



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2022 – 03:27 PM JST

PDB ID : 7WCS  
Title : Structure of the lactoperoxidase with bound nitric oxide and nitrite in the substrate binding site at 1.98 Å resolution.  
Authors : Viswanathan, V.; Kumar, M.; Singh, R.P.; Singh, A.K.; Sinha, M.; Kaur, P.; Sharma, P.; Sharma, S.; Singh, T.P.  
Deposited on : 2021-12-20  
Resolution : 1.98 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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.27  
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) : 2.27

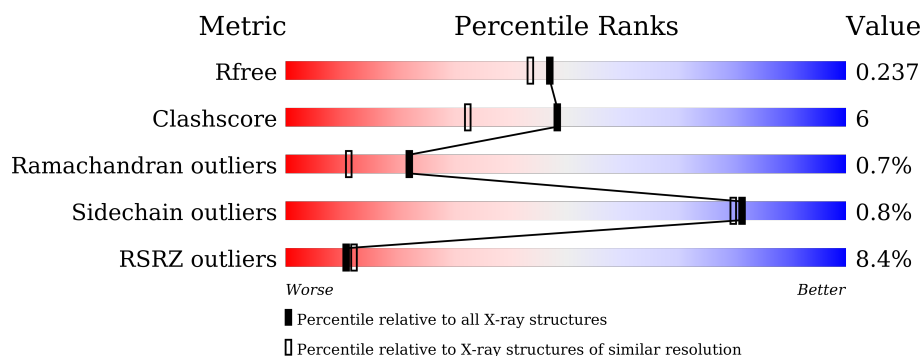
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.98 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	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

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	595	<div> <div>8%</div> <div>89%</div> <div>11%</div> </div>
2	B	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
10	IOD	A	625	-	-	X	-
4	NO	A	604	-	-	X	-
7	SCN	A	614	-	-	X	-
9	OSM	A	613	-	-	X	-

## 2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 5346 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 Lactoperoxidase.

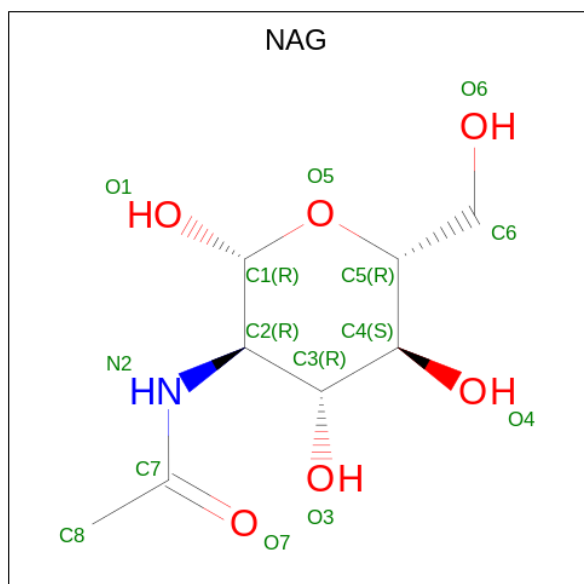
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	P	S	0	2	0
			4774	3035	849	863	1	26			

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



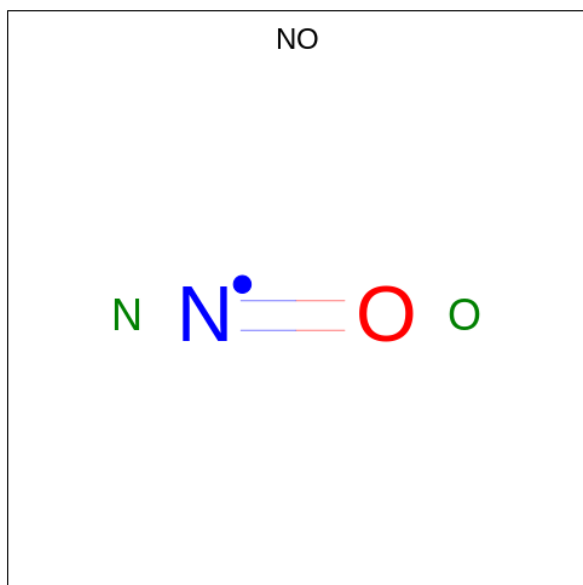
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 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).



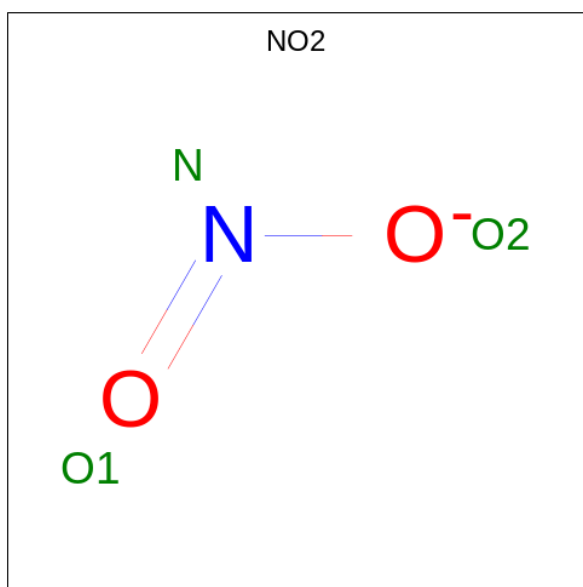
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is NITRIC OXIDE (three-letter code: NO) (formula: NO) (labeled as "Ligand of Interest" by depositor).



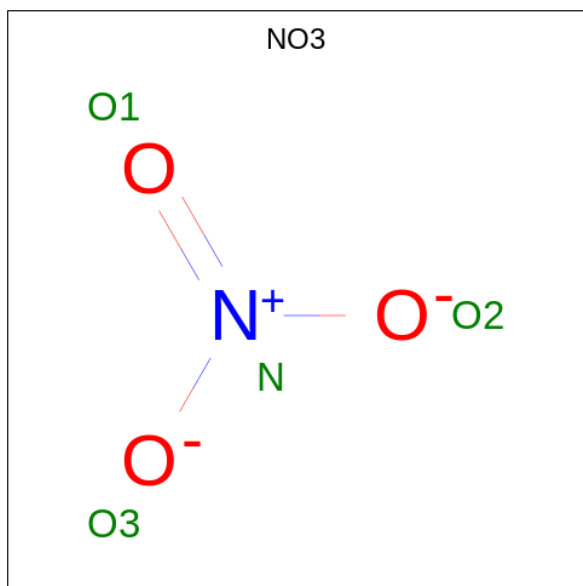
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	N	O	0	0
			2	1	1		

- Molecule 5 is NITRITE ION (three-letter code: NO2) (formula: NO<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	N	O	0	0
			3	1	2		

- Molecule 6 is NITRATE ION (three-letter code: NO3) (formula: NO<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



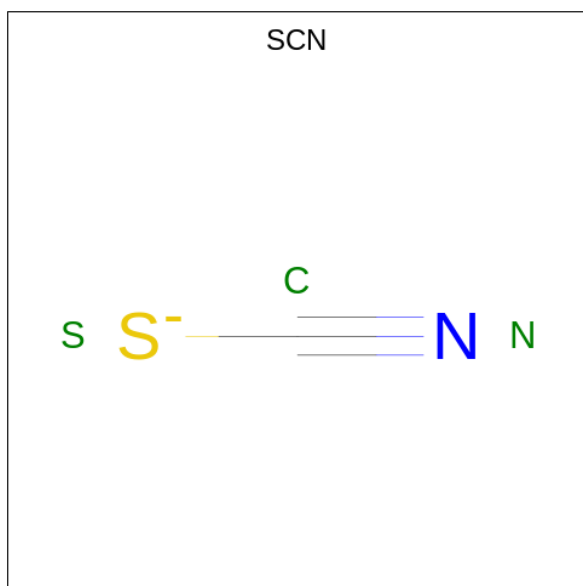
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	N	O	0	0
			4	1	3		
6	A	1	Total	N	O	0	0
			4	1	3		

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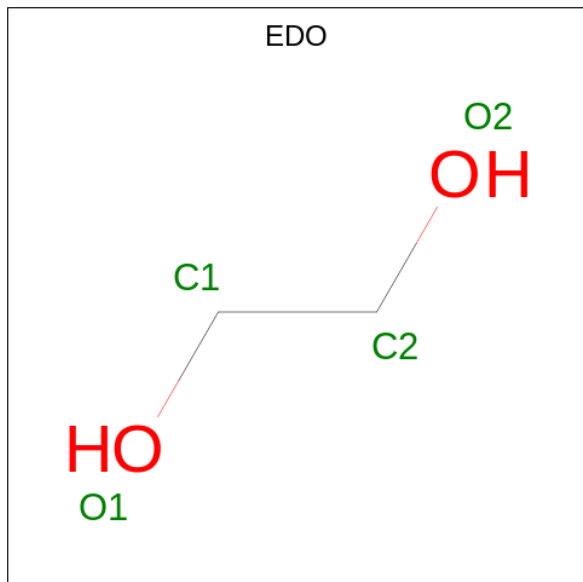
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	N	O	0	0
			4	1	3		
6	A	1	Total	N	O	0	0
			4	1	3		
6	A	1	Total	N	O	0	0
			4	1	3		
6	A	1	Total	N	O	0	0
			4	1	3		
6	A	1	Total	N	O	0	0
			4	1	3		
6	A	1	Total	N	O	0	0
			4	1	3		

- Molecule 7 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	S	0	0
			3	1	1	1		
7	A	1	Total	C	N	S	0	0
			3	1	1	1		
7	A	1	Total	C	N	S	0	0
			3	1	1	1		
7	A	1	Total	C	N	S	0	0
			3	1	1	1		

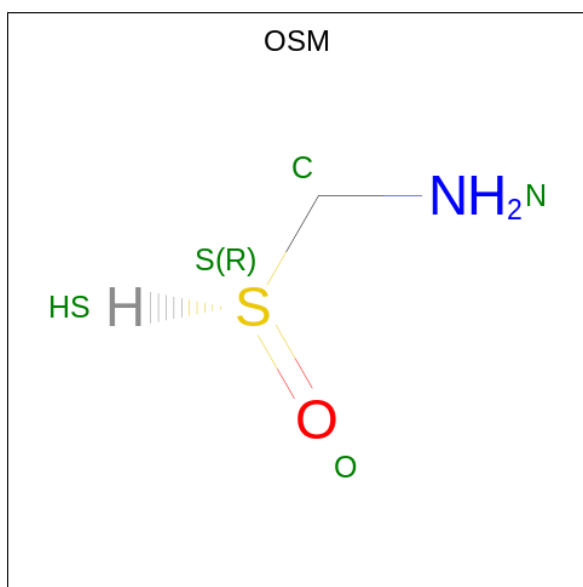
- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 9 is 1-(OXIDOSULFANYL)METHANAMINE (three-letter code: OSM) (formula:  $CH_5NOS$ ) (labeled as "Ligand of Interest" by depositor).





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

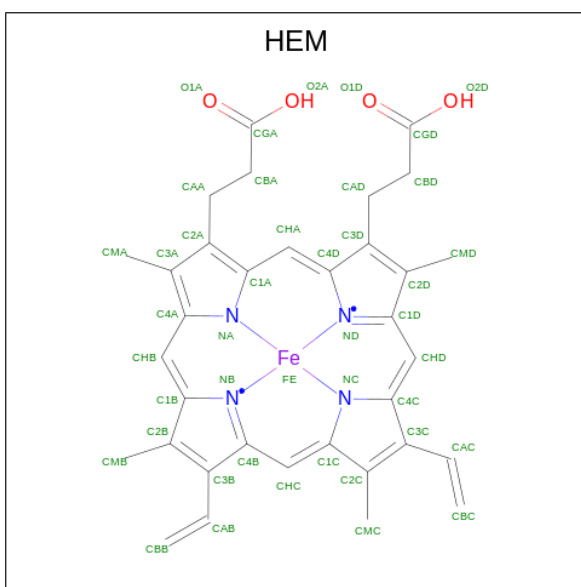
- Molecule 10 is IODIDE ION (three-letter code: IOD) (formula: I) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	10	Total	I	0	0
			10	10		

- Molecule 11 is SODIUM ION (three-letter code: NA) (formula: Na) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	3	Total	Na	0	0
			3	3		

- Molecule 12 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C<sub>34</sub>H<sub>32</sub>FeN<sub>4</sub>O<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 13 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	A	1	Total Ca 1 1	0	0

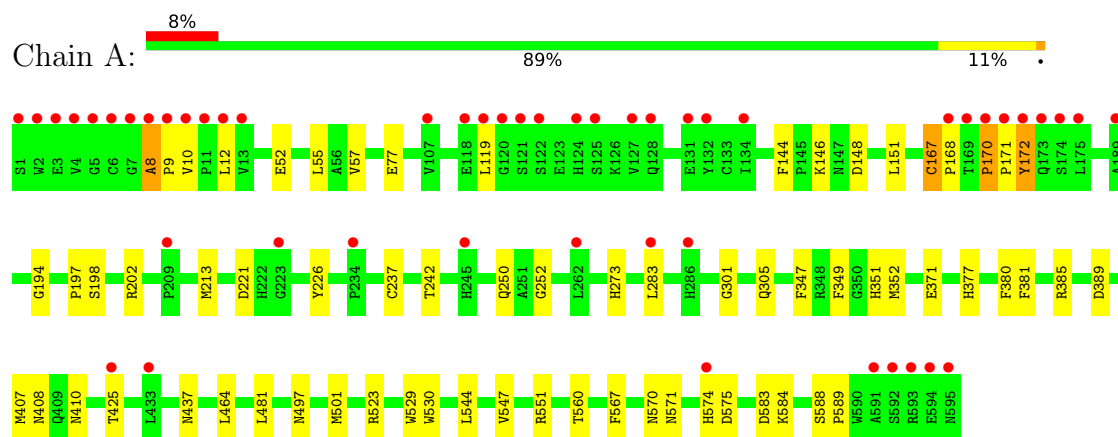
- Molecule 14 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	A	363	Total O 364 364	0	1

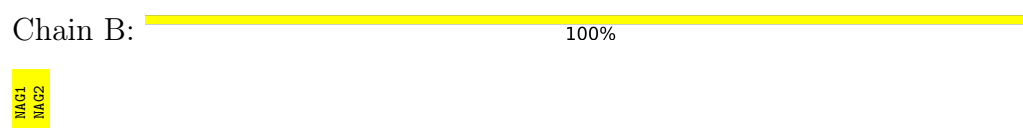
### 3 Residue-property plots [i](#)

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: Lactoperoxidase



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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.05Å 80.34Å 76.12Å 90.00° 102.82° 90.00°	Depositor
Resolution (Å)	35.33 – 1.98 35.33 – 1.98	Depositor EDS
% Data completeness (in resolution range)	98.3 (35.33-1.98) 98.3 (35.33-1.98)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.06 (at 1.98Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, $R_{free}$	0.176 , 0.235 0.183 , 0.237	Depositor DCC
$R_{free}$ test set	2188 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	29.9	Xtriage
Anisotropy	0.133	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 51.8	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	0.96	EDS
Total number of atoms	5346	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.42% 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: NO3, SCN, NO, EDO, SEP, NO2, HEM, IOD, OSM, CA, NAG, NA

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	0.71	0/4898	0.82	0/6647

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4774	0	4683	49	0
2	B	28	0	25	0	0
3	A	42	0	39	2	0
4	A	2	0	0	2	0
5	A	3	0	0	1	0
6	A	36	0	0	4	0
7	A	12	0	0	2	0
8	A	16	0	22	1	0
9	A	12	0	15	5	0
10	A	10	0	0	3	0
11	A	3	0	0	0	0
12	A	43	0	30	1	0
13	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	A	364	0	0	10	0
All	All	5346	0	4814	59	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (59) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:ASN:OD1	10:A:625:IOD:I	2.45	1.03
6:A:609:NO3:O3	9:A:621[A]:OSM:S	2.22	0.97
1:A:560:THR:N	6:A:616:NO3:O2	2.00	0.93
3:A:602:NAG:O4	14:A:701:HOH:O	2.04	0.76
1:A:351:HIS:HD1	1:A:437:ASN:HD21	1.32	0.75
1:A:77:GLU:HG3	6:A:618:NO3:O2	1.87	0.74
1:A:551:ARG:HD3	1:A:584:LYS:HA	1.72	0.71
3:A:601:NAG:O6	9:A:613:OSM:N	2.23	0.71
1:A:167:CYS:HB3	1:A:168:PRO:HD3	1.72	0.70
4:A:604:NO:O	10:A:623:IOD:I	2.80	0.70
4:A:604:NO:O	5:A:605:NO2:O2	2.10	0.69
9:A:613:OSM:H2	14:A:864:HOH:O	1.92	0.68
1:A:146:LYS:O	14:A:702:HOH:O	2.10	0.68
1:A:167:CYS:CB	1:A:168:PRO:HD3	2.28	0.62
1:A:9:PRO:HD3	14:A:993:HOH:O	2.01	0.59
1:A:407:MET:HB3	1:A:501:MET:HE2	1.84	0.59
1:A:237:CYS:HA	1:A:381:PHE:O	2.04	0.58
7:A:614:SCN:N	14:A:707:HOH:O	2.32	0.58
12:A:636:HEM:HMC2	12:A:636:HEM:HBC2	1.88	0.56
1:A:567:PHE:H	9:A:613:OSM:HS	1.54	0.55
1:A:523:ARG:HG3	1:A:529:TRP:CE2	2.41	0.55
1:A:167:CYS:CB	1:A:168:PRO:CD	2.85	0.54
1:A:588:SER:HB2	1:A:589:PRO:HD3	1.90	0.54
1:A:352:MET:HB3	1:A:407:MET:HG2	1.91	0.53
1:A:464:LEU:HA	1:A:481:LEU:HD12	1.89	0.53
9:A:621[B]:OSM:S	14:A:804:HOH:O	2.37	0.53
1:A:213:MET:HG2	1:A:273:HIS:CD2	2.44	0.52
1:A:551:ARG:HD3	1:A:583:ASP:O	2.09	0.52
1:A:377:HIS:HA	1:A:380:PHE:CE2	2.46	0.51
1:A:8:ALA:CB	1:A:167:CYS:O	2.59	0.51
1:A:10:VAL:HG13	1:A:12:LEU:HD13	1.93	0.50
7:A:614:SCN:C	14:A:707:HOH:O	2.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:MET:HB3	1:A:501:MET:CE	2.45	0.47
1:A:570:ASN:HD22	1:A:575:ASP:HB3	1.79	0.47
1:A:301:GLY:O	1:A:305:GLN:HG3	2.15	0.46
1:A:221:ASP:HB2	1:A:226:TYR:CZ	2.51	0.46
1:A:194:GLY:HA2	1:A:252:GLY:O	2.16	0.45
1:A:410:ASN:CG	10:A:625:IOD:I	3.21	0.44
1:A:551:ARG:CD	1:A:583:ASP:O	2.65	0.44
1:A:144:PHE:HB2	1:A:151:LEU:HD13	1.99	0.44
1:A:52:GLU:CG	1:A:57:VAL:HG12	2.47	0.43
1:A:202:ARG:NH2	1:A:250:GLN:OE1	2.51	0.43
1:A:371:GLU:OE2	14:A:703:HOH:O	2.21	0.43
1:A:349:PHE:HA	1:A:497:ASN:HD21	1.84	0.43
1:A:352:MET:CB	1:A:407:MET:HG2	2.49	0.42
1:A:385:ARG:O	1:A:389:ASP:HB3	2.19	0.42
1:A:530:TRP:NE1	8:A:622:EDO:O2	2.52	0.42
1:A:148:ASP:O	1:A:151:LEU:HB2	2.19	0.42
1:A:574:HIS:C	1:A:574:HIS:ND1	2.73	0.41
1:A:481:LEU:HD23	1:A:481:LEU:HA	1.87	0.41
1:A:197:PRO:HD2	6:A:617:NO3:O2	2.21	0.41
1:A:544:LEU:O	1:A:547:VAL:HG22	2.20	0.41
1:A:407:MET:SD	1:A:408:ASN:N	2.93	0.41
1:A:571:ASN:HB3	14:A:1001:HOH:O	2.21	0.41
1:A:8:ALA:HB3	1:A:9:PRO:CD	2.51	0.40
1:A:52:GLU:HG2	1:A:57:VAL:HG12	2.03	0.40
1:A:242:THR:HB	14:A:898:HOH:O	2.21	0.40
1:A:55:LEU:HD13	1:A:172:TYR:OH	2.21	0.40
1:A:170:PRO:HD2	1:A:171:PRO:HD2	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	594/595 (100%)	567 (96%)	23 (4%)	4 (1%)	22	11

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	CYS
1	A	170	PRO
1	A	8	ALA
1	A	425	THR

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	518/516 (100%)	514 (99%)	4 (1%)	81	80

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	119	LEU
1	A	172	TYR
1	A	283	LEU
1	A	347	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	GLN
1	A	329	GLN
1	A	419	ASN
1	A	468	GLN
1	A	497	ASN
1	A	570	ASN



### 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	SEP	A	198	11,1	8,9,10	1.38	1 (12%)	8,12,14	1.30	2 (25%)

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	SEP	A	198	11,1	-	5/5/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	198	SEP	P-OG	2.99	1.69	1.60

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	SEP	P-OG-CB	2.73	125.83	118.30
1	A	198	SEP	OG-CB-CA	2.09	110.18	108.14

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	198	SEP	CA-CB-OG-P
1	A	198	SEP	CB-OG-P-O3P
1	A	198	SEP	CB-OG-P-O1P
1	A	198	SEP	CB-OG-P-O2P
1	A	198	SEP	N-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

2 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	B	1	2,1	14,14,15	0.56	0	17,19,21	1.64	4 (23%)
2	NAG	B	2	2	14,14,15	0.38	0	17,19,21	1.82	5 (29%)

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	B	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	NAG	C4-C3-C2	-4.47	104.46	111.02
2	B	2	NAG	C1-O5-C5	3.58	117.04	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	NAG	C6-C5-C4	3.51	121.23	113.00
2	B	1	NAG	O5-C5-C4	-3.17	103.11	110.83
2	B	2	NAG	O5-C5-C6	2.85	111.67	107.20
2	B	1	NAG	O5-C1-C2	-2.66	107.09	111.29
2	B	1	NAG	C1-O5-C5	-2.31	109.07	112.19
2	B	2	NAG	C2-N2-C7	-2.19	119.79	122.90
2	B	2	NAG	O3-C3-C2	2.14	113.89	109.47

There are no chirality outliers.

