



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 4, 2026 – 11:19 PM UTC

PDB ID : 9M0B / pdb\_00009m0b  
Title : Crystal structure of alpha-agarase AGA from *Catenovulum maritimum*  
Authors : Zhang, X.M.; Li, W.H.; Han, X.D.  
Deposited on : 2025-02-24  
Resolution : 1.64 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

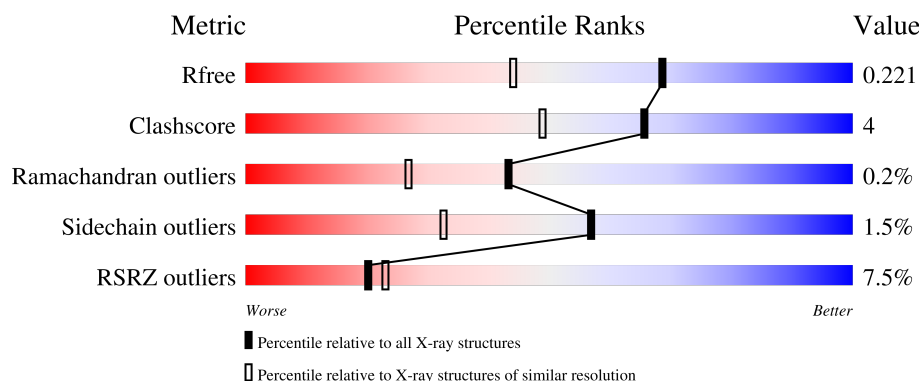
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.64 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1141 (1.64-1.64)
Clashscore	190562	1171 (1.64-1.64)
Ramachandran outliers	187476	1151 (1.64-1.64)
Sidechain outliers	187428	1150 (1.64-1.64)
RSRZ outliers	180081	1141 (1.64-1.64)

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	773	<div> <div>5%</div> <div>92%</div> <div>7%</div> </div>
1	B	773	<div> <div>10%</div> <div>90%</div> <div>9%</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	EDO	B	1504	-	-	X	-
7	CL	B	1520	-	-	X	-
9	PEG	B	1503	-	-	X	-

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 13781 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 Alpha-agarase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	773	Total	C	N	O	S	0	6	0
			6136	3916	1028	1179	13			
1	B	772	Total	C	N	O	S	0	6	0
			6116	3903	1020	1180	13			

There are 8 discrepancies between the modelled and reference sequences:

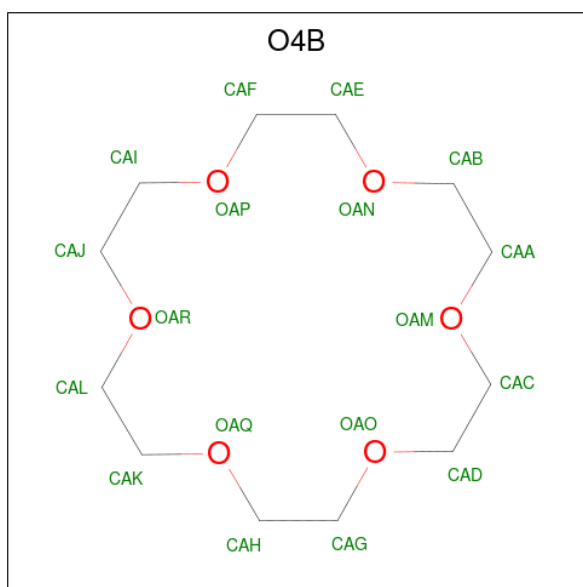
Chain	Residue	Modelled	Actual	Comment	Reference
A	1440	HIS	-	expression tag	UNP A0A0J8H064
A	1441	HIS	-	expression tag	UNP A0A0J8H064
A	1442	HIS	-	expression tag	UNP A0A0J8H064
A	1443	HIS	-	expression tag	UNP A0A0J8H064
B	1440	HIS	-	expression tag	UNP A0A0J8H064
B	1441	HIS	-	expression tag	UNP A0A0J8H064
B	1442	HIS	-	expression tag	UNP A0A0J8H064
B	1443	HIS	-	expression tag	UNP A0A0J8H064

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is 1,4,7,10,13,16-HEXAOXACYCLOOCTADECANE (CCD ID: O4B) (formula:  $C_{12}H_{24}O_6$ ) (labeled as "Ligand of Interest" by depositor).

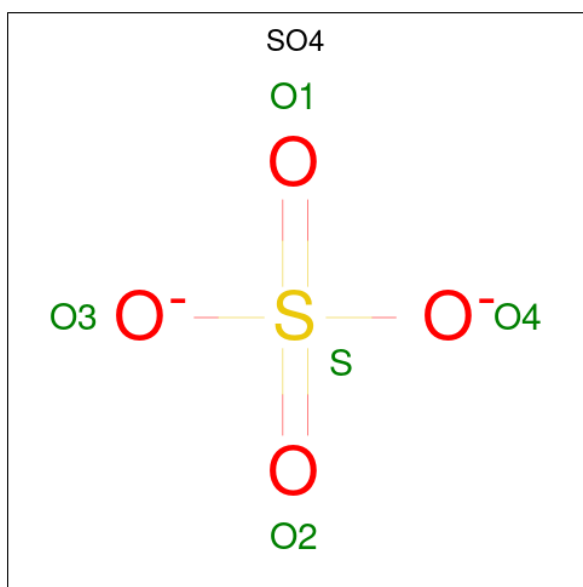


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			18	12	6		
3	B	1	Total	C	O	0	0
			18	12	6		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	Mg	0	0
			3	3		
4	B	2	Total	Mg	0	0
			2	2		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	4	Total	Na	0	0
			4	4		

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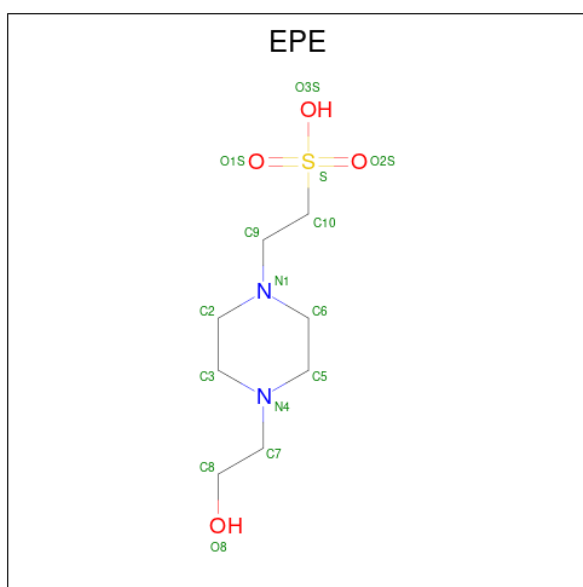
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	2	Total	Na	0	0
			2	2		

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

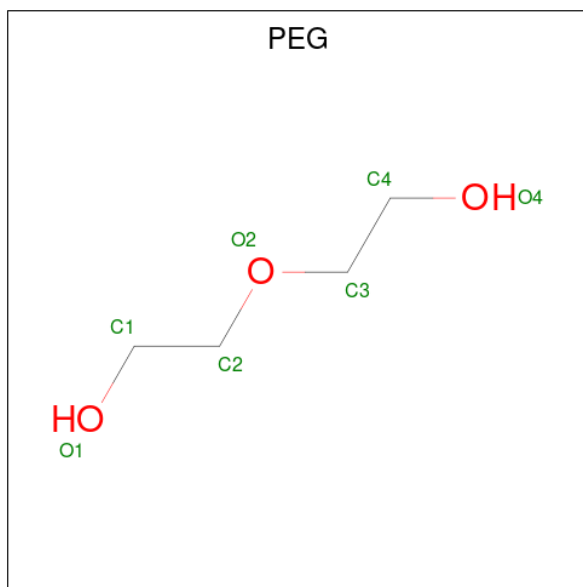
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Cl	0	0
			1	1		
7	B	2	Total	Cl	0	0
			2	2		

- Molecule 8 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C<sub>8</sub>H<sub>18</sub>N<sub>2</sub>O<sub>4</sub>S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 9 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			7	4	3		

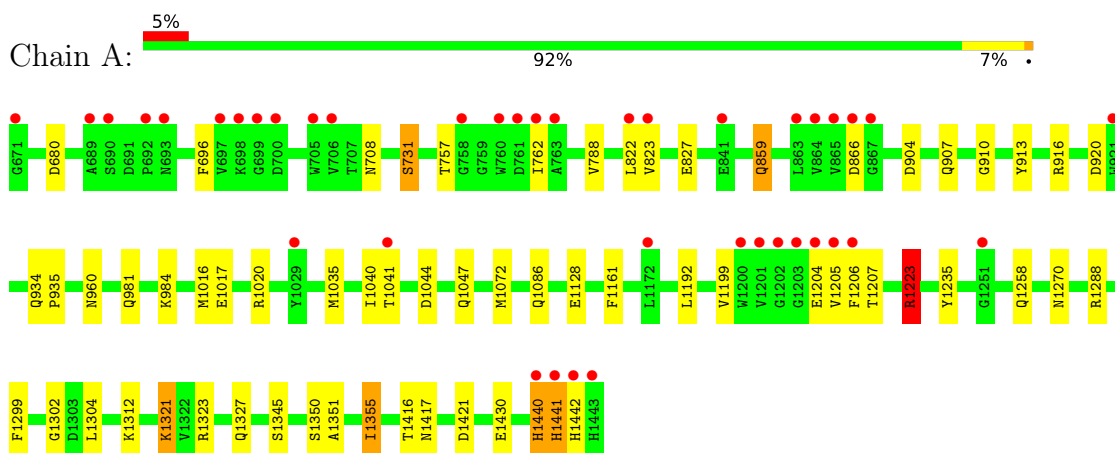
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	686	Total	O	0	0
			686	686		
10	B	681	Total	O	0	0
			681	681		

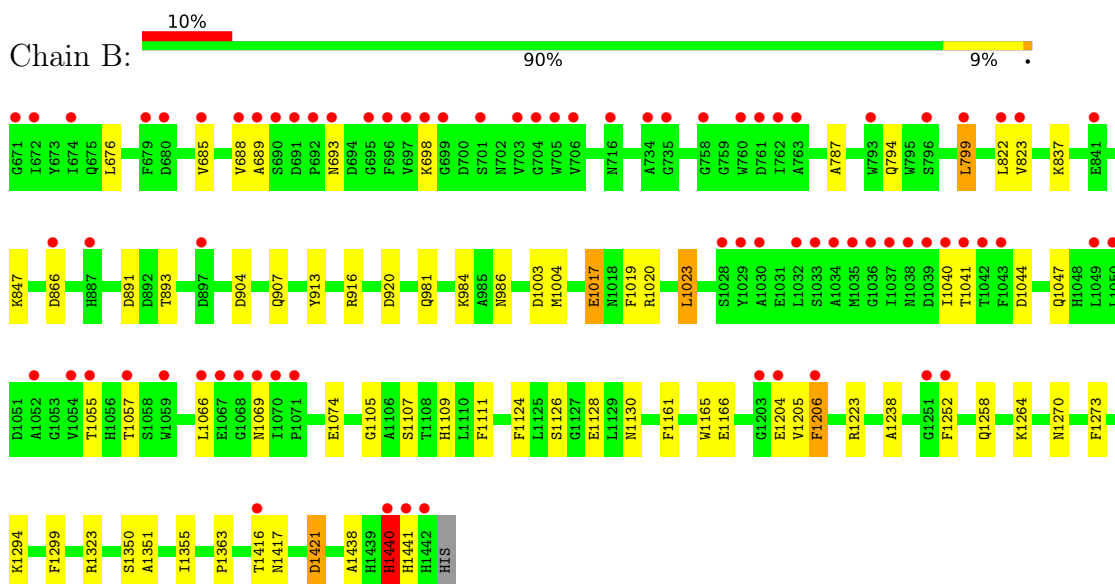
### 3 Residue-property plots [i](#)

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: Alpha-agarase



- Molecule 1: Alpha-agarase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	129.24Å 136.06Å 109.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	109.17 – 1.64 109.17 – 1.64	Depositor EDS
% Data completeness (in resolution range)	99.8 (109.17-1.64) 99.8 (109.17-1.64)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.47 (at 1.64Å)	Xtriage
Refinement program	PHENIX v1.2	Depositor
R, $R_{free}$	0.187 , 0.220 0.192 , 0.221	Depositor DCC
$R_{free}$ test set	11632 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.0	Xtriage
Anisotropy	0.062	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 39.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.010 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	13781	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% 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: NA, CL, PEG, MG, SO4, EPE, EDO, O4B

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	0.63	0/6334	1.06	9/8639 (0.1%)
1	B	0.63	0/6313	1.07	16/8612 (0.2%)
All	All	0.63	0/12647	1.06	25/17251 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	1
All	All	0	3

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1321	LYS	CB-CA-C	-8.30	94.35	110.46
1	B	1441	HIS	CA-CB-CG	7.98	121.78	113.80
1	B	1003	ASP	CA-CB-CG	7.96	120.56	112.60
1	B	916	ARG	CB-CA-C	-7.92	97.20	110.19
1	A	1441	HIS	CA-CB-CG	7.77	121.57	113.80
1	B	698	LYS	CB-CA-C	-7.33	99.60	110.16
1	B	866	ASP	CB-CA-C	7.33	122.95	111.95
1	B	1440	HIS	CB-CA-C	-7.31	98.02	110.22
1	B	920	ASP	CA-CB-CG	6.89	119.49	112.60
1	A	1440	HIS	CB-CA-C	6.82	121.24	110.19
1	B	1441	HIS	CB-CA-C	6.65	119.31	110.06
1	A	696	PHE	CA-CB-CG	5.89	119.69	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1258	GLN	N-CA-CB	-5.80	101.58	110.16
1	B	866	ASP	CA-CB-CG	5.61	118.21	112.60
1	B	1421	ASP	CA-CB-CG	5.58	118.18	112.60
1	B	698	LYS	N-CA-CB	5.51	118.22	109.51
1	B	847	LYS	CB-CA-C	-5.46	99.42	109.46
1	A	866	ASP	CA-CB-CG	5.45	118.05	112.60
1	B	685	VAL	N-CA-C	-5.42	107.70	112.90
1	A	680	ASP	CA-CB-CG	5.35	117.95	112.60
1	B	1017	GLU	CB-CG-CD	5.34	121.67	112.60
1	B	891	ASP	CA-CB-CG	5.26	117.86	112.60
1	A	916	ARG	CB-CA-C	-5.10	101.33	109.75
1	A	920	ASP	CA-CB-CG	5.09	117.69	112.60
1	A	1223	ARG	CD-NE-CZ	5.09	131.52	124.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1223	ARG	Sidechain
1	A	1288	ARG	Sidechain
1	B	1223	ARG	Sidechain

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6136	0	5757	46	0
1	B	6116	0	5734	50	0
2	A	20	0	30	0	0
2	B	20	0	30	6	0
3	A	18	0	24	0	0
3	B	18	0	24	0	0
4	A	3	0	0	0	0
4	B	2	0	0	0	0
5	A	20	0	0	0	0
5	B	30	0	0	0	0
6	A	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	2	0	0	0	0
7	A	1	0	0	0	0
7	B	2	0	0	3	0
8	B	15	0	18	0	0
9	B	7	0	10	5	0
10	A	686	0	0	2	0
10	B	681	0	0	8	0
All	All	13781	0	11627	92	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 4.

All (92) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1055:THR:HB	2:B:1504:EDO:H12	1.42	0.99
1:B:1165:TRP:NE1	7:B:1520:CL:CL	2.54	0.75
1:A:907:GLN:HE21	1:A:913:TYR:H	1.32	0.75
1:B:907:GLN:HE21	1:B:913:TYR:H	1.33	0.74
1:A:827:GLU:H	1:A:1086:GLN:HE22	1.37	0.73
1:A:1235:TYR:HB2	1:A:1355[A]:ILE:HG23	1.73	0.70
1:A:1270:ASN:HD21	1:A:1350:SER:HA	1.57	0.70
1:B:1130:ASN:OD1	7:B:1520:CL:CL	2.51	0.65
1:A:1020[B]:ARG:NH1	1:A:1041:THR:HA	2.11	0.65
1:A:1440:HIS:HE2	1:B:904:ASP:HA	1.62	0.64
1:B:1438:ALA:HA	9:B:1503:PEG:H11	1.80	0.63
1:B:893:THR:HA	2:B:1505:EDO:H22	1.80	0.62
1:A:859:GLN:H	1:A:859:GLN:HE21	1.47	0.62
1:A:910:GLY:O	9:B:1503:PEG:H31	2.00	0.62
9:B:1503:PEG:H32	10:B:1988:HOH:O	1.99	0.61
1:B:893:THR:HG22	2:B:1505:EDO:H21	1.83	0.60
1:B:1055:THR:HB	2:B:1504:EDO:C1	2.26	0.60
1:B:1270:ASN:HD21	1:B:1350:SER:HA	1.66	0.59
1:A:708:ASN:ND2	1:A:960:ASN:HD21	2.02	0.58
1:A:1441:HIS:CD2	1:B:986:ASN:HD21	2.22	0.58
1:A:1020[B]:ARG:HH11	1:A:1041:THR:HA	1.68	0.57
1:A:1270:ASN:ND2	1:A:1351:ALA:H	2.03	0.57
1:B:1057:THR:OG1	2:B:1504:EDO:O1	2.13	0.57
1:A:859:GLN:H	1:A:859:GLN:NE2	2.03	0.57
1:B:1270:ASN:ND2	1:B:1351:ALA:H	2.03	0.56
1:B:981:GLN:HE22	1:B:984:LYS:NZ	2.02	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1107[B]:SER:HA	1:B:1126:SER:O	2.06	0.56
1:A:1321:LYS:HG3	10:A:1966:HOH:O	2.05	0.56
1:B:1107[A]:SER:HA	1:B:1126:SER:O	2.06	0.55
1:B:1416:THR:HG22	1:B:1417:ASN:H	1.72	0.54
1:B:1166:GLU:OE1	7:B:1520:CL:CL	2.64	0.53
1:A:708:ASN:HD21	1:A:960:ASN:HD21	1.57	0.53
1:A:1416:THR:HG22	1:A:1417:ASN:H	1.74	0.52
1:B:837:LYS:HE3	10:B:2127:HOH:O	2.09	0.52
1:B:1109:HIS:HE1	10:B:2107:HOH:O	1.93	0.51
1:A:907:GLN:NE2	1:A:913:TYR:H	2.05	0.51
1:A:731:SER:HB3	1:A:762:ILE:O	2.10	0.51
1:A:1016:MET:HA	1:A:1016:MET:HE2	1.93	0.50
1:B:1004[B]:MET:SD	1:B:1252:PHE:CD1	3.05	0.50
1:A:910:GLY:CA	9:B:1503:PEG:H31	2.41	0.49
1:A:1323:ARG:HD3	1:A:1327:GLN:HB2	1.95	0.49
1:B:1020:ARG:HG2	1:B:1040:ILE:O	2.12	0.49
1:B:1270:ASN:HD21	1:B:1351:ALA:H	1.61	0.49
1:A:1044:ASP:OD2	1:A:1047:GLN:HB2	2.13	0.49
1:A:981:GLN:HE22	1:A:984:LYS:NZ	2.11	0.49
1:B:907:GLN:NE2	1:B:913:TYR:H	2.07	0.49
1:B:1109:HIS:HD2	1:B:1111:PHE:H	1.60	0.49
1:B:1363:PRO:HD3	9:B:1503:PEG:H41	1.94	0.48
1:B:1055:THR:CB	2:B:1504:EDO:H12	2.29	0.48
1:A:1017:GLU:OE1	1:A:1020[A]:ARG:NE	2.46	0.47
1:A:859:GLN:NE2	10:A:1625:HOH:O	2.47	0.47
1:B:981:GLN:HE22	1:B:984:LYS:HZ2	1.61	0.47
1:B:1416:THR:HG23	1:B:1421:ASP:O	2.15	0.46
1:B:676:LEU:HG	1:B:799:LEU:HA	1.98	0.46
1:A:859:GLN:HE21	1:A:859:GLN:N	2.11	0.46
1:B:1264:LYS:HD2	10:B:1660:HOH:O	2.15	0.46
1:B:1020:ARG:NH1	1:B:1041:THR:HA	2.31	0.46
1:A:1258:GLN:HE21	1:A:1302:GLY:H	1.64	0.45
1:A:1017:GLU:OE1	1:A:1020[A]:ARG:NH2	2.50	0.45
1:A:981:GLN:HE22	1:A:984:LYS:HZ2	1.64	0.45
1:B:787:ALA:HB1	1:B:794:GLN:HG3	1.98	0.45
1:B:1238:ALA:O	1:B:1273:PHE:HA	2.16	0.45
1:A:1235:TYR:CB	1:A:1355[A]:ILE:HG23	2.44	0.45
1:A:1440:HIS:CE1	1:B:904:ASP:OD1	2.70	0.45
1:B:1066:LEU:HD13	1:B:1074:GLU:HG3	1.98	0.45
1:A:1304:LEU:HD21	1:A:1312[A]:LYS:HE2	1.99	0.45
1:B:1264:LYS:NZ	10:B:1615:HOH:O	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1128:GLU:HA	1:B:1161:PHE:O	2.18	0.43
1:A:1299:PHE:HA	1:A:1323:ARG:O	2.17	0.43
1:B:799:LEU:C	1:B:799:LEU:HD22	2.44	0.43
1:A:827:GLU:H	1:A:1086:GLN:NE2	2.11	0.43
1:A:1199:VAL:O	1:A:1207:THR:HA	2.18	0.43
1:B:1299:PHE:HA	1:B:1323:ARG:O	2.19	0.43
1:A:1416:THR:HG23	1:A:1421:ASP:O	2.19	0.42
1:B:1270:ASN:HD22	1:B:1270:ASN:HA	1.65	0.42
1:A:934:GLN:HB3	1:A:935:PRO:HD3	2.02	0.42
1:A:1128:GLU:HA	1:A:1161:PHE:O	2.20	0.42
1:B:1105:GLY:HA2	1:B:1124:PHE:O	2.19	0.42
1:B:1355[B]:ILE:HD11	10:B:2238:HOH:O	2.20	0.42
1:A:731:SER:HA	1:A:757:THR:HG21	2.02	0.41
1:A:1035:MET:HE1	1:A:1072:MET:HE3	2.02	0.41
1:B:688:VAL:HG12	10:B:1800:HOH:O	2.20	0.41
1:A:708:ASN:HD21	1:A:788:VAL:HA	1.86	0.41
1:B:1294:LYS:HD3	10:B:2128:HOH:O	2.20	0.41
1:B:1205:VAL:O	1:B:1206:PHE:HB2	2.21	0.41
1:A:904:ASP:HB3	1:B:1440:HIS:NE2	2.36	0.41
1:B:1044:ASP:OD2	1:B:1047:GLN:HB2	2.21	0.41
1:A:1020[B]:ARG:CG	1:A:1040:ILE:O	2.68	0.40
1:A:1440:HIS:NE2	1:B:904:ASP:HA	2.33	0.40
1:B:1019:PHE:O	1:B:1023:LEU:HB2	2.21	0.40
1:A:1205:VAL:O	1:A:1206:PHE:HB2	2.21	0.40
1:A:1270:ASN:HD22	1:A:1270:ASN:HA	1.65	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	777/773 (100%)	757 (97%)	19 (2%)	1 (0%)	48 29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	776/773 (100%)	753 (97%)	21 (3%)	2 (0%)	36	20
All	All	1553/1546 (100%)	1510 (97%)	40 (3%)	3 (0%)	43	27

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	689	ALA
1	A	1442	HIS
1	B	1206	PHE

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	649/643 (101%)	637 (98%)	12 (2%)	51	26
1	B	648/643 (101%)	639 (99%)	9 (1%)	59	35
All	All	1297/1286 (101%)	1276 (98%)	21 (2%)	57	30

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	731	SER
1	A	822	LEU
1	A	823	VAL
1	A	859	GLN
1	A	1192	LEU
1	A	1204	GLU
1	A	1223	ARG
1	A	1345[A]	SER
1	A	1345[B]	SER
1	A	1355[A]	ILE
1	A	1355[B]	ILE
1	A	1430	GLU
1	B	693	ASN

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Mol	Chain	Res	Type
1	B	799	LEU
1	B	822	LEU
1	B	823	VAL
1	B	1017	GLU
1	B	1023	LEU
1	B	1069	ASN
1	B	1204	GLU
1	B	1440	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	675	GLN
1	A	708	ASN
1	A	859	GLN
1	A	887	HIS
1	A	907	GLN
1	A	981	GLN
1	A	1086	GLN
1	A	1097	GLN
1	A	1098	GLN
1	A	1185	GLN
1	A	1258	GLN
1	A	1270	ASN
1	A	1441	HIS
1	A	1443	HIS
1	B	812	GLN
1	B	887	HIS
1	B	907	GLN
1	B	966	ASN
1	B	981	GLN
1	B	1098	GLN
1	B	1109	HIS
1	B	1130	ASN
1	B	1185	GLN
1	B	1225	GLN
1	B	1258	GLN
1	B	1270	ASN
1	B	1335	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 ⓘ

Of 38 ligands modelled in this entry, 14 are monoatomic - leaving 24 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$
5	SO4	B	1512	-	4,4,4	0.45	0	6,6,6	0.26	0
2	EDO	A	1504	-	3,3,3	0.16	0	2,2,2	0.41	0
2	EDO	A	1506	-	3,3,3	0.08	0	2,2,2	0.43	0
5	SO4	B	1515	-	4,4,4	0.29	0	6,6,6	0.13	0
8	EPE	B	1501	-	15,15,15	0.79	1 (6%)	19,20,20	0.97	2 (10%)
2	EDO	A	1501	-	3,3,3	0.13	0	2,2,2	0.30	0
2	EDO	B	1508	-	3,3,3	0.30	0	2,2,2	0.40	0
5	SO4	A	1511	-	4,4,4	0.24	0	6,6,6	0.15	0
5	SO4	A	1513	-	4,4,4	0.32	0	6,6,6	0.10	0
9	PEG	B	1503	-	6,6,6	0.84	0	5,5,5	0.96	0
2	EDO	B	1504	-	3,3,3	0.60	0	2,2,2	0.65	0
5	SO4	A	1512	-	4,4,4	0.33	0	6,6,6	0.08	0
2	EDO	B	1506	-	3,3,3	0.16	0	2,2,2	0.16	0
2	EDO	B	1507	-	3,3,3	0.14	0	2,2,2	0.66	0
5	SO4	B	1514	-	4,4,4	0.31	0	6,6,6	0.13	0
2	EDO	A	1505	-	3,3,3	0.17	0	2,2,2	0.12	0
5	SO4	B	1511	-	4,4,4	0.40	0	6,6,6	0.25	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	SO4	B	1513	-	4,4,4	0.28	0	6,6,6	0.14	0
2	EDO	A	1503	-	3,3,3	0.22	0	2,2,2	0.16	0
3	O4B	A	1502	-	18,18,18	0.50	0	18,18,18	0.37	0
3	O4B	B	1502	-	18,18,18	0.51	0	18,18,18	0.40	0
2	EDO	B	1505	-	3,3,3	0.55	0	2,2,2	0.77	0
5	SO4	A	1510	-	4,4,4	0.24	0	6,6,6	0.13	0
5	SO4	B	1516	-	4,4,4	0.26	0	6,6,6	0.18	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
2	EDO	B	1504	-	-	1/1/1/1	-
2	EDO	A	1504	-	-	1/1/1/1	-
2	EDO	A	1506	-	-	1/1/1/1	-
3	O4B	A	1502	-	-	12/18/18/18	0/1/1/1
8	EPE	B	1501	-	-	3/9/19/19	0/1/1/1
3	O4B	B	1502	-	-	9/18/18/18	0/1/1/1
2	EDO	A	1501	-	-	1/1/1/1	-
2	EDO	B	1505	-	-	0/1/1/1	-
2	EDO	A	1505	-	-	0/1/1/1	-
2	EDO	B	1508	-	-	1/1/1/1	-
9	PEG	B	1503	-	-	3/4/4/4	-
2	EDO	B	1506	-	-	0/1/1/1	-
2	EDO	A	1503	-	-	0/1/1/1	-
2	EDO	B	1507	-	-	1/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	1501	EPE	O3S-S	2.71	1.57	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	1501	EPE	O3S-S-O2S	-2.57	104.97	111.40
8	B	1501	EPE	O3S-S-O1S	2.17	116.82	111.40

There are no chirality outliers.

