



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:51 AM UTC

PDB ID : 22GA / pdb\_000022ga  
Title : Crystal structure of sorghum sulfotransferase LGS1 reveals sulfation-assisted BC-ring formation in strigolactone biosynthesis  
Authors : Asano, H.; Teramoto, T.; Kakuta, Y.  
Deposited on : 2026-01-09  
Resolution : 1.94 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](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.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

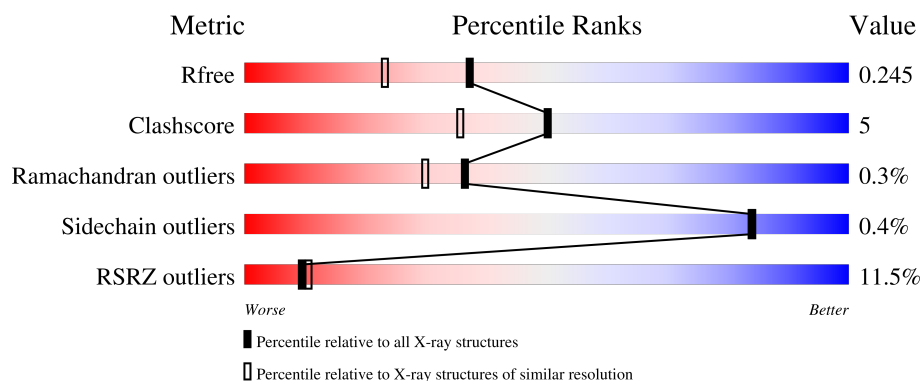
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.94 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))
$R_{free}$	180053	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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  $\geq 3$ , 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	375	<div> <div>8%</div> <div> <div></div> <div>75%</div> <div>13%</div> <div>13%</div> </div> </div>
1	B	375	<div> <div>12%</div> <div> <div></div> <div>81%</div> <div>6%</div> <div>13%</div> </div> </div>

## 2 Entry composition [i](#)

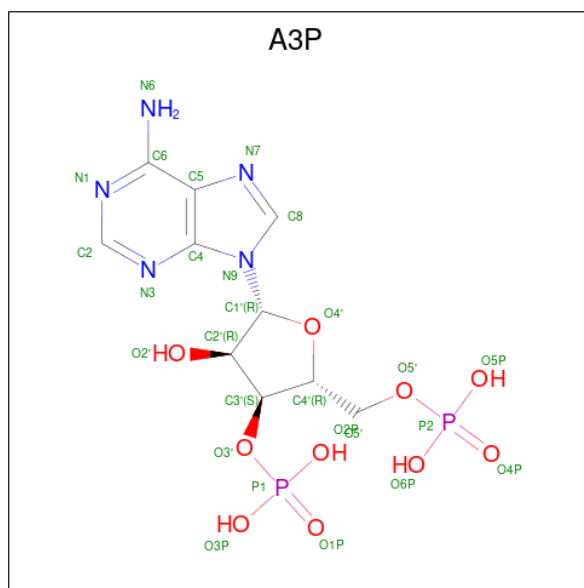
There are 4 unique types of molecules in this entry. The entry contains 5726 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Sulfotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	3	14	0
			2694	1722	471	484	17			
1	B	327	Total	C	N	O	S	8	8	0
			2619	1674	454	474	17			

- Molecule 2 is ADENOSINE-3'-5'-DIPHOSPHATE (CCD ID: A3P) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula:  $C_3H_8O_3$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	1
			12	6	6		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

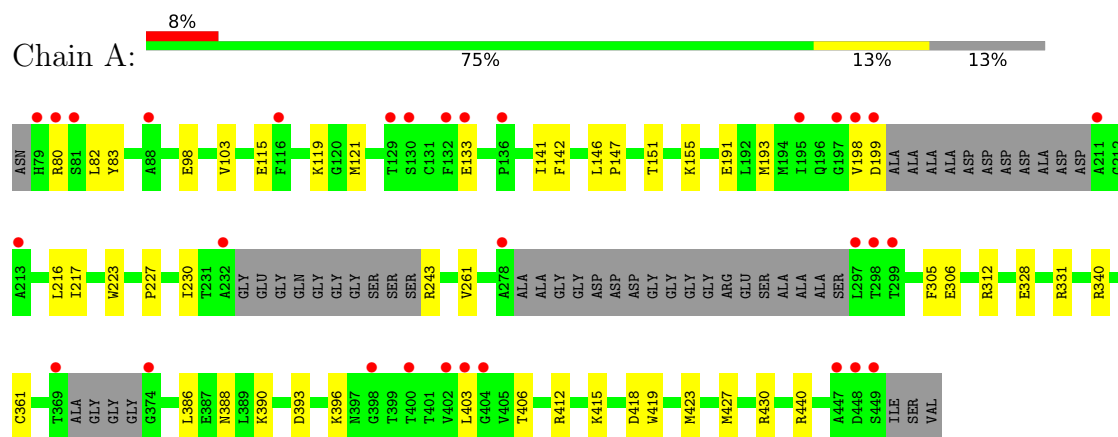
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	183	Total	O	0	0
			183	183		
4	B	128	Total	O	0	0
			128	128		

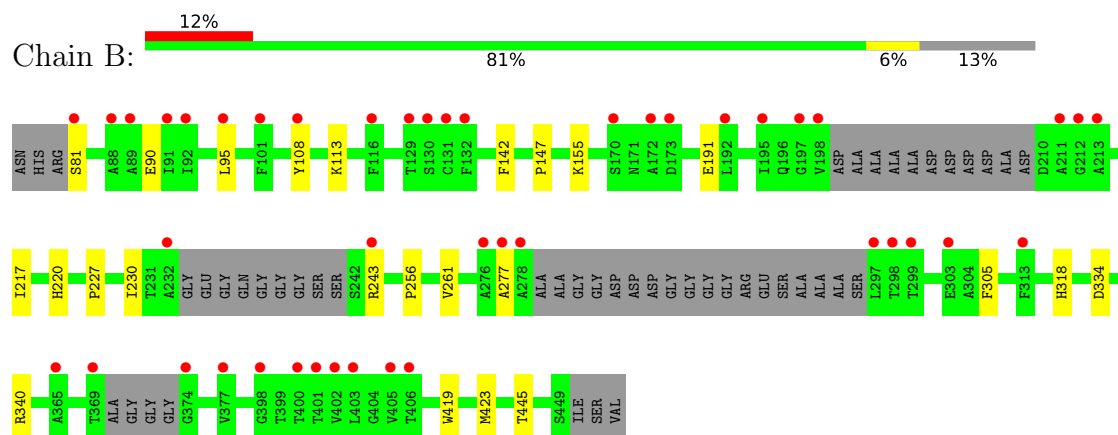
### 3 Residue-property plots [i](#)

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: Sulfotransferase



#### • Molecule 1: Sulfotransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	40.92Å 96.50Å 179.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.25 – 1.94 48.25 – 1.94	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.25-1.94) 99.7 (48.25-1.94)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.16 (at 1.94Å)	Xtriage
Refinement program	PHENIX (1.21.1_5286: ???)	Depositor
R, $R_{free}$	0.226 , 0.266 (Not available) , 0.245	Depositor DCC
$R_{free}$ test set	1994 reflections (3.70%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.6	Xtriage
Anisotropy	0.504	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 55.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5726	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	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 48.44 % 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 8.6028e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: A3P, GOL

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	0.13	0/2766	0.27	0/3747
1	B	0.12	0/2687	0.27	0/3643
All	All	0.13	0/5453	0.27	0/7390

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

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	2694	0	2629	35	0
1	B	2619	0	2556	19	0
2	A	27	0	11	2	0
2	B	27	0	11	2	0
3	A	24	0	32	5	0
3	B	24	0	32	4	0
4	A	183	0	0	5	0
4	B	128	0	0	4	0
All	All	5726	0	5271	57	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 5.

