



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 17, 2024 – 02:11 PM EDT

PDB ID : 8TE1  
Title : Crystal structure of the methyltransferase domain of R882H/R676K DNMT3A homotetramer  
Authors : Lu, J.W.; Song, J.K.  
Deposited on : 2023-07-05  
Resolution : 2.48 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.002 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.38.3

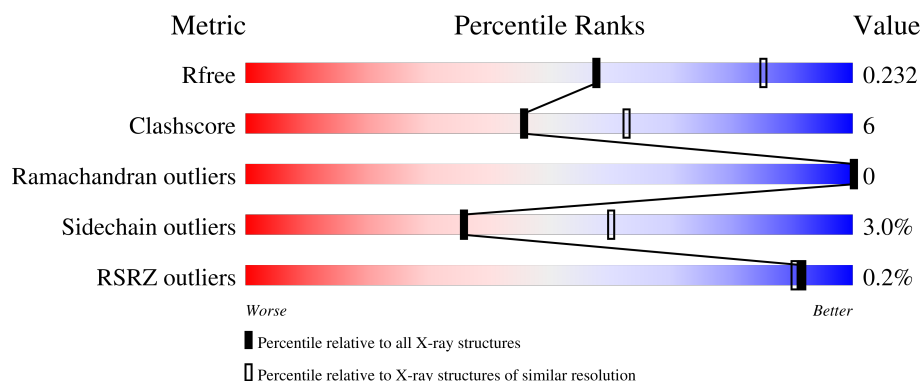
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.48 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



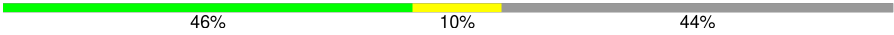
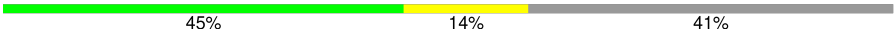
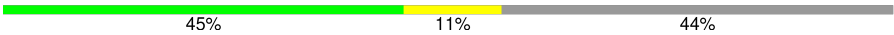
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	164625	7106 (2.50-2.46)
Clashscore	180529	7991 (2.50-2.46)
Ramachandran outliers	177936	7888 (2.50-2.46)
Sidechain outliers	177891	7890 (2.50-2.46)
RSRZ outliers	164620	7106 (2.50-2.46)

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	287	 83% 12% 5%
1	B	287	 80% 15% 5%
1	C	287	 86% 10% 4%
1	D	287	 81% 15% 4%
1	E	287	 44% 12% 45%

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Mol	Chain	Length	Quality of chain
1	F	287	 46% 10% 44%
1	G	287	 45% 14% 41%
1	H	287	 45% 11% 44%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14743 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 DNA (cytosine-5)-methyltransferase 3A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	273	Total	C	N	O	S	0	2	0
			2195	1406	390	386	13			
1	B	275	Total	C	N	O	S	0	4	0
			2218	1422	395	387	14			
1	C	275	Total	C	N	O	S	0	3	0
			2199	1411	388	386	14			
1	E	159	Total	C	N	O	S	0	0	0
			1265	829	218	212	6			
1	H	161	Total	C	N	O	S	0	0	0
			1272	829	220	217	6			
1	F	160	Total	C	N	O	S	0	0	0
			1273	834	215	218	6			
1	D	275	Total	C	N	O	S	0	3	0
			2205	1414	388	389	14			
1	G	170	Total	C	N	O	S	0	0	0
			1336	871	232	227	6			

There are 32 discrepancies between the modelled and reference sequences:

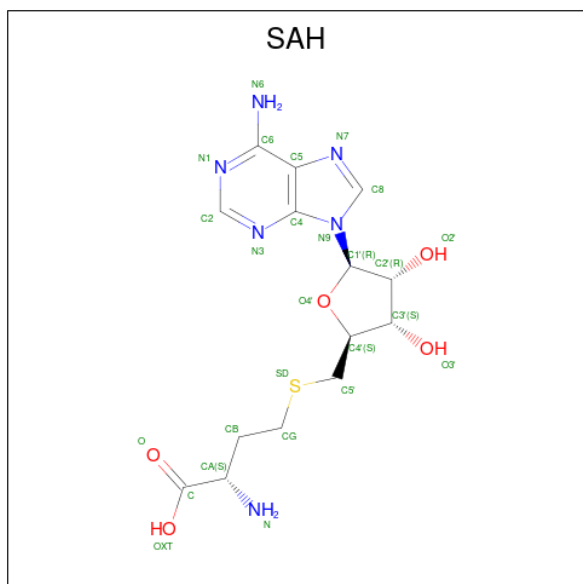
Chain	Residue	Modelled	Actual	Comment	Reference
A	626	GLY	-	expression tag	UNP Q9Y6K1
A	627	SER	-	expression tag	UNP Q9Y6K1
A	676	LYS	ARG	engineered mutation	UNP Q9Y6K1
A	882	HIS	ARG	engineered mutation	UNP Q9Y6K1
B	626	GLY	-	expression tag	UNP Q9Y6K1
B	627	SER	-	expression tag	UNP Q9Y6K1
B	676	LYS	ARG	engineered mutation	UNP Q9Y6K1
B	882	HIS	ARG	engineered mutation	UNP Q9Y6K1
C	626	GLY	-	expression tag	UNP Q9Y6K1
C	627	SER	-	expression tag	UNP Q9Y6K1
C	676	LYS	ARG	engineered mutation	UNP Q9Y6K1
C	882	HIS	ARG	engineered mutation	UNP Q9Y6K1
E	626	GLY	-	expression tag	UNP Q9Y6K1

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Chain	Residue	Modelled	Actual	Comment	Reference
E	627	SER	-	expression tag	UNP Q9Y6K1
E	676	LYS	ARG	engineered mutation	UNP Q9Y6K1
E	882	HIS	ARG	engineered mutation	UNP Q9Y6K1
H	626	GLY	-	expression tag	UNP Q9Y6K1
H	627	SER	-	expression tag	UNP Q9Y6K1
H	676	LYS	ARG	engineered mutation	UNP Q9Y6K1
H	882	HIS	ARG	engineered mutation	UNP Q9Y6K1
F	626	GLY	-	expression tag	UNP Q9Y6K1
F	627	SER	-	expression tag	UNP Q9Y6K1
F	676	LYS	ARG	engineered mutation	UNP Q9Y6K1
F	882	HIS	ARG	engineered mutation	UNP Q9Y6K1
D	626	GLY	-	expression tag	UNP Q9Y6K1
D	627	SER	-	expression tag	UNP Q9Y6K1
D	676	LYS	ARG	engineered mutation	UNP Q9Y6K1
D	882	HIS	ARG	engineered mutation	UNP Q9Y6K1
G	626	GLY	-	expression tag	UNP Q9Y6K1
G	627	SER	-	expression tag	UNP Q9Y6K1
G	676	LYS	ARG	engineered mutation	UNP Q9Y6K1
G	882	HIS	ARG	engineered mutation	UNP Q9Y6K1

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula:  $C_{14}H_{20}N_6O_5S$ ) (labeled as "Ligand of Interest" by depositor).



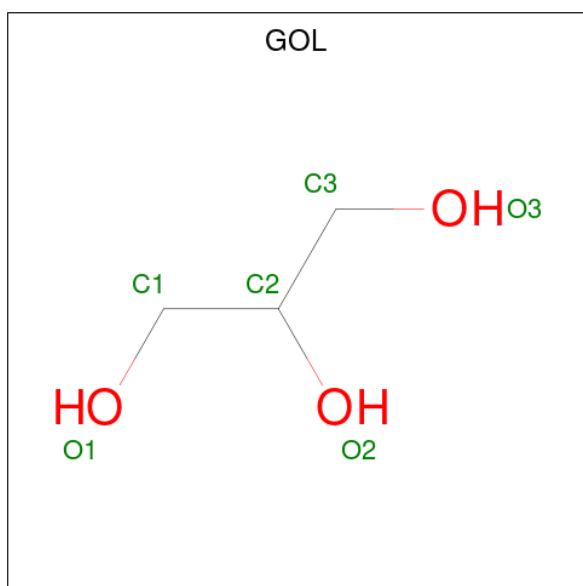
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			26	14	6	5		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	C	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
2	D	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- 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 depositor).



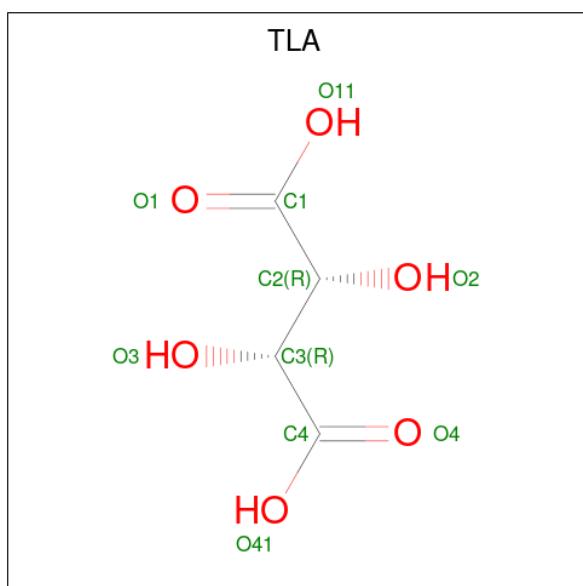
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		

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

- Molecule 4 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula:  $C_4H_6O_6$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			10	4	6		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	129	Total	O	0	0
			129	129		
5	B	115	Total	O	0	0
			115	115		
5	C	113	Total	O	0	0
			113	113		
5	E	38	Total	O	0	0
			38	38		
5	H	32	Total	O	0	0
			32	32		

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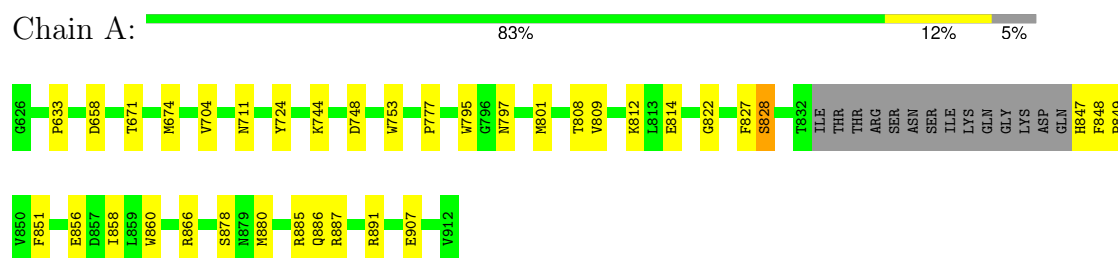
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	F	35	Total 35	O 35	0	0
5	D	108	Total 108	O 108	0	0
5	G	30	Total 30	O 30	0	0



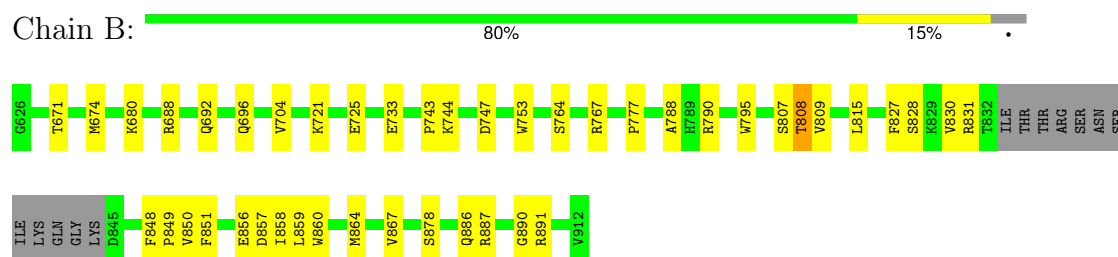
### 3 Residue-property plots [i](#)

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.

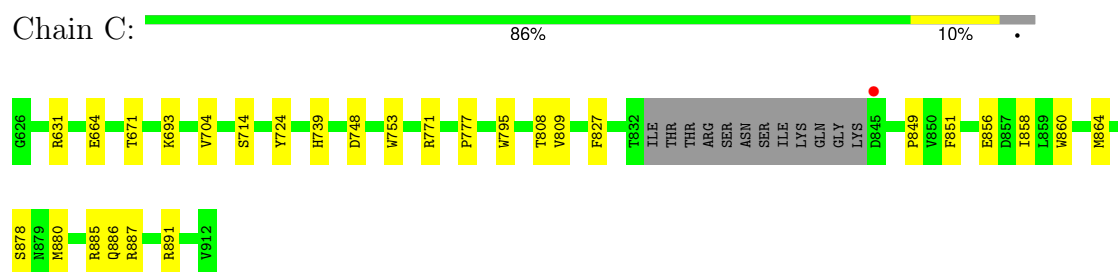
- Molecule 1: DNA (cytosine-5)-methyltransferase 3A



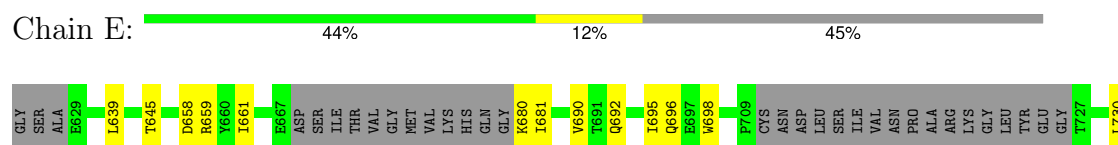
- Molecule 1: DNA (cytosine-5)-methyltransferase 3A

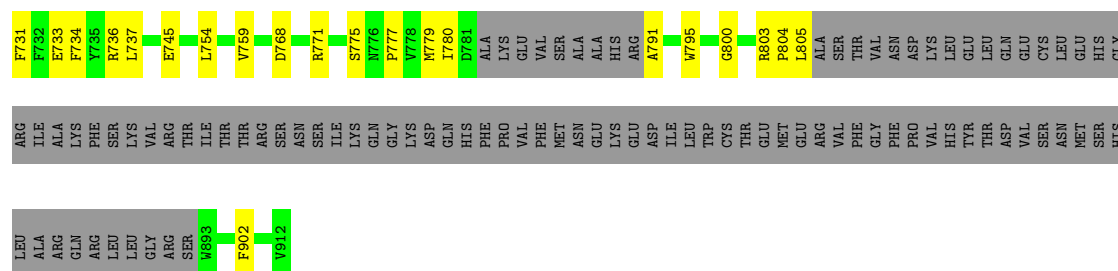


- Molecule 1: DNA (cytosine-5)-methyltransferase 3A



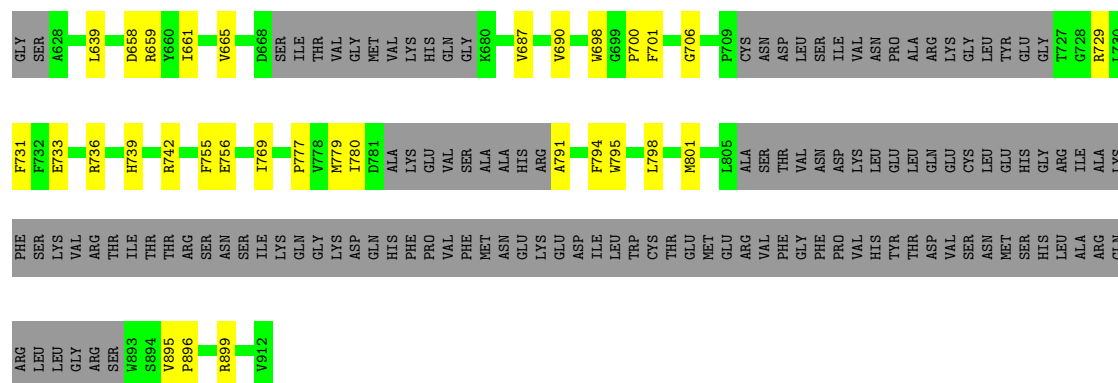
- Molecule 1: DNA (cytosine-5)-methyltransferase 3A





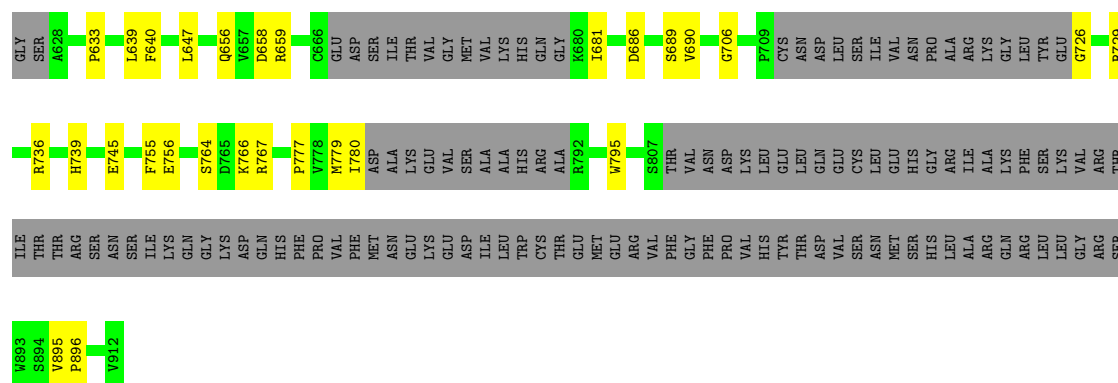
- Molecule 1: DNA (cytosine-5)-methyltransferase 3A

Chain H: 45% 11% 44%



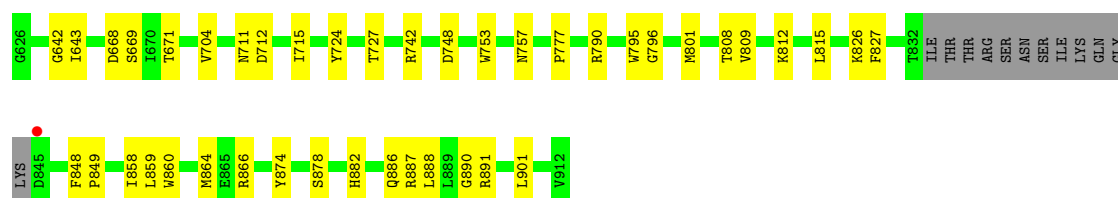
- Molecule 1: DNA (cytosine-5)-methyltransferase 3A