All (33) torsion outliers are listed below:

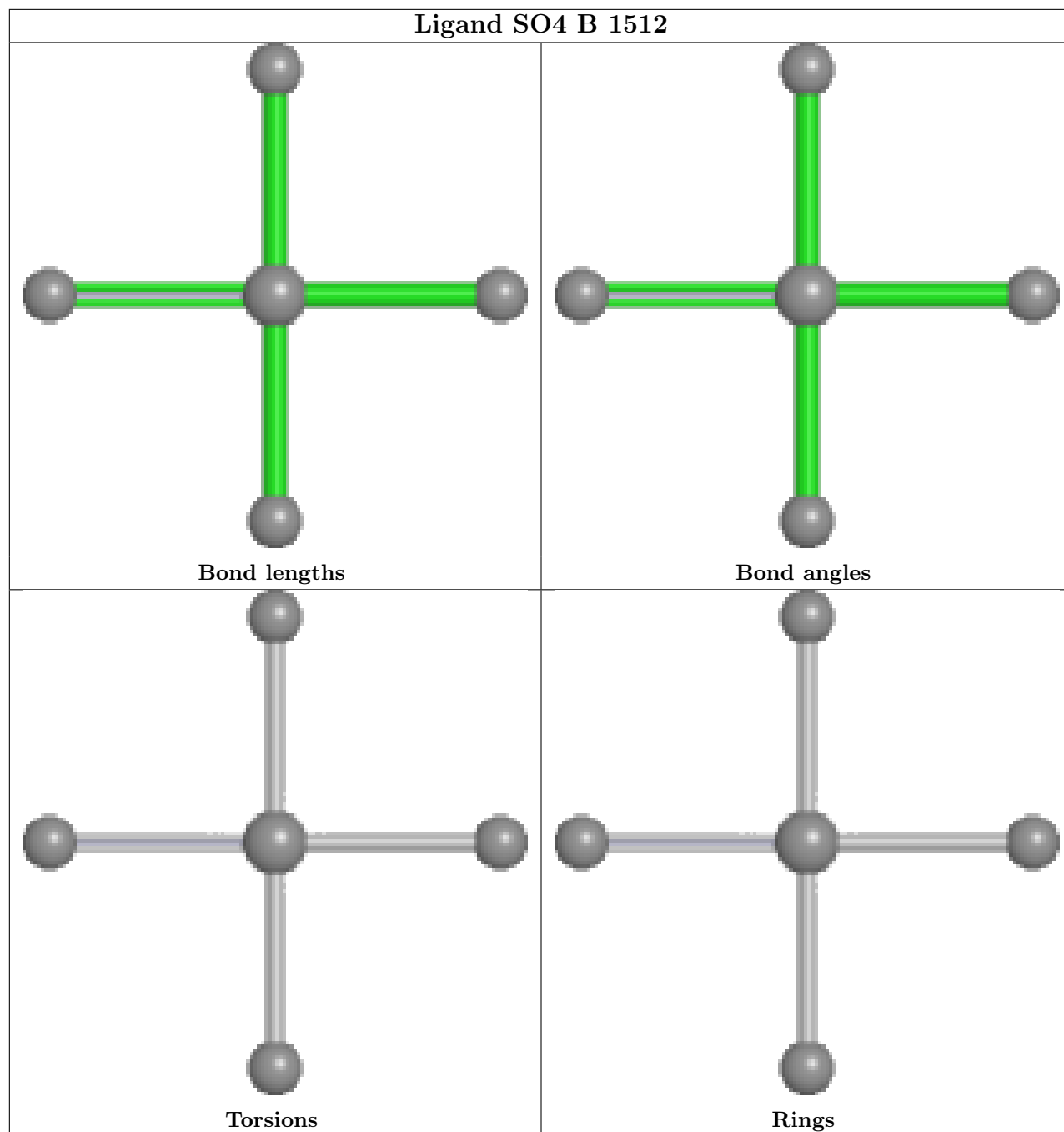
Mol	Chain	Res	Type	Atoms
9	B	1503	PEG	C4-C3-O2-C2
8	B	1501	EPE	N4-C7-C8-O8
3	B	1502	O4B	OAN-CAE-CAF-OAP
3	B	1502	O4B	OAM-CAC-CAD-OAO
3	A	1502	O4B	OAM-CAA-CAB-OAN
3	B	1502	O4B	OAM-CAA-CAB-OAN
9	B	1503	PEG	O2-C3-C4-O4
3	A	1502	O4B	OAO-CAG-CAH-OAQ
2	A	1501	EDO	O1-C1-C2-O2
2	B	1504	EDO	O1-C1-C2-O2
2	B	1507	EDO	O1-C1-C2-O2
3	B	1502	O4B	CAB-CAA-OAM-CAC
3	A	1502	O4B	OAM-CAC-CAD-OAO
3	A	1502	O4B	OAN-CAE-CAF-OAP
8	B	1501	EPE	C9-C10-S-O3S
3	A	1502	O4B	CAE-CAF-OAP-CAI
3	A	1502	O4B	CAK-CAL-OAR-CAJ
3	B	1502	O4B	CAC-CAD-OAO-CAG
3	B	1502	O4B	CAI-CAJ-OAR-CAL
3	A	1502	O4B	CAG-CAH-OAQ-CAK
3	A	1502	O4B	CAH-CAG-OAO-CAD
3	A	1502	O4B	CAL-CAK-OAQ-CAH
2	A	1504	EDO	O1-C1-C2-O2
3	B	1502	O4B	CAJ-CAI-OAP-CAF
3	B	1502	O4B	CAD-CAC-OAM-CAA
3	A	1502	O4B	CAC-CAD-OAO-CAG
3	A	1502	O4B	OAP-CAI-CAJ-OAR
2	B	1508	EDO	O1-C1-C2-O2
2	A	1506	EDO	O1-C1-C2-O2
8	B	1501	EPE	C9-C10-S-O1S
3	A	1502	O4B	CAB-CAA-OAM-CAC
9	B	1503	PEG	C1-C2-O2-C3
3	B	1502	O4B	CAA-CAB-OAN-CAE

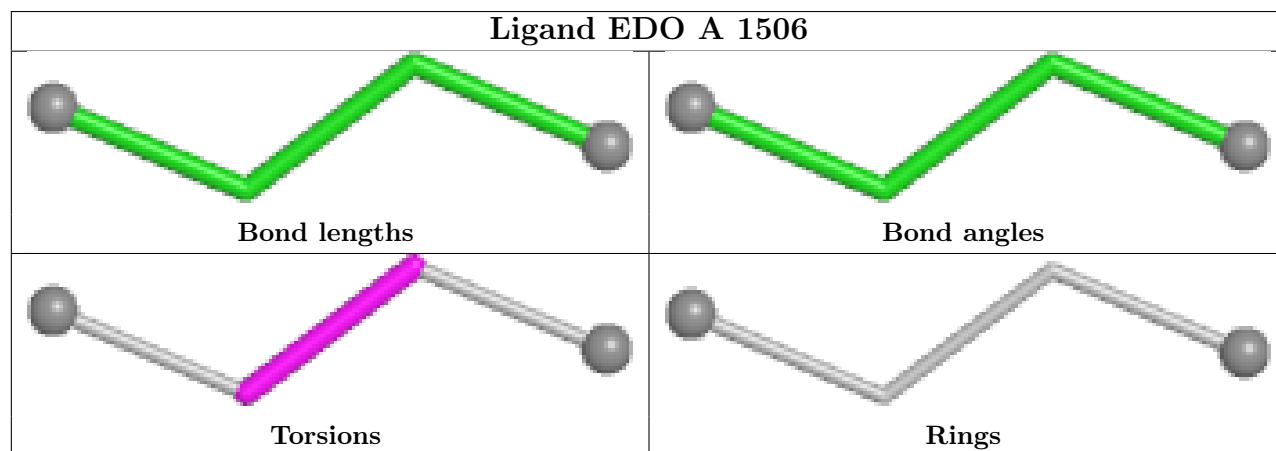
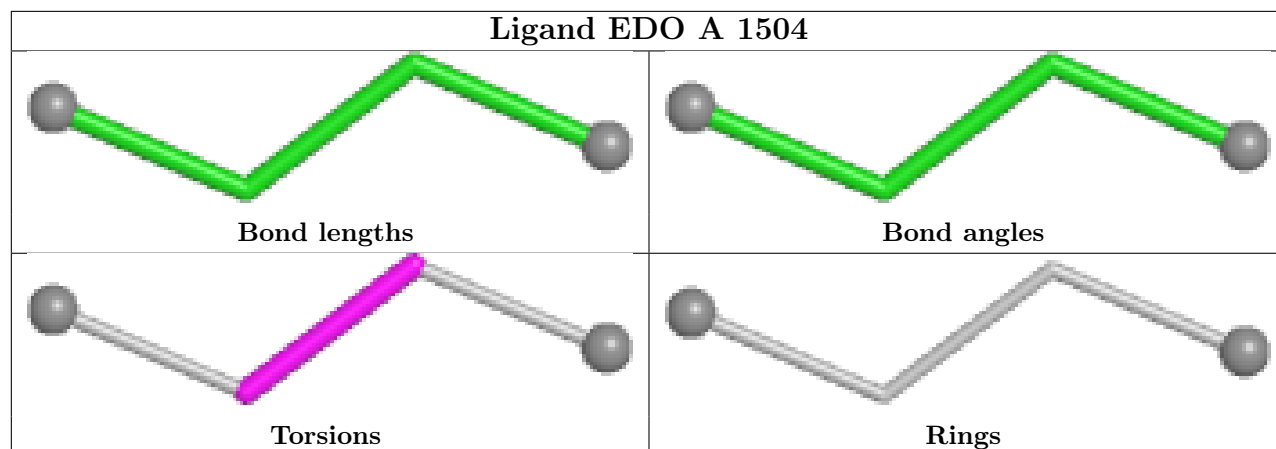
There are no ring outliers.

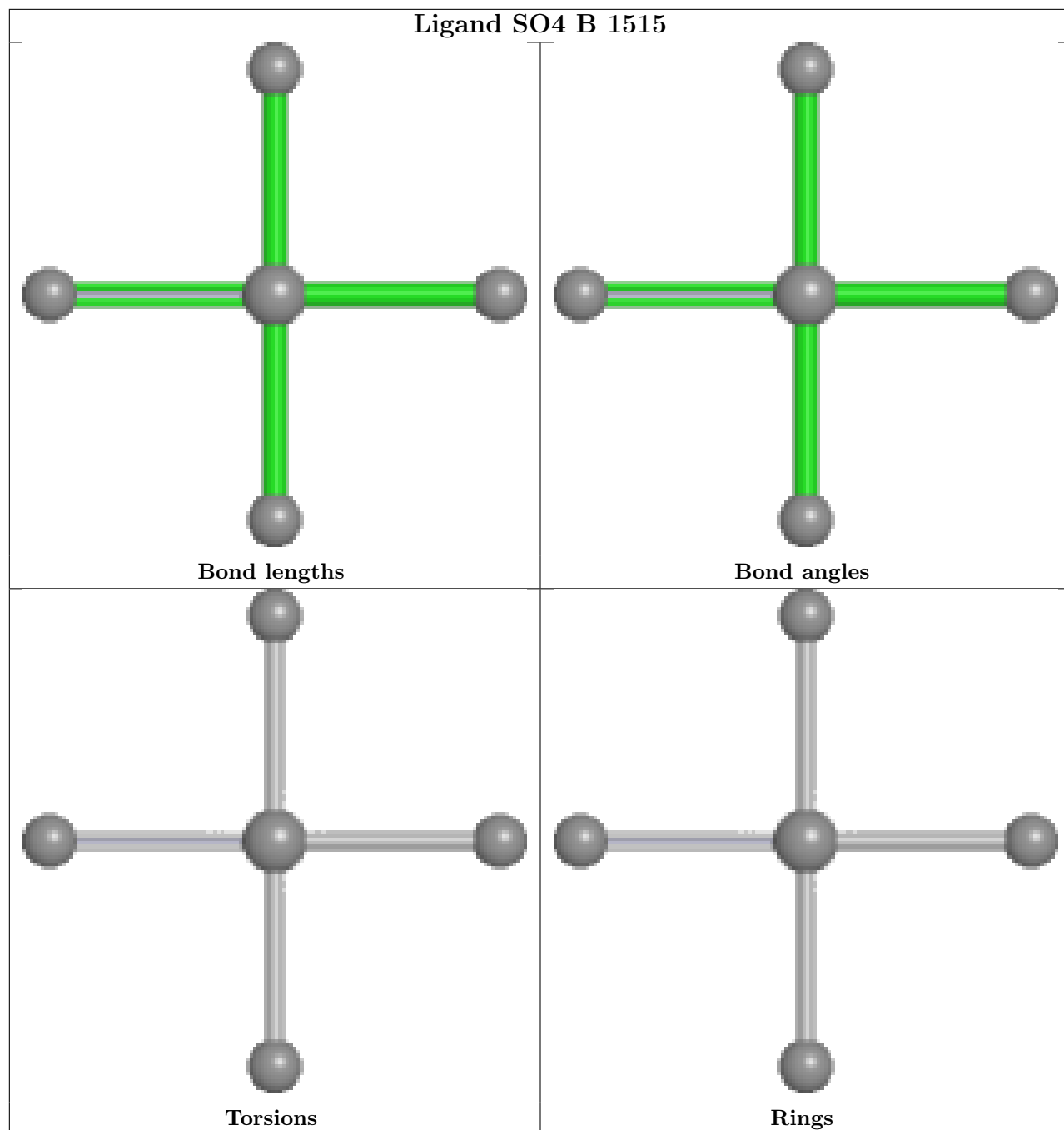
3 monomers are involved in 11 short contacts:

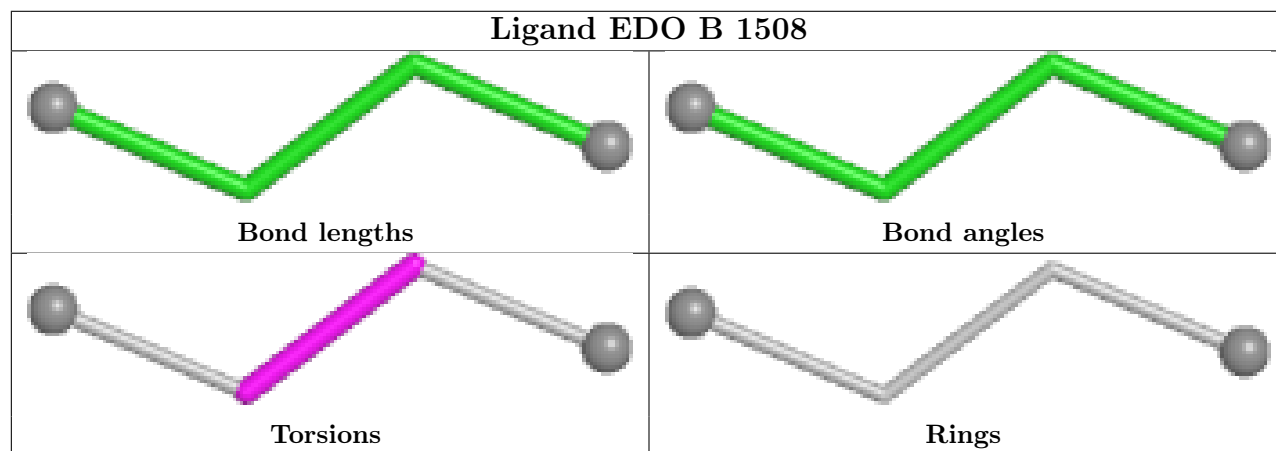
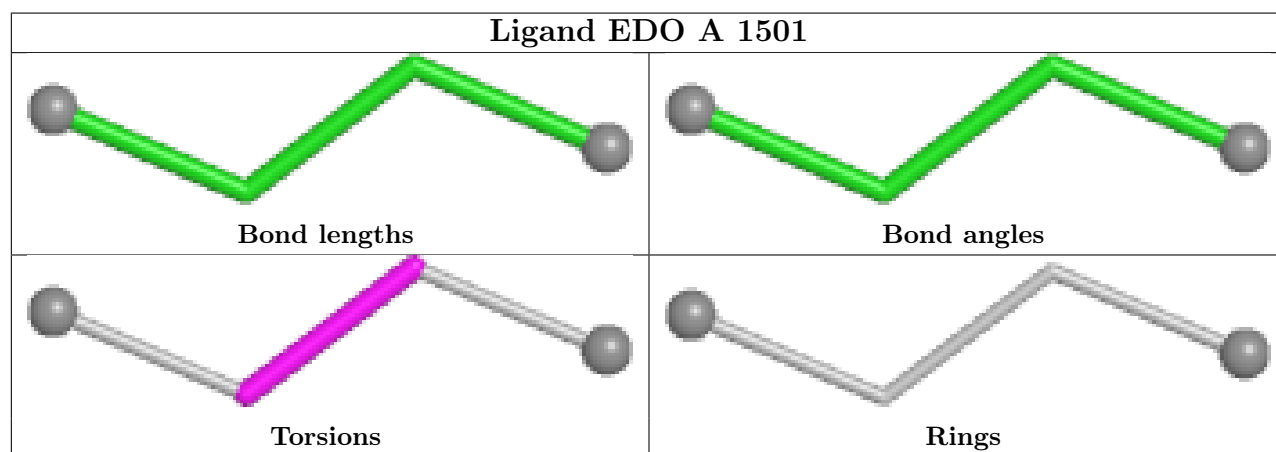
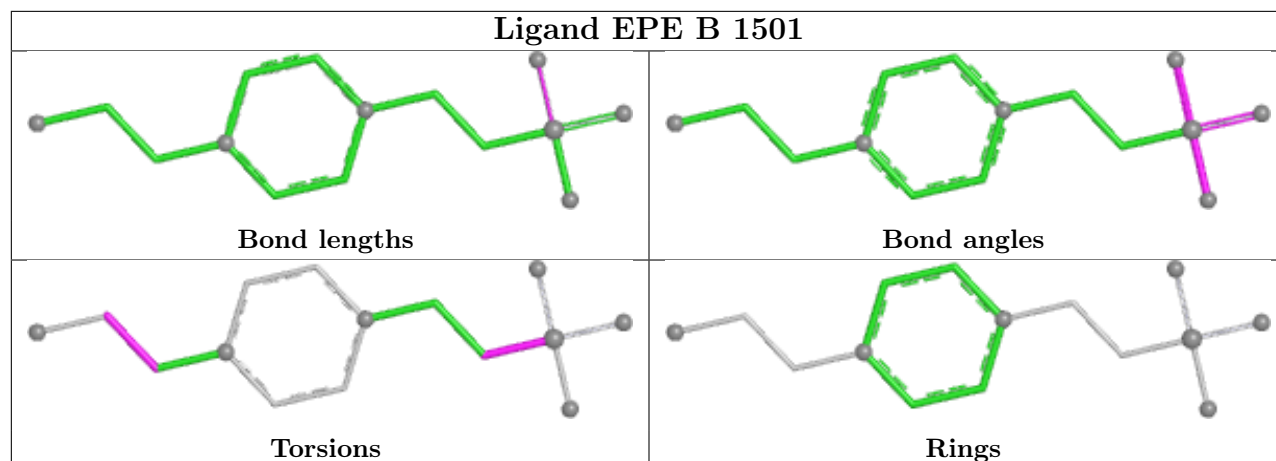
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	1503	PEG	5	0
2	B	1504	EDO	4	0
2	B	1505	EDO	2	0

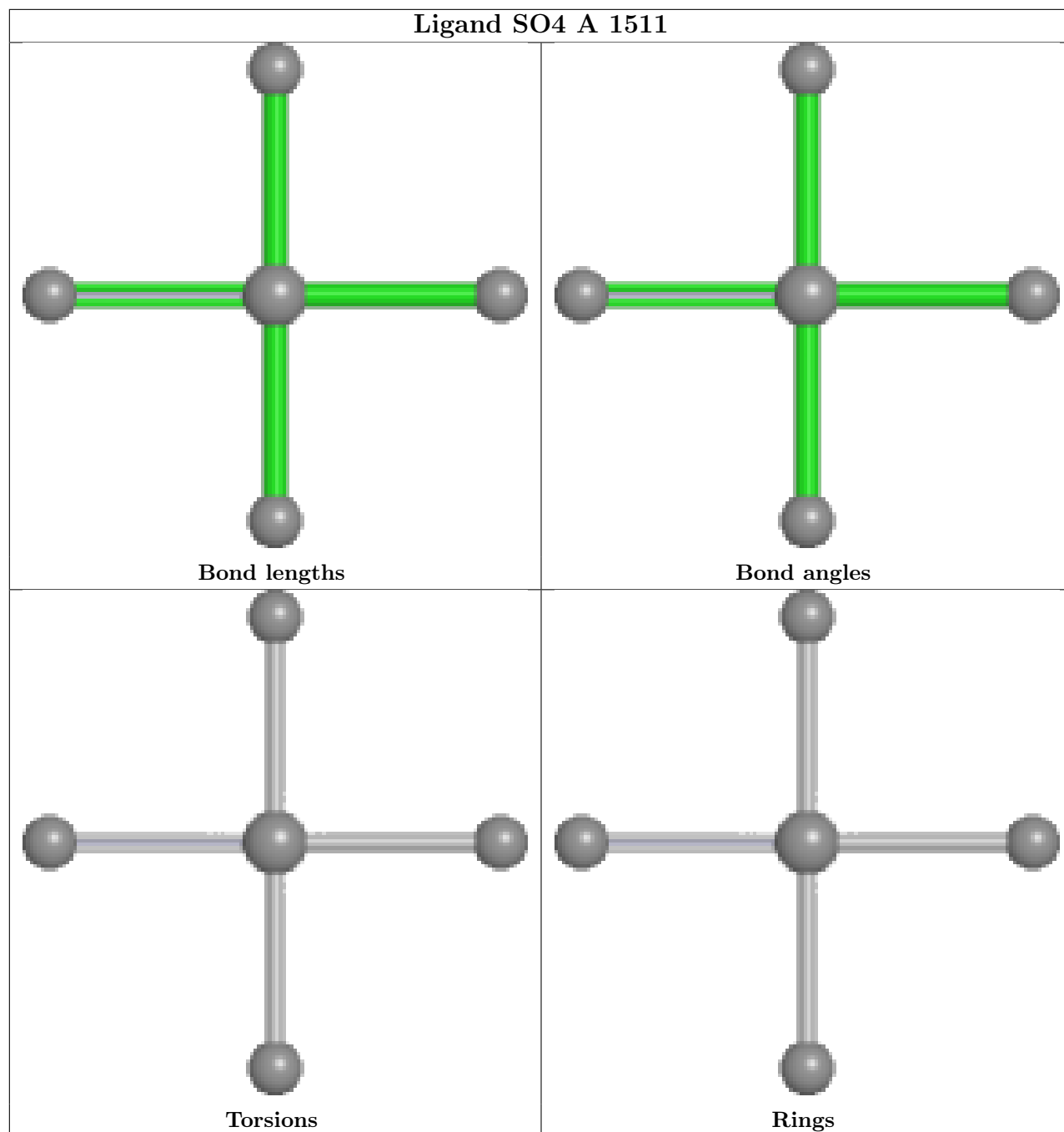
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

