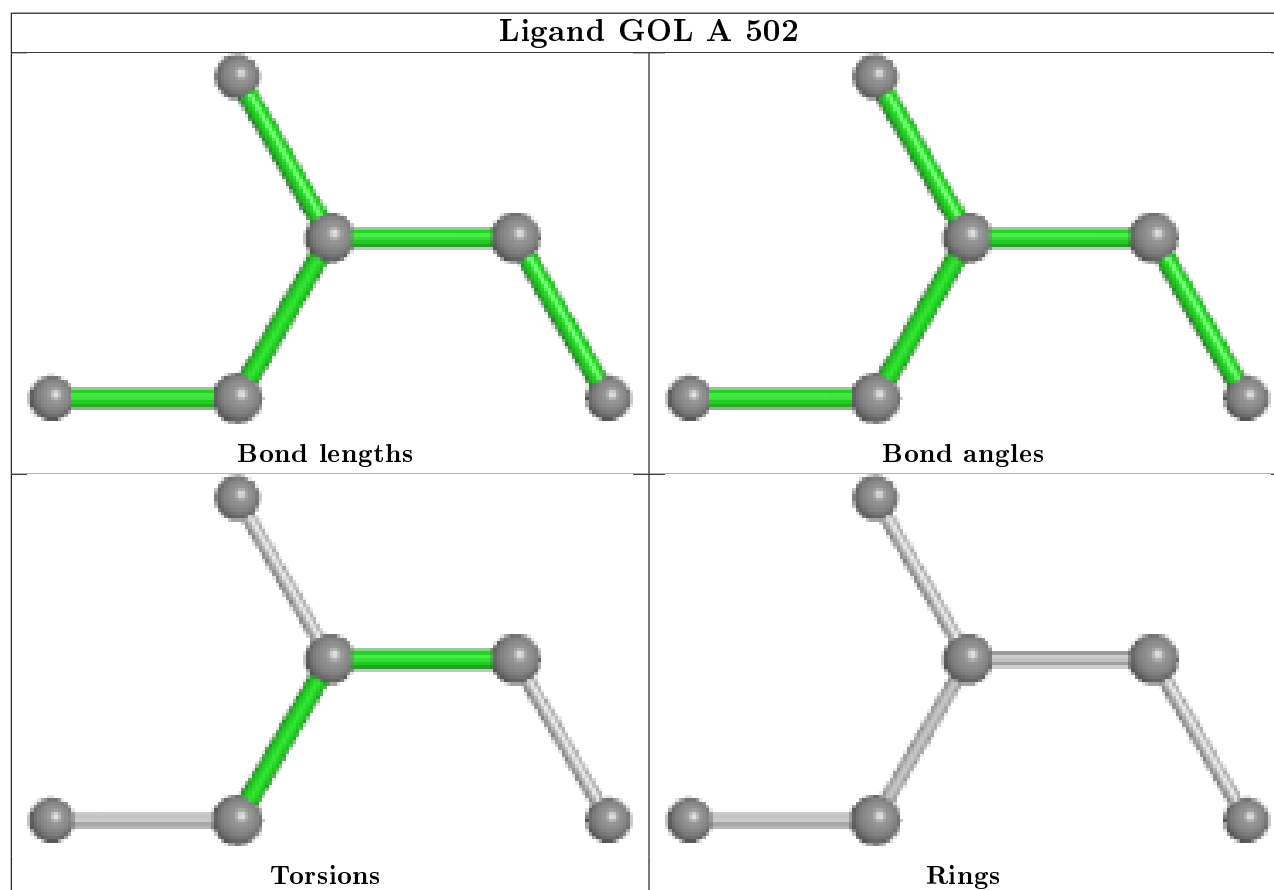
Mol	Chain	Res	Type	Atoms
3	D	504	GOL	C1-C2-C3-O3
3	D	504	GOL	O2-C2-C3-O3

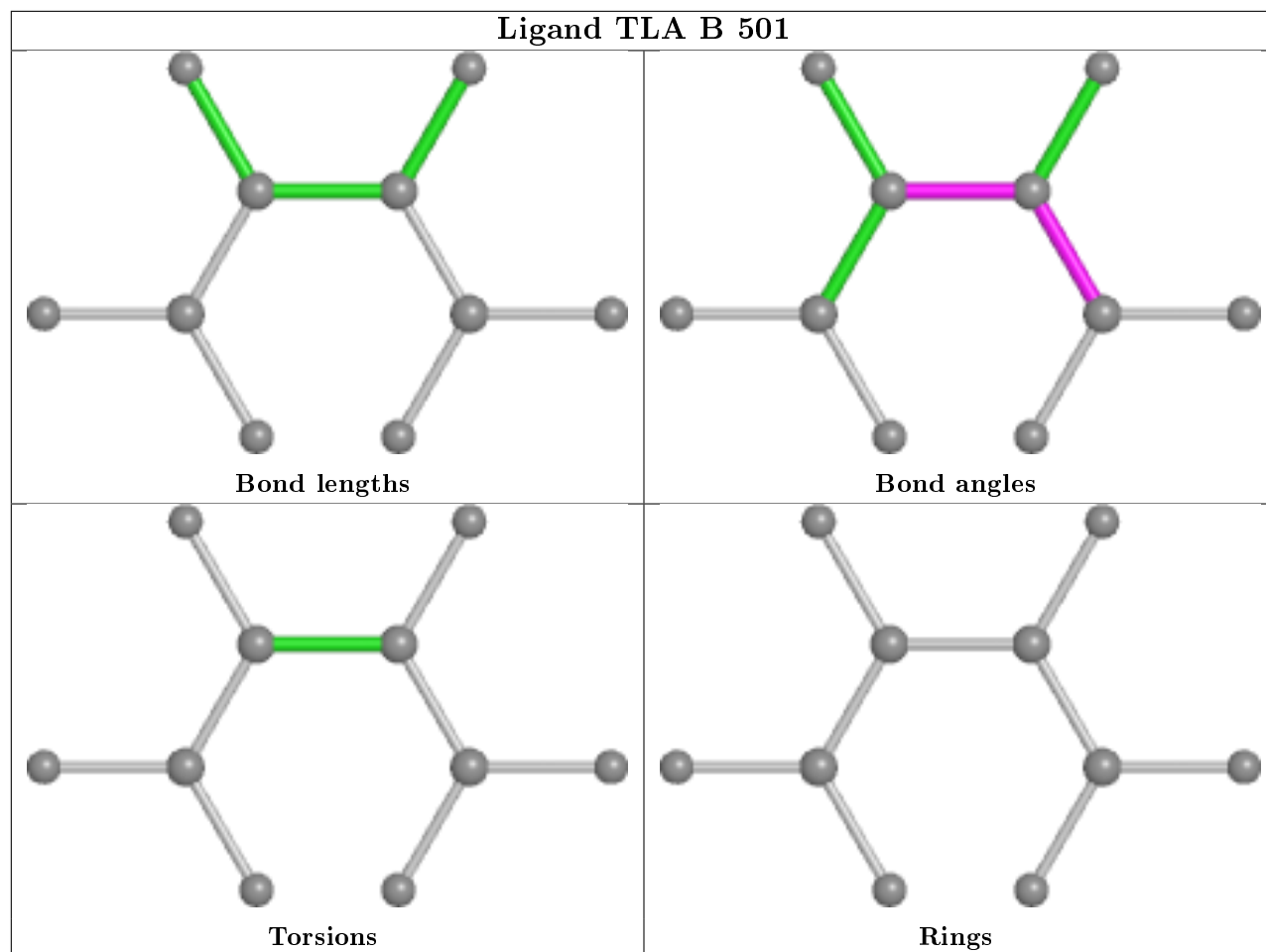
There are no ring outliers.