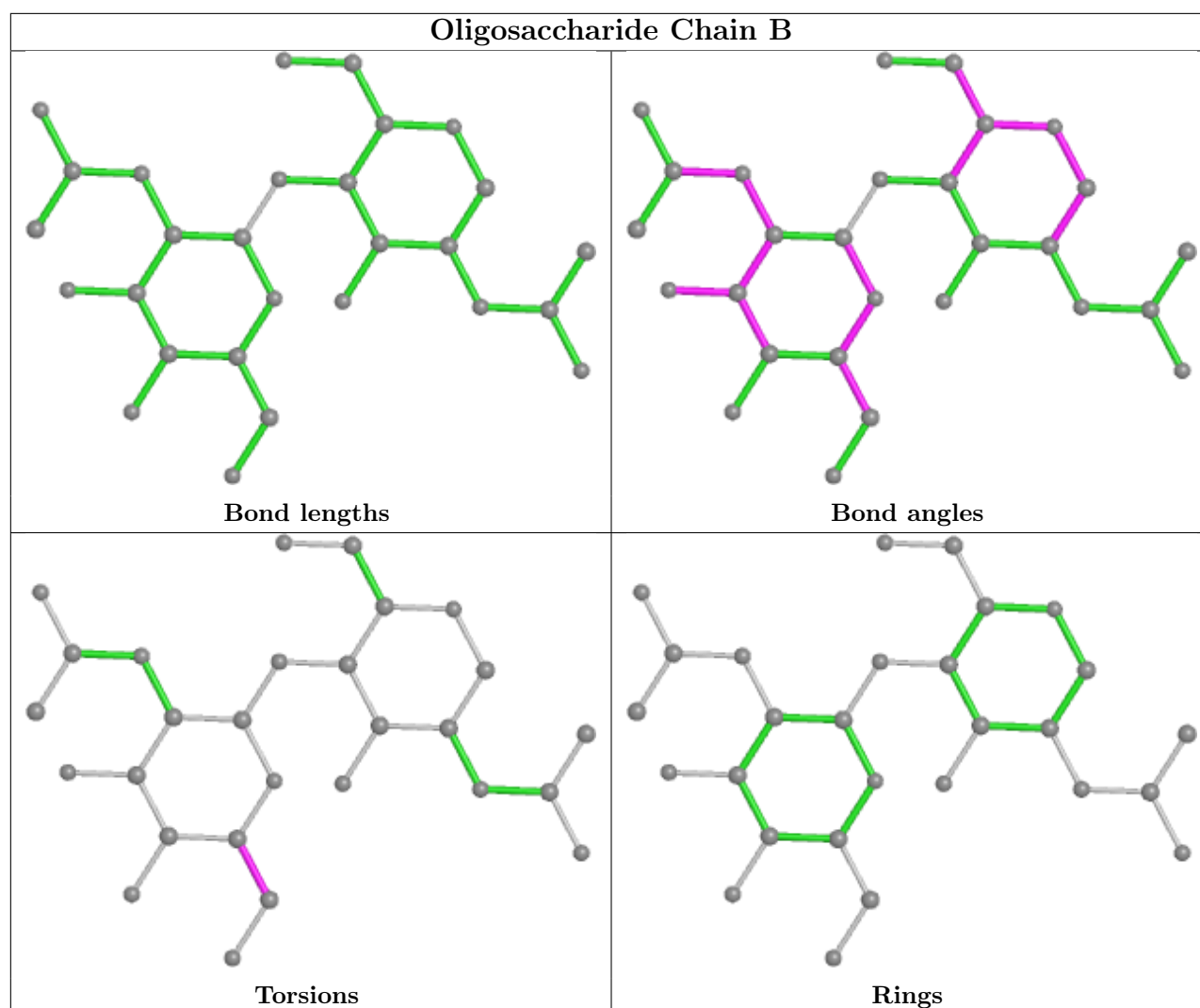
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NAG	O5-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.



## 5.6 Ligand geometry [i](#)

Of 40 ligands modelled in this entry, 14 are monoatomic - leaving 26 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	$\# Z  > 2$
6	NO3	A	620	-	1,3,3	1.00	0	0,3,3	-	-
6	NO3	A	618	-	1,3,3	0.29	0	0,3,3	-	-
4	NO	A	604	12	0,1,1	-	-	-	-	-
9	OSM	A	613	-	1,3,3	0.07	0	0,2,2	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
12	HEM	A	636	4,1	27,50,50	0.86	1 (3%)	17,82,82	1.80	6 (35%)
9	OSM	A	621[A]	-	1,3,3	0.03	0	0,2,2	-	-
5	NO2	A	605	-	1,2,2	0.10	0	0,1,1	-	-
6	NO3	A	616	-	1,3,3	0.13	0	0,3,3	-	-
6	NO3	A	615	11	1,3,3	0.46	0	0,3,3	-	-
7	SCN	A	614	-	1,2,2	0.91	0	0,1,1	-	-
6	NO3	A	619	-	1,3,3	0.10	0	0,3,3	-	-
6	NO3	A	607	-	1,3,3	0.23	0	0,3,3	-	-
8	EDO	A	622	10	3,3,3	0.98	0	2,2,2	0.86	0
9	OSM	A	621[B]	-	1,3,3	0.04	0	0,2,2	-	-
7	SCN	A	610	-	1,2,2	1.12	0	0,1,1	-	-
6	NO3	A	609	-	1,3,3	0.22	0	0,3,3	-	-
7	SCN	A	608	-	1,2,2	0.49	0	0,1,1	-	-
6	NO3	A	606	-	1,3,3	0.50	0	0,3,3	-	-
8	EDO	A	611	-	3,3,3	0.16	0	2,2,2	0.12	0
8	EDO	A	639	-	3,3,3	0.14	0	2,2,2	0.24	0
3	NAG	A	601	1	14,14,15	0.77	0	17,19,21	1.31	2 (11%)
7	SCN	A	612	-	1,2,2	1.33	0	0,1,1	-	-
3	NAG	A	603	1	14,14,15	0.35	0	17,19,21	1.51	3 (17%)
8	EDO	A	637	-	3,3,3	0.48	0	2,2,2	0.10	0
6	NO3	A	617	-	1,3,3	0.30	0	0,3,3	-	-
3	NAG	A	602	1	14,14,15	0.72	0	17,19,21	1.12	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
9	OSM	A	613	-	-	0/0/1/1	-
12	HEM	A	636	4,1	-	0/6/54/54	-
9	OSM	A	621[B]	-	-	0/0/1/1	-
9	OSM	A	621[A]	-	-	0/0/1/1	-
8	EDO	A	639	-	-	0/1/1/1	-
3	NAG	A	601	1	-	0/6/23/26	0/1/1/1
3	NAG	A	603	1	-	2/6/23/26	0/1/1/1
8	EDO	A	637	-	-	1/1/1/1	-
8	EDO	A	611	-	-	1/1/1/1	-
3	NAG	A	602	1	-	0/6/23/26	0/1/1/1
8	EDO	A	622	10	-	1/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	A	636	HEM	C3D-C4D	2.57	1.48	1.42

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	603	NAG	C1-O5-C5	3.93	117.52	112.19
12	A	636	HEM	CBD-CAD-C3D	-3.68	105.69	112.48
12	A	636	HEM	CMC-C2C-C3C	2.85	130.01	124.68
12	A	636	HEM	C1D-C2D-C3D	-2.79	105.05	107.00
12	A	636	HEM	C4A-C3A-C2A	2.76	108.92	107.00
3	A	601	NAG	C2-N2-C7	2.55	126.54	122.90
3	A	603	NAG	O5-C5-C6	2.53	111.17	107.20
12	A	636	HEM	CMB-C2B-C3B	2.24	128.87	124.68
3	A	603	NAG	O5-C5-C4	-2.18	105.52	110.83
12	A	636	HEM	CMA-C3A-C4A	-2.10	125.23	128.46
3	A	601	NAG	C3-C4-C5	-2.07	106.55	110.24

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	603	NAG	C4-C5-C6-O6
3	A	603	NAG	O5-C5-C6-O6
8	A	611	EDO	O1-C1-C2-O2
8	A	622	EDO	O1-C1-C2-O2
8	A	637	EDO	O1-C1-C2-O2

There are no ring outliers.

14 monomers are involved in 15 short contacts:

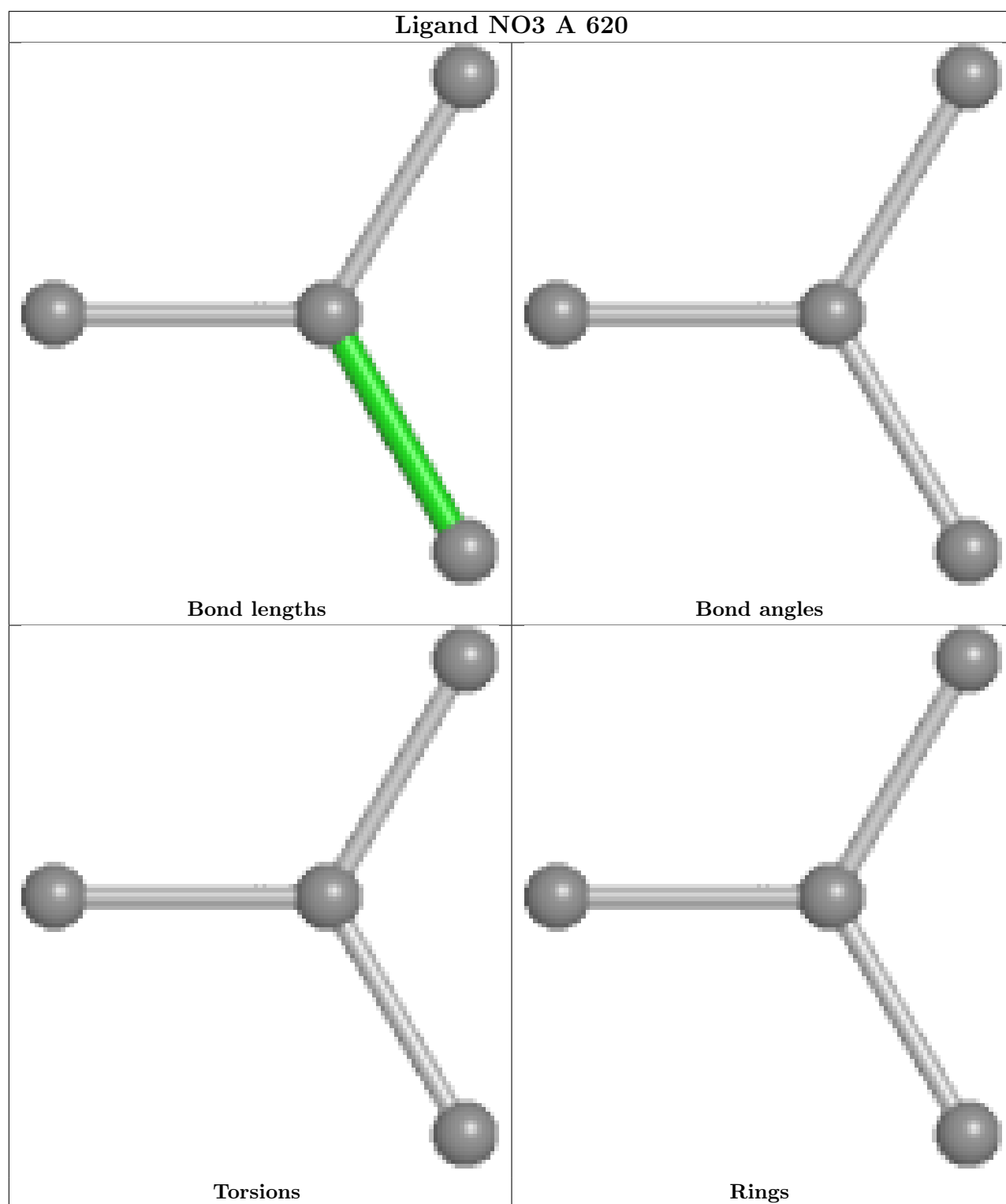
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	618	NO3	1	0
4	A	604	NO	2	0
9	A	613	OSM	3	0
12	A	636	HEM	1	0
9	A	621[A]	OSM	1	0
5	A	605	NO2	1	0
6	A	616	NO3	1	0
7	A	614	SCN	2	0
8	A	622	EDO	1	0
9	A	621[B]	OSM	1	0
6	A	609	NO3	1	0

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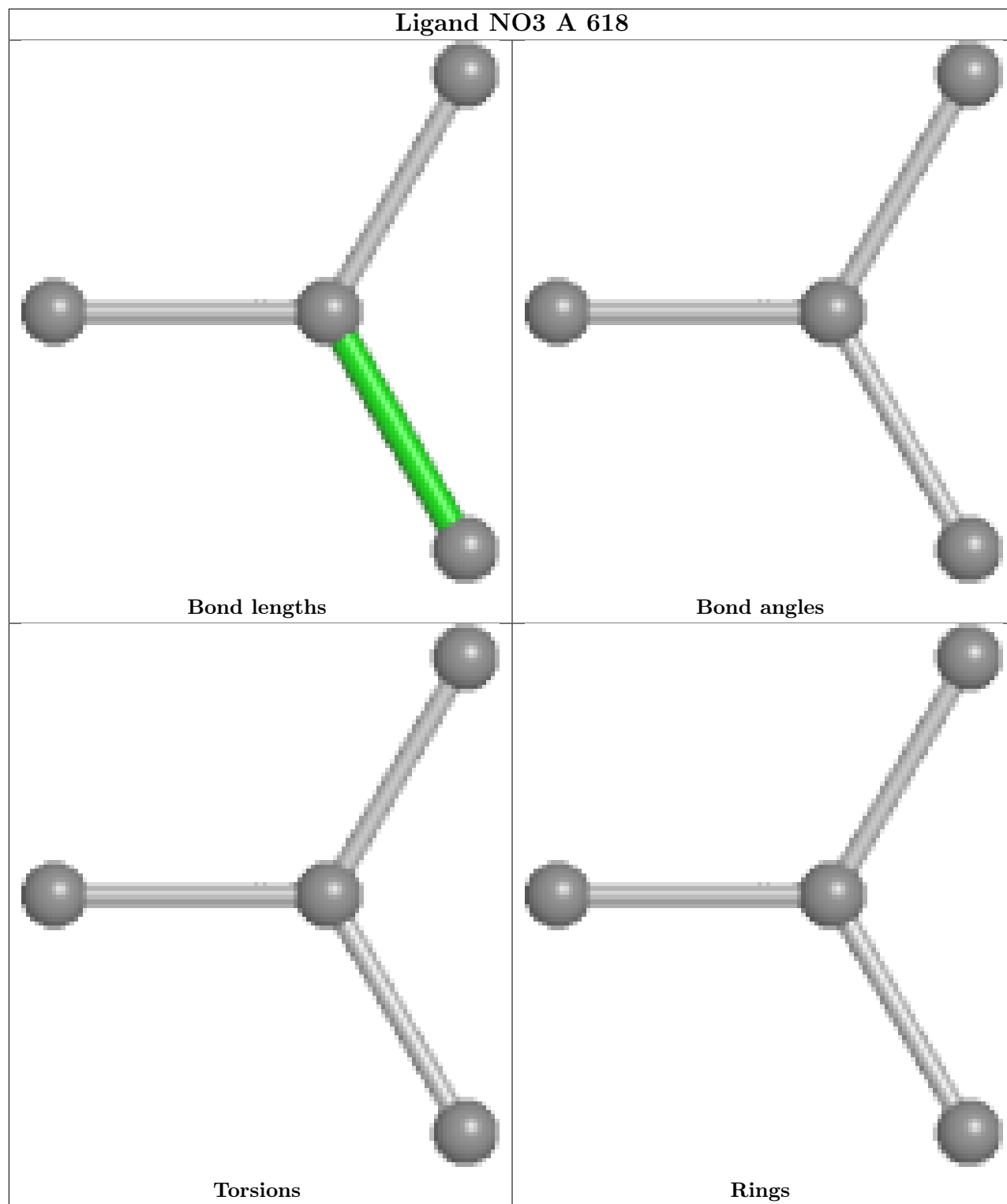
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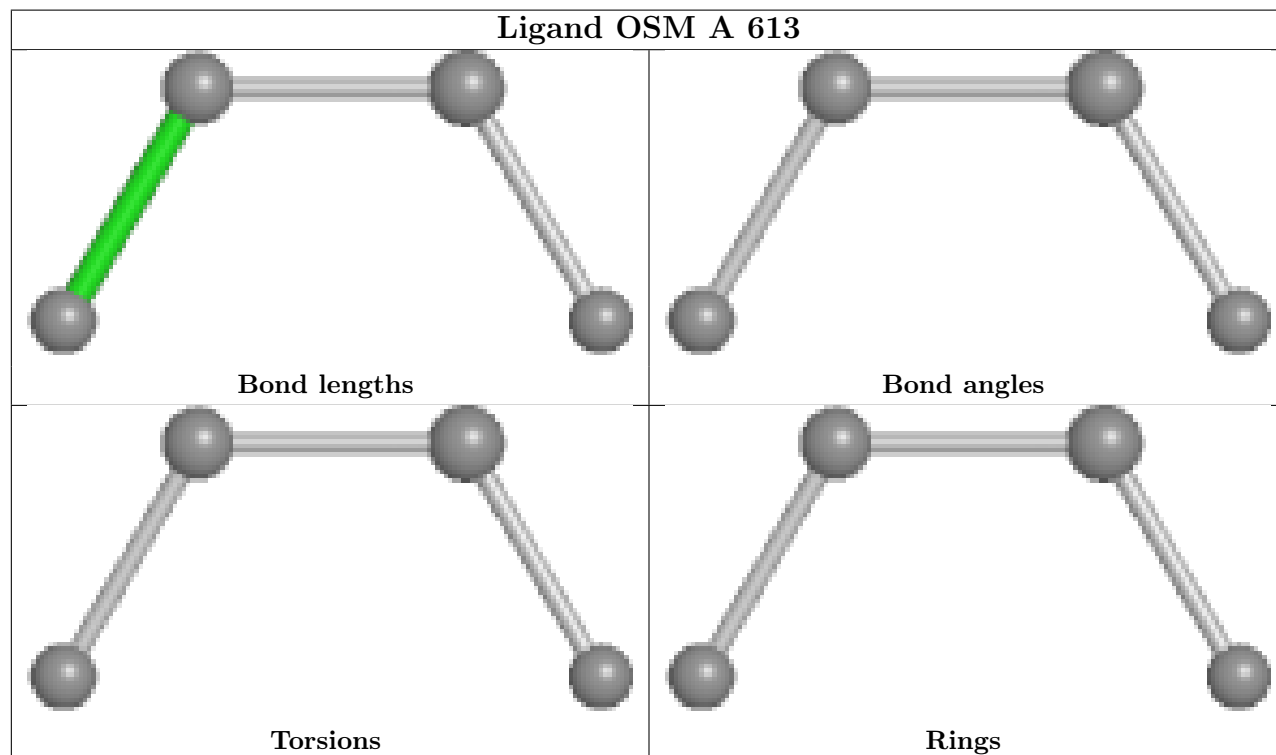
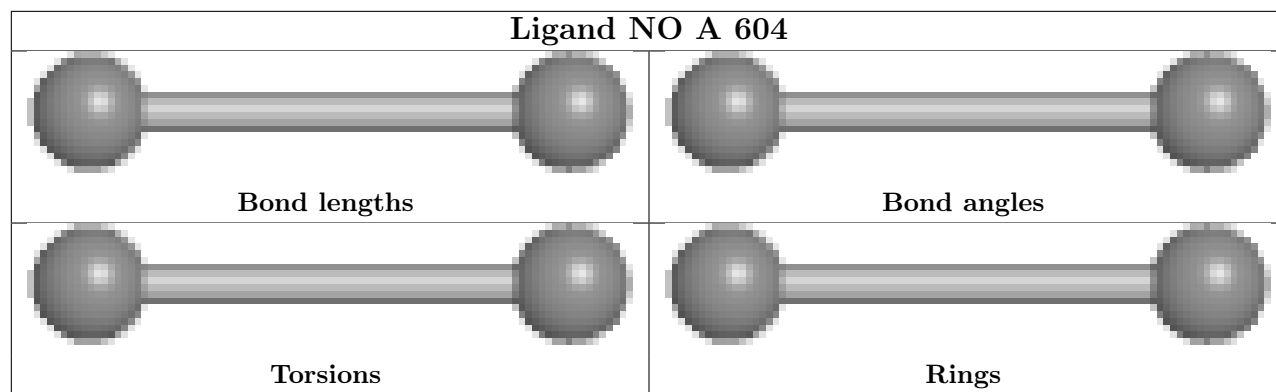
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	NAG	1	0
6	A	617	NO3	1	0
3	A	602	NAG	1	0