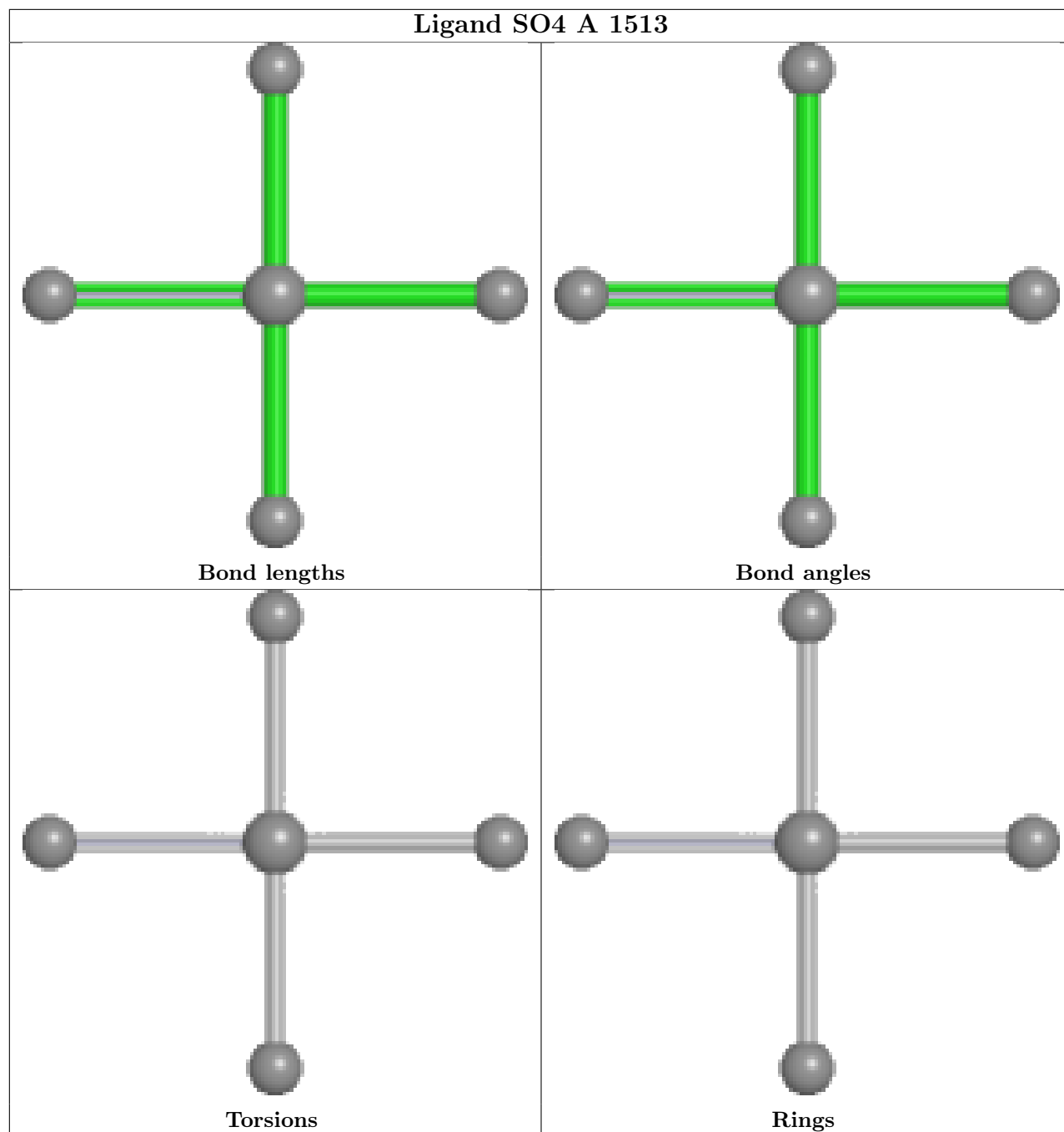


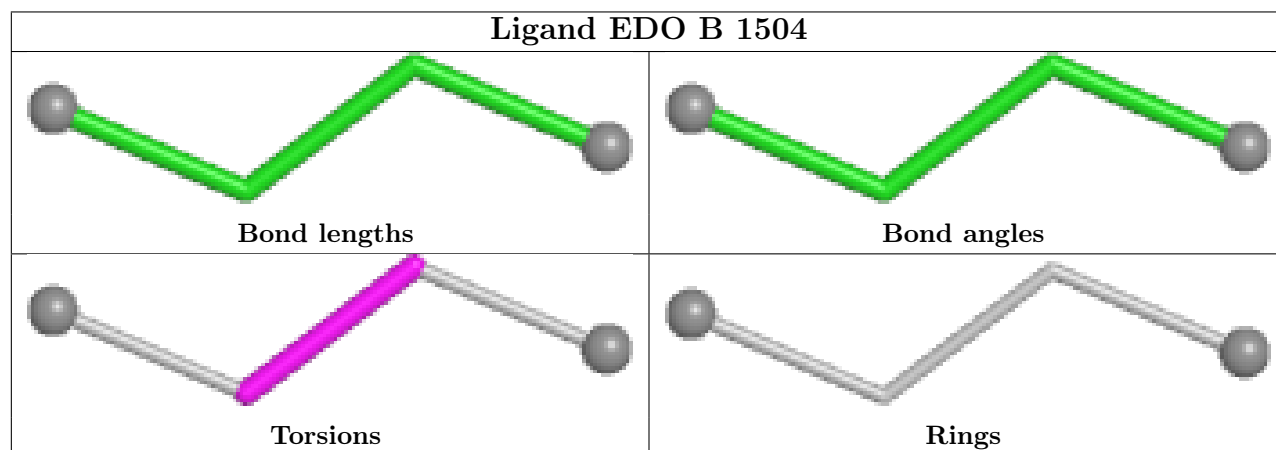
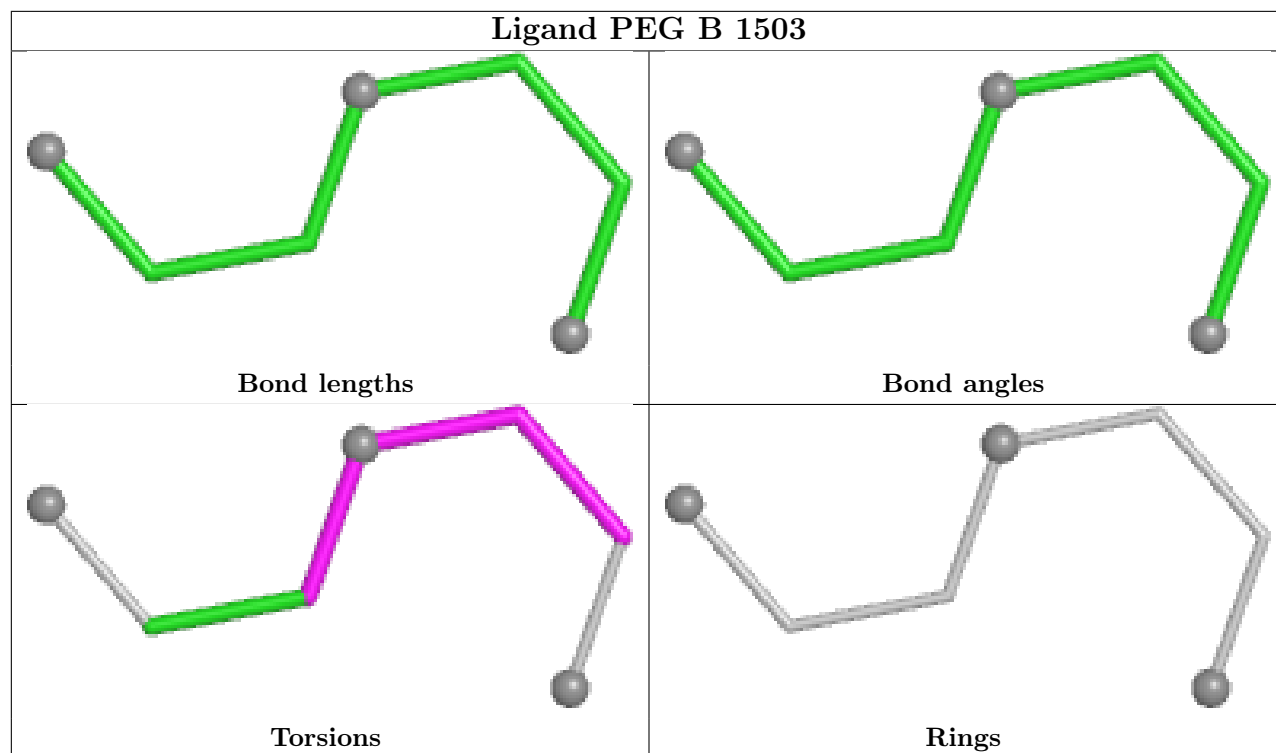


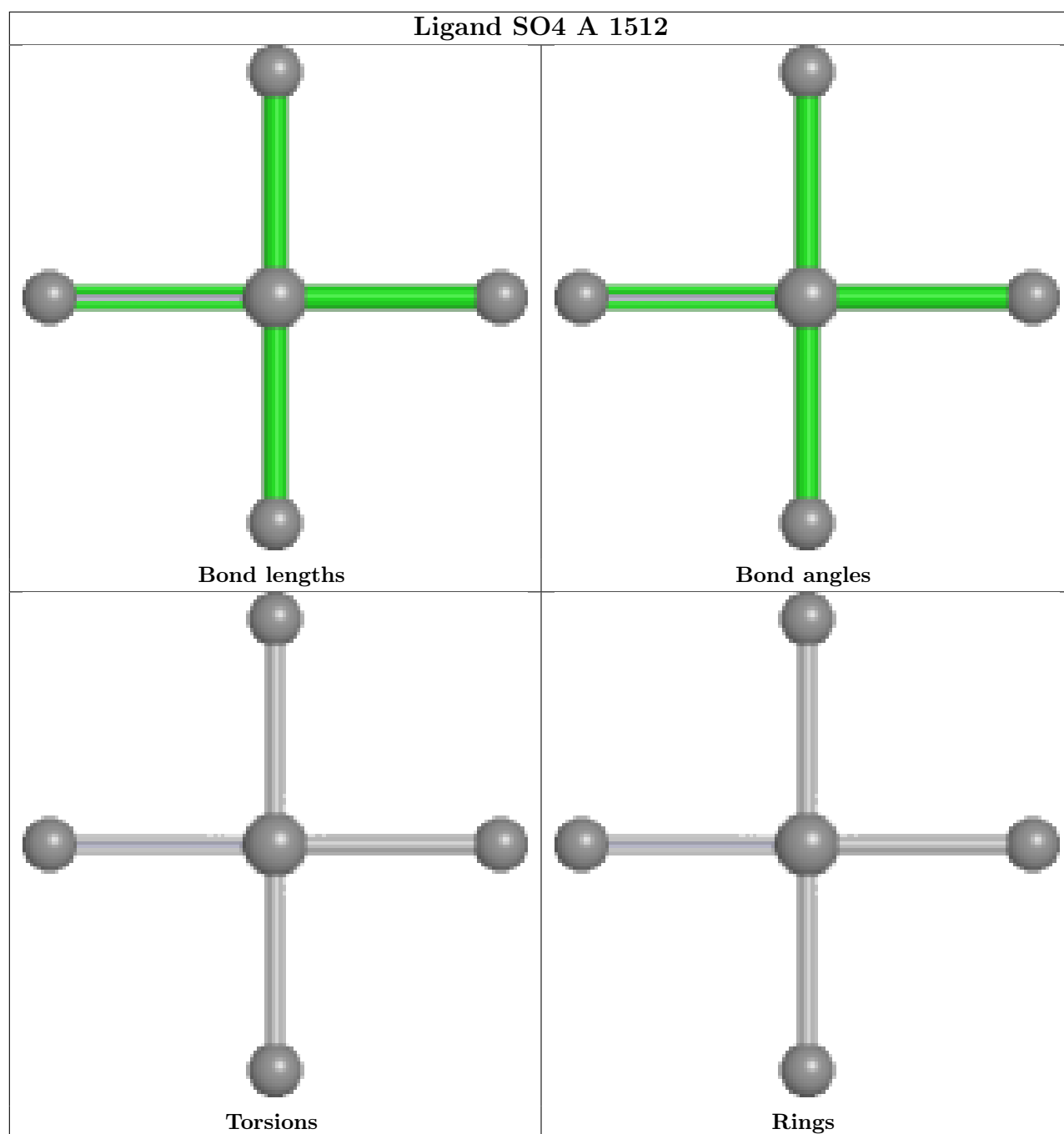


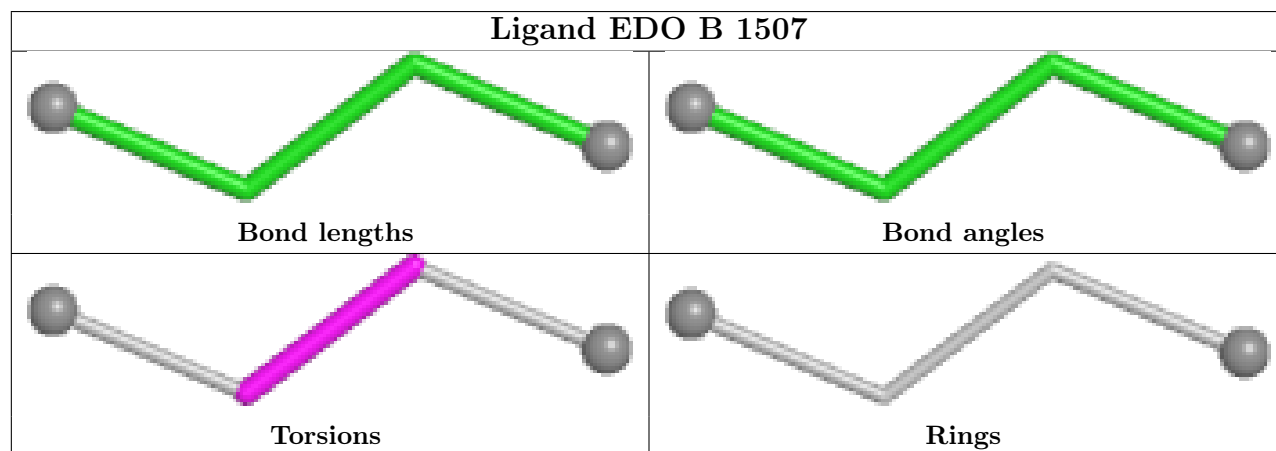
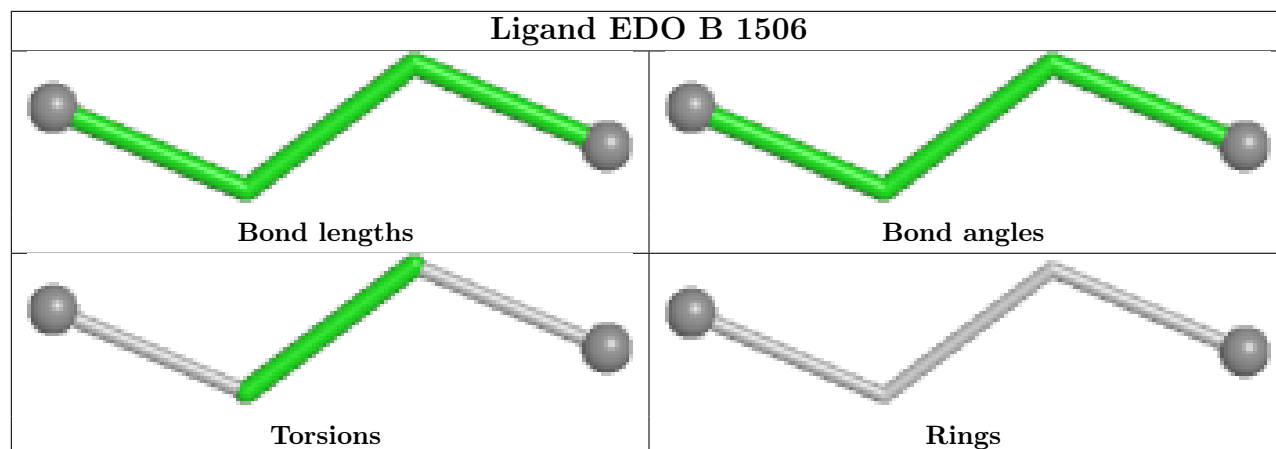