All (57) 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:340[B]:ARG:NH2	4:A:601:HOH:O	2.23	0.71
1:B:340:ARG:NH1	4:B:604:HOH:O	2.28	0.66
1:B:340:ARG:NH2	1:B:445:THR:O	2.30	0.65
1:A:147[B]:PRO:HB3	3:A:504[B]:GOL:H11	1.77	0.65
1:B:155:LYS:NZ	4:B:605:HOH:O	2.30	0.64
1:B:81:SER:N	3:B:504:GOL:HO2	1.97	0.62
1:B:261:VAL:HG21	1:B:419:TRP:HA	1.80	0.62
1:B:256:PRO:HG3	1:B:318:HIS:CE1	2.36	0.60
1:A:261:VAL:HG21	1:A:419:TRP:HA	1.83	0.59
1:B:147:PRO:HB3	3:B:502:GOL:H32	1.84	0.59
1:A:227:PRO:HD2	1:A:230[A]:ILE:HD12	1.85	0.58
1:A:403:LEU:HD22	3:A:504[A]:GOL:H31	1.88	0.56
1:A:115:GLU:HG2	1:A:119:LYS:HD2	1.88	0.56
1:B:90:GLU:N	1:B:90:GLU:OE2	2.40	0.55
1:A:440:ARG:NH1	4:A:614:HOH:O	2.39	0.55
1:A:80:ARG:HD3	1:A:133:GLU:HG2	1.88	0.54
1:B:81:SER:N	4:B:612:HOH:O	2.41	0.52
1:A:423:MET:HA	1:A:427[B]:MET:HE3	1.91	0.52
2:A:501:A3P:O3P	2:A:501:A3P:O2'	2.28	0.51
1:A:328:GLU:OE2	1:A:331:ARG:NH2	2.33	0.51
1:B:305:PHE:CE1	1:B:423:MET:HE3	2.47	0.50
1:A:121:MET:HE1	1:A:191:GLU:HG3	1.93	0.49
1:A:142:PHE:CZ	1:A:230[B]:ILE:HD12	2.48	0.49
1:A:390:LYS:NZ	1:A:412:ARG:O	2.40	0.49
2:B:501:A3P:O3P	2:B:501:A3P:O2'	2.30	0.48
1:B:95:LEU:HD13	1:B:108:TYR:HB2	1.96	0.48
1:A:393:ASP:HA	1:A:396[B]:LYS:HE3	1.97	0.47
1:A:415[B]:LYS:HE2	4:A:633:HOH:O	2.14	0.46
1:A:243:ARG:NH2	4:A:622:HOH:O	2.48	0.46
1:A:98:GLU:OE1	1:A:312:ARG:NH1	2.49	0.45
2:A:501:A3P:O6P	3:A:504[A]:GOL:O1	2.28	0.45
1:B:220:HIS:NE2	3:B:502:GOL:H11	2.31	0.45
1:A:227:PRO:HB2	1:A:230[B]:ILE:HG12	1.98	0.45
1:B:227:PRO:HD2	1:B:230:ILE:HD12	1.99	0.45
1:A:193:MET:HG2	1:A:199:ASP:HA	1.99	0.44
1:A:306:GLU:CD	1:A:430:ARG:HH12	2.26	0.44
1:A:386:LEU:O	1:A:390:LYS:HB2	2.17	0.44
1:B:142:PHE:HA	1:B:217:ILE:O	2.18	0.44
1:B:113:LYS:NZ	4:B:611:HOH:O	2.41	0.44
1:A:216:LEU:H	3:A:503:GOL:H2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:388:ASN:OD1	3:A:502:GOL:H32	2.18	0.44
1:A:415[B]:LYS:NZ	1:A:418:ASP:OD1	2.52	0.43
1:A:223:TRP:CE2	1:A:328:GLU:HG3	2.53	0.42
1:A:82[B]:LEU:HA	1:A:227:PRO:HB3	2.01	0.42
1:A:146:LEU:HD12	1:A:146:LEU:HA	1.91	0.42
1:A:142:PHE:HA	1:A:217:ILE:O	2.20	0.42
2:B:501:A3P:O6P	3:B:502:GOL:H31	2.19	0.42
1:A:305:PHE:CE1	1:A:423:MET:HE3	2.55	0.42
1:B:305:PHE:HE1	1:B:423:MET:HE3	1.84	0.42
1:A:80:ARG:HD2	1:A:83:TYR:HE1	1.84	0.41
1:B:191:GLU:OE1	1:B:191:GLU:N	2.52	0.41
1:A:141:ILE:HB	1:A:216:LEU:HD23	2.02	0.41
1:A:306:GLU:OE2	1:A:430:ARG:NH1	2.46	0.41
1:A:151:THR:HG22	1:A:155:LYS:HE3	2.03	0.41
1:A:361:CYS:HB3	1:B:243:ARG:HG2	2.01	0.41
1:B:334:ASP:OD1	1:B:334:ASP:N	2.49	0.40
1:A:155:LYS:NZ	4:A:626:HOH:O	2.51	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	332/375 (88%)	327 (98%)	4 (1%)	1 (0%)	36	30
1	B	324/375 (86%)	316 (98%)	6 (2%)	2 (1%)	21	11
All	All	656/750 (88%)	643 (98%)	10 (2%)	3 (0%)	36	15

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	277[A]	ALA

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Mol	Chain	Res	Type
1	B	277[B]	ALA
1	A	198	VAL

### 5.3.2 Protein sidechains ⓘ

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	267/292 (91%)	265 (99%)	2 (1%)	76	74
1	B	274/292 (94%)	274 (100%)	0	100	100
All	All	541/584 (93%)	539 (100%)	2 (0%)	84	84

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	VAL
1	A	406	THR

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

Mol	Chain	Res	Type
1	B	85	ASN
1	B	379	GLN
1	B	407	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

10 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	504[B]	-	5,5,5	0.34	0	5,5,5	0.45	0
3	GOL	A	503	-	5,5,5	0.34	0	5,5,5	0.36	0
3	GOL	B	502	-	5,5,5	0.33	0	5,5,5	0.44	0
3	GOL	B	505	-	5,5,5	0.34	0	5,5,5	0.39	0
3	GOL	A	502	-	5,5,5	0.33	0	5,5,5	0.37	0
3	GOL	B	504	-	5,5,5	0.35	0	5,5,5	0.39	0
2	A3P	B	501	-	29,29,29	0.69	0	44,45,45	0.73	1 (2%)
2	A3P	A	501	-	29,29,29	0.71	0	44,45,45	0.81	1 (2%)
3	GOL	B	503	-	5,5,5	0.35	0	5,5,5	0.44	0
3	GOL	A	504[A]	-	5,5,5	0.33	0	5,5,5	0.48	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
3	GOL	A	504[B]	-	-	0/4/4/4	-
3	GOL	A	503	-	-	2/4/4/4	-
3	GOL	B	502	-	-	2/4/4/4	-
3	GOL	B	505	-	-	0/4/4/4	-
3	GOL	A	502	-	-	0/4/4/4	-
3	GOL	B	504	-	-	0/4/4/4	-
2	A3P	B	501	-	-	2/15/31/31	0/3/3/3
2	A3P	A	501	-	-	1/15/31/31	0/3/3/3
3	GOL	B	503	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	504[A]	-	-	0/4/4/4	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	A3P	P1-O3'-C3'	-3.55	113.95	123.43
2	B	501	A3P	P1-O3'-C3'	-3.21	114.87	123.43

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	503	GOL	C1-C2-C3-O3
3	B	502	GOL	O1-C1-C2-C3
3	A	503	GOL	O2-C2-C3-O3
3	B	502	GOL	O1-C1-C2-O2
2	B	501	A3P	C5'-O5'-P2-O4P
2	B	501	A3P	C3'-O3'-P1-O3P
2	A	501	A3P	C3'-O3'-P1-O3P

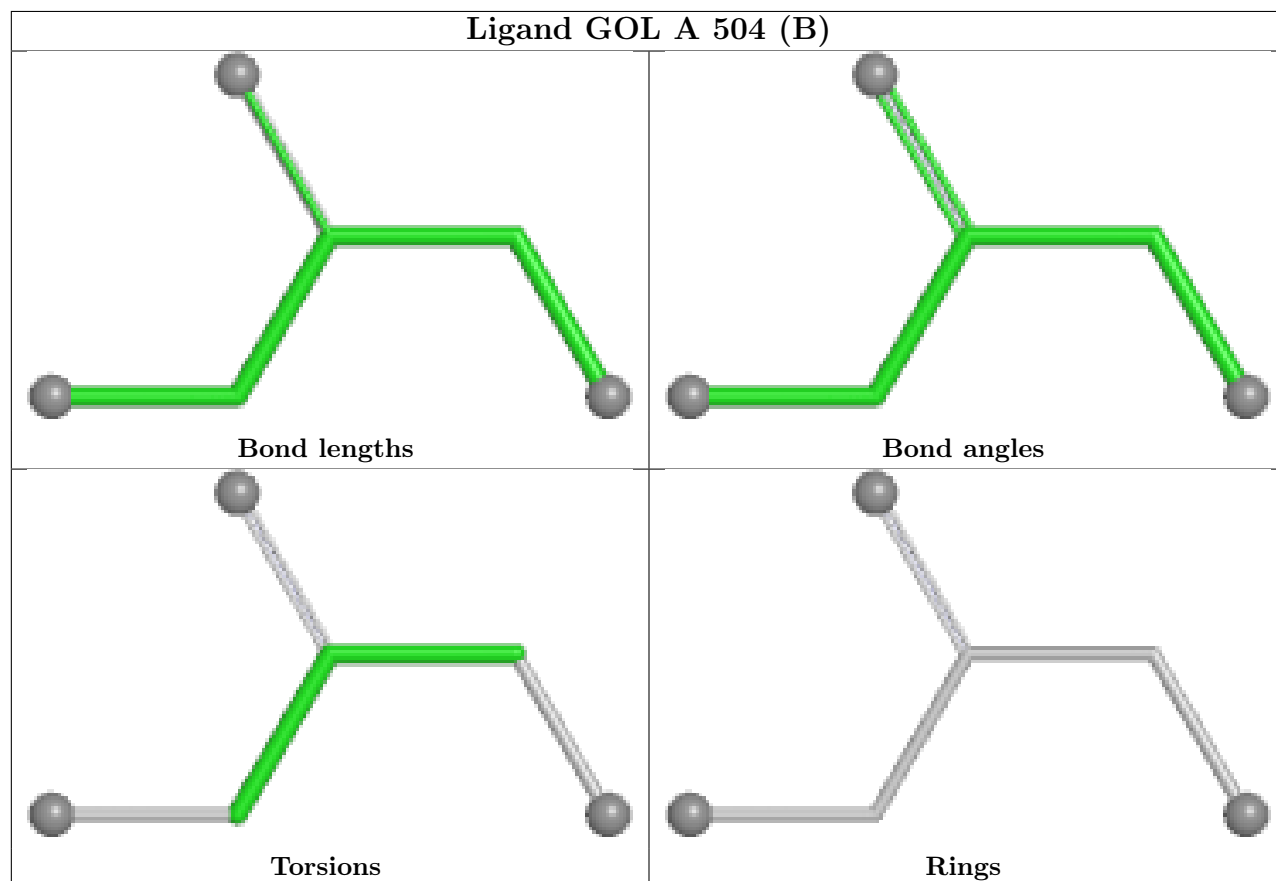
There are no ring outliers.