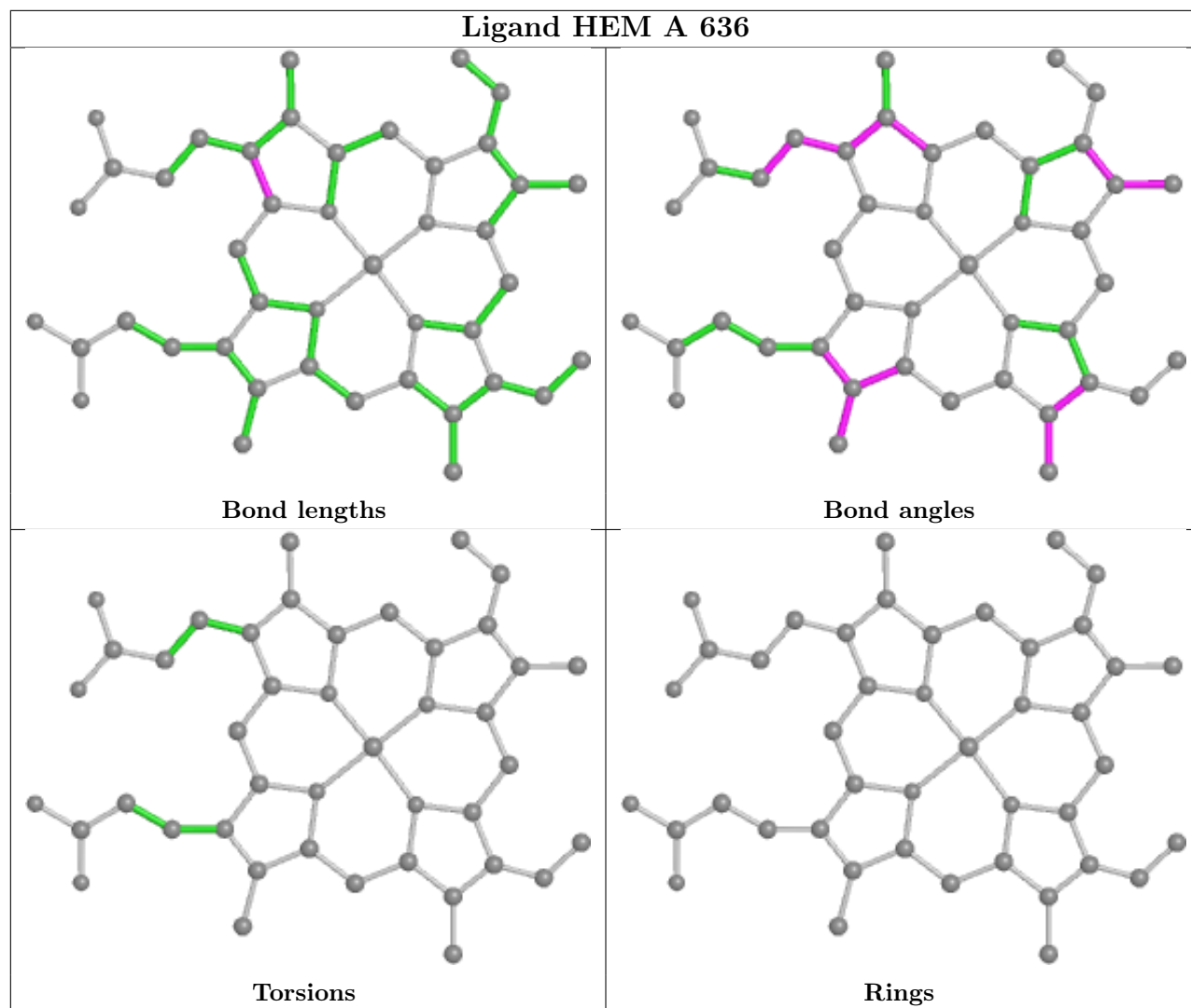
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

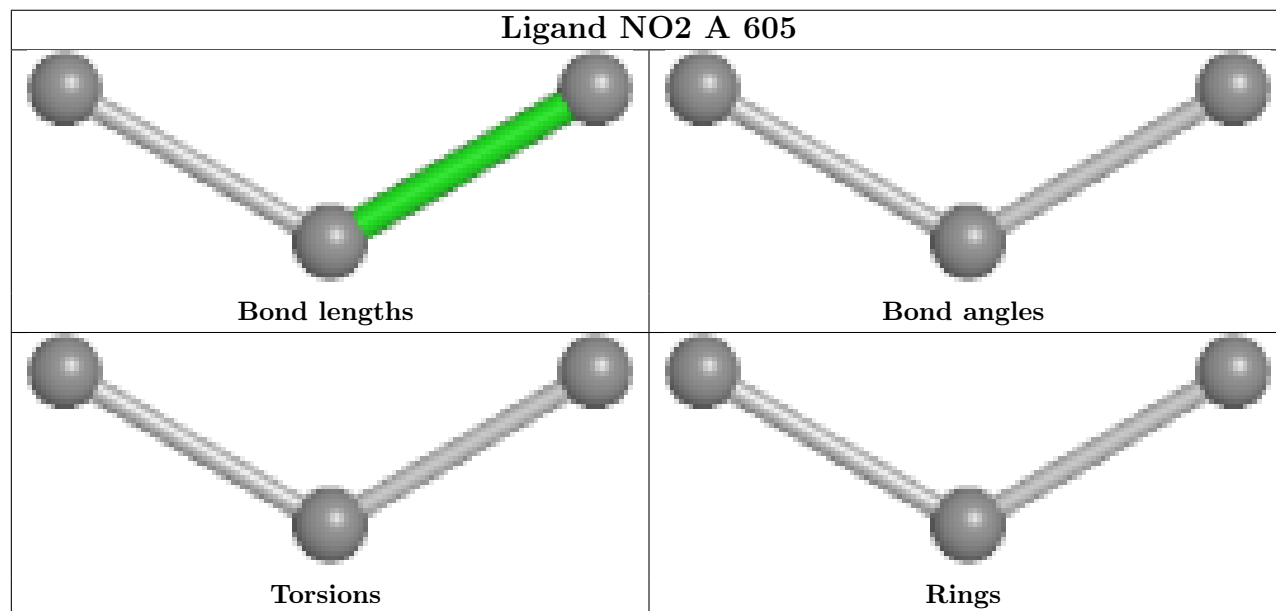
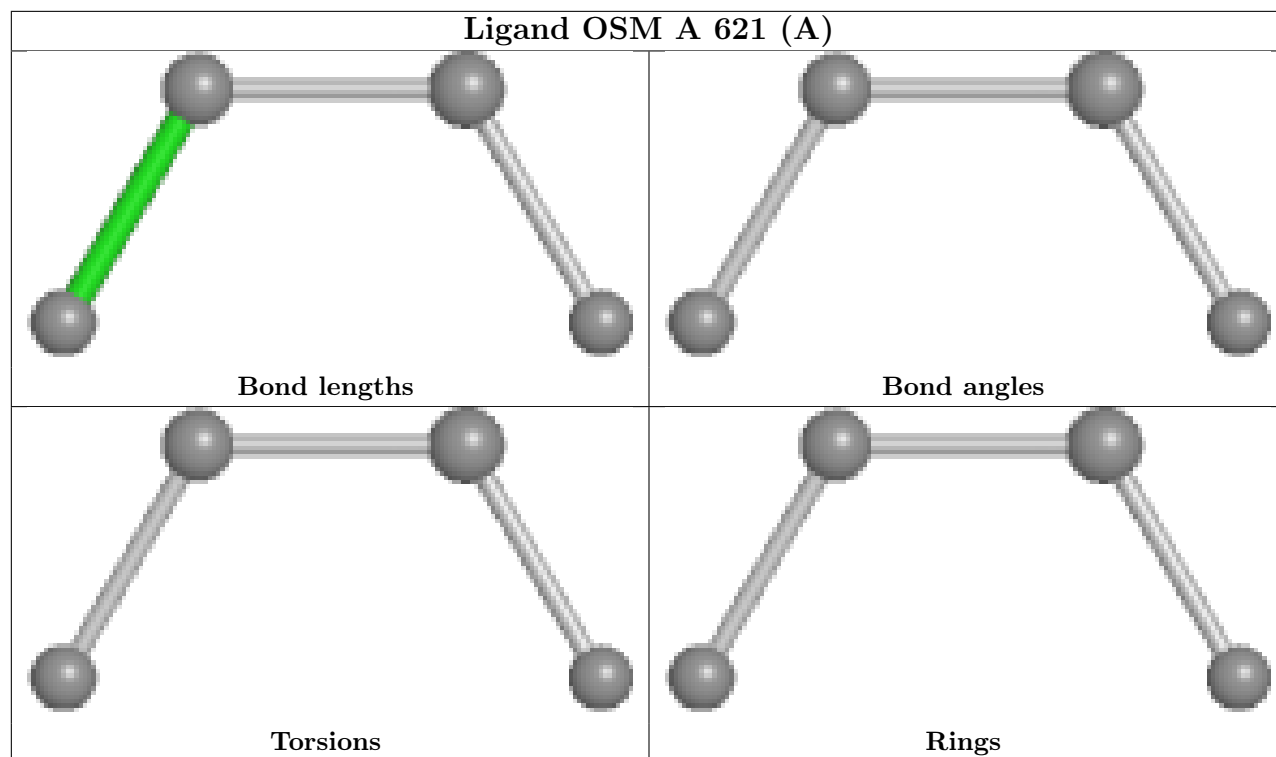