Chain F: 46% 10% 44%

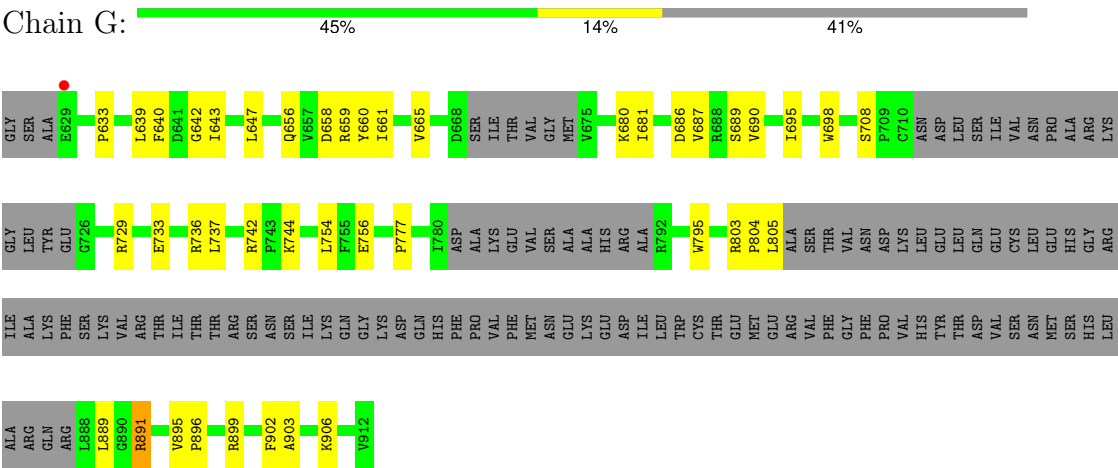


- Molecule 1: DNA (cytosine-5)-methyltransferase 3A

Chain D: 81% 15% 4%



● Molecule 1: DNA (cytosine-5)-methyltransferase 3A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	177.83Å 177.83Å 110.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.06 – 2.48 47.06 – 2.48	Depositor EDS
% Data completeness (in resolution range)	98.9 (47.06-2.48) 98.9 (47.06-2.48)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.06 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.193 , 0.226 0.200 , 0.232	Depositor DCC
$R_{free}$ test set	135512 reflections (1.44%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	52.5	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 40.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.467 for -h,-k,l 0.480 for h,-h-k,-l 0.467 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	14743	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% 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, SAH

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	0.25	0/2255	0.51	0/3045
1	B	0.28	0/2284	0.53	0/3082
1	C	0.25	0/2261	0.51	0/3054
1	D	0.25	0/2267	0.52	0/3061
1	E	0.26	0/1298	0.51	0/1753
1	F	0.27	0/1306	0.51	0/1763
1	G	0.29	0/1368	0.53	0/1846
1	H	0.30	0/1303	0.55	0/1758
All	All	0.27	0/14342	0.52	0/19362

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	2195	0	2162	20	0
1	B	2218	0	2193	27	0
1	C	2199	0	2159	19	0
1	D	2205	0	2168	27	0
1	E	1265	0	1230	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1273	0	1235	16	0
1	G	1336	0	1298	24	0
1	H	1272	0	1238	21	0
2	A	26	0	19	0	0
2	B	26	0	19	0	0
2	C	26	0	19	2	0
2	D	26	0	19	0	0
3	A	24	0	32	3	0
3	B	12	0	16	1	0
3	C	24	0	32	1	0
3	D	6	0	8	1	0
4	C	10	0	4	0	0
5	A	129	0	0	0	0
5	B	115	0	0	2	0
5	C	113	0	0	1	0
5	D	108	0	0	0	0
5	E	38	0	0	1	0
5	F	35	0	0	1	0
5	G	30	0	0	1	0
5	H	32	0	0	0	0
All	All	14743	0	13851	159	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 6.

All (159) 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:G:896:PRO:O	1:G:899:ARG:HB3	1.86	0.75
1:B:790:ARG:NH2	1:B:890:GLY:O	2.23	0.71
1:H:896:PRO:HA	1:H:899:ARG:HG2	1.74	0.70
1:G:804:PRO:HB2	1:G:805:LEU:HD23	1.74	0.69
1:G:661:ILE:HD13	1:G:698:TRP:HB3	1.73	0.69
1:G:690:VAL:O	1:G:736:ARG:NH2	2.26	0.69
1:A:849:PRO:HD2	1:A:858:ILE:HA	1.74	0.69
1:B:680:LYS:HE2	3:B:1002:GOL:H2	1.73	0.68
1:C:849:PRO:HD2	1:C:858:ILE:HA	1.76	0.68
1:E:690:VAL:O	1:E:736:ARG:NH2	2.26	0.67
1:D:790:ARG:NH2	1:D:890:GLY:O	2.28	0.66
1:H:690:VAL:O	1:H:736:ARG:NH2	2.29	0.66
1:D:643:ILE:HG23	1:D:874:TYR:HE2	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:647:LEU:HD21	1:G:681:ILE:HD13	1.79	0.65
1:G:633:PRO:HB3	1:G:656:GLN:HB3	1.79	0.64
1:C:693:LYS:NZ	5:C:1103:HOH:O	2.29	0.64
1:D:643:ILE:HD11	1:D:888:LEU:HD13	1.80	0.63
1:A:671:THR:HG21	1:A:878:SER:HB2	1.81	0.63
1:F:647:LEU:HD21	1:F:681:ILE:HD13	1.80	0.62
1:E:680:LYS:N	5:E:1003:HOH:O	2.33	0.61
1:A:812:LYS:HE2	1:A:866[B]:ARG:HH11	1.66	0.61
1:C:671:THR:HG21	1:C:878:SER:HB2	1.83	0.61
1:B:831[A]:ARG:NH1	5:B:1104:HOH:O	2.35	0.59
1:C:771:ARG:NH2	1:H:733:GLU:OE1	2.35	0.59
1:C:880:MET:HG3	1:C:885:ARG:HG3	1.87	0.57
1:D:808:THR:OG1	1:D:809:VAL:N	2.37	0.57
1:B:671:THR:HG21	1:B:878:SER:HB2	1.85	0.57
1:E:692:GLN:NE2	1:E:696:GLN:OE1	2.37	0.57
1:A:808:THR:OG1	1:A:809:VAL:N	2.38	0.57
1:B:733:GLU:OE2	1:E:771:ARG:NH2	2.38	0.56
1:G:642:GLY:HA2	1:G:889:LEU:HB3	1.88	0.56
1:C:808:THR:OG1	1:C:809:VAL:N	2.39	0.56
1:F:895:VAL:N	1:F:896:PRO:HD2	2.21	0.56
1:B:864:MET:HE1	1:B:886:GLN:HG2	1.89	0.55
1:D:671:THR:HG21	1:D:878:SER:HB2	1.89	0.55
1:H:798:LEU:HB2	1:H:801:MET:HE3	1.88	0.54
1:D:812:LYS:HE2	1:D:866[B]:ARG:HH11	1.72	0.54
1:B:830:VAL:HG21	1:B:859:LEU:HD11	1.90	0.54
1:D:849:PRO:HD2	1:D:858:ILE:HA	1.90	0.54
1:G:903:ALA:O	1:G:906:LYS:HG2	2.08	0.53
1:A:744:LYS:NZ	1:F:745:GLU:OE1	2.42	0.53
1:D:712:ASP:HB2	1:D:727:THR:HG22	1.91	0.52
1:H:780:ILE:O	1:H:791:ALA:HA	2.10	0.52
1:D:864:MET:HE1	1:D:886:GLN:HA	1.90	0.52
1:E:639:LEU:O	1:E:639:LEU:HD13	2.10	0.52
1:F:690:VAL:O	1:F:736:ARG:NH2	2.43	0.51
1:B:851:PHE:CE1	1:B:856:GLU:HG3	2.46	0.51
1:G:640:PHE:HZ	1:G:756:GLU:OE2	1.93	0.51
1:G:899:ARG:NH2	5:G:1002:HOH:O	2.36	0.51
1:C:851:PHE:CE1	1:C:856:GLU:HG3	2.45	0.51
1:A:907:GLU:HG3	3:A:1005:GOL:H32	1.91	0.50
1:H:661:ILE:CD1	1:H:698:TRP:HB3	2.42	0.50
1:A:724:TYR:CD1	1:F:729:ARG:HA	2.46	0.50
1:A:814:GLU:OE2	1:A:828:SER:OG	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:639:LEU:HD13	1:F:639:LEU:O	2.10	0.50
1:B:815:LEU:HD11	1:B:859:LEU:HD21	1.94	0.50
1:A:860:TRP:CE2	1:B:878:SER:HA	2.47	0.50
1:C:864:MET:CE	1:C:886:GLN:HG2	2.42	0.49
1:A:880:MET:HE2	1:A:885:ARG:HG3	1.93	0.49
1:E:695:ILE:HD11	1:E:737:LEU:HD22	1.93	0.49
1:H:639:LEU:O	1:H:639:LEU:HD13	2.12	0.49
1:F:777:PRO:HB3	1:F:795:TRP:CE2	2.47	0.49
1:E:777:PRO:HB3	1:E:795:TRP:CE2	2.47	0.49
1:H:665:VAL:HB	1:H:729:ARG:NH1	2.27	0.49
1:D:724:TYR:CD1	1:G:729:ARG:HA	2.48	0.49
1:H:665:VAL:HG12	1:H:687:VAL:HG11	1.95	0.49
1:E:754:LEU:HD13	1:E:902:PHE:CE1	2.49	0.48
1:G:686:ASP:O	1:G:689:SER:OG	2.32	0.48
1:C:878:SER:HA	1:D:860:TRP:CE2	2.49	0.48
1:G:805:LEU:HD23	1:G:805:LEU:N	2.28	0.48
1:B:808:THR:OG1	1:B:809:VAL:N	2.47	0.48
1:D:777:PRO:HB3	1:D:795:TRP:CE2	2.49	0.48
1:A:851:PHE:CE1	1:A:856:GLU:HG3	2.49	0.48
1:B:849:PRO:HD2	1:B:858:ILE:HA	1.95	0.48
1:D:826:LYS:HE3	1:D:848:PHE:O	2.14	0.48
1:A:797:ASN:HA	3:A:1002:GOL:H11	1.96	0.47
1:F:633:PRO:HB3	1:F:656:GLN:HB3	1.96	0.47
1:A:633:PRO:HB2	1:A:658:ASP:HB2	1.95	0.47
1:D:668:ASP:HB3	1:D:888:LEU:HD11	1.96	0.47
1:G:665:VAL:HG22	1:G:687:VAL:HG11	1.94	0.47
1:C:864:MET:HE1	1:C:886:GLN:HG2	1.97	0.47
1:C:724:TYR:CD2	1:H:729:ARG:HA	2.49	0.47
1:H:779:MET:HE3	1:H:780:ILE:N	2.30	0.47
1:A:822:GLY:HA3	1:B:674[B]:MET:HE1	1.97	0.47
1:H:777:PRO:HB3	1:H:795:TRP:CE2	2.50	0.47
1:A:777:PRO:HB3	1:A:795:TRP:CE2	2.50	0.46
1:G:754:LEU:HD13	1:G:902:PHE:CE1	2.50	0.46
1:B:864:MET:HE1	1:B:886:GLN:CG	2.45	0.46
1:F:686:ASP:O	1:F:689:SER:OG	2.32	0.46
1:G:777:PRO:HB3	1:G:795:TRP:CE2	2.51	0.46
1:D:711:ASN:ND2	1:D:727:THR:HG21	2.31	0.46
1:H:899:ARG:HH11	1:H:899:ARG:HG3	1.81	0.46
1:E:779:MET:SD	1:E:780:ILE:N	2.89	0.45
1:C:860:TRP:CE2	1:D:878:SER:HA	2.51	0.45
1:A:878:SER:HA	1:B:860:TRP:CE2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:777:PRO:HB3	1:C:795:TRP:CE2	2.52	0.45
1:E:754:LEU:HD13	1:E:902:PHE:HE1	1.82	0.45
1:D:878:SER:O	1:D:878:SER:OG	2.31	0.45
1:G:695:ILE:HD11	1:G:737:LEU:HD22	1.98	0.45
1:C:739:HIS:HD1	1:H:739:HIS:CD2	2.35	0.45
1:C:887:ARG:O	1:C:891:ARG:HG3	2.15	0.45
1:E:759:VAL:HG11	1:E:791:ALA:HB3	1.98	0.45
1:D:796:GLY:O	3:D:1002:GOL:H2	2.17	0.45
1:B:886:GLN:NE2	5:B:1101:HOH:O	2.29	0.45
1:G:803:ARG:HA	1:G:804:PRO:HD3	1.72	0.44
1:F:706:GLY:O	1:F:755:PHE:HA	2.17	0.44
1:F:779:MET:SD	1:F:780:ILE:N	2.90	0.44
1:D:815:LEU:HD11	1:D:859:LEU:HD21	2.00	0.44
1:F:726:GLY:N	5:F:1002:HOH:O	2.50	0.44
1:A:801:MET:SD	3:A:1003:GOL:H32	2.58	0.44
1:E:733:GLU:OE1	1:E:736:ARG:NH1	2.51	0.44
1:C:704:VAL:O	1:C:753:TRP:HA	2.18	0.43
1:H:661:ILE:HD12	1:H:701:PHE:CZ	2.53	0.43
1:B:721:LYS:HB3	1:B:725:GLU:HB2	2.00	0.43
1:B:743:PRO:HB2	1:B:747:ASP:HB3	1.99	0.43
1:C:664:GLU:OE2	2:C:1001:SAH:O2'	2.33	0.43
1:H:895:VAL:N	1:H:896:PRO:HD2	2.32	0.43
1:F:895:VAL:H	1:F:896:PRO:HD2	1.83	0.43
1:E:804:PRO:O	1:E:805:LEU:HB2	2.18	0.43
1:C:631:ARG:NH2	3:C:1006:GOL:O1	2.51	0.43
1:H:798:LEU:HB2	1:H:801:MET:CE	2.49	0.43
1:B:788:ALA:HB2	1:B:867:VAL:HG13	2.00	0.43
1:C:771:ARG:HH22	1:H:733:GLU:CD	2.22	0.43
1:A:847:HIS:HB3	1:A:848:PHE:H	1.55	0.43
1:E:768:ASP:OD1	1:E:771:ARG:NH1	2.51	0.42
1:G:660:TYR:HB3	1:G:681:ILE:HG23	2.01	0.42
1:B:692:GLN:O	1:B:696:GLN:HG3	2.19	0.42
1:F:640:PHE:HZ	1:F:756:GLU:OE1	2.02	0.42
1:B:704:VAL:O	1:B:753:TRP:HA	2.19	0.42
1:B:850:VAL:HG13	1:B:857:ASP:HB3	2.00	0.42
1:E:661:ILE:CD1	1:E:698:TRP:HB3	2.50	0.42
1:D:887:ARG:O	1:D:891:ARG:HG3	2.19	0.42
1:G:661:ILE:CD1	1:G:698:TRP:HB3	2.46	0.42
1:D:704:VAL:O	1:D:753:TRP:HA	2.19	0.42
1:B:688:ARG:HG2	1:E:771:ARG:NH2	2.34	0.42
1:D:642:GLY:O	1:D:669:SER:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:801:MET:HG2	1:D:901:LEU:HD22	2.02	0.42
1:G:733:GLU:OE1	1:G:736:ARG:NH1	2.53	0.42
1:E:731:PHE:O	1:E:734:PHE:HB3	2.20	0.41
1:A:887:ARG:O	1:A:891:ARG:HG3	2.20	0.41
1:B:744:LYS:HA	1:B:744:LYS:HD3	1.76	0.41
1:F:895:VAL:N	1:F:896:PRO:CD	2.83	0.41
1:G:891:ARG:O	1:G:895:VAL:HG23	2.20	0.41
1:B:777:PRO:HB3	1:B:795:TRP:CE2	2.55	0.41
2:C:1001:SAH:HN1	2:C:1001:SAH:HG1	1.75	0.41
1:H:706:GLY:O	1:H:755:PHE:HA	2.21	0.41
1:D:882:HIS:O	1:D:886:GLN:HG3	2.19	0.41
1:F:767:ARG:HE	1:F:767:ARG:HB2	1.76	0.41
1:D:790:ARG:HH11	1:D:790:ARG:HG3	1.84	0.41
1:G:729:ARG:NH1	1:G:733:GLU:OE2	2.54	0.41
1:B:848:PHE:HB2	1:B:856:GLU:HG2	2.03	0.40
1:H:756:GLU:HB2	1:H:794:PHE:CE2	2.57	0.40
1:D:715:ILE:H	1:D:715:ILE:HG12	1.77	0.40
1:G:643:ILE:HD12	1:G:889:LEU:HD22	2.03	0.40
1:H:731:PHE:CE1	1:H:769:ILE:HG23	2.57	0.40
1:A:704:VAL:O	1:A:753:TRP:HA	2.21	0.40
1:B:887:ARG:O	1:B:891:ARG:HG3	2.22	0.40
1:E:800:GLY:O	1:E:803:ARG:NH1	2.50	0.40
1:D:643:ILE:HD11	1:D:888:LEU:HB3	2.04	0.40

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	271/287 (94%)	267 (98%)	4 (2%)	0	100	100
1	B	275/287 (96%)	269 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	274/287 (96%)	266 (97%)	8 (3%)	0	100	100
1	D	274/287 (96%)	267 (97%)	7 (3%)	0	100	100
1	E	149/287 (52%)	145 (97%)	4 (3%)	0	100	100
1	F	150/287 (52%)	148 (99%)	2 (1%)	0	100	100
1	G	160/287 (56%)	155 (97%)	5 (3%)	0	100	100
1	H	151/287 (53%)	149 (99%)	2 (1%)	0	100	100
All	All	1704/2296 (74%)	1666 (98%)	38 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	232/251 (92%)	226 (97%)	6 (3%)	41	65
1	B	234/251 (93%)	228 (97%)	6 (3%)	41	65
1	C	230/251 (92%)	227 (99%)	3 (1%)	65	83
1	D	232/251 (92%)	228 (98%)	4 (2%)	56	77
1	E	128/251 (51%)	121 (94%)	7 (6%)	18	34
1	F	129/251 (51%)	124 (96%)	5 (4%)	27	49
1	G	135/251 (54%)	127 (94%)	8 (6%)	16	31
1	H	129/251 (51%)	125 (97%)	4 (3%)	35	59
All	All	1449/2008 (72%)	1406 (97%)	43 (3%)	36	60