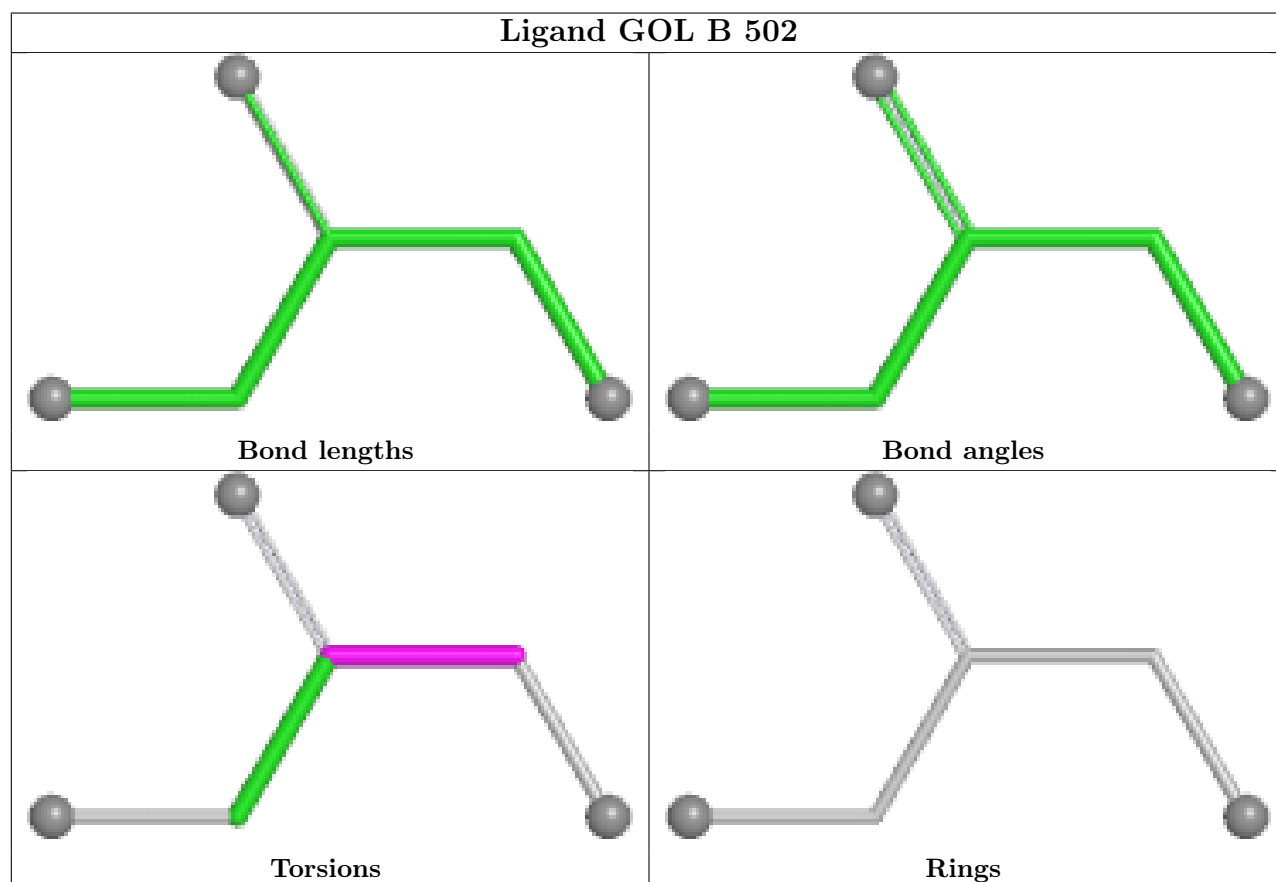
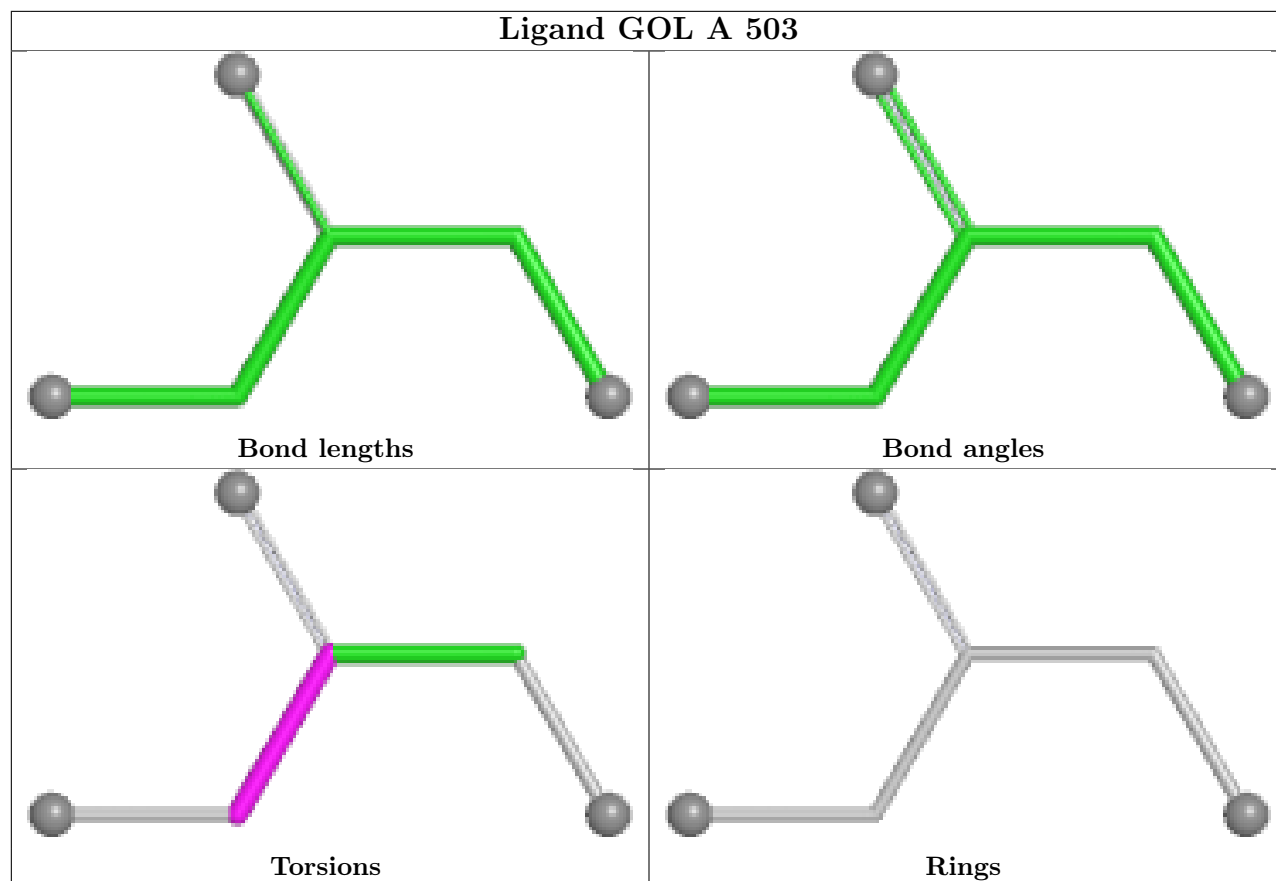
8 monomers are involved in 11 short contacts:

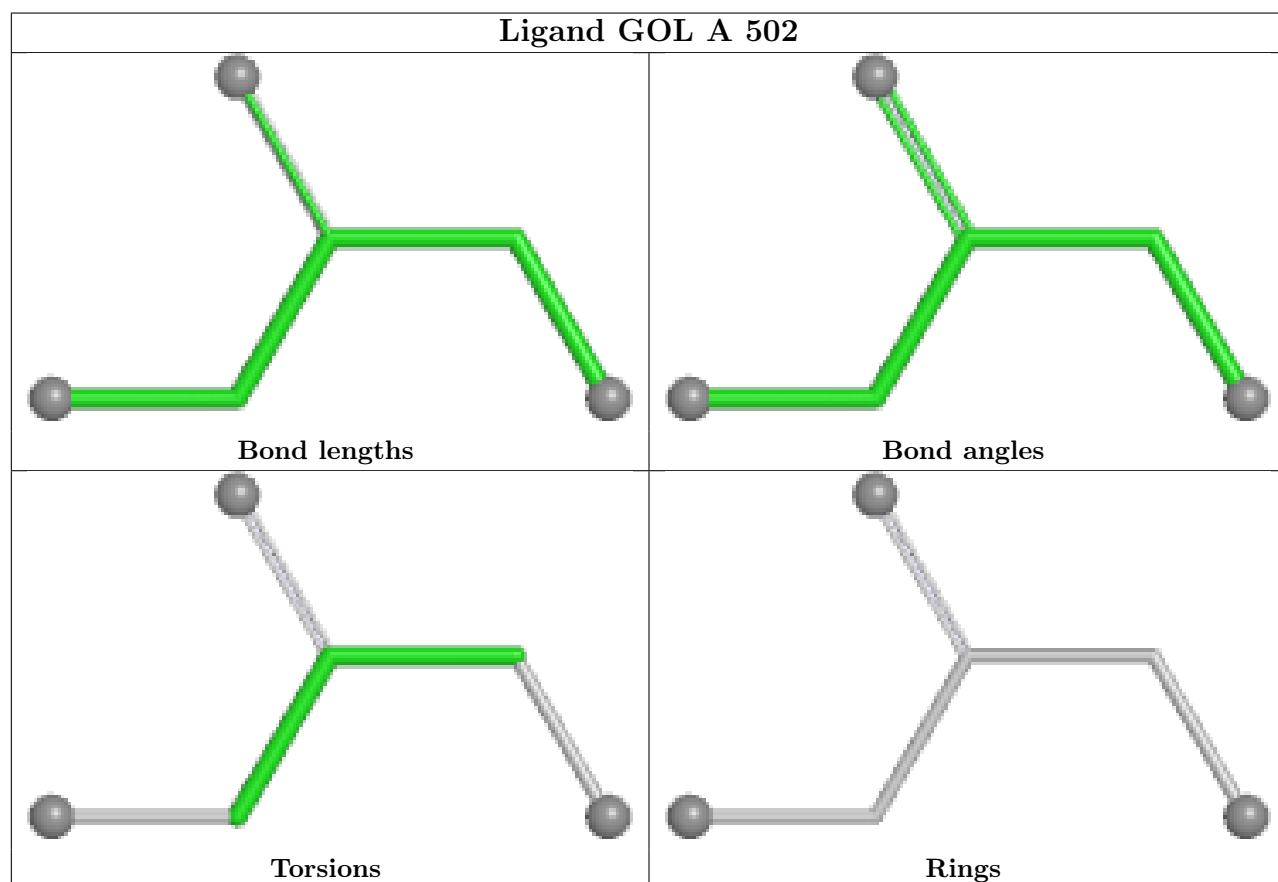
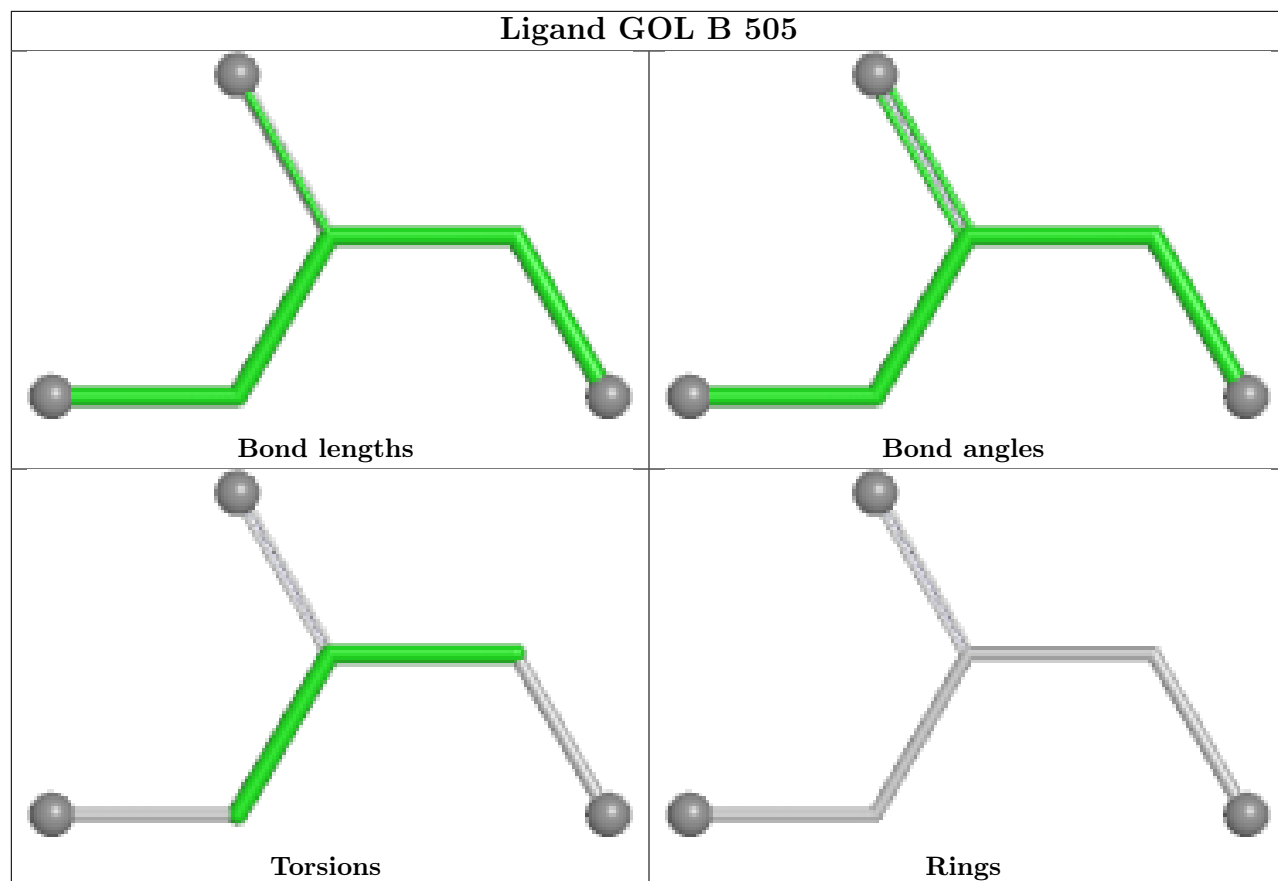
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	504[B]	GOL	1	0
3	A	503	GOL	1	0
3	B	502	GOL	3	0
3	A	502	GOL	1	0
3	B	504	GOL	1	0
2	B	501	A3P	2	0
2	A	501	A3P	2	0
3	A	504[A]	GOL	2	0

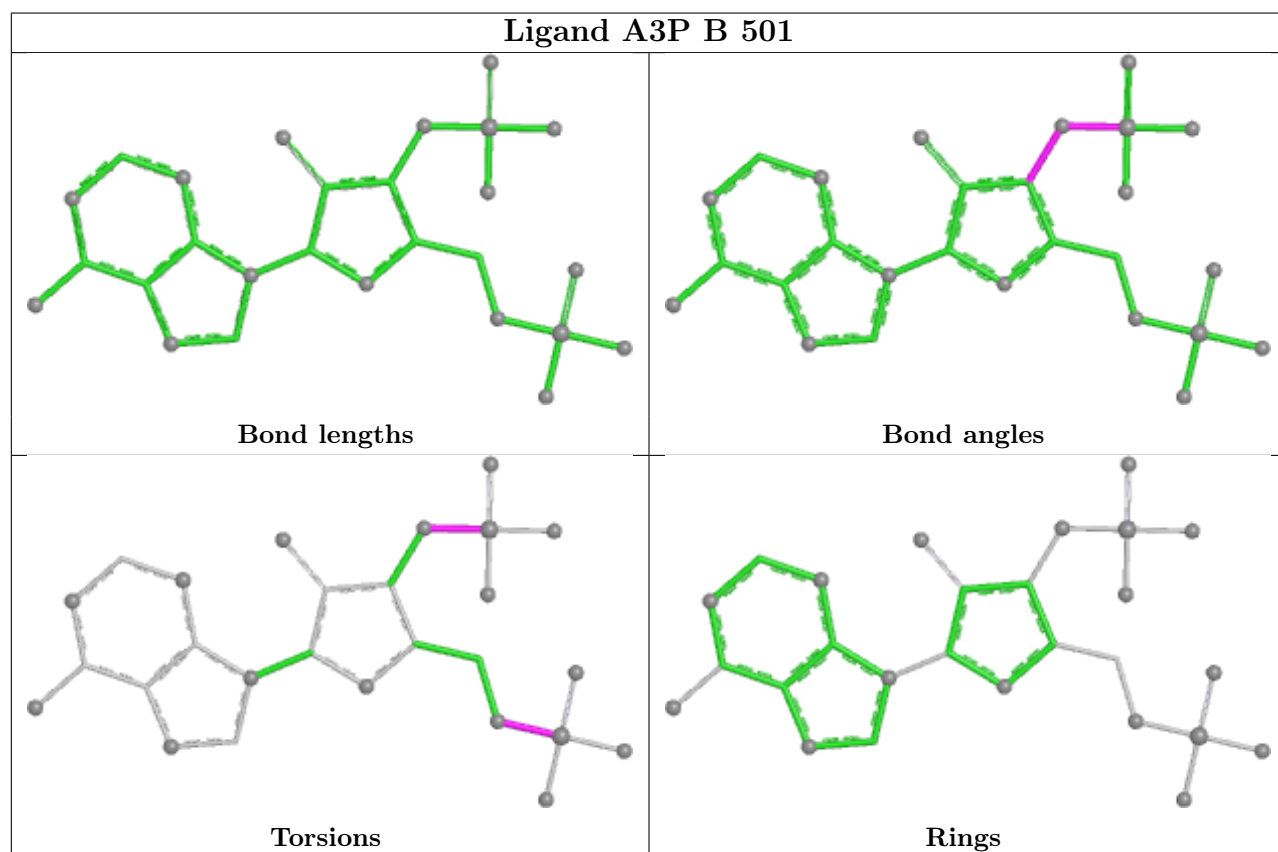
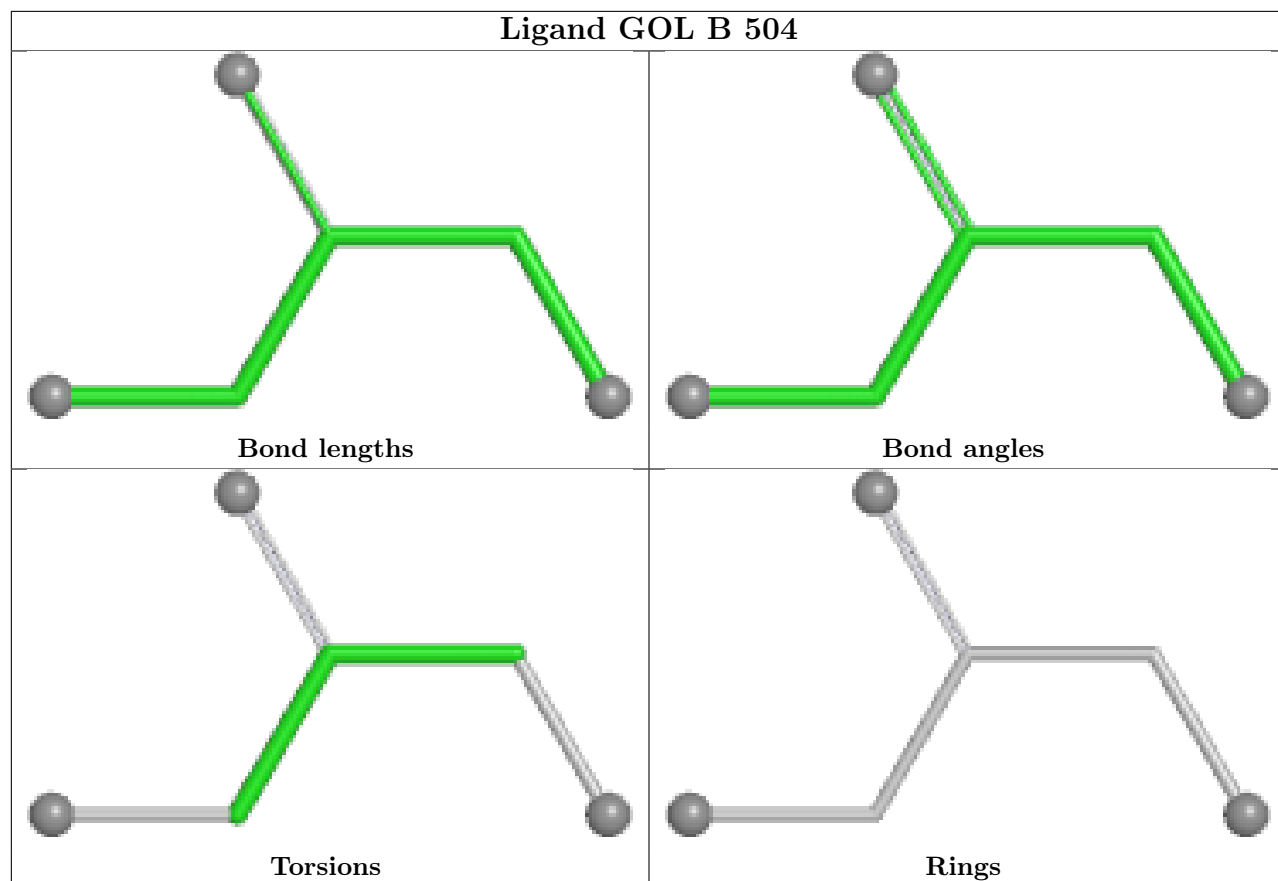
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