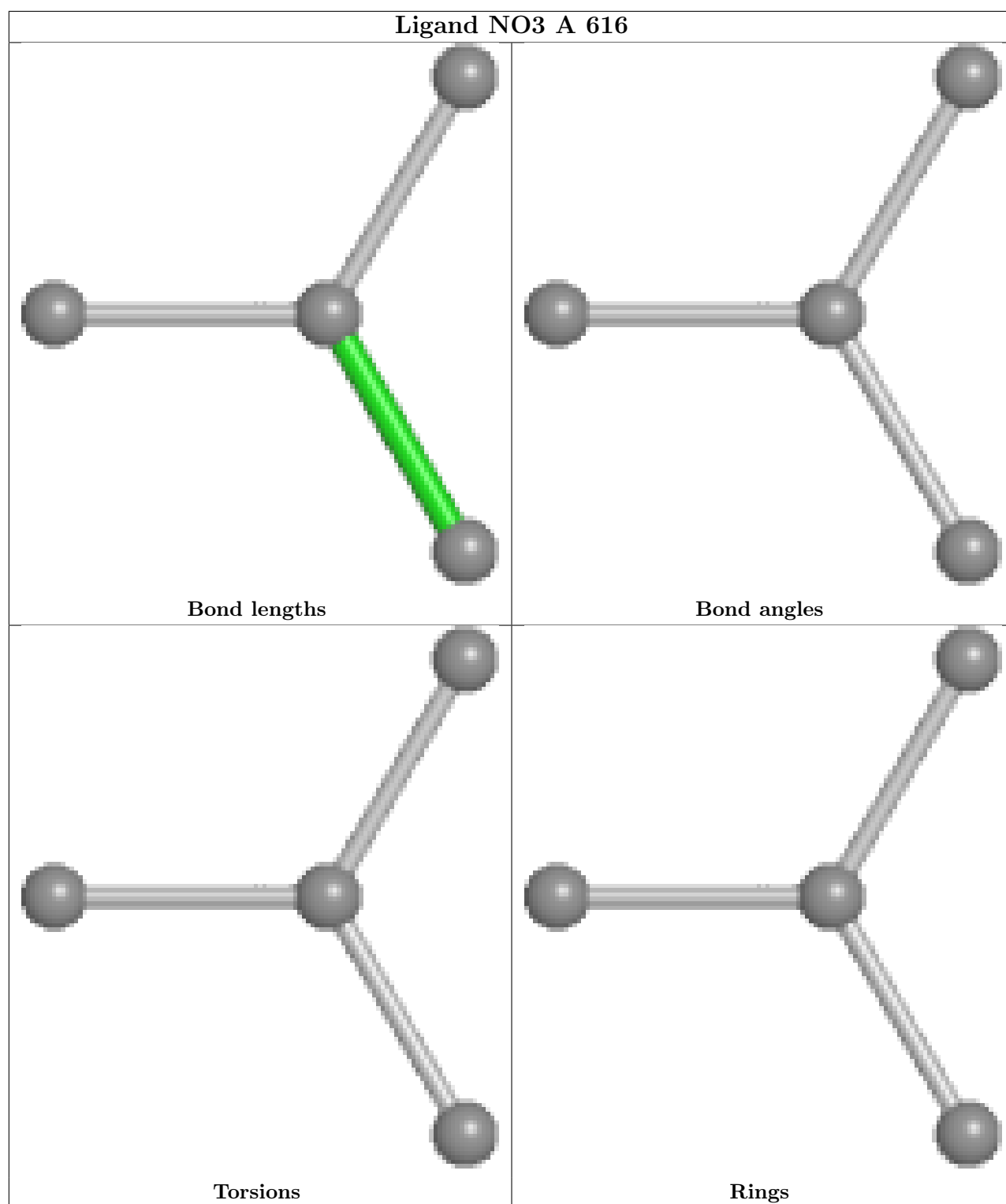


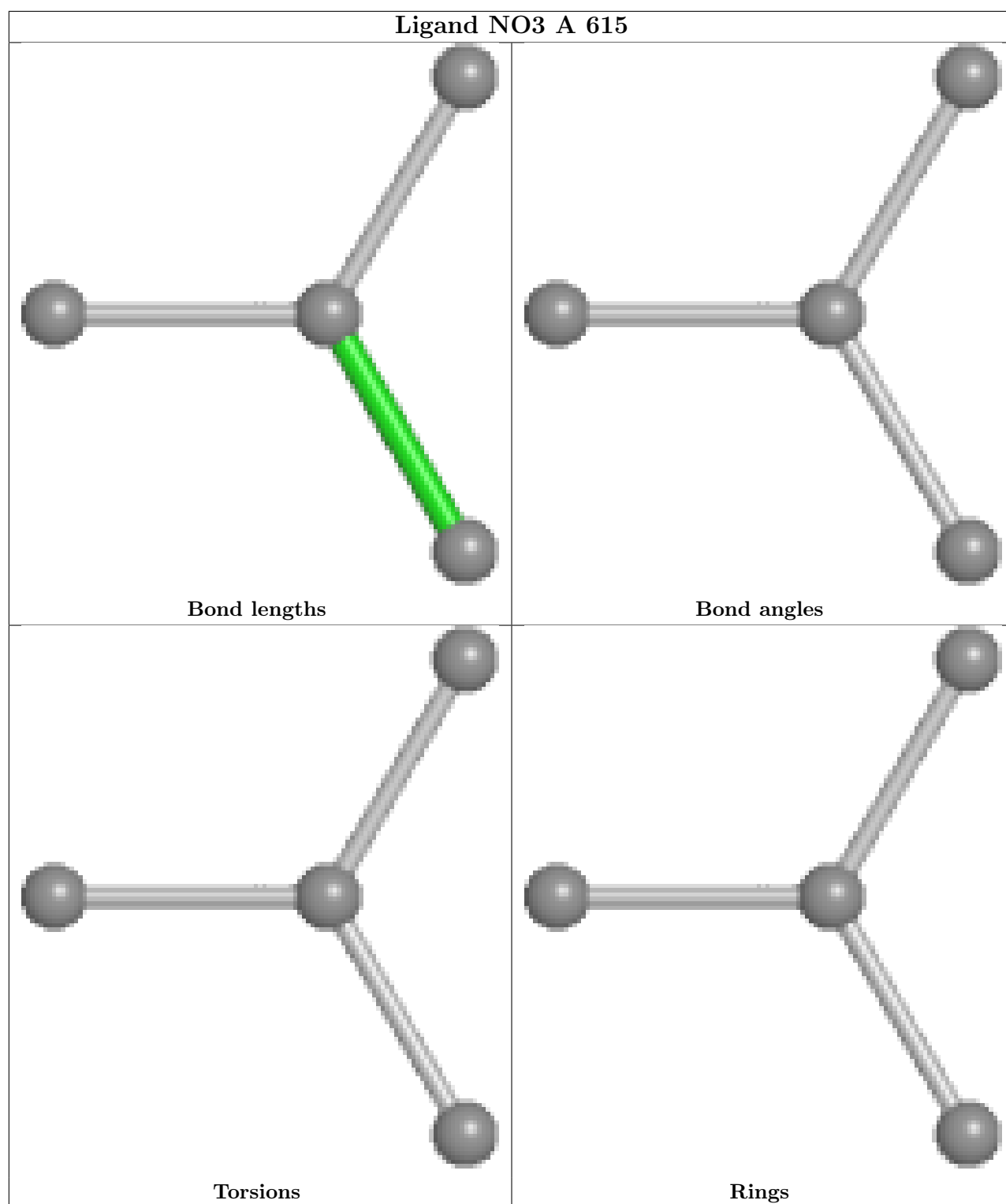


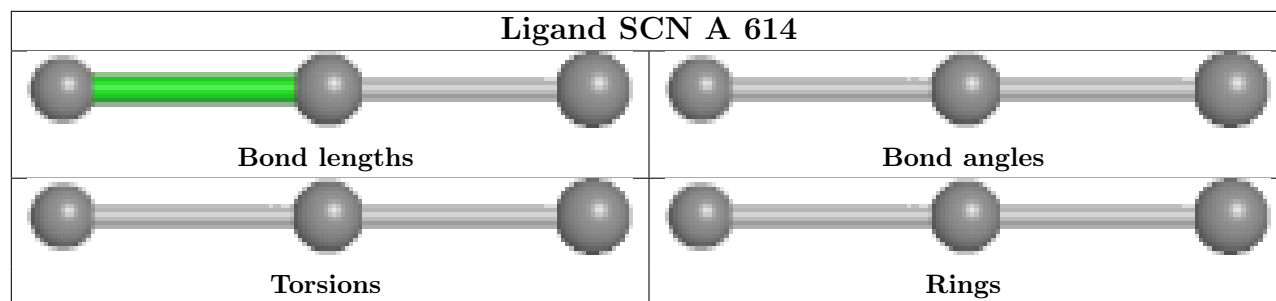


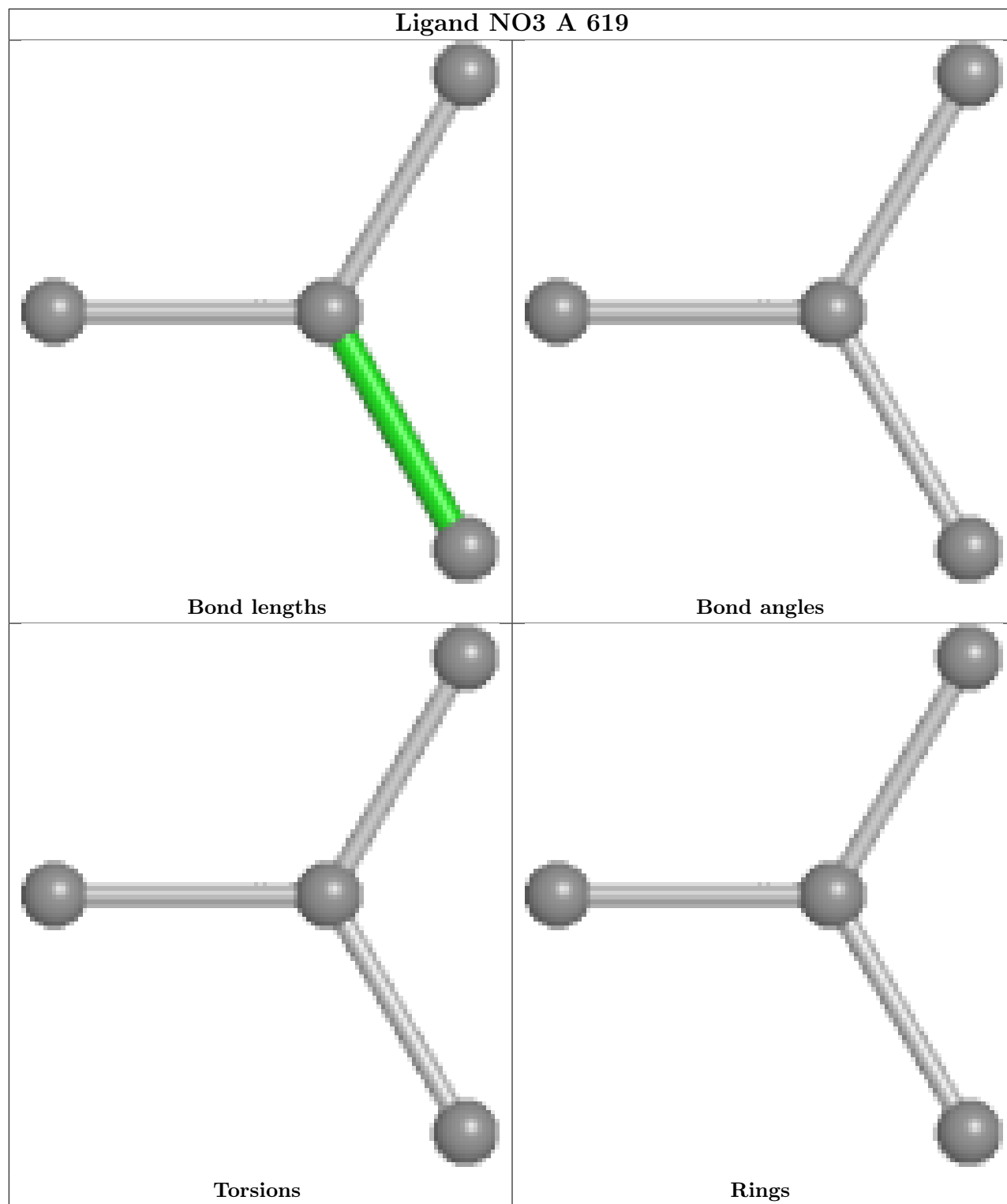




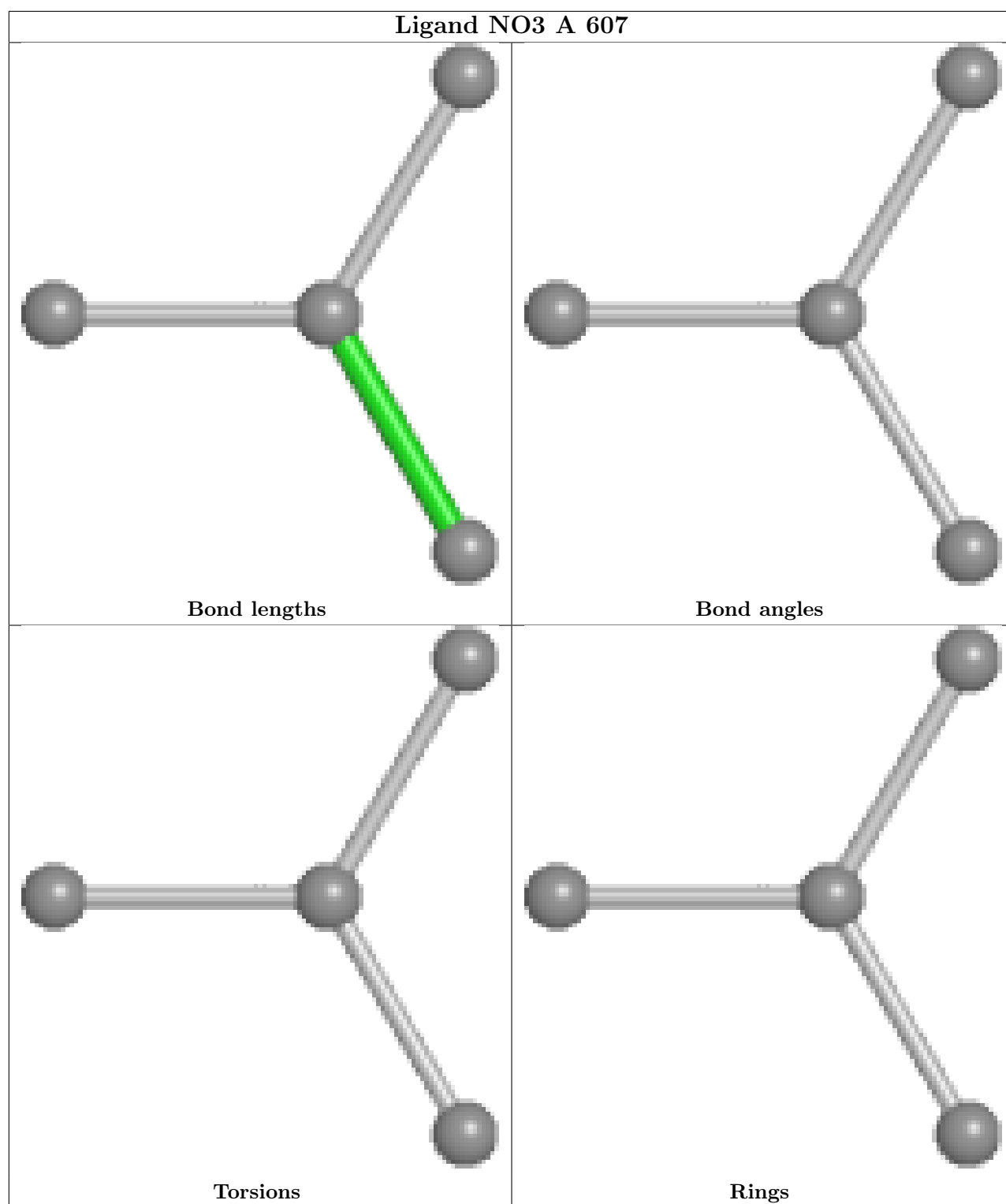


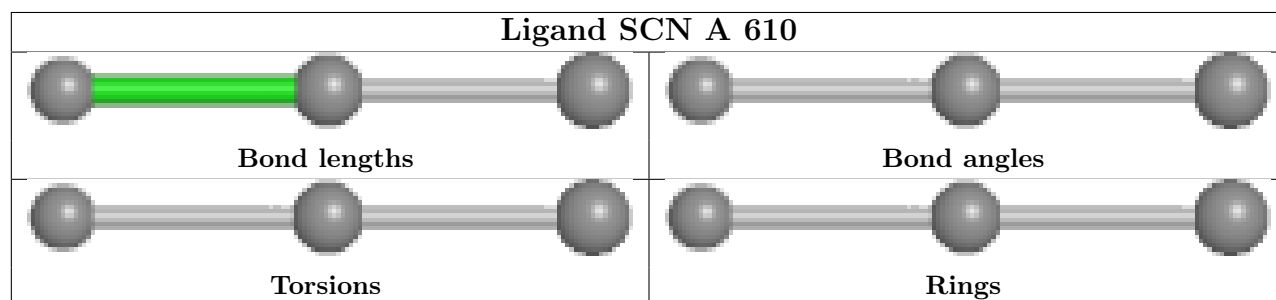
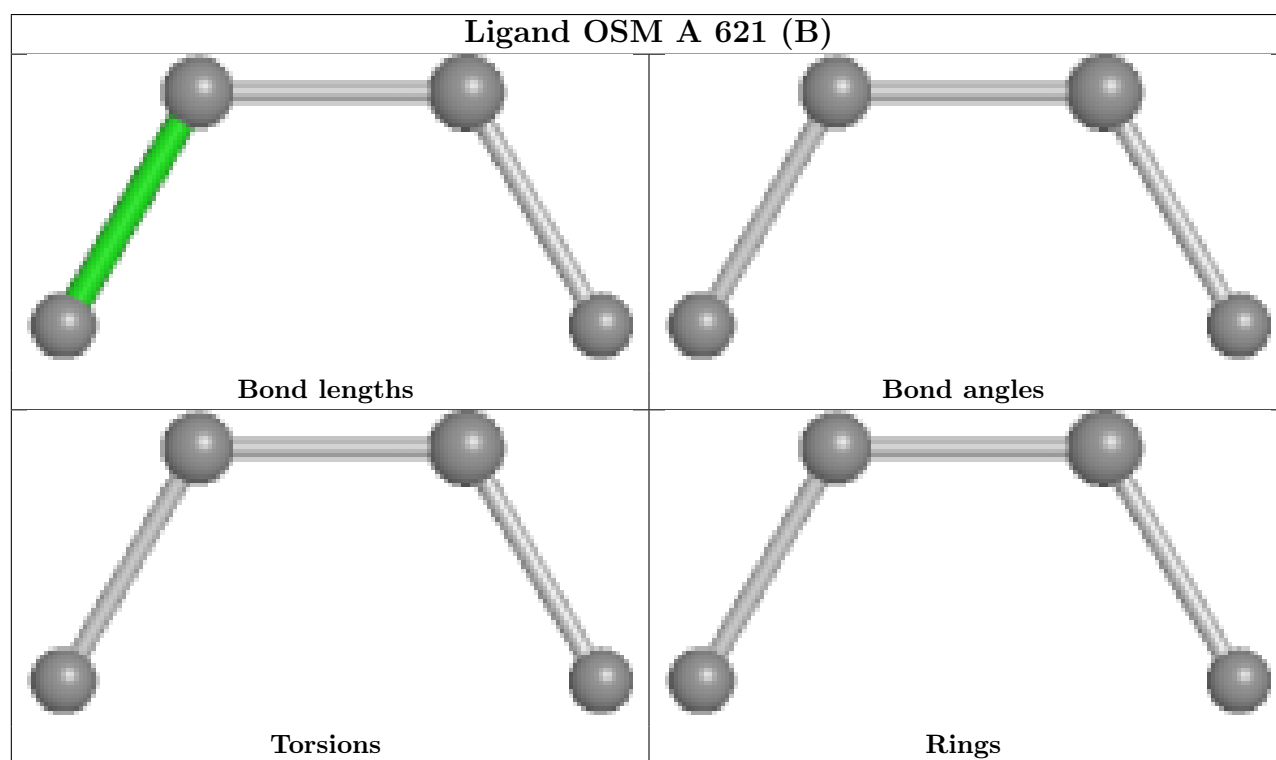
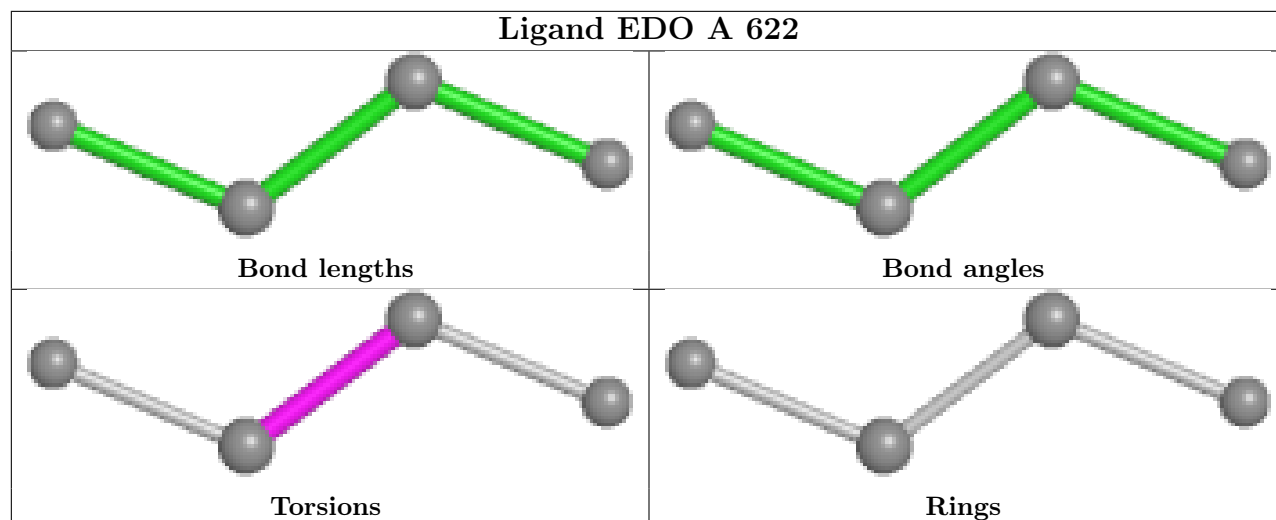


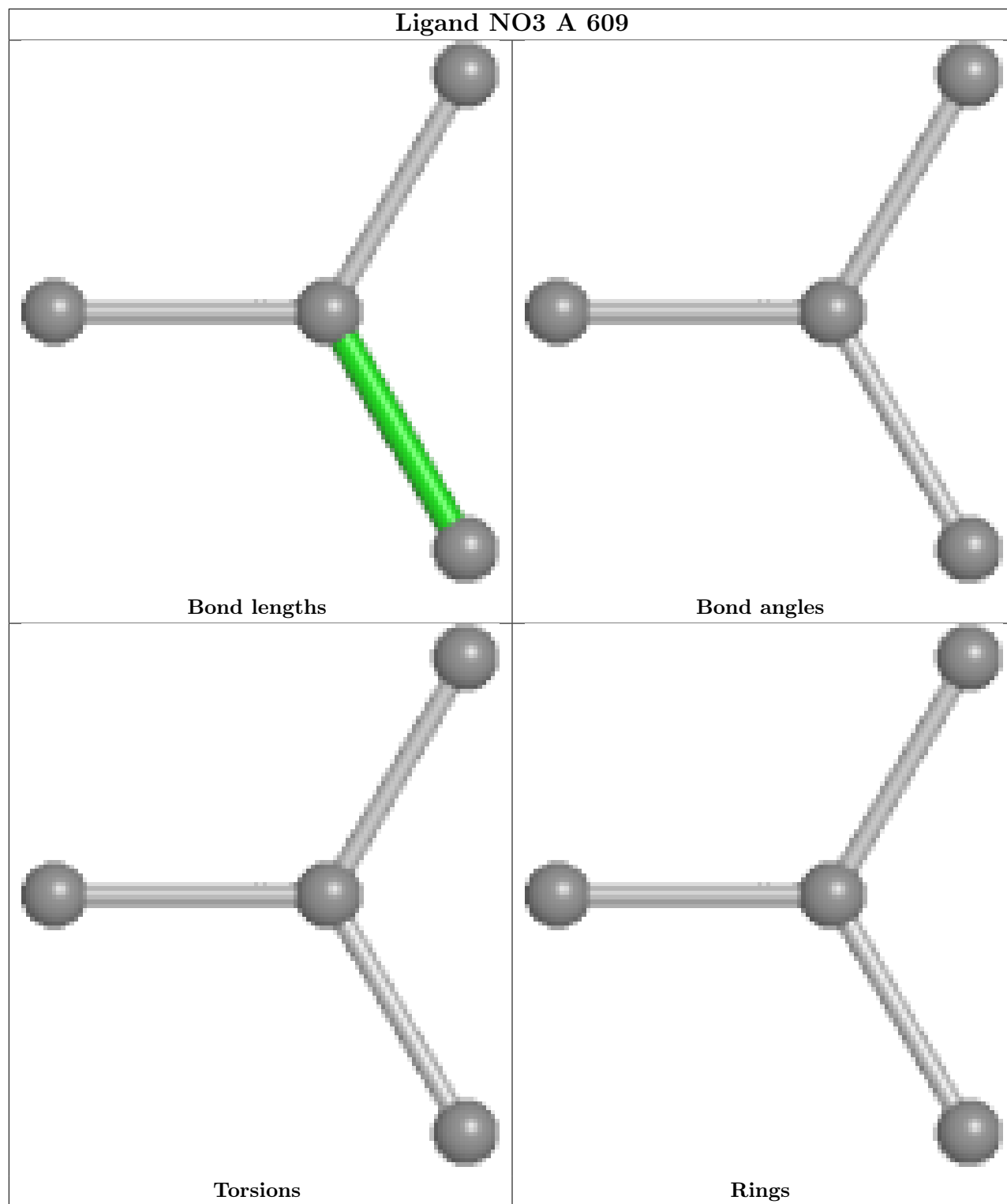


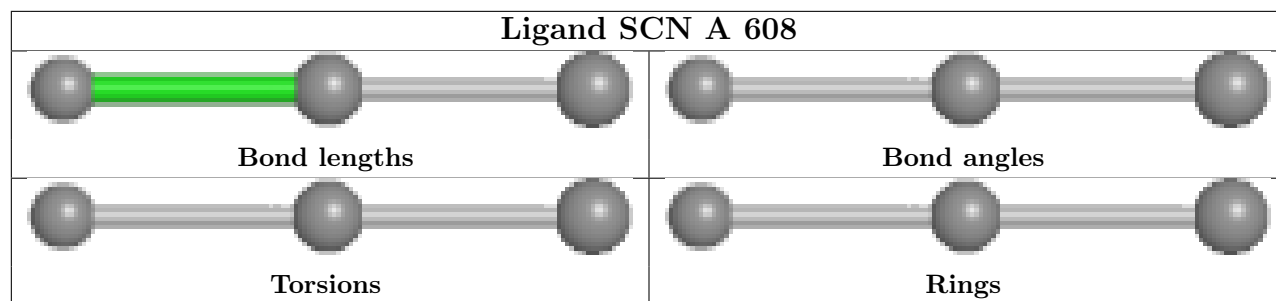


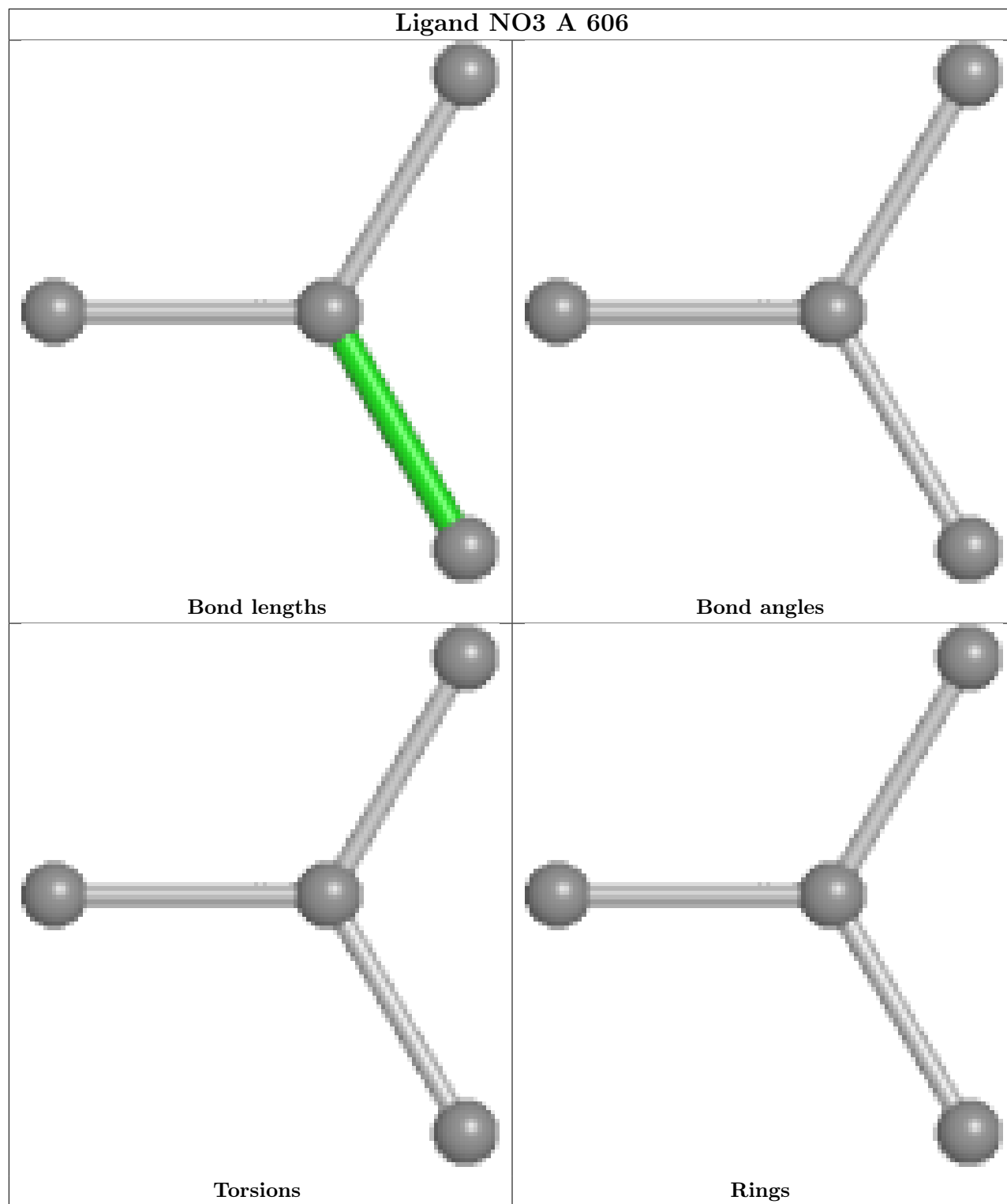


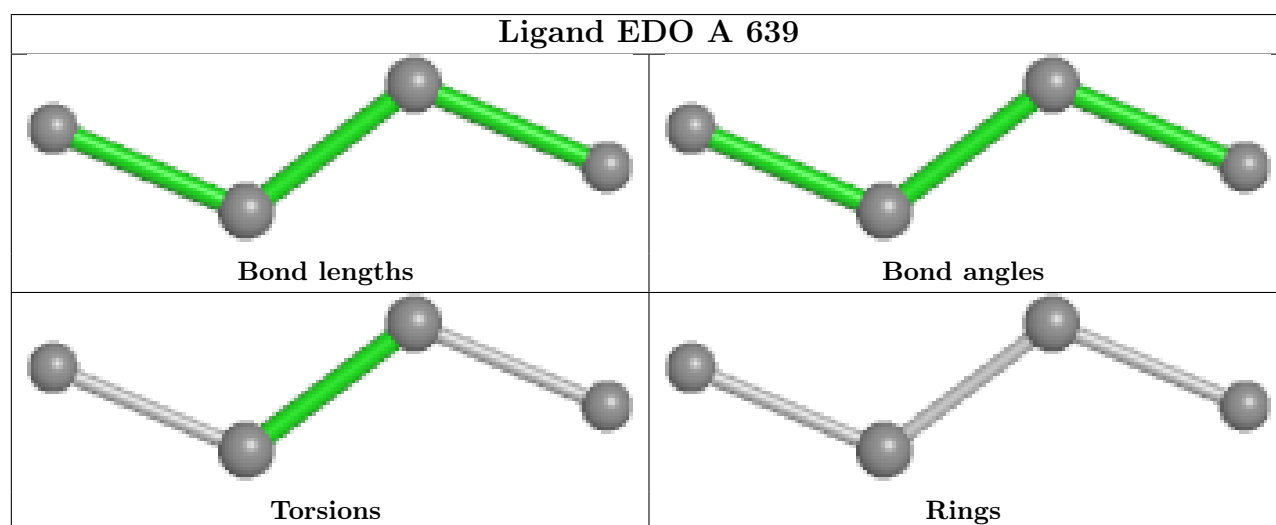
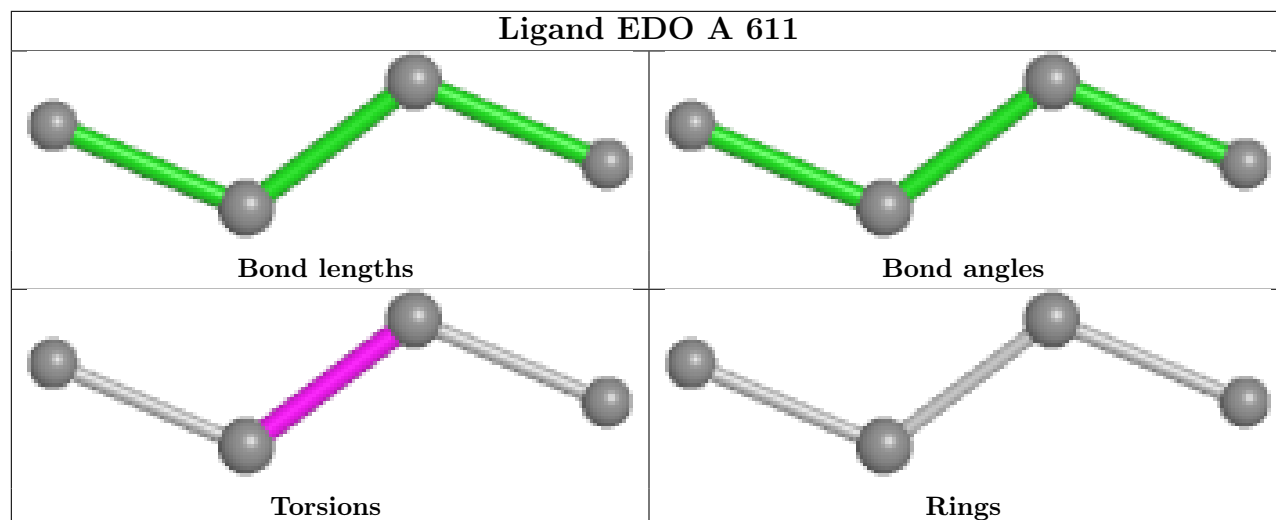