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	674	MET
1	A	711	ASN
1	A	748	ASP
1	A	827	PHE

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Mol	Chain	Res	Type
1	A	828	SER
1	A	886	GLN
1	B	764	SER
1	B	767	ARG
1	B	807	SER
1	B	808	THR
1	B	827	PHE
1	B	828	SER
1	C	714	SER
1	C	748	ASP
1	C	827	PHE
1	E	645	THR
1	E	658	ASP
1	E	659	ARG
1	E	681	ILE
1	E	730	LEU
1	E	745	GLU
1	E	775	SER
1	H	658	ASP
1	H	659	ARG
1	H	700	PRO
1	H	742	ARG
1	F	658	ASP
1	F	659	ARG
1	F	739	HIS
1	F	764	SER
1	F	766	LYS
1	D	742	ARG
1	D	748	ASP
1	D	757	ASN
1	D	827	PHE
1	G	639	LEU
1	G	658	ASP
1	G	659	ARG
1	G	680	LYS
1	G	708	SER
1	G	742	ARG
1	G	744	LYS
1	G	891	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	692	GLN
1	E	696	GLN
1	E	757	ASN
1	H	757	ASN
1	F	757	ASN
1	D	711	ASN
1	G	656	GLN

### 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 ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

16 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	GOL	C	1006	-	5,5,5	0.95	0	5,5,5	1.08	0
4	TLA	C	1002	-	9,9,9	1.22	0	12,12,12	1.21	1 (8%)
2	SAH	A	1001	-	23,28,28	1.28	3 (13%)	22,40,40	1.78	4 (18%)
2	SAH	C	1001	-	23,28,28	1.25	3 (13%)	22,40,40	1.82	4 (18%)
3	GOL	C	1004	-	5,5,5	0.92	0	5,5,5	1.07	0
3	GOL	C	1003	-	5,5,5	0.87	0	5,5,5	1.09	0
3	GOL	A	1003	-	5,5,5	0.91	0	5,5,5	1.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SAH	D	1001	-	23,28,28	1.25	3 (13%)	22,40,40	1.81	4 (18%)
3	GOL	B	1003	-	5,5,5	0.97	0	5,5,5	1.05	0
3	GOL	C	1005	-	5,5,5	0.99	0	5,5,5	1.00	0
3	GOL	A	1005	-	5,5,5	0.90	0	5,5,5	1.06	0
3	GOL	D	1002	-	5,5,5	0.85	0	5,5,5	1.15	0
3	GOL	A	1002	-	5,5,5	0.95	0	5,5,5	0.99	0
3	GOL	A	1004	-	5,5,5	1.01	0	5,5,5	1.01	0
3	GOL	B	1002	-	5,5,5	0.96	0	5,5,5	1.04	0
2	SAH	B	1001	-	23,28,28	1.26	3 (13%)	22,40,40	1.81	4 (18%)

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	C	1006	-	-	2/4/4/4	-
4	TLA	C	1002	-	-	9/12/12/12	-
2	SAH	A	1001	-	-	2/11/31/31	0/3/3/3
2	SAH	C	1001	-	-	2/11/31/31	0/3/3/3
3	GOL	C	1004	-	-	2/4/4/4	-
3	GOL	C	1003	-	-	4/4/4/4	-
3	GOL	A	1003	-	-	1/4/4/4	-
2	SAH	D	1001	-	-	2/11/31/31	0/3/3/3
3	GOL	B	1003	-	-	4/4/4/4	-
3	GOL	C	1005	-	-	4/4/4/4	-
3	GOL	A	1005	-	-	2/4/4/4	-
3	GOL	D	1002	-	-	0/4/4/4	-
3	GOL	A	1002	-	-	2/4/4/4	-
3	GOL	A	1004	-	-	2/4/4/4	-
3	GOL	B	1002	-	-	0/4/4/4	-
2	SAH	B	1001	-	-	2/11/31/31	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	SAH	C2-N3	4.21	1.38	1.32
2	B	1001	SAH	C2-N3	4.16	1.38	1.32
2	D	1001	SAH	C2-N3	4.12	1.38	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1001	SAH	C2-N3	4.11	1.38	1.32
2	A	1001	SAH	C2-N1	2.63	1.38	1.33
2	C	1001	SAH	C2-N1	2.54	1.38	1.33
2	B	1001	SAH	C2-N1	2.51	1.38	1.33
2	D	1001	SAH	C2-N1	2.51	1.38	1.33
2	B	1001	SAH	OXT-C	-2.23	1.23	1.30
2	C	1001	SAH	OXT-C	-2.19	1.23	1.30
2	A	1001	SAH	OXT-C	-2.19	1.23	1.30
2	D	1001	SAH	OXT-C	-2.17	1.23	1.30

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1001	SAH	N3-C2-N1	-6.37	120.02	128.67
2	C	1001	SAH	N3-C2-N1	-6.33	120.08	128.67
2	A	1001	SAH	N3-C2-N1	-6.31	120.10	128.67
2	B	1001	SAH	N3-C2-N1	-6.28	120.14	128.67
2	C	1001	SAH	C5'-SD-CG	-3.16	92.88	102.26
2	A	1001	SAH	C5'-SD-CG	-2.93	93.57	102.26
2	B	1001	SAH	C5'-SD-CG	-2.88	93.73	102.26
2	D	1001	SAH	OXT-C-O	-2.85	117.61	124.08
2	D	1001	SAH	C5'-SD-CG	-2.84	93.83	102.26
2	B	1001	SAH	OXT-C-O	-2.83	117.66	124.08
2	A	1001	SAH	OXT-C-O	-2.76	117.81	124.08
2	C	1001	SAH	OXT-C-O	-2.74	117.86	124.08
2	B	1001	SAH	O4'-C1'-N9	2.56	112.14	108.75
4	C	1002	TLA	O1-C1-C2	-2.47	115.03	121.62
2	C	1001	SAH	O4'-C1'-N9	2.31	111.80	108.75
2	A	1001	SAH	O4'-C1'-N9	2.04	111.45	108.75
2	D	1001	SAH	O4'-C1'-N9	2.02	111.42	108.75

There are no chirality outliers.

All (40) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1001	SAH	N-CA-CB-CG
2	D	1001	SAH	N-CA-CB-CG
3	A	1002	GOL	O1-C1-C2-O2
3	A	1002	GOL	O1-C1-C2-C3
3	A	1005	GOL	C1-C2-C3-O3
3	B	1003	GOL	C1-C2-C3-O3
3	C	1004	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
3	C	1005	GOL	O1-C1-C2-C3
4	C	1002	TLA	C2-C3-C4-O41
4	C	1002	TLA	C2-C3-C4-O4
3	A	1004	GOL	O1-C1-C2-C3
3	C	1003	GOL	O1-C1-C2-C3
3	C	1005	GOL	C1-C2-C3-O3
3	C	1006	GOL	C1-C2-C3-O3
3	A	1005	GOL	O2-C2-C3-O3
3	C	1004	GOL	O2-C2-C3-O3
3	C	1005	GOL	O1-C1-C2-O2
4	C	1002	TLA	O3-C3-C4-O41
3	B	1003	GOL	O2-C2-C3-O3
3	C	1005	GOL	O2-C2-C3-O3
3	C	1006	GOL	O2-C2-C3-O3
4	C	1002	TLA	O1-C1-C2-C3
3	B	1003	GOL	O1-C1-C2-C3
4	C	1002	TLA	O3-C3-C4-O4
4	C	1002	TLA	O11-C1-C2-C3
3	A	1003	GOL	C1-C2-C3-O3
2	A	1001	SAH	N-CA-CB-CG
2	C	1001	SAH	N-CA-CB-CG
2	A	1001	SAH	CB-CG-SD-C5'
2	C	1001	SAH	CB-CG-SD-C5'
2	D	1001	SAH	CB-CG-SD-C5'
4	C	1002	TLA	O2-C2-C3-C4
2	B	1001	SAH	CB-CG-SD-C5'
4	C	1002	TLA	O2-C2-C3-O3
4	C	1002	TLA	C1-C2-C3-O3
3	C	1003	GOL	C1-C2-C3-O3
3	C	1003	GOL	O1-C1-C2-O2
3	A	1004	GOL	O1-C1-C2-O2
3	B	1003	GOL	O1-C1-C2-O2
3	C	1003	GOL	O2-C2-C3-O3

There are no ring outliers.

7 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1006	GOL	1	0
2	C	1001	SAH	2	0
3	A	1003	GOL	1	0
3	A	1005	GOL	1	0

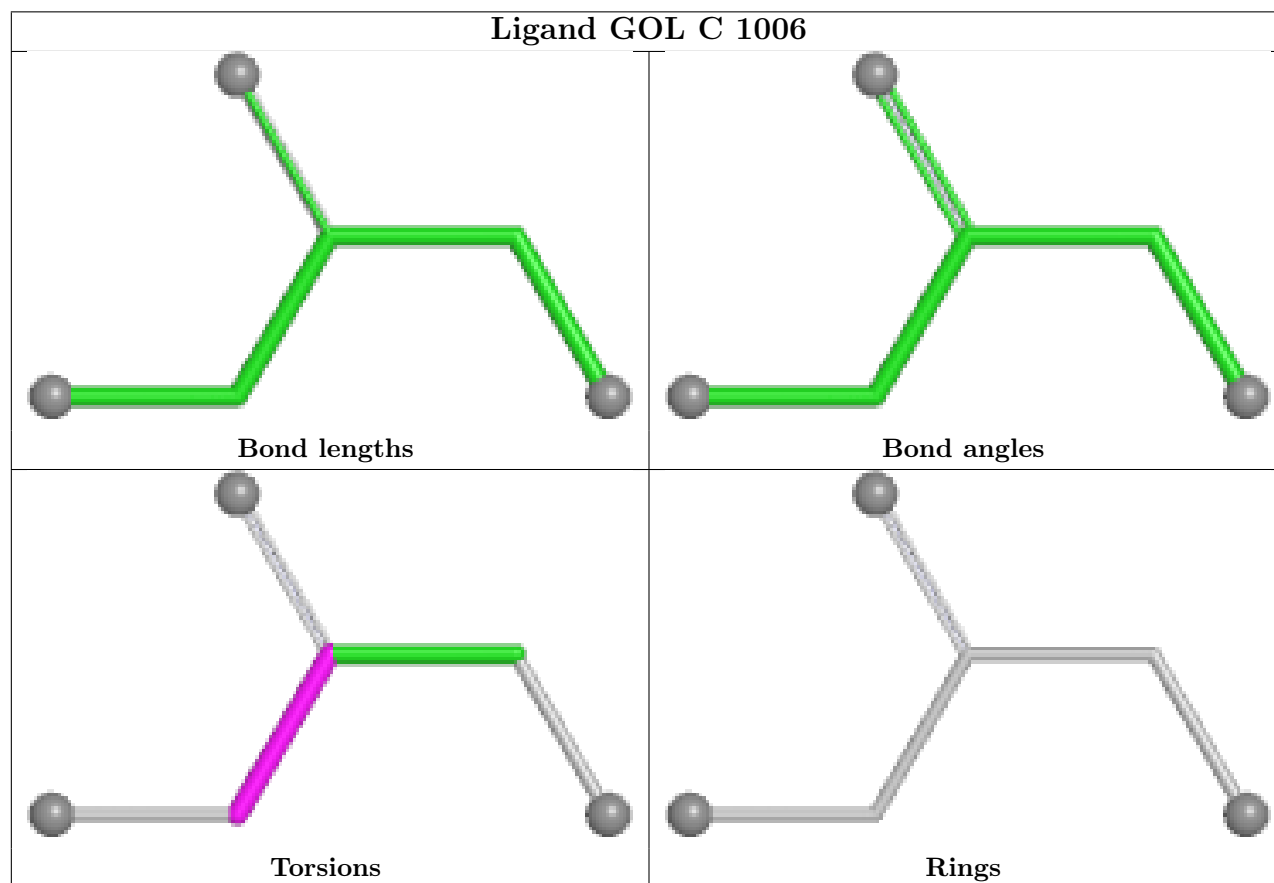
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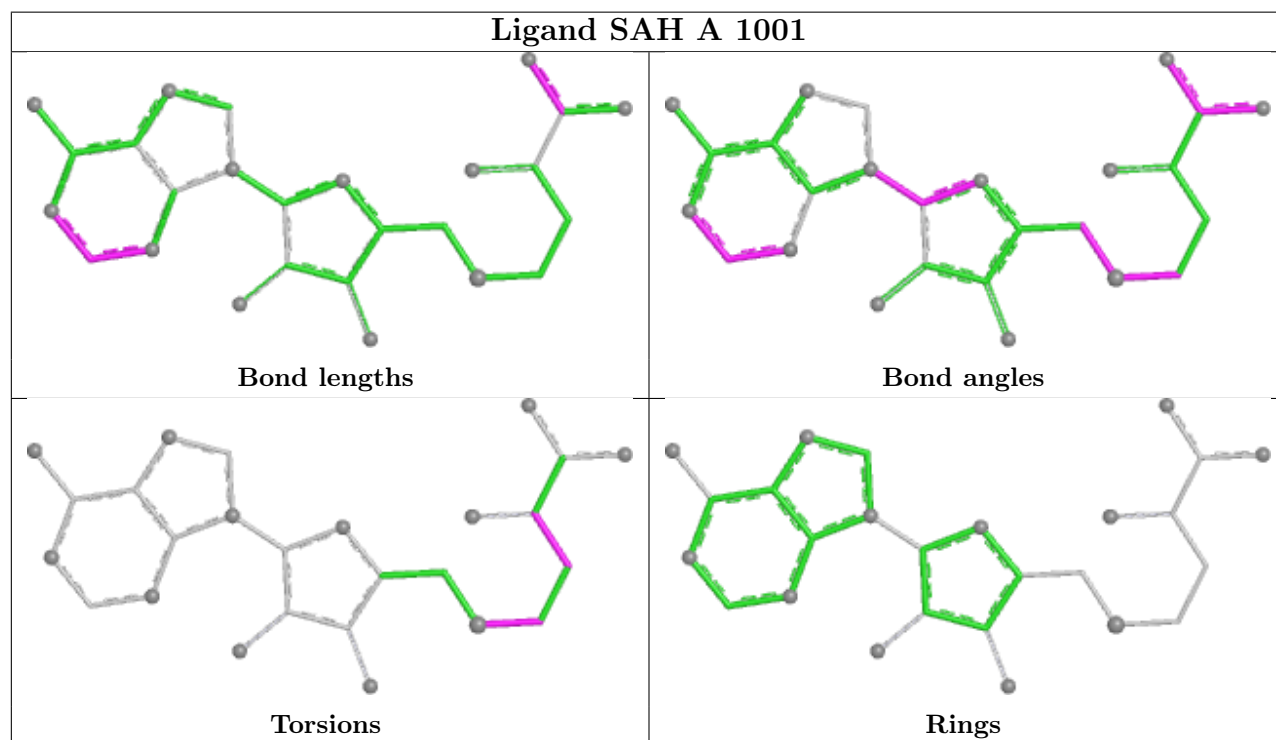
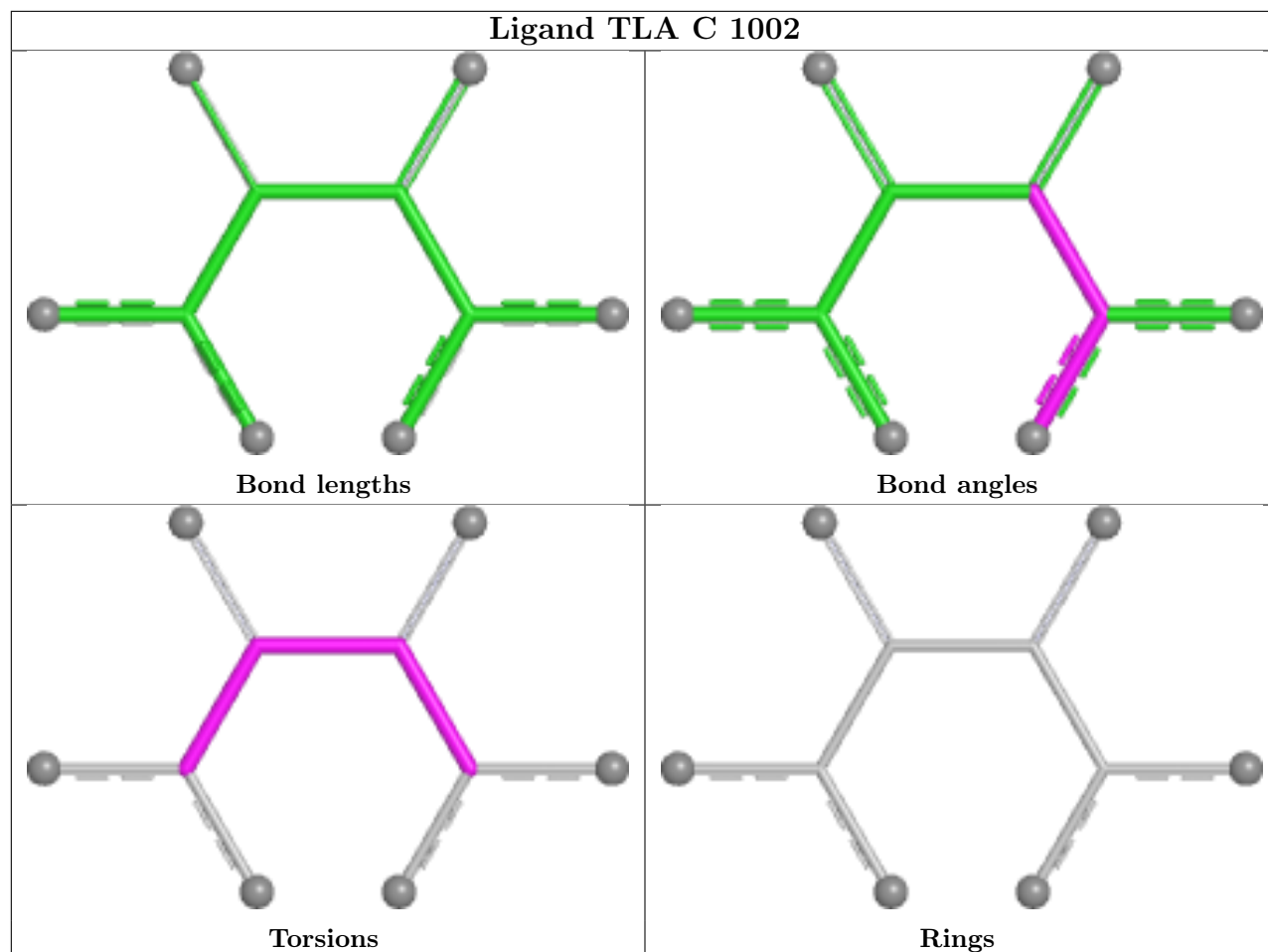