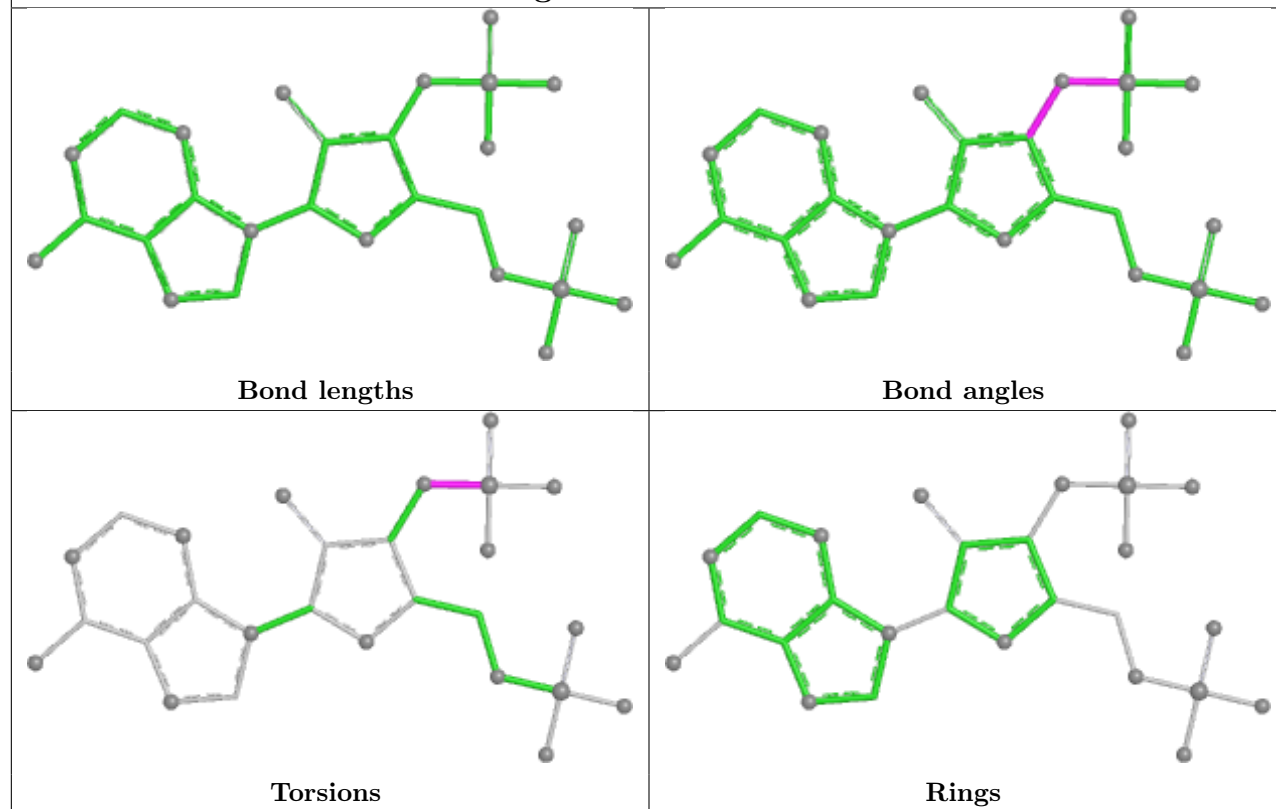




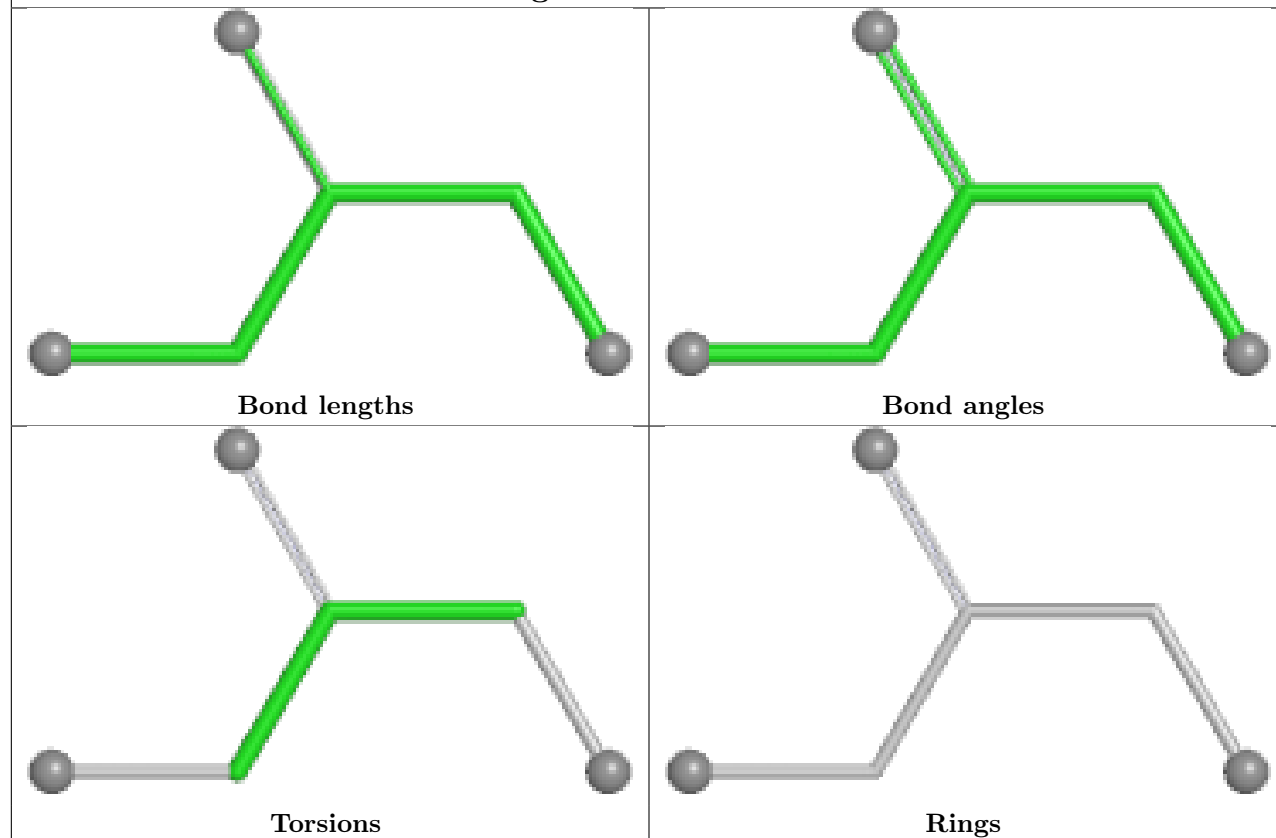


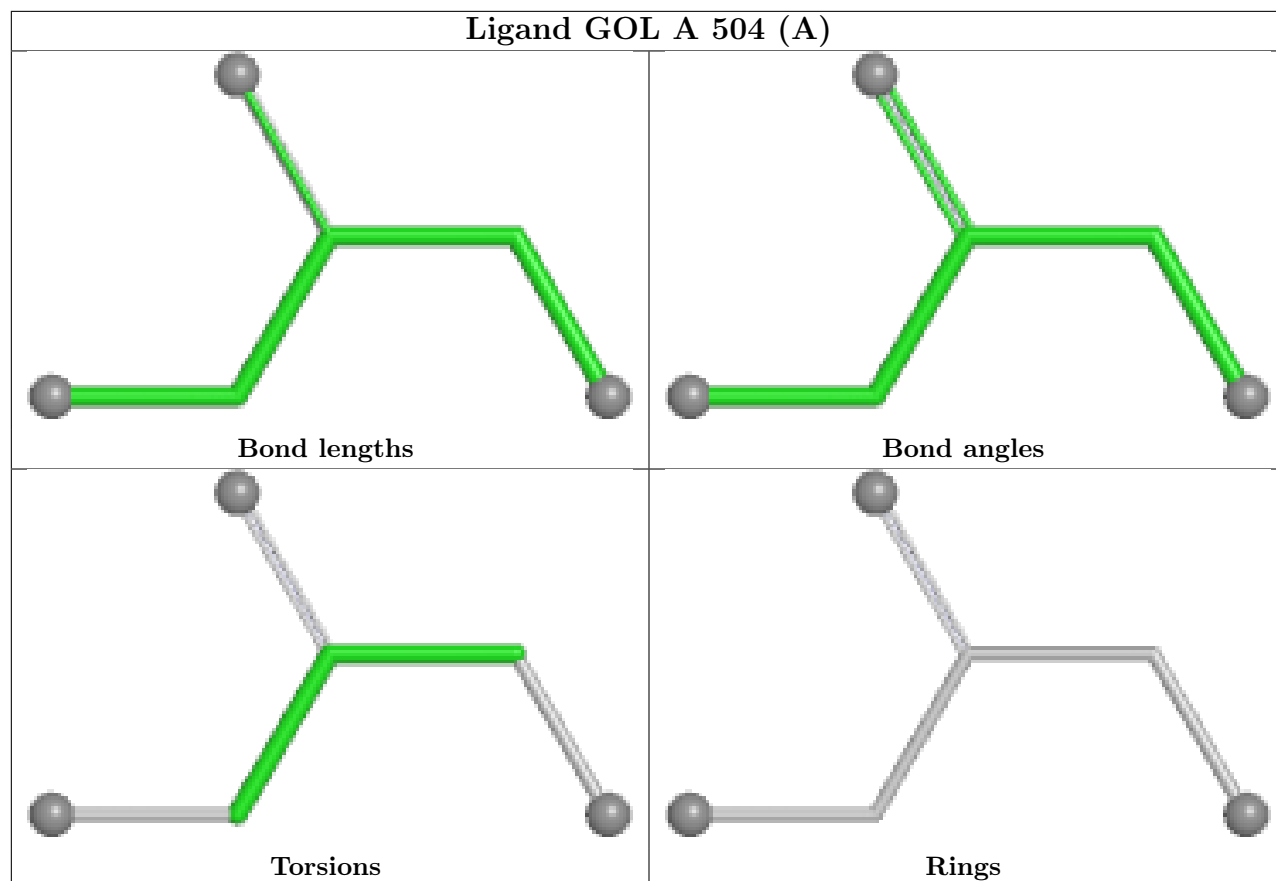


## Ligand A3P A 501



## Ligand GOL B 503





## 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, 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	328/375 (87%)	0.58	31 (9%) 14 15	15, 43, 90, 150	16 (4%)
1	B	327/375 (87%)	0.91	44 (13%) 7 7	18, 54, 98, 137	8 (2%)
All	All	655/750 (87%)	0.74	75 (11%) 9 10	15, 49, 98, 150	24 (3%)

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	278[A]	ALA	11.4
1	A	136[A]	PRO	6.6
1	A	297	LEU	6.0
1	A	403	LEU	5.6
1	B	297	LEU	5.3
1	B	89	ALA	5.2
1	B	277[A]	ALA	5.0
1	B	91	ILE	4.7
1	A	404	GLY	4.6
1	B	88	ALA	4.3
1	B	198	VAL	4.3
1	A	211	ALA	3.9
1	B	402	VAL	3.8
1	B	405	VAL	3.8
1	A	402	VAL	3.7
1	B	212	GLY	3.6
1	A	132	PHE	3.5
1	B	298	THR	3.4
1	B	213	ALA	3.4
1	A	80	ARG	3.3
1	A	369	THR	3.3
1	A	449	SER	3.3
1	A	198	VAL	3.2
1	B	116	PHE	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	129	THR	3.2
1	B	400	THR	3.1
1	A	199	ASP	3.1
1	B	403	LEU	3.1
1	B	132	PHE	3.1
1	A	213	ALA	3.0
1	B	211	ALA	3.0
1	A	298	THR	3.0
1	A	195	ILE	2.9
1	A	197	GLY	2.9
1	B	398	GLY	2.9
1	B	276[A]	ALA	2.8
1	A	88	ALA	2.8
1	A	116	PHE	2.7
1	B	406	THR	2.7
1	A	278	ALA	2.6
1	A	374	GLY	2.6
1	B	131	CYS	2.6
1	A	130	SER	2.6
1	B	172	ALA	2.6
