



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 22, 2024 – 01:10 pm BST

PDB ID : 7P32  
Title : Crystal structure of human lysosomal acid-alpha-glucosidase, GAA, in complex with cyclosulfamidate 6  
Authors : Roig-Zamboni, V.; Kok, K.; Overkleeft, H.; Artola, M.; Sulzenbacher, G.  
Deposited on : 2021-07-06  
Resolution : 1.82 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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
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)	:	2.37.1

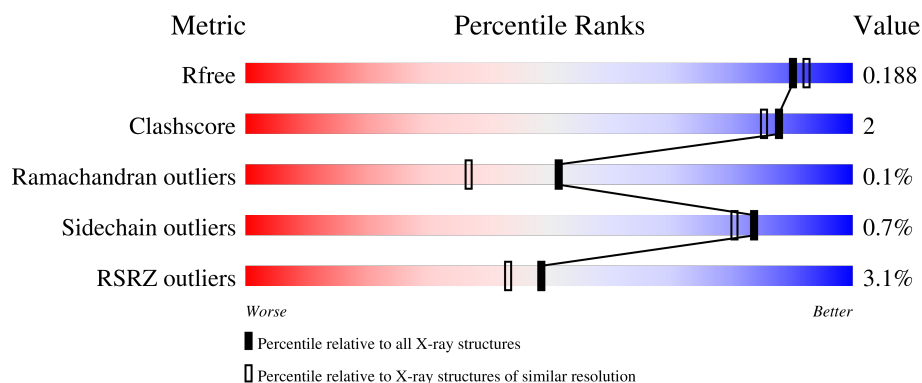
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.82 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	7484 (1.84-1.80)
Clashscore	141614	8401 (1.84-1.80)
Ramachandran outliers	138981	8290 (1.84-1.80)
Sidechain outliers	138945	8290 (1.84-1.80)
RSRZ outliers	127900	7371 (1.84-1.80)

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	AAA	872	<div> <div>3%</div> <div>93%</div> </div>
2	BBB	3	<div> <div>33%</div> <div>67%</div> </div>
3	BcB	2	<div> <div>100%</div> </div>
4	BfB	3	<div> <div>100%</div> </div>
5	BiB	2	<div> <div>100%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	BBB	2	-	-	-	X

## 2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 7681 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.

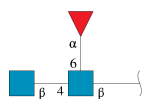
- Molecule 1 is a protein called Lysosomal alpha-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	847	Total	C	N	O	S	0	17	0
			6764	4341	1137	1252	34			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	199	ARG	HIS	variant	UNP P10253
AAA	223	HIS	ARG	variant	UNP P10253
AAA	780	ILE	VAL	variant	UNP P10253

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	BBB	3	Total	C	N	O	0	0	0
			38	22	2	14			

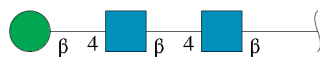
- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	BcB	2	Total	C	N	O	0	0	0
			28	16	2	10			



- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



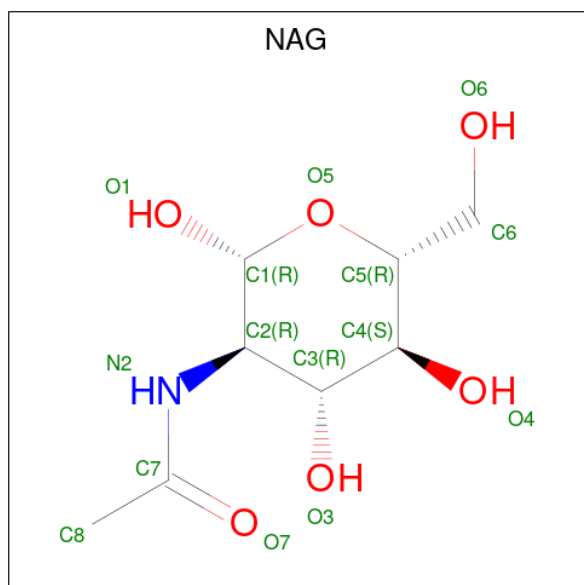
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	BfB	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 5 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



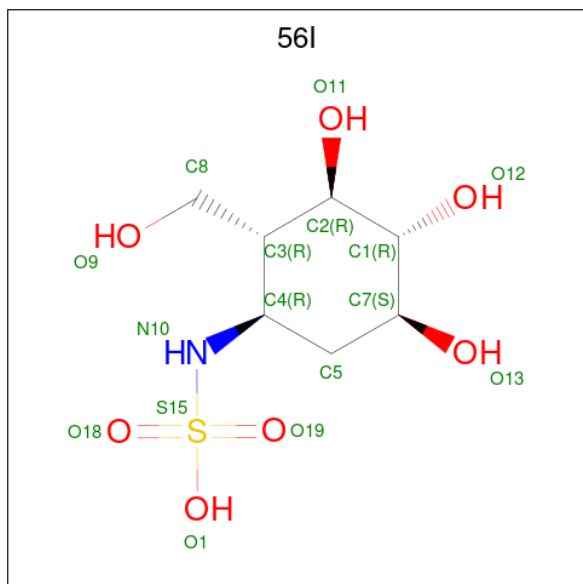
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	BiB	2	Total	C	N	O	0	0	0
			24	14	1	9			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>) (labeled as "Ligand of Interest" by depositor).



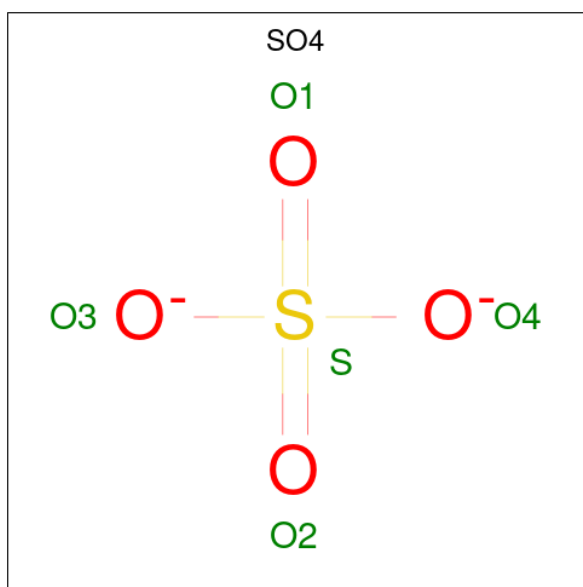
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	AAA	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is [(1R,2R,3R,4R,5S)-2-(hydroxymethyl)-3,4,5-tris(oxidanyl)cyclohexyl]sulfamic acid (three-letter code: 56I) (formula:  $C_7H_{15}NO_7S$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
7	AAA	1	16	7	1	7	1	0	0

- Molecule 8 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ) (labeled as "Ligand of Interest" by depositor).

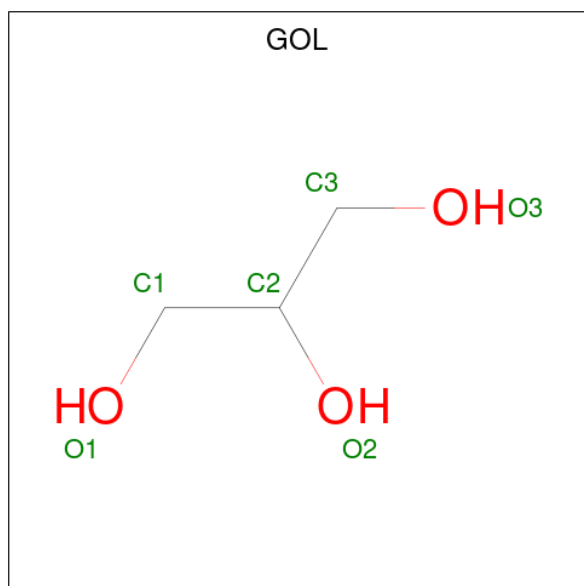


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	AAA	1	Total O S 5 4 1	0	0
8	AAA	1	Total O S 5 4 1	0	0
8	AAA	1	Total O S 5 4 1	0	0
8	AAA	1	Total O S 5 4 1	0	0
8	AAA	1	Total O S 5 4 1	0	0

- Molecule 9 is CHLORIDE ION (three-letter code: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

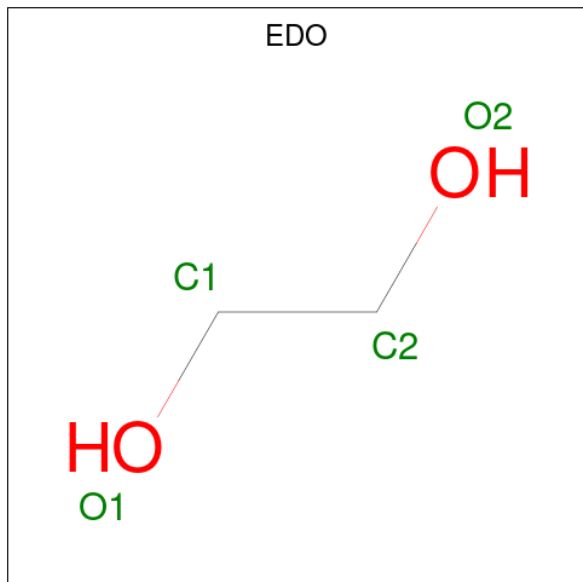
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	AAA	9	Total Cl 9 9	0	0

- Molecule 10 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).



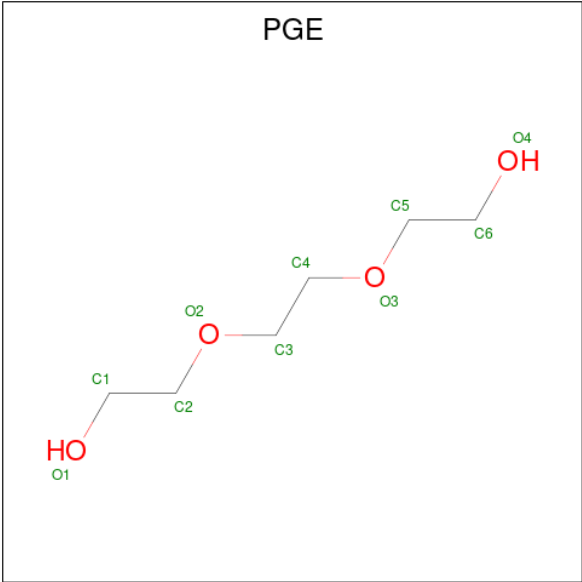
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	AAA	1	Total C O 6 3 3	0	0
10	AAA	1	Total C O 6 3 3	0	0
10	AAA	1	Total C O 6 3 3	0	0

- Molecule 11 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	AAA	1	Total	C	O	0	0
			4	2	2		
11	AAA	1	Total	C	O	0	0
			4	2	2		
11	AAA	1	Total	C	O	0	0
			4	2	2		
11	AAA	1	Total	C	O	0	0
			4	2	2		

- Molecule 12 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula:  $C_6H_{14}O_4$ ) (labeled as "Ligand of Interest" by depositor).



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

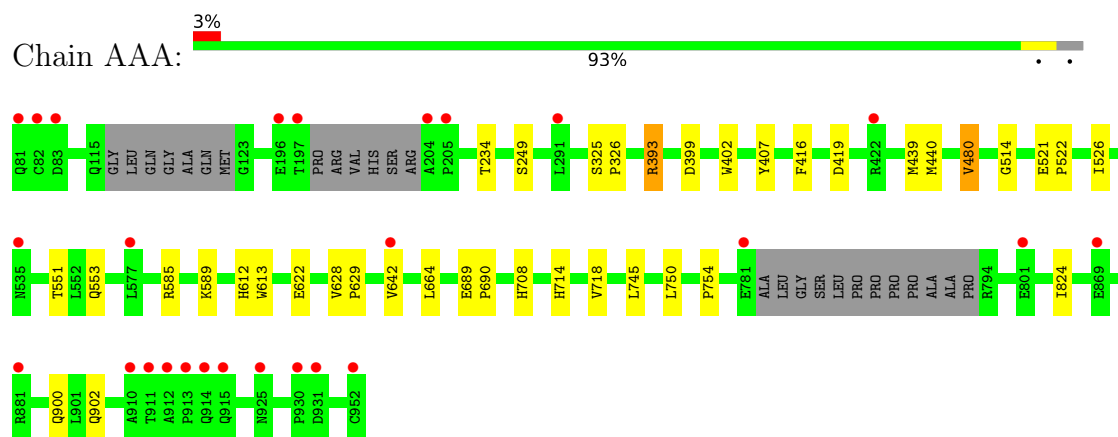
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	AAA	680	Total	O	0	0
			680	680		

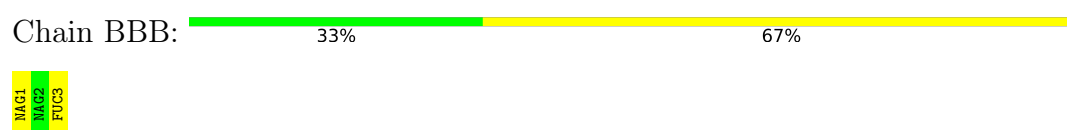
### 3 Residue-property plots [i](#)

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: Lysosomal alpha-glucosidase



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



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 4: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 5: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain BiB:

100%

MAG1  
FUC2

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	97.04Å 102.61Å 129.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.00 – 1.82 47.68 – 1.82	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.00-1.82) 99.8 (47.68-1.82)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.13 (at 1.82Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.150 , 0.175 0.164 , 0.188	Depositor DCC
$R_{free}$ test set	5791 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.1	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 45.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7681	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NAG, CL, 56I, PGE, BMA, CSO, EDO, FUC, SO4

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	AAA	0.65	0/6997	0.77	0/9554

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	AAA	6764	0	6572	26	0
2	BBB	38	0	34	0	0
3	BcB	28	0	25	0	0
4	BfB	39	0	34	0	0
5	BiB	24	0	22	0	0
6	AAA	14	0	13	0	0
7	AAA	16	0	0	0	0
8	AAA	25	0	0	0	0
9	AAA	9	0	0	0	0
10	AAA	18	0	24	0	0
11	AAA	16	0	24	3	0
12	AAA	10	0	14	0	0
13	AAA	680	0	0	4	0
All	All	7681	0	6762	27	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (27) 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:AAA:393[A]:ARG:HG3	1:AAA:393[A]:ARG:HH21	1.36	0.90
1:AAA:393[A]:ARG:NH2	13:AAA:1101:HOH:O	2.15	0.77
1:AAA:393[A]:ARG:HH21	1:AAA:393[A]:ARG:CG	2.01	0.73
1:AAA:393[A]:ARG:HG3	1:AAA:393[A]:ARG:NH2	2.00	0.70
1:AAA:551:THR:OG1	1:AAA:553[B]:GLN:OE1	2.17	0.61
1:AAA:900:GLN:HE22	11:AAA:1023:EDO:H12	1.67	0.60
1:AAA:708:HIS:CE1	1:AAA:824[B]:ILE:HD12	2.38	0.58
11:AAA:1021:EDO:H11	13:AAA:1354:HOH:O	2.09	0.53
1:AAA:900:GLN:HE22	11:AAA:1023:EDO:C1	2.22	0.52
1:AAA:526:ILE:C	1:AAA:526:ILE:HD12	2.31	0.52
1:AAA:234:THR:HA	1:AAA:249:SER:O	2.13	0.48
1:AAA:622:GLU:HG2	13:AAA:1193:HOH:O	2.13	0.48
1:AAA:664:LEU:HD13	1:AAA:754:PRO:HG3	1.96	0.47
1:AAA:585[B]:ARG:NE	1:AAA:589:LYS:HE3	2.30	0.46
1:AAA:628:VAL:HB	1:AAA:629:PRO:HD3	1.96	0.46
1:AAA:439[B]:MET:SD	1:AAA:514:GLY:HA3	2.57	0.45
1:AAA:419:ASP:HB2	13:AAA:1199:HOH:O	2.17	0.44
1:AAA:521:GLU:N	1:AAA:522:PRO:HA	2.33	0.43
1:AAA:612:HIS:O	1:AAA:642:VAL:HA	2.18	0.43
1:AAA:745:LEU:HA	1:AAA:750:LEU:O	2.19	0.43
1:AAA:689:GLU:HB3	1:AAA:690:PRO:HD3	2.01	0.42
1:AAA:407:TYR:O	1:AAA:416:PHE:HA	2.20	0.41
1:AAA:714:HIS:CE1	1:AAA:718:VAL:HG11	2.57	0.40
1:AAA:325:SER:N	1:AAA:326:PRO:HA	2.37	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	AAA	855/872 (98%)	835 (98%)	19 (2%)	1 (0%)	51 37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	480	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	AAA	740/741 (100%)	734 (99%)	6 (1%)	81 77

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	393[A]	ARG
1	AAA	393[B]	ARG
1	AAA	399	ASP
1	AAA	440	MET
1	AAA	480	VAL
1	AAA	613	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
1	CSO	AAA	938	1	3,6,7	0.72	0	0,6,8	-	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSO	AAA	938	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates ⓘ

10 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	NAG	BBB	1	2,1	14,14,15	0.69	0	17,19,21	1.13	1 (5%)
2	NAG	BBB	2	2	14,14,15	0.61	0	17,19,21	0.72	0
2	FUC	BBB	3	2	10,10,11	0.68	0	14,14,16	1.16	2 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	BcB	1	3,1	14,14,15	0.69	0	17,19,21	1.23	2 (11%)
3	NAG	BcB	2	3	14,14,15	0.51	0	17,19,21	1.39	3 (17%)
4	NAG	BfB	1	4,1	14,14,15	0.64	0	17,19,21	1.11	1 (5%)
4	NAG	BfB	2	4	14,14,15	0.61	0	17,19,21	1.16	2 (11%)
4	BMA	BfB	3	4	11,11,12	0.55	0	15,15,17	1.37	2 (13%)
5	NAG	BiB	1	5,1	14,14,15	0.74	0	17,19,21	1.22	1 (5%)
5	FUC	BiB	2	5	10,10,11	0.62	0	14,14,16	1.42	3 (21%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	BBB	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	BBB	2	2	-	0/6/23/26	0/1/1/1
2	FUC	BBB	3	2	-	-	0/1/1/1
3	NAG	BcB	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	BcB	2	3	-	0/6/23/26	0/1/1/1
4	NAG	BfB	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	BfB	2	4	-	0/6/23/26	0/1/1/1
4	BMA	BfB	3	4	-	2/2/19/22	0/1/1/1
5	NAG	BiB	1	5,1	-	0/6/23/26	0/1/1/1
5	FUC	BiB	2	5	-	-	0/1/1/1

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	BfB	3	BMA	O5-C5-C6	3.78	113.14	107.20
2	BBB	1	NAG	O5-C1-C2	-3.63	105.55	111.29
5	BiB	2	FUC	O5-C5-C4	3.08	115.05	109.52
4	BfB	1	NAG	O5-C1-C2	-2.59	107.20	111.29
2	BBB	3	FUC	C1-O5-C5	2.39	118.19	112.78
3	BcB	1	NAG	C1-O5-C5	-2.35	109.01	112.19
5	BiB	1	NAG	O5-C5-C6	2.34	110.86	107.20
4	BfB	2	NAG	O7-C7-N2	-2.34	117.66	121.95
5	BiB	2	FUC	C1-O5-C5	2.31	118.02	112.78
3	BcB	2	NAG	C1-C2-N2	-2.31	106.54	110.49
3	BcB	1	NAG	O5-C5-C6	2.24	110.71	107.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	BcB	2	NAG	C3-C4-C5	-2.19	106.33	110.24
3	BcB	2	NAG	O5-C5-C4	-2.19	105.51	110.83
4	BfB	3	BMA	O2-C2-C1	-2.10	104.85	109.15
5	BiB	2	FUC	O5-C1-C2	-2.09	107.54	110.77
4	BfB	2	NAG	C6-C5-C4	-2.02	108.27	113.00
2	BBB	3	FUC	C2-C3-C4	2.02	114.39	110.89

There are no chirality outliers.