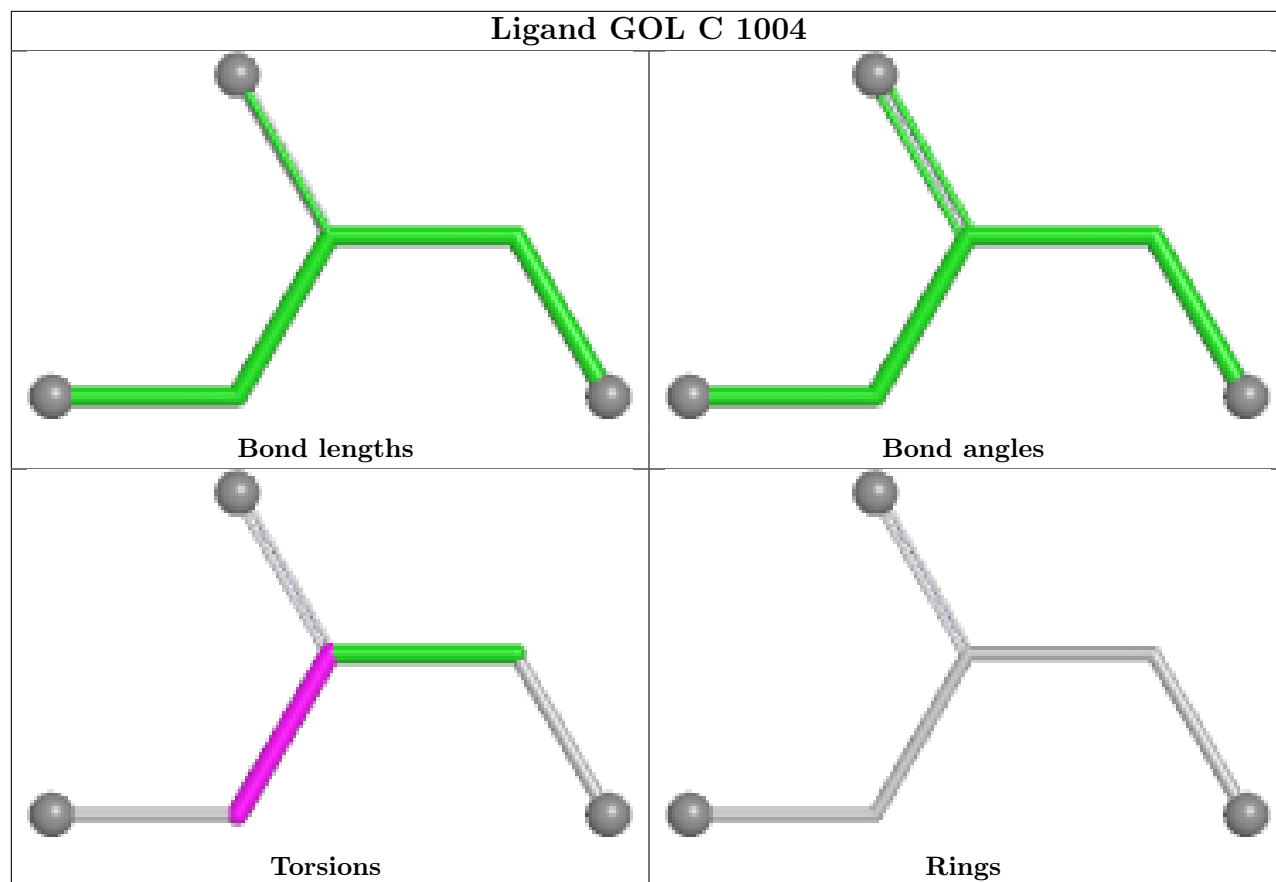
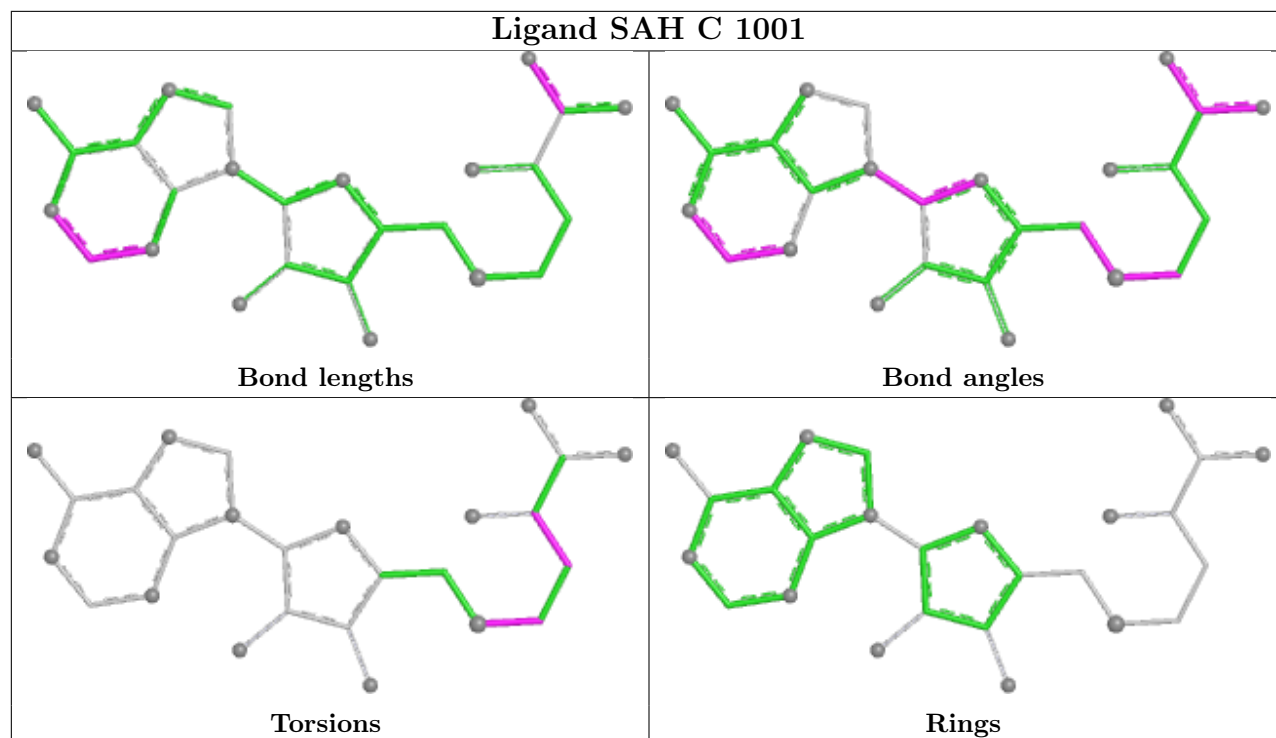
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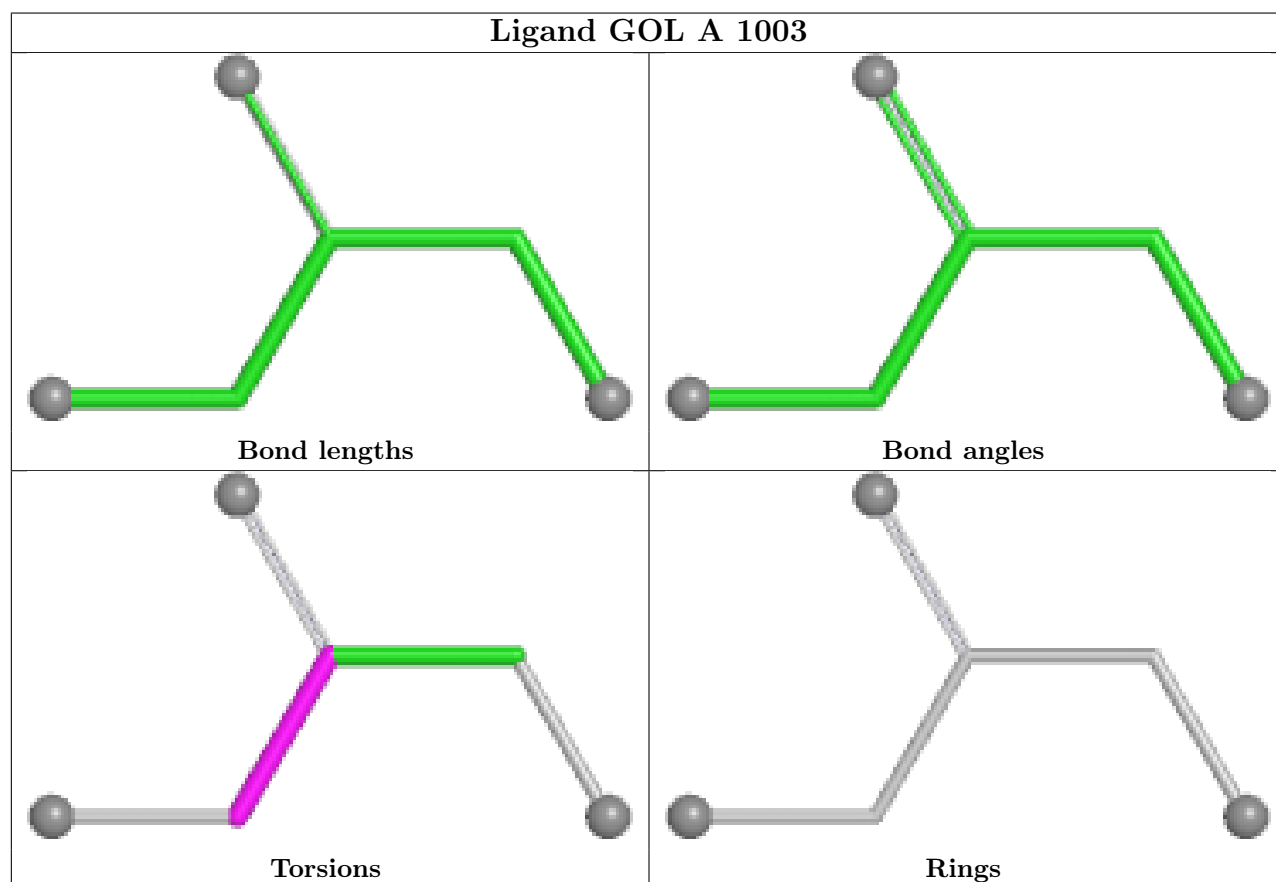
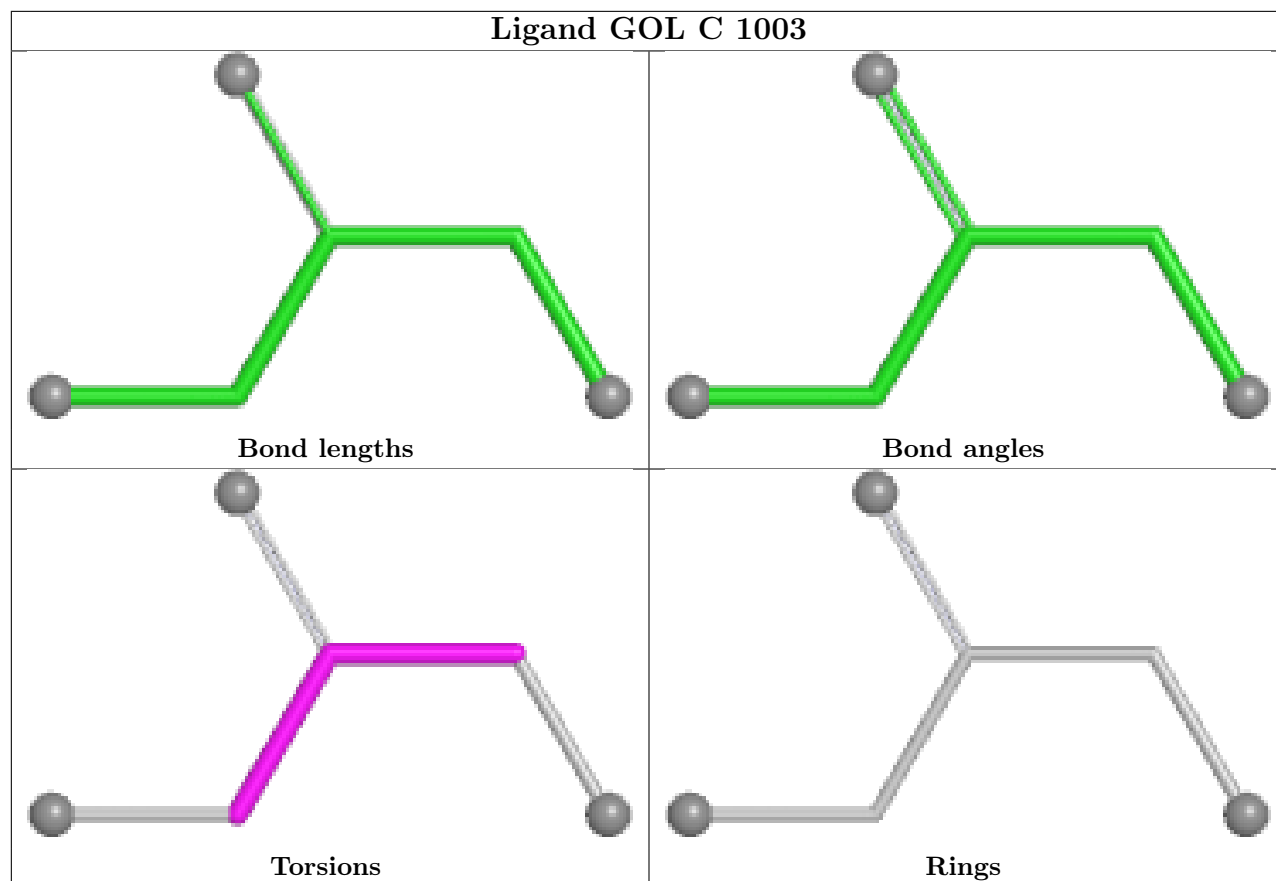
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1002	GOL	1	0
3	A	1002	GOL	1	0
3	B	1002	GOL	1	0