1 monomer is involved in 1 short contact:

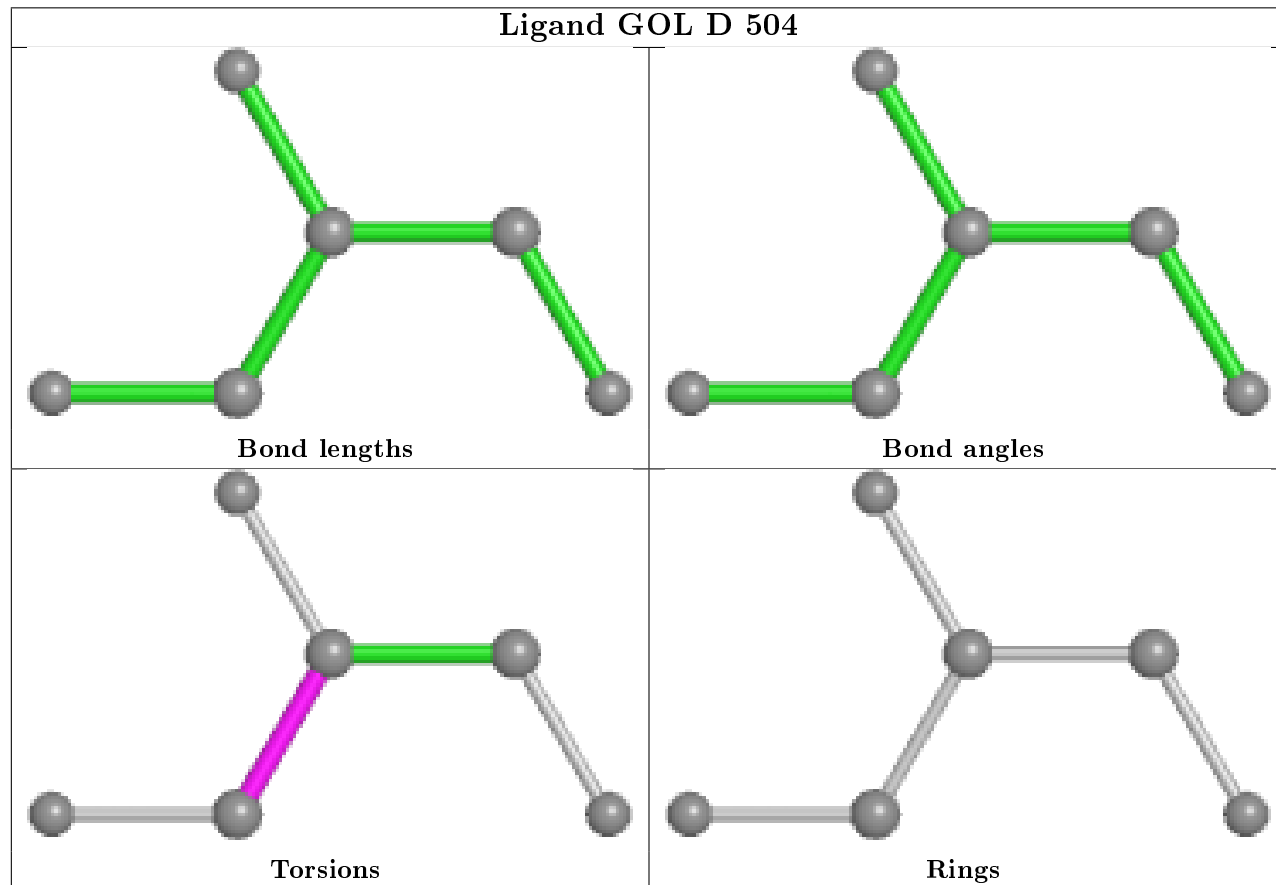
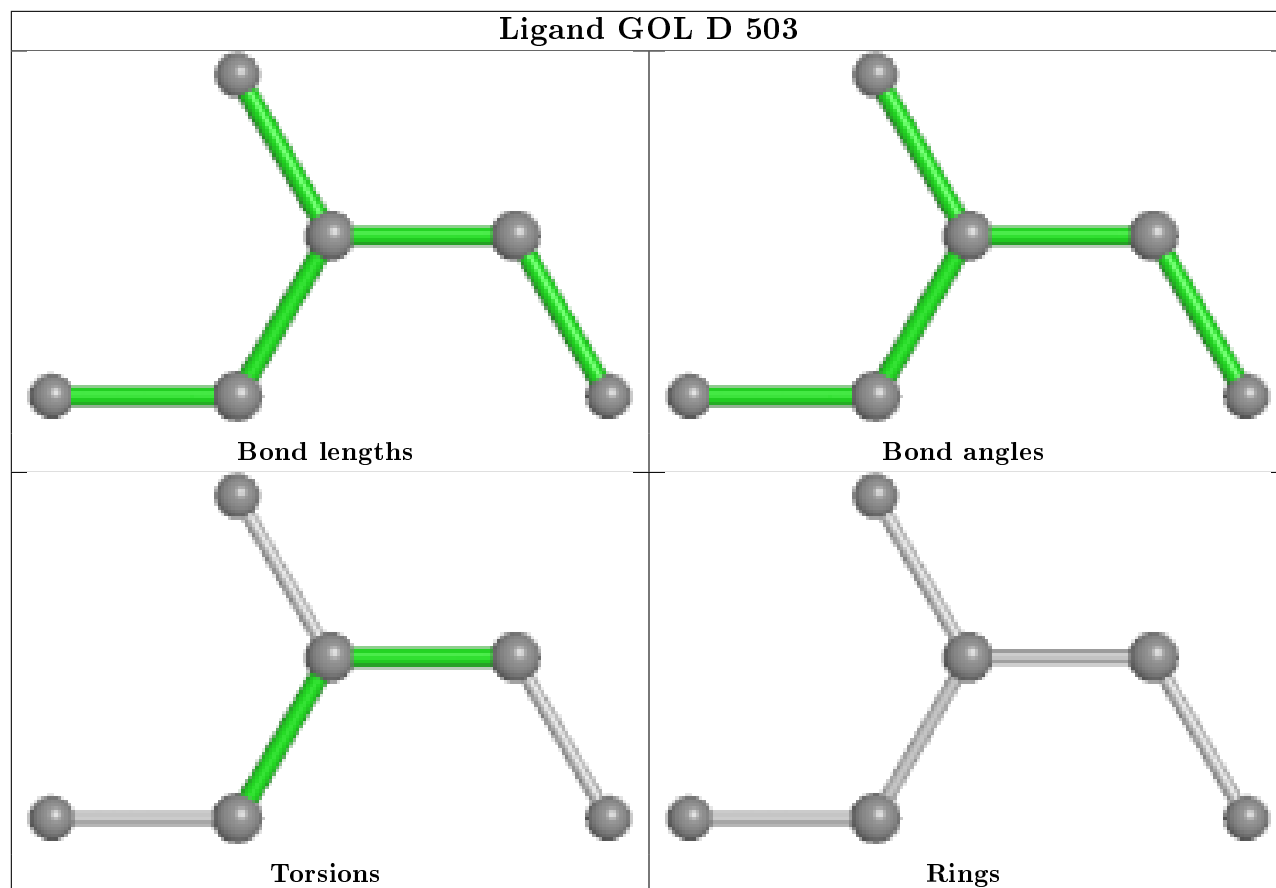
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	TLA	1	0