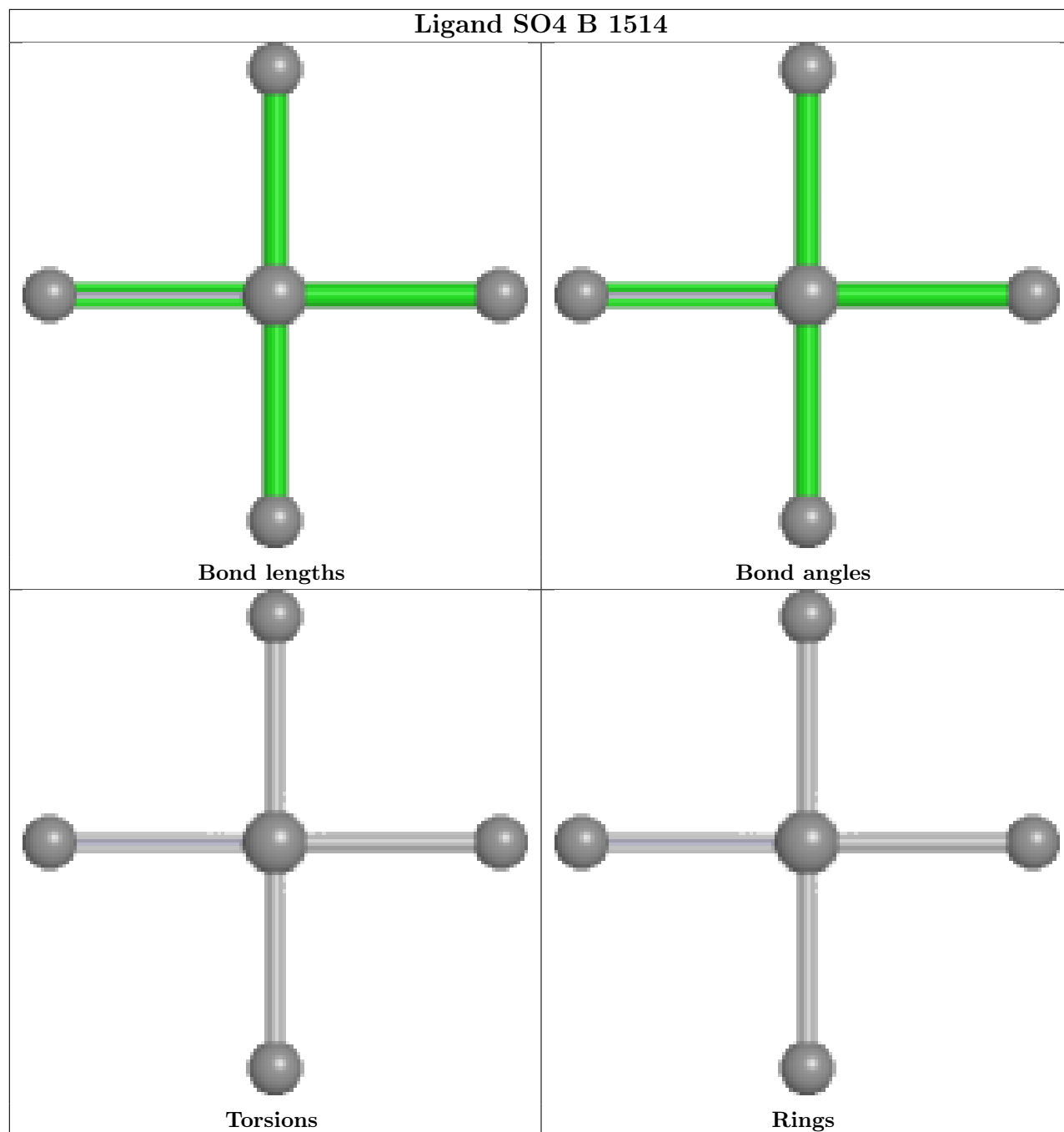


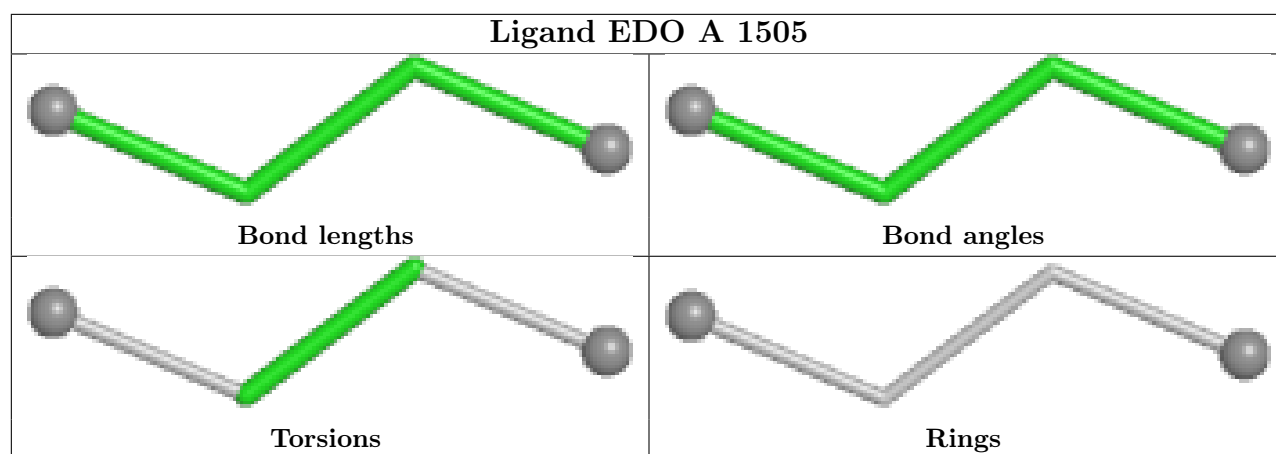


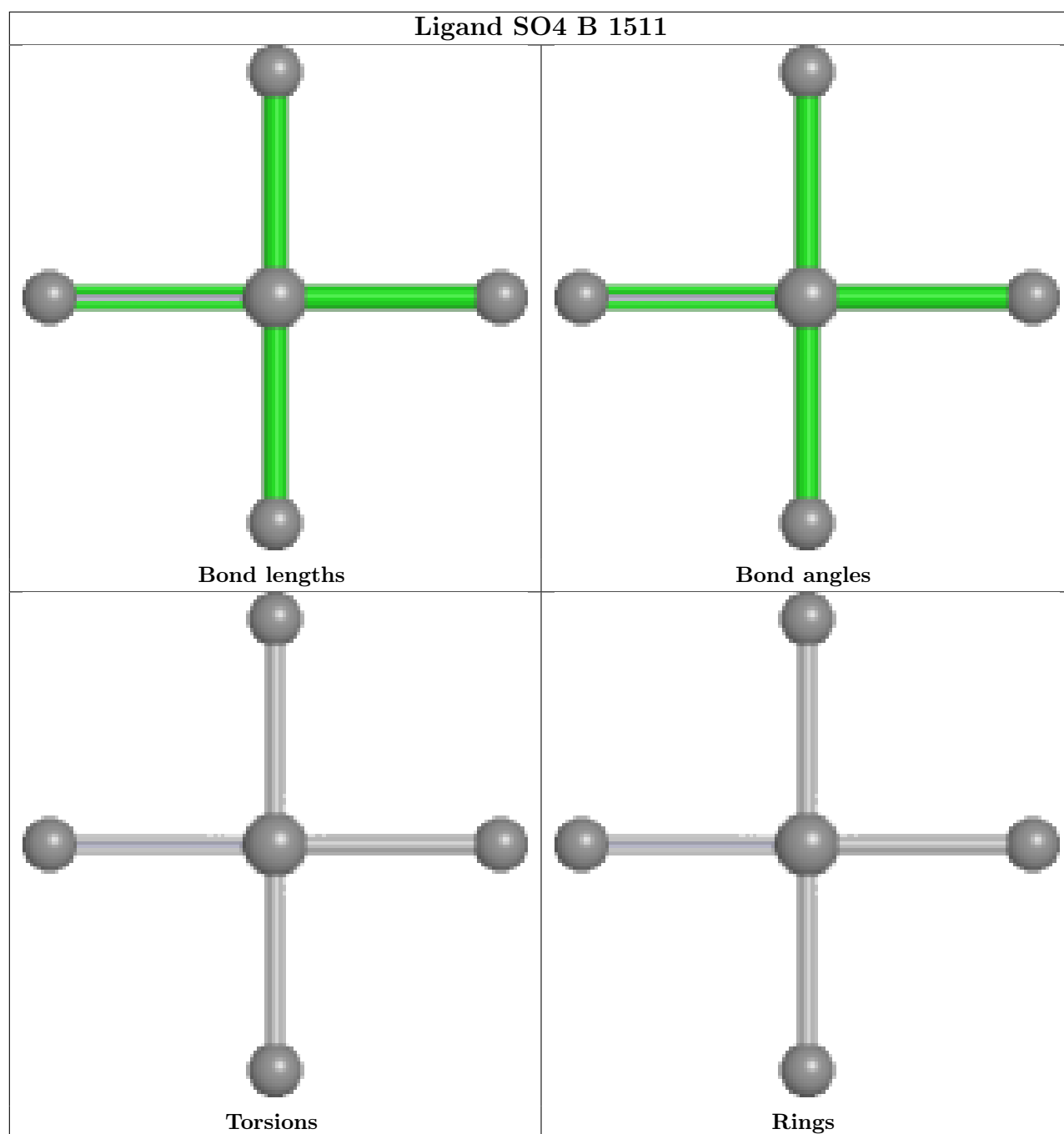


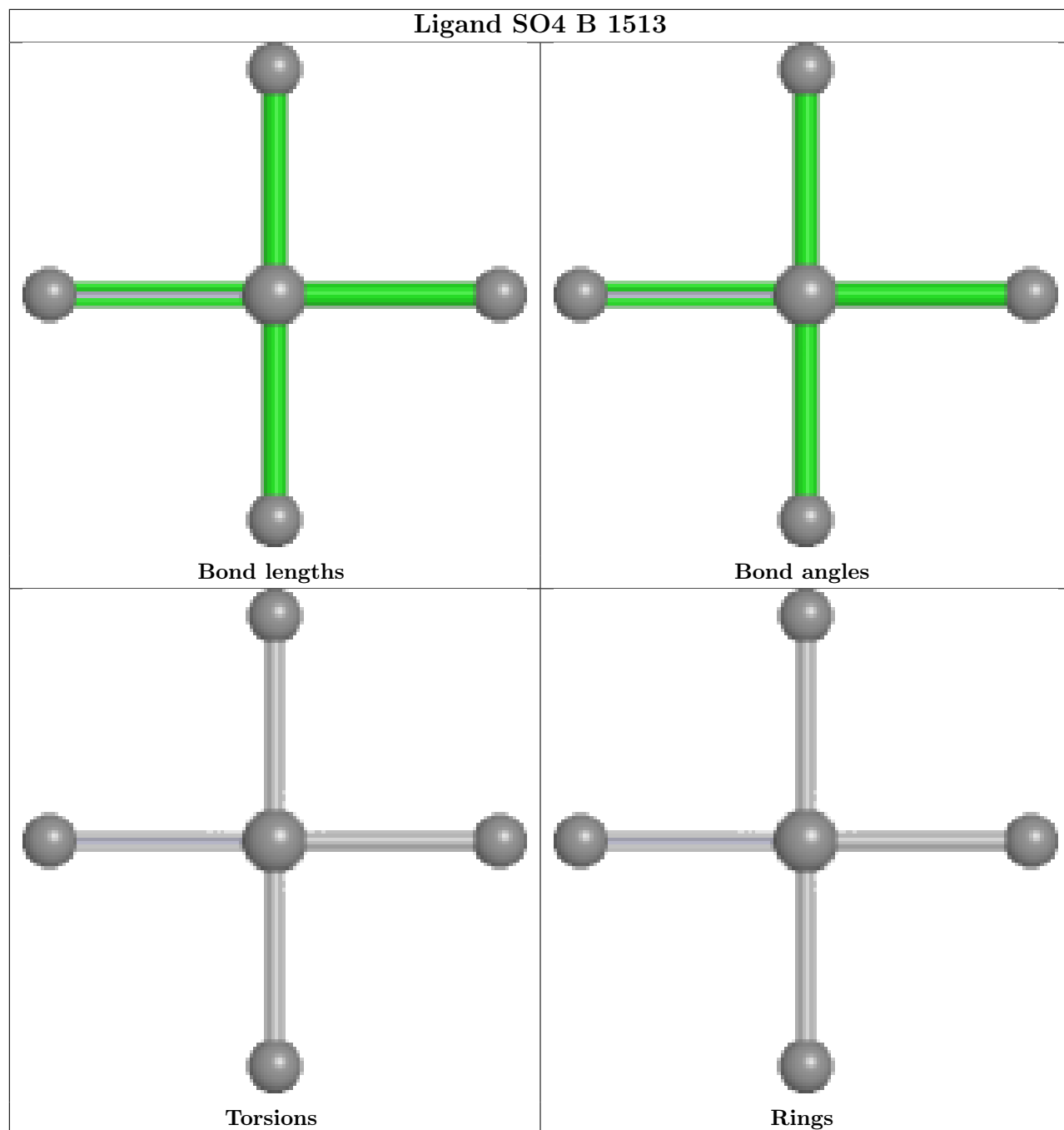


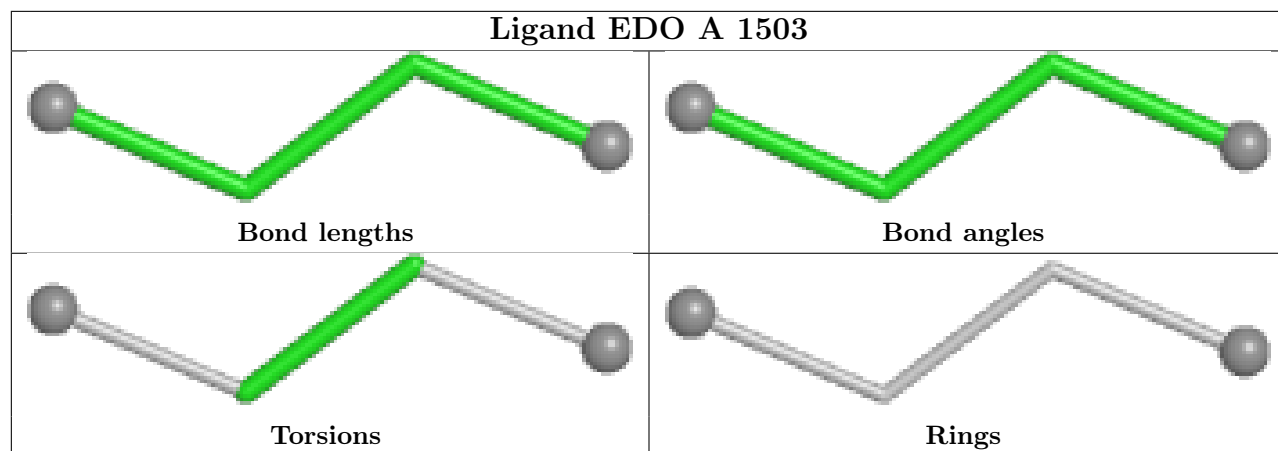


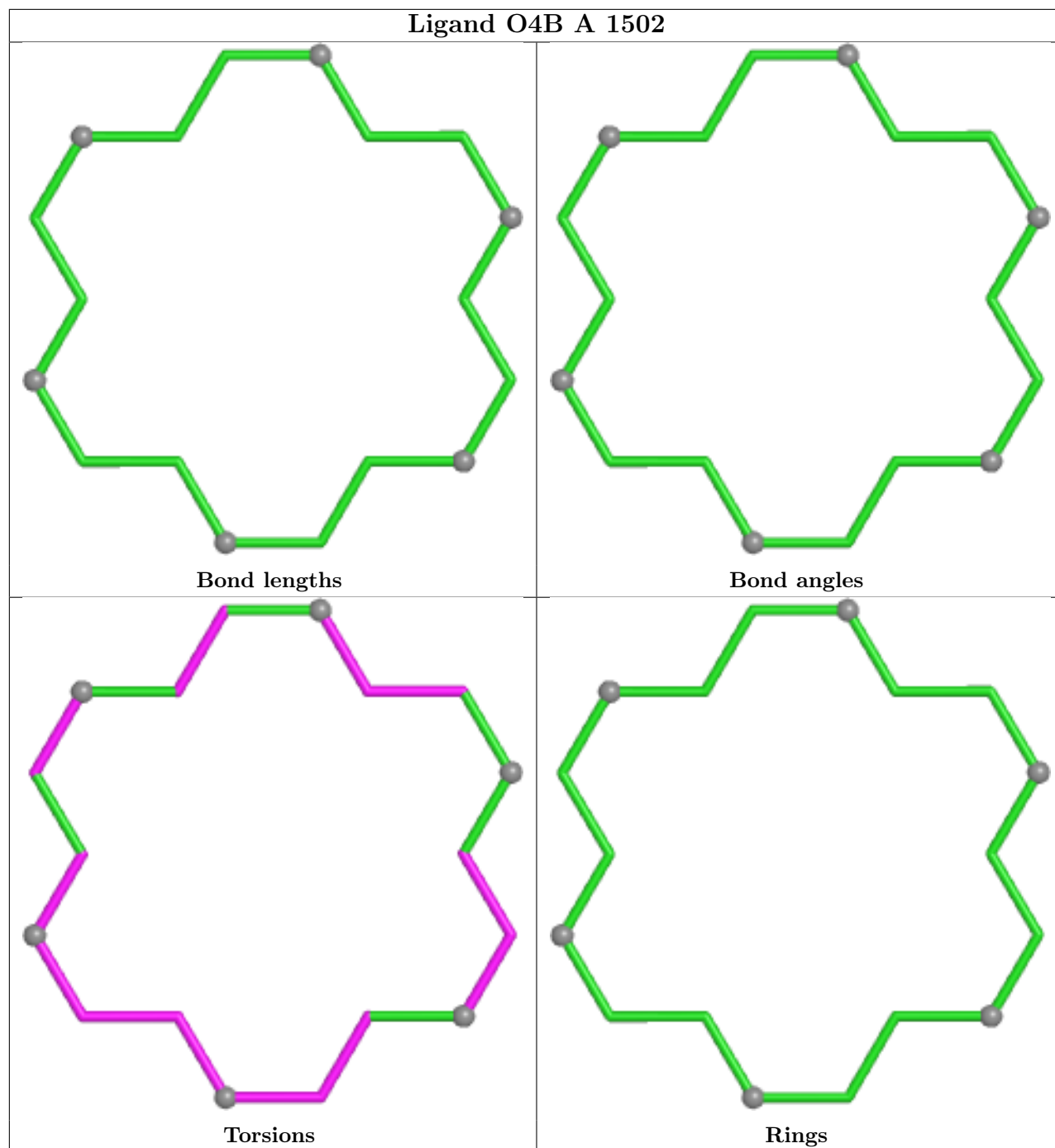


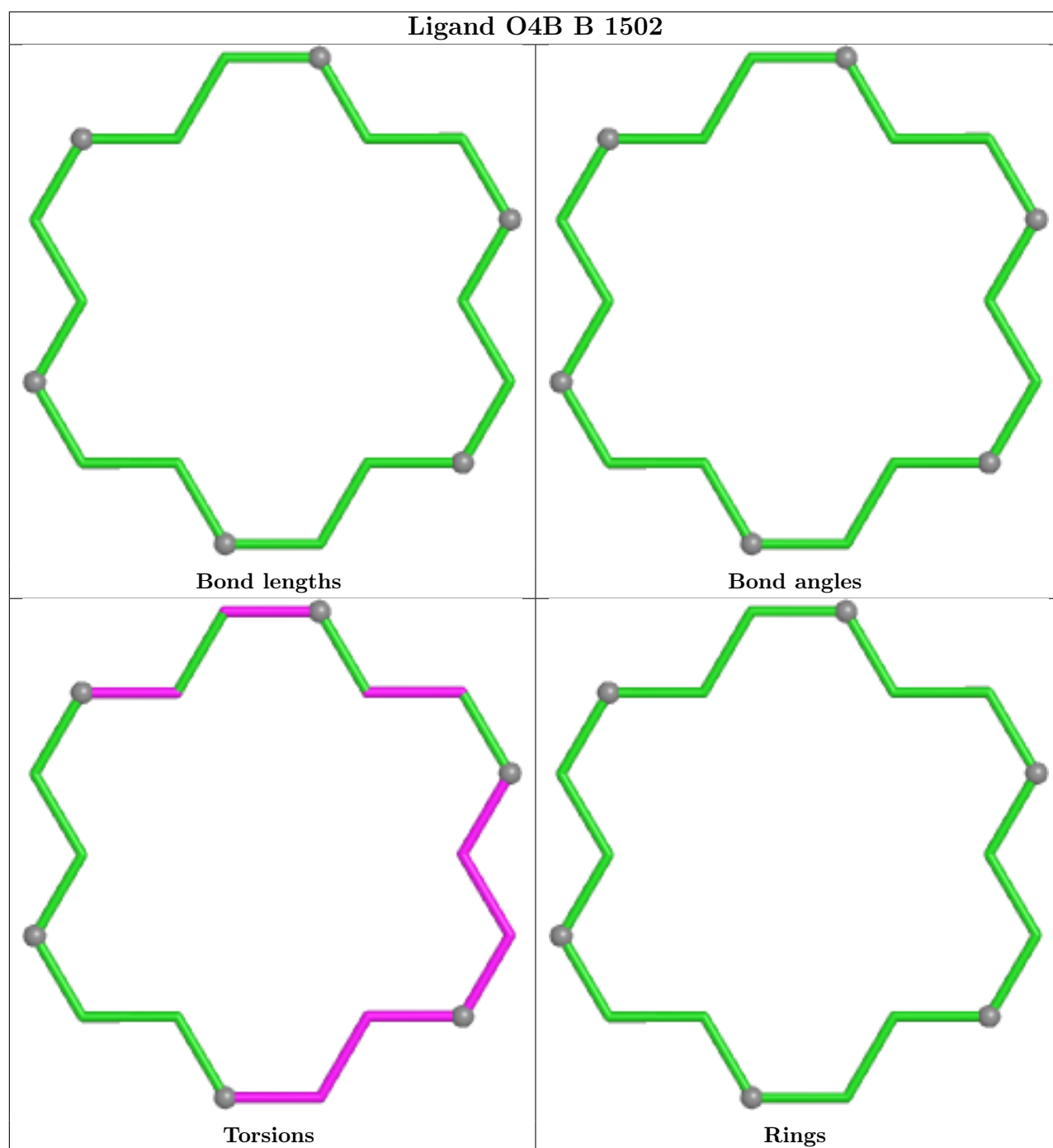


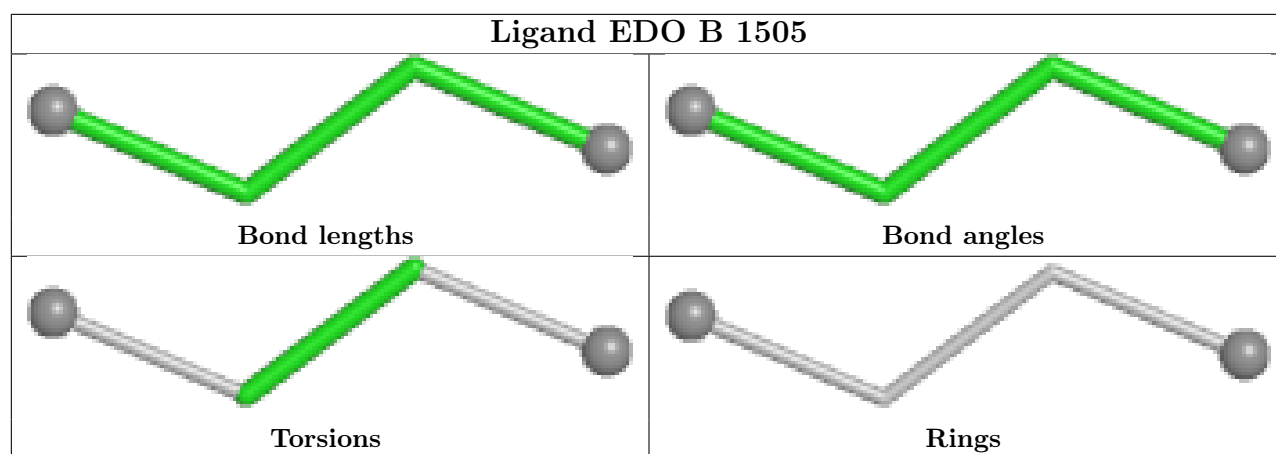


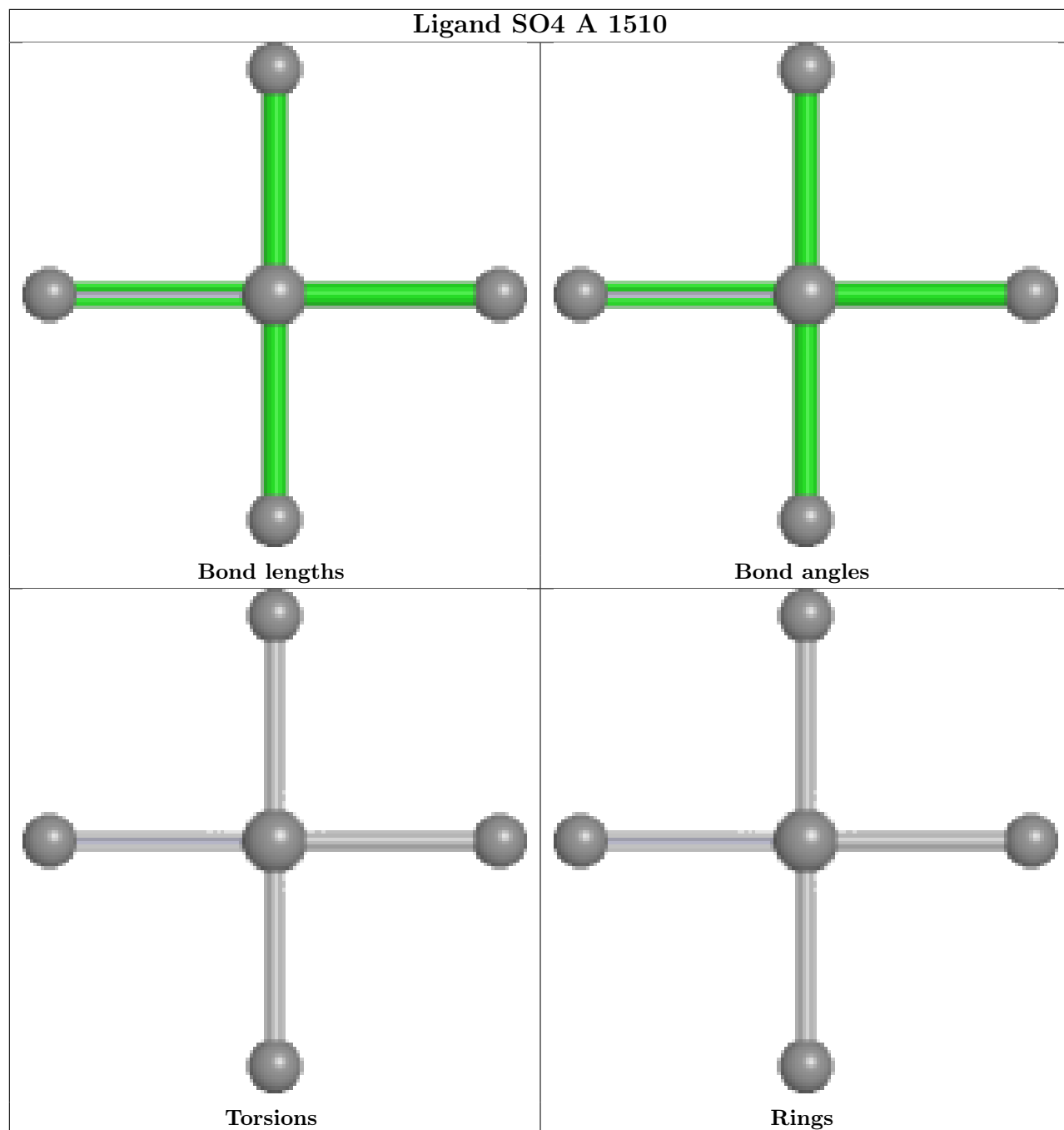


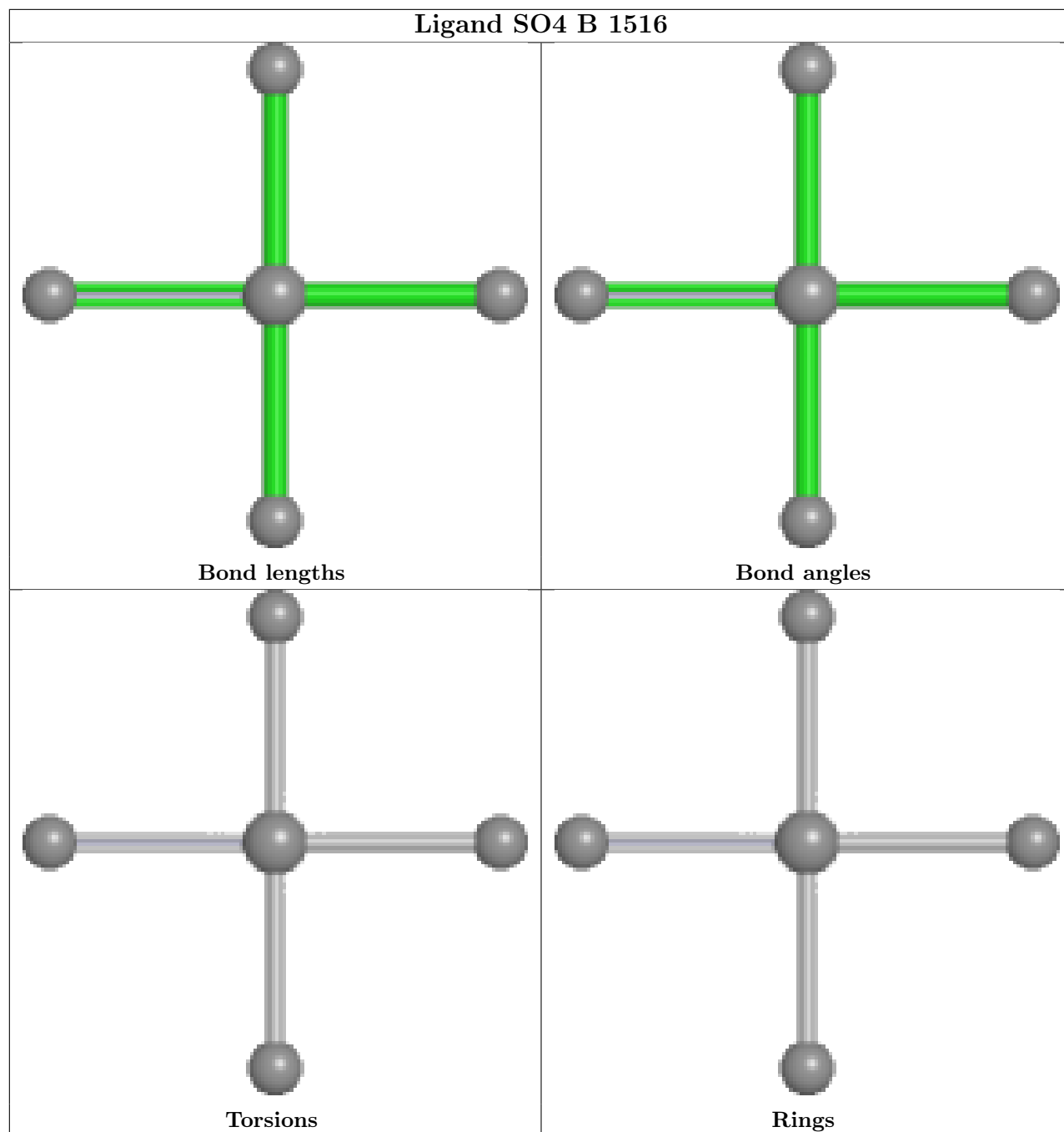












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
1	A	773/773 (100%)	0.10	40 (5%)	33 37	10, 21, 42, 85	6 (0%)
1	B	772/773 (99%)	0.26	76 (9%)	13 14	9, 21, 50, 90	6 (0%)
All	All	1545/1546 (99%)	0.18	116 (7%)	20 23	9, 21, 47, 90	12 (0%)

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1029	TYR	7.0
1	A	1203	GLY	6.4
1	A	1206	PHE	5.6
1	B	705	TRP	5.5
1	B	1442	HIS	5.2
1	B	734	ALA	5.1
1	A	1440	HIS	5.1
1	A	705	TRP	4.9
1	A	865	VAL	4.8
1	A	822	LEU	4.7
1	B	823	VAL	4.6
1	A	1443	HIS	4.6
1	A	1200	TRP	4.5
1	A	1201	VAL	4.5
1	B	760	TRP	4.4
1	B	1069	ASN	4.3
1	B	1041	THR	4.3
1	B	671	GLY	4.3
1	B	697	VAL	4.3
1	A	689	ALA	4.2
1	A	760	TRP	4.2
1	A	866	ASP	4.1
1	B	1040	ILE	4.1
1	B	1030	ALA	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	1203	GLY	3.8
1	B	761	ASP	3.8
1	B	822	LEU	3.7
1	B	689	ALA	3.7
1	B	1034	ALA	3.7
1	B	1037	ILE	3.7
1	B	672	ILE	3.6
1	B	1440	HIS	3.6
1	A	1202	GLY	3.6
1	A	1442	HIS	3.6
1	B	1206	PHE	3.6
1	B	692	PRO	3.6
1	B	1441	HIS	3.5
1	B	1036	GLY	3.4
1	A	1204	GLU	3.4
1	A	671	GLY	3.3
1	B	763	ALA	3.2
1	B	796	SER	3.2
1	A	1441	HIS	3.2
1	B	1050	LEU	3.2
1	A	762	ILE	3.1
1	B	762	ILE	3.1
1	B	680	ASP	3.1
1	A	867	GLY	3.1
1	A	690	SER	3.0
1	A	700	ASP	3.0
1	B	1066	LEU	3.0
1	B	1033	SER	3.0
1	A	841	GLU	3.0
1	A	697	VAL	2.9
1	B	1042	THR	2.9
1	B	1251	GLY	2.9
1	B	1032	LEU	2.9
1	B	897	ASP	2.8
1	B	699	GLY	2.8
1	B	706	VAL	2.8
1	B	693	ASN	2.7
1	B	799	LEU	2.7
1	B	1071	PRO	2.6
1	B	701	SER	2.6
1	A	699	GLY	2.6
1	A	823	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	761	ASP	2.6
1	A	1041	THR	2.6
1	A	864	VAL	2.6
1	A	763	ALA	2.6
1	B	690	SER	2.6
1	B	698	LYS	2.6
1	B	735	GLY	2.6
1	B	1038	ASN	2.6
1	B	1054	VAL	2.5
1	B	1204	GLU	2.5
1	B	695	GLY	2.5
1	B	1068	GLY	2.5
1	B	866	ASP	2.4
1	B	758	GLY	2.4
1	B	1070	ILE	2.4
1	B	1039	ASP	2.4
1	B	793	TRP	2.4
1	B	1049	LEU	2.4
1	B	1043	PHE	2.4
1	B	1252	PHE	2.4
1	A	693	ASN	2.4
1	B	704	GLY	2.4
1	B	679	PHE	2.4
1	B	1067	GLU	2.3
1	B	696	PHE	2.3
1	B	703	VAL	2.3
1	B	841	GLU	2.3
1	A	698	LYS	2.3
1	B	1416	THR	2.3
1	A	1205	VAL	2.3
1	A	692	PRO	2.3
1	B	674	ILE	2.3
1	A	758	GLY	2.2
1	B	1028	SER	2.2
1	A	706	VAL	2.2
1	B	685	VAL	2.2
1	B	1052	ALA	2.2
1	B	887	HIS	2.1
1	B	1035	MET	2.1
1	A	863	LEU	2.1
1	B	1055	THR	2.1
1	A	1029	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	1251	GLY	2.1
1	B	688	VAL	2.1
1	B	716	ASN	2.1
1	B	691	ASP	2.1
1	B	1059	TRP	2.1
1	A	1172	LEU	2.0
1	B	1057	THR	2.0
1	A	921	TRP	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	SO4	B	1515	5/5	0.70	0.16	74,76,85,88	0
7	CL	B	1520	1/1	0.73	0.34	73,73,73,73	0
3	O4B	A	1502	18/18	0.74	0.26	47,61,94,101	0
5	SO4	A	1512	5/5	0.74	0.17	62,83,85,91	0
5	SO4	B	1516	5/5	0.77	0.15	69,86,88,90	0
5	SO4	B	1513	5/5	0.78	0.14	55,70,75,75	0
9	PEG	B	1503	7/7	0.79	0.18	31,33,43,46	0
5	SO4	B	1514	5/5	0.80	0.13	79,80,84,85	0
6	NA	A	1517	1/1	0.81	0.22	49,49,49,49	0
2	EDO	B	1506	4/4	0.81	0.16	43,44,45,48	0
2	EDO	B	1508	4/4	0.81	0.17	45,46,46,48	0
5	SO4	B	1512	5/5	0.83	0.15	42,45,56,62	0
5	SO4	A	1511	5/5	0.83	0.12	54,70,72,78	0
3	O4B	B	1502	18/18	0.84	0.20	36,45,79,83	0
2	EDO	B	1504	4/4	0.85	0.15	37,40,40,46	0

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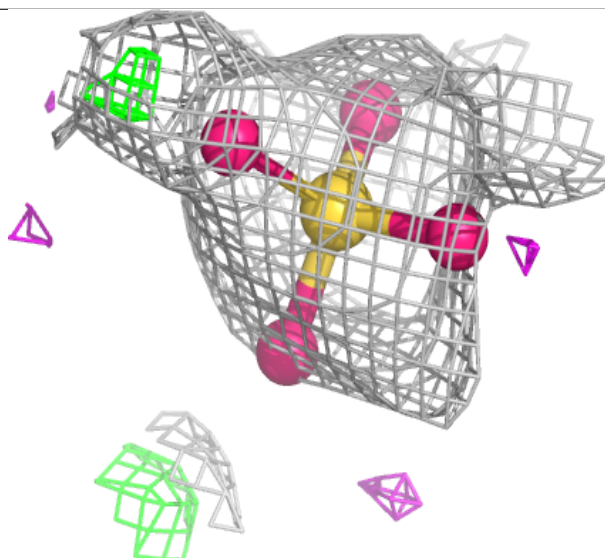
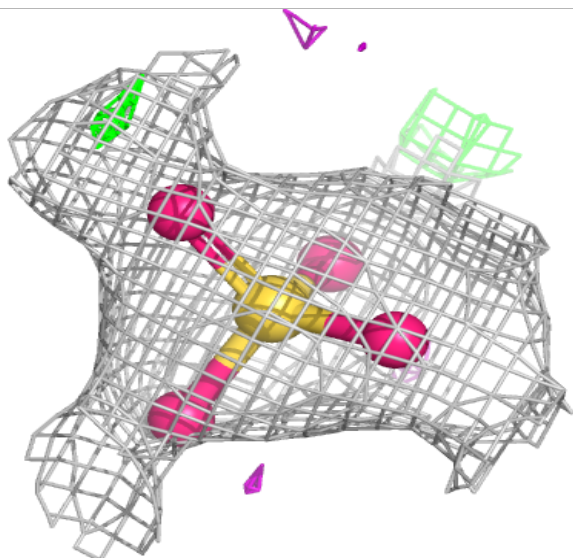
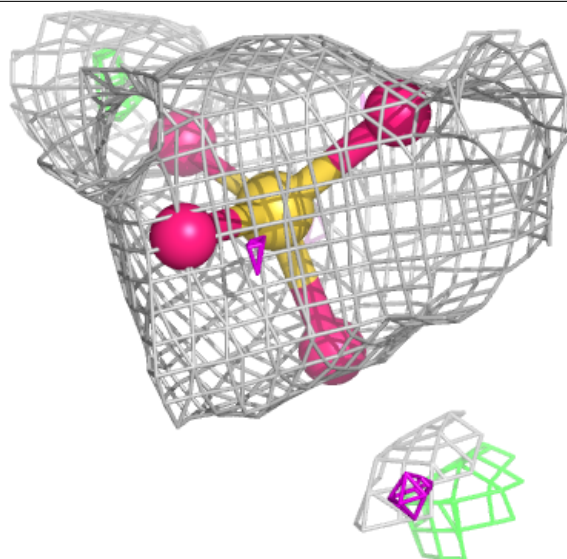
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	SO4	A	1510	5/5	0.85	0.12	43,56,60,68	0
2	EDO	A	1505	4/4	0.85	0.16	49,52,53,56	0
2	EDO	B	1505	4/4	0.86	0.14	34,38,40,41	0
8	EPE	B	1501	15/15	0.87	0.19	17,23,26,30	15
5	SO4	A	1513	5/5	0.87	0.14	46,49,68,70	0
2	EDO	A	1506	4/4	0.88	0.14	40,44,45,46	0
2	EDO	A	1503	4/4	0.88	0.16	36,37,43,46	0
2	EDO	B	1507	4/4	0.89	0.14	23,35,42,43	0
6	NA	B	1518	1/1	0.90	0.16	42,42,42,42	0
2	EDO	A	1504	4/4	0.90	0.14	28,35,42,43	0
6	NA	A	1516	1/1	0.90	0.12	48,48,48,48	0
2	EDO	A	1501	4/4	0.90	0.14	39,46,48,50	0
4	MG	B	1510	1/1	0.92	0.11	38,38,38,38	0
4	MG	A	1508	1/1	0.92	0.09	39,39,39,39	0
6	NA	A	1515	1/1	0.92	0.21	40,40,40,40	0
6	NA	A	1514	1/1	0.95	0.13	41,41,41,41	0
6	NA	B	1517	1/1	0.95	0.10	41,41,41,41	0
4	MG	A	1509	1/1	0.97	0.06	23,23,23,23	0
5	SO4	B	1511	5/5	0.97	0.07	31,35,42,49	0
4	MG	A	1507	1/1	0.99	0.03	17,17,17,17	0
4	MG	B	1509	1/1	0.99	0.02	17,17,17,17	0
7	CL	B	1519	1/1	1.00	0.01	17,17,17,17	0
7	CL	A	1518	1/1	1.00	0.03	17,17,17,17	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.