1	B	299	THR	2.5
1	B	173	ASP	2.5
1	B	130	SER	2.5
1	B	232	ALA	2.5
1	B	365	ALA	2.5
1	A	447	ALA	2.4
1	B	377	VAL	2.4
1	A	81	SER	2.4
1	B	195	ILE	2.4
1	A	79	HIS	2.3
1	A	398	GLY	2.3
1	A	448	ASP	2.3
1	A	299	THR	2.3
1	A	400	THR	2.3
1	B	95	LEU	2.3
1	B	192	LEU	2.3
1	B	369	THR	2.3
1	A	133	GLU	2.2
1	B	170	SER	2.2
1	A	232	ALA	2.2
1	B	108	TYR	2.2
1	B	92	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	81	SER	2.2
1	B	101	PHE	2.1
1	B	129	THR	2.1
1	B	401	THR	2.1
1	B	243	ARG	2.1
1	B	374	GLY	2.1
1	B	303	GLU	2.0
1	B	197	GLY	2.0
1	B	313	PHE	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](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

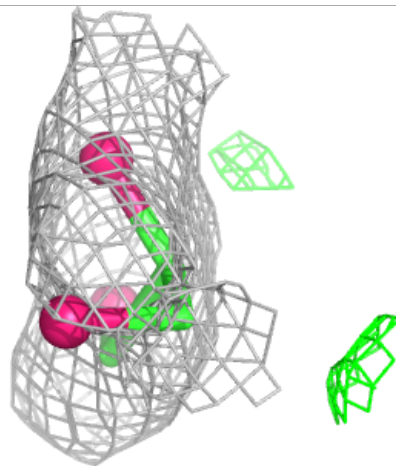
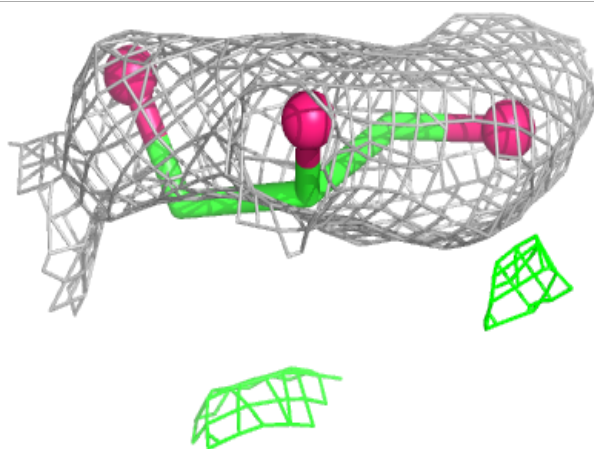
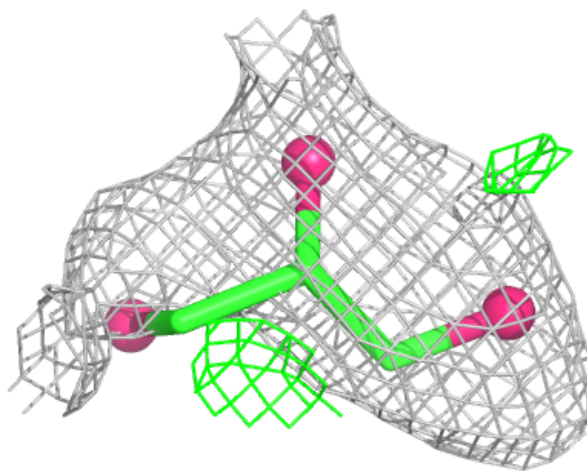
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	GOL	B	504	6/6	0.70	0.15	75,90,92,96	0
3	GOL	A	502	6/6	0.73	0.13	55,64,73,75	0
3	GOL	B	505	6/6	0.74	0.14	79,86,101,105	0
3	GOL	A	503	6/6	0.75	0.17	57,77,79,80	0
3	GOL	B	503	6/6	0.84	0.12	75,81,85,91	0
3	GOL	A	504[B]	6/6	0.85	0.12	40,42,44,45	6
3	GOL	A	504[A]	6/6	0.85	0.12	34,42,46,49	6
3	GOL	B	502	6/6	0.89	0.12	59,61,69,73	0
2	A3P	A	501	27/27	0.97	0.06	27,32,34,37	0
2	A3P	B	501	27/27	0.97	0.06	33,40,42,47	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.