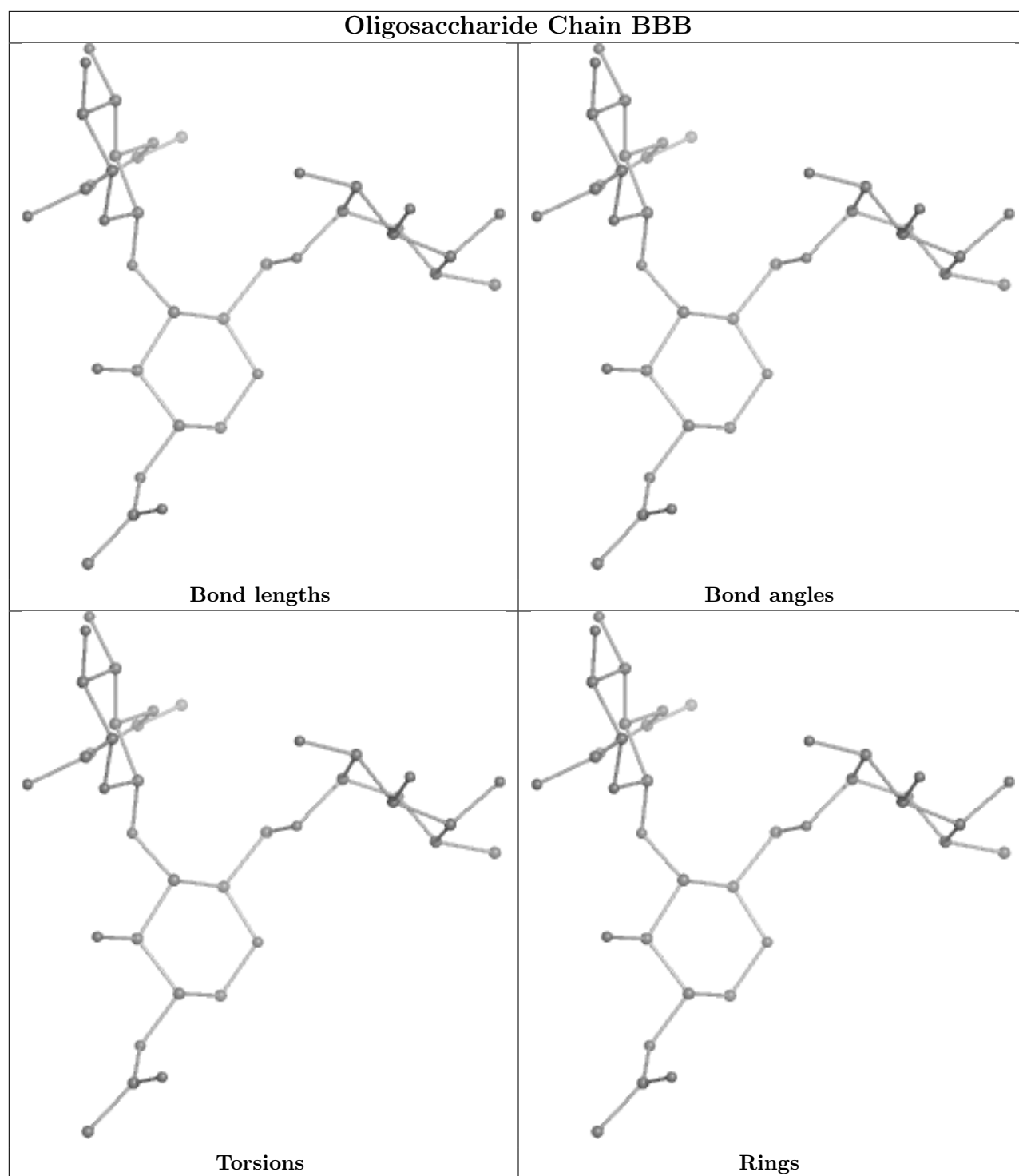
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	BfB	3	BMA	O5-C5-C6-O6
4	BfB	3	BMA	C4-C5-C6-O6

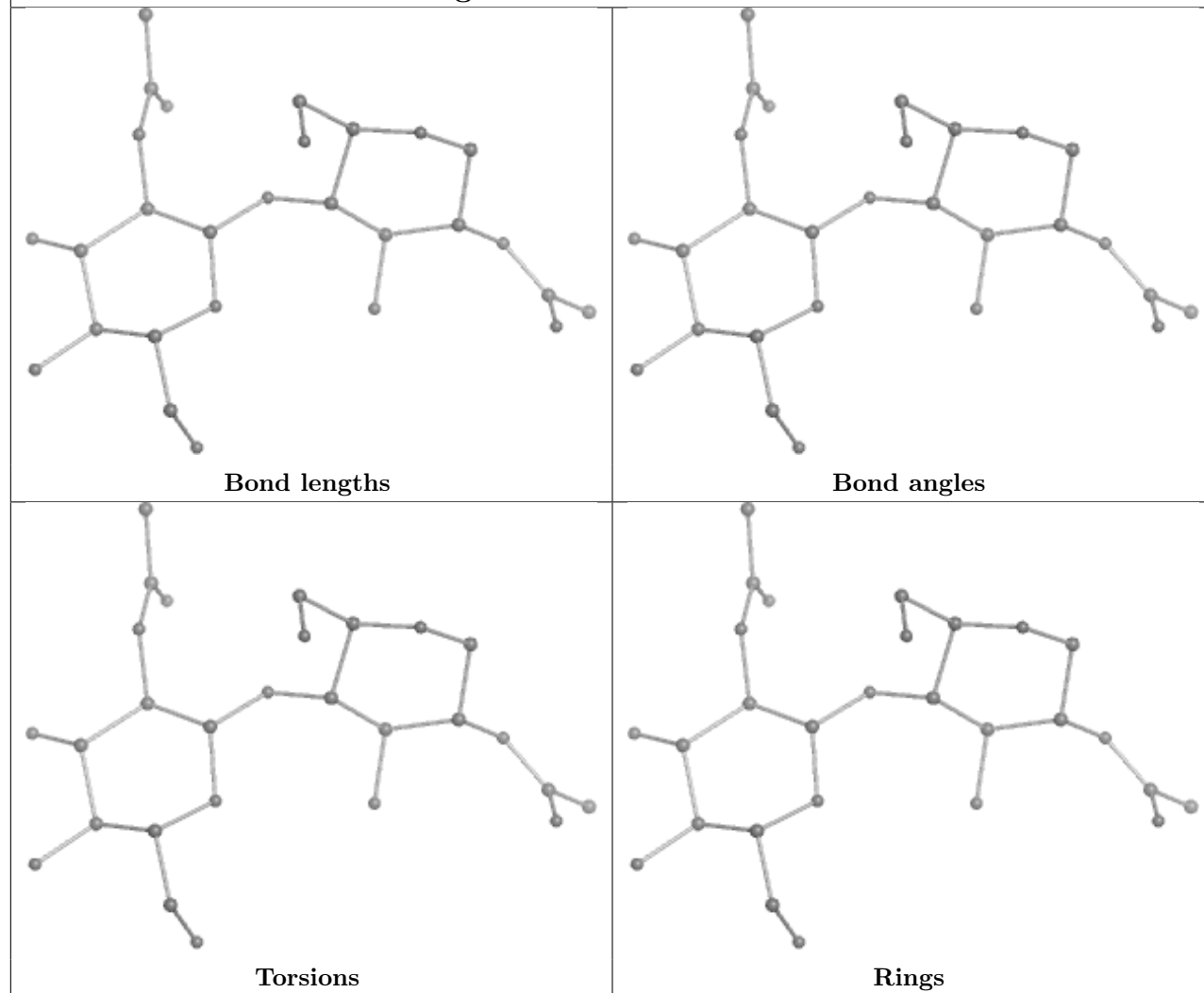
There are no ring outliers.

No monomer is involved in short contacts.

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

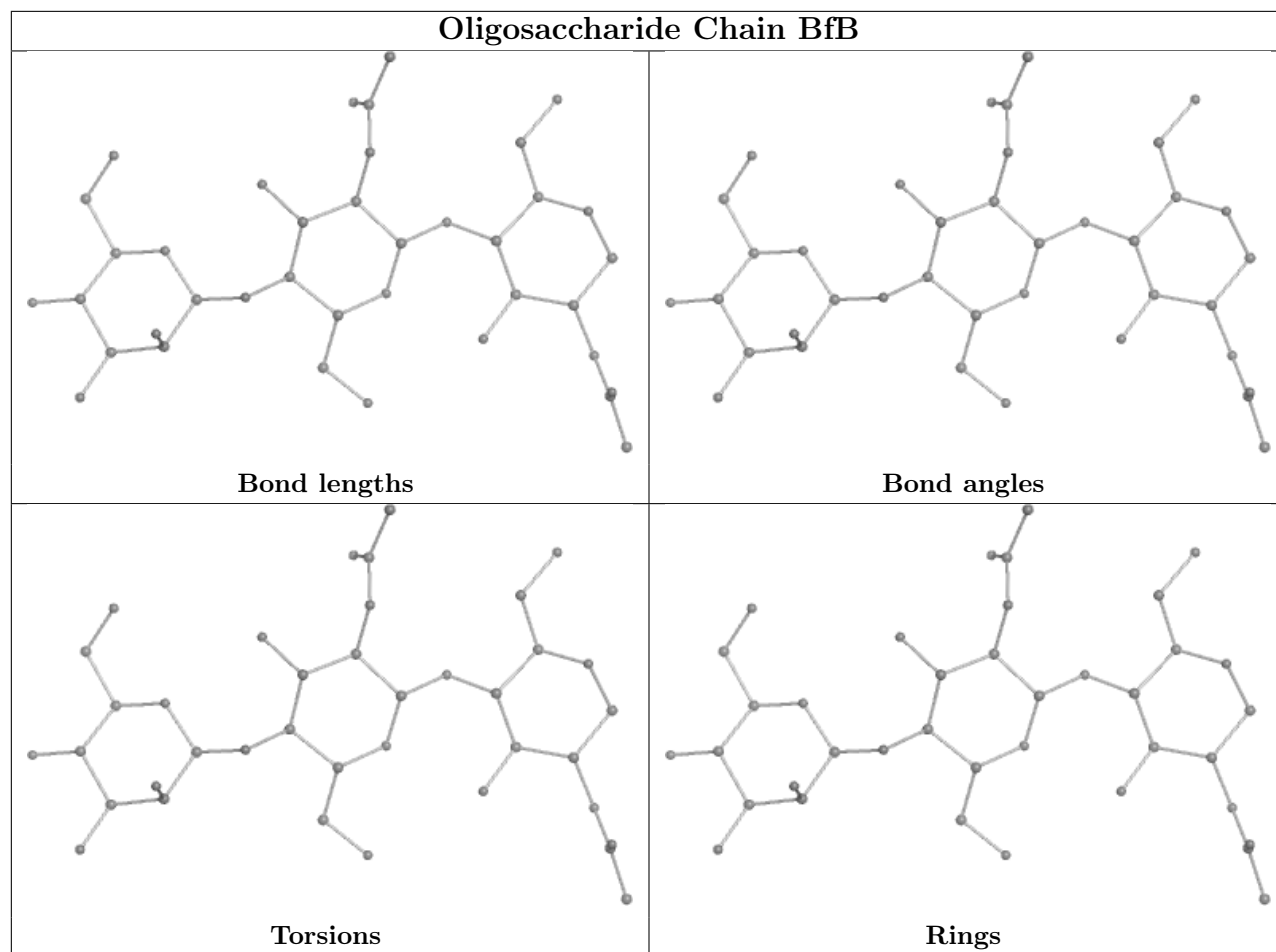


## Oligosaccharide Chain BcB

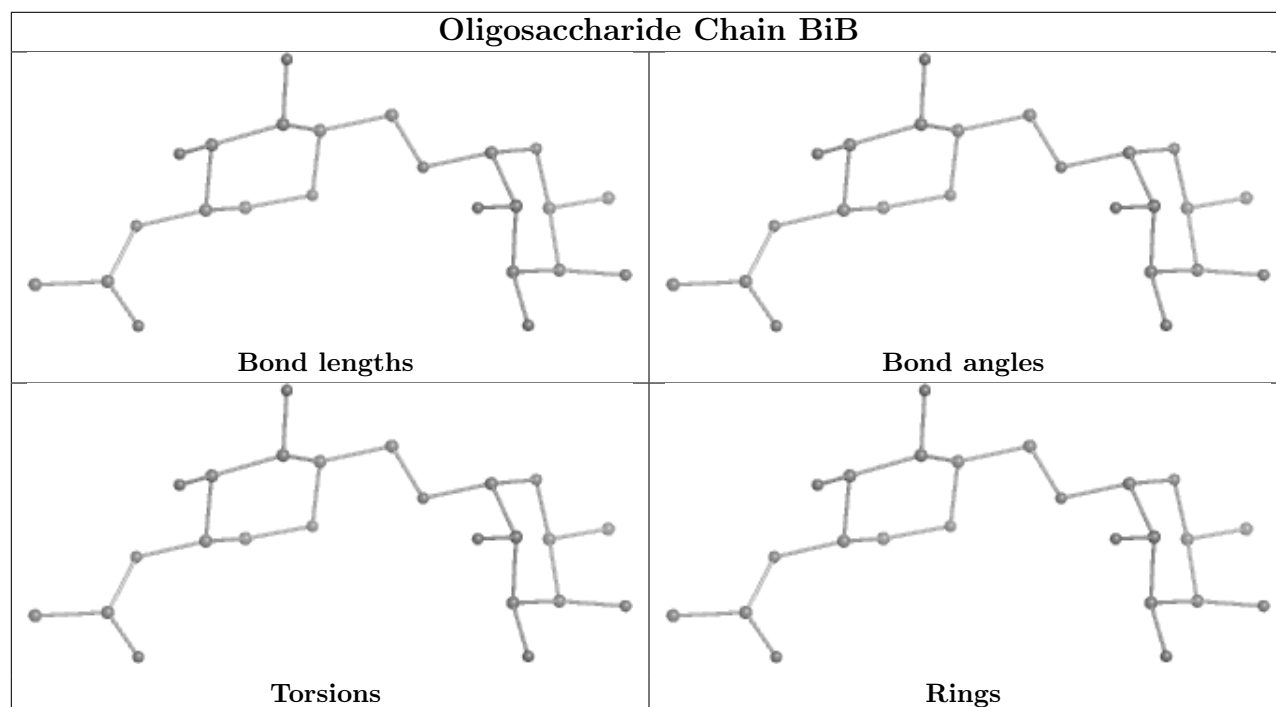




## Oligosaccharide Chain BfB



## Oligosaccharide Chain BiB



## 5.6 Ligand geometry

Of 24 ligands modelled in this entry, 9 are monoatomic - leaving 15 for Mogul analysis.

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	$\# Z  > 2$
8	SO4	AAA	1006	-	4,4,4	0.41	0	6,6,6	0.22	0
10	GOL	AAA	1018	-	5,5,5	0.21	0	5,5,5	0.62	0
8	SO4	AAA	1005	-	4,4,4	0.43	0	6,6,6	0.12	0
7	56I	AAA	1002	1	15,16,16	2.64	3 (20%)	18,24,24	1.67	2 (11%)
8	SO4	AAA	1003	-	4,4,4	0.28	0	6,6,6	0.19	0
10	GOL	AAA	1019	-	5,5,5	0.18	0	5,5,5	0.36	0
6	NAG	AAA	1001	1	14,14,15	0.66	0	17,19,21	1.56	4 (23%)
8	SO4	AAA	1004	-	4,4,4	0.27	0	6,6,6	0.15	0
11	EDO	AAA	1022	-	3,3,3	0.20	0	2,2,2	0.20	0
11	EDO	AAA	1023	-	3,3,3	0.37	0	2,2,2	0.20	0
12	PGE	AAA	1024	-	9,9,9	0.23	0	8,8,8	0.13	0
11	EDO	AAA	1021	-	3,3,3	0.20	0	2,2,2	0.11	0
11	EDO	AAA	1020	-	3,3,3	0.13	0	2,2,2	0.50	0
10	GOL	AAA	1017	-	5,5,5	0.13	0	5,5,5	0.24	0
8	SO4	AAA	1007	-	4,4,4	0.31	0	6,6,6	0.38	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
10	GOL	AAA	1018	-	-	2/4/4/4	-
7	56I	AAA	1002	1	-	1/7/27/27	0/1/1/1
10	GOL	AAA	1019	-	-	1/4/4/4	-
6	NAG	AAA	1001	1	-	0/6/23/26	0/1/1/1
11	EDO	AAA	1023	-	-	0/1/1/1	-
11	EDO	AAA	1022	-	-	0/1/1/1	-
12	PGE	AAA	1024	-	-	1/7/7/7	-
11	EDO	AAA	1021	-	-	0/1/1/1	-
10	GOL	AAA	1017	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	EDO	AAA	1020	-	-	1/1/1/1	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	AAA	1002	56I	O19-S15	8.37	1.51	1.42
7	AAA	1002	56I	O18-S15	3.83	1.46	1.42
7	AAA	1002	56I	C3-C2	-3.26	1.49	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	AAA	1002	56I	O19-S15-O18	-4.77	108.90	120.16
6	AAA	1001	NAG	O5-C1-C2	-3.65	105.53	111.29
7	AAA	1002	56I	C5-C4-C3	3.45	115.45	111.49
6	AAA	1001	NAG	C3-C4-C5	-2.88	105.11	110.24
6	AAA	1001	NAG	O6-C6-C5	-2.32	103.32	111.29
6	AAA	1001	NAG	C1-O5-C5	-2.05	109.41	112.19

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	AAA	1018	GOL	O1-C1-C2-O2
10	AAA	1018	GOL	O1-C1-C2-C3
7	AAA	1002	56I	C4-N10-S15-O19
11	AAA	1020	EDO	O1-C1-C2-O2
12	AAA	1024	PGE	O2-C3-C4-O3
10	AAA	1019	GOL	O2-C2-C3-O3

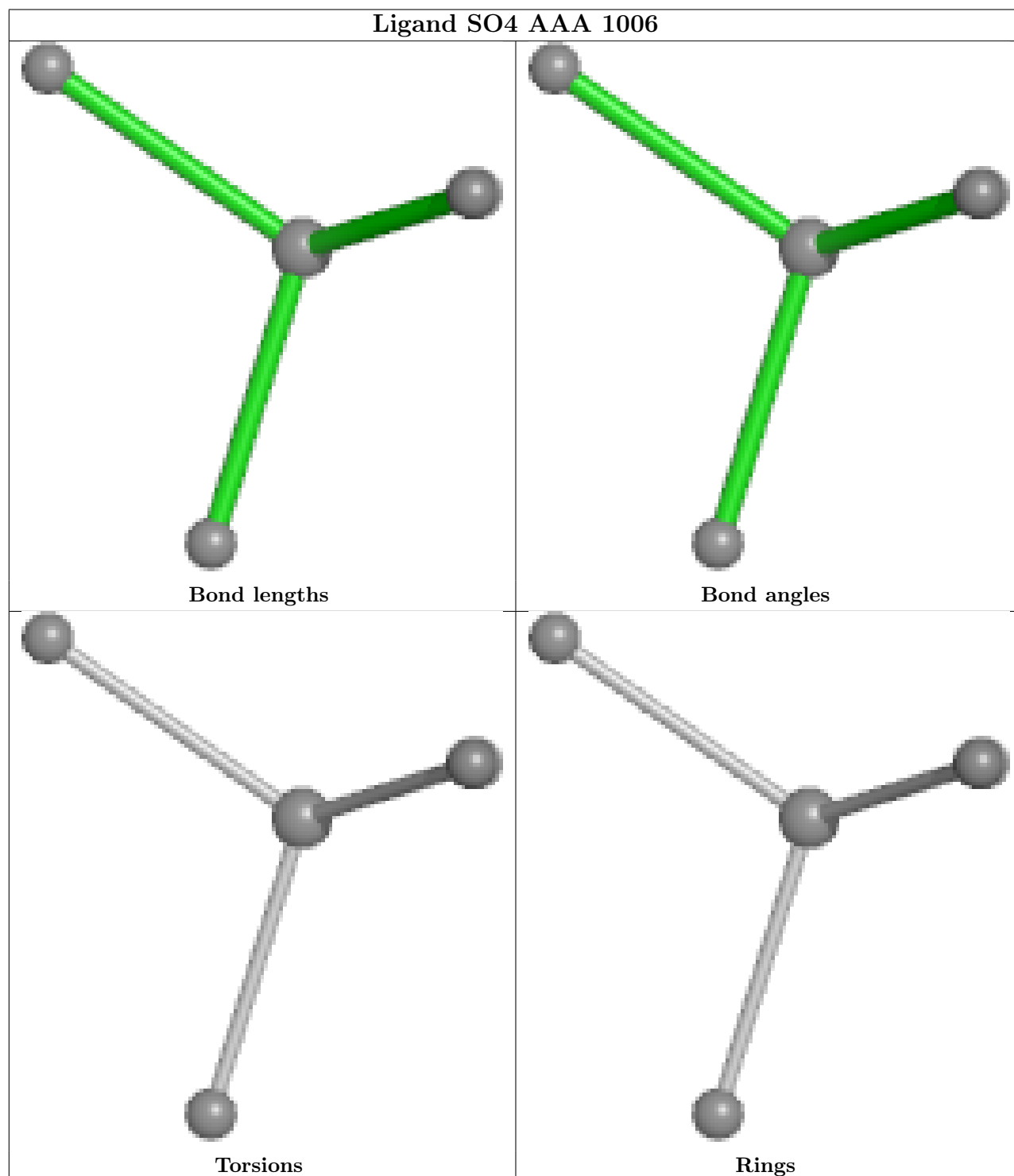
There are no ring outliers.