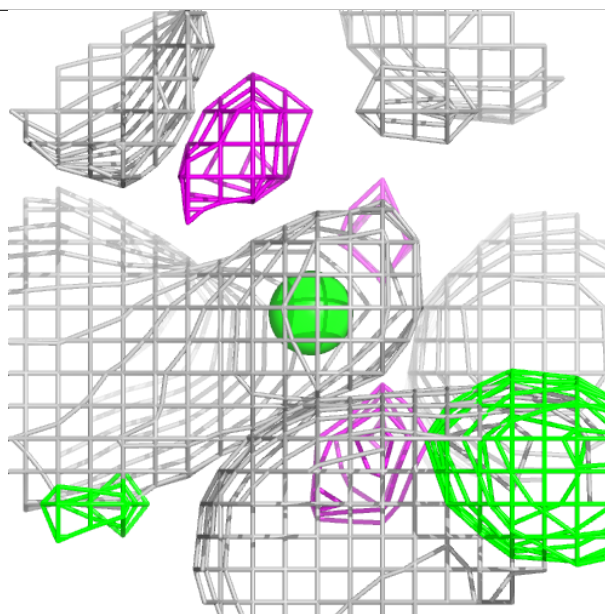
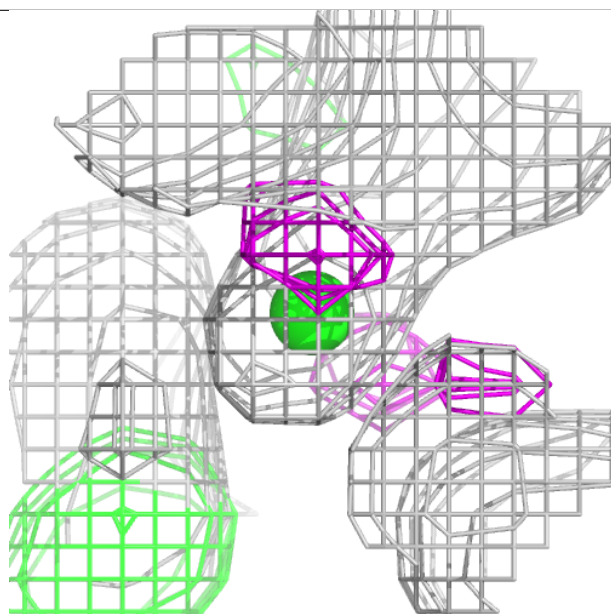
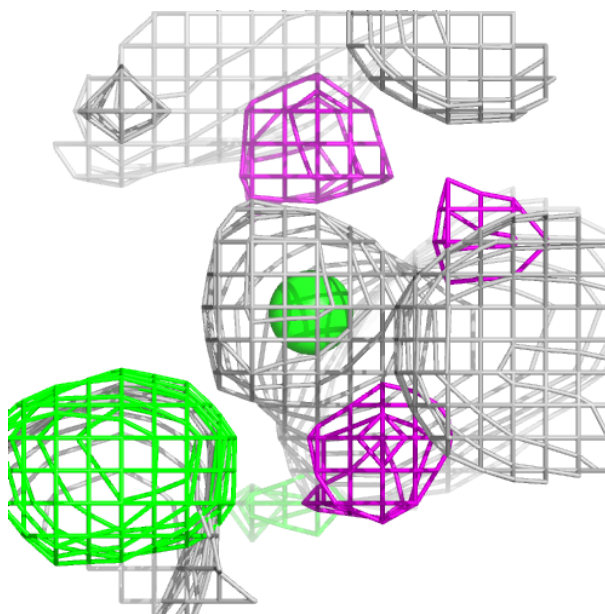
**Electron density around SO4 B 1515:**

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



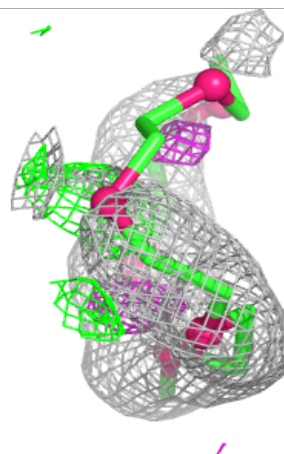
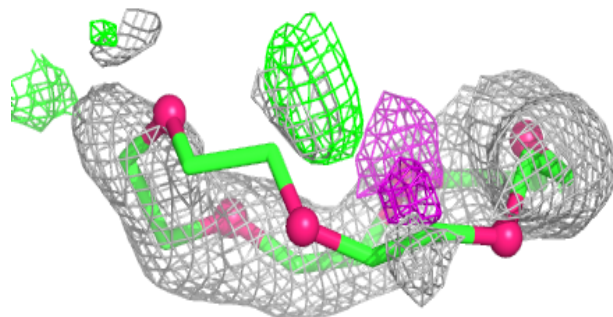
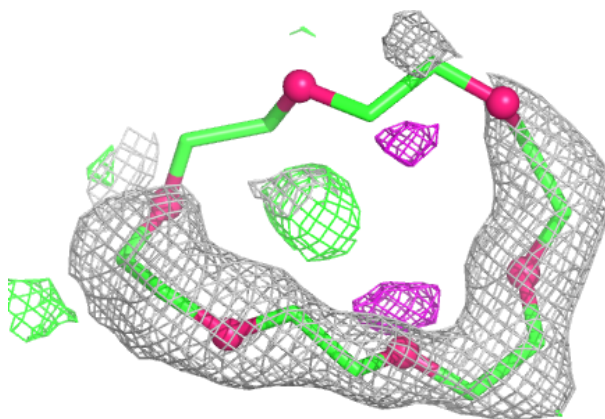
**Electron density around CL B 1520:**

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



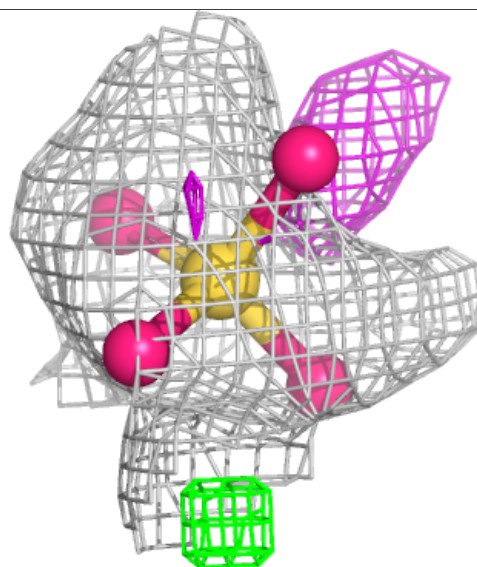
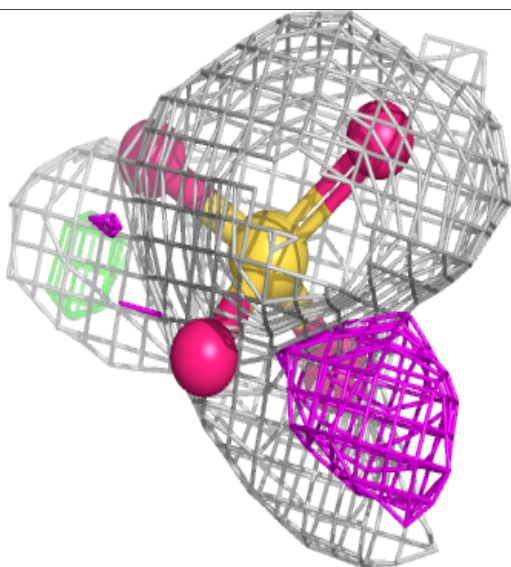
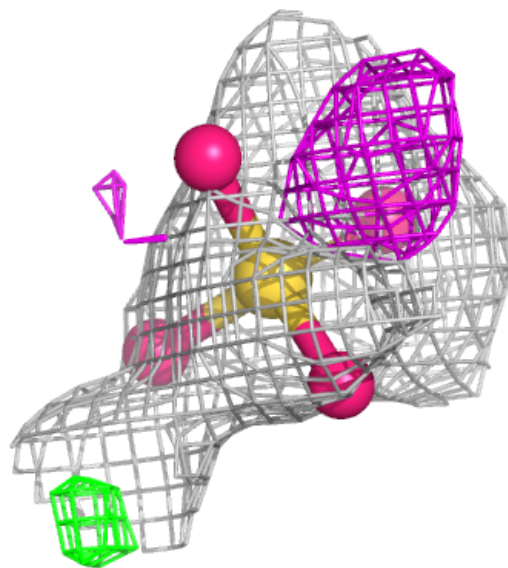
**Electron density around O4B A 1502:**

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



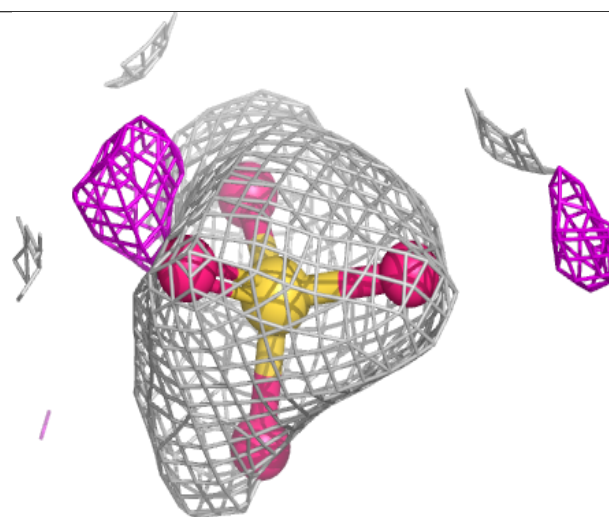
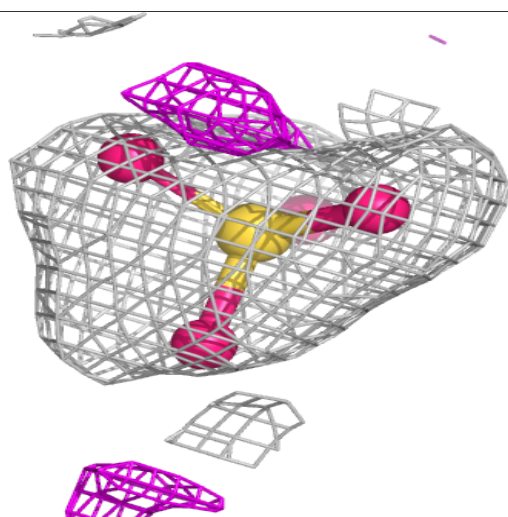
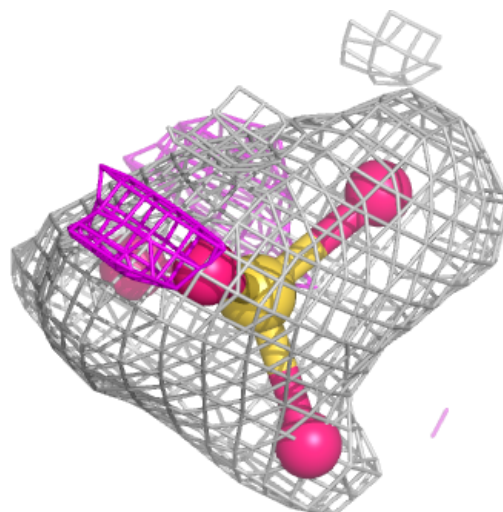
**Electron density around SO4 A 1512:**

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



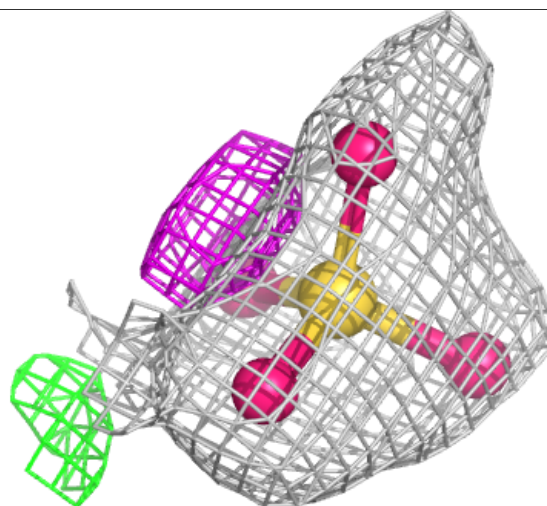
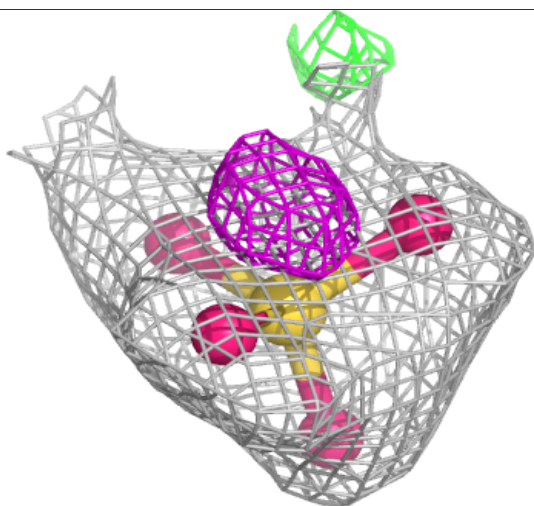
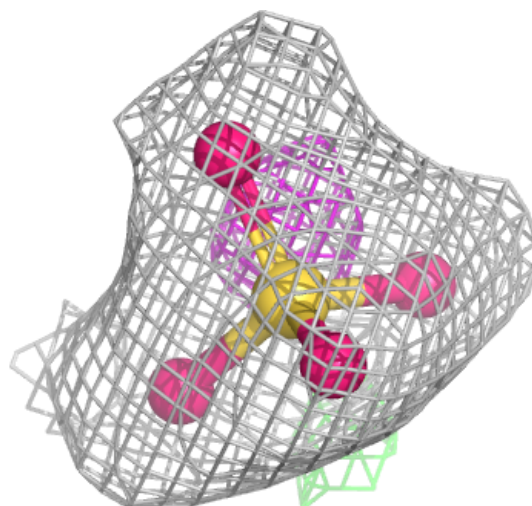
**Electron density around SO4 B 1516:**

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



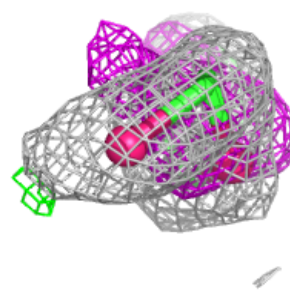
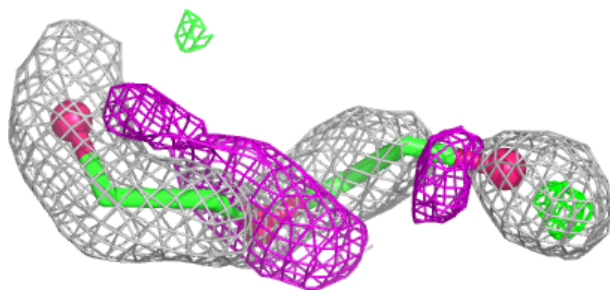
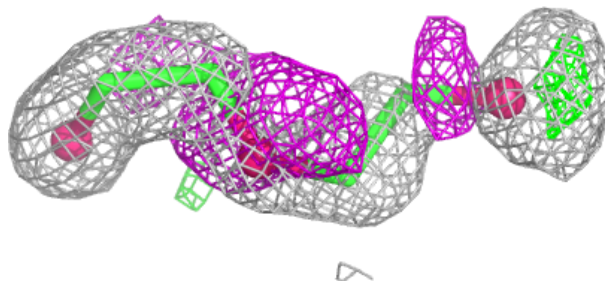
**Electron density around SO4 B 1513:**

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



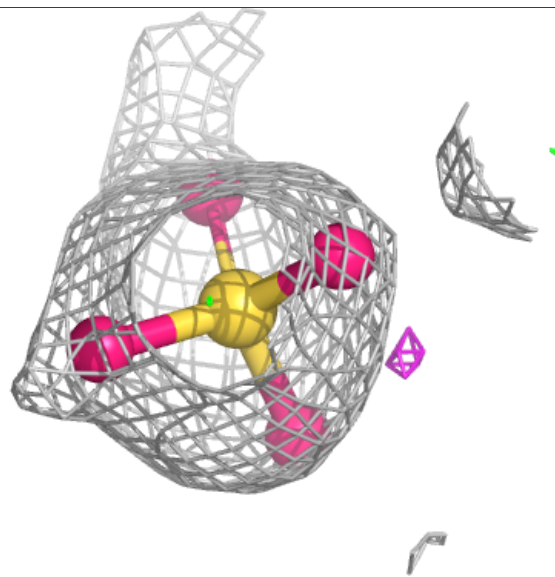
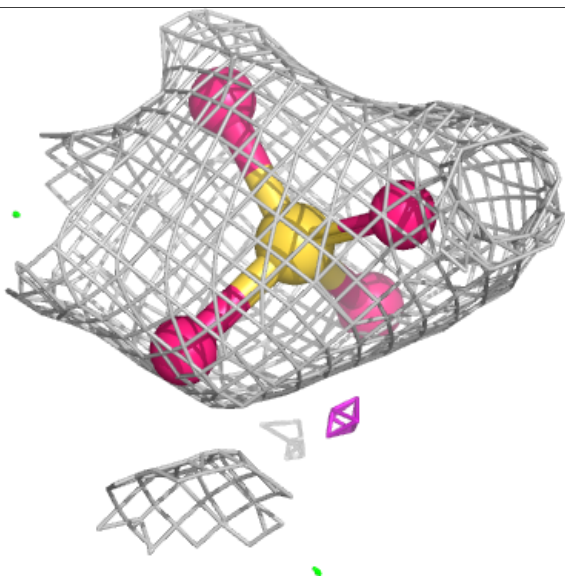
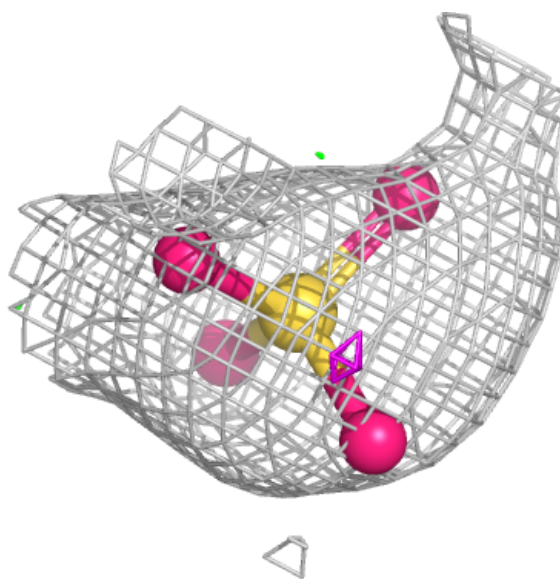
**Electron density around PEG B 1503:**

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



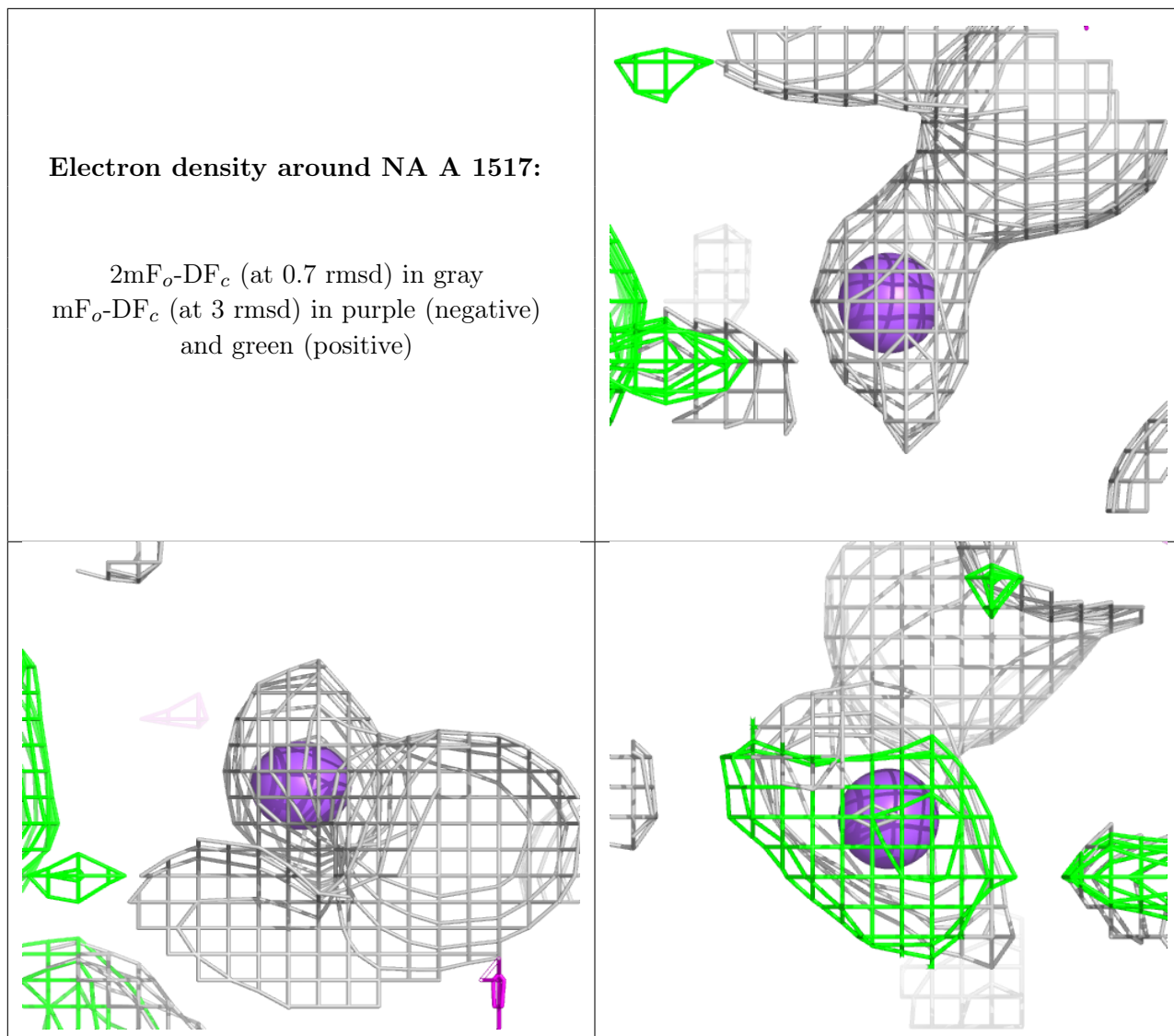
**Electron density around SO4 B 1514:**

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



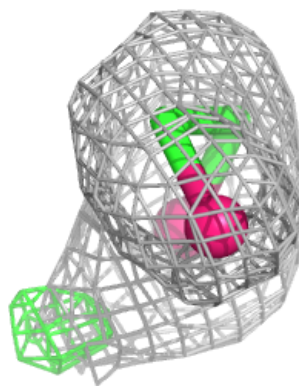
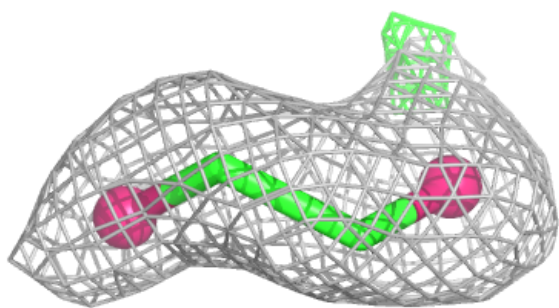
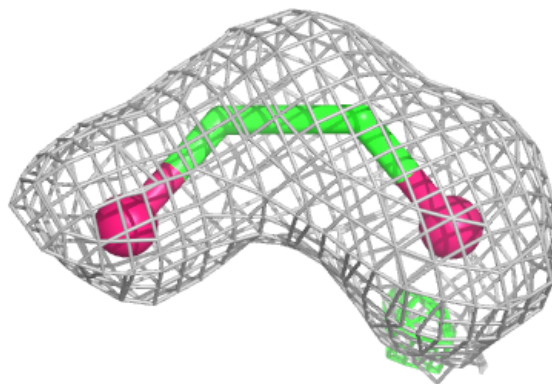
**Electron density around NA A 1517:**

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



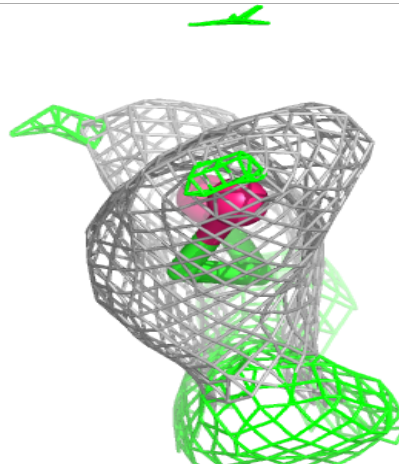
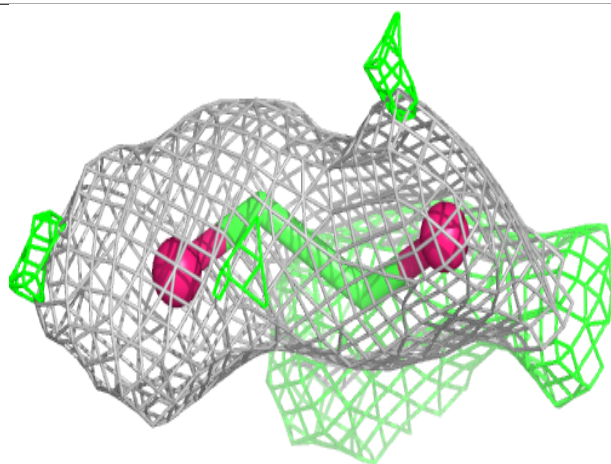
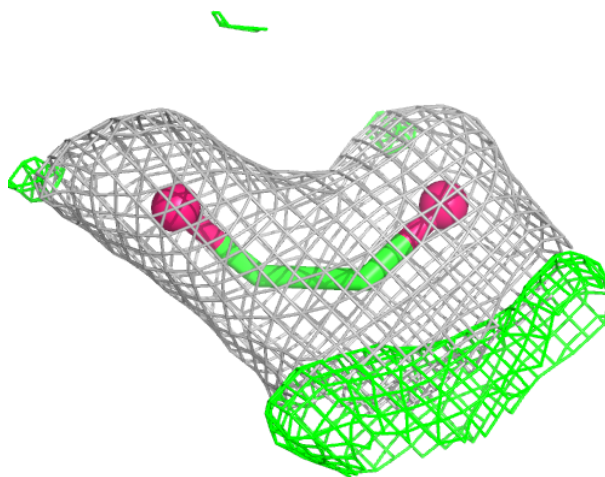
**Electron density around EDO B 1506:**