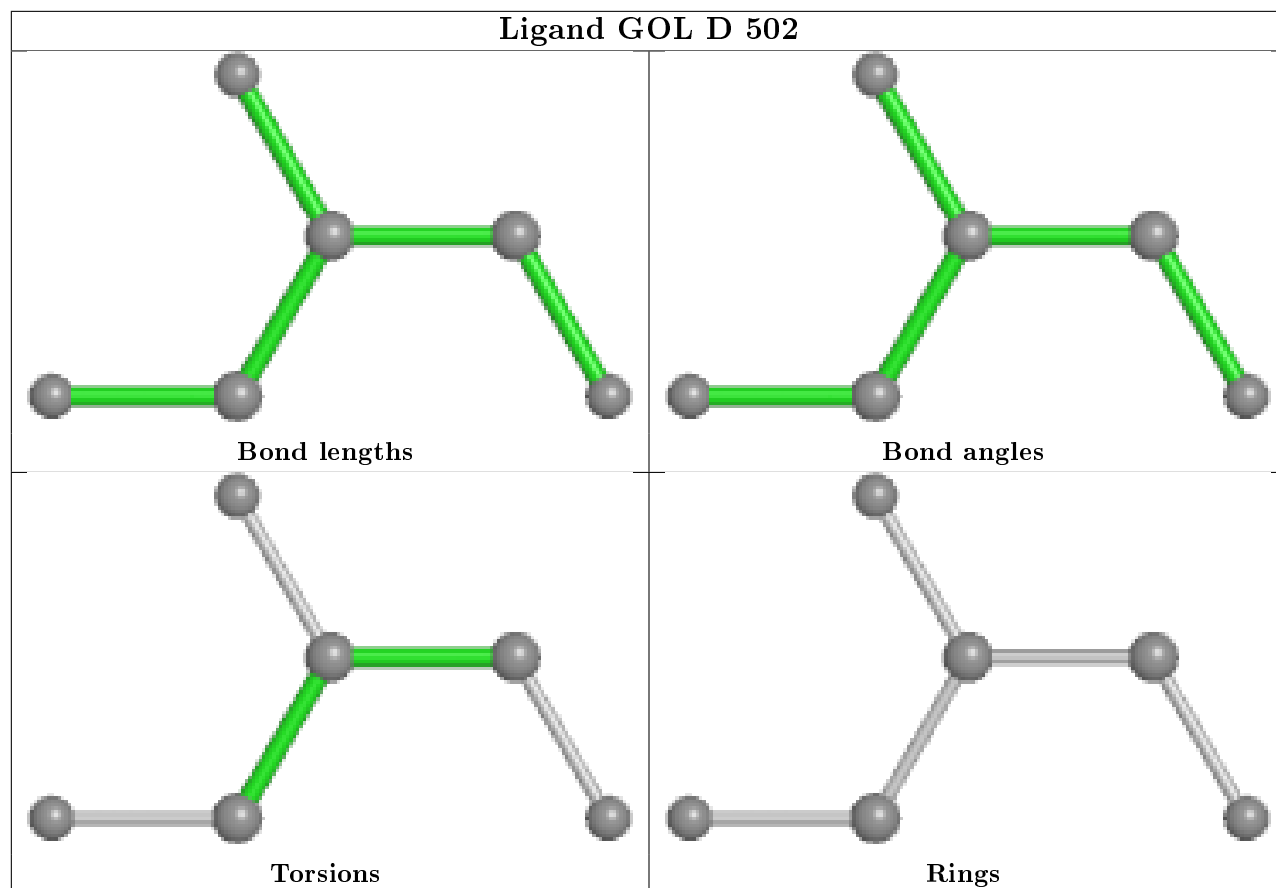
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