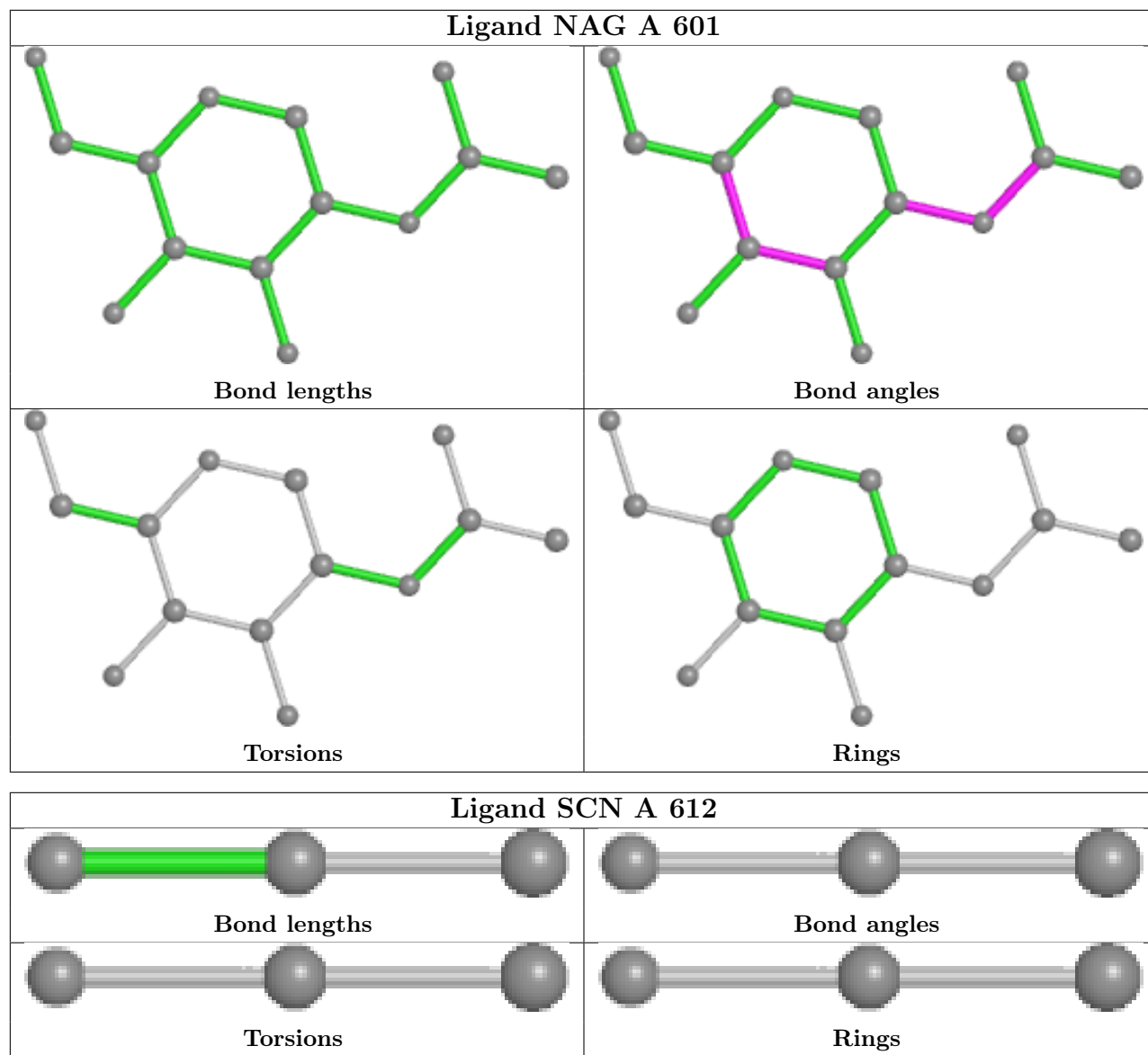


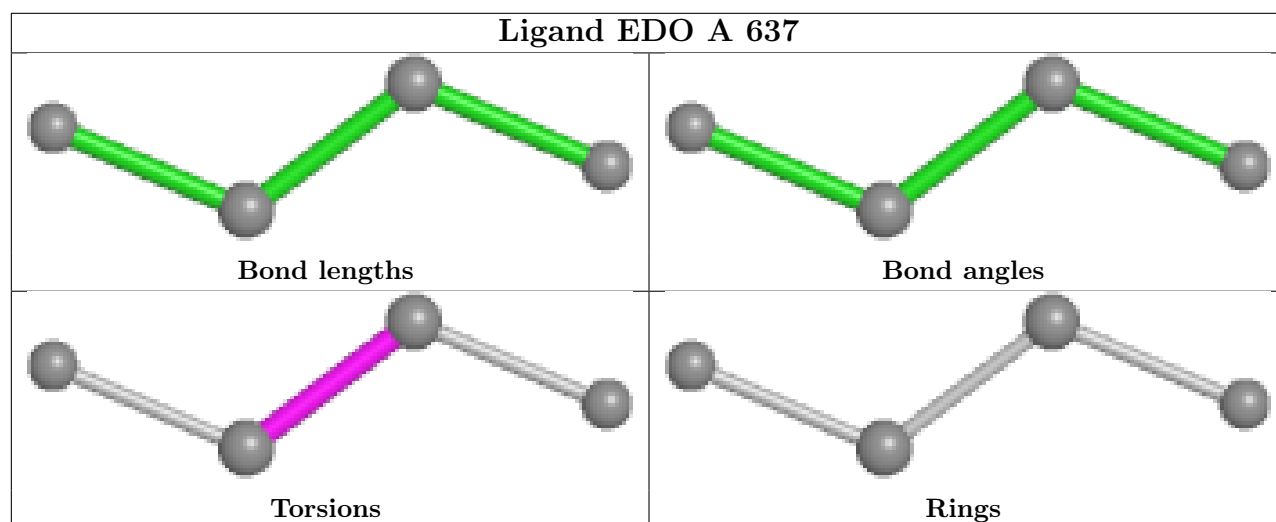
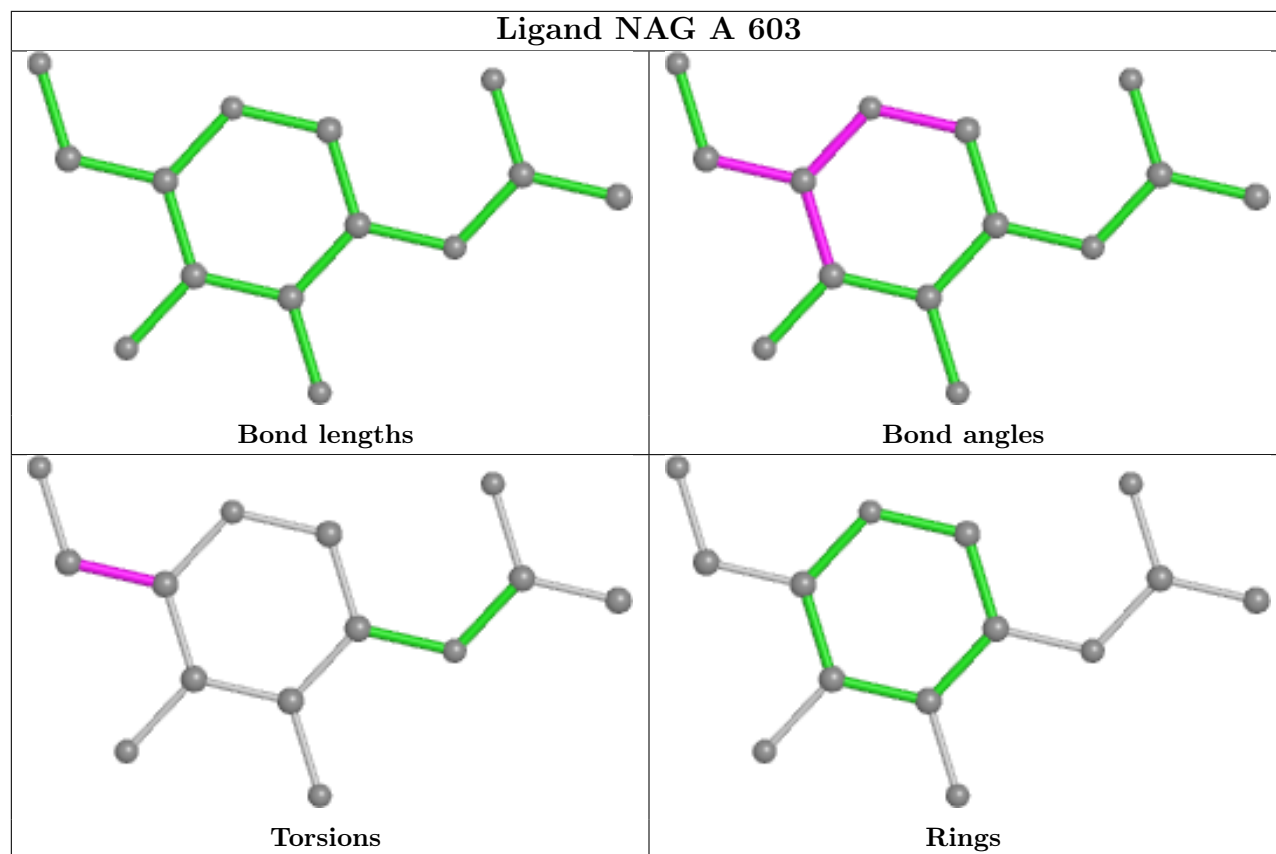




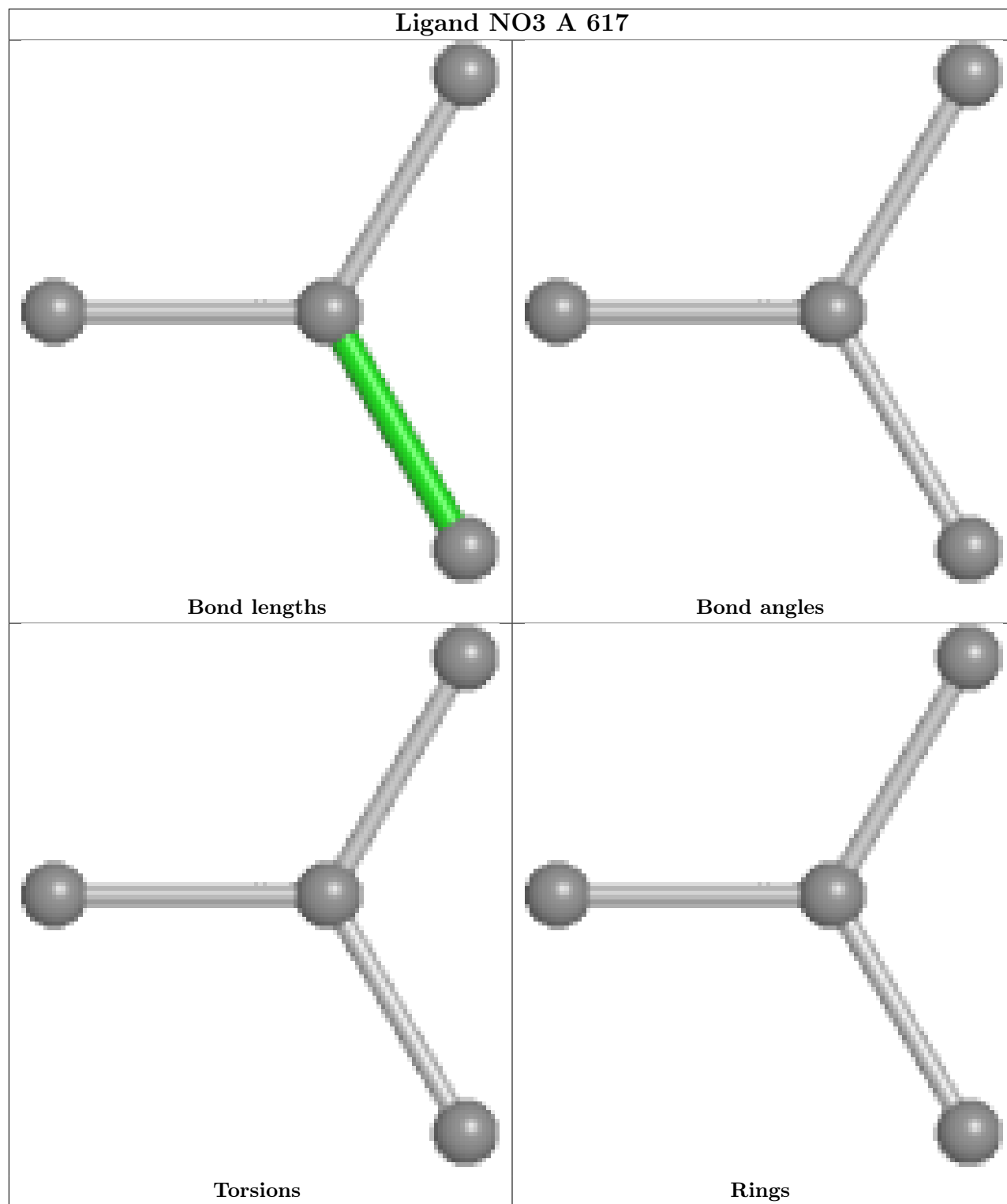


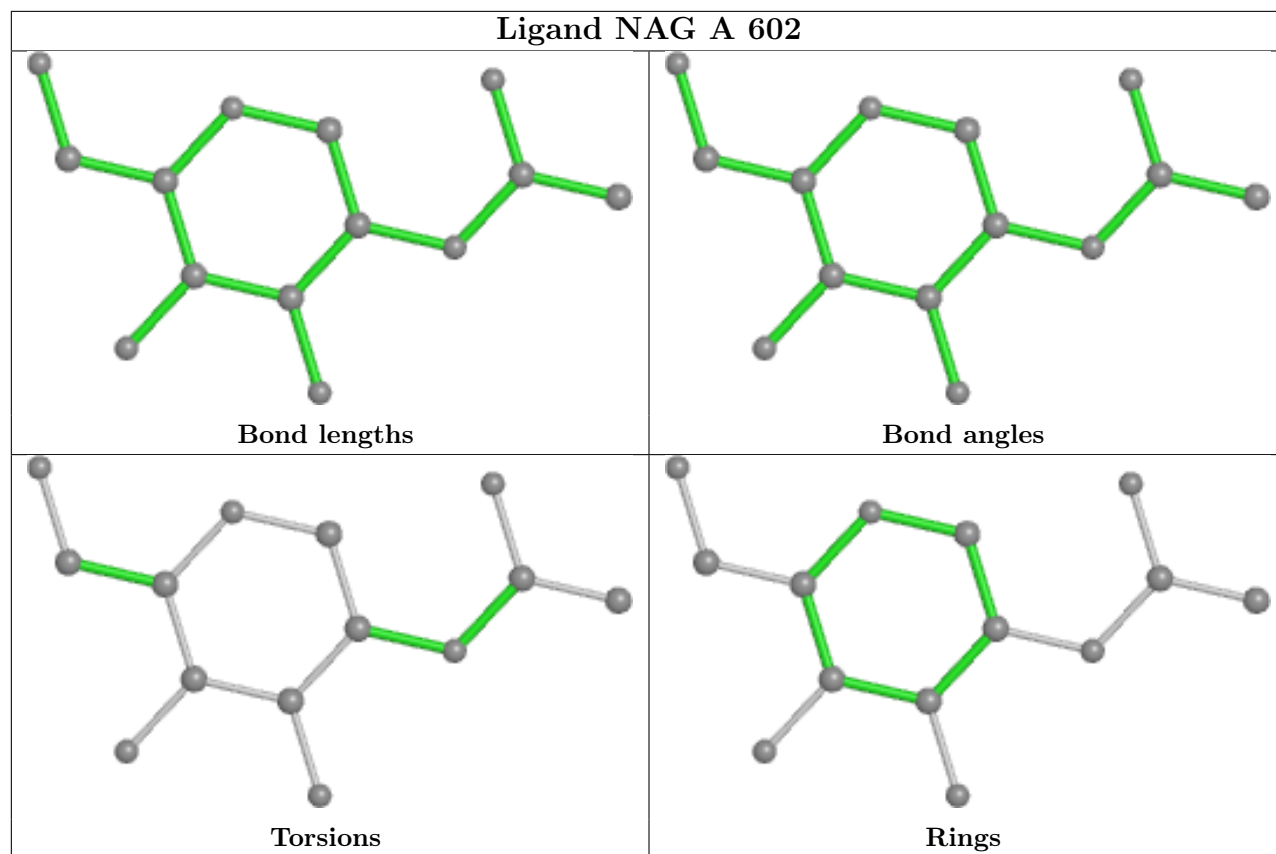












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data

### 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	594/595 (99%)	0.61	50 (8%) <b>11</b> <b>12</b>	18, 35, 91, 184	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	TRP	27.4
1	A	122	SER	17.4
1	A	172	TYR	16.1
1	A	1	SER	14.2
1	A	7	GLY	12.5
1	A	121	SER	11.2
1	A	120	GLY	11.0
1	A	5	GLY	10.3
1	A	594	GLU	9.4
1	A	173	GLN	9.3
1	A	4	VAL	9.0
1	A	593	ARG	8.8
1	A	119	LEU	8.4
1	A	9	PRO	8.3
1	A	595	ASN	8.2
1	A	11	PRO	8.2
1	A	174	SER	8.2
1	A	10	VAL	8.0
1	A	171	PRO	7.7
1	A	13	VAL	7.6
1	A	6	CYS	7.3
1	A	8	ALA	6.8
1	A	12	LEU	6.1
1	A	3	GLU	5.8
1	A	127	VAL	5.4
1	A	170	PRO	5.4
1	A	118	GLU	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	124	HIS	4.8
1	A	125	SER	4.7
1	A	283	LEU	4.6
1	A	132	TYR	4.5
1	A	169	THR	4.2
1	A	128	GLN	4.1
1	A	175	LEU	4.0
1	A	168	PRO	3.3
1	A	592	SER	3.2
1	A	209	PRO	3.0
1	A	131	GLU	2.8
1	A	134	ILE	2.7
1	A	591	ALA	2.6
1	A	223	GLY	2.6
1	A	286	HIS	2.5
1	A	425	THR	2.4
1	A	574	HIS	2.3
1	A	234	PRO	2.3
1	A	107	VAL	2.2
1	A	433	LEU	2.1
1	A	245	HIS	2.1
1	A	262	LEU	2.0
1	A	189	ALA	2.0

## 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.

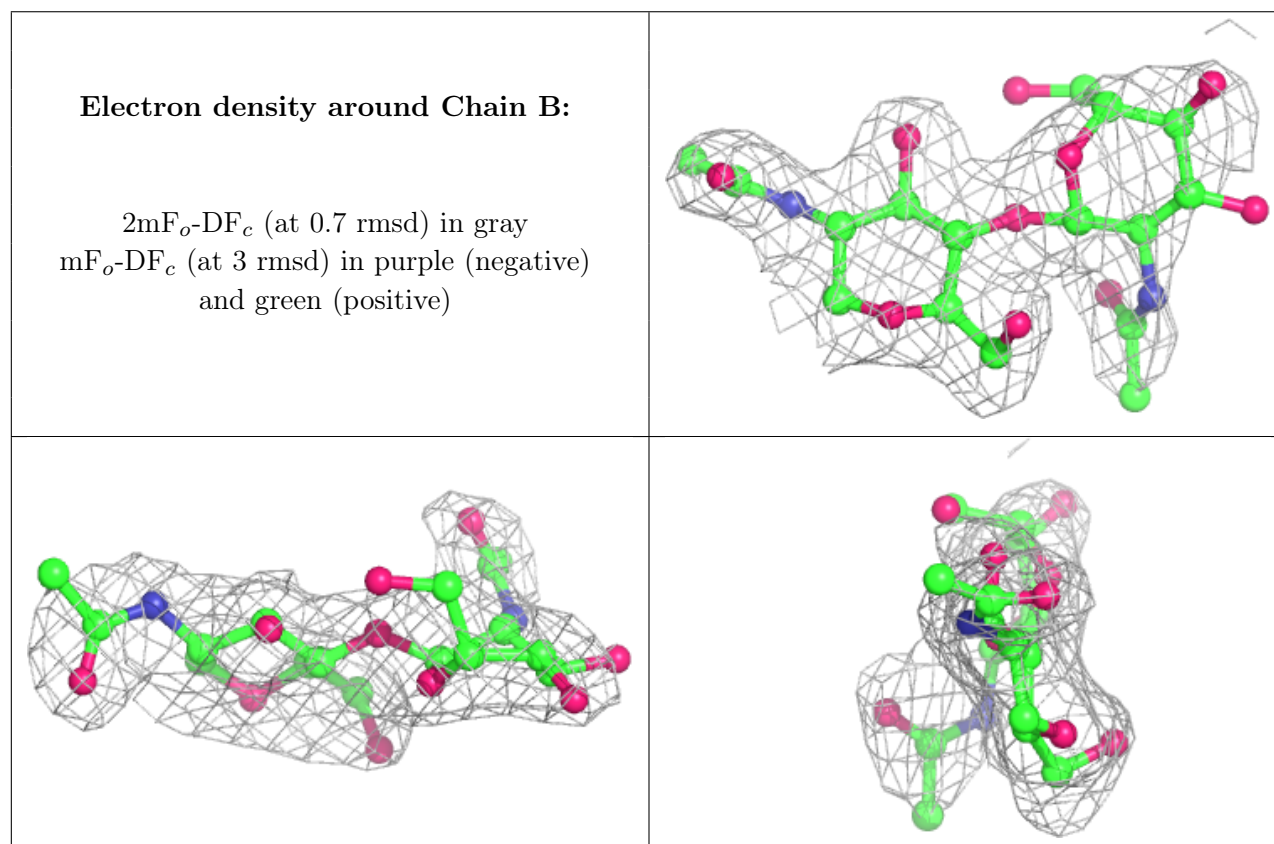
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
1	SEP	A	198	10/11	0.91	0.14	34,42,56,56	0

## 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( $\text{\AA}^2$ )	Q<0.9
2	NAG	B	2	14/15	0.87	0.25	62,67,70,77	14
2	NAG	B	1	14/15	0.94	0.11	38,45,53,54	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.