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



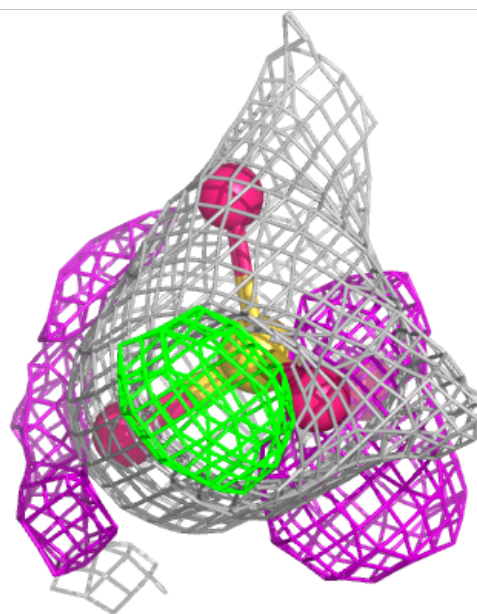
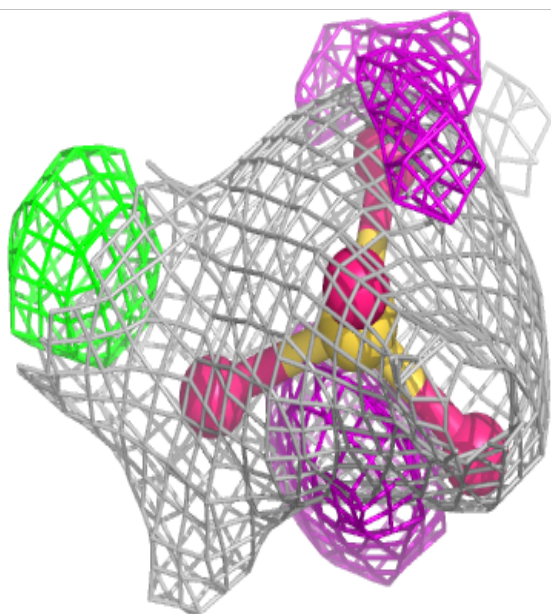
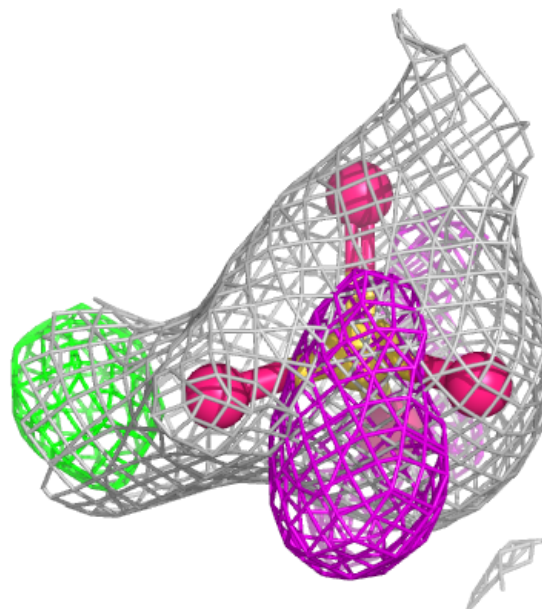
**Electron density around EDO B 1508:**

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



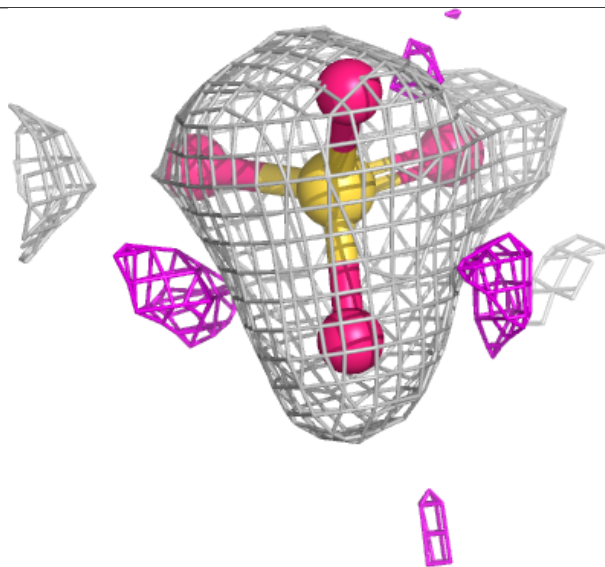
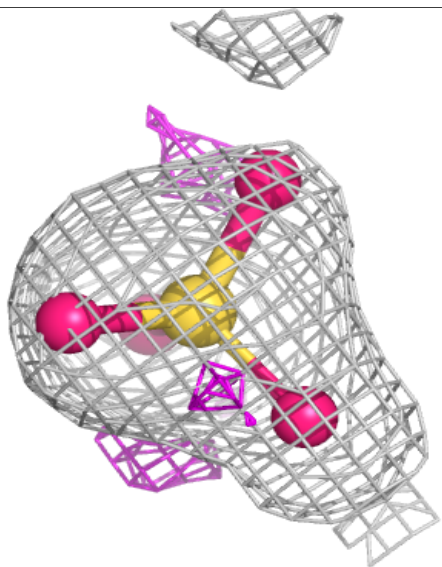
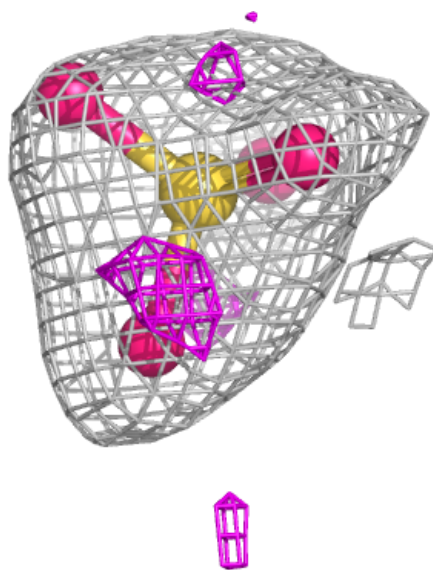
**Electron density around SO4 B 1512:**

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



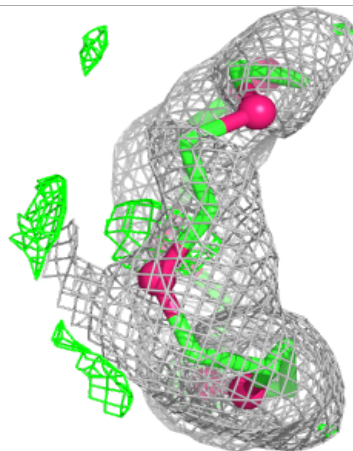
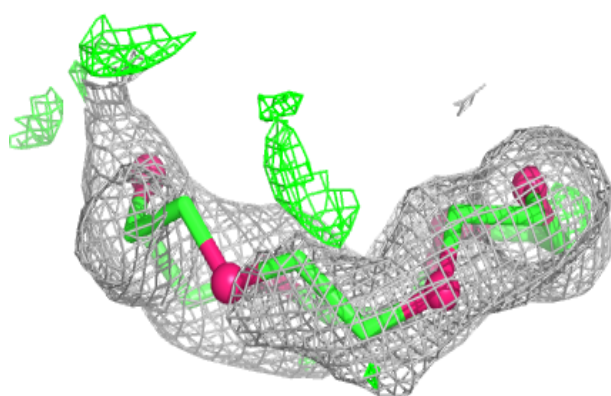
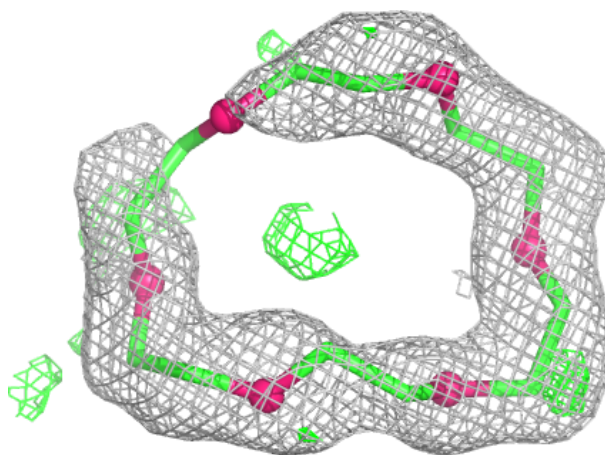
**Electron density around SO4 A 1511:**

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and green (positive)



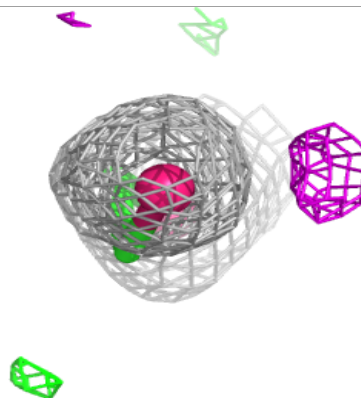
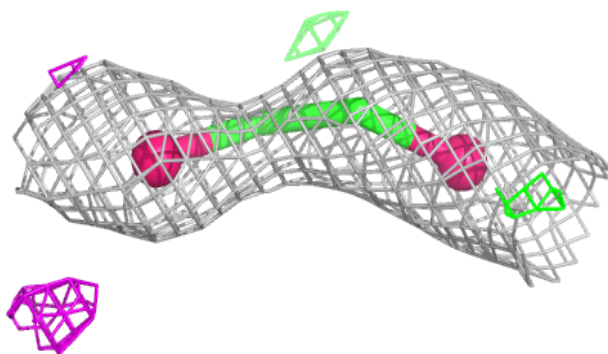
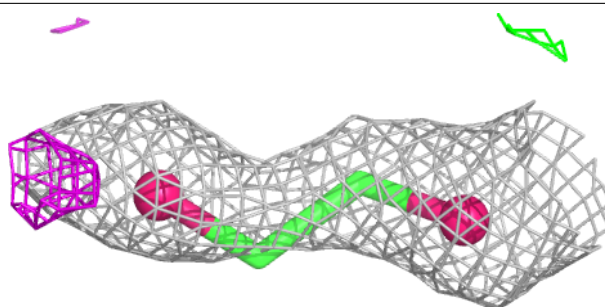
**Electron density around O4B B 1502:**

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



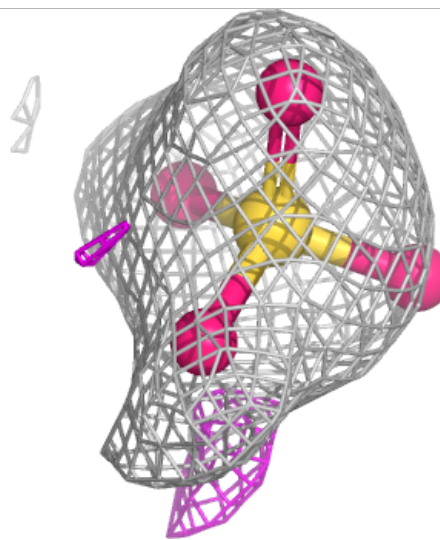
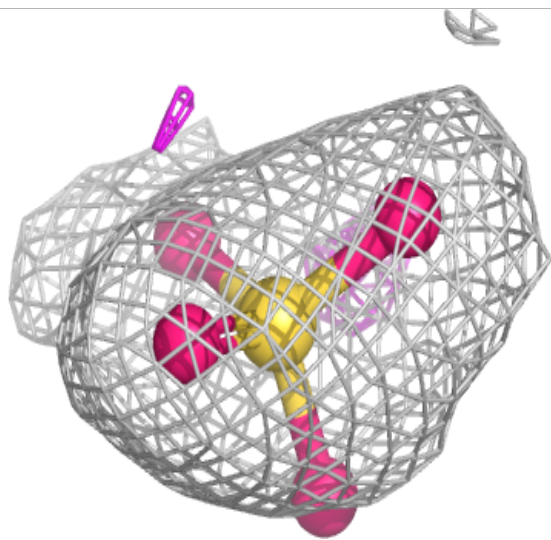
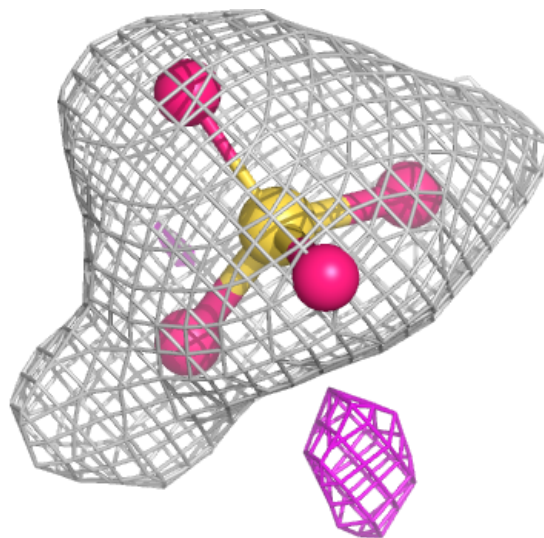
**Electron density around EDO B 1504:**

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



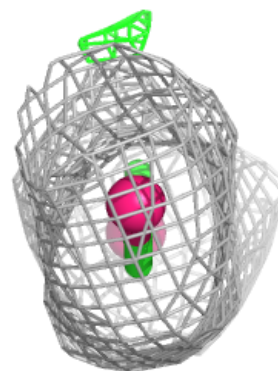
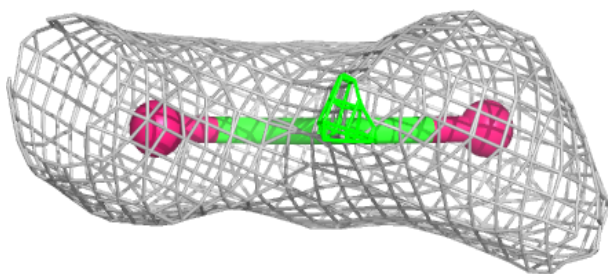
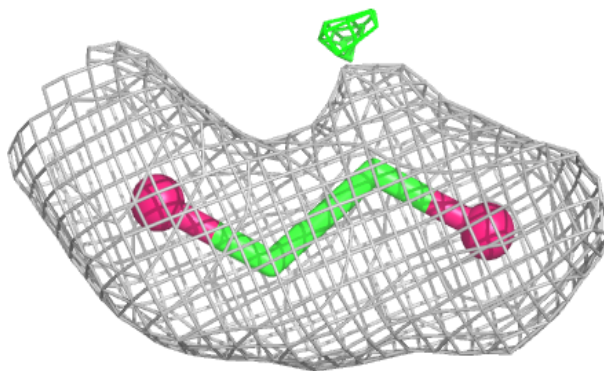
**Electron density around SO4 A 1510:**

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and green (positive)

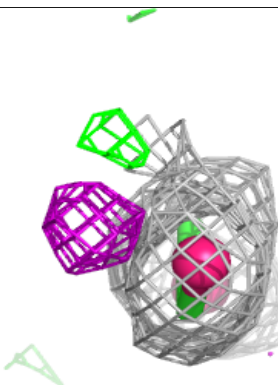
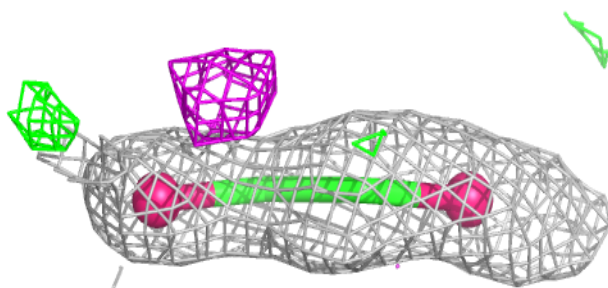
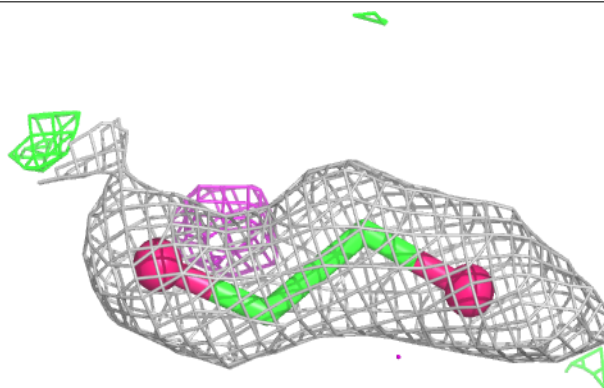


**Electron density around EDO A 1505:**

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

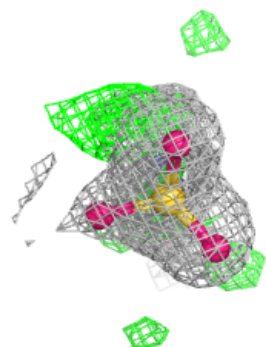
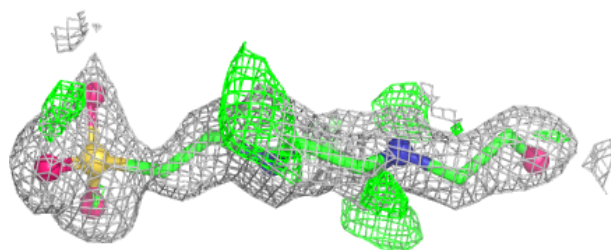
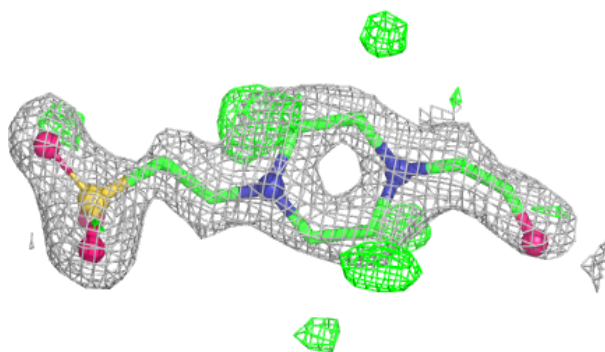
**Electron density around EDO B 1505:**

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



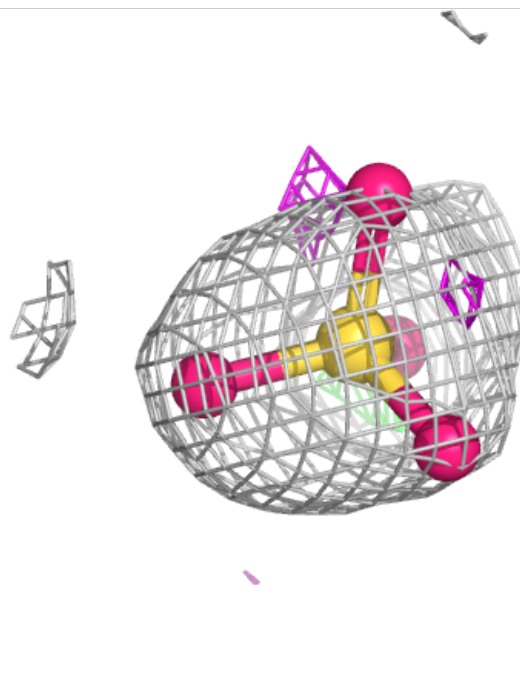
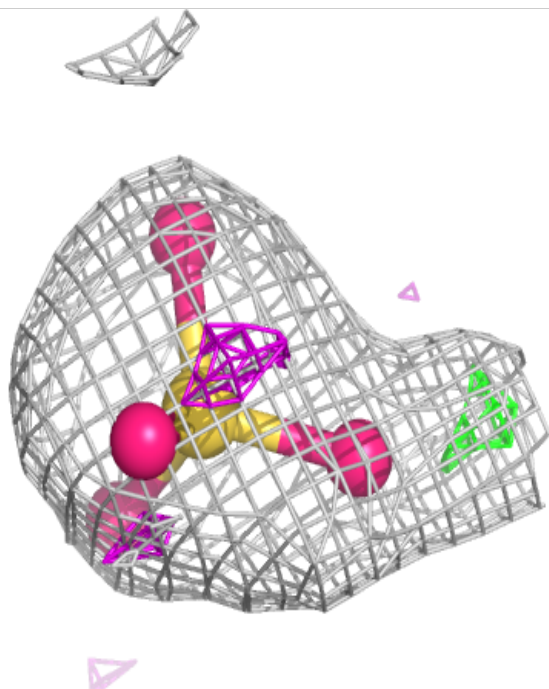
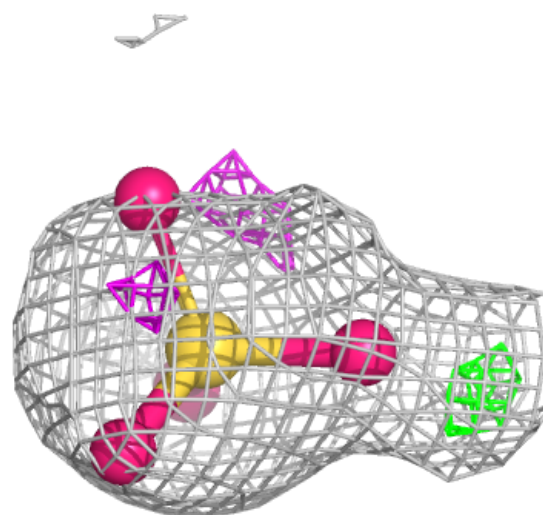
**Electron density around EPE B 1501:**

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



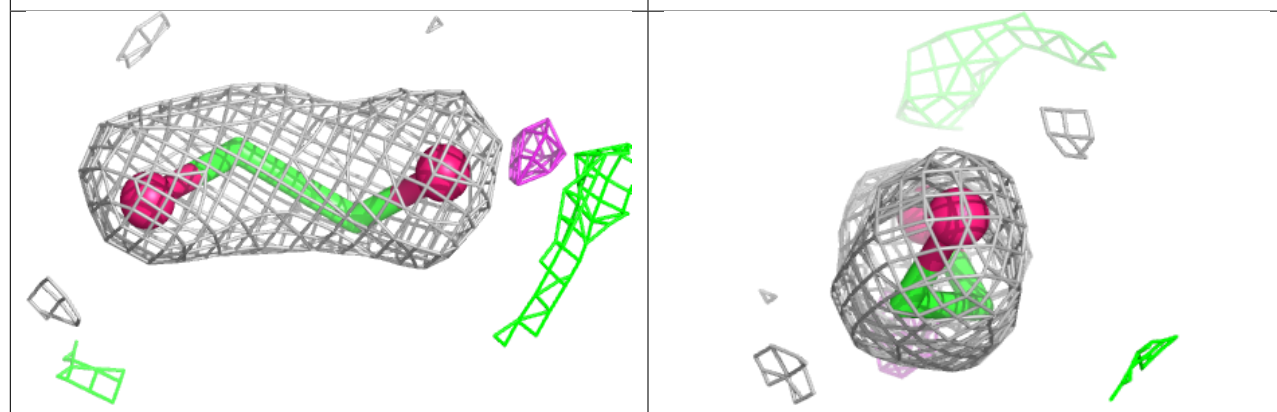
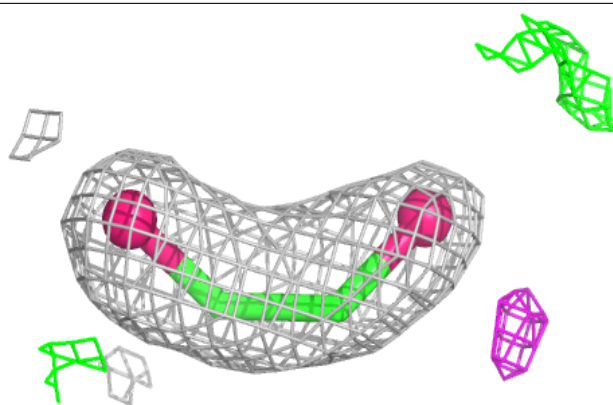
**Electron density around SO4 A 1513:**

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



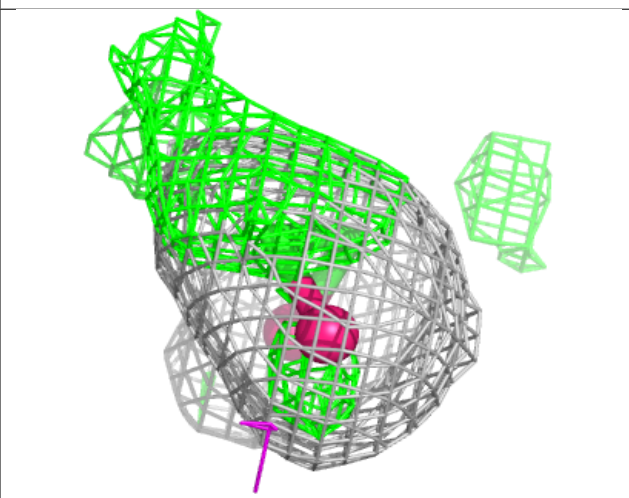
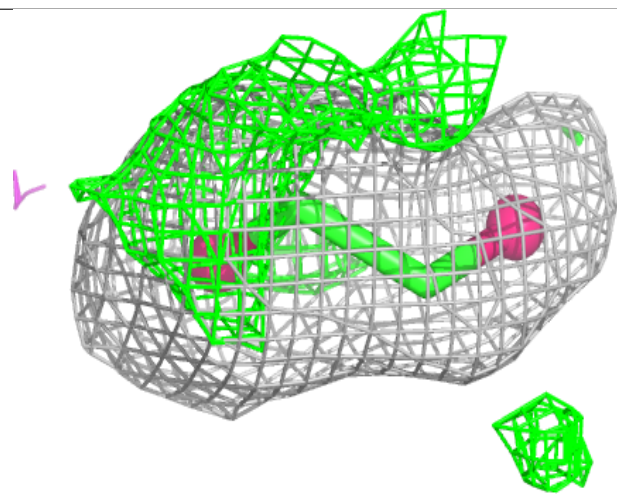
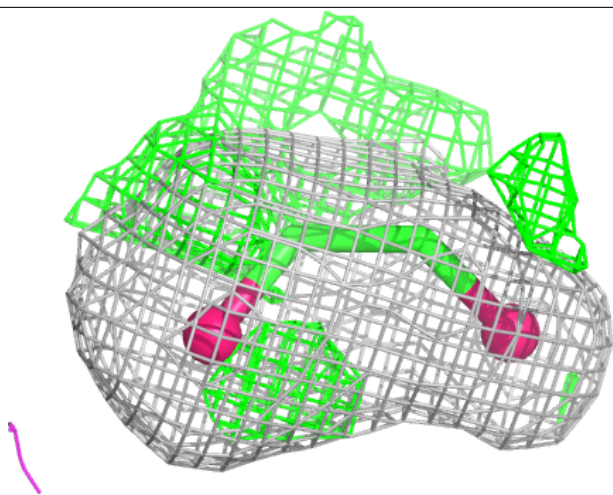
**Electron density around EDO A 1506:**