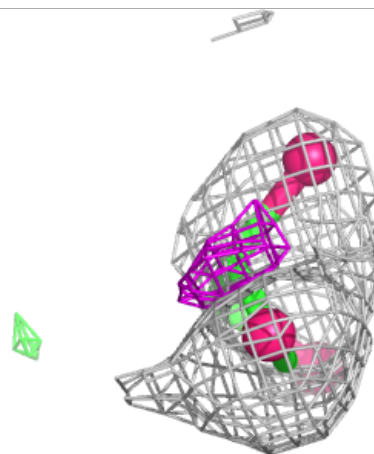
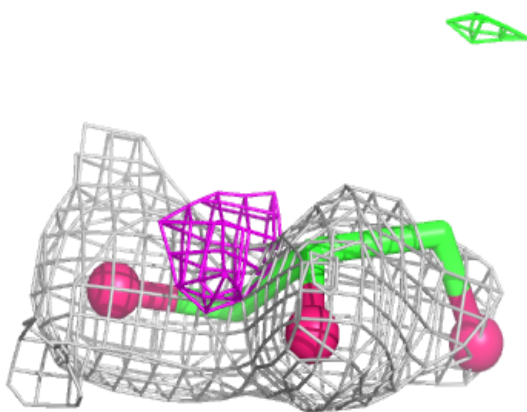
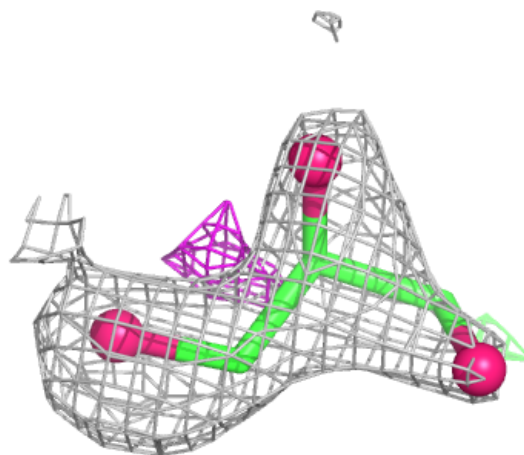
**Electron density around GOL B 504:**

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



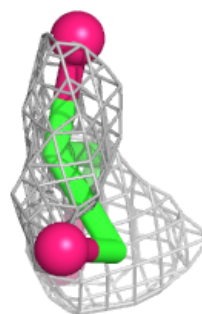
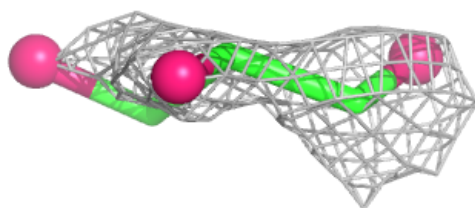
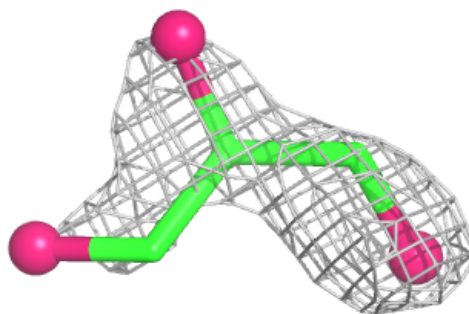
**Electron density around GOL A 502:**

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



**Electron density around GOL B 505:**

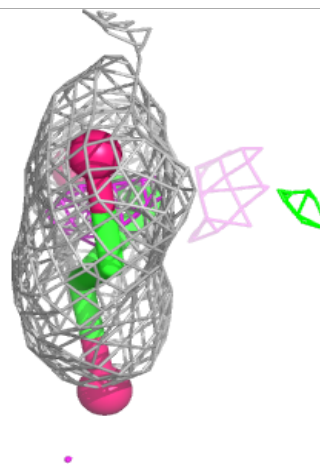
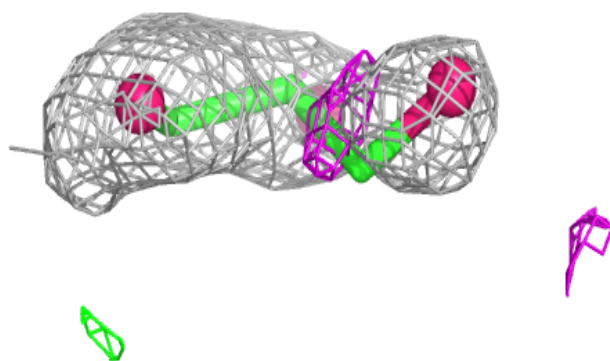
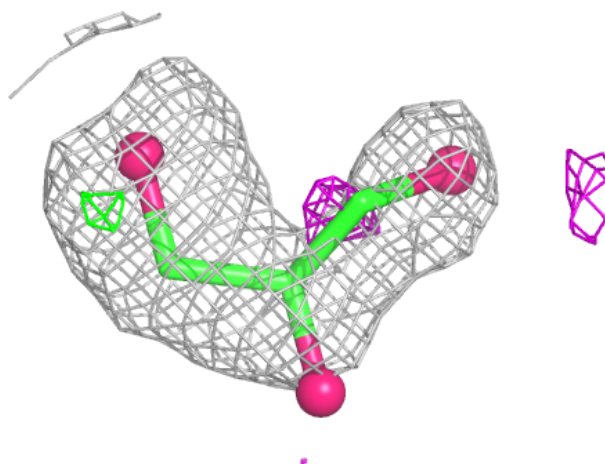
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





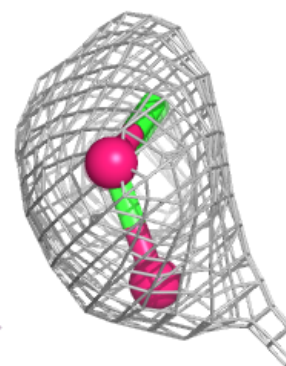
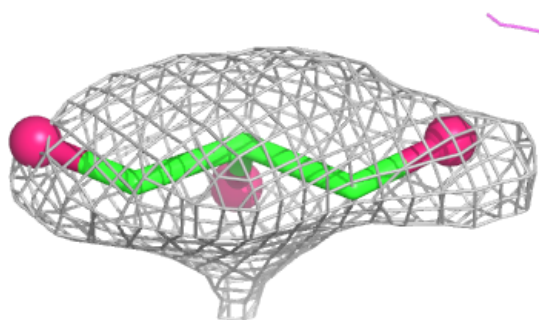
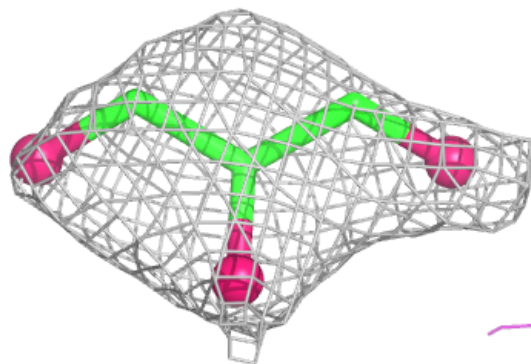
**Electron density around GOL A 503:**

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and green (positive)

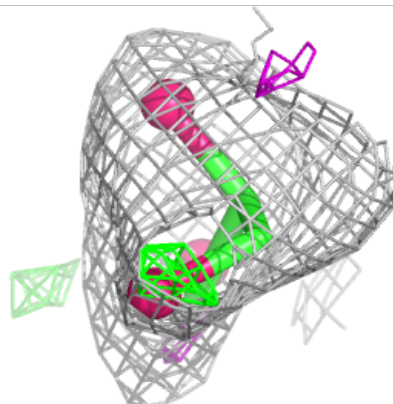
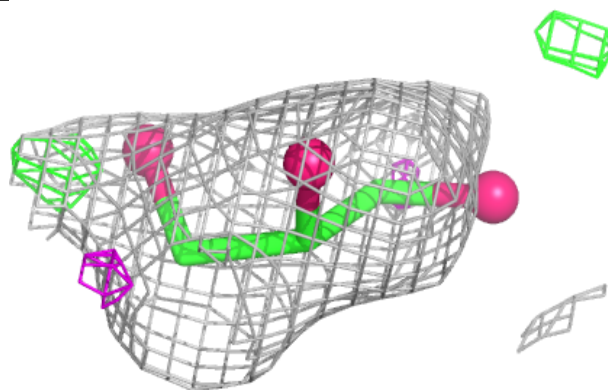
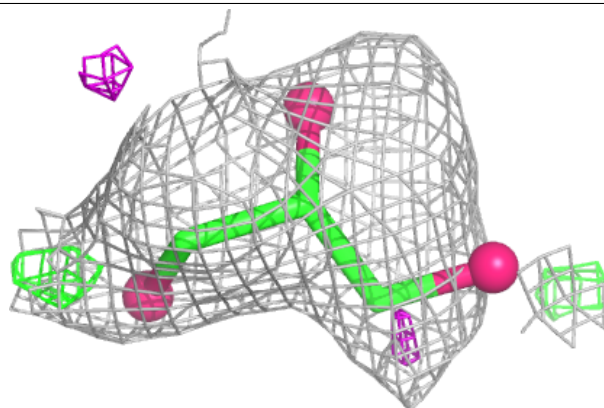