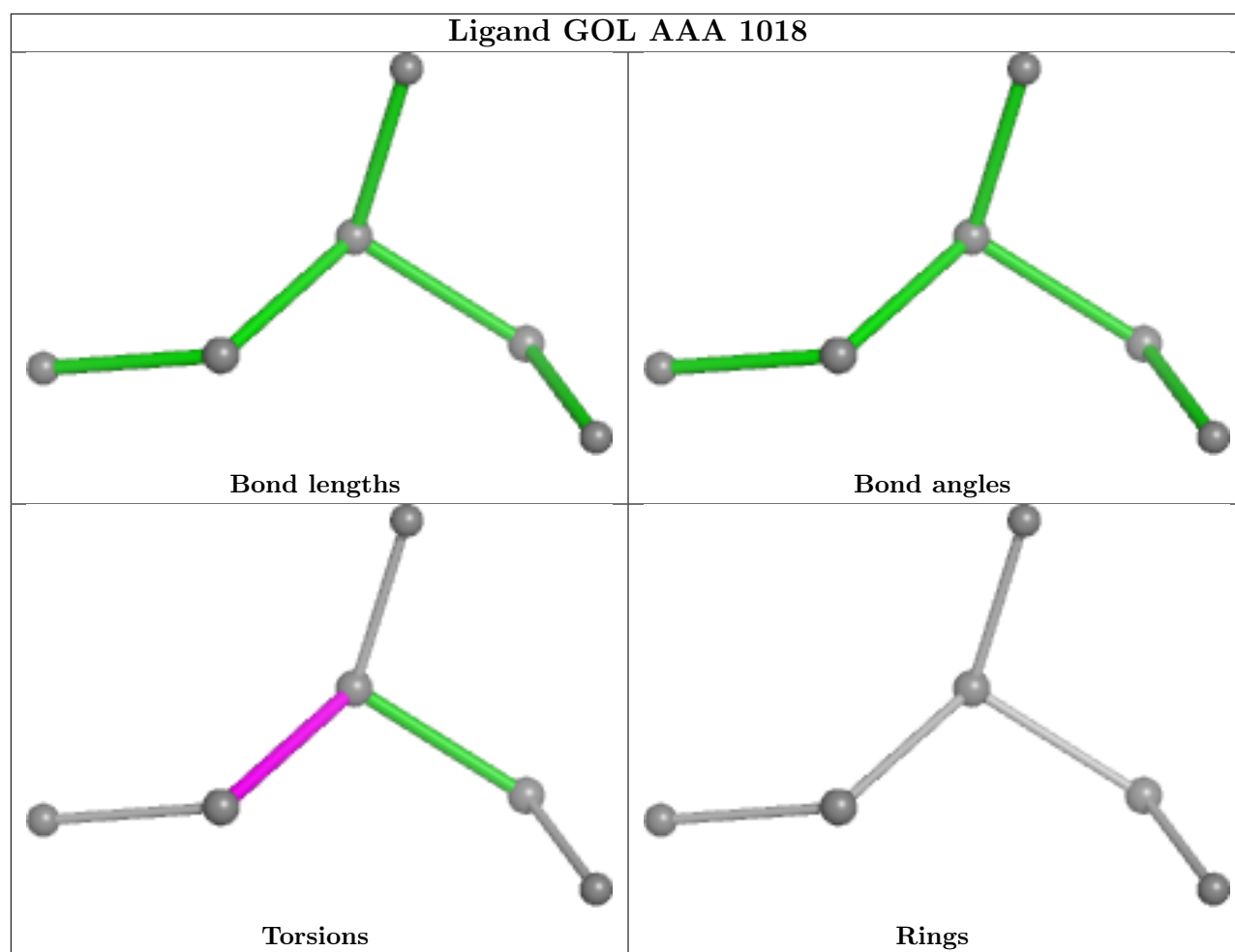
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	AAA	1023	EDO	2	0
11	AAA	1021	EDO	1	0

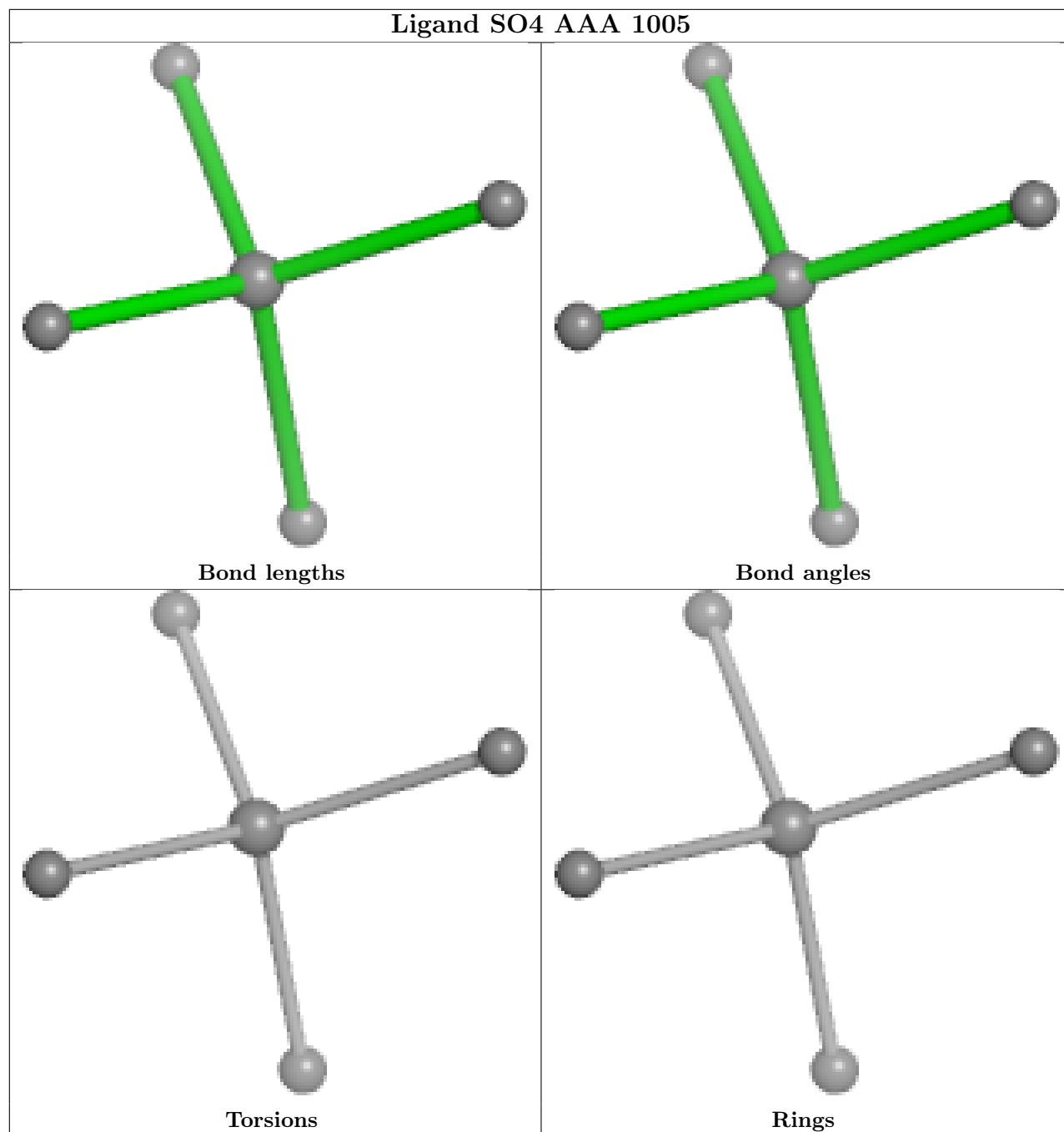
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

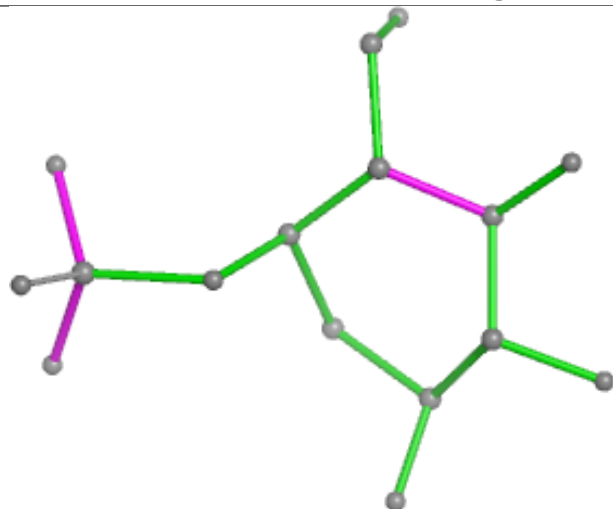




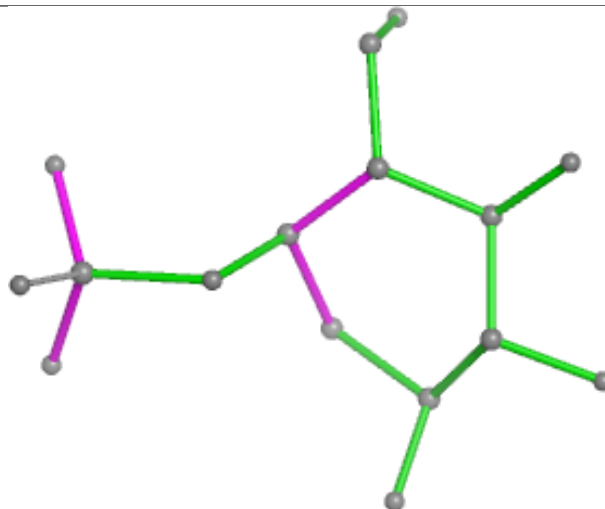
## Ligand SO4 AAA 1005



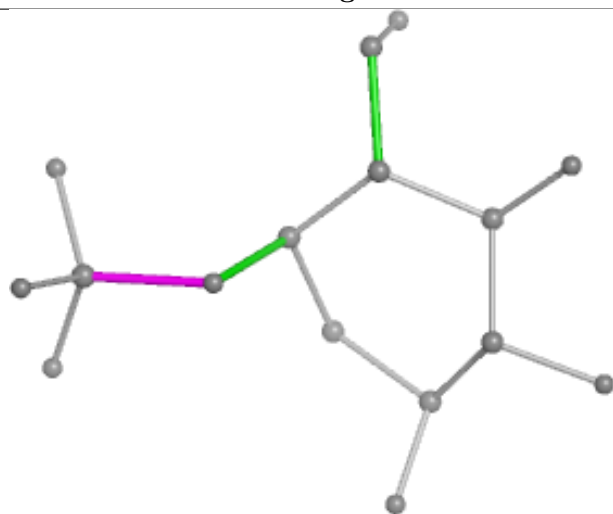
## Ligand 56I AAA 1002



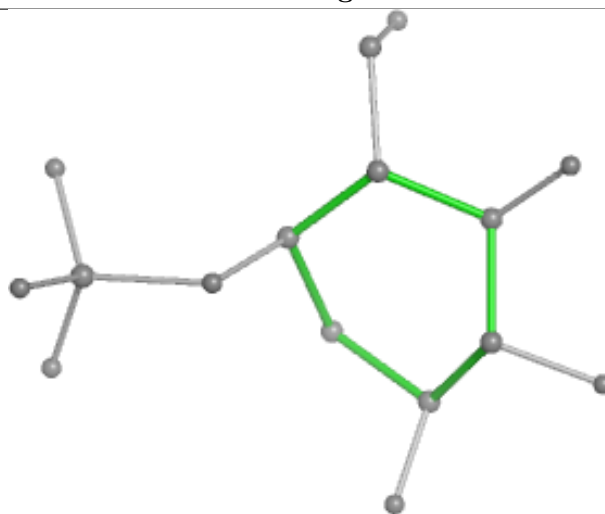
Bond lengths



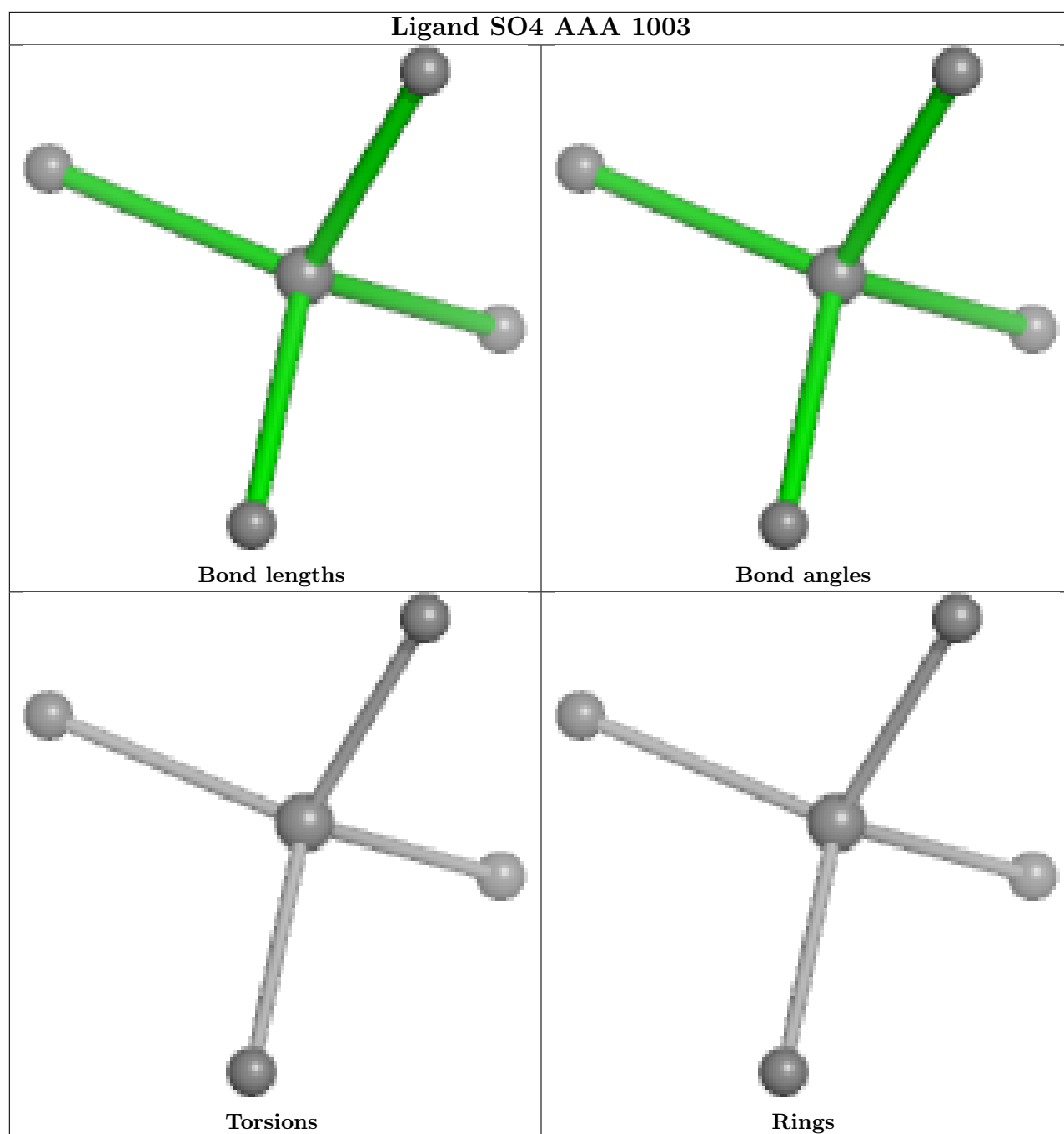
Bond angles



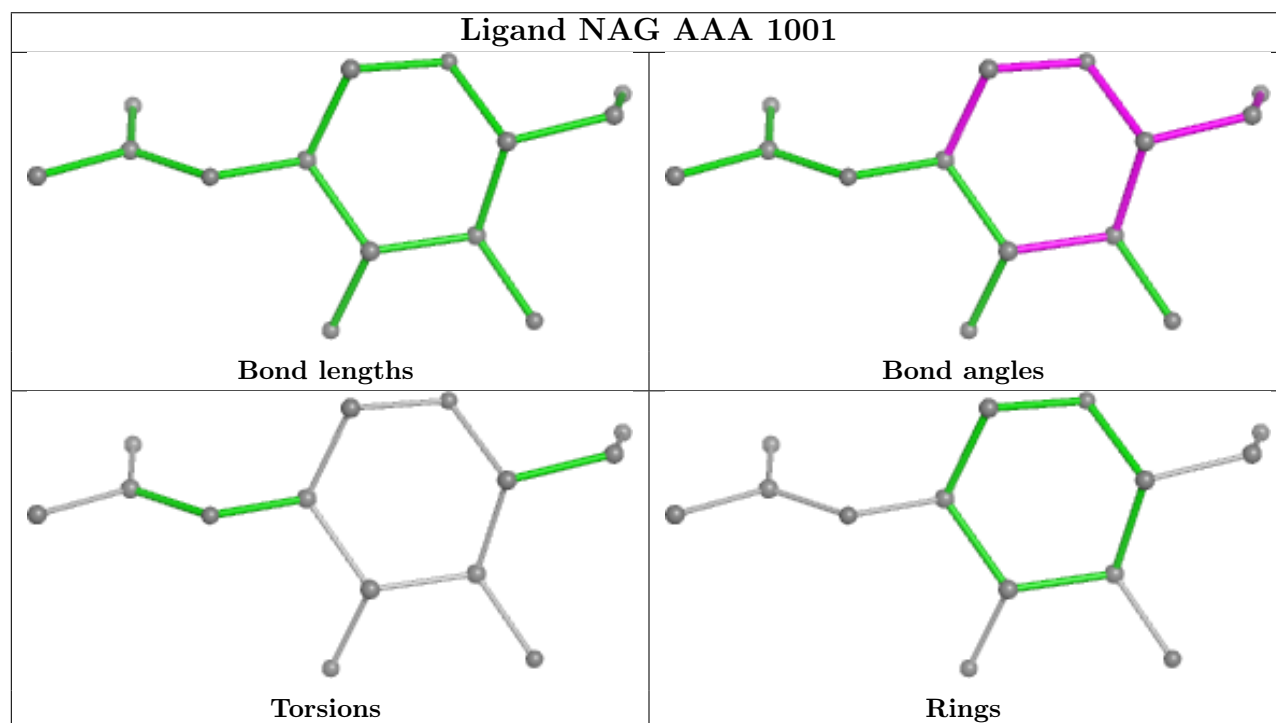
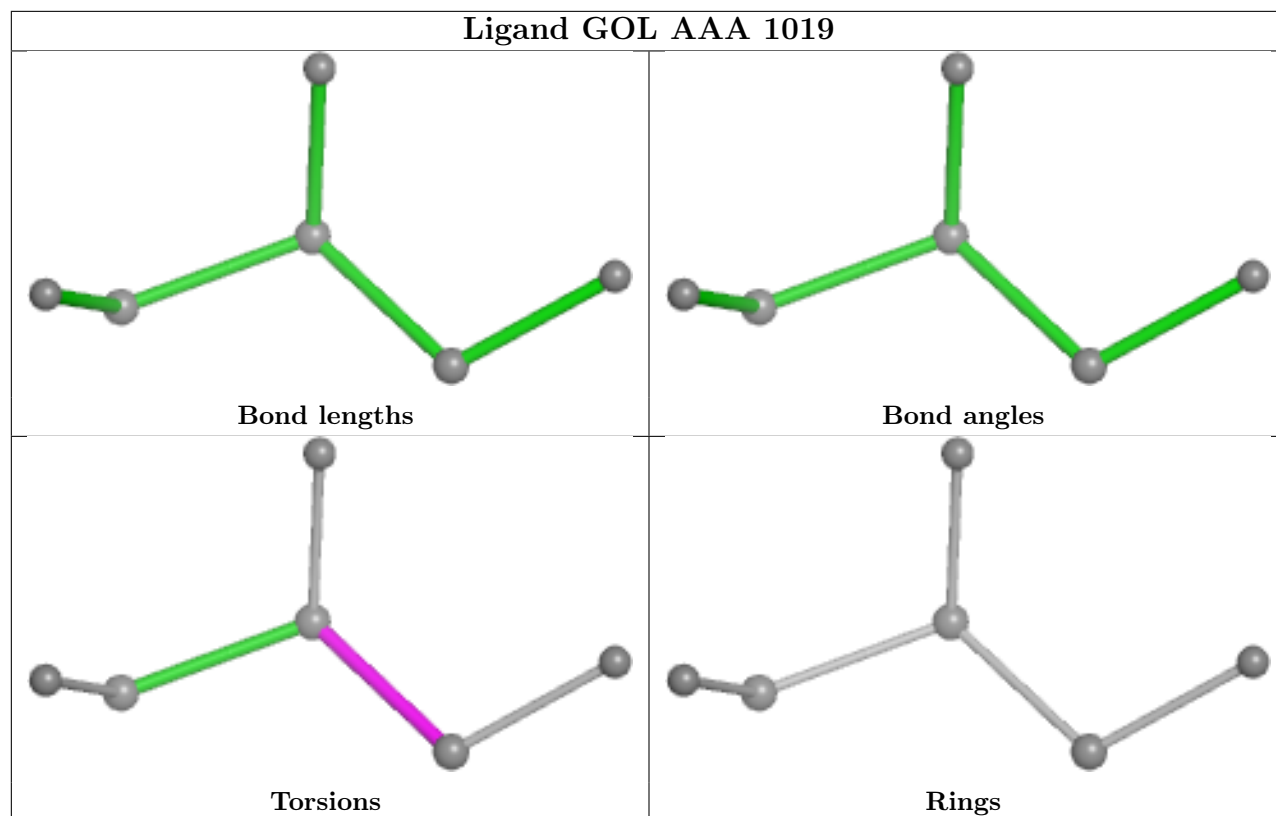
Torsions