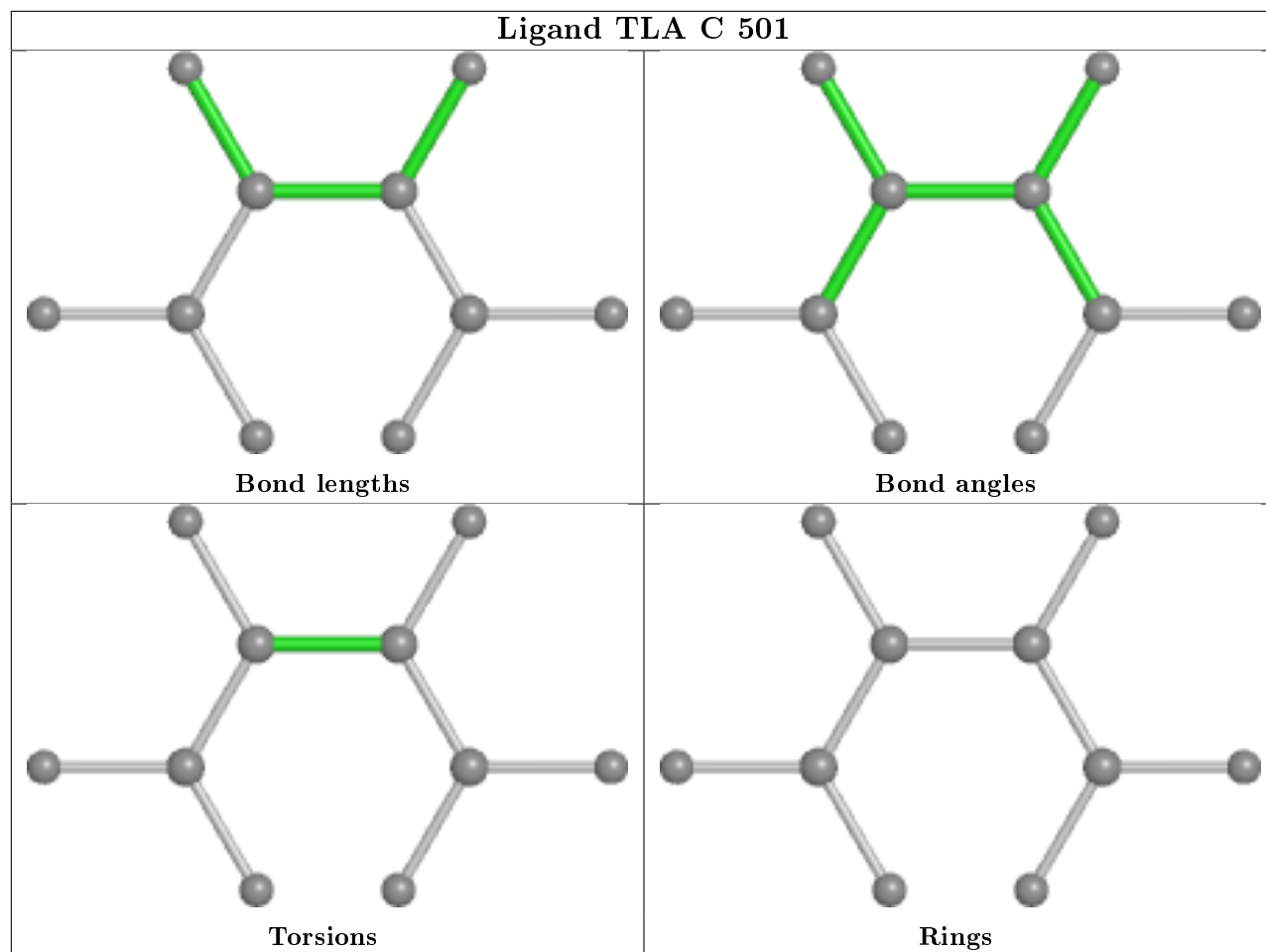


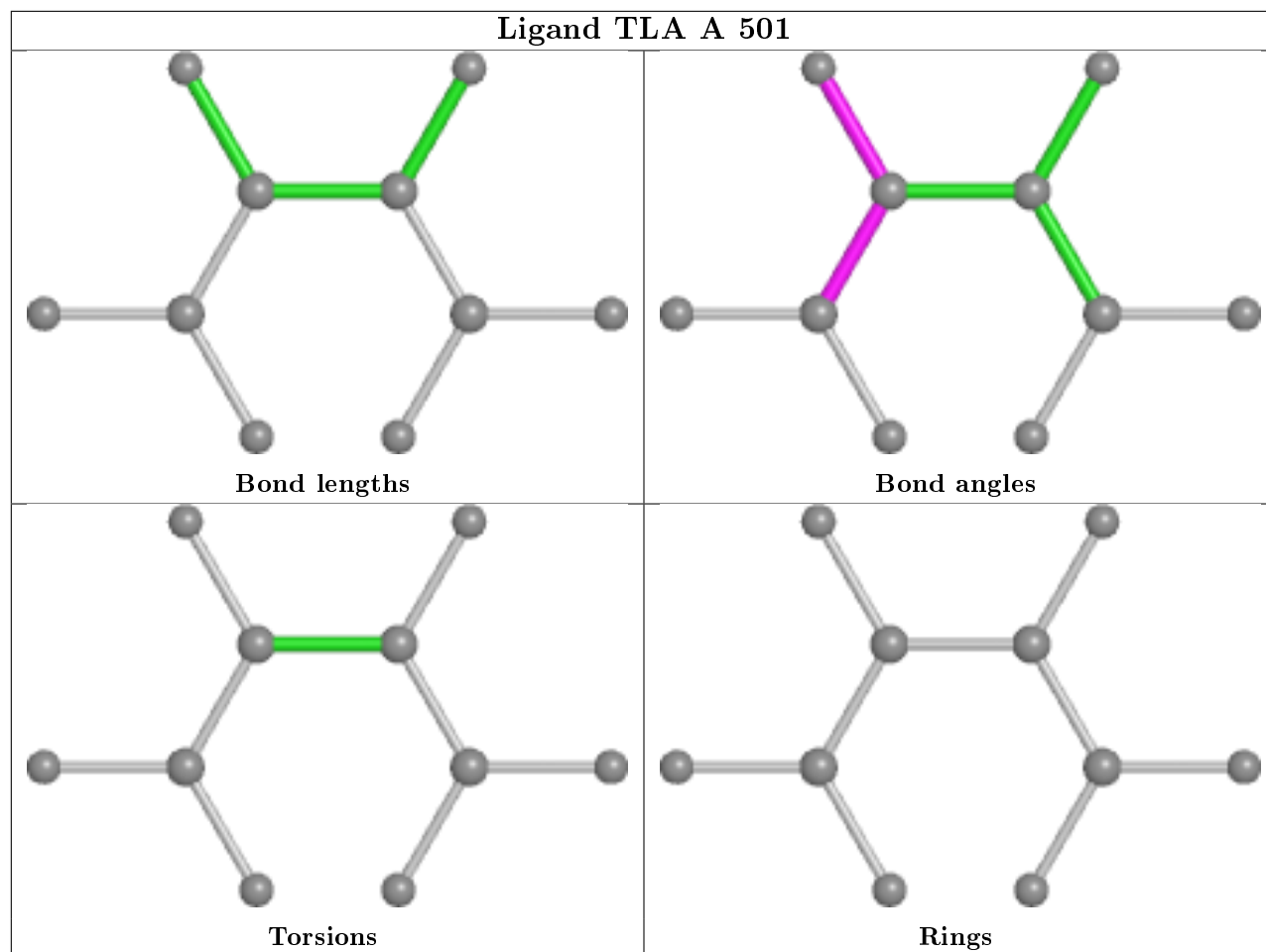


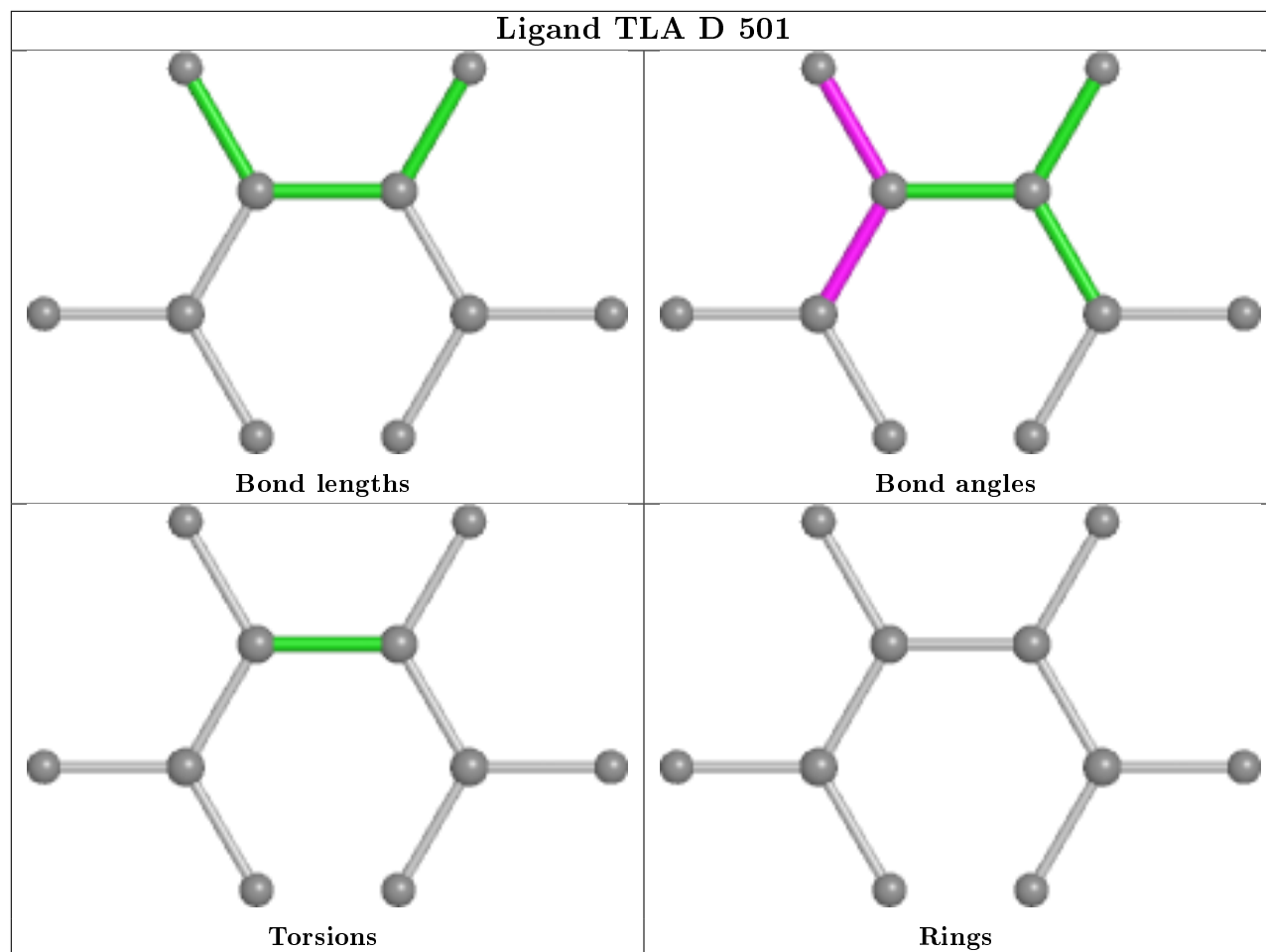












## 5.7 Other polymers [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	171/191 (89%)	-0.46	2 (1%) 79 79	15, 21, 40, 80	0
1	B	170/191 (89%)	-0.46	1 (0%) 89 89	16, 24, 41, 70	0
1	C	170/191 (89%)	-0.44	4 (2%) 59 58	16, 24, 40, 78	0
1	D	169/191 (88%)	-0.47	2 (1%) 79 79	16, 23, 43, 62	0
All	All	680/764 (89%)	-0.46	9 (1%) 77 77	15, 23, 41, 80	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	449	ILE	4.6
1	C	449	ILE	3.8
1	C	450	HIS	3.8
1	B	450	HIS	3.5
1	C	448	ARG	3.1