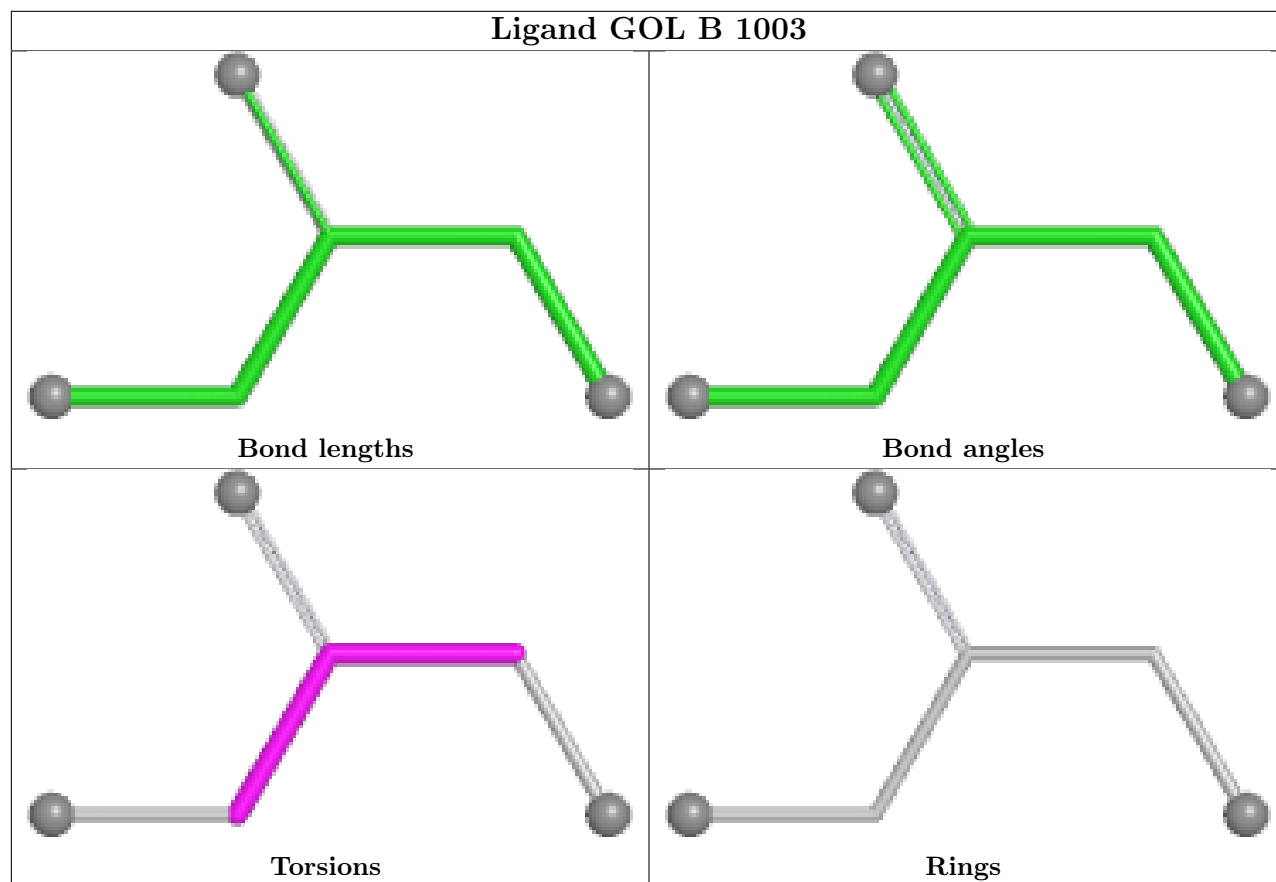
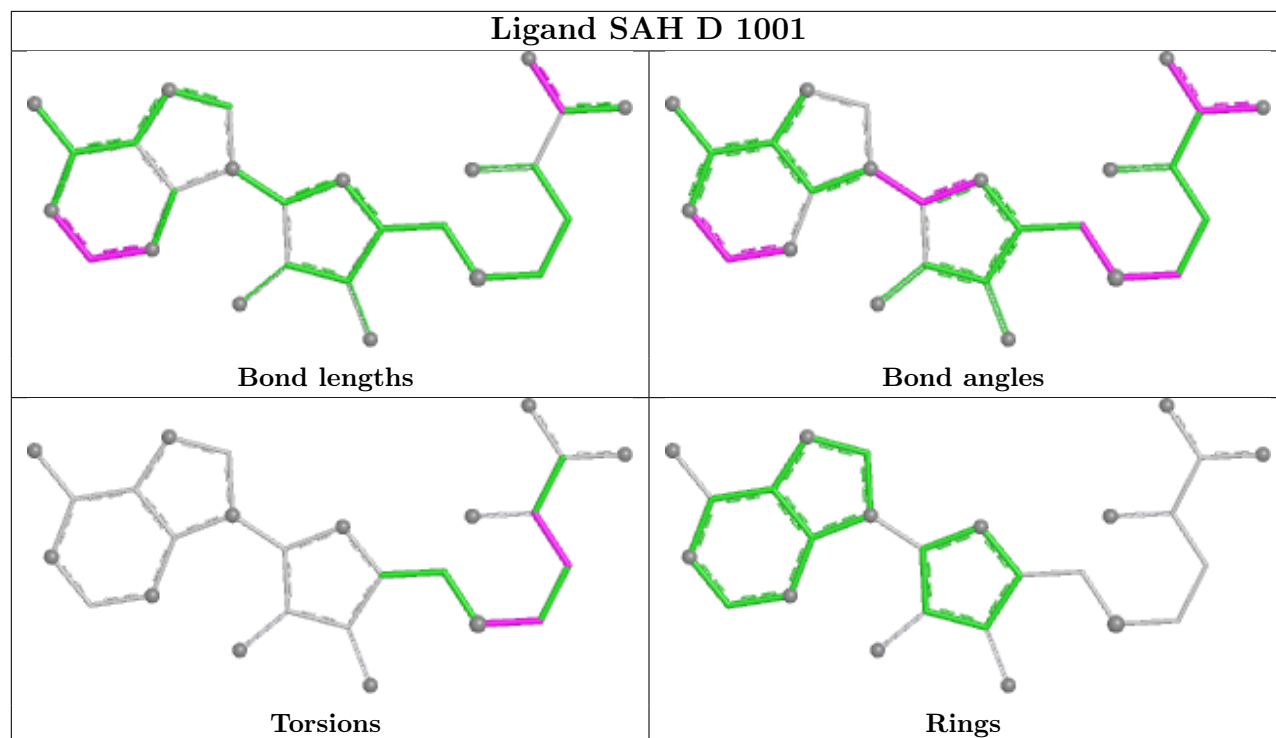
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

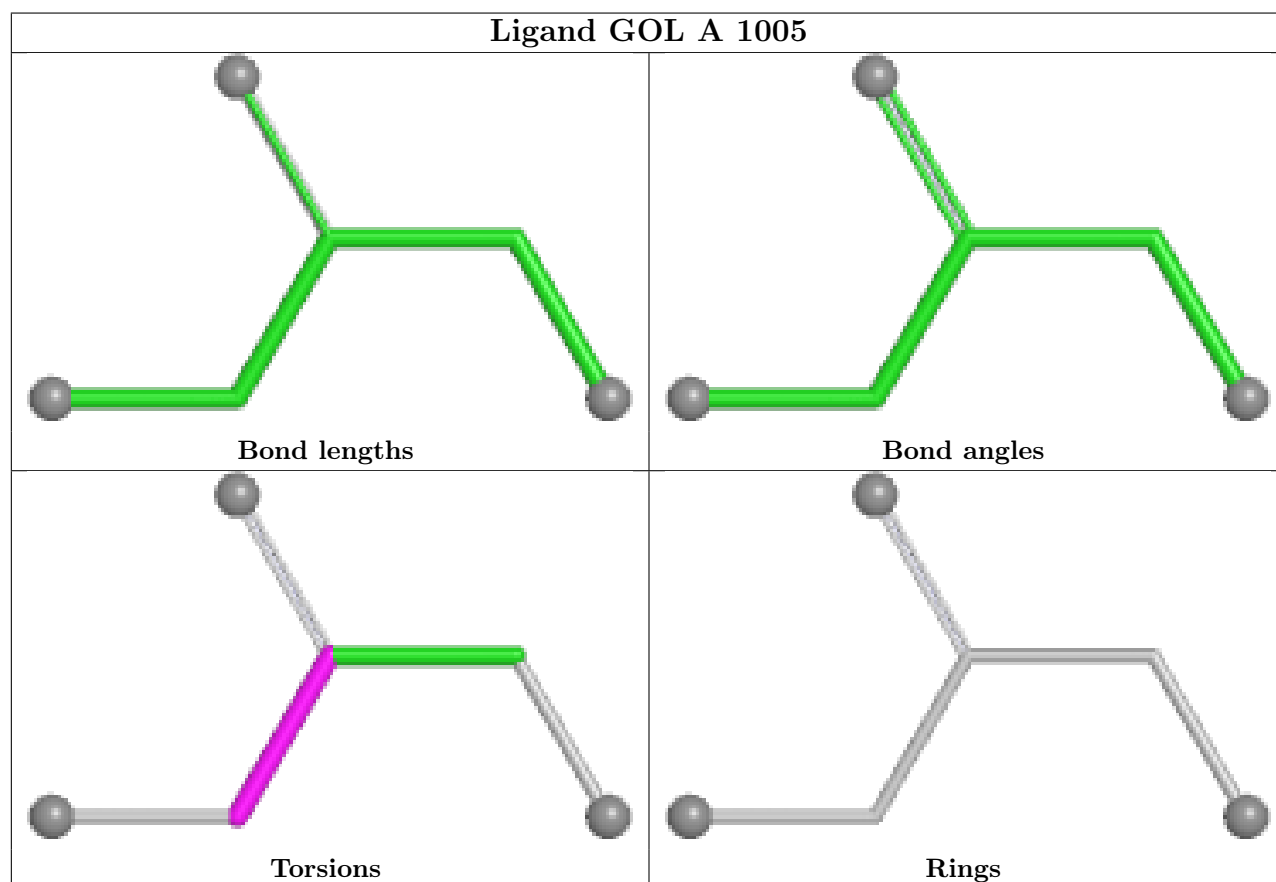
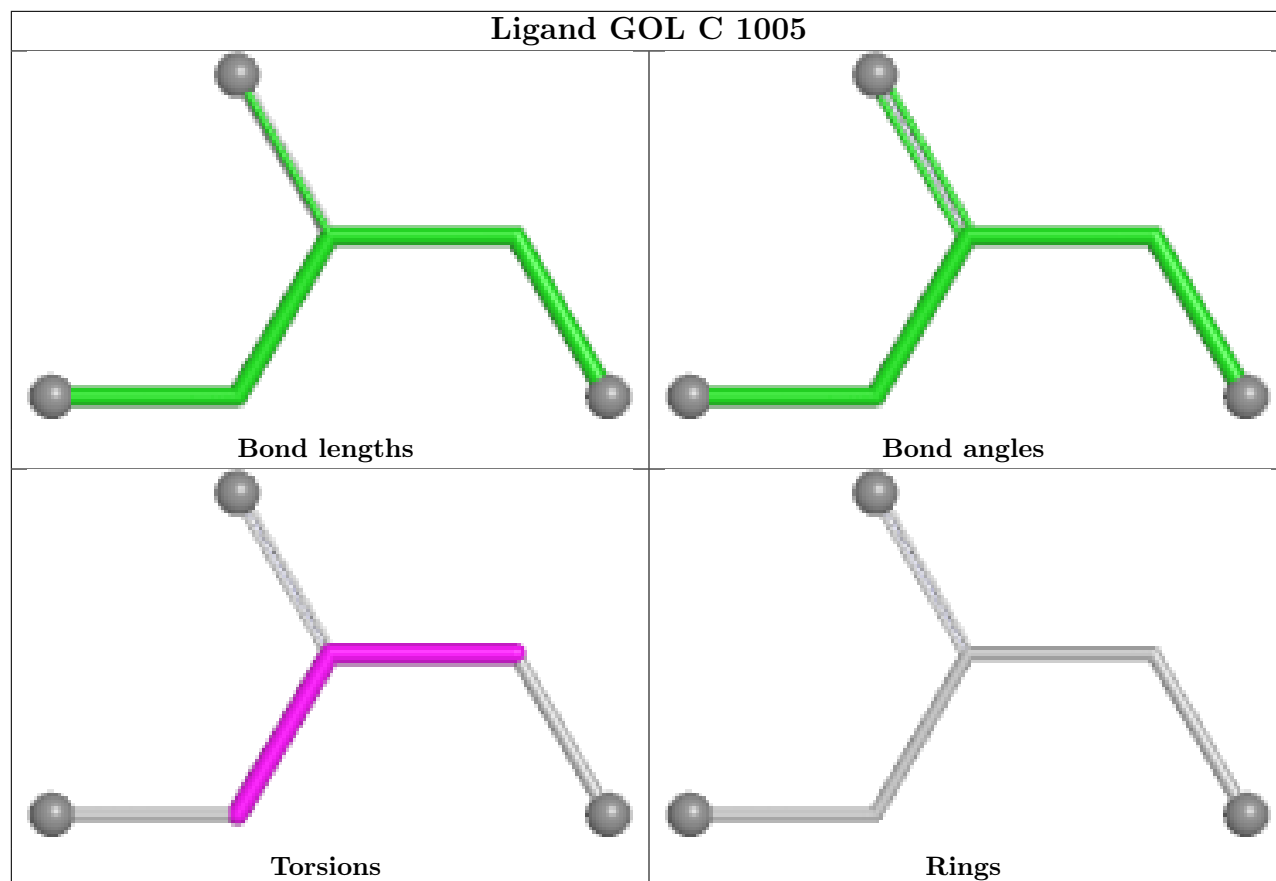


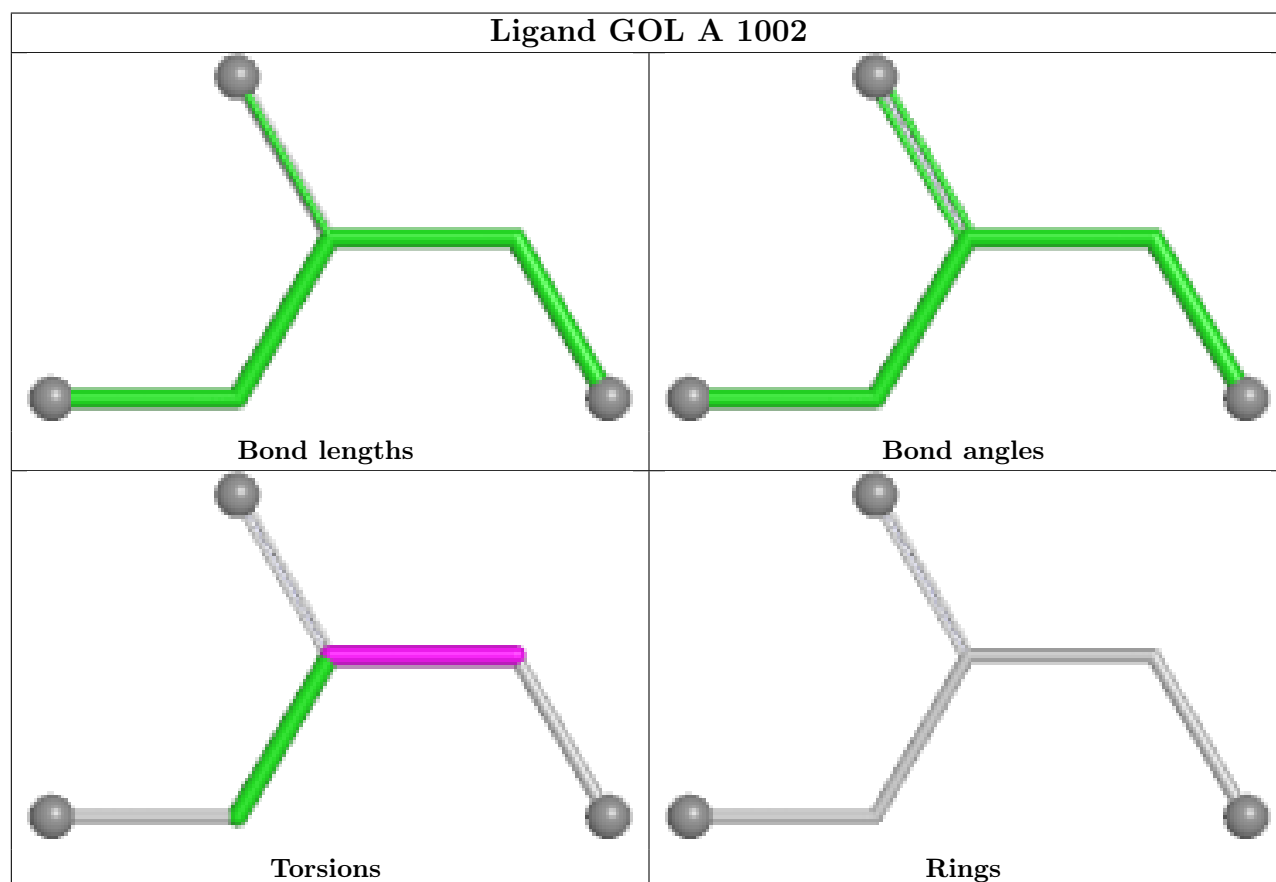
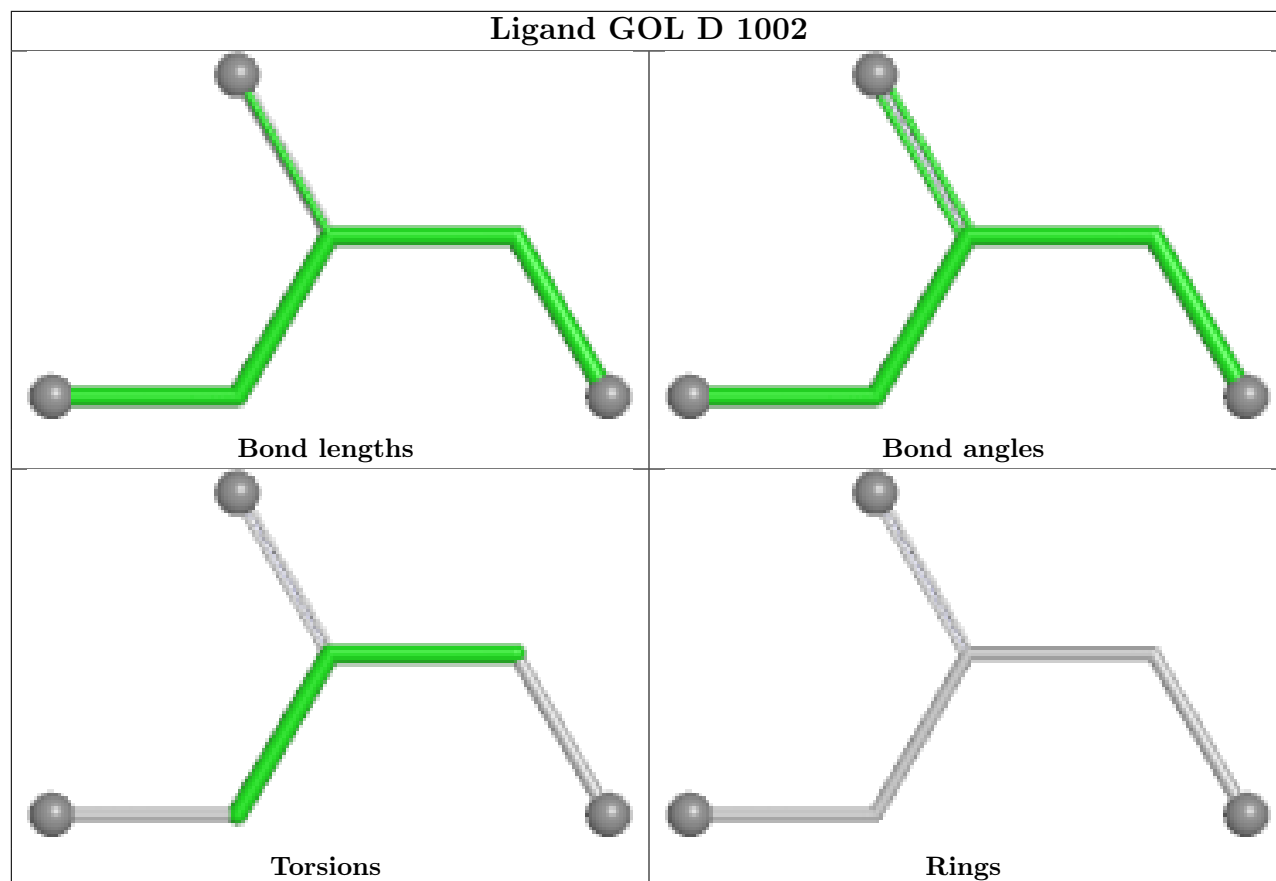