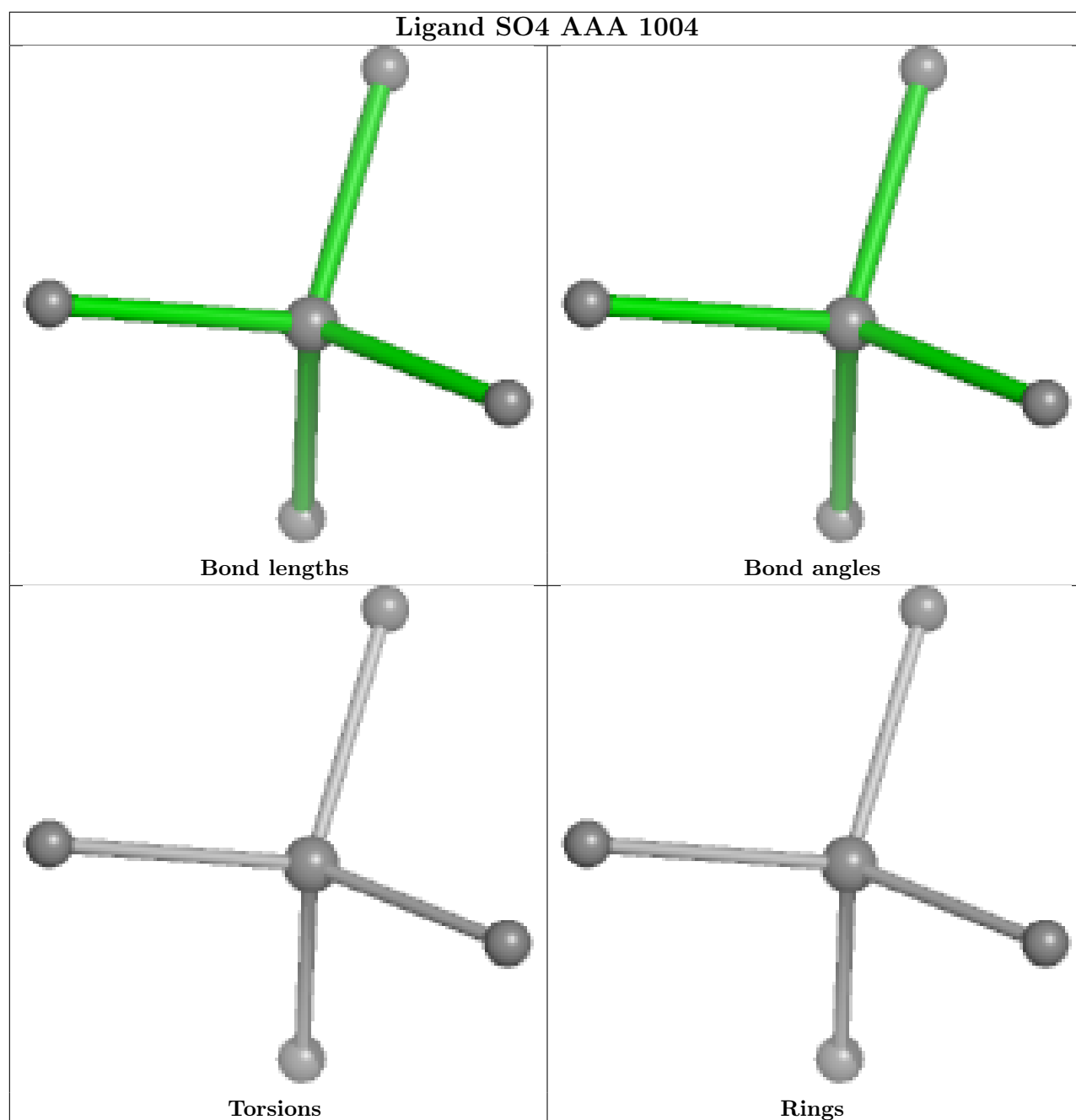


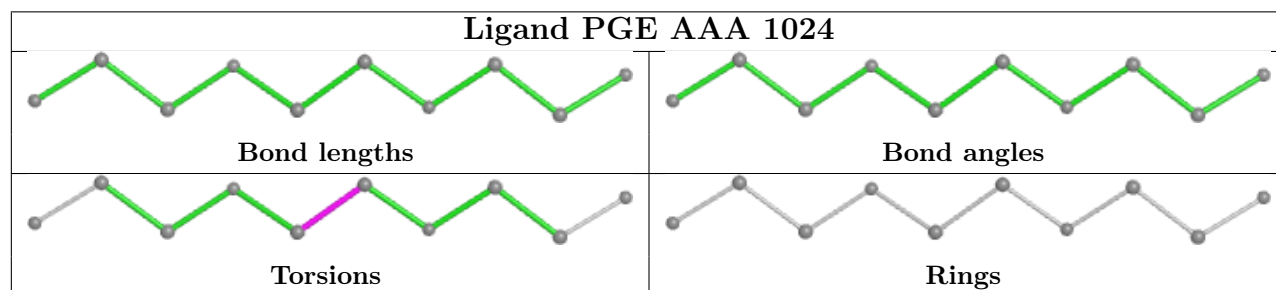
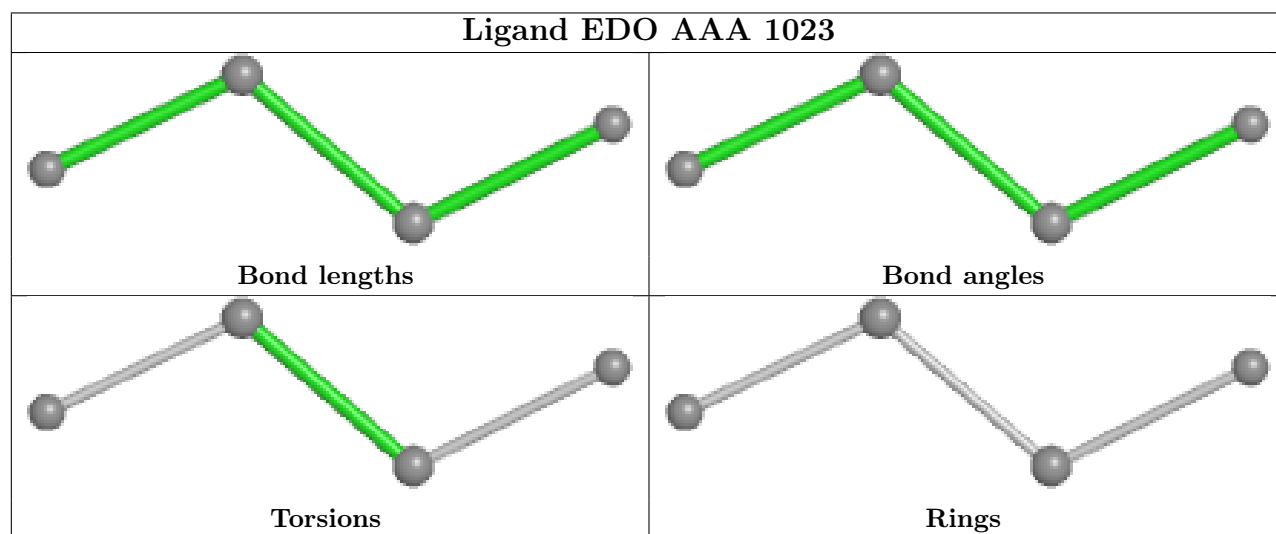
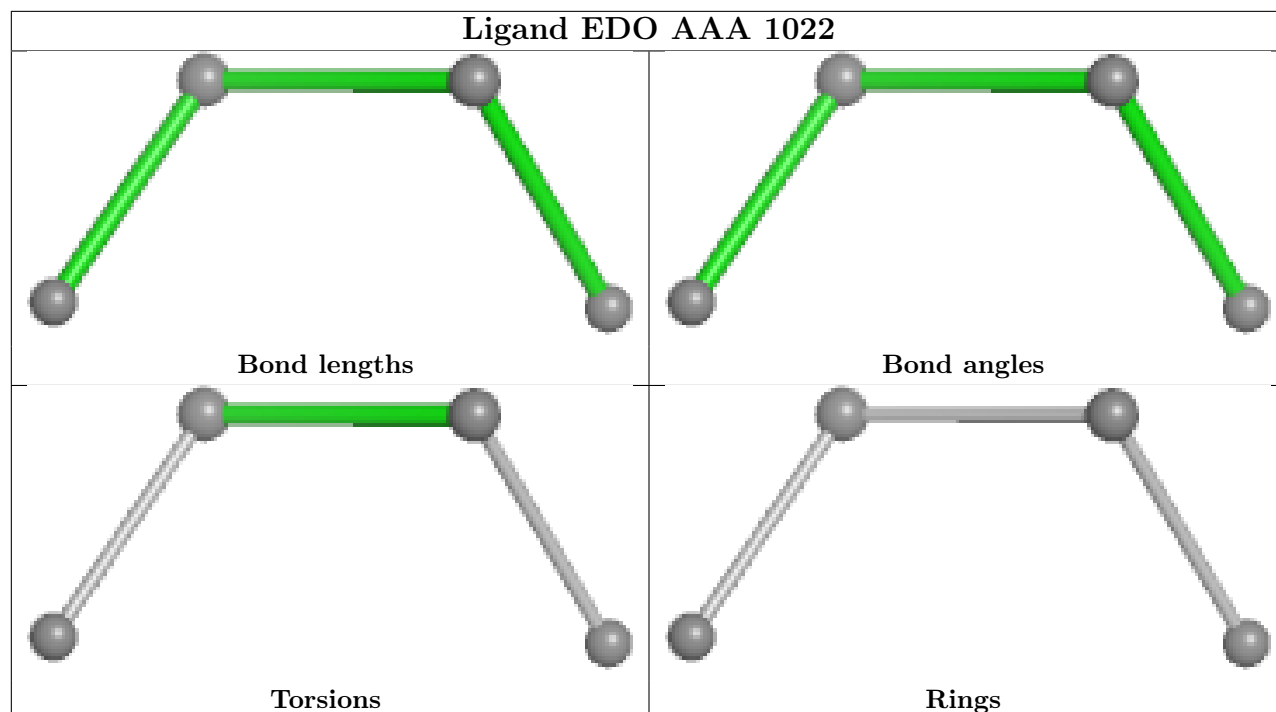
Rings

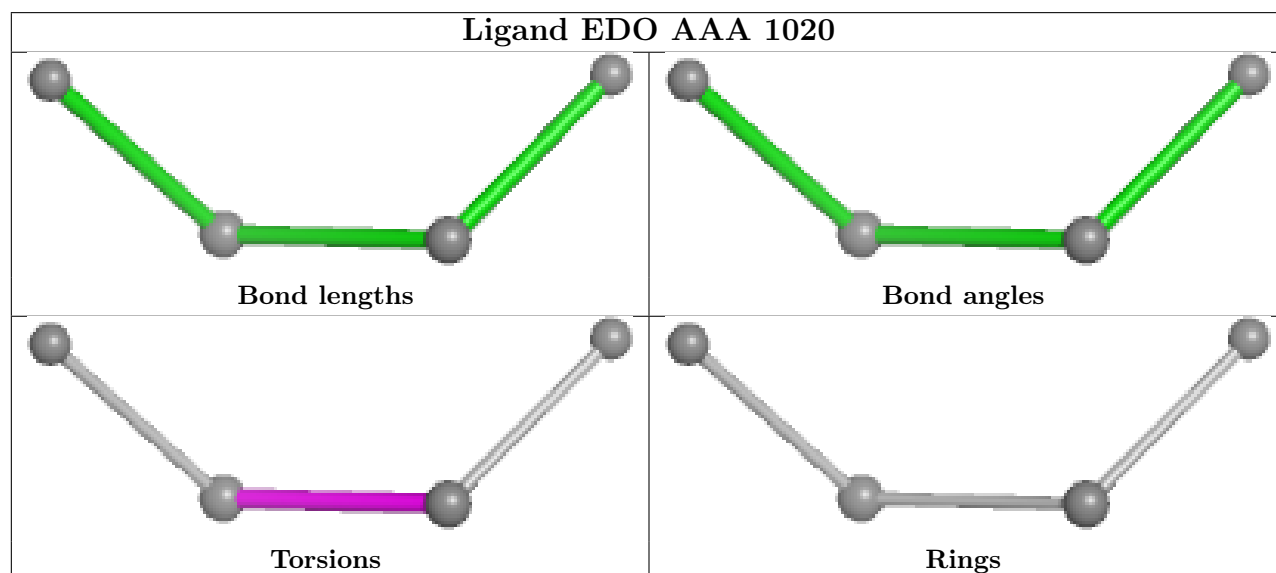
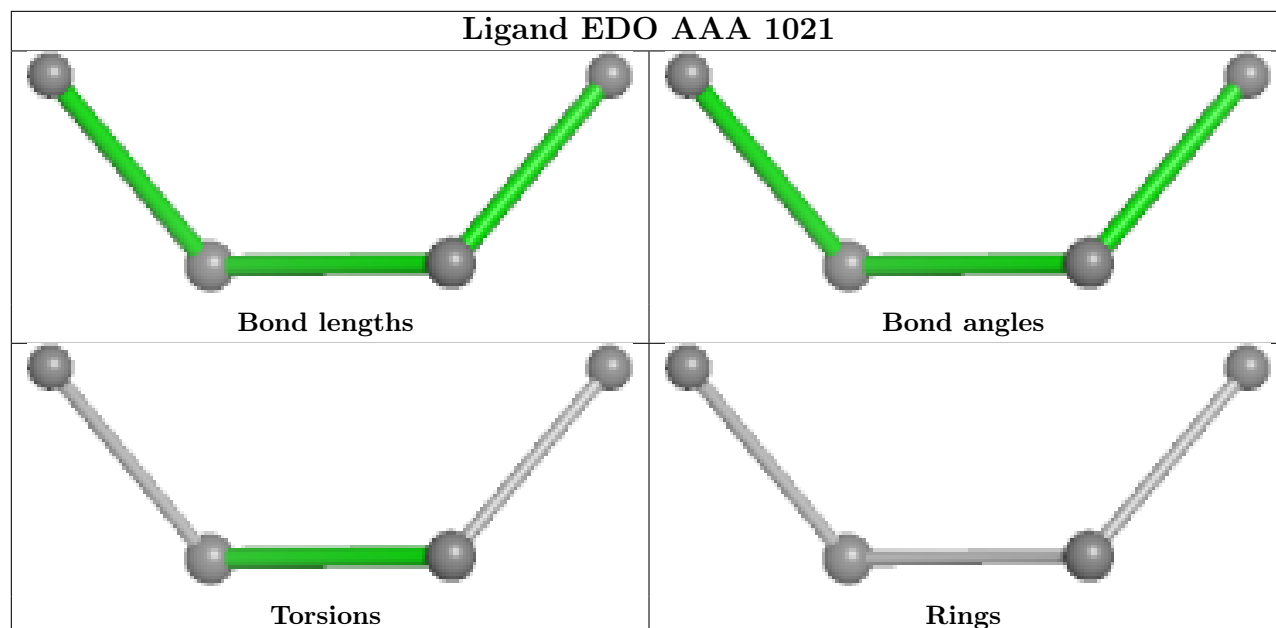