### 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](#)

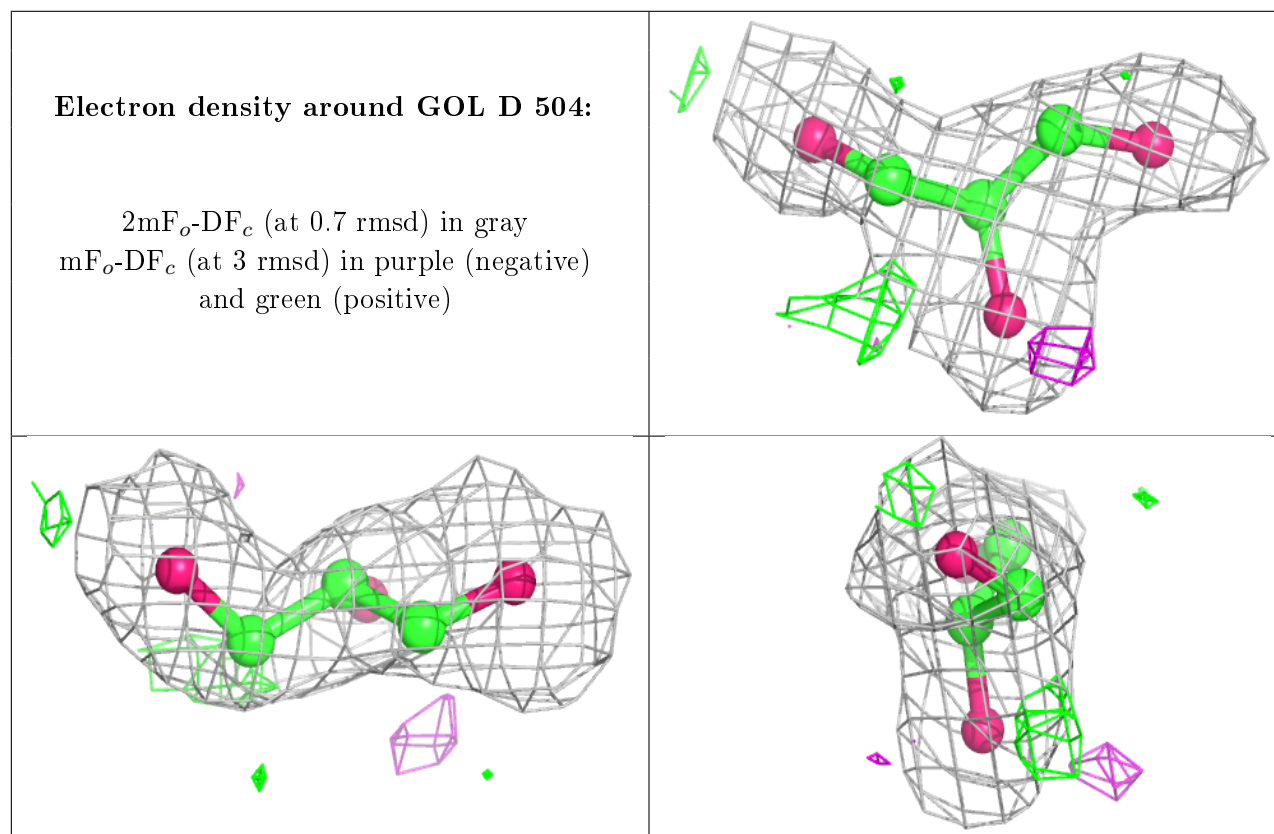
There are no carbohydrates in this entry.

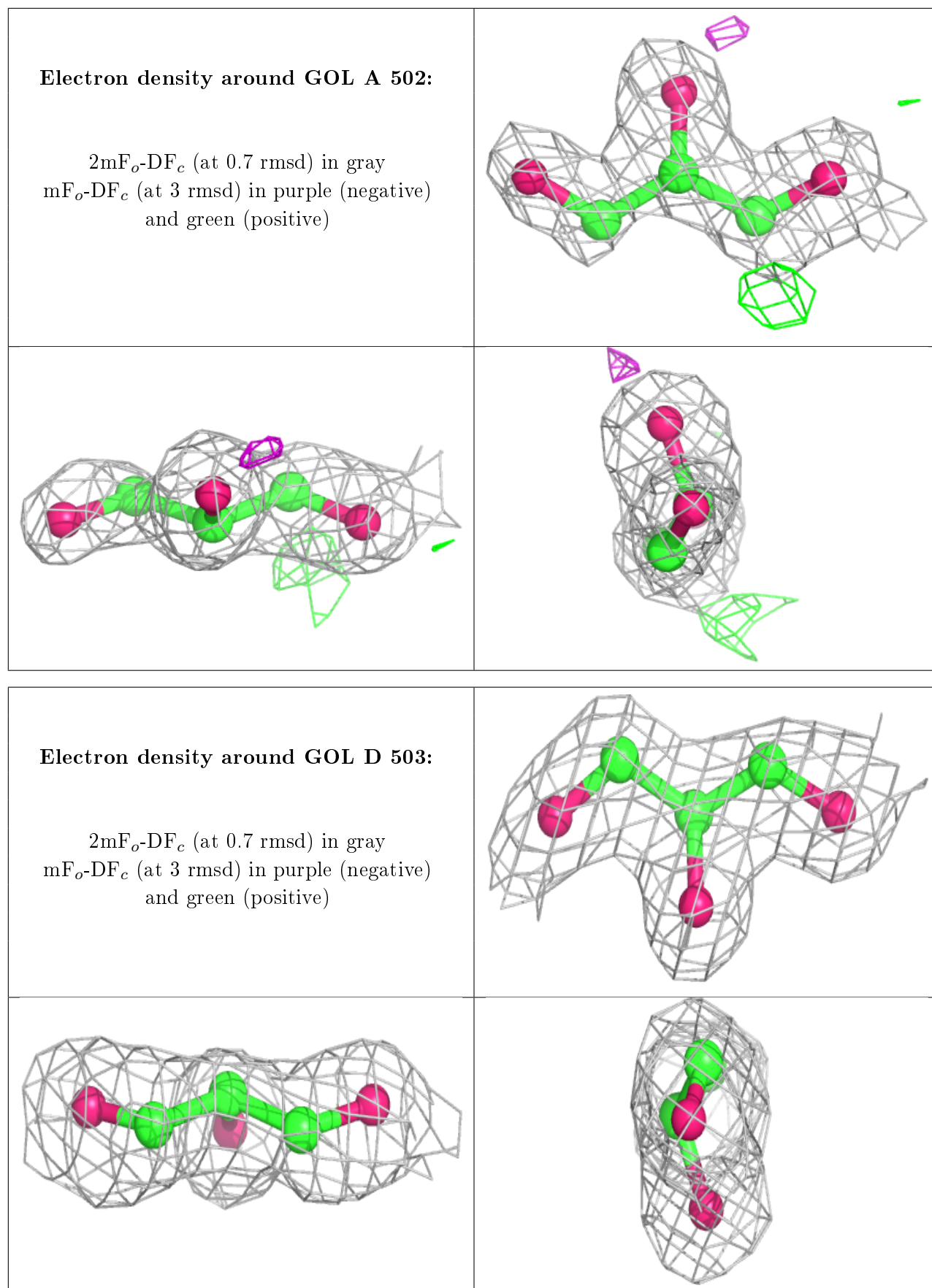
### 6.4 Ligands [i](#)