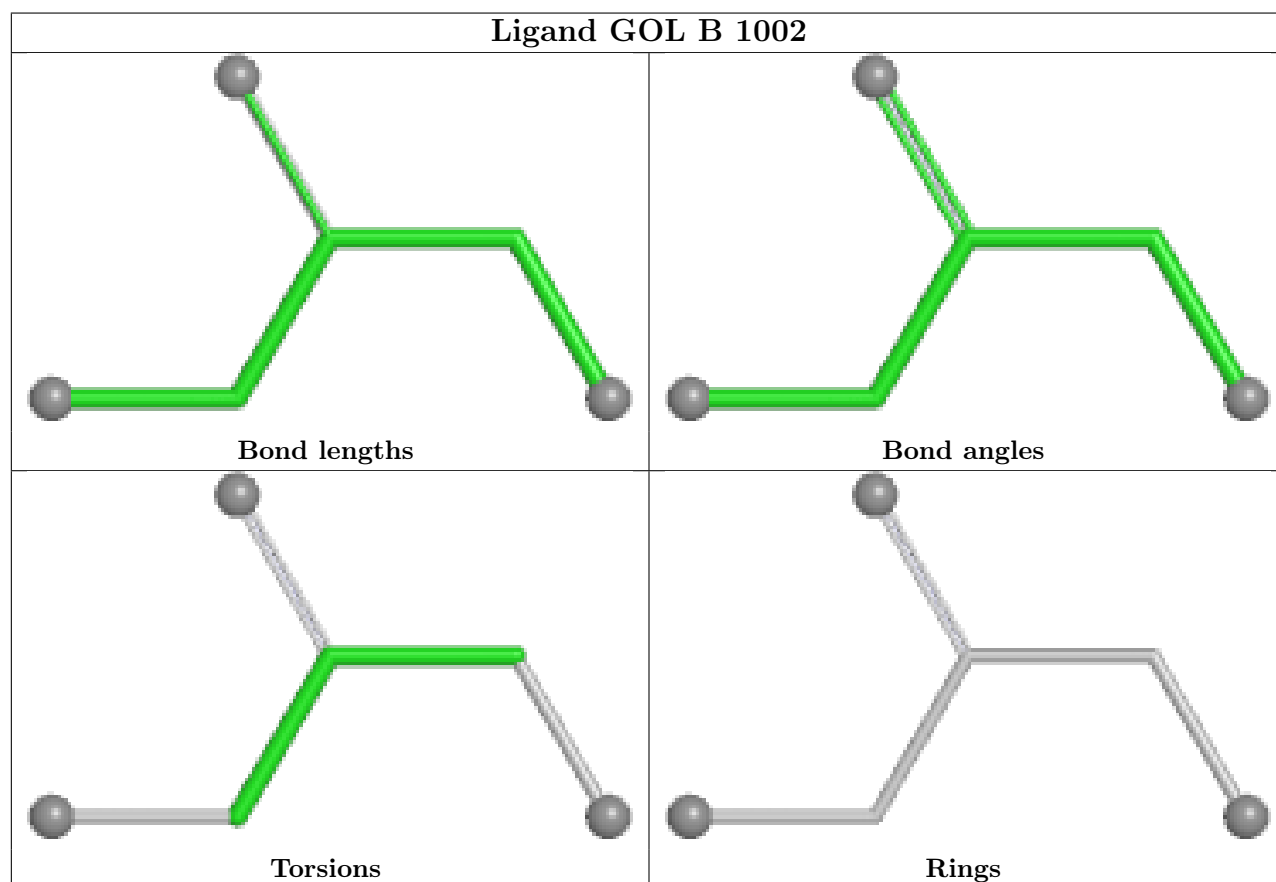
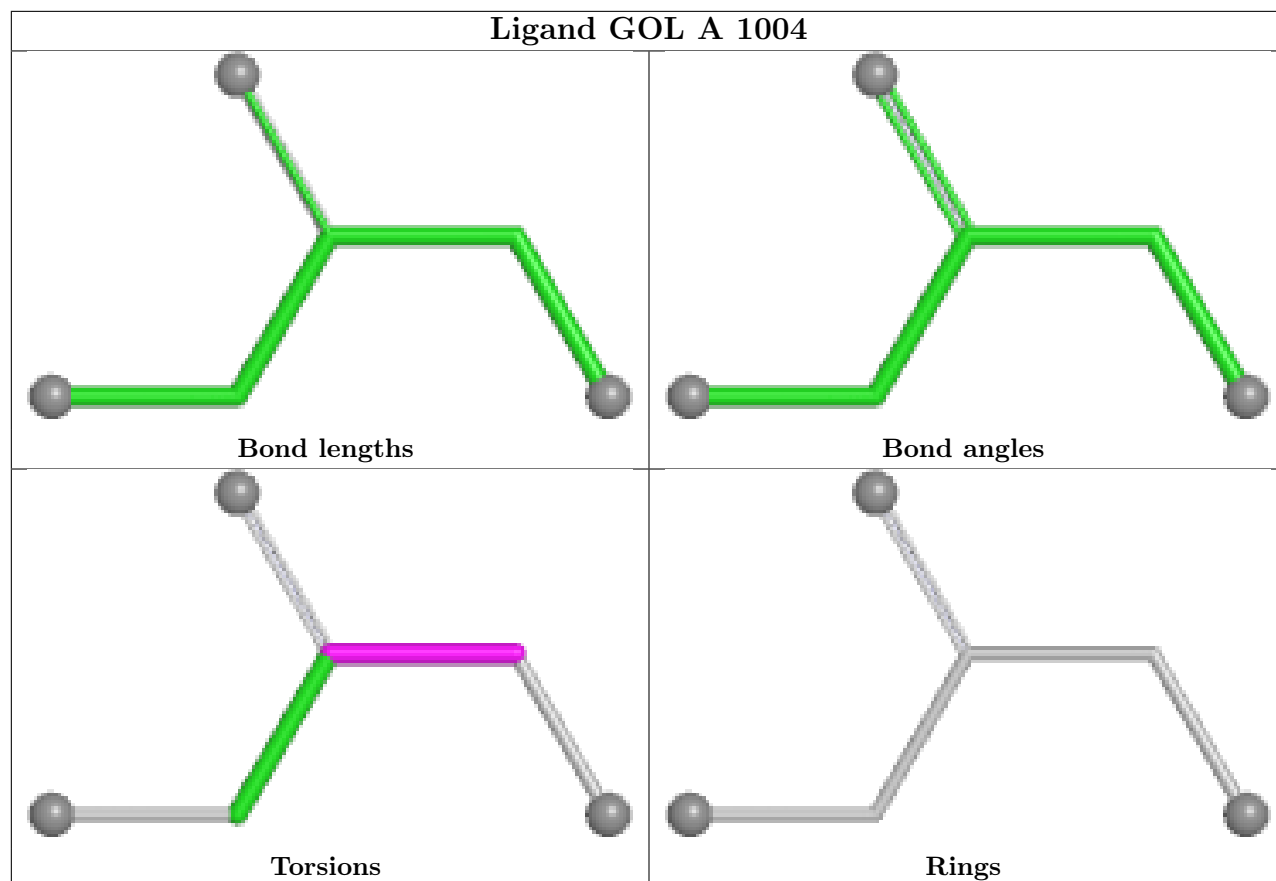




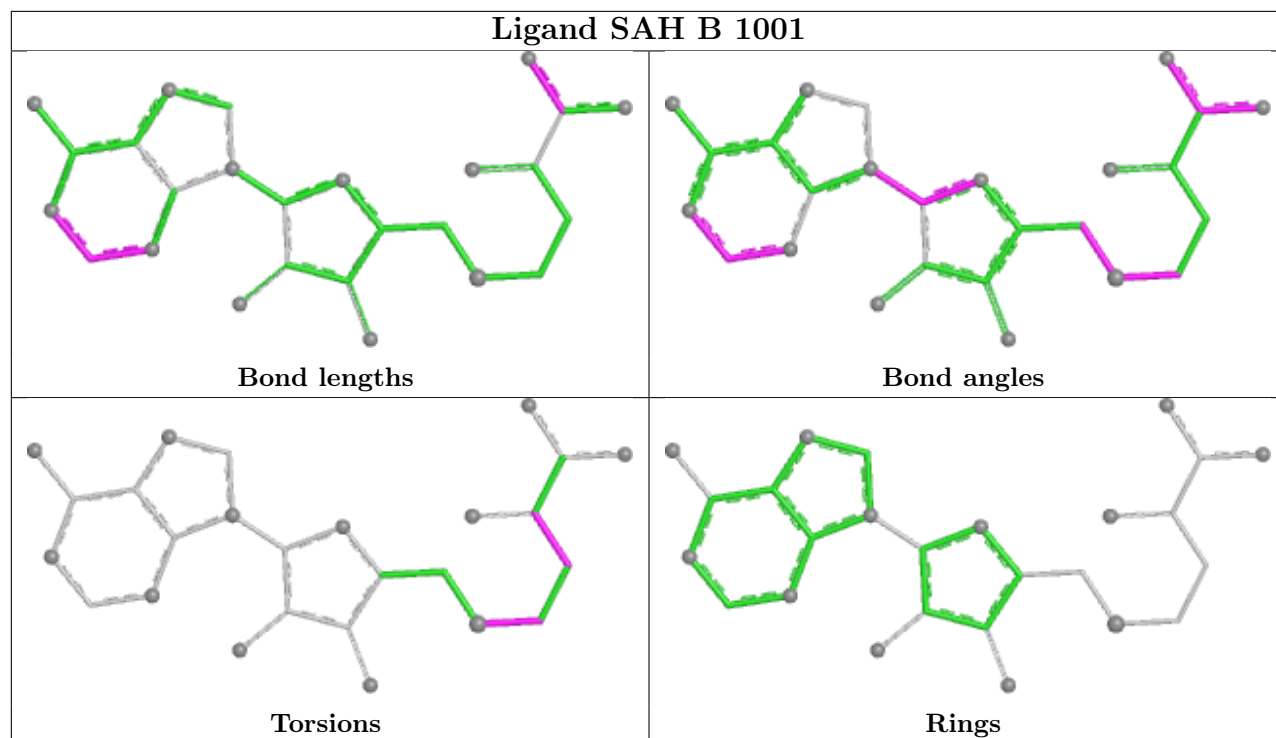












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [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	273/287 (95%)	-1.44	0	100	100	24, 48, 88, 123	2 (0%)
1	B	275/287 (95%)	-1.42	0	100	100	25, 47, 88, 136	4 (1%)
1	C	275/287 (95%)	-1.42	1 (0%)	89	87	25, 48, 90, 127	3 (1%)
1	D	275/287 (95%)	-1.40	1 (0%)	89	87	25, 48, 94, 130	3 (1%)
1	E	159/287 (55%)	-1.21	0	100	100	39, 67, 107, 135	0
1	F	160/287 (55%)	-1.20	0	100	100	42, 67, 109, 140	0
1	G	170/287 (59%)	-1.16	1 (0%)	85	83	44, 71, 133, 158	0
1	H	161/287 (56%)	-1.19	0	100	100	38, 67, 110, 143	0
All	All	1748/2296 (76%)	-1.33	3 (0%)	92	90	24, 54, 106, 158	12 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	845	ASP	2.9
1	C	845	ASP	2.6
1	G	629	GLU	2.4

### 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 monosaccharides in this entry.

## 6.4 Ligands

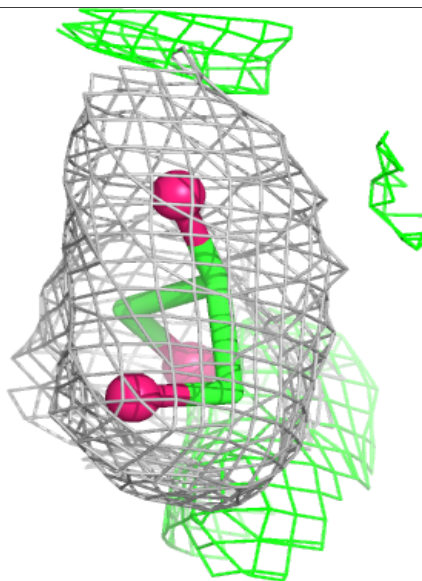
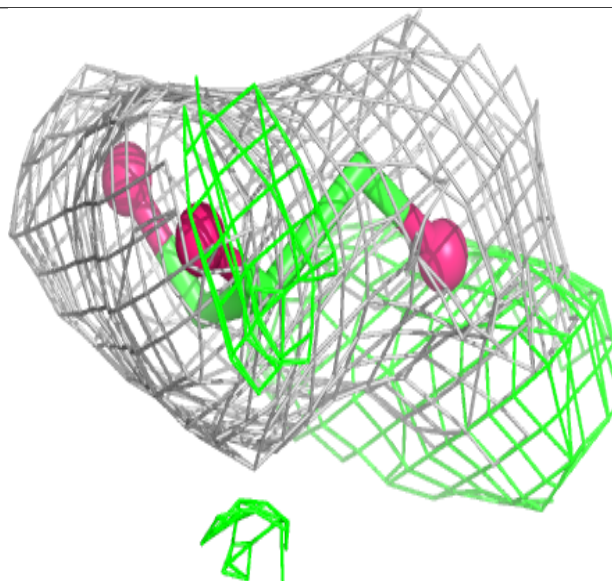
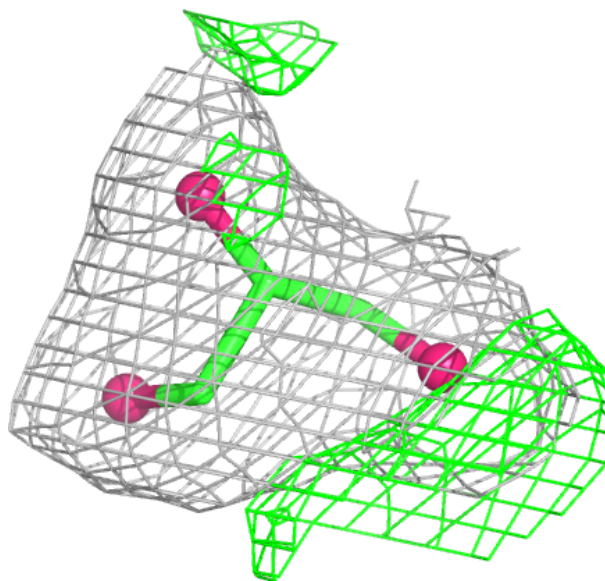
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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	C	1003	6/6	0.96	0.09	56,73,77,79	0
3	GOL	A	1002	6/6	0.97	0.08	60,65,77,85	0
3	GOL	A	1004	6/6	0.98	0.10	55,73,82,86	0
3	GOL	A	1005	6/6	0.98	0.07	49,69,91,106	0
3	GOL	B	1002	6/6	0.98	0.10	59,86,91,93	0
3	GOL	B	1003	6/6	0.98	0.11	39,64,88,92	0
3	GOL	A	1003	6/6	0.98	0.08	63,93,98,104	0
4	TLA	C	1002	10/10	0.98	0.07	81,96,119,127	0
2	SAH	A	1001	26/26	0.99	0.04	40,47,55,58	0
2	SAH	B	1001	26/26	0.99	0.04	39,48,54,58	0
2	SAH	C	1001	26/26	0.99	0.04	41,52,55,58	0
3	GOL	C	1004	6/6	0.99	0.05	44,89,94,108	0
3	GOL	C	1005	6/6	0.99	0.06	54,69,85,88	0
3	GOL	C	1006	6/6	0.99	0.09	50,62,75,82	0
3	GOL	D	1002	6/6	0.99	0.06	44,81,95,101	0
2	SAH	D	1001	26/26	0.99	0.03	36,48,57,57	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.