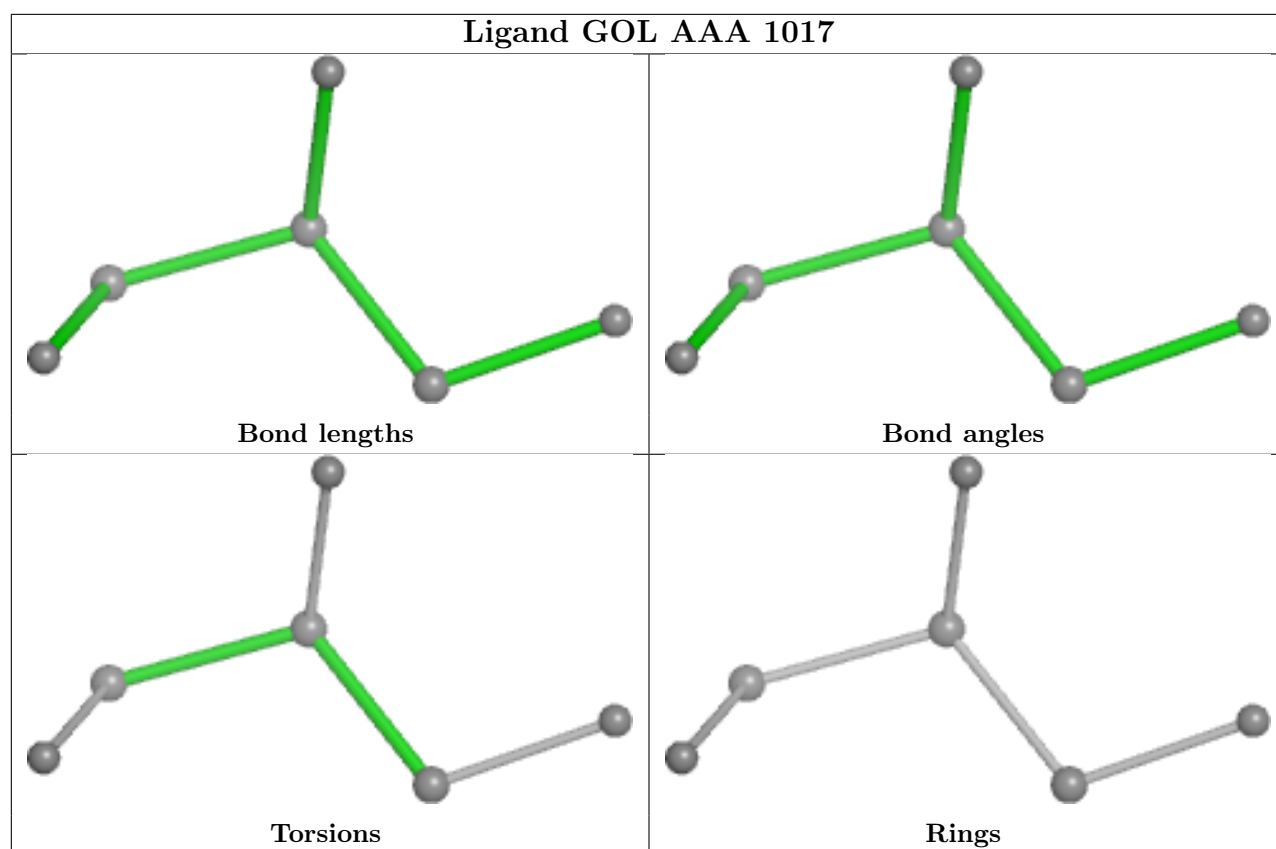


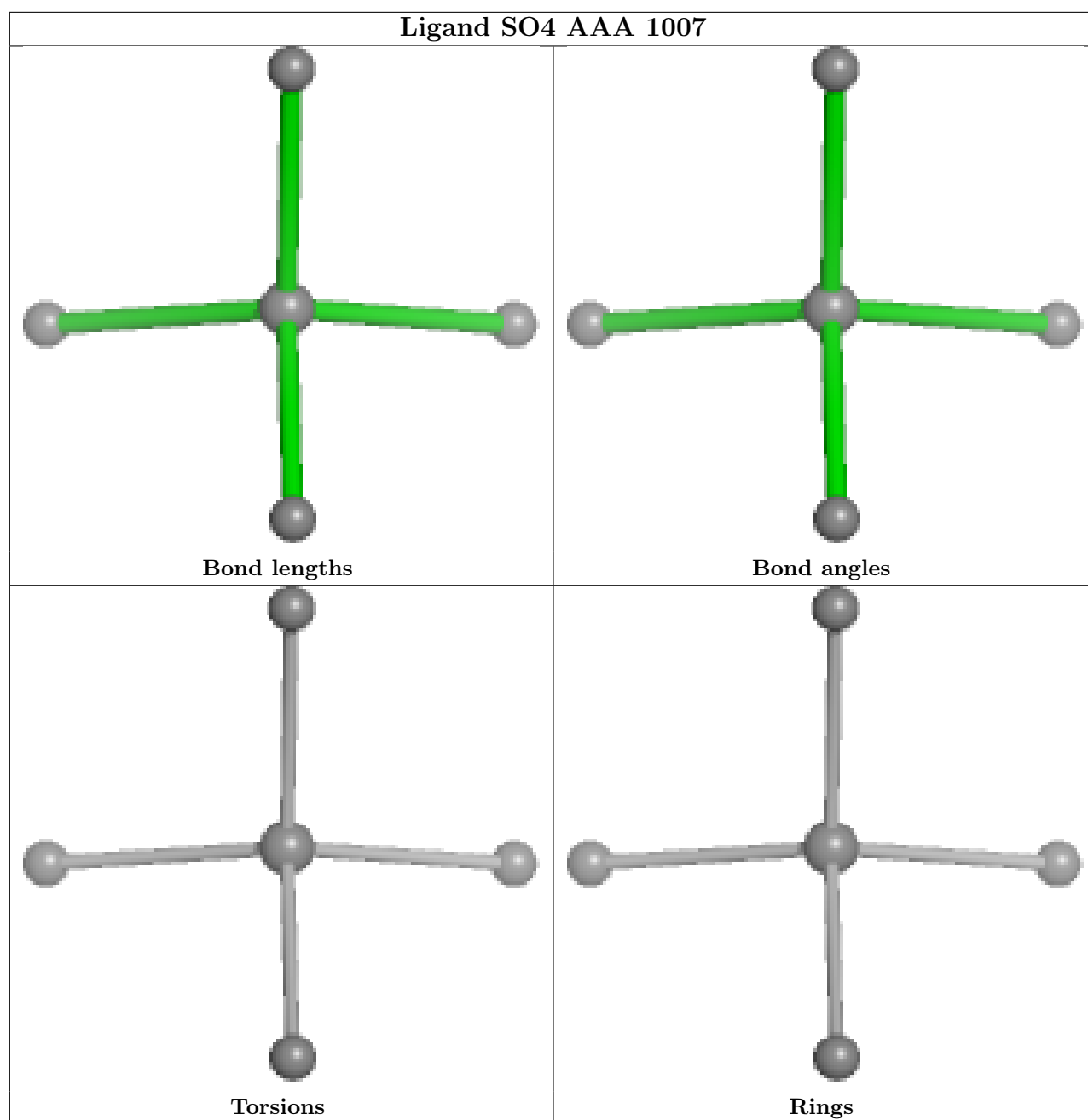












## 5.7 Other polymers [i](#)

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	AAA	846/872 (97%)	-0.02	26 (3%)	49 43	19, 27, 46, 80	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	205	PRO	4.6
1	AAA	952	CYS	4.0
1	AAA	914	GLN	3.6
1	AAA	912	ALA	3.6
1	AAA	83	ASP	3.4
1	AAA	81	GLN	3.2
1	AAA	911	THR	3.2
1	AAA	197	THR	3.1
1	AAA	291	LEU	2.9
1	AAA	422	ARG	2.7
1	AAA	535	ASN	2.5
1	AAA	910	ALA	2.5
1	AAA	204	ALA	2.5
1	AAA	869	GLU	2.5
1	AAA	931	ASP	2.4
1	AAA	781	GLU	2.4
1	AAA	196	GLU	2.4
1	AAA	913	PRO	2.3
1	AAA	801	GLU	2.3
1	AAA	915	GLN	2.2
1	AAA	577	LEU	2.2
1	AAA	930	PRO	2.2
1	AAA	925	ASN	2.2
1	AAA	82	CYS	2.2
1	AAA	642	VAL	2.1
1	AAA	881	ARG	2.1

## 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CSO	AAA	938	7/8	0.95	0.09	31,34,45,60	0

## 6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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.

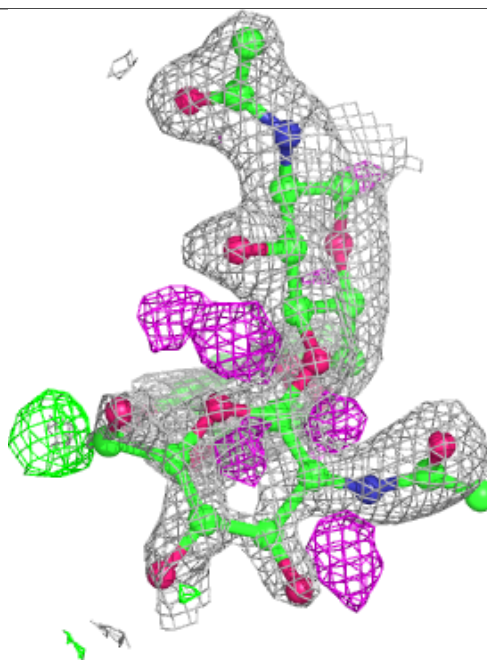
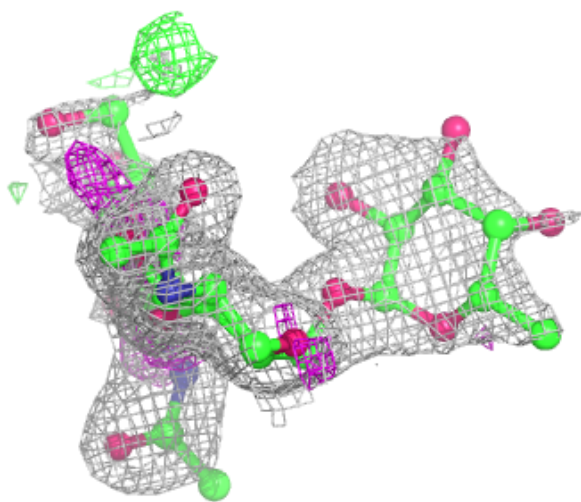
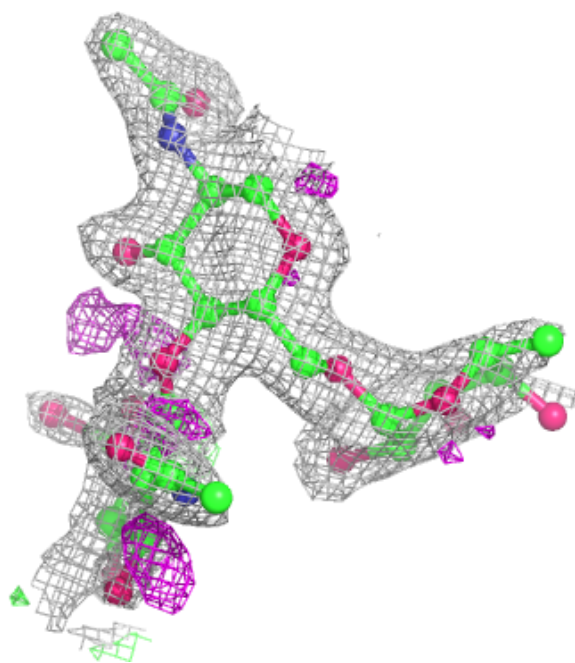
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	BcB	2	14/15	0.76	0.36	51,58,74,79	0
2	NAG	BBB	2	14/15	0.79	0.46	54,67,88,90	0
4	BMA	BfB	3	11/12	0.79	0.26	52,72,82,93	0
5	NAG	BiB	1	14/15	0.81	0.23	37,52,58,62	0
5	FUC	BiB	2	10/11	0.85	0.48	69,81,89,94	0
2	FUC	BBB	3	10/11	0.88	0.37	63,70,80,87	0
3	NAG	BcB	1	14/15	0.93	0.12	24,32,40,42	0
2	NAG	BBB	1	14/15	0.94	0.27	34,40,51,53	0
4	NAG	BfB	2	14/15	0.95	0.12	29,36,50,54	0
4	NAG	BfB	1	14/15	0.96	0.08	26,30,34,39	0

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



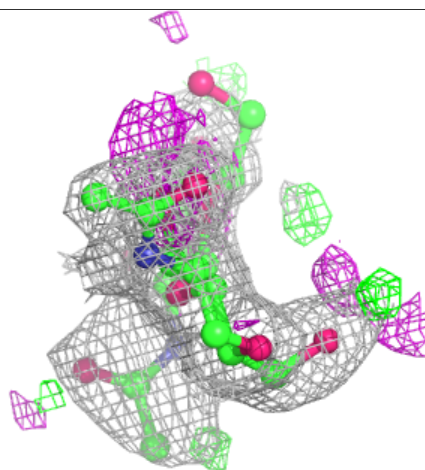
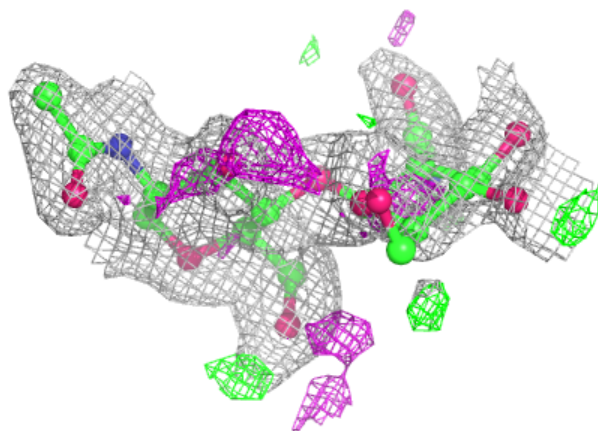
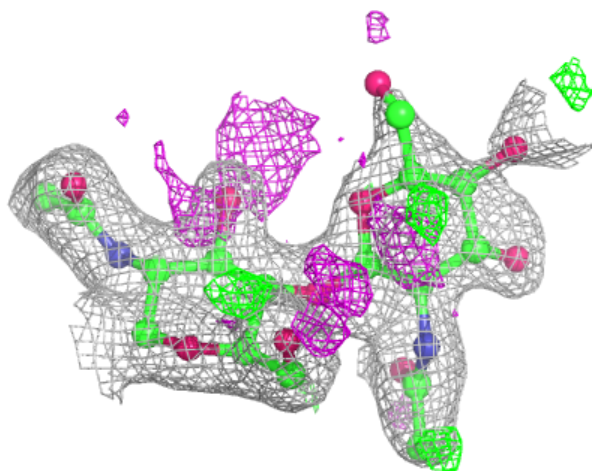
**Electron density around Chain BBB:**

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



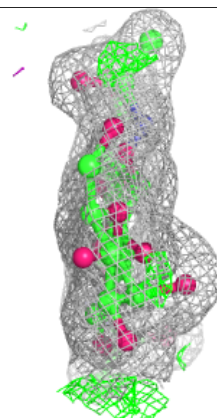
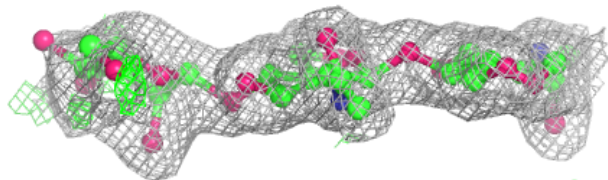
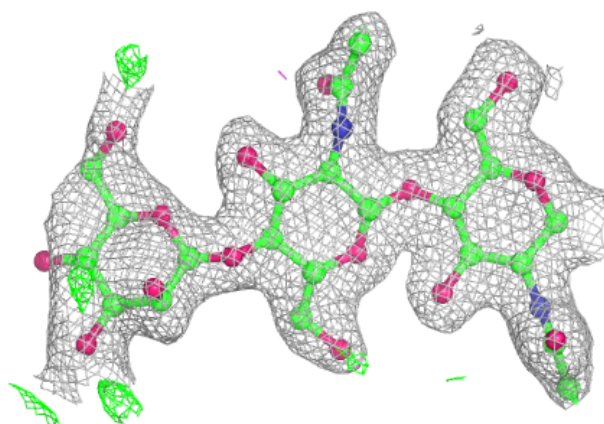
**Electron density around Chain BcB:**

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

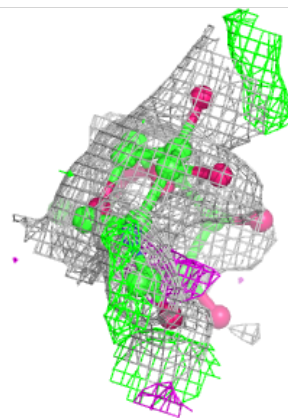
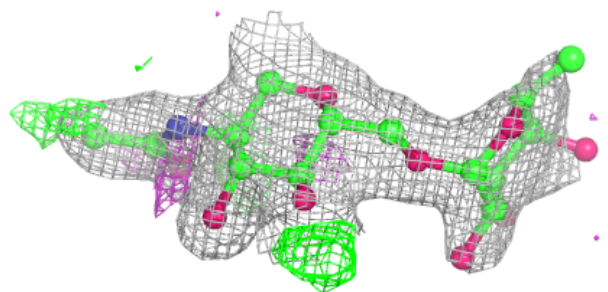
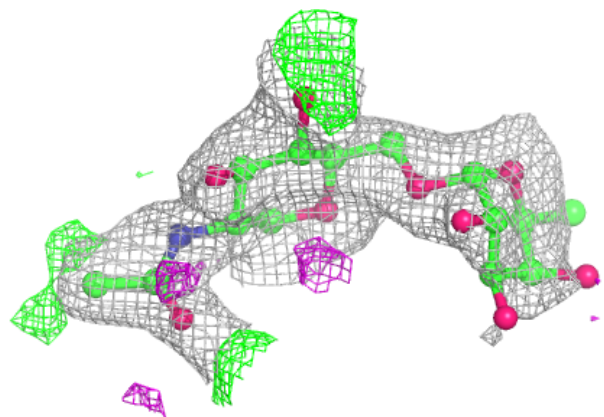


**Electron density around Chain BfB:**

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

**Electron density around Chain BiB:**

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



## 6.4 Ligands ⓘ

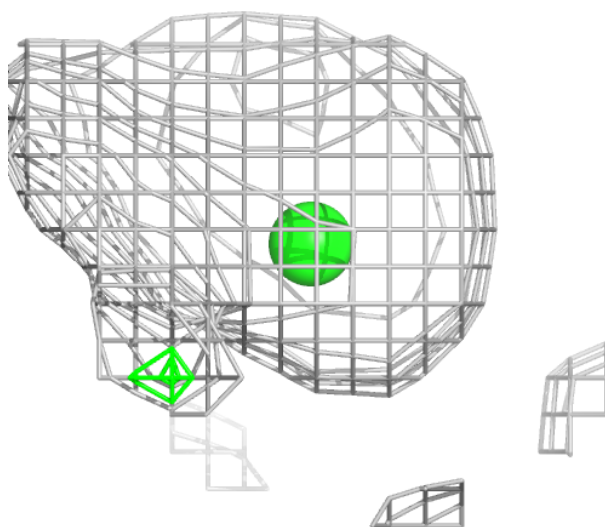
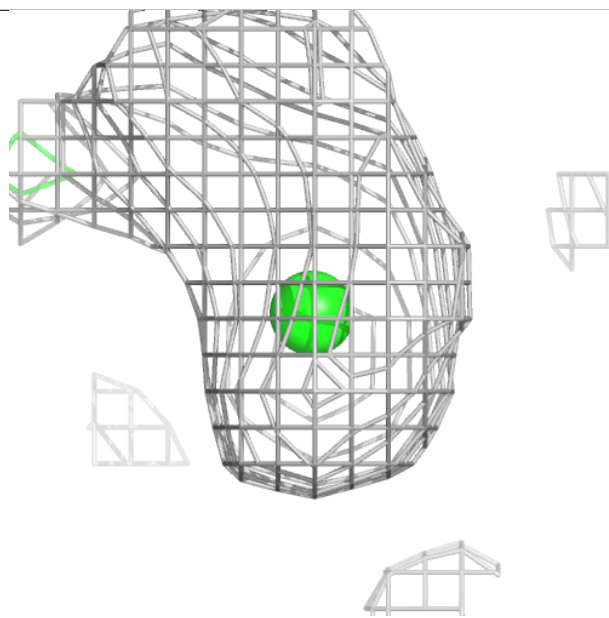
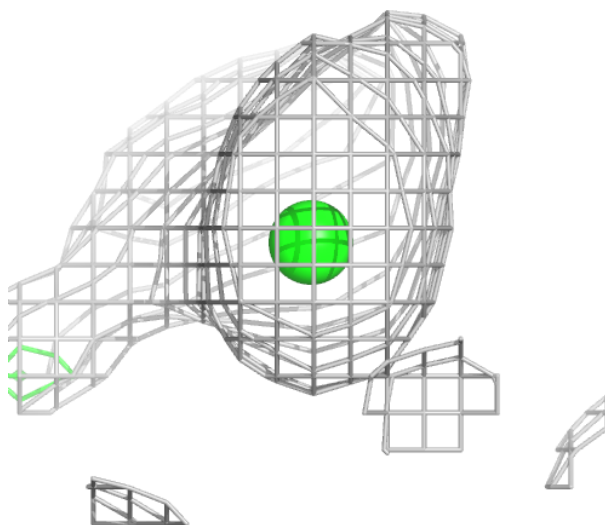
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
9	CL	AAA	1016	1/1	0.66	0.16	77,77,77,77	0
12	PGE	AAA	1024	10/10	0.70	0.20	62,67,73,74	0
9	CL	AAA	1010	1/1	0.78	0.12	71,71,71,71	0
9	CL	AAA	1008	1/1	0.86	0.12	61,61,61,61	0
9	CL	AAA	1011	1/1	0.86	0.08	63,63,63,63	0
11	EDO	AAA	1020	4/4	0.87	0.11	53,56,57,59	0
8	SO4	AAA	1004	5/5	0.88	0.20	54,65,75,80	0
10	GOL	AAA	1018	6/6	0.88	0.17	32,42,45,47	0
9	CL	AAA	1014	1/1	0.90	0.06	69,69,69,69	0
10	GOL	AAA	1019	6/6	0.91	0.15	28,31,34,34	6
9	CL	AAA	1013	1/1	0.91	0.15	74,74,74,74	0
9	CL	AAA	1012	1/1	0.91	0.09	66,66,66,66	0
8	SO4	AAA	1005	5/5	0.92	0.17	38,39,42,46	5
10	GOL	AAA	1017	6/6	0.92	0.12	32,35,38,39	0
11	EDO	AAA	1023	4/4	0.92	0.12	38,38,39,42	0
9	CL	AAA	1015	1/1	0.92	0.18	75,75,75,75	0
6	NAG	AAA	1001	14/15	0.93	0.17	31,39,51,53	0
11	EDO	AAA	1021	4/4	0.93	0.12	32,47,50,52	0
8	SO4	AAA	1006	5/5	0.94	0.20	43,47,52,64	5
9	CL	AAA	1009	1/1	0.94	0.03	68,68,68,68	0
11	EDO	AAA	1022	4/4	0.96	0.21	40,43,50,56	0
7	56I	AAA	1002	16/16	0.96	0.09	20,22,31,32	0
8	SO4	AAA	1007	5/5	0.96	0.09	25,28,35,39	5
8	SO4	AAA	1003	5/5	0.99	0.14	39,40,41,44	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 CL AAA 1016:**

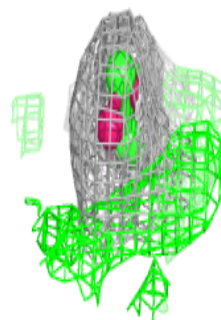
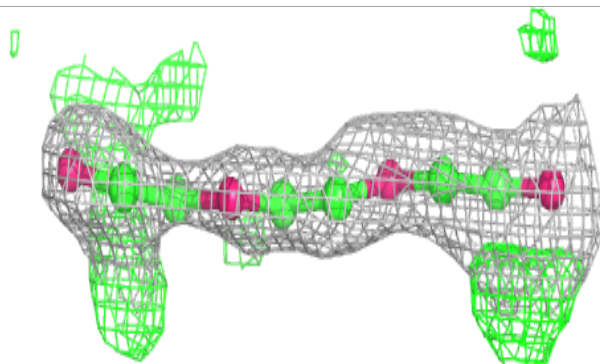
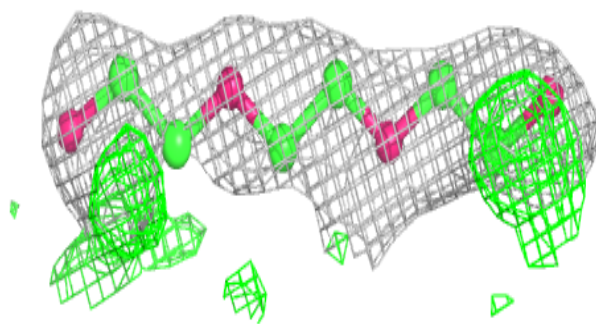
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