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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
3	GOL	D	504	6/6	0.70	0.11	47,51,54,59	0
3	GOL	A	502	6/6	0.91	0.17	31,33,36,40	0
3	GOL	D	503	6/6	0.96	0.09	25,28,29,36	0
2	TLA	D	501	10/10	0.97	0.06	16,17,18,19	0
3	GOL	D	502	6/6	0.98	0.07	18,20,20,22	0
2	TLA	C	501	10/10	0.98	0.06	17,18,19,20	0
2	TLA	B	501	10/10	0.98	0.06	18,19,19,20	0
2	TLA	A	501	10/10	0.99	0.06	16,17,20,20	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.

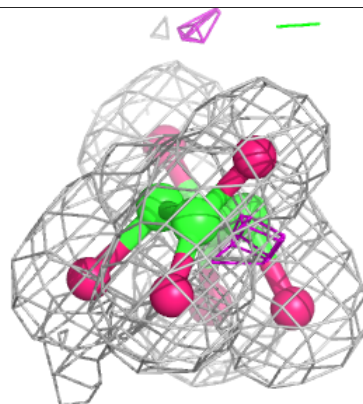
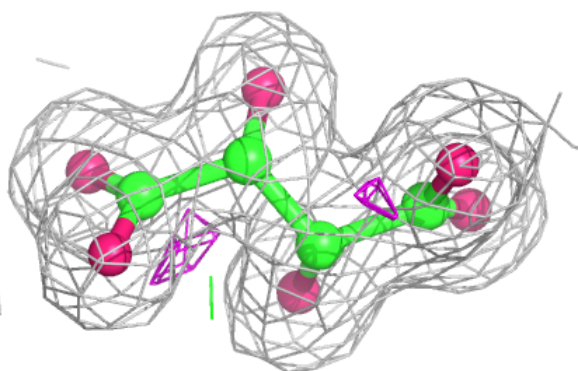
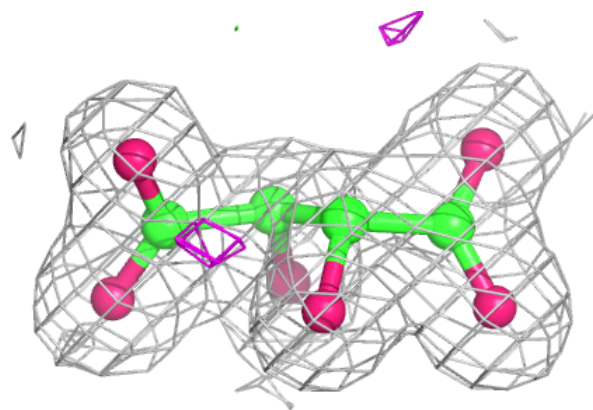




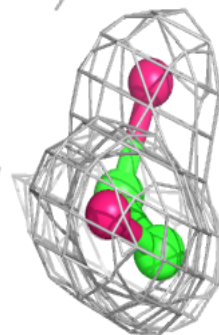
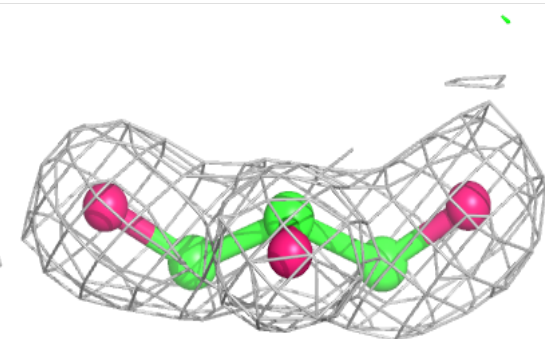
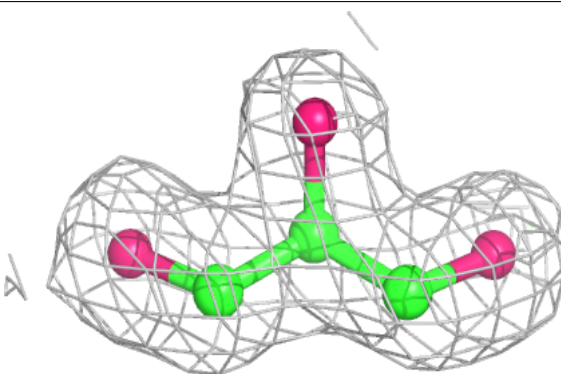


**Electron density around TLA D 501:**

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

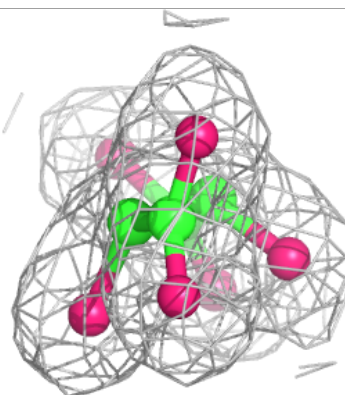
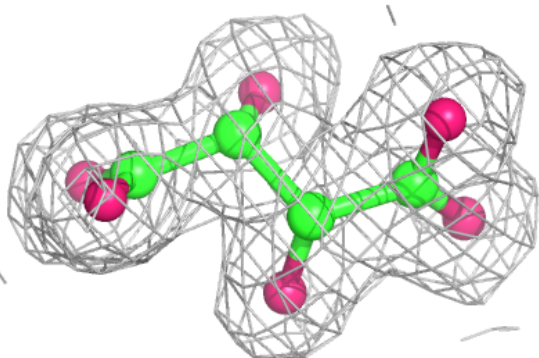
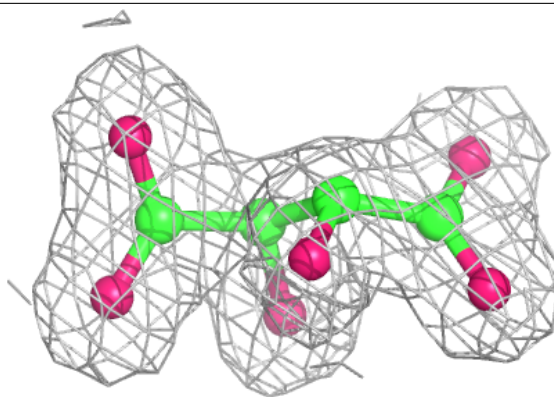
**Electron density around GOL D 502:**