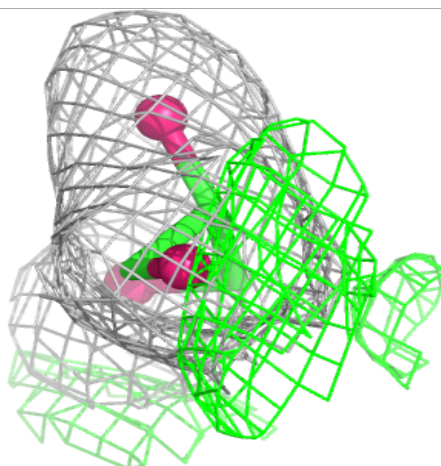
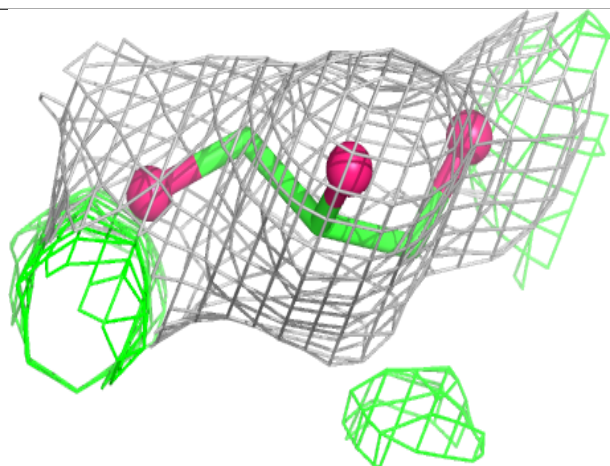
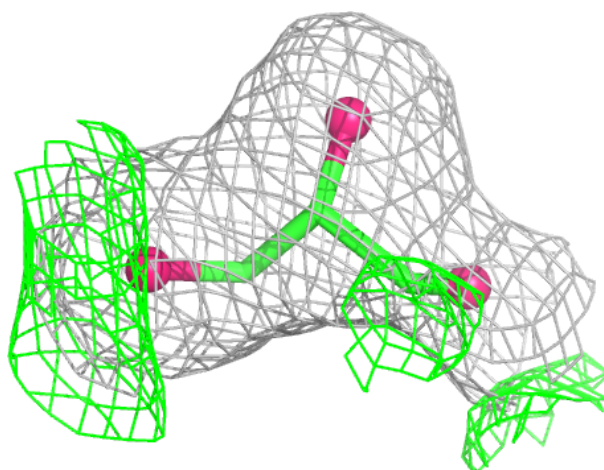
**Electron density around GOL C 1003:**

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



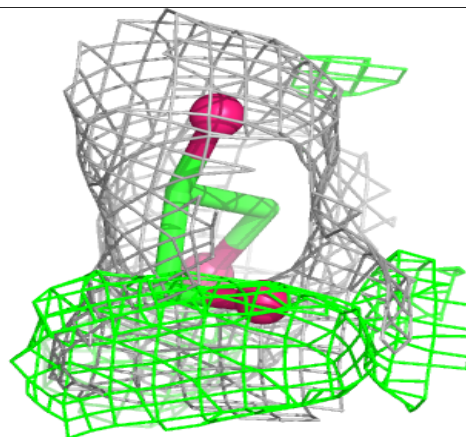
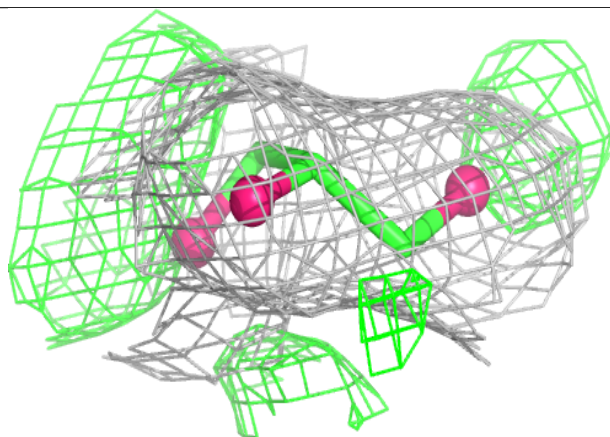
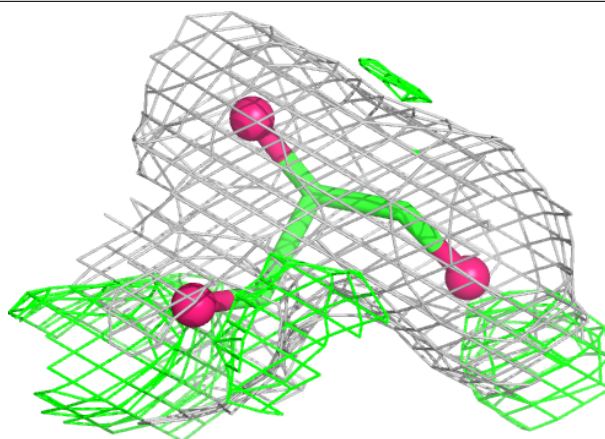
**Electron density around GOL A 1002:**

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



**Electron density around GOL A 1004:**

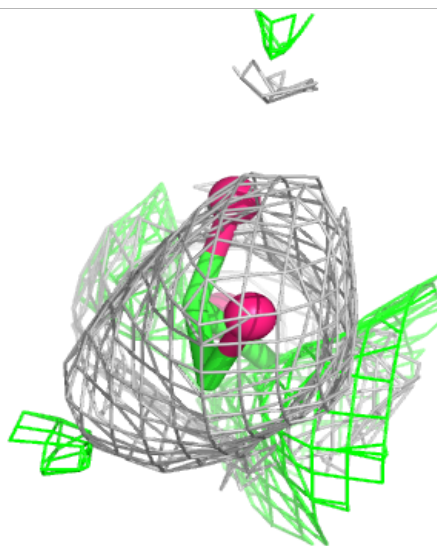
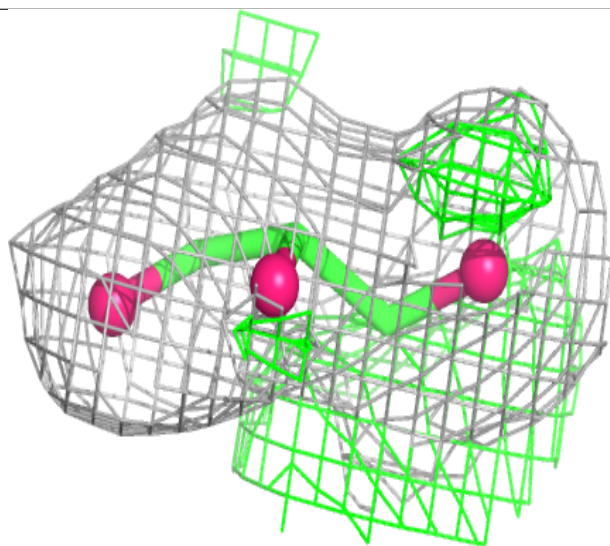
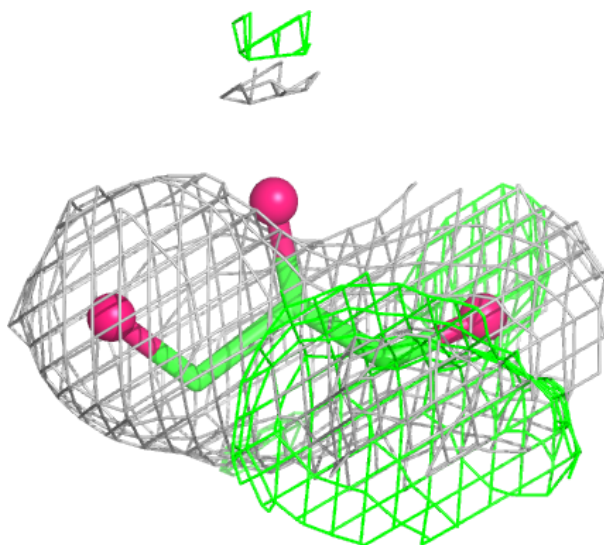
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





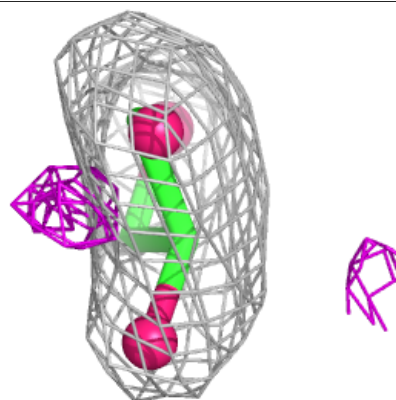
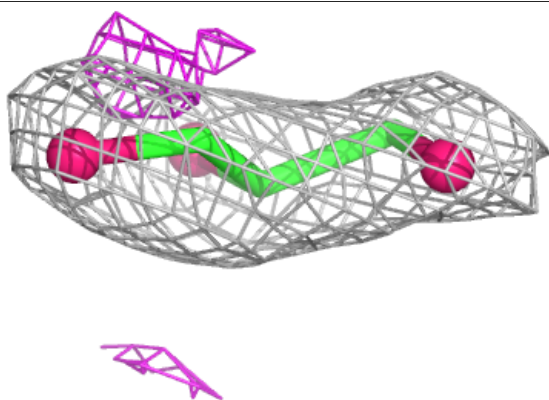
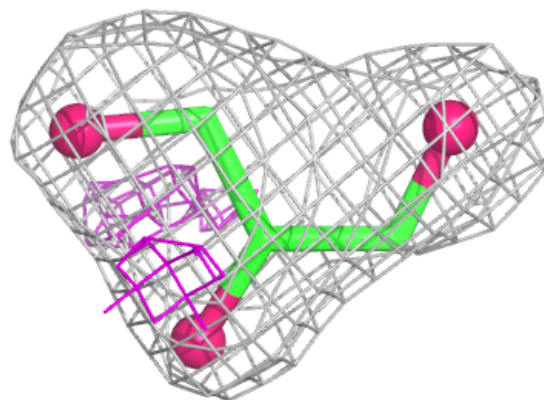
**Electron density around GOL A 1005:**

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



**Electron density around GOL B 1002:**

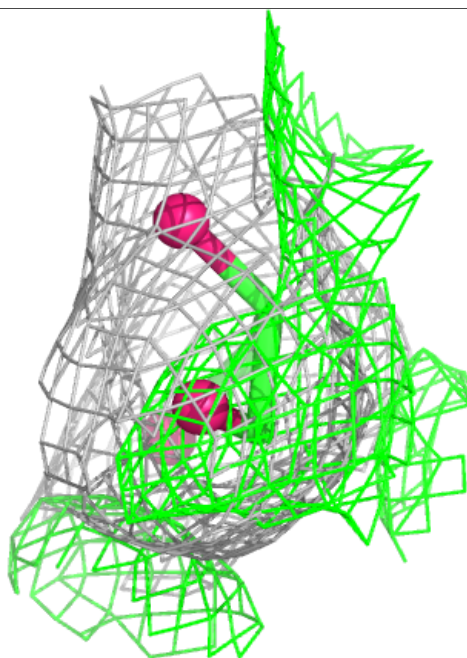
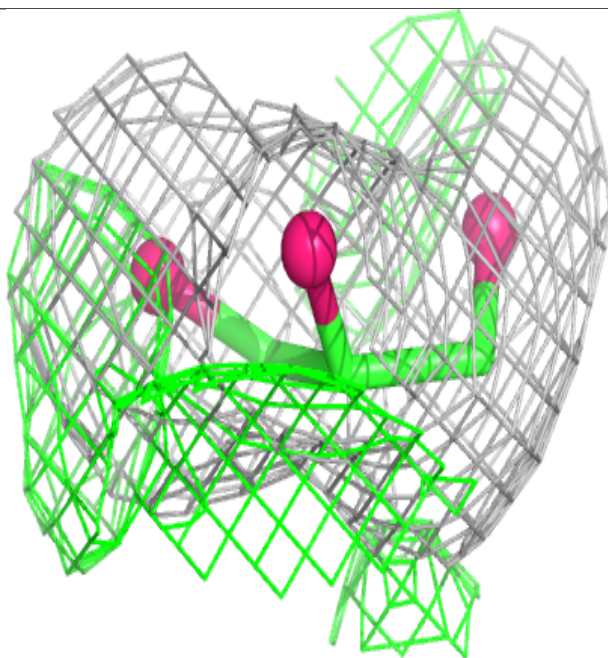
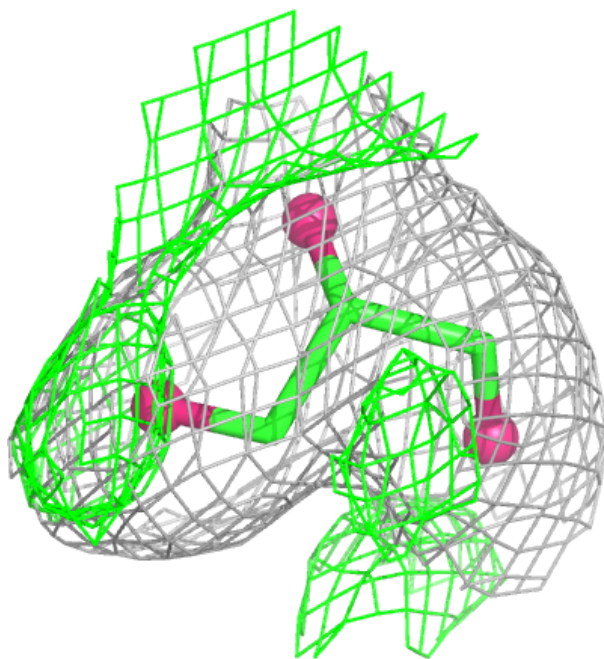
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 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





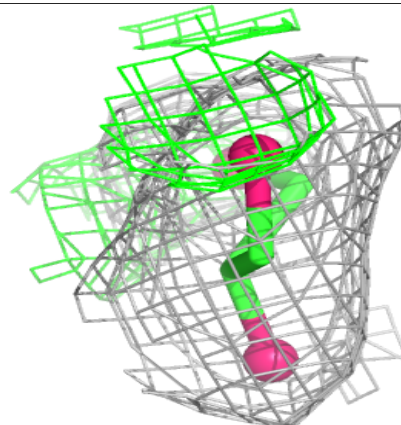
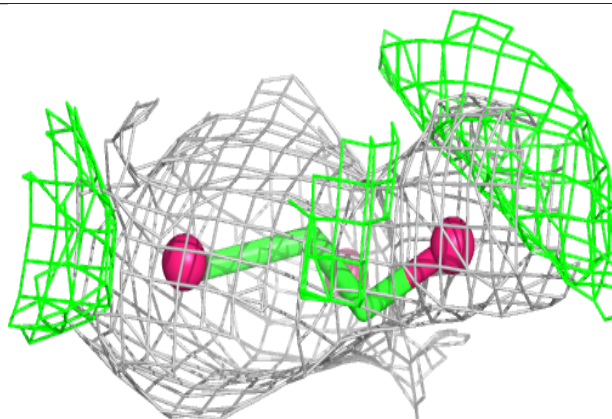
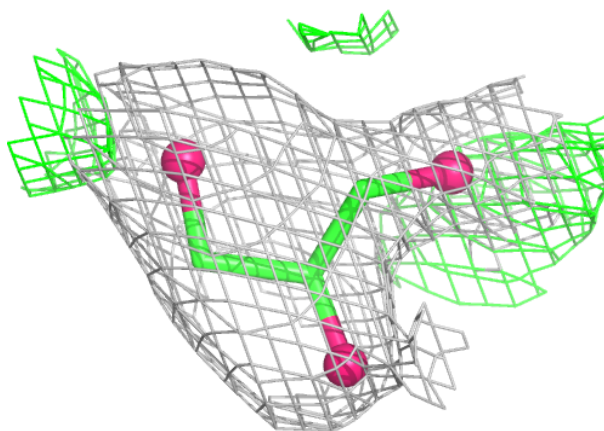
**Electron density around GOL B 1003:**

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and green (positive)

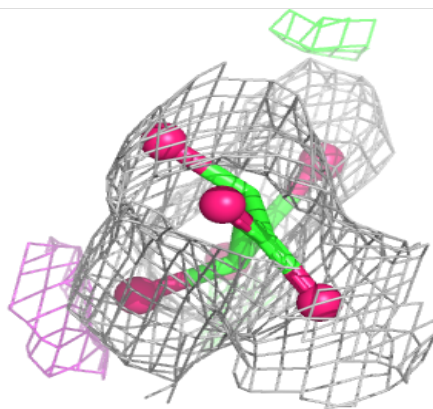
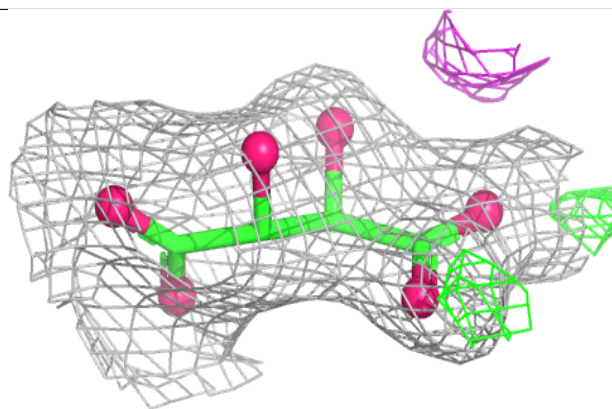
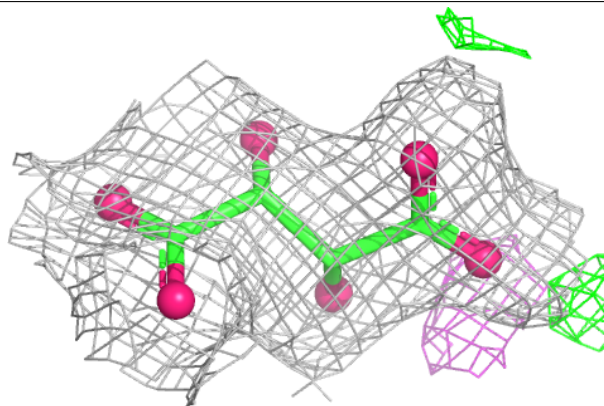


**Electron density around GOL A 1003:**

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

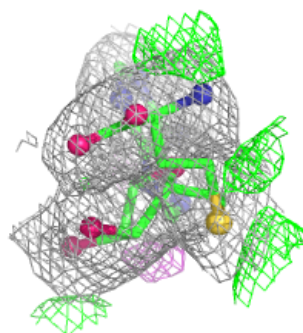
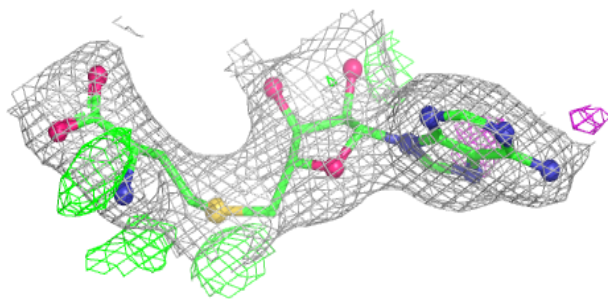
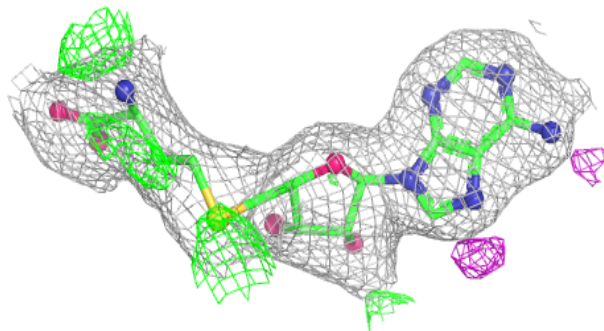
**Electron density around TLA C 1002:**

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and green (positive)