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



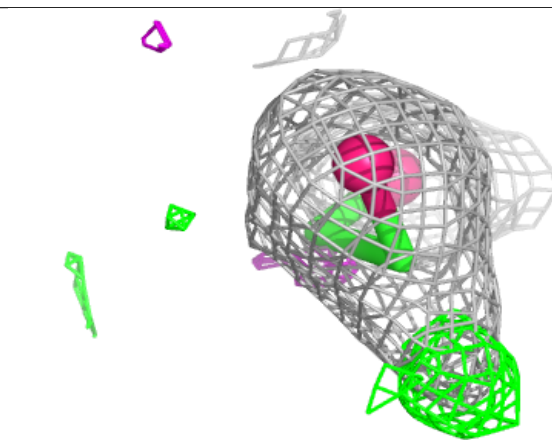
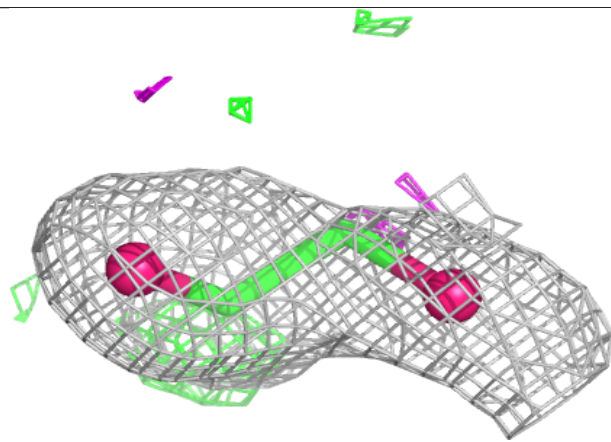
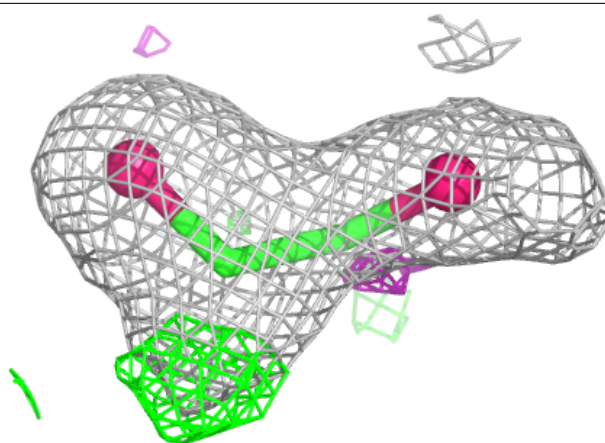
**Electron density around EDO A 1503:**

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



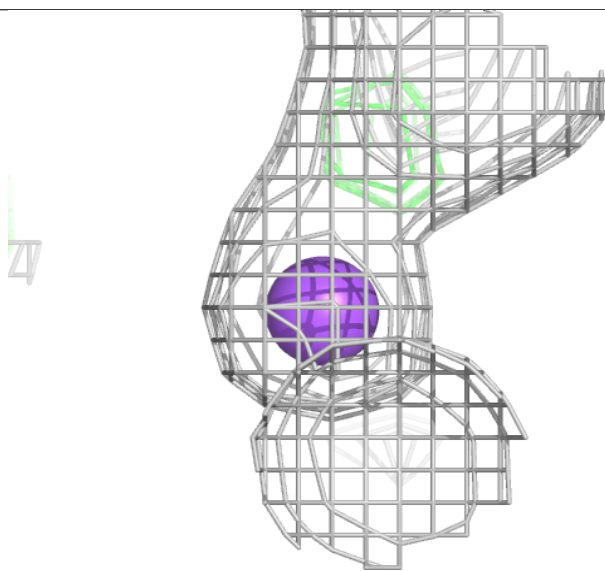
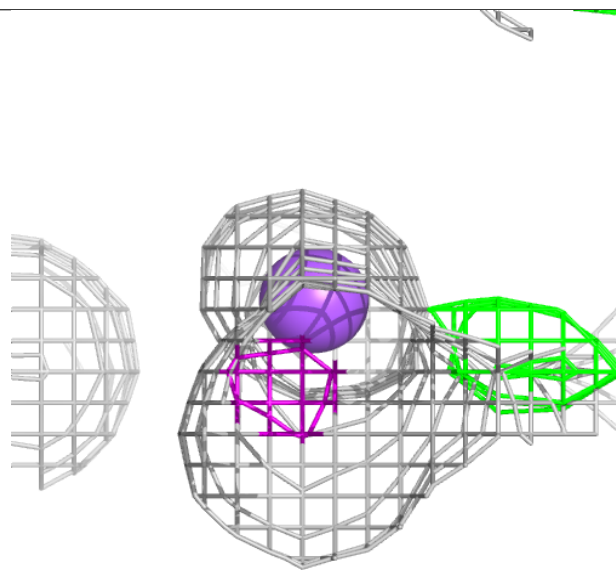
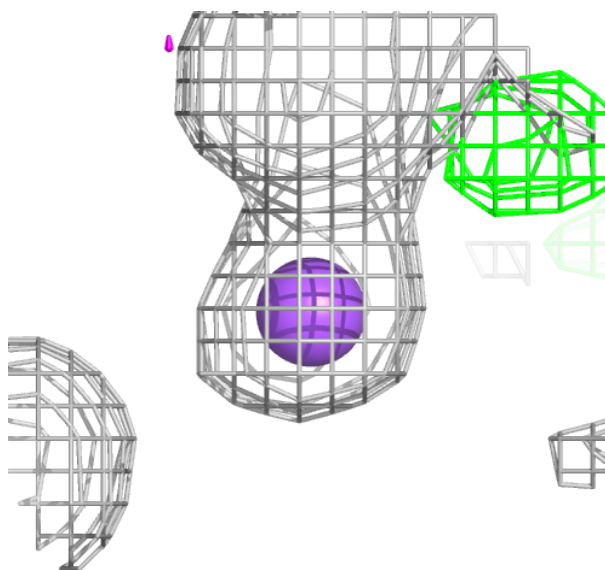
**Electron density around EDO B 1507:**

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



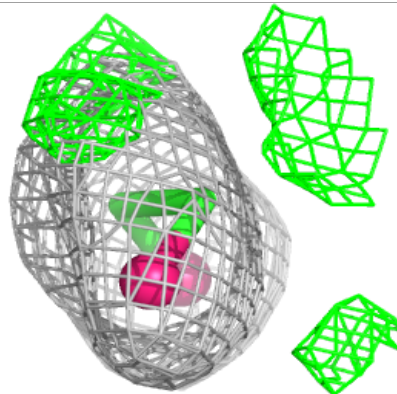
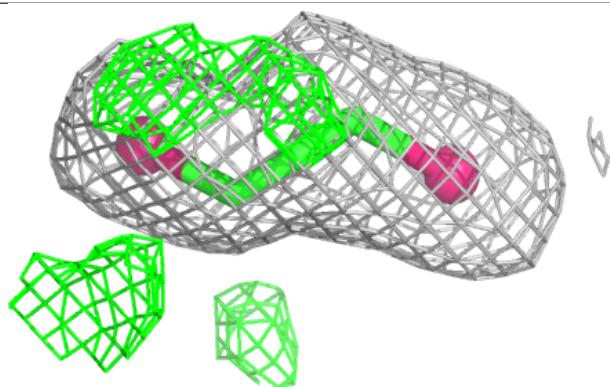
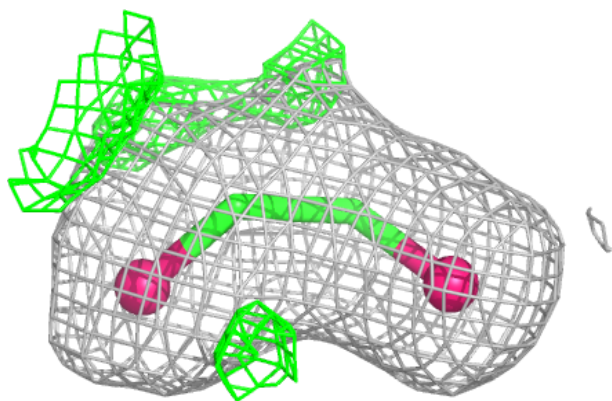
**Electron density around NA B 1518:**

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



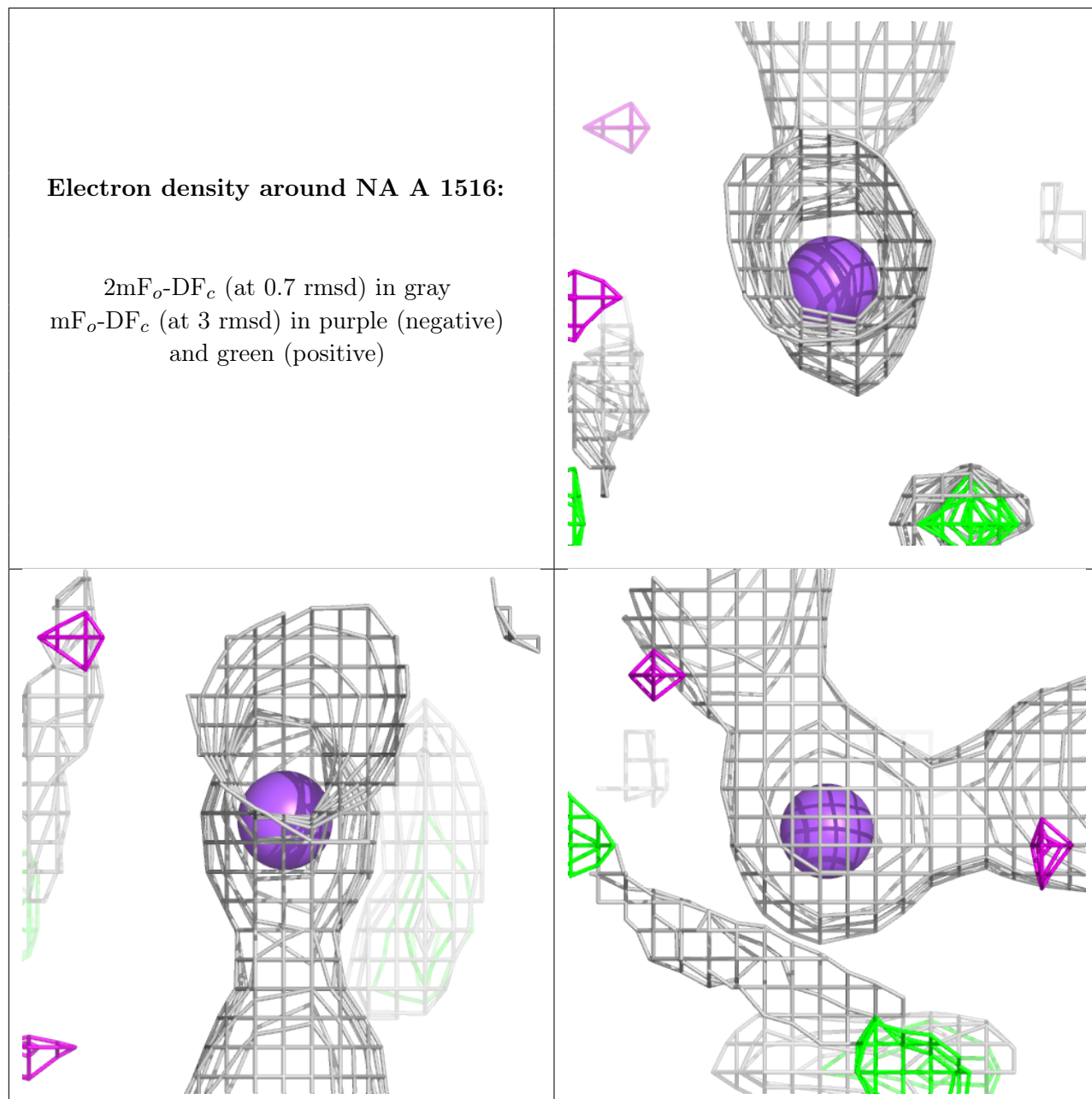
**Electron density around EDO A 1504:**

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



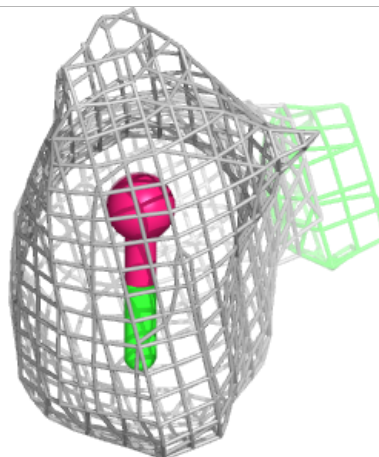
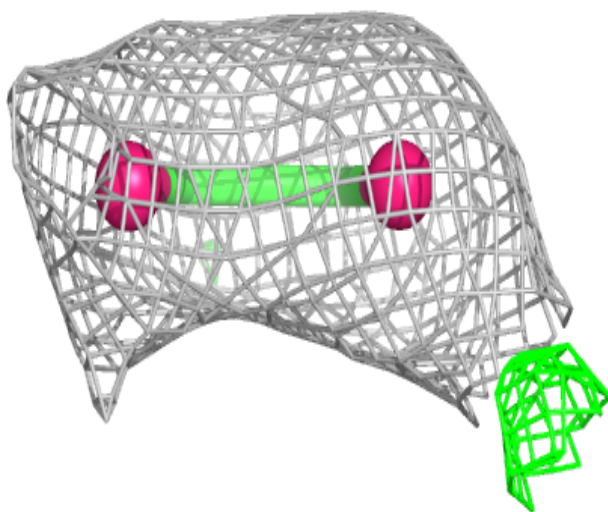
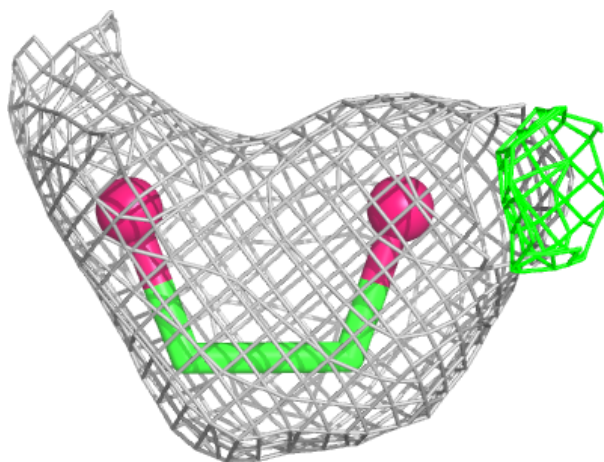
**Electron density around NA A 1516:**

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



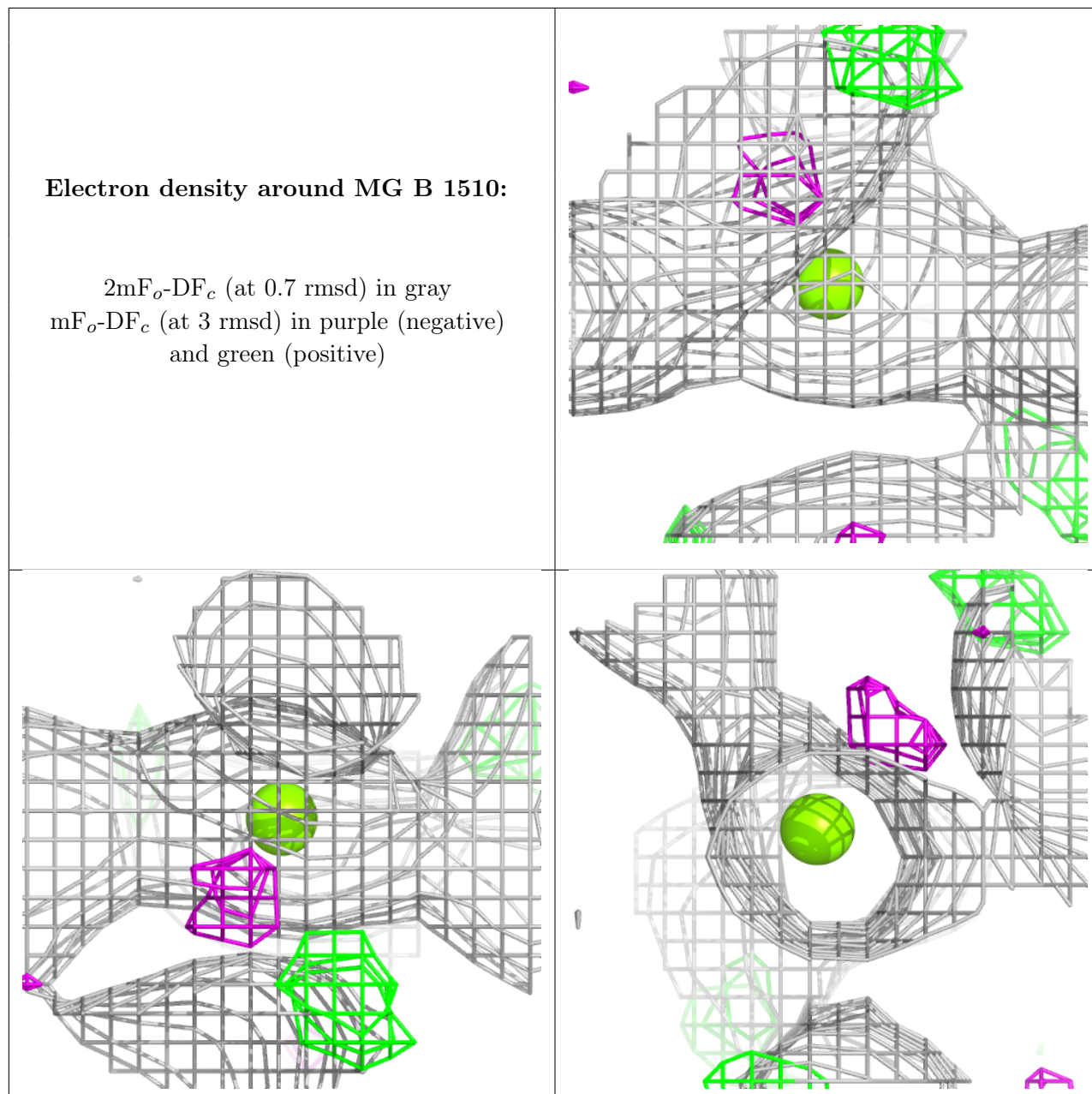
**Electron density around EDO A 1501:**

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



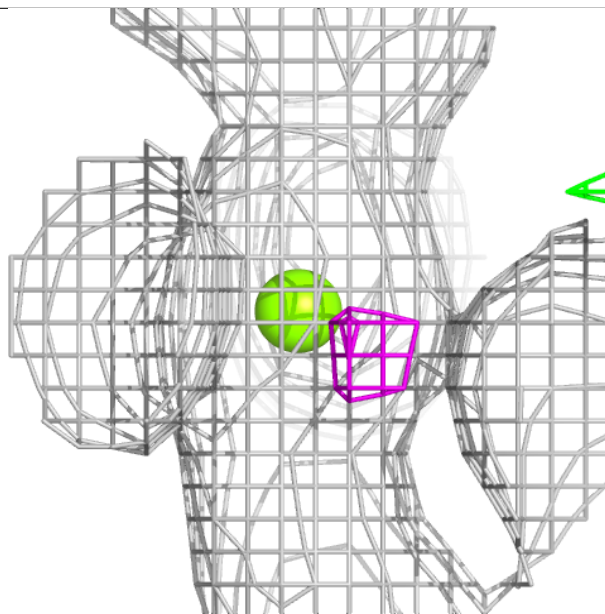
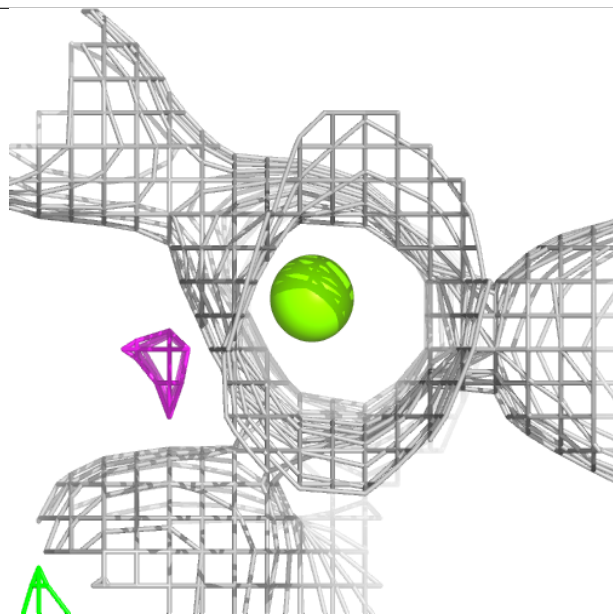
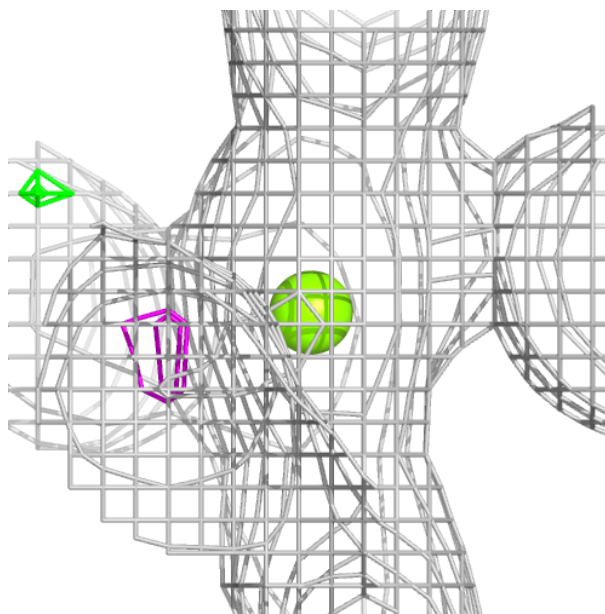
**Electron density around MG B 1510:**

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



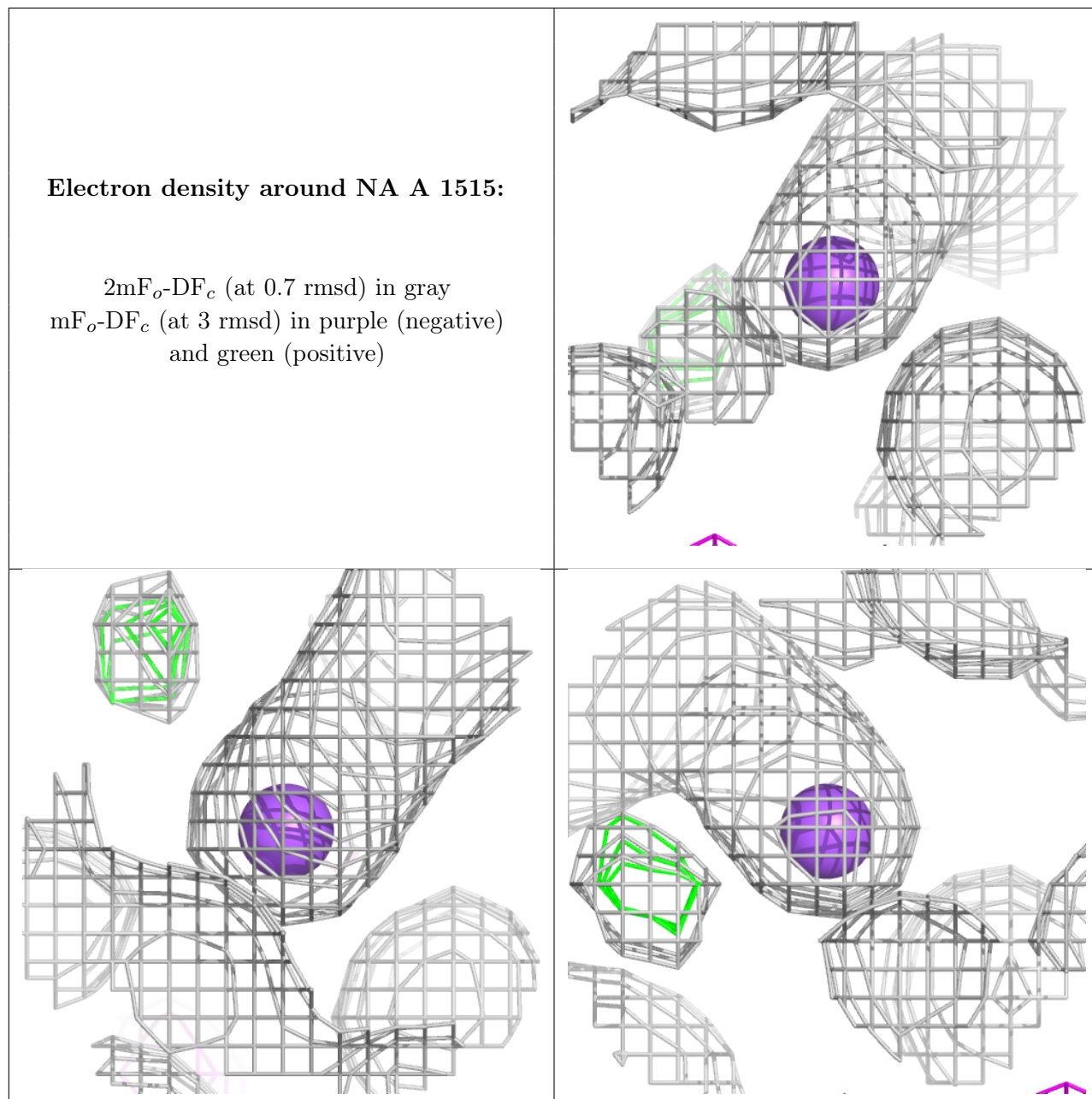
**Electron density around MG A 1508:**

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



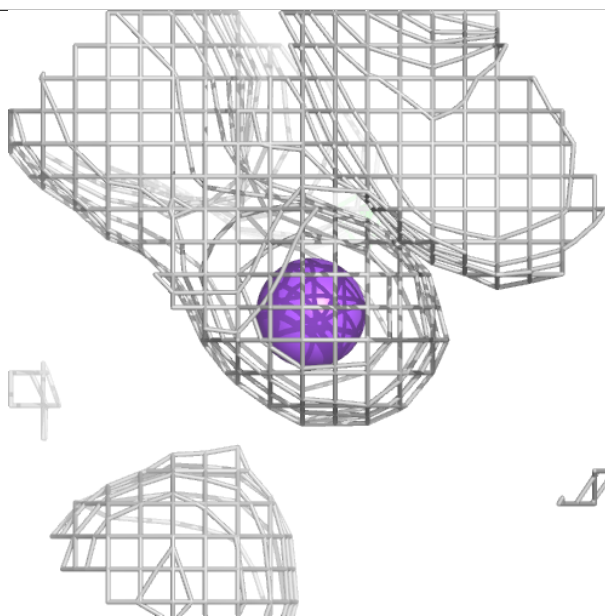
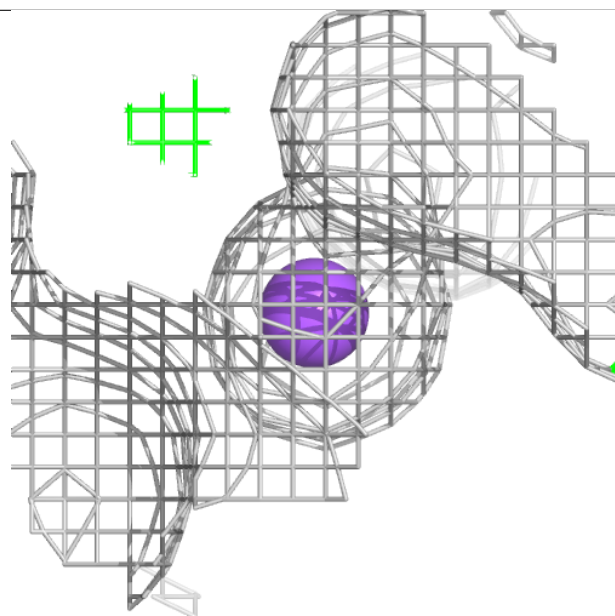
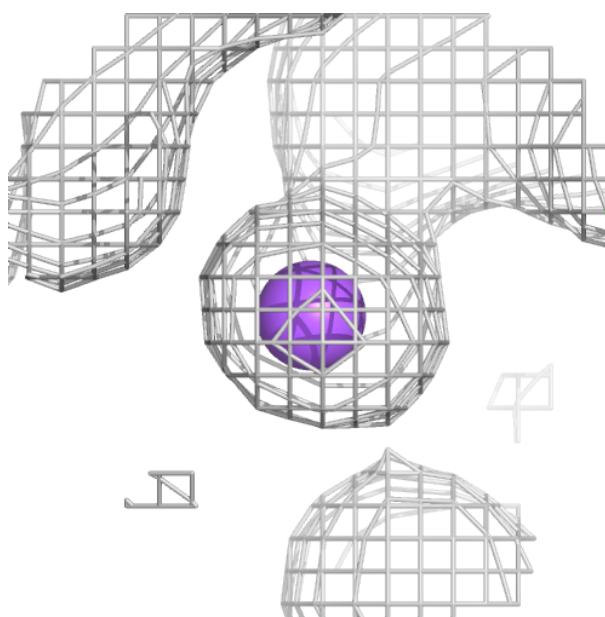
**Electron density around NA A 1515:**