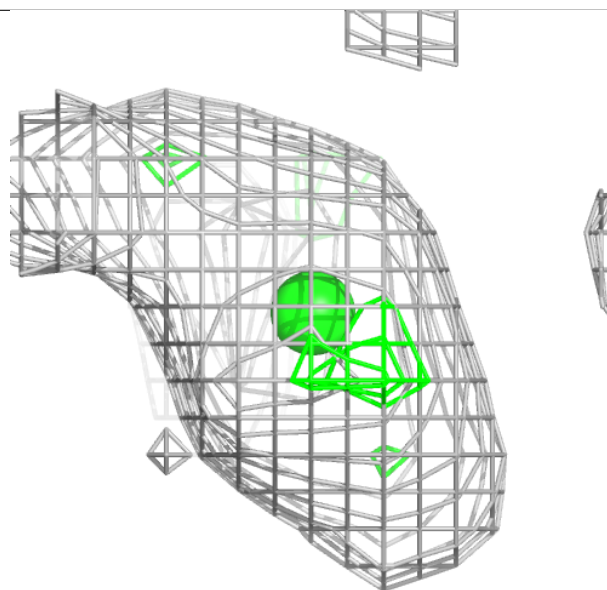
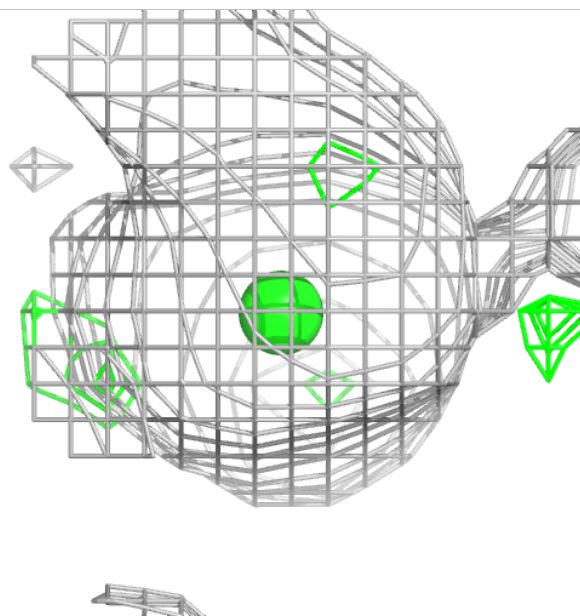
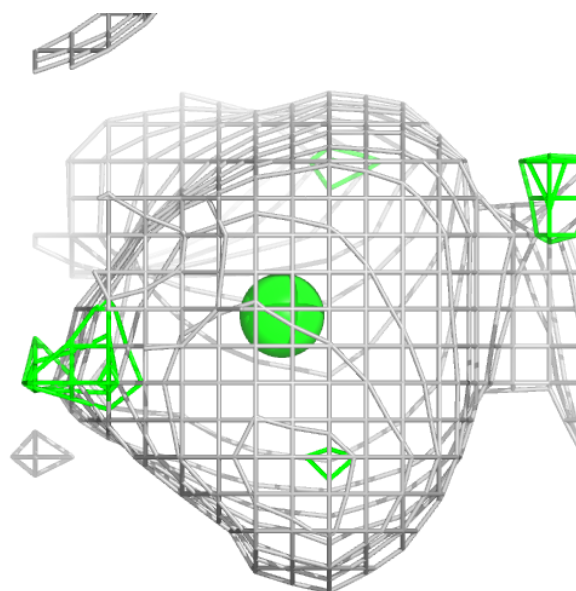
**Electron density around PGE AAA 1024:**

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



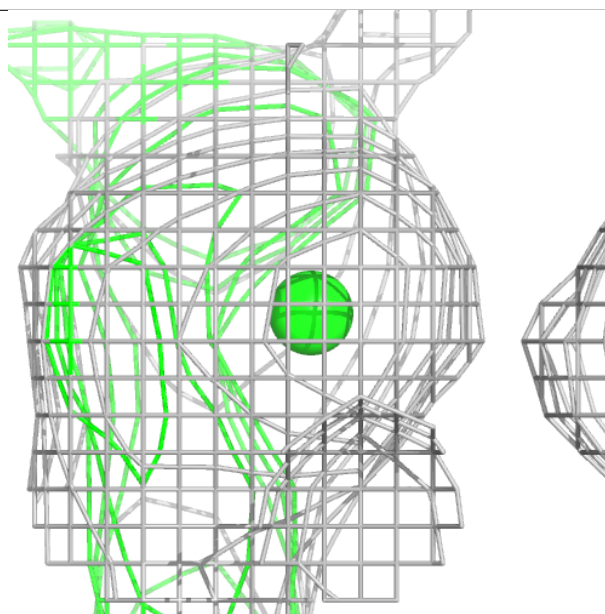
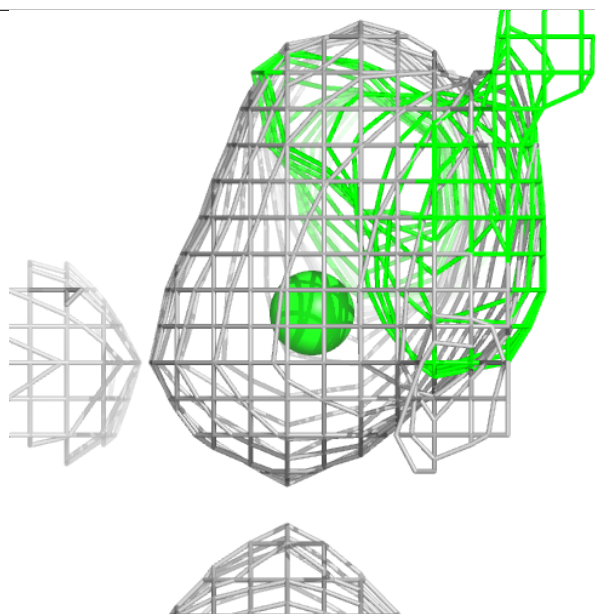
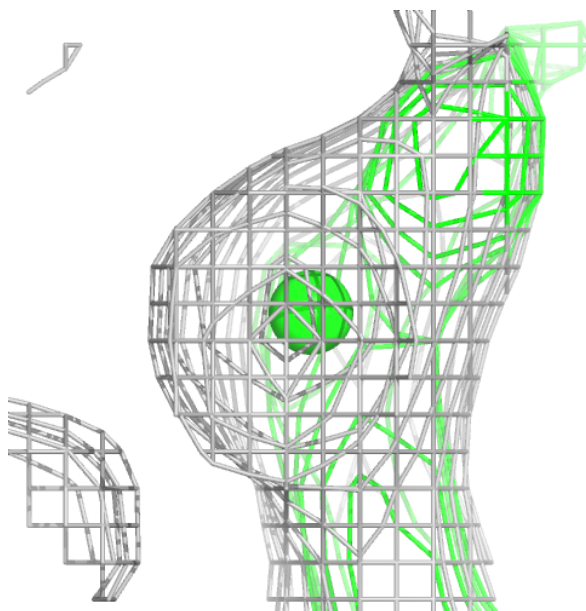
**Electron density around CL AAA 1010:**

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



**Electron density around CL AAA 1008:**

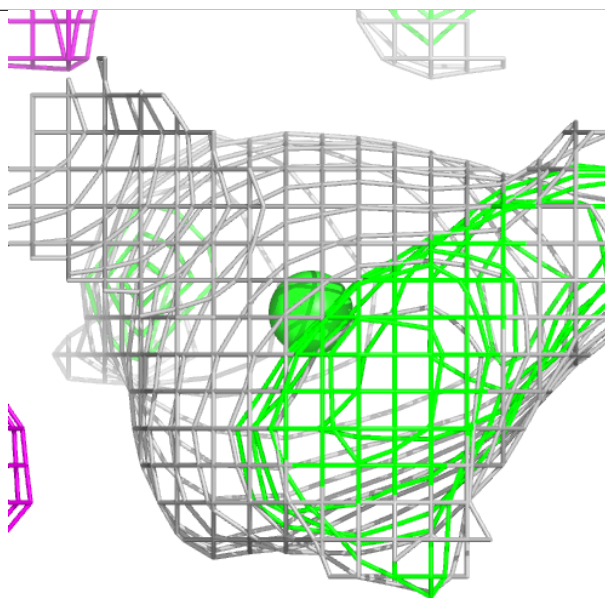
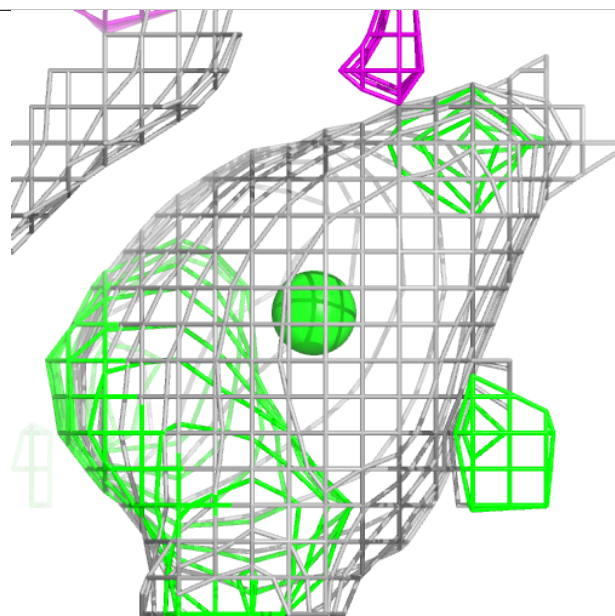
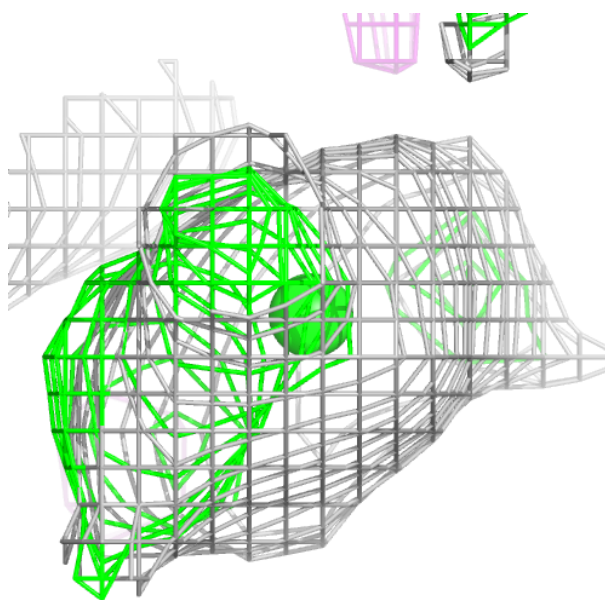
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





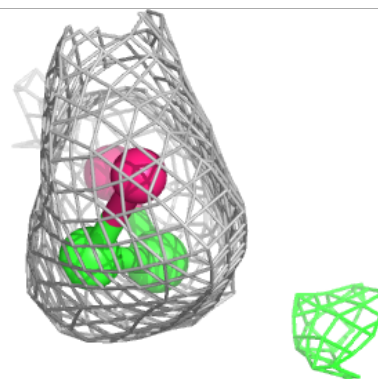
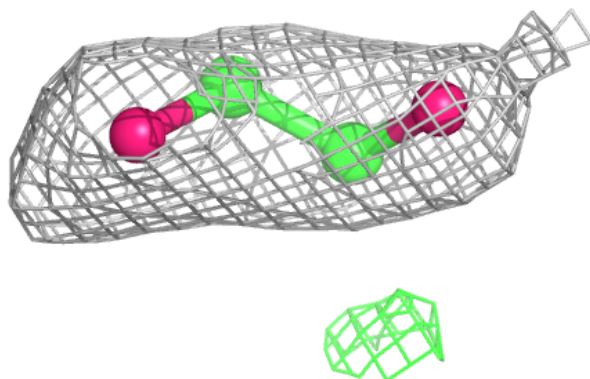
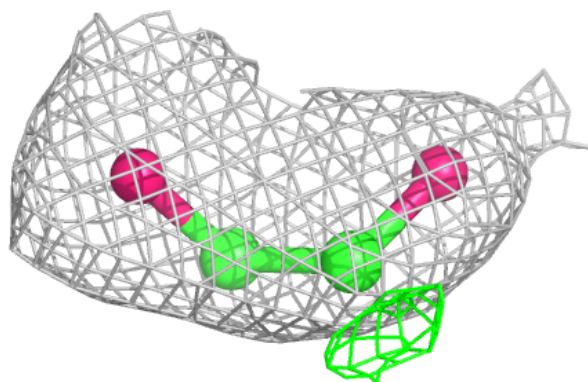
**Electron density around CL AAA 1011:**

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



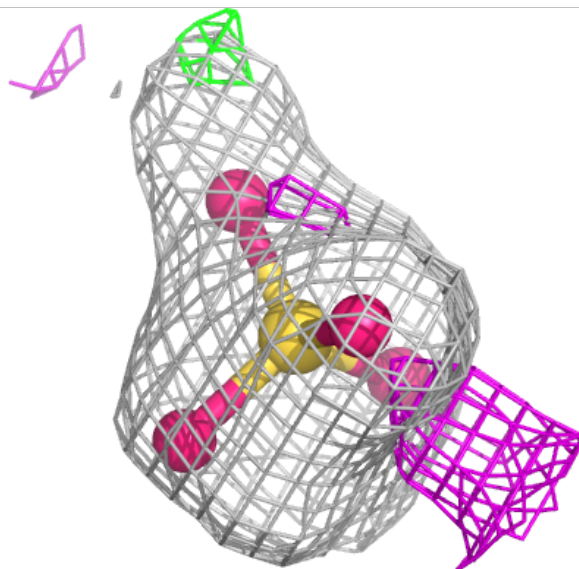
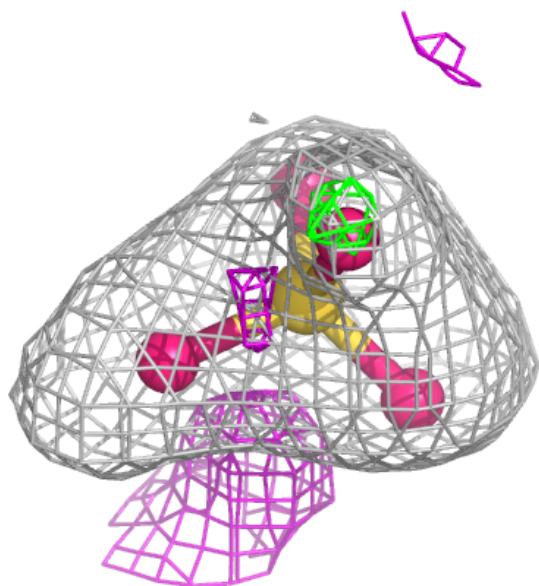
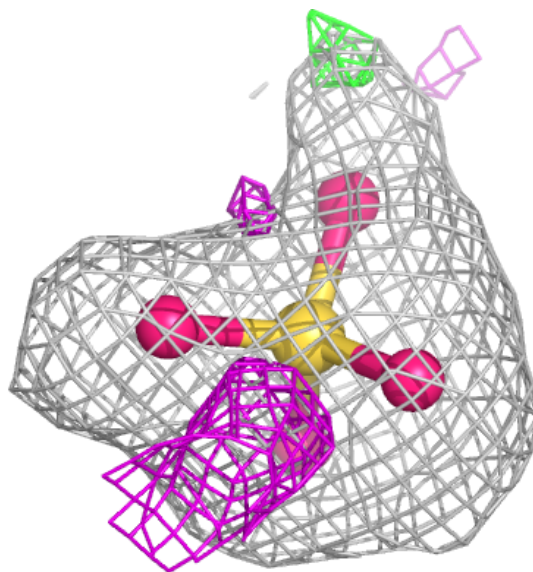
**Electron density around EDO AAA 1020:**

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



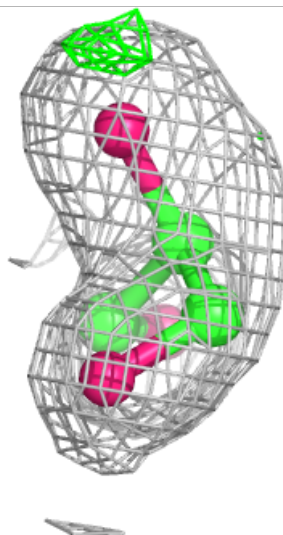
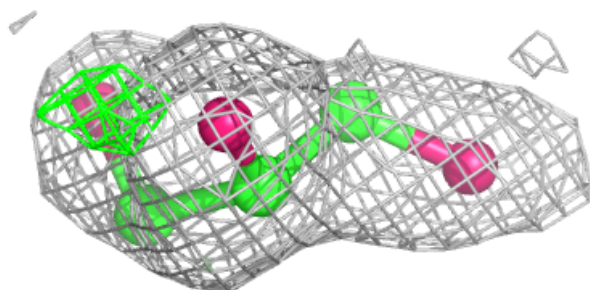
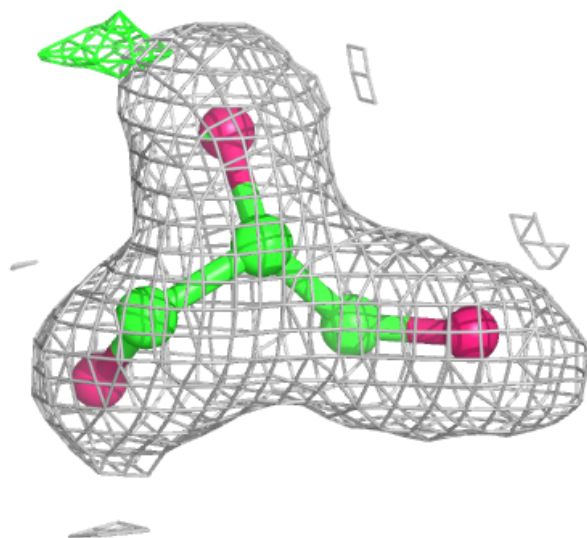
**Electron density around SO4 AAA 1004:**

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



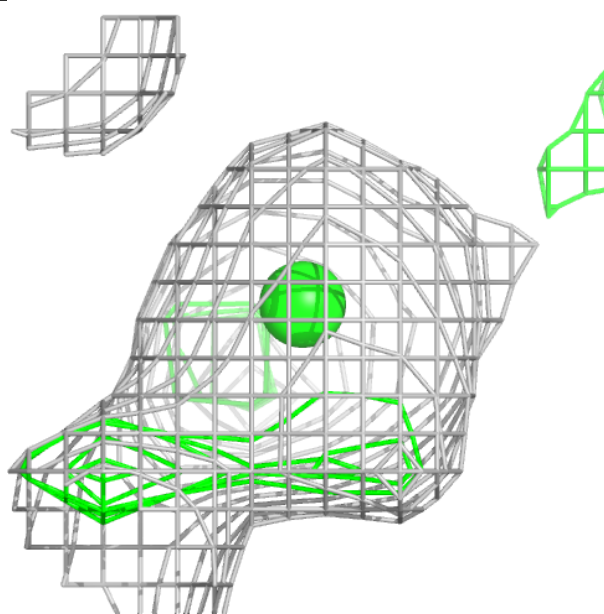
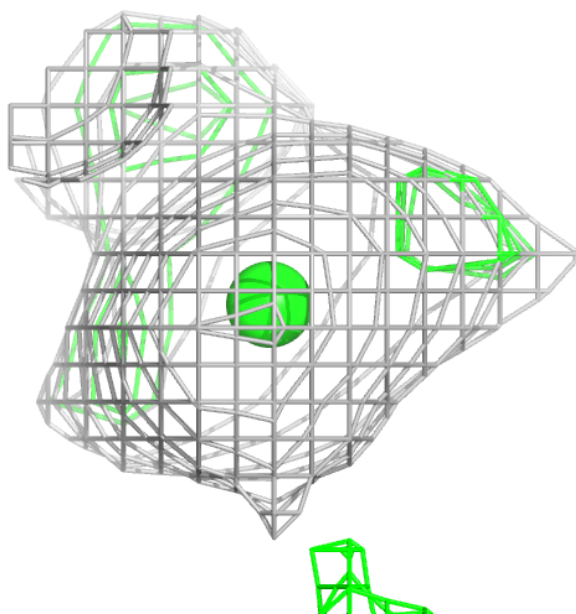
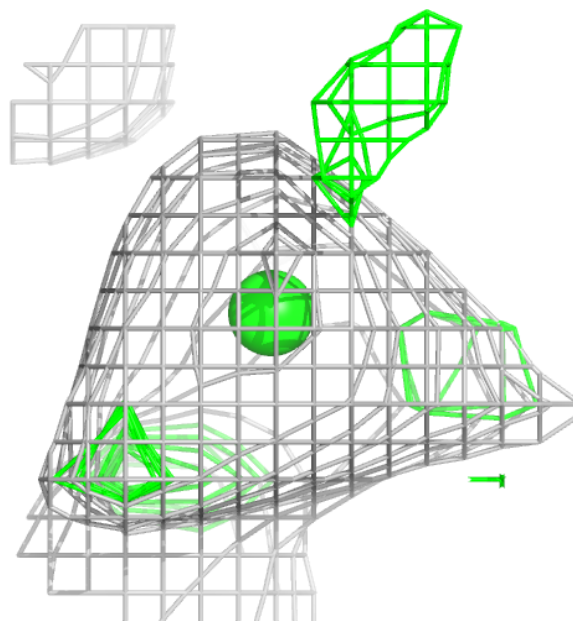
**Electron density around GOL AAA 1018:**