## 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	A	603	14/15	0.76	0.22	59,69,76,85	14
3	NAG	A	601	14/15	0.81	0.29	49,60,66,71	0
8	EDO	A	639	4/4	0.88	0.17	42,43,44,48	0
8	EDO	A	637	4/4	0.89	0.17	34,35,41,52	0
9	OSM	A	621[A]	4/4	0.89	0.23	34,36,37,40	4
9	OSM	A	621[B]	4/4	0.89	0.23	41,43,44,45	4
8	EDO	A	611	4/4	0.90	0.13	48,49,49,50	0

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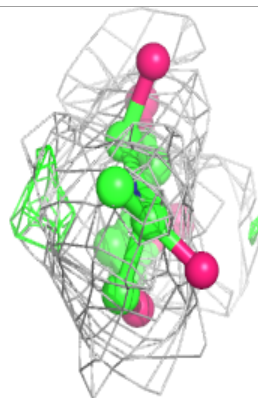
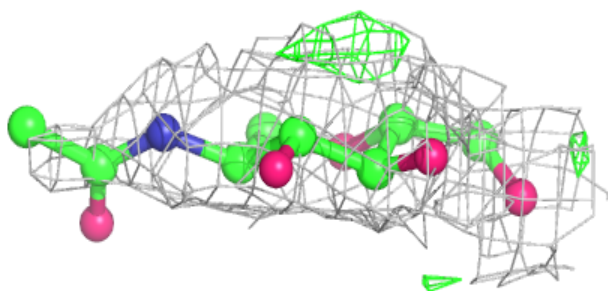
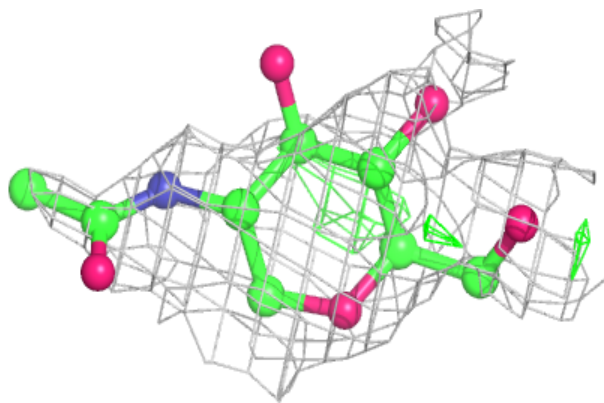
*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
7	SCN	A	614	3/3	0.91	0.18	36,36,44,45	0
3	NAG	A	602	14/15	0.93	0.12	43,48,52,52	0
6	NO3	A	609	4/4	0.94	0.29	52,54,61,62	0
7	SCN	A	608	3/3	0.94	0.13	38,38,40,45	3
10	IOD	A	625	1/1	0.95	0.09	55,55,55,55	1
7	SCN	A	610	3/3	0.96	0.09	39,39,47,48	0
6	NO3	A	615	4/4	0.96	0.11	21,26,34,42	0
11	NA	A	633	1/1	0.96	0.06	38,38,38,38	0
11	NA	A	634	1/1	0.96	0.05	38,38,38,38	0
9	OSM	A	613	4/4	0.97	0.09	28,35,38,38	4
6	NO3	A	606	4/4	0.97	0.17	32,32,43,48	0
7	SCN	A	612	3/3	0.97	0.09	26,26,26,34	0
4	NO	A	604	2/2	0.98	0.12	33,33,33,41	0
6	NO3	A	620	4/4	0.98	0.12	28,35,37,57	0
10	IOD	A	624	1/1	0.98	0.03	51,51,51,51	1
12	HEM	A	636	43/43	0.98	0.16	17,22,26,28	0
13	CA	A	638	1/1	0.98	0.08	25,25,25,25	0
6	NO3	A	617	4/4	0.99	0.08	22,23,24,25	4
10	IOD	A	627	1/1	0.99	0.02	51,51,51,51	1
10	IOD	A	628	1/1	0.99	0.07	34,34,34,34	1
10	IOD	A	629	1/1	0.99	0.05	31,31,31,31	1
10	IOD	A	631	1/1	0.99	0.07	30,30,30,30	1
10	IOD	A	632	1/1	0.99	0.02	42,42,42,42	1
6	NO3	A	618	4/4	0.99	0.07	15,16,17,20	4
6	NO3	A	619	4/4	0.99	0.08	17,18,19,24	4
11	NA	A	635	1/1	0.99	0.06	38,38,38,38	0
6	NO3	A	607	4/4	0.99	0.11	33,35,38,43	4
6	NO3	A	616	4/4	0.99	0.10	19,20,20,22	4
8	EDO	A	622	4/4	1.00	0.09	3,3,3,4	4
5	NO2	A	605	3/3	1.00	0.13	17,17,18,18	3
10	IOD	A	630	1/1	1.00	0.03	36,36,36,36	1
10	IOD	A	626	1/1	1.00	0.06	26,26,26,26	0
10	IOD	A	623	1/1	1.00	0.11	22,22,22,22	1

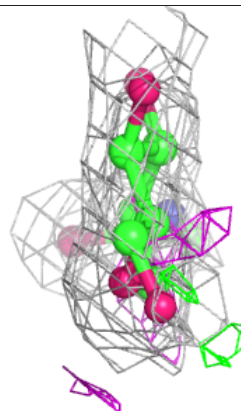
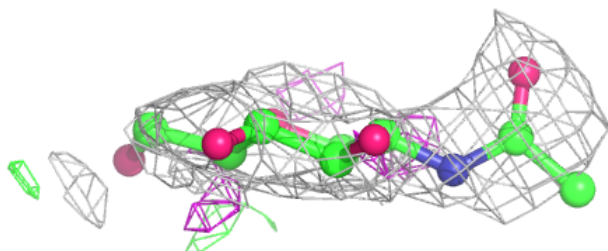
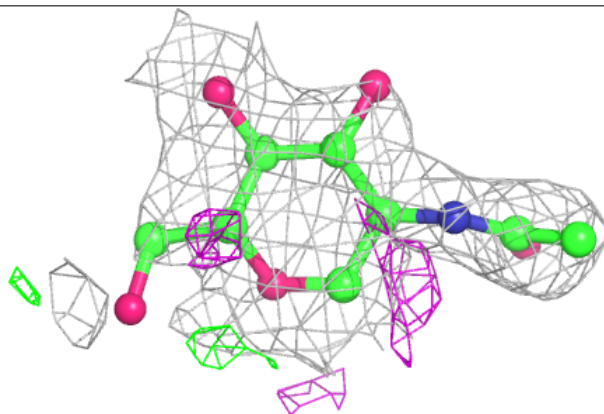
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around NAG A 603:**

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

**Electron density around NAG A 601:**

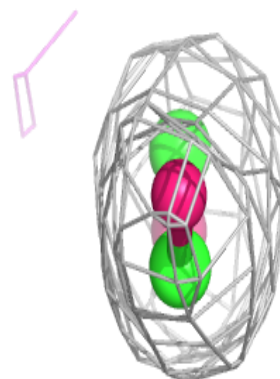
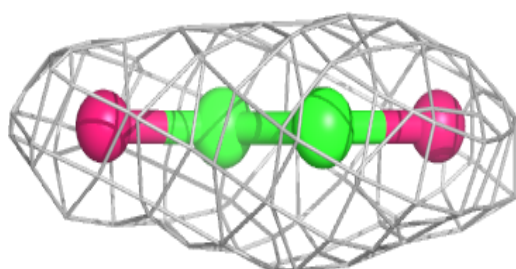
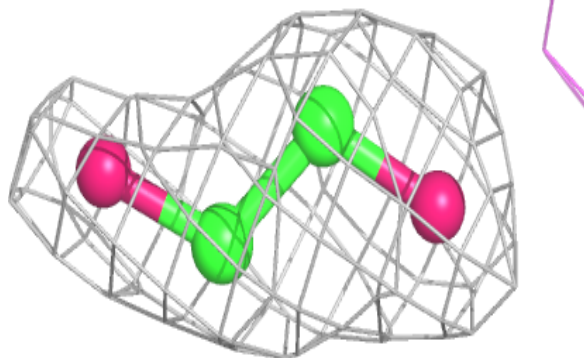
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



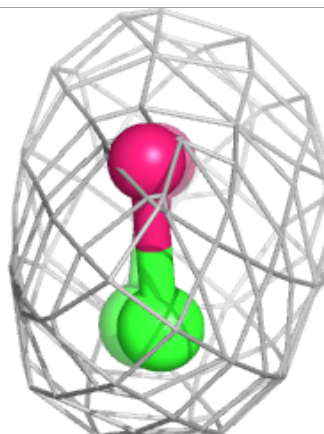
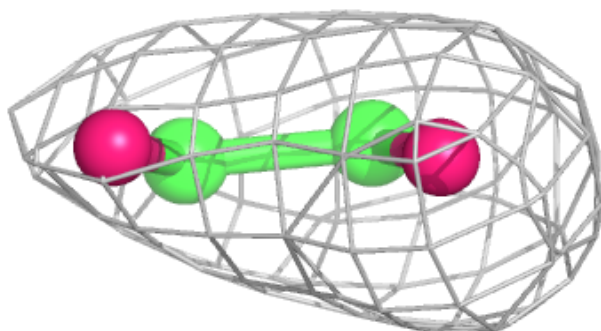
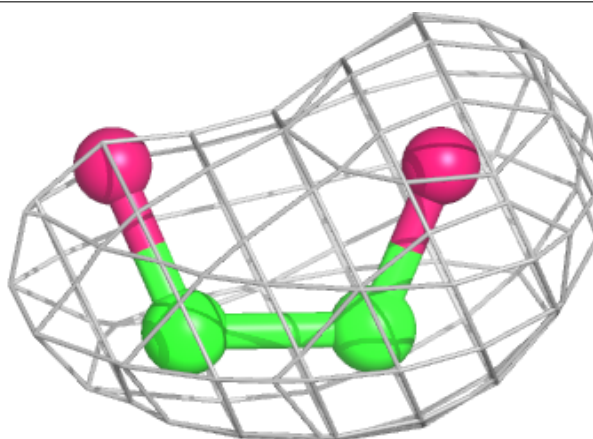


**Electron density around EDO A 639:**

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

**Electron density around EDO A 637:**

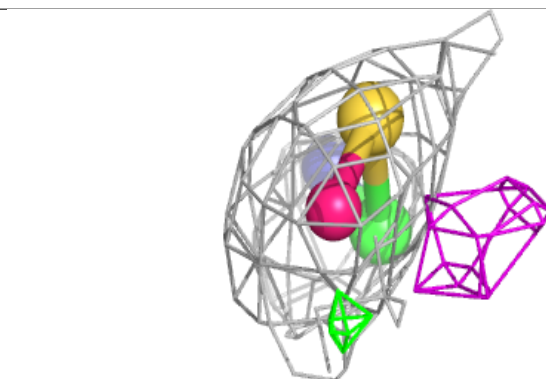
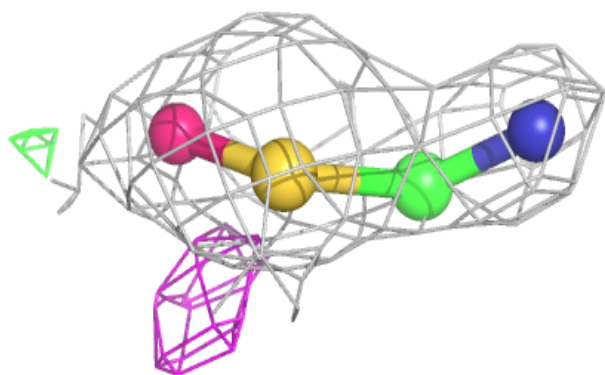
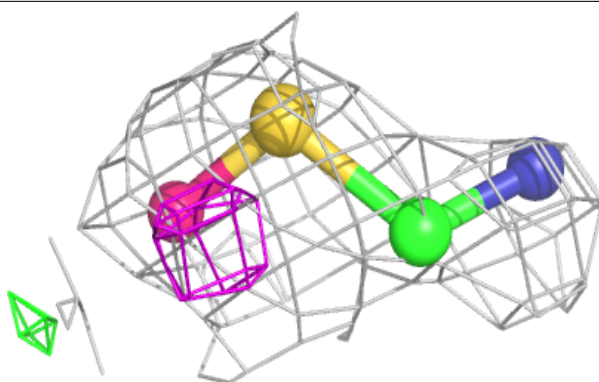
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



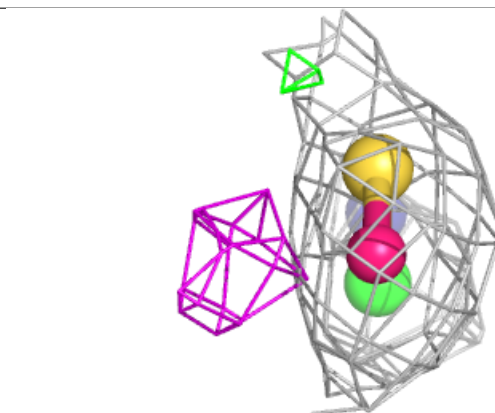
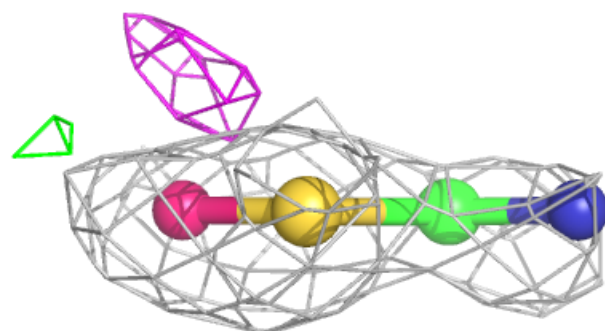
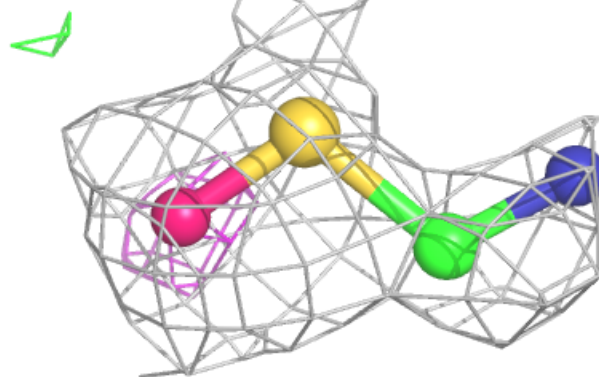


**Electron density around OSM A 621 (A):**

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

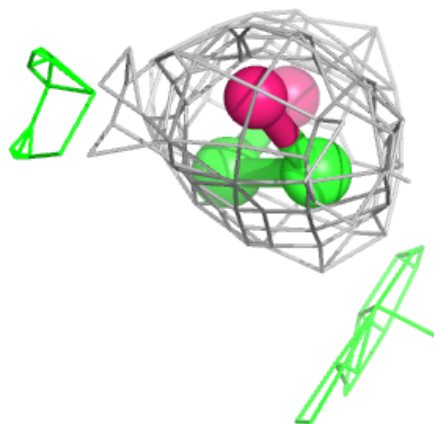
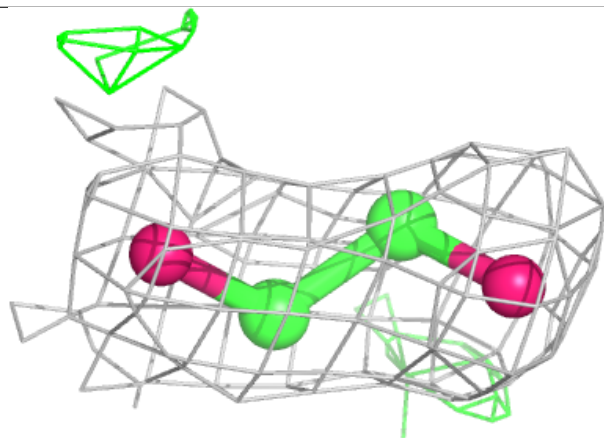
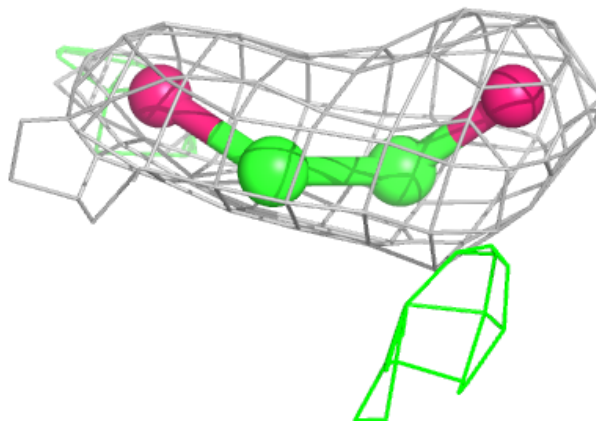
**Electron density around OSM A 621 (B):**

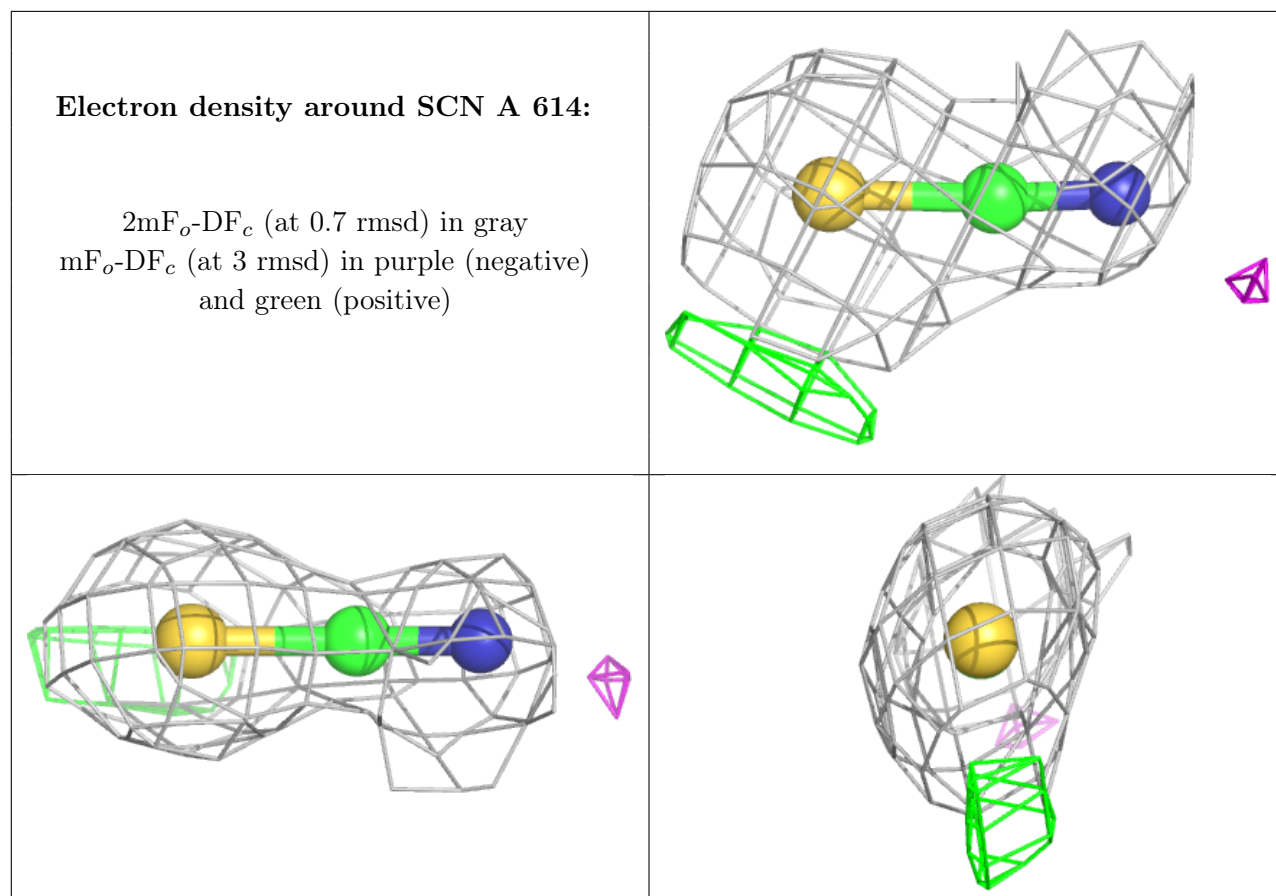
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around EDO A 611:**