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



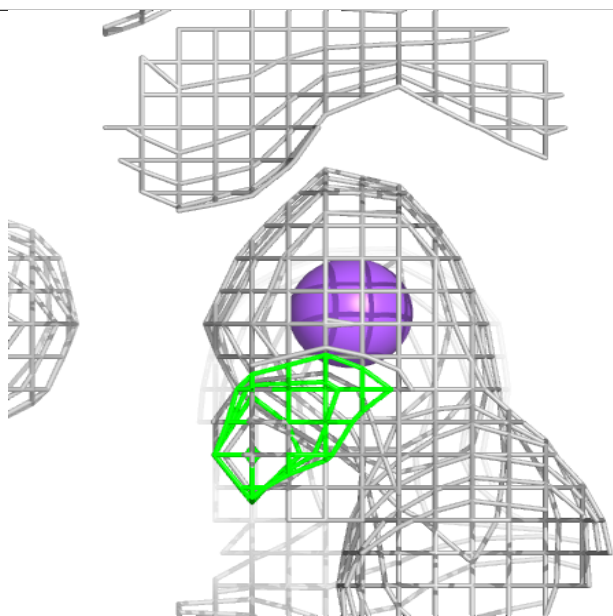
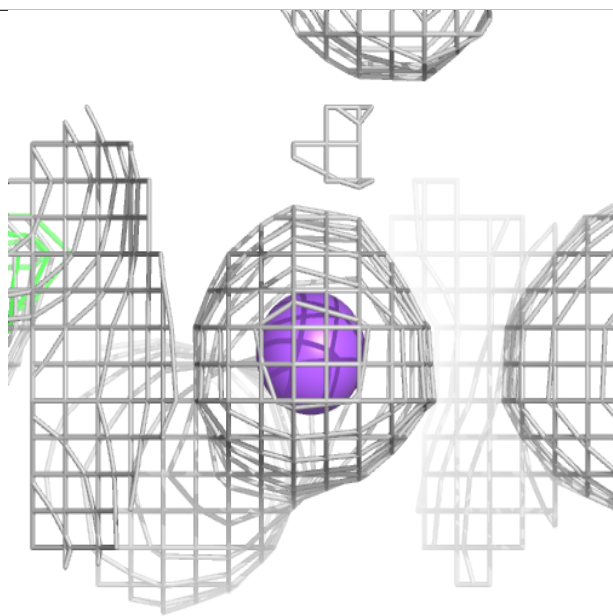
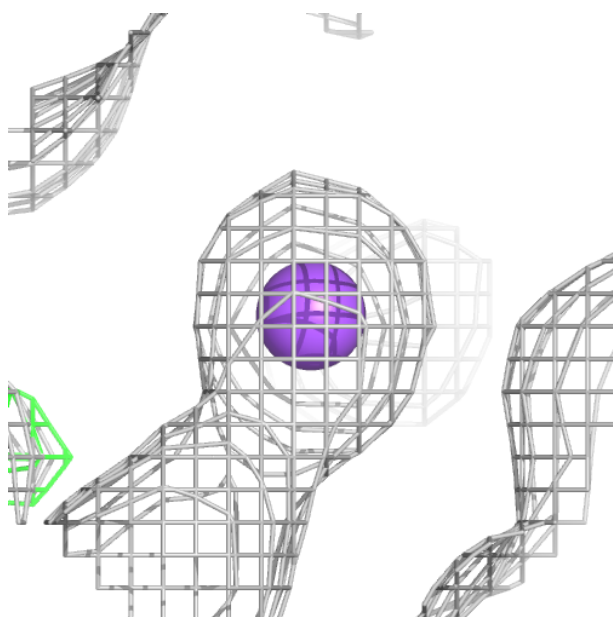
**Electron density around NA A 1514:**

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



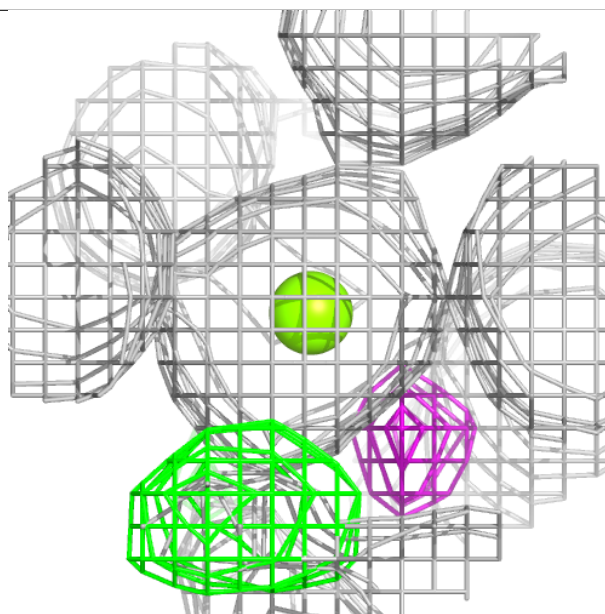
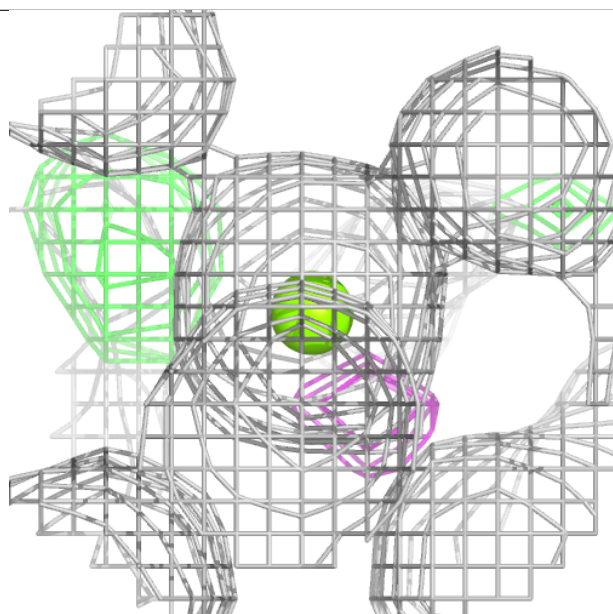
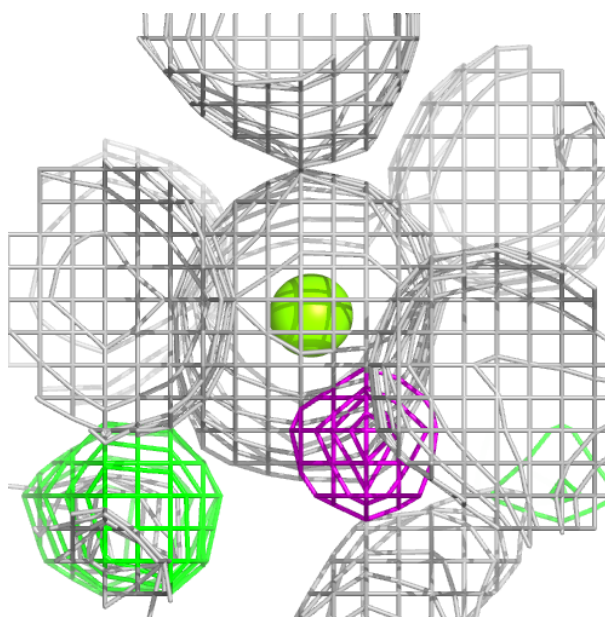
**Electron density around NA B 1517:**

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



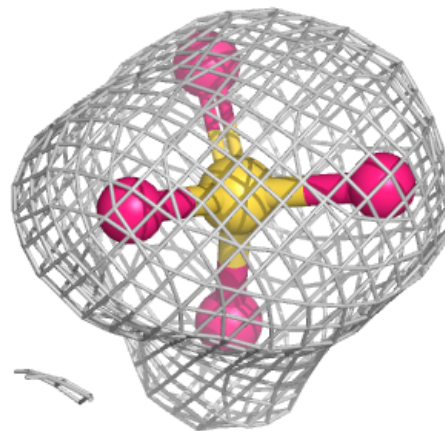
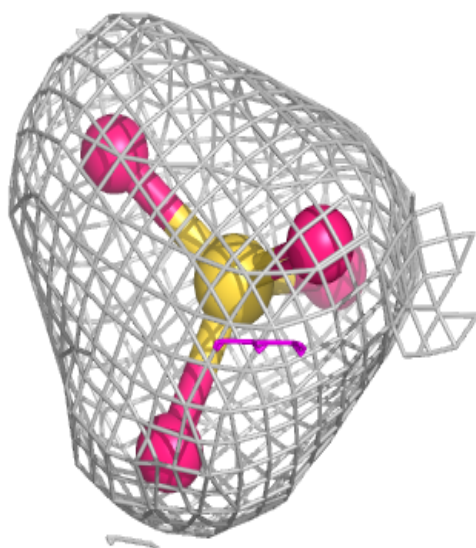
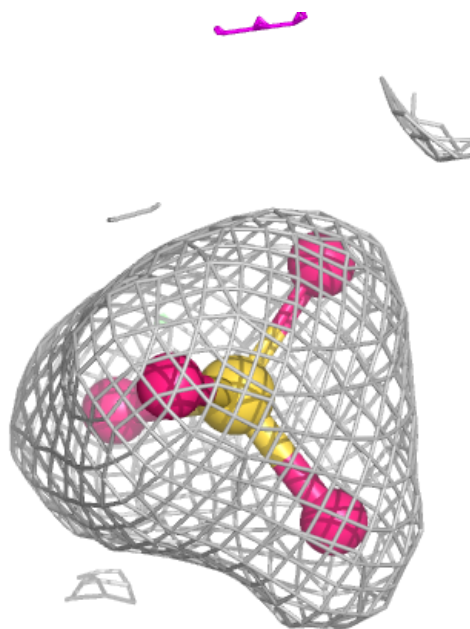
**Electron density around MG A 1509:**

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



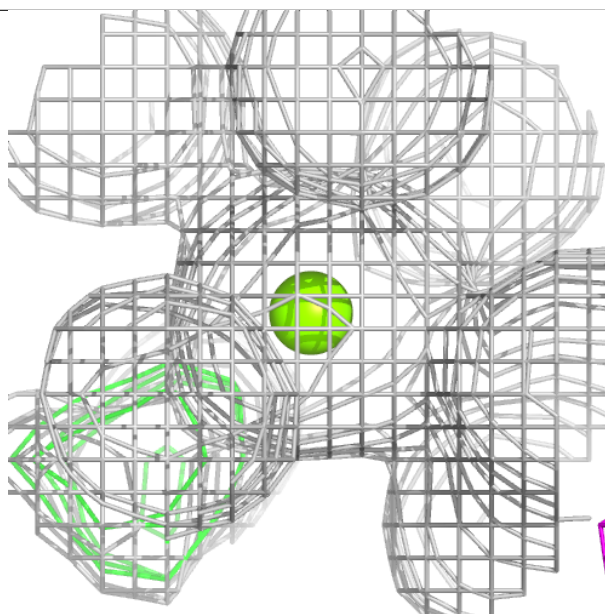
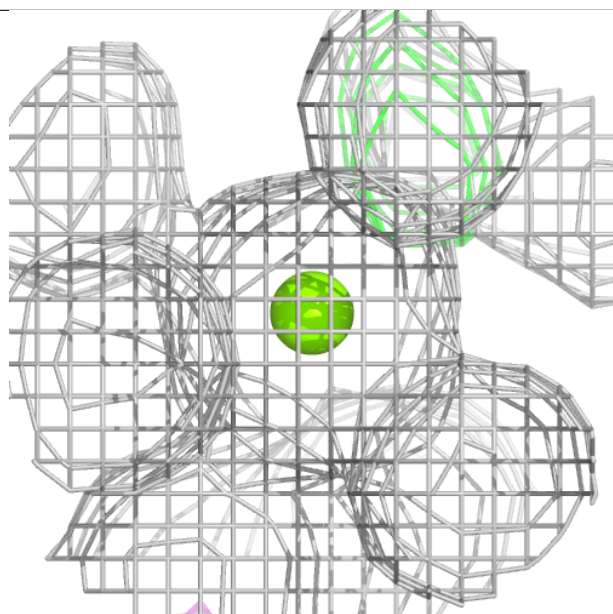
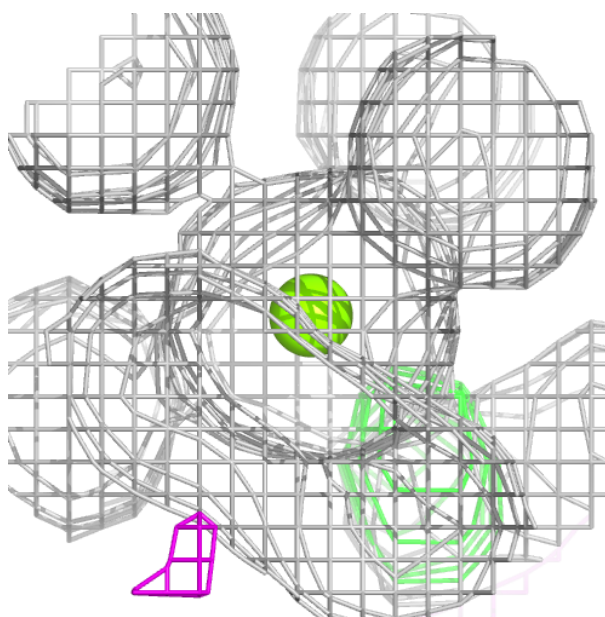
**Electron density around SO4 B 1511:**

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



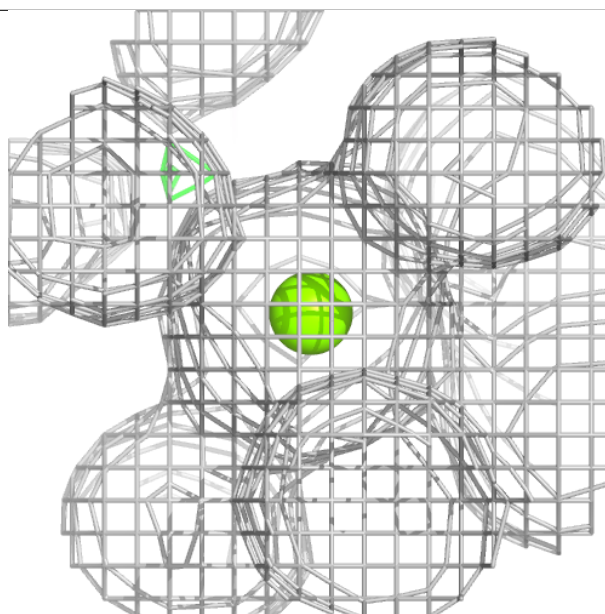
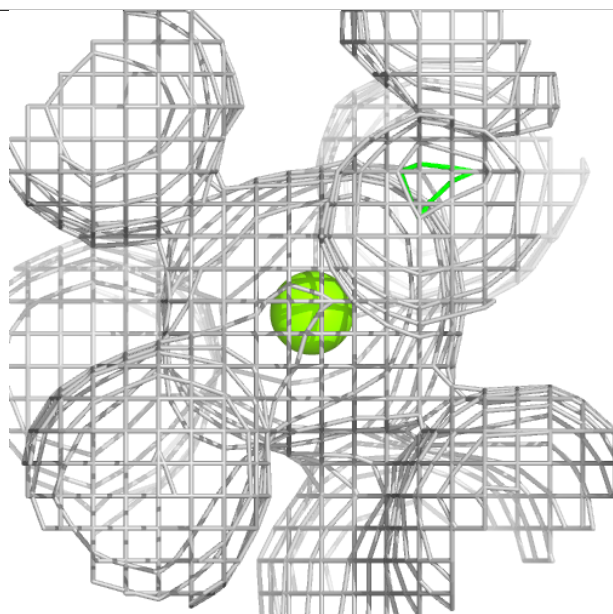
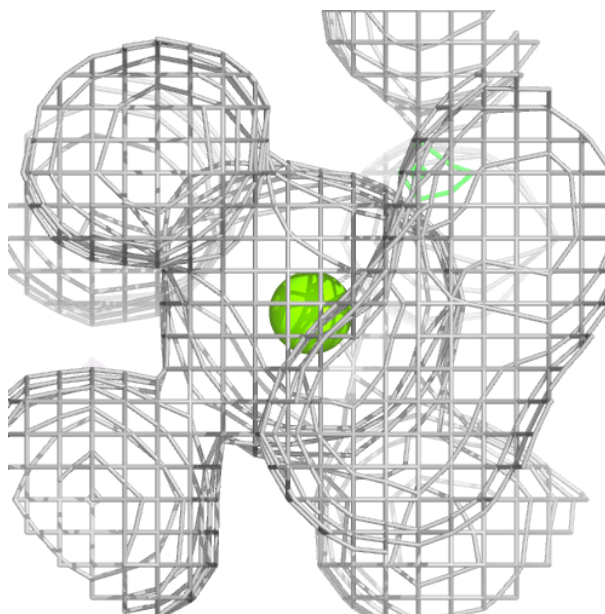
**Electron density around MG A 1507:**

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



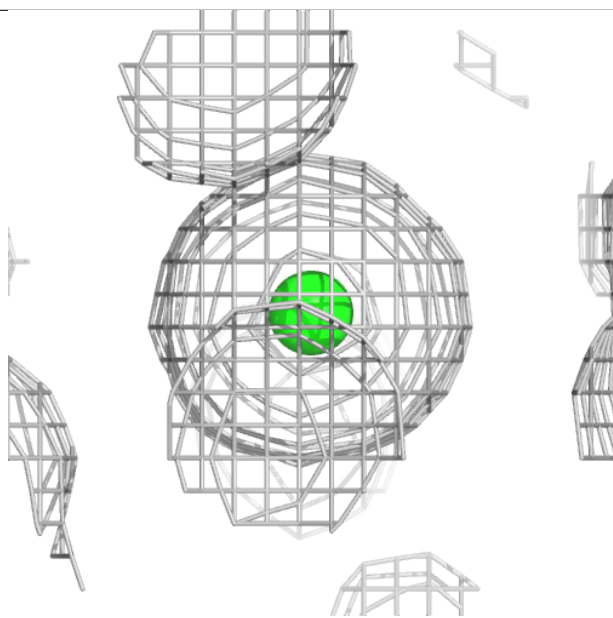
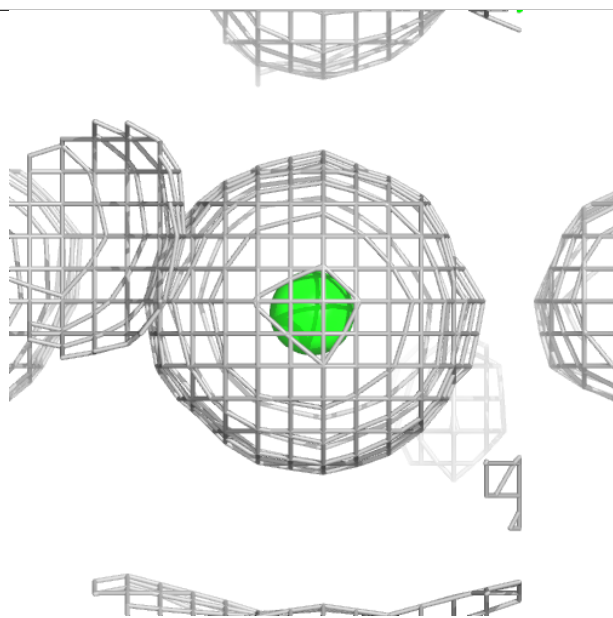
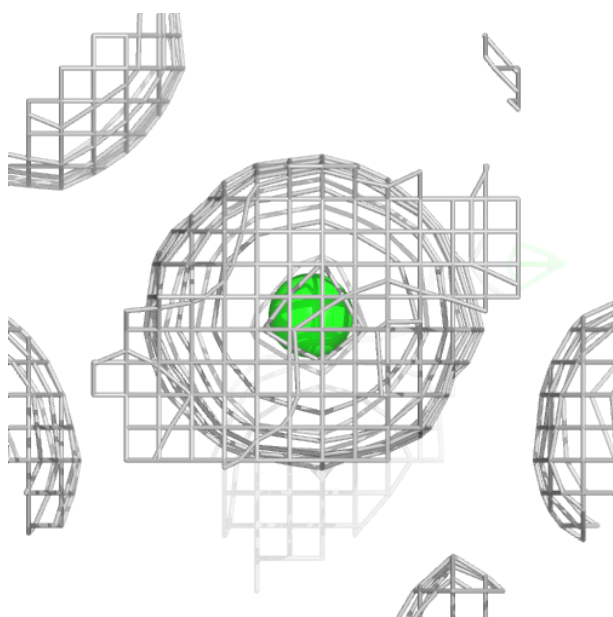
**Electron density around MG B 1509:**

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



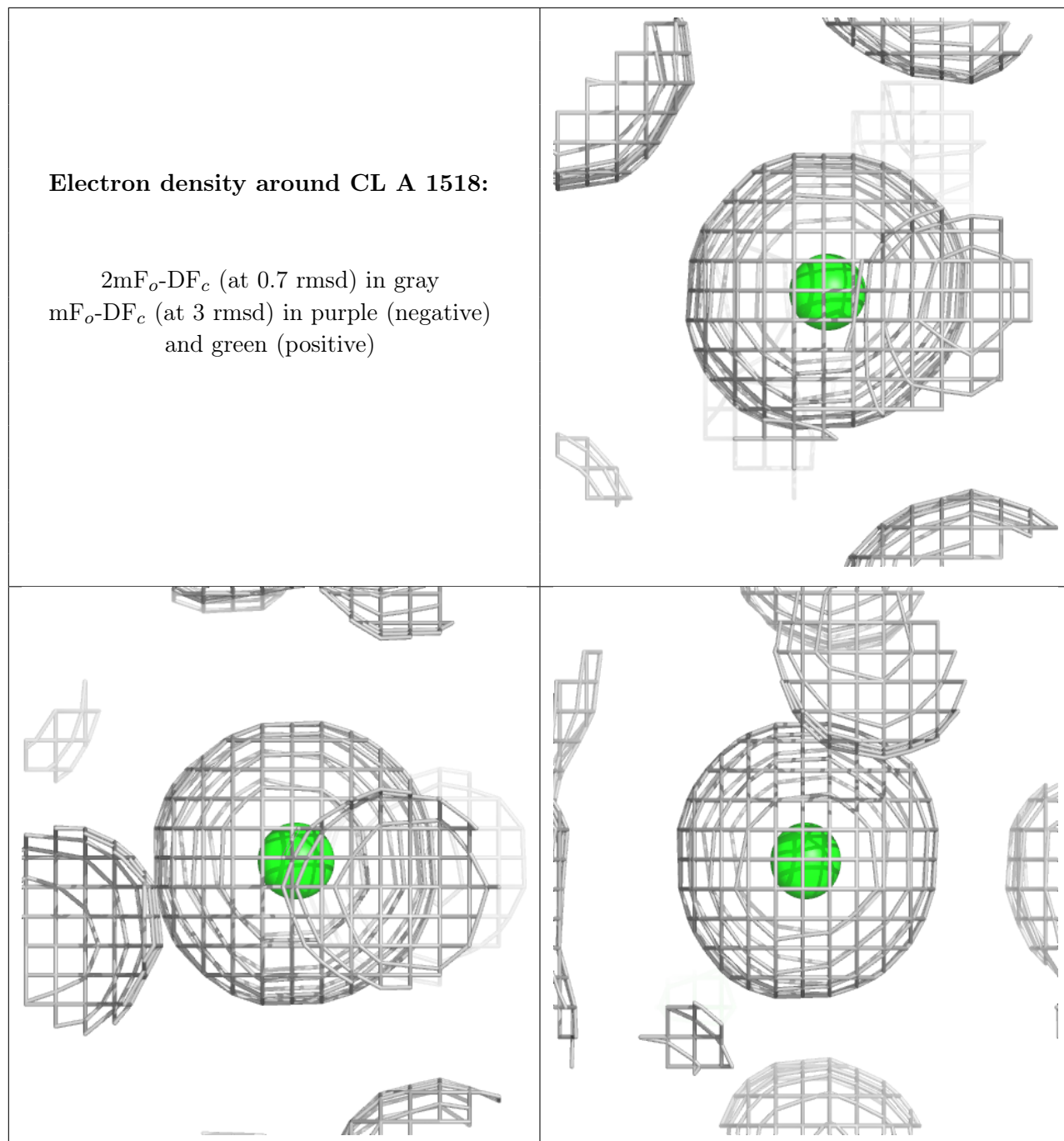
**Electron density around CL B 1519:**

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



**Electron density around CL A 1518:**

$2mF_o-DF_c$  (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.