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



**Electron density around CL AAA 1014:**

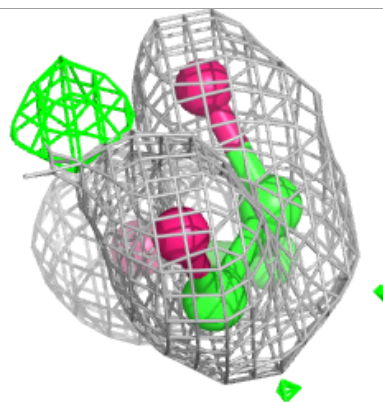
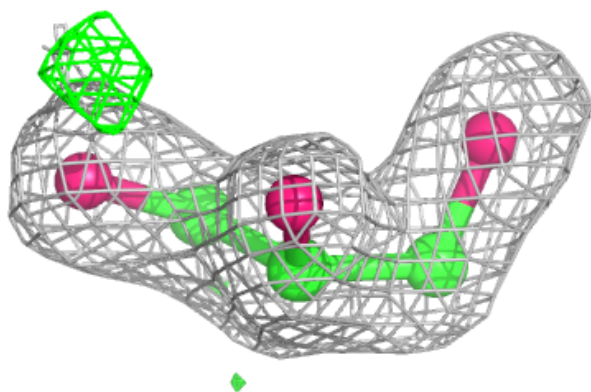
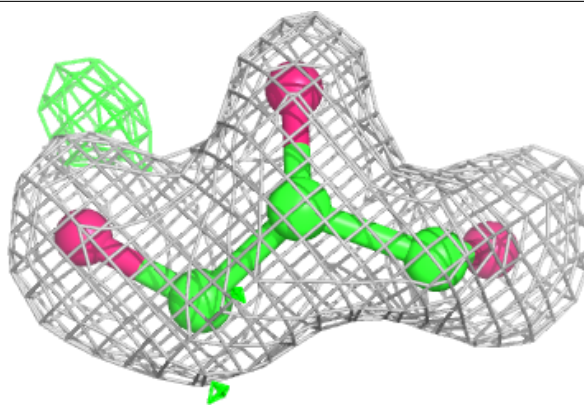
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





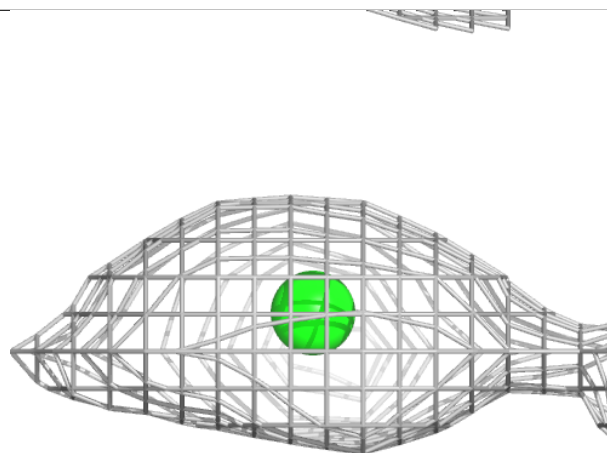
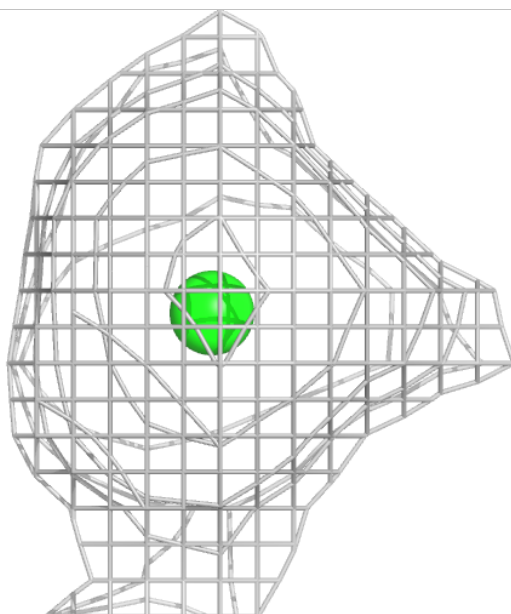
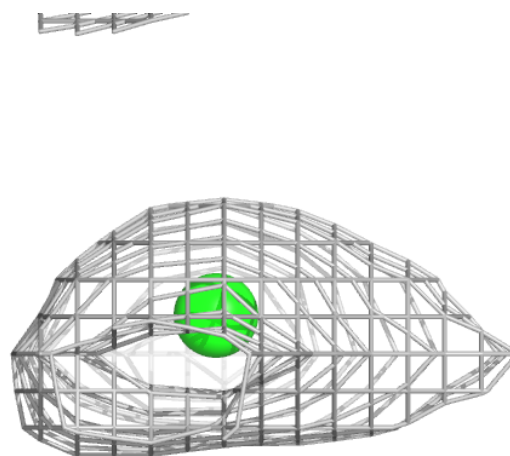
**Electron density around GOL AAA 1019:**

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



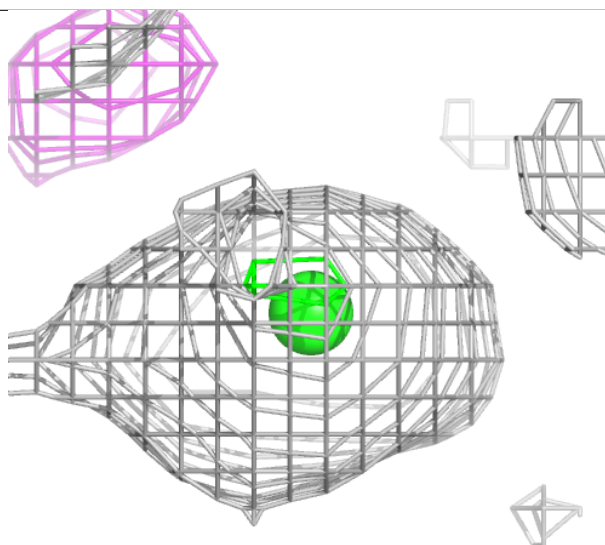
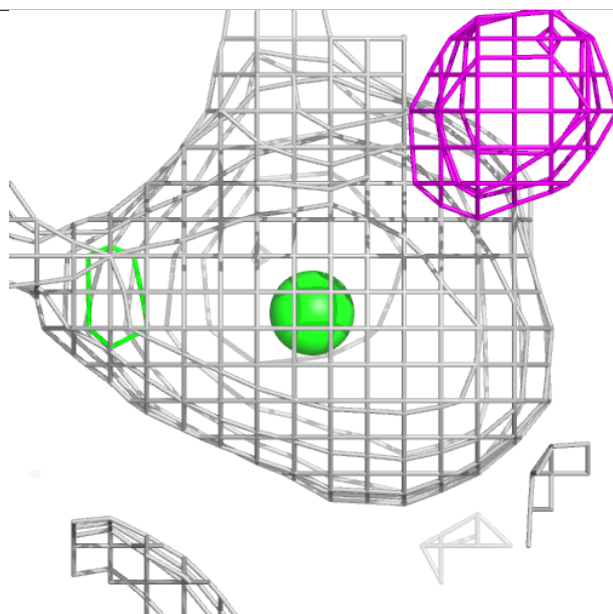
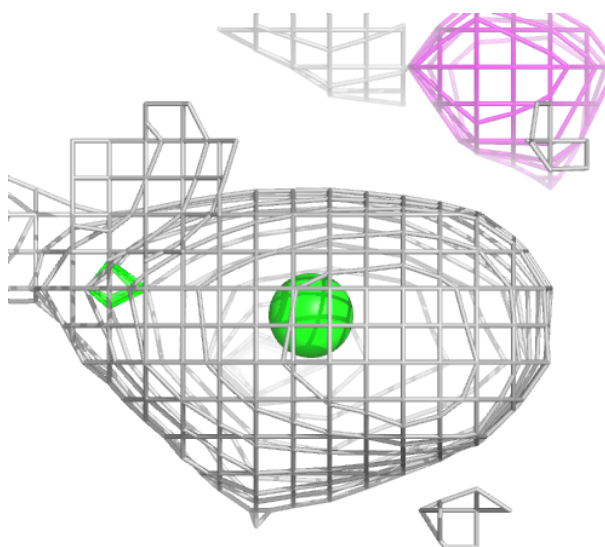
**Electron density around CL AAA 1013:**

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



**Electron density around CL AAA 1012:**

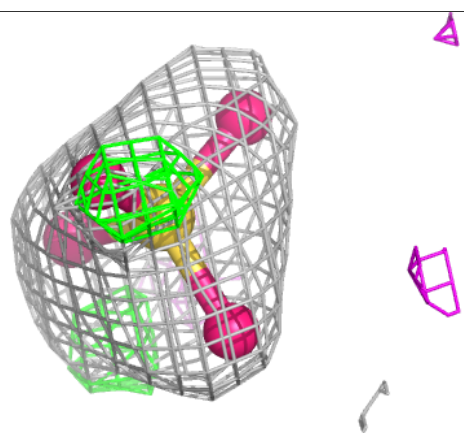
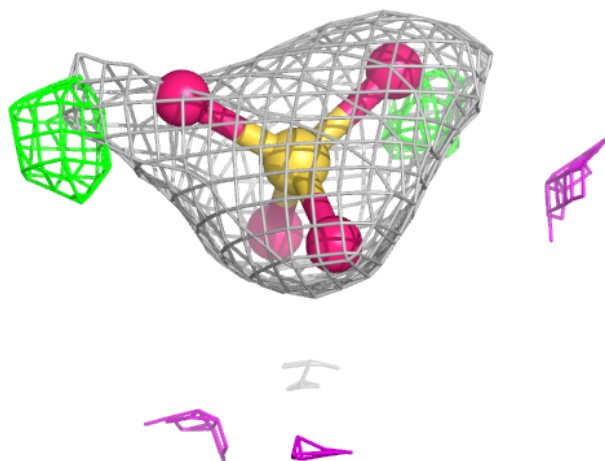
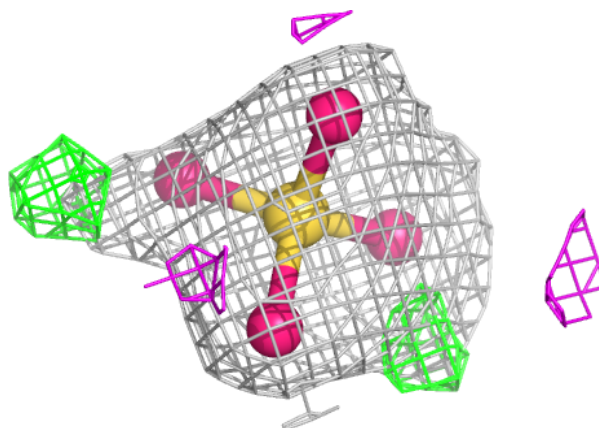
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





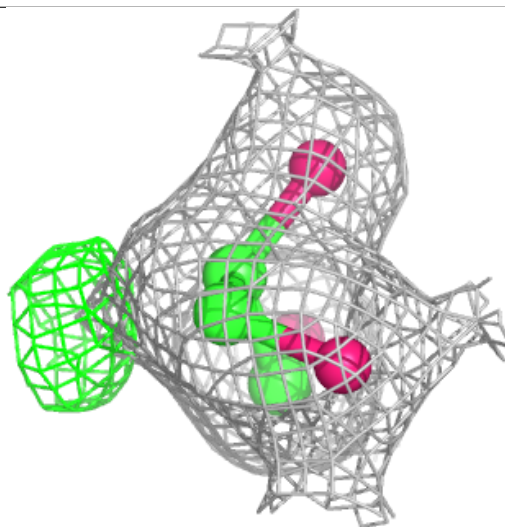
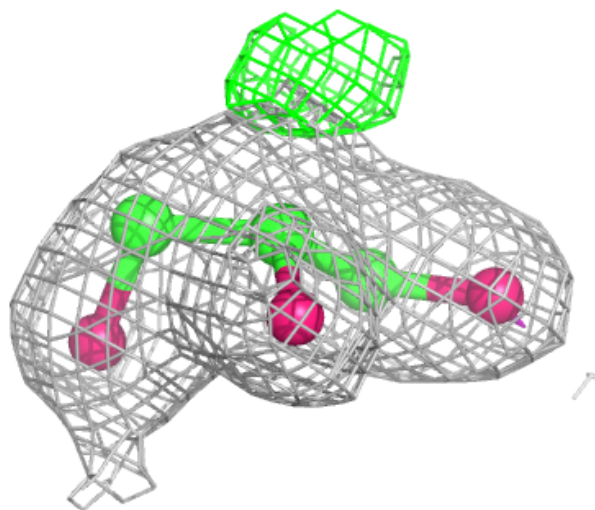
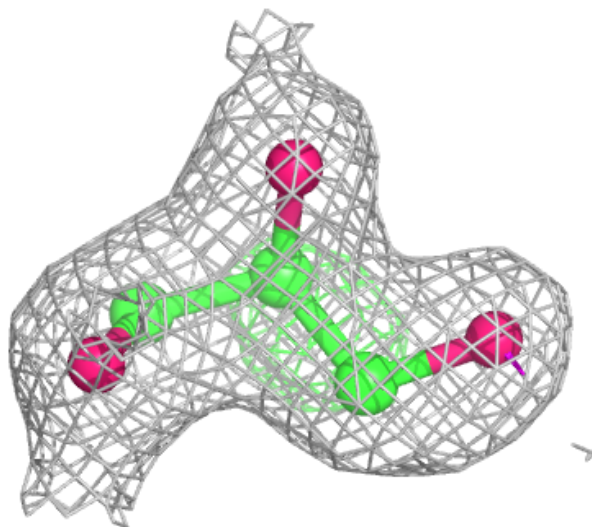
**Electron density around SO4 AAA 1005:**

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



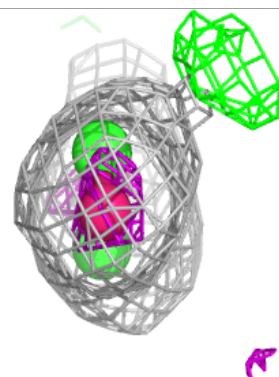
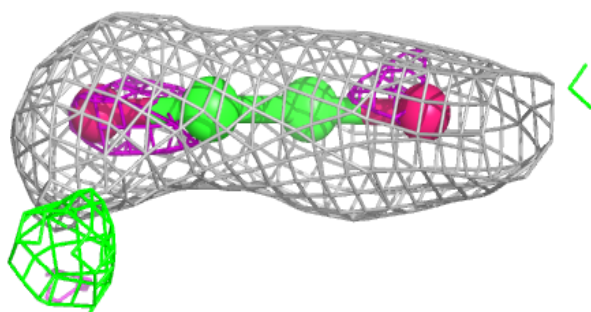
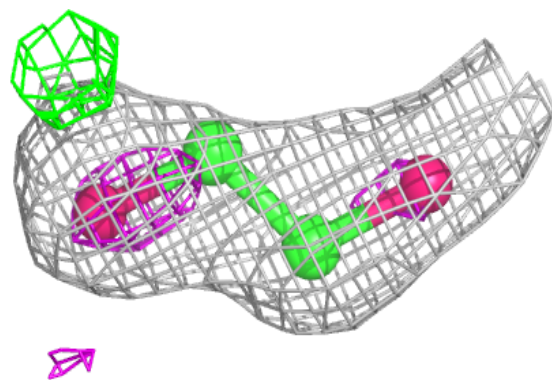
**Electron density around GOL AAA 1017:**

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



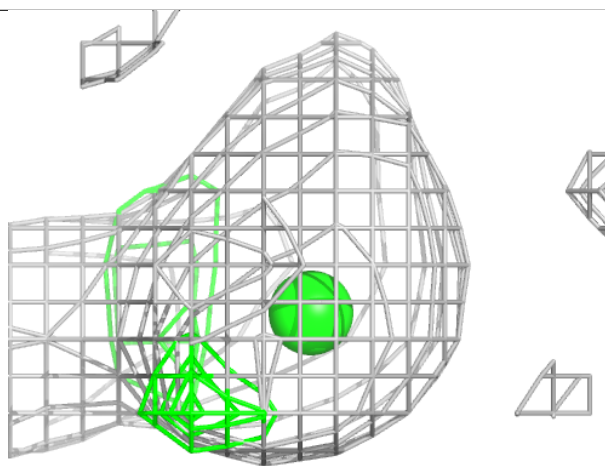
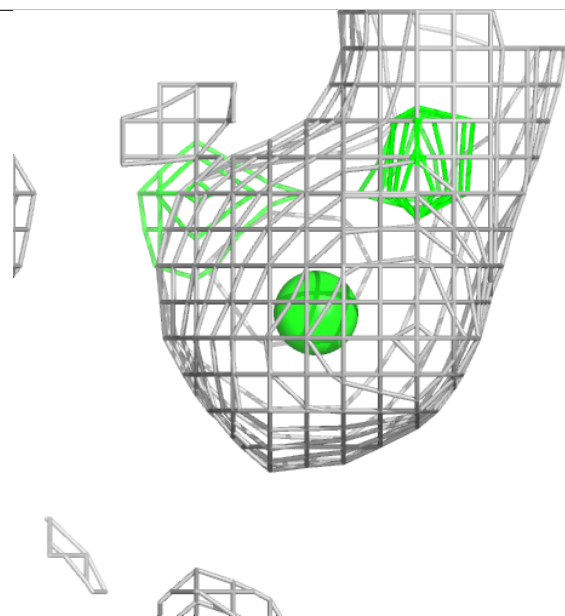
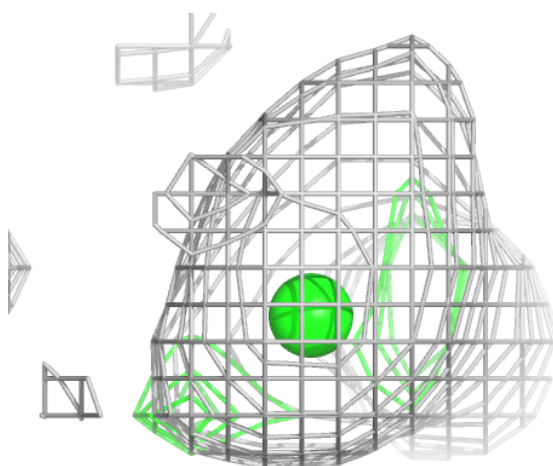
**Electron density around EDO AAA 1023:**

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



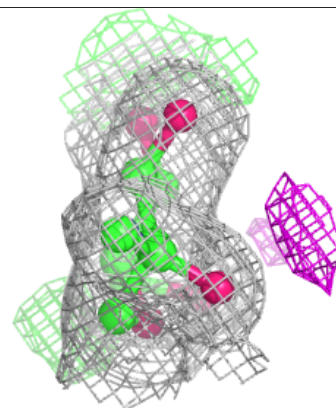
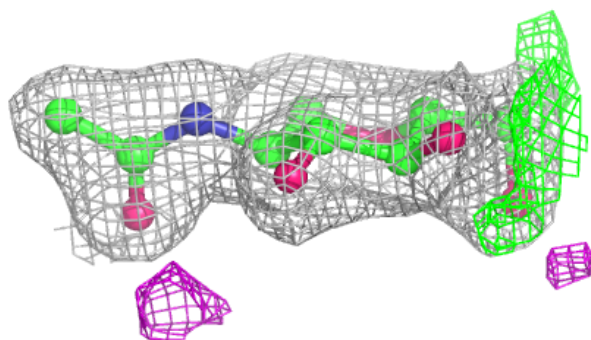
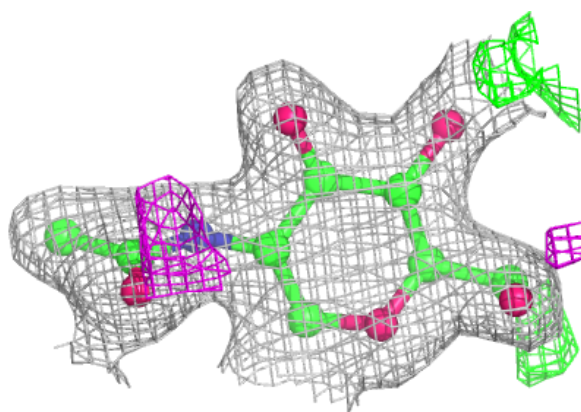
**Electron density around CL AAA 1015:**