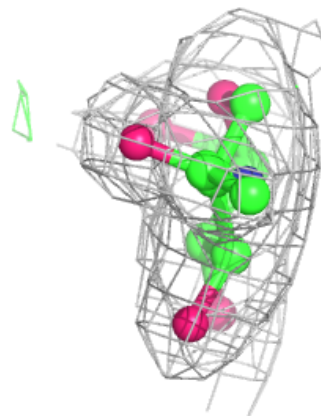
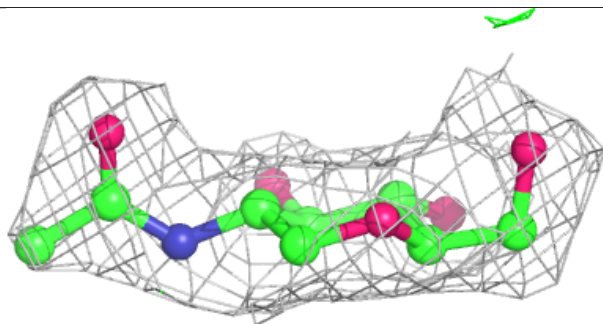
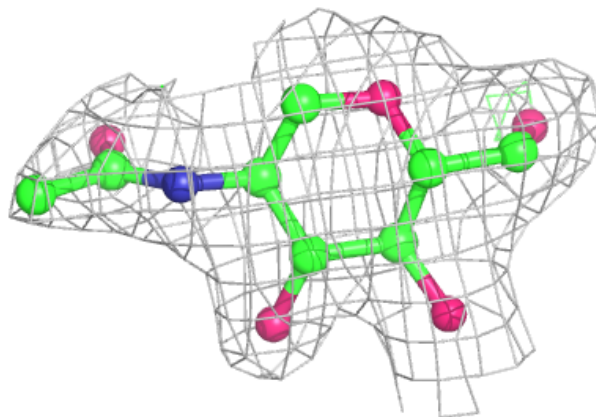
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





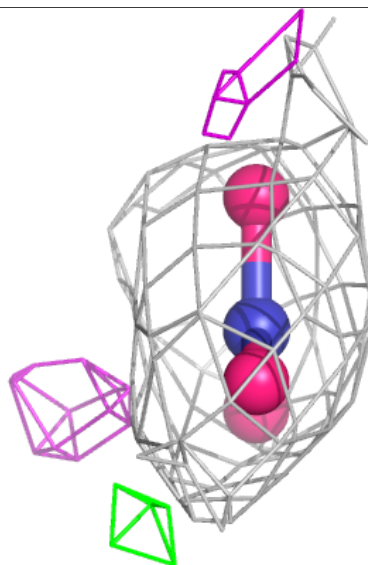
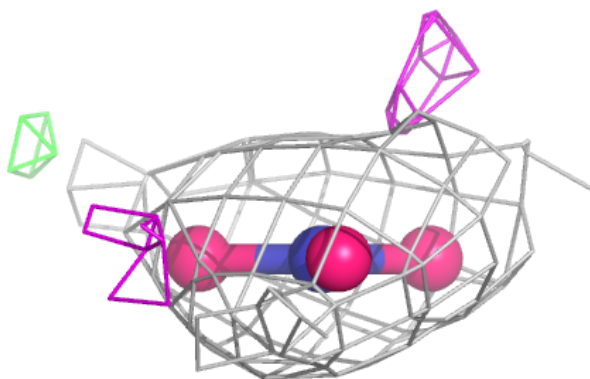
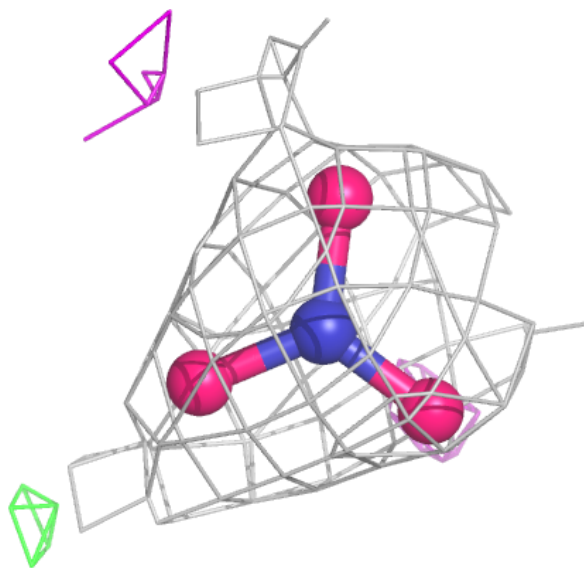
**Electron density around NAG A 602:**

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



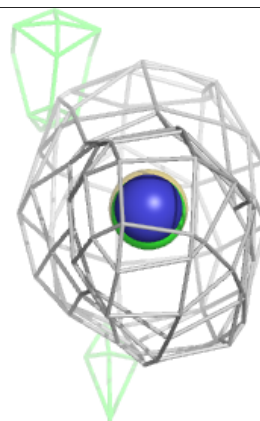
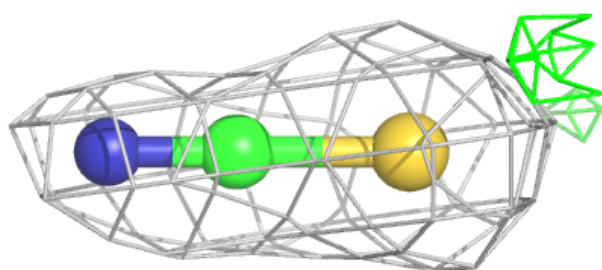
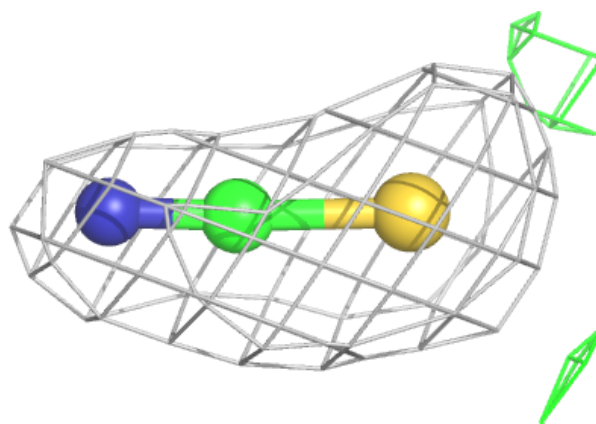
**Electron density around NO3 A 609:**

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



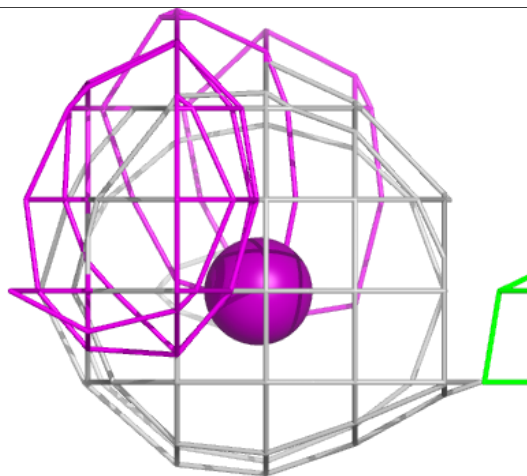
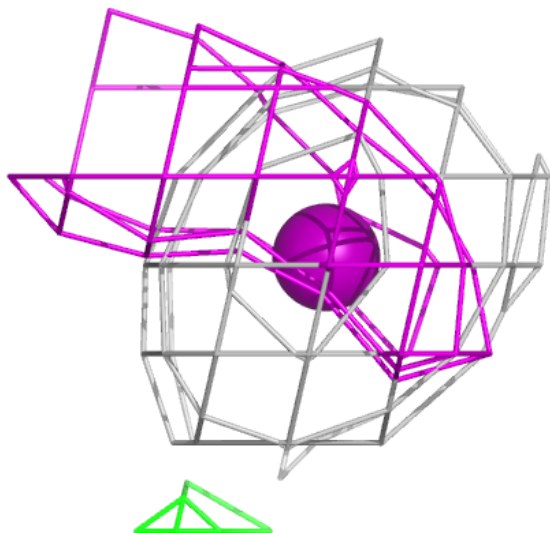
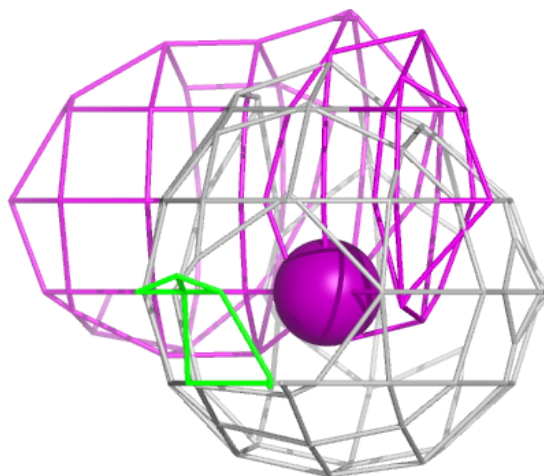
**Electron density around SCN A 608:**

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



**Electron density around IOD A 625:**

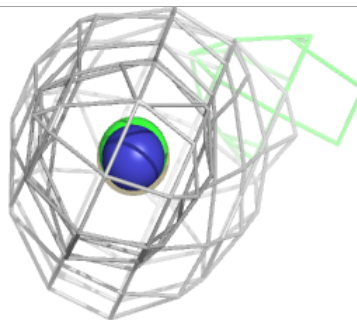
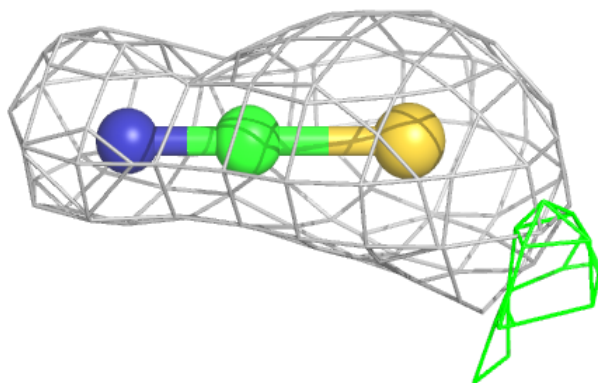
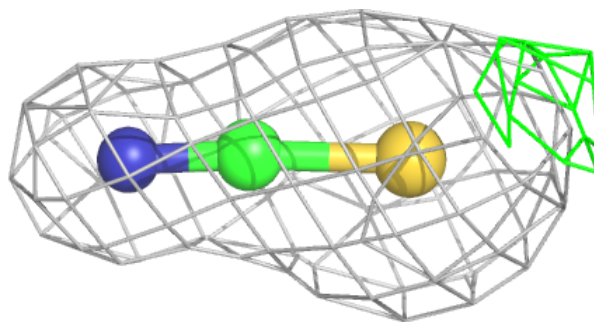
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around SCN A 610:**

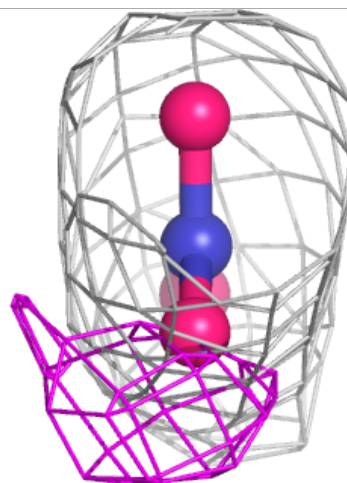
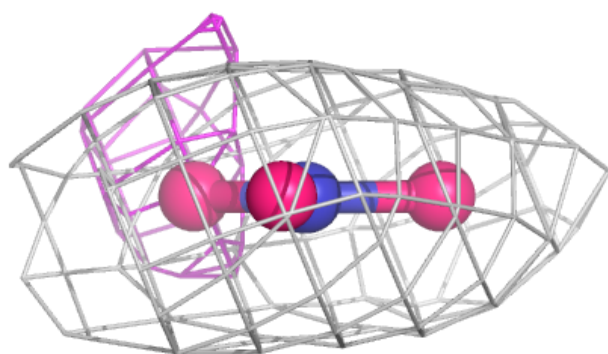
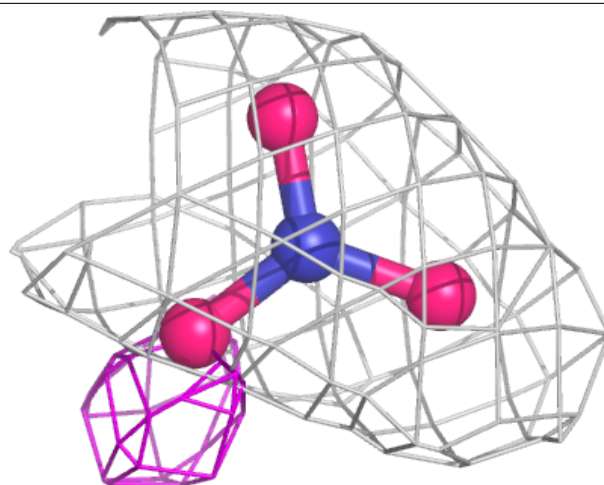
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





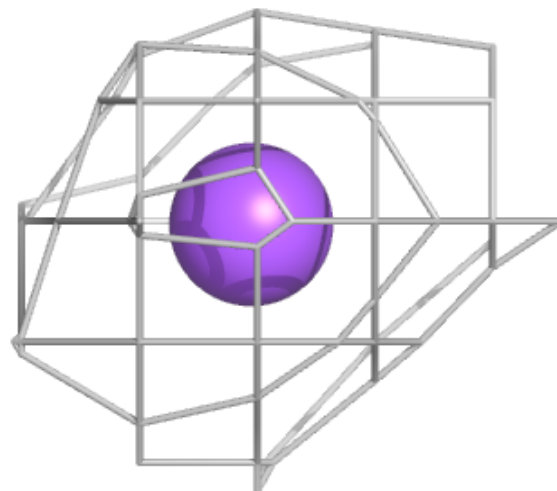
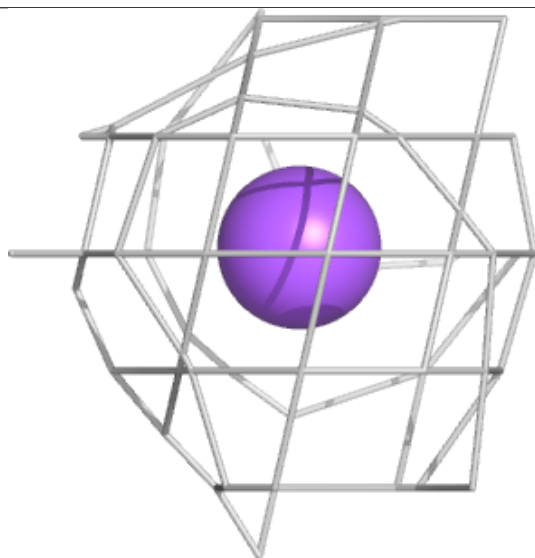
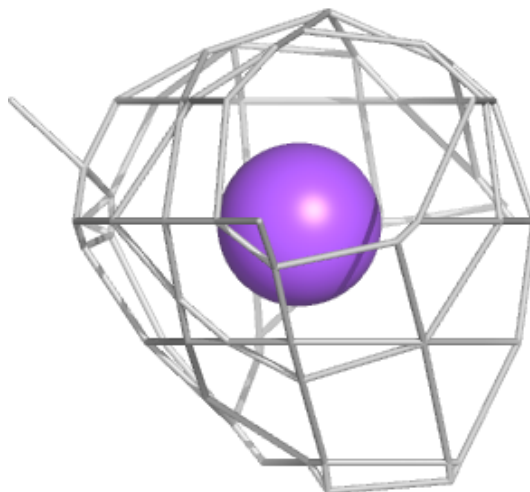
**Electron density around NO3 A 615:**

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



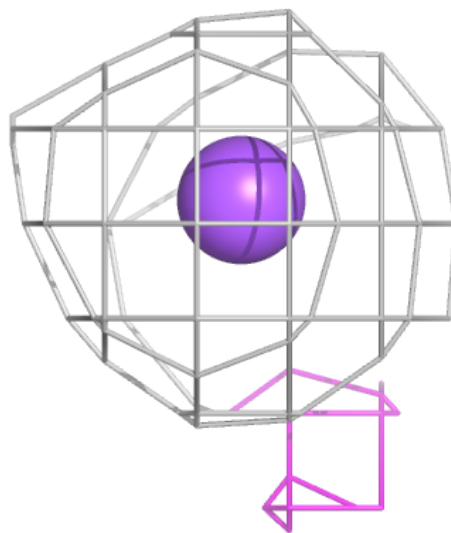
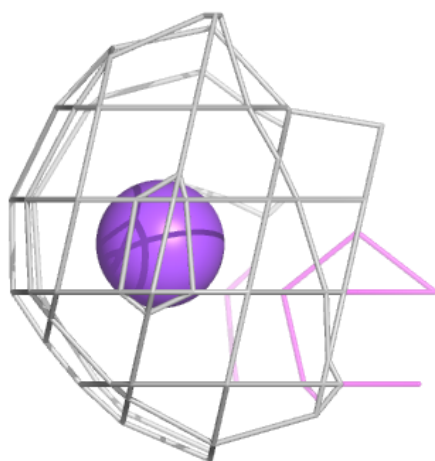
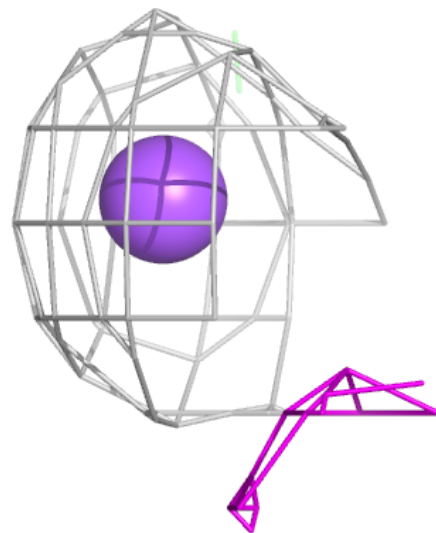
**Electron density around NA A 633:**

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



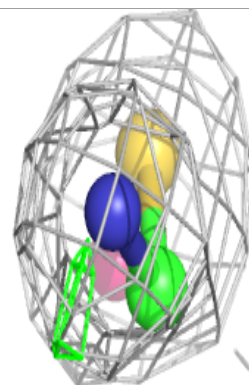
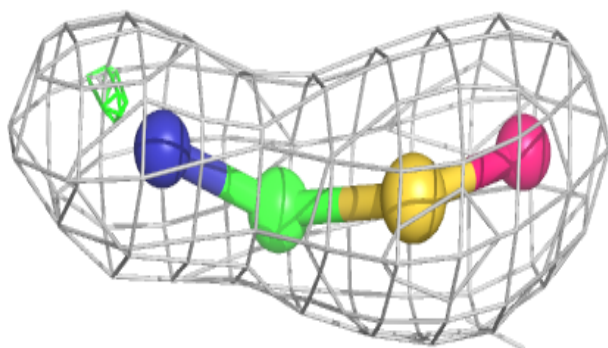
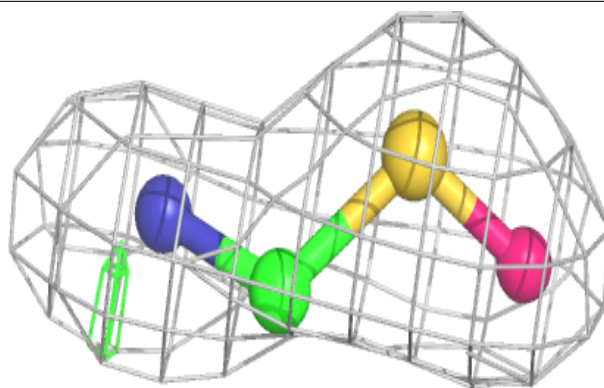
**Electron density around NA A 634:**

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



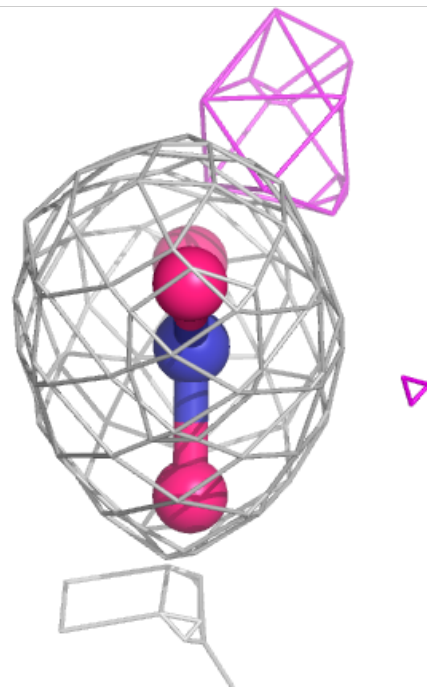
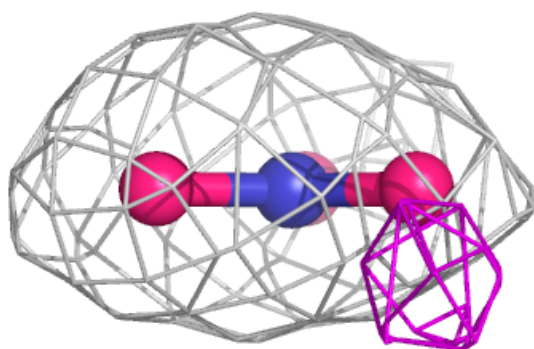
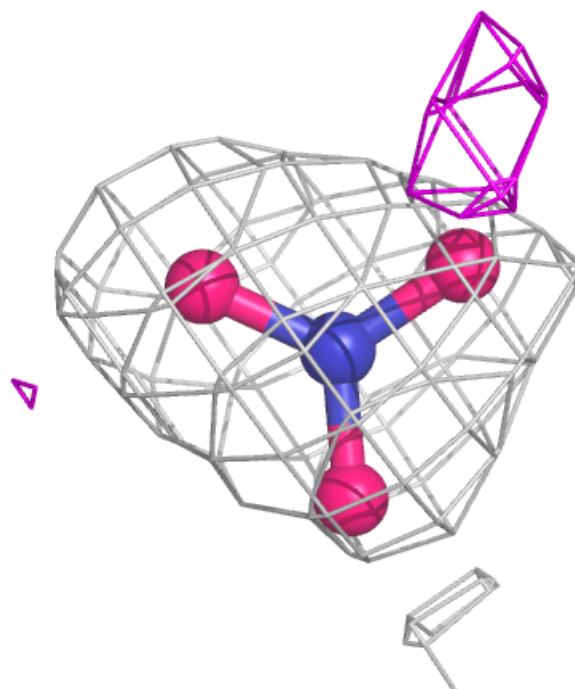
**Electron density around OSM A 613:**