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

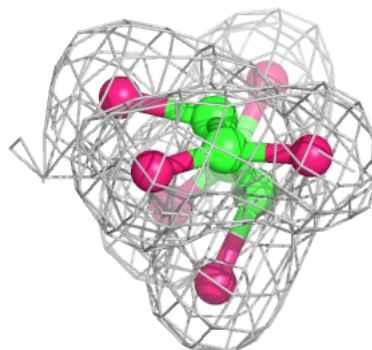
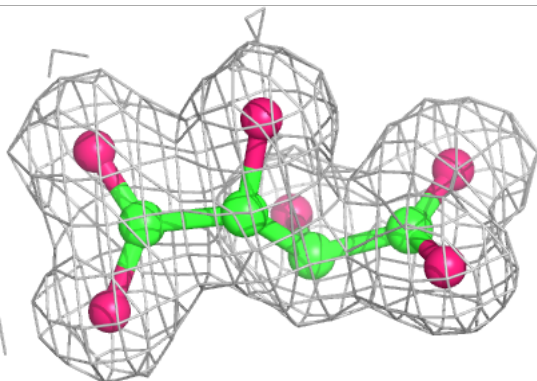
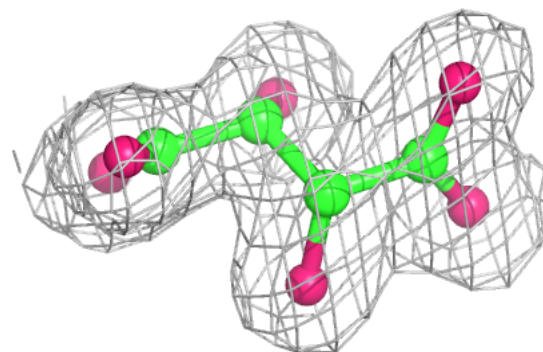


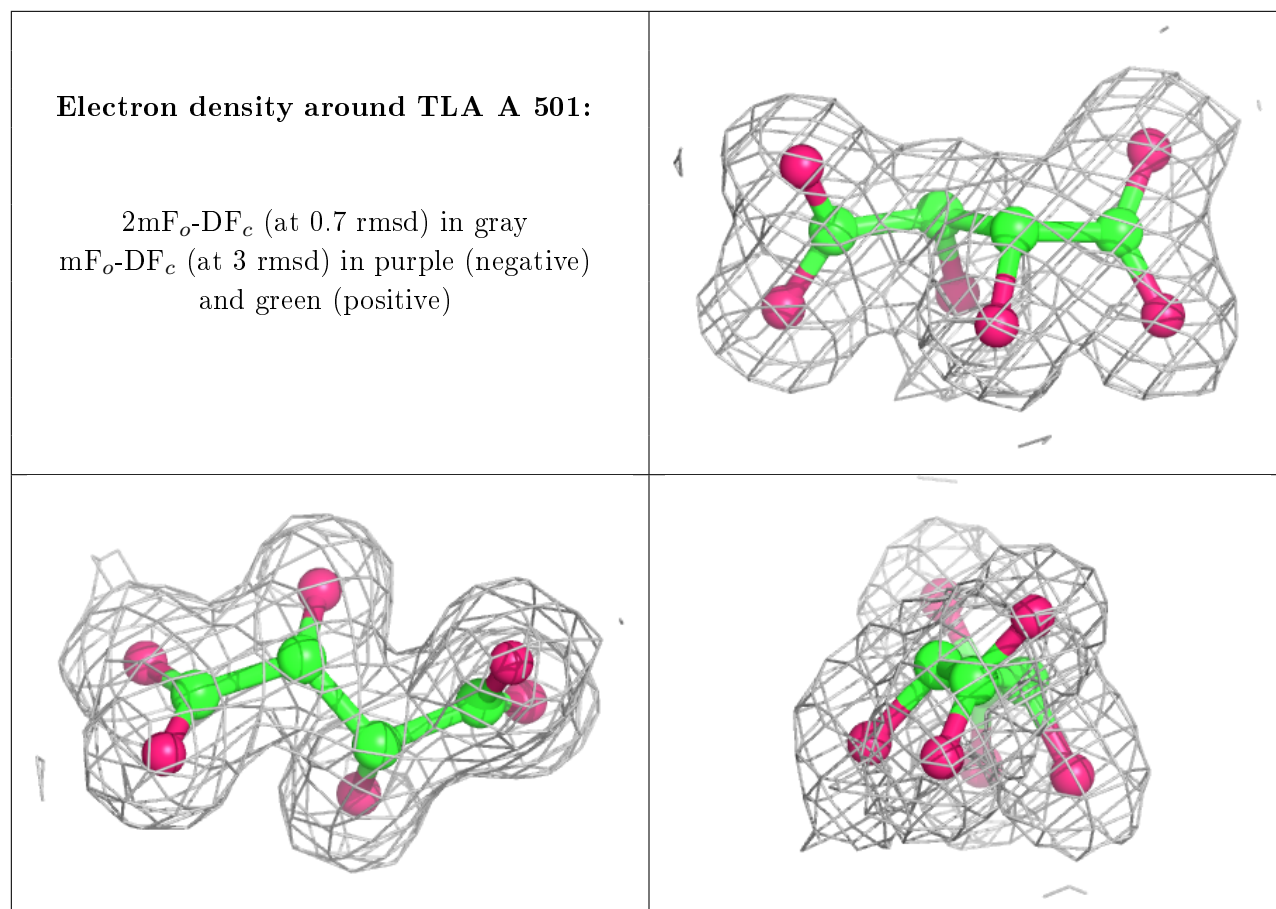
**Electron density around TLA C 501:**

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

**Electron density around TLA B 501:**

$2mF_o-DF_c$  (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.