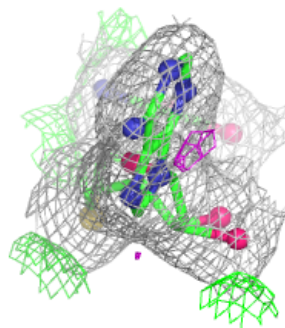
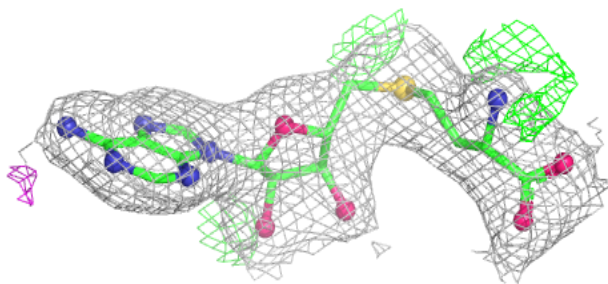
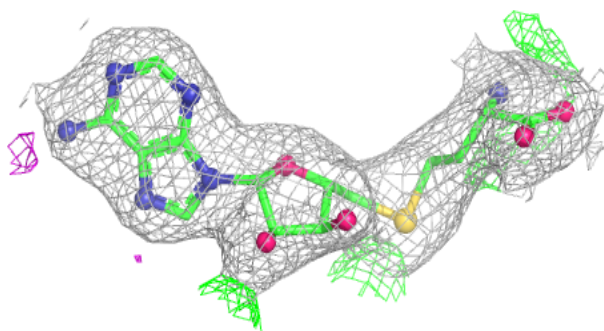


**Electron density around SAH A 1001:**

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

**Electron density around SAH B 1001:**

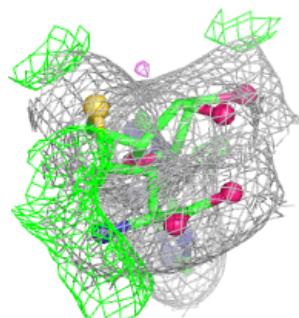
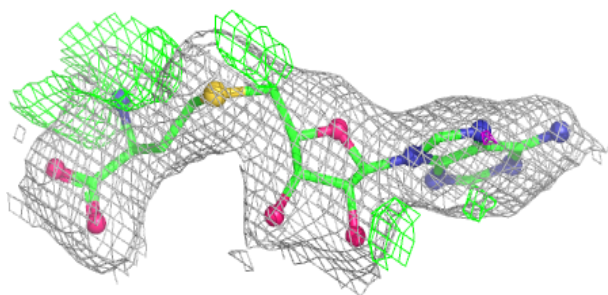
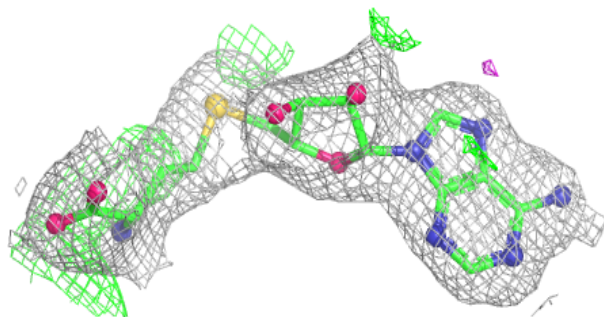
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





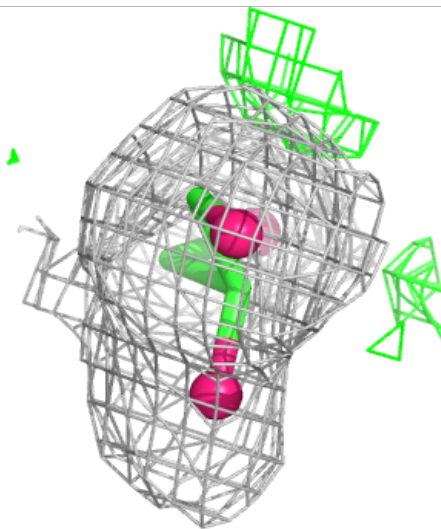
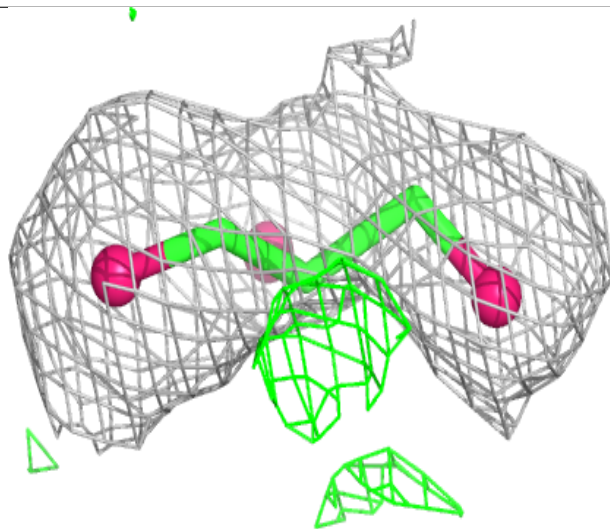
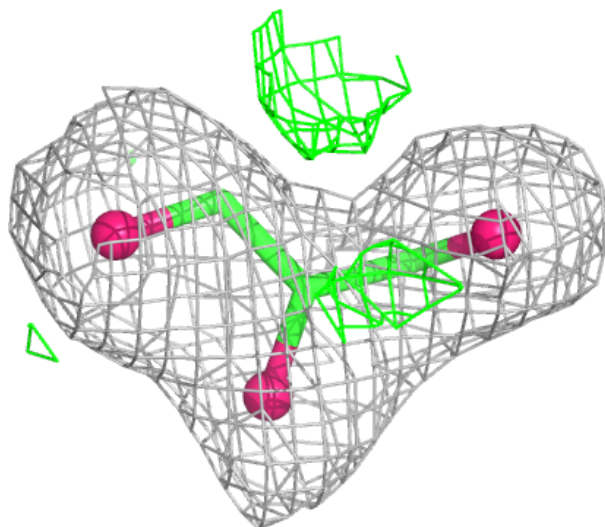
**Electron density around SAH C 1001:**

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



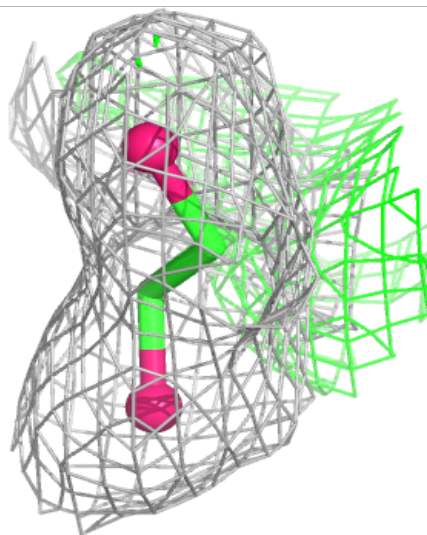
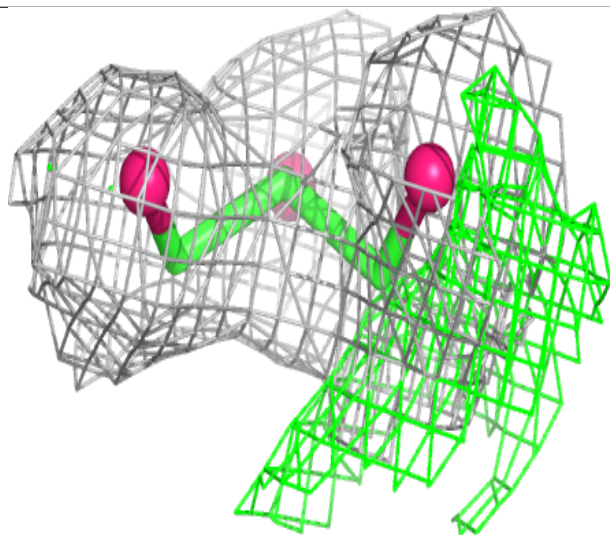
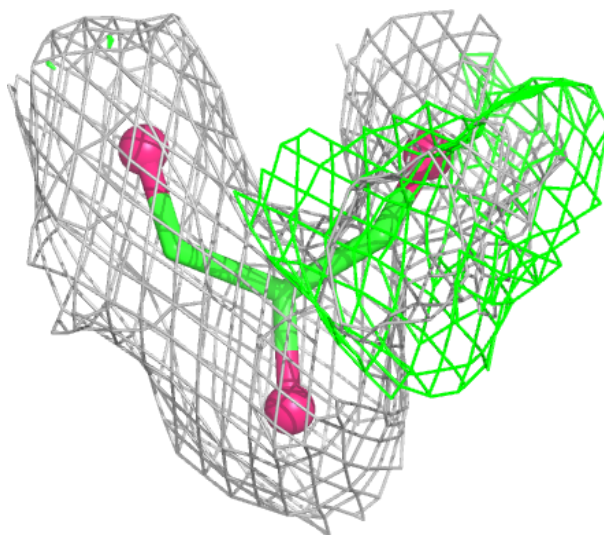
**Electron density around GOL C 1004:**

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



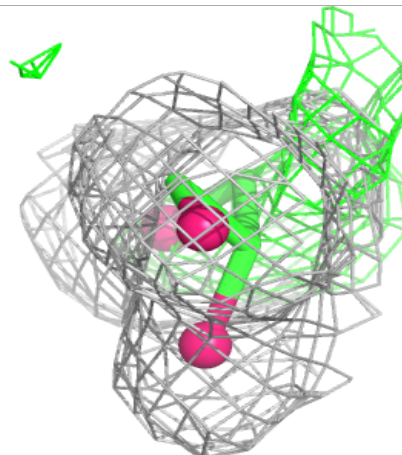
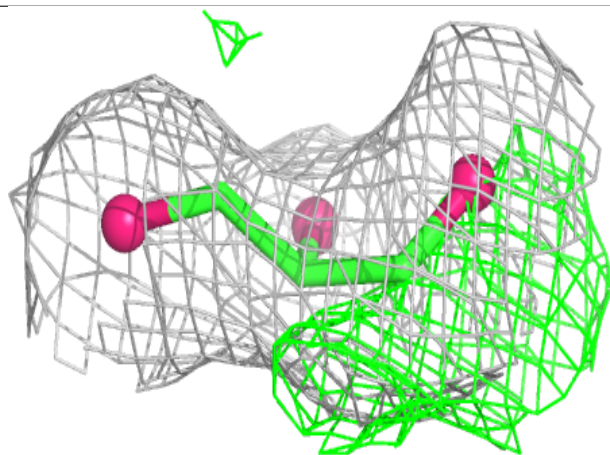
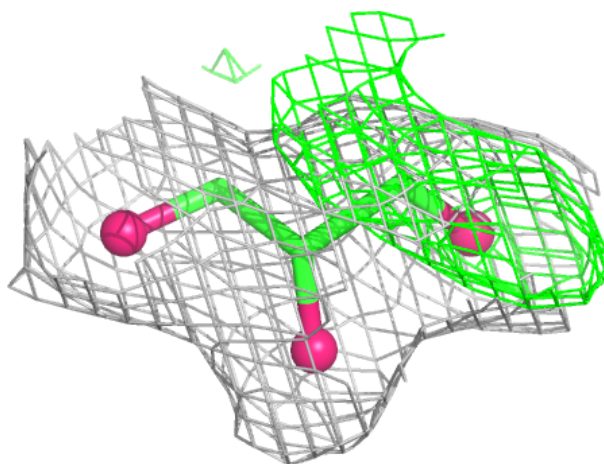
**Electron density around GOL C 1005:**

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and green (positive)



**Electron density around GOL C 1006:**

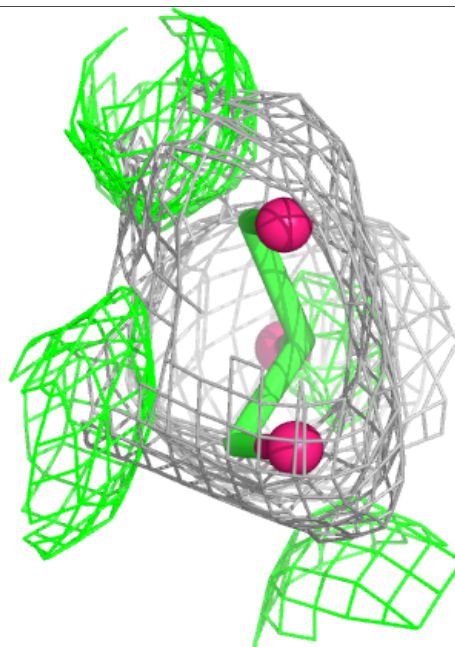
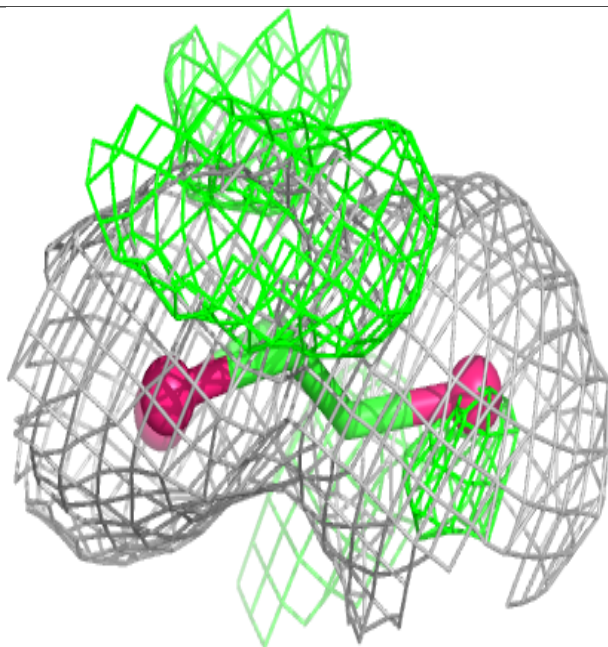
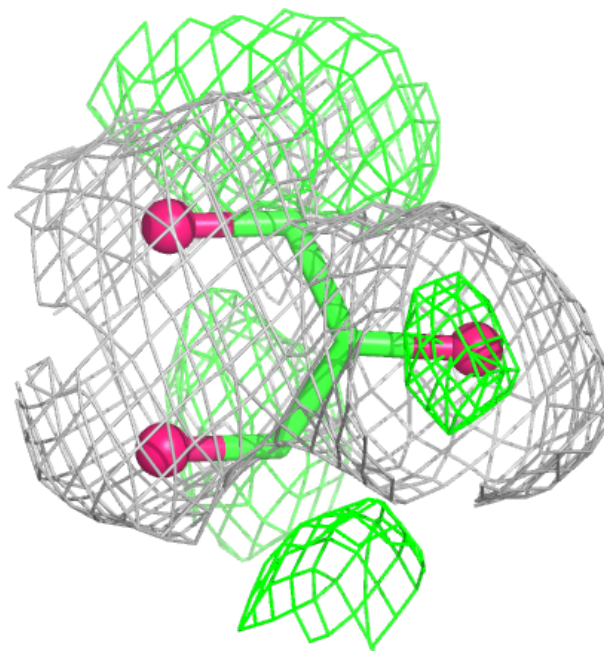
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



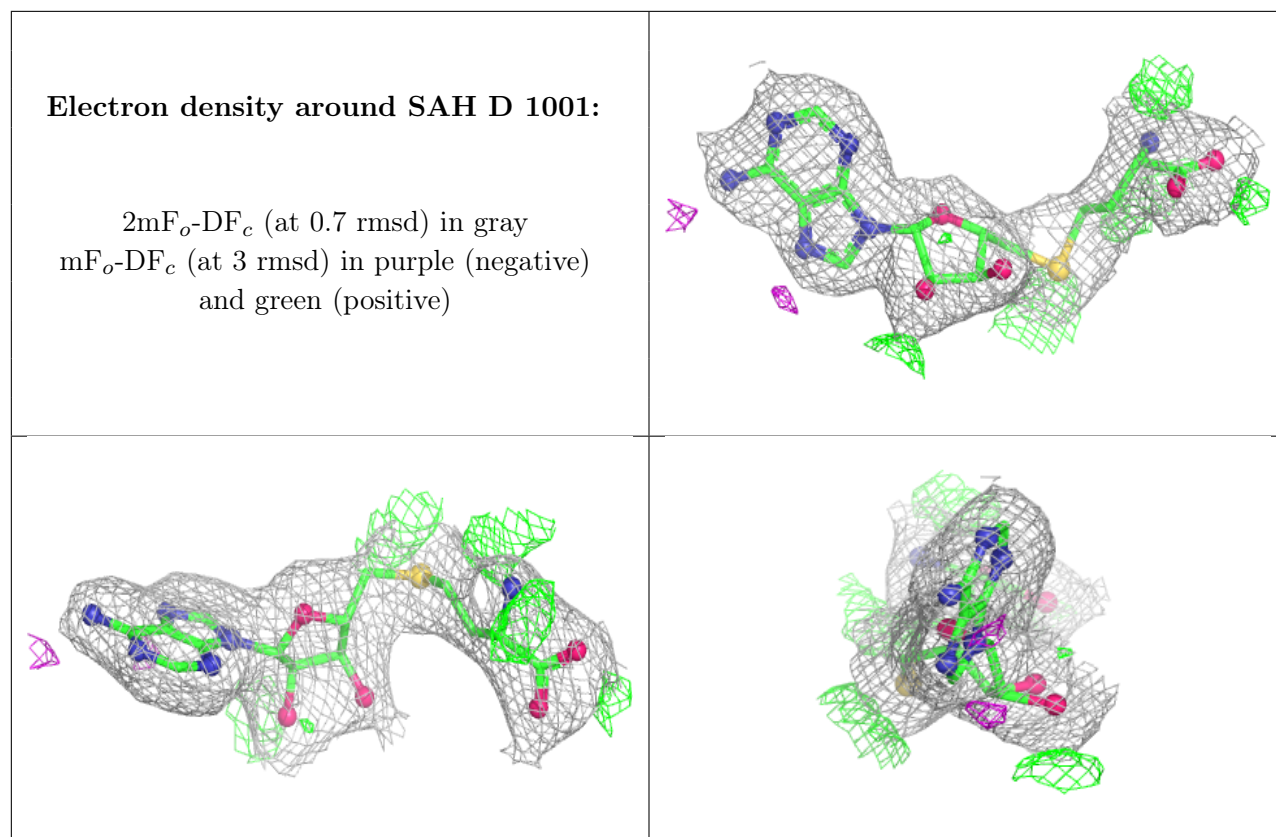


**Electron density around GOL D 1002:**

$2mF_o-DF_c$  (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.