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



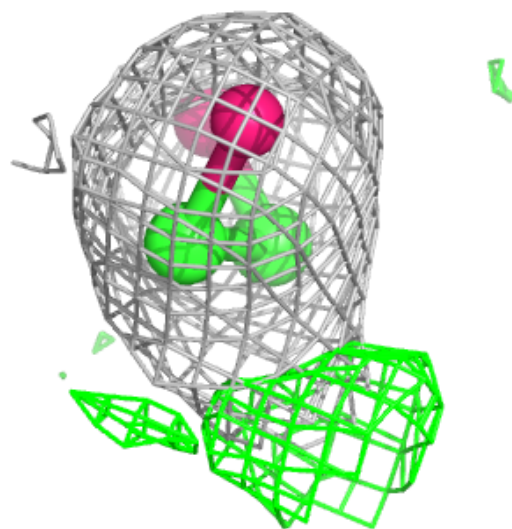
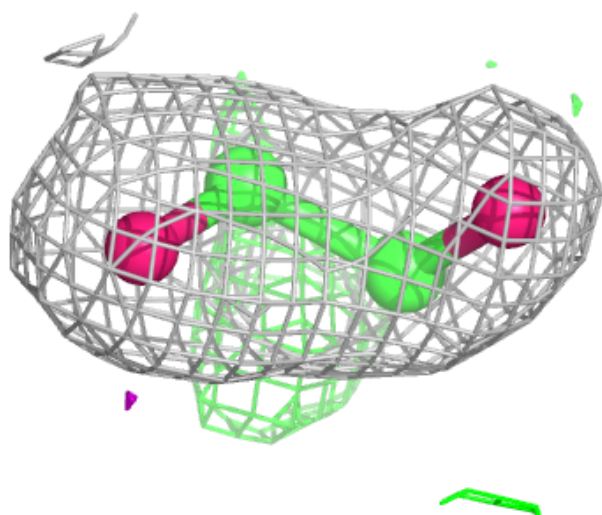
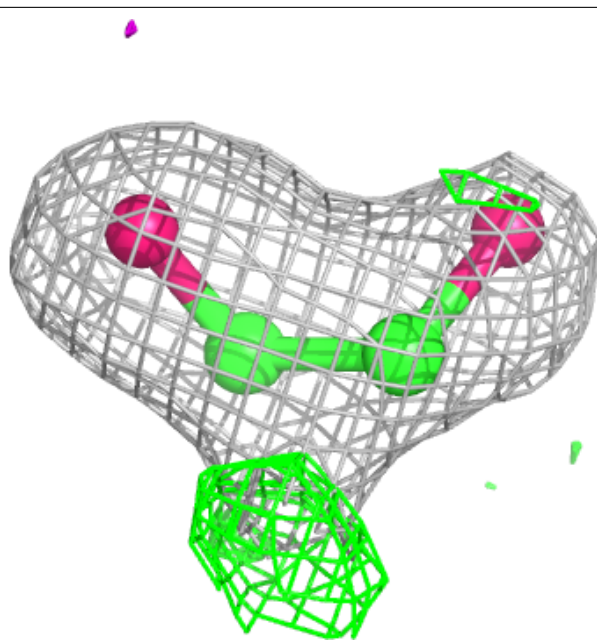
**Electron density around NAG AAA 1001:**

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



**Electron density around EDO AAA 1021:**

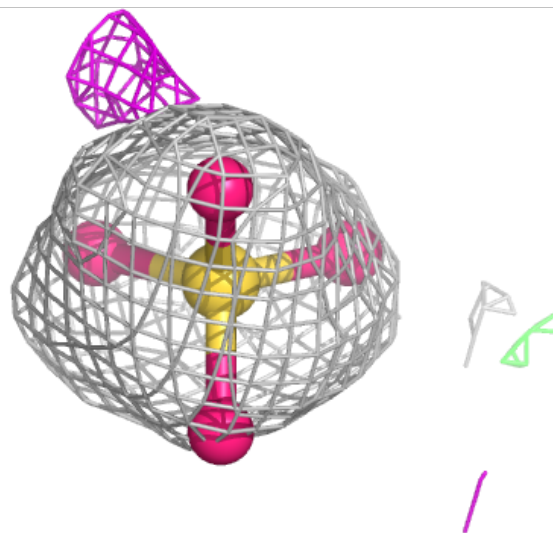
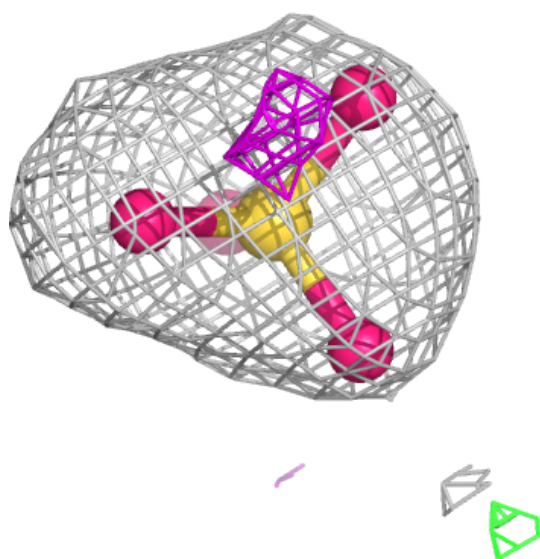
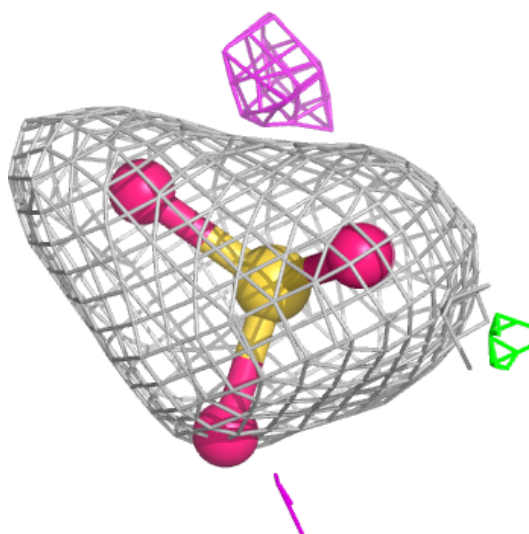
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





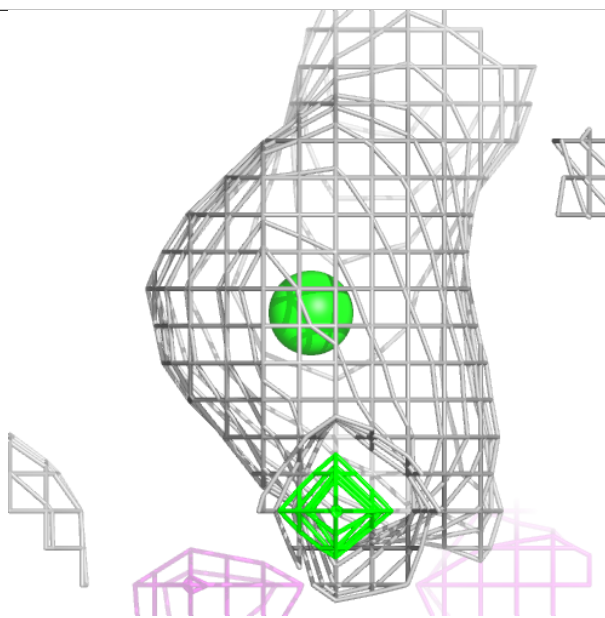
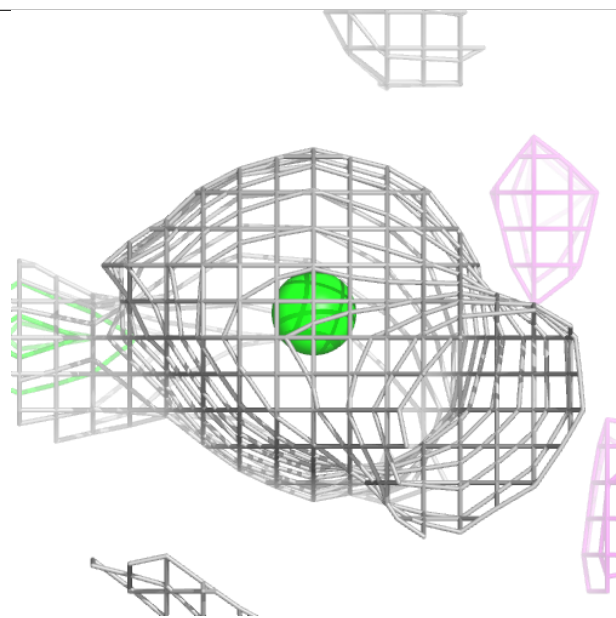
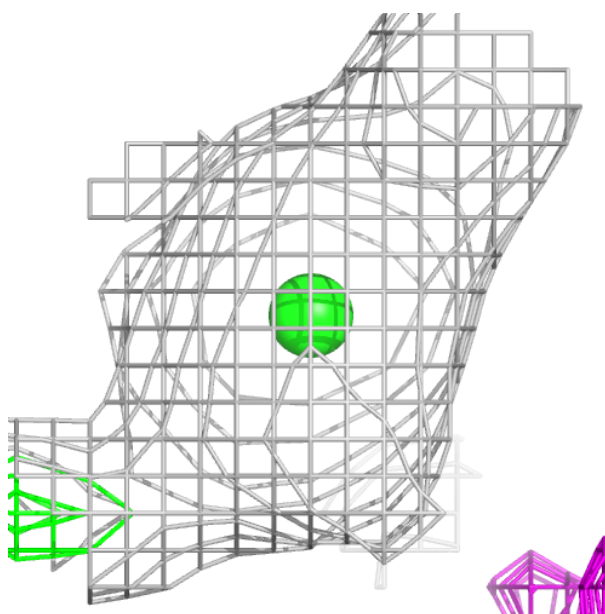
**Electron density around SO4 AAA 1006:**

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



**Electron density around CL AAA 1009:**

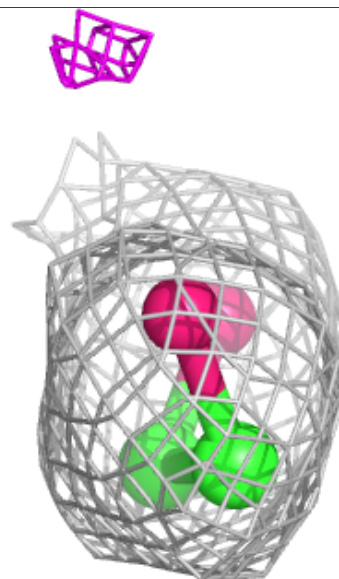
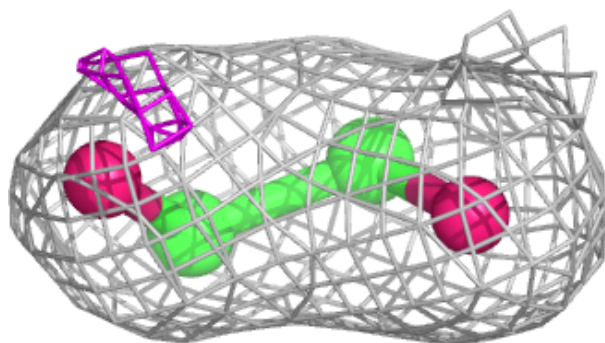
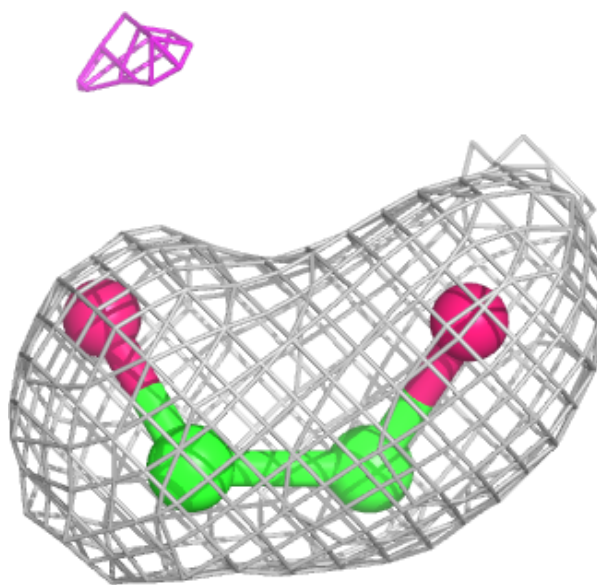
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





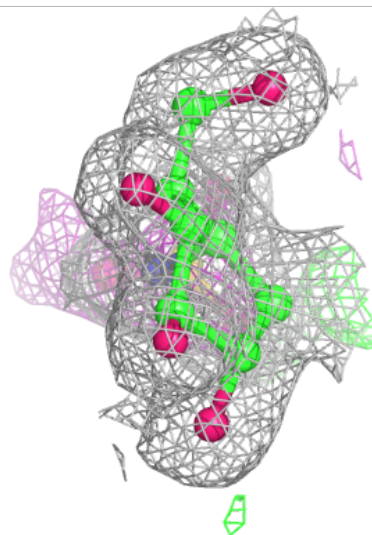
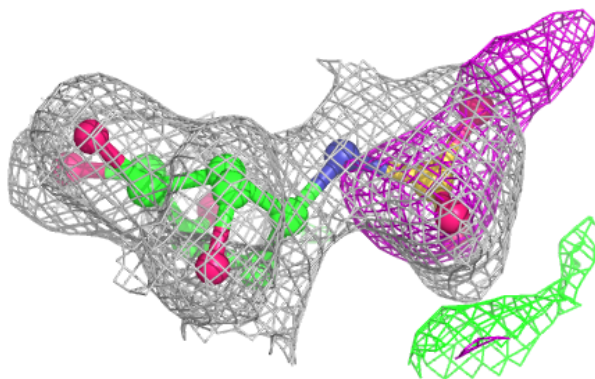
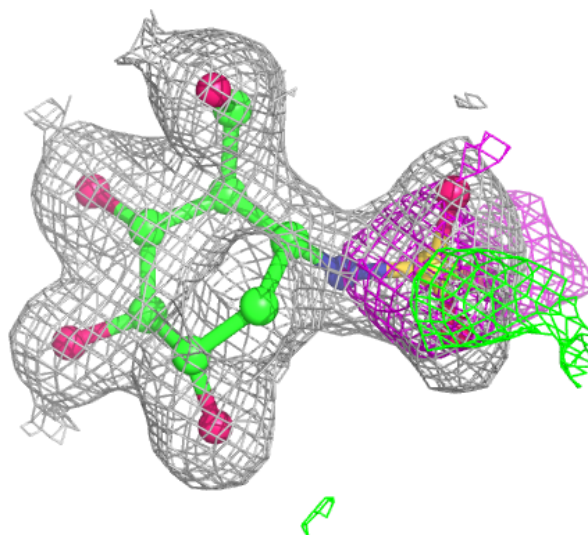
**Electron density around EDO AAA 1022:**

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



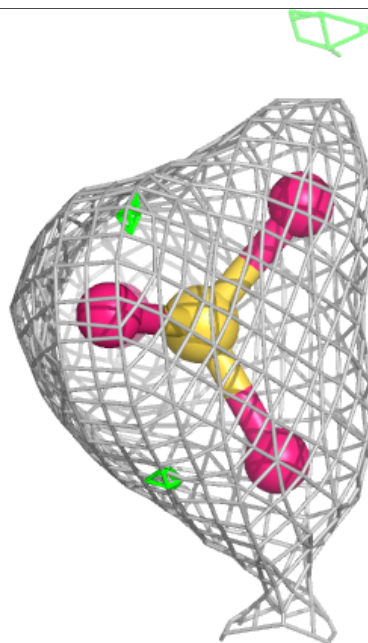
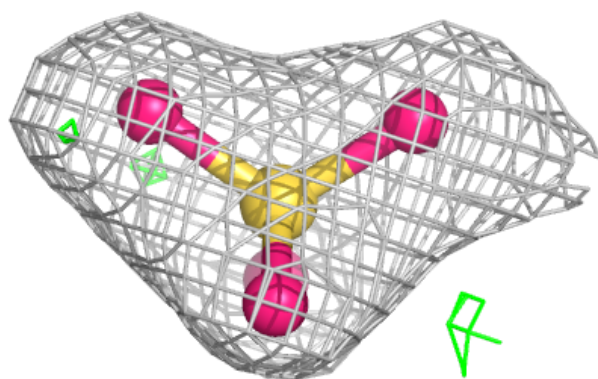
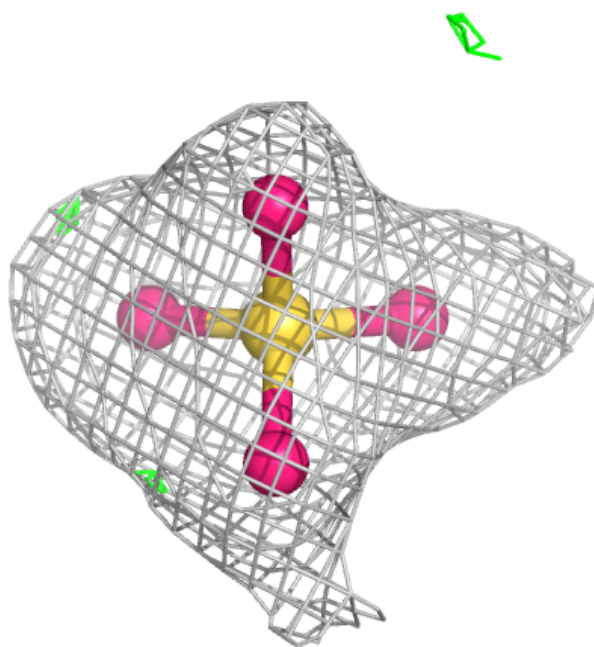
**Electron density around 56I AAA 1002:**

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



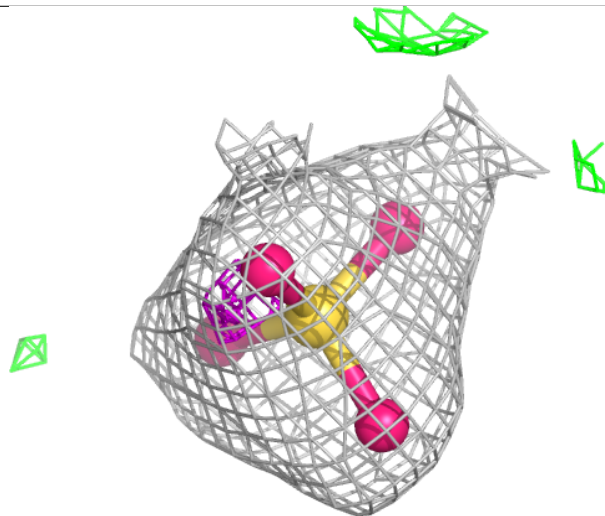
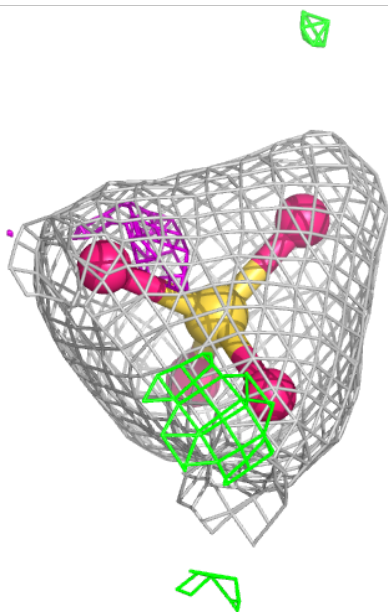
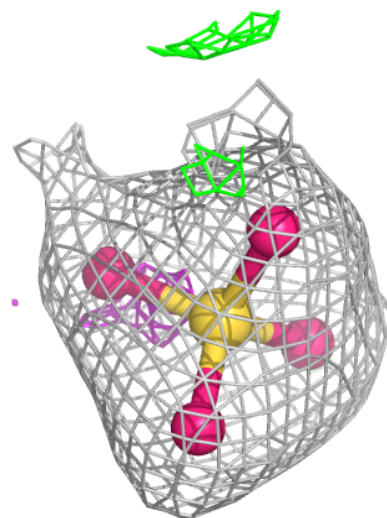
**Electron density around SO4 AAA 1007:**

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



**Electron density around SO4 AAA 1003:**

$2mF_o-DF_c$  (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.