**Electron density around GOL B 503:**

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

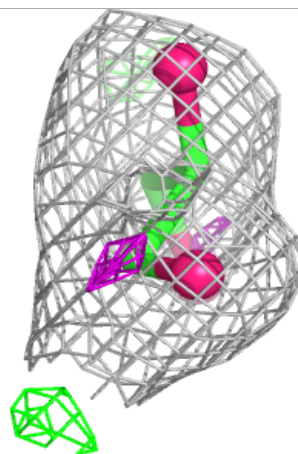
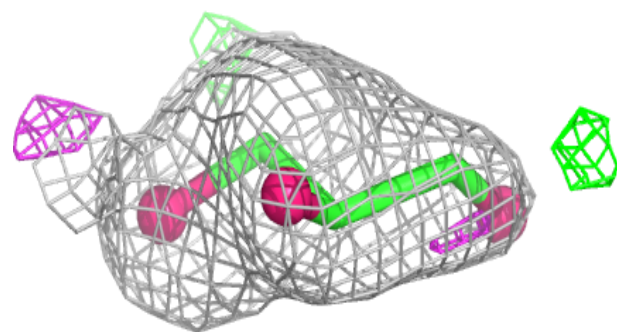
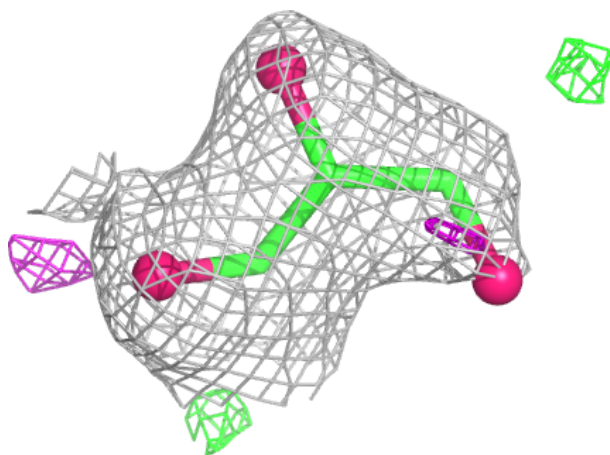
**Electron density around GOL A 504 (B):**

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and green (positive)



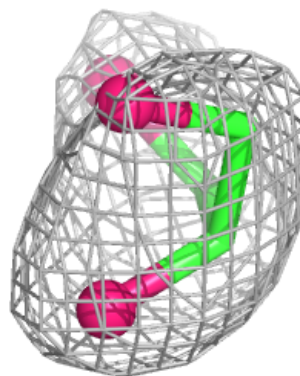
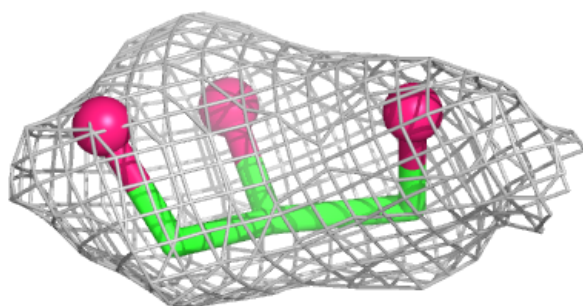
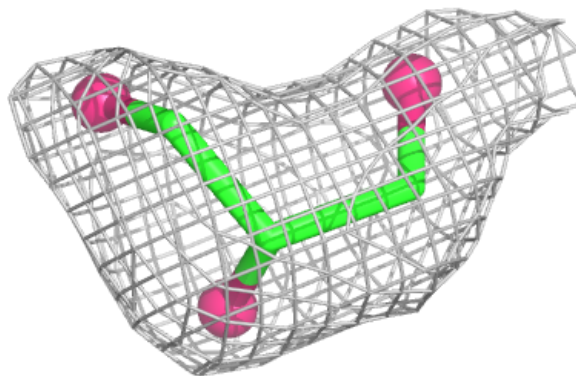
**Electron density around GOL A 504 (A):**

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



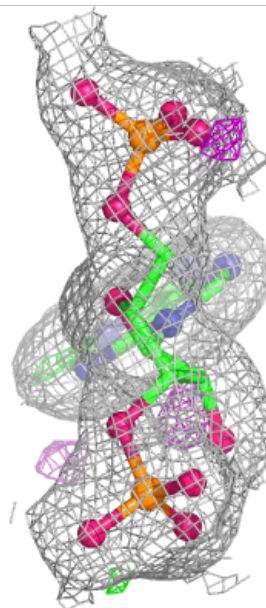
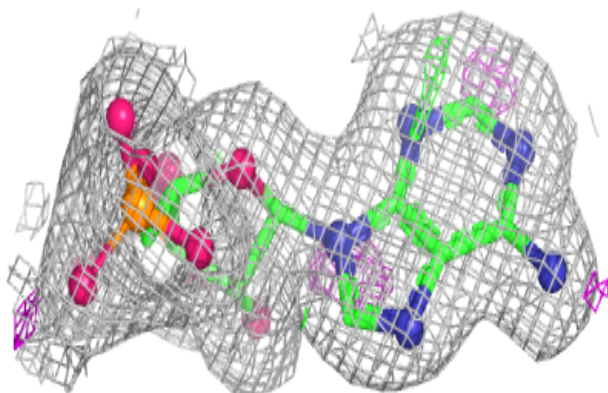
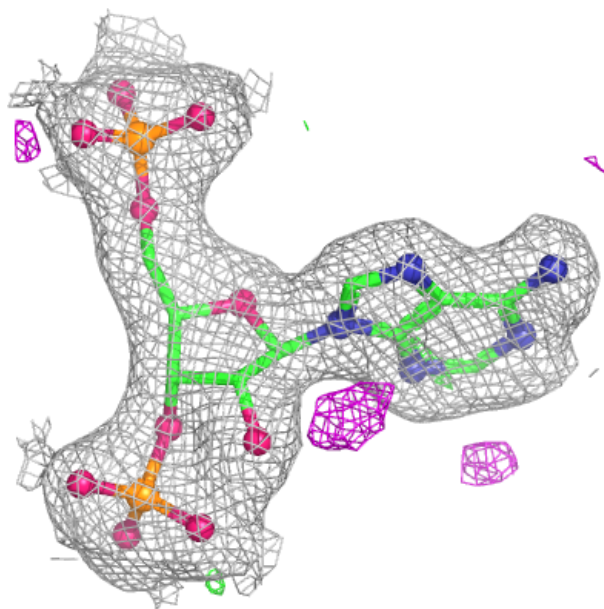
**Electron density around GOL B 502:**

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



**Electron density around A3P A 501:**

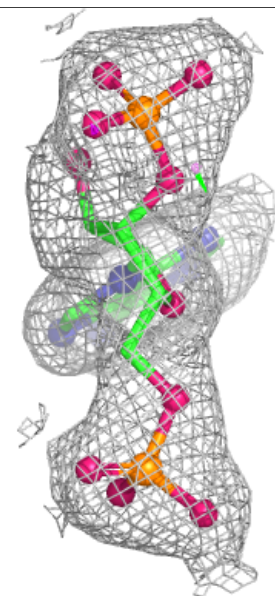
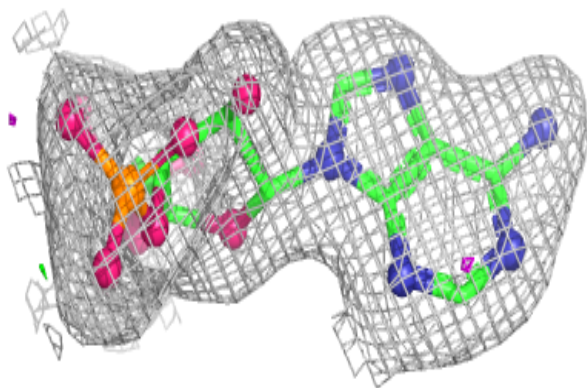
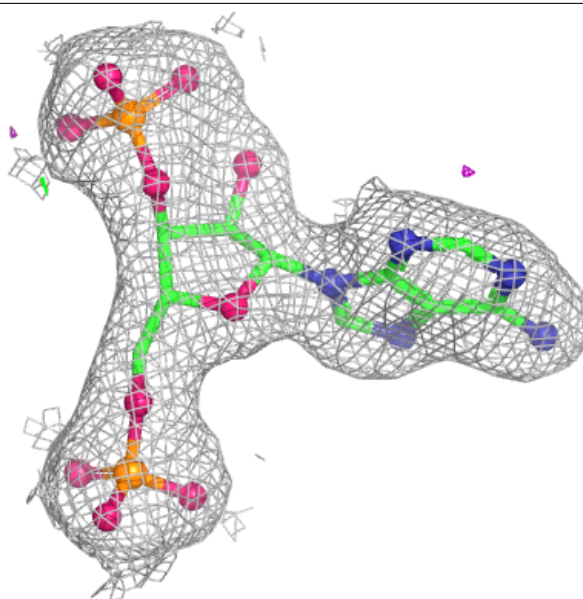
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around A3P 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 ⓘ

There are no such residues in this entry.