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



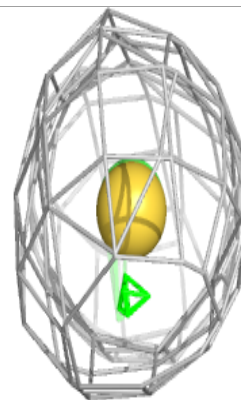
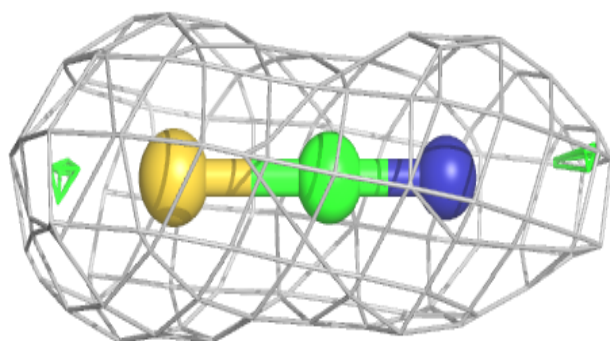
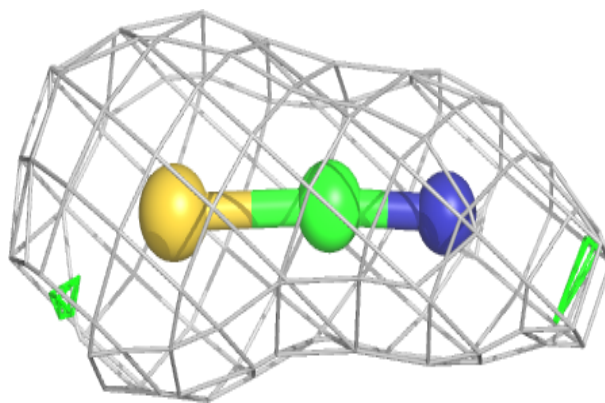
**Electron density around NO3 A 606:**

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

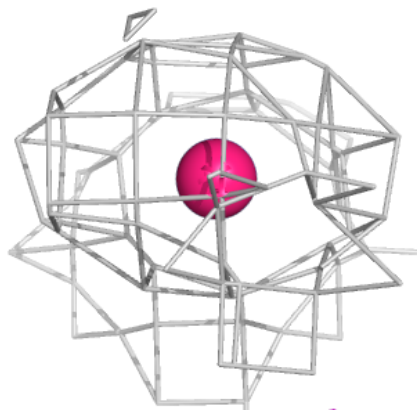
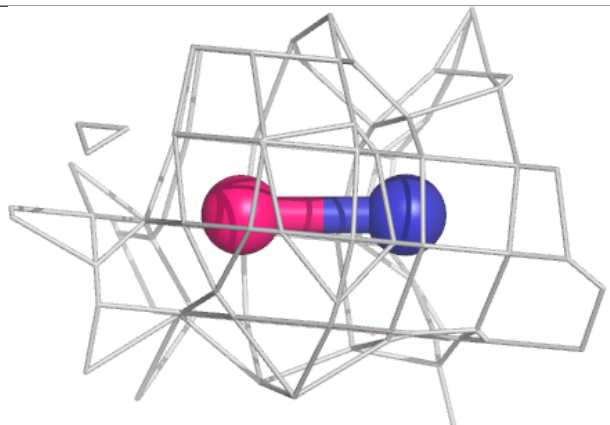
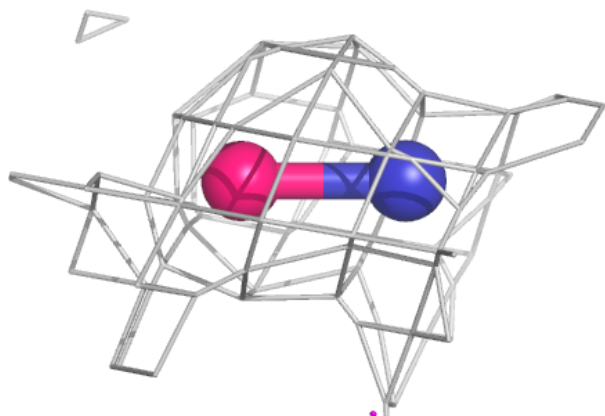


**Electron density around SCN A 612:**

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

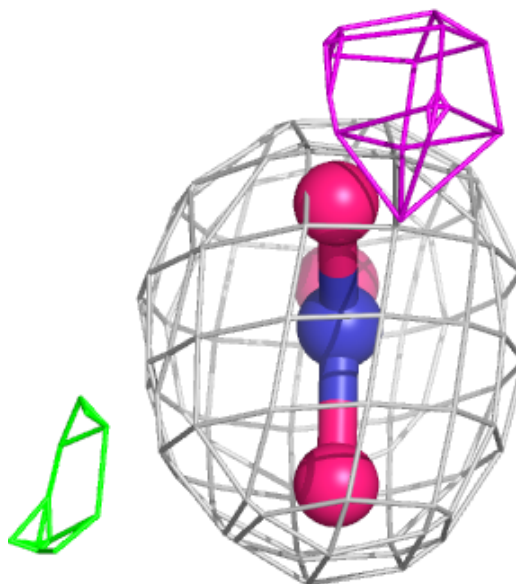
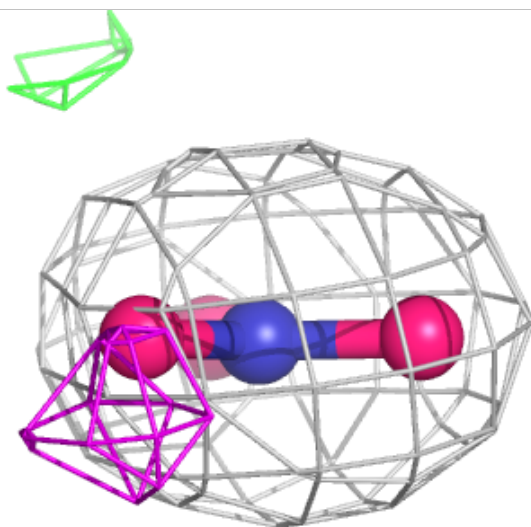
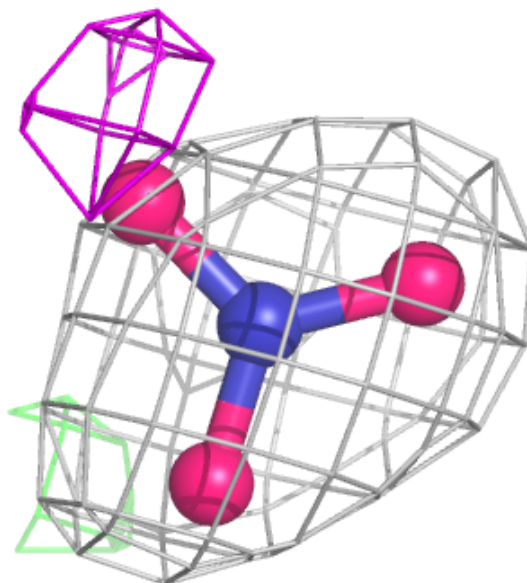
**Electron density around NO A 604:**

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



**Electron density around NO3 A 620:**

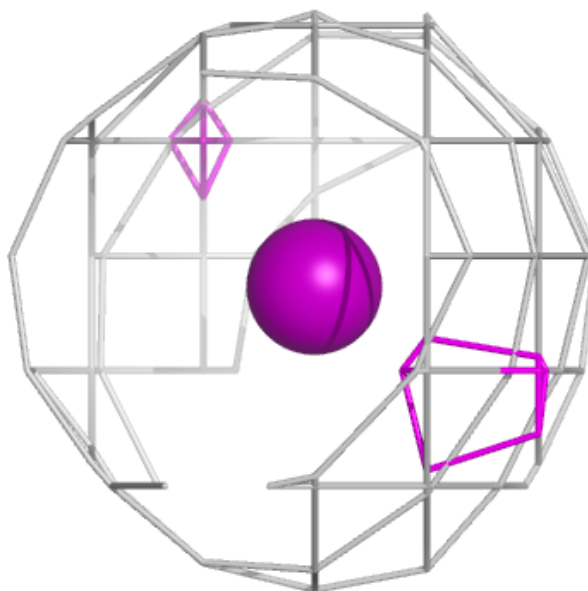
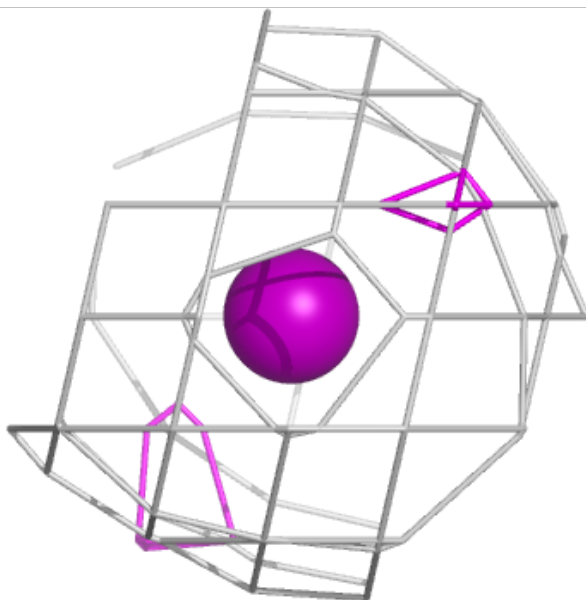
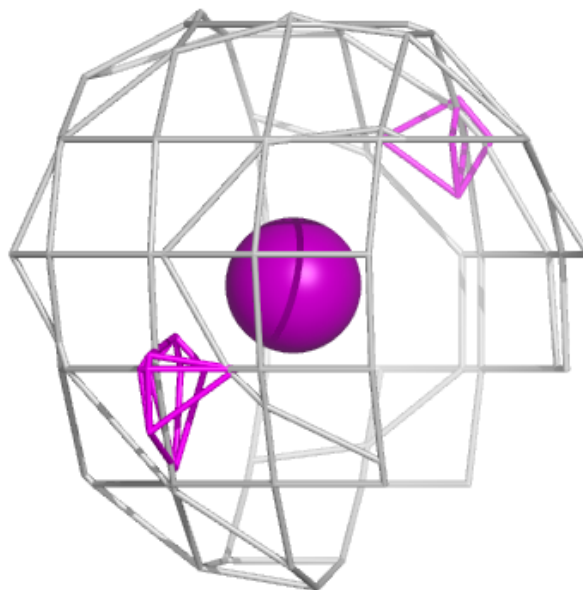
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around IOD A 624:**

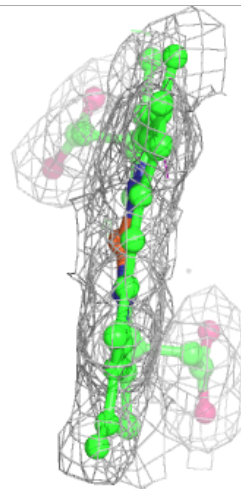
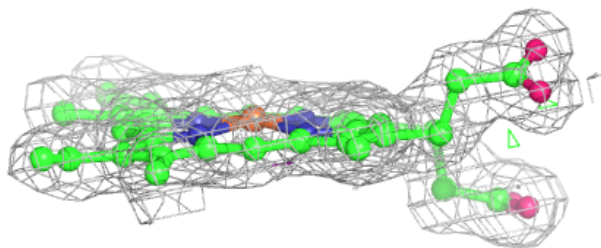
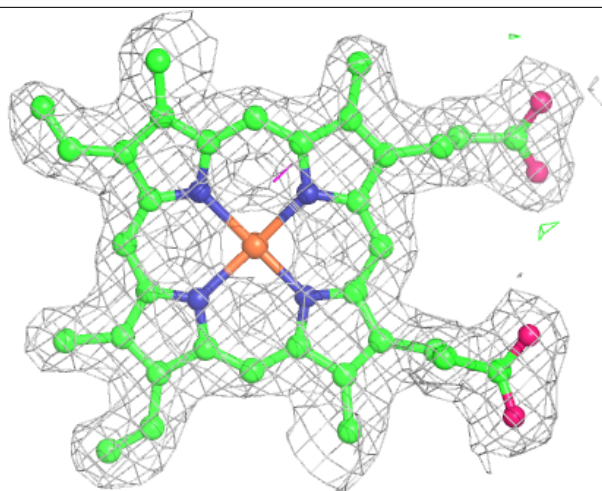
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





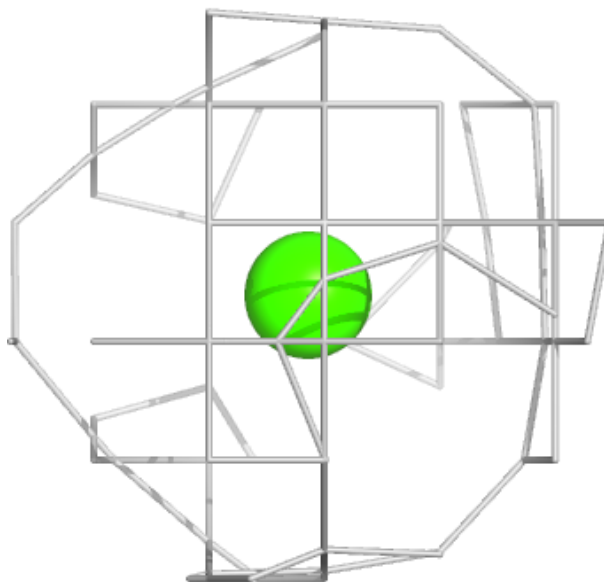
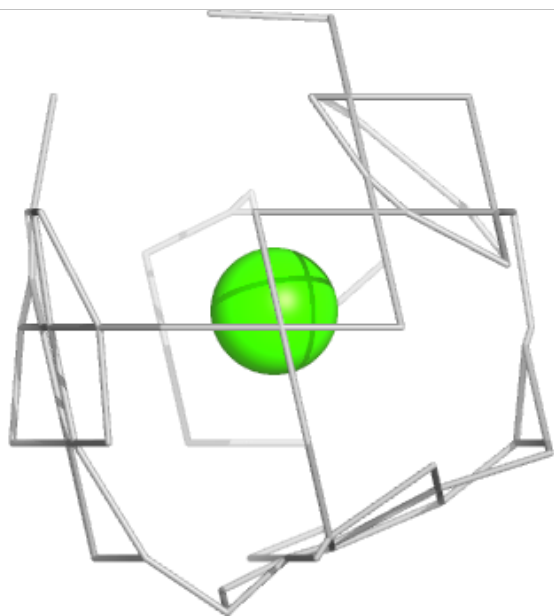
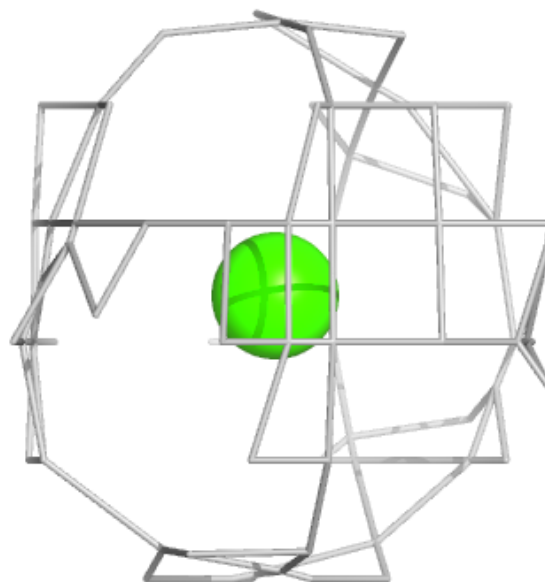
**Electron density around HEM A 636:**

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



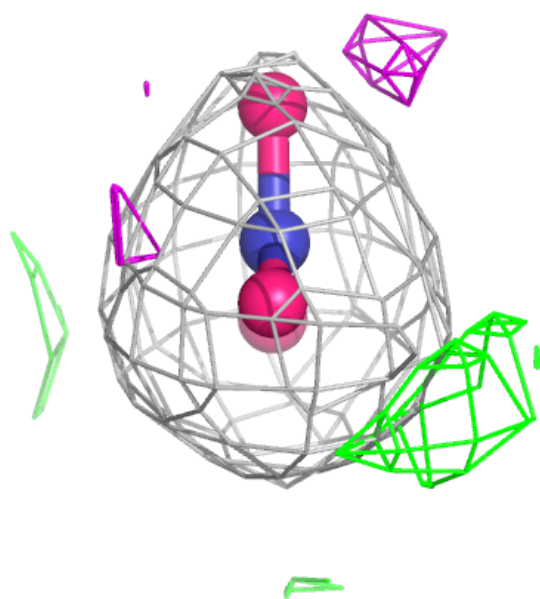
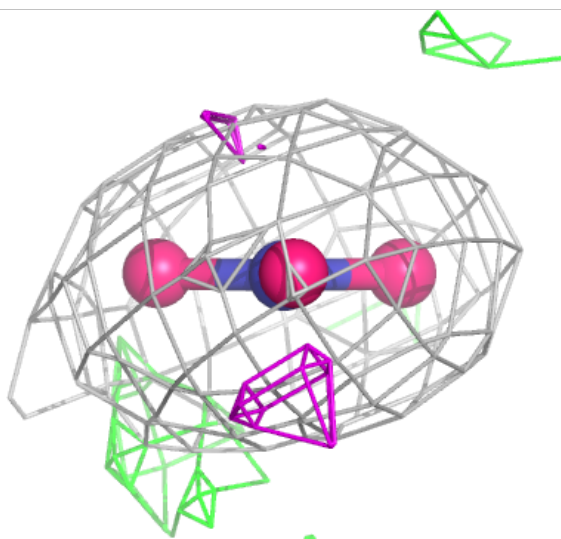
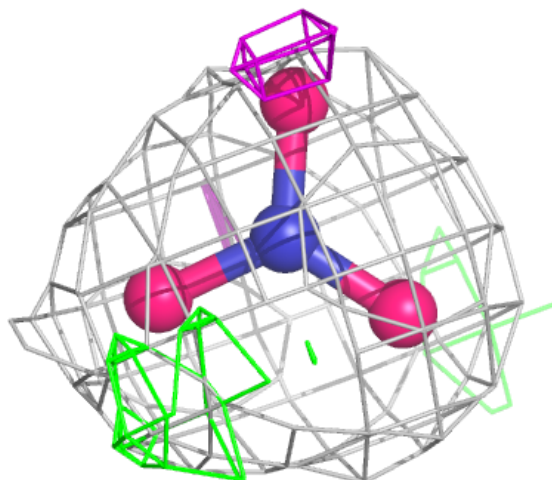
**Electron density around CA A 638:**

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



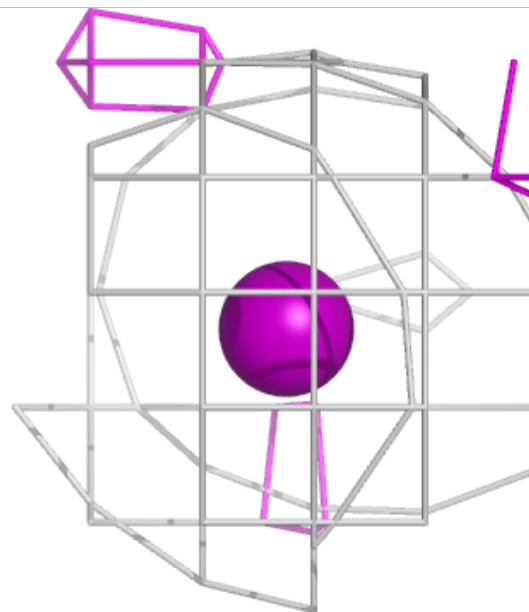
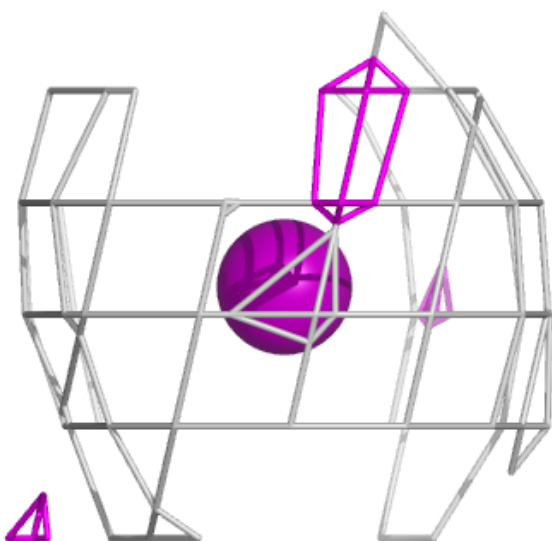
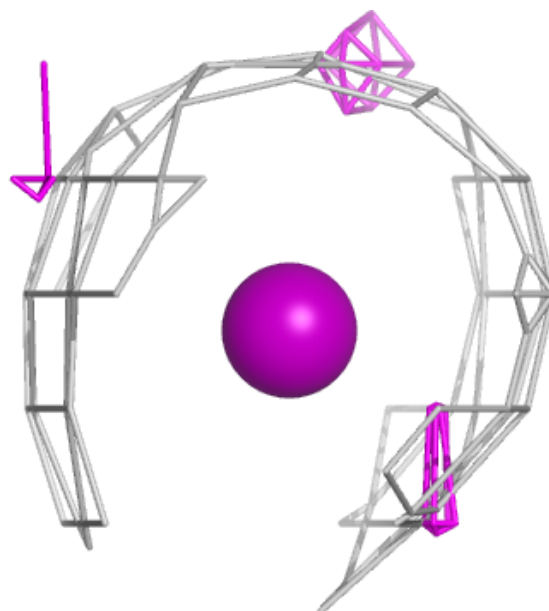
**Electron density around NO3 A 617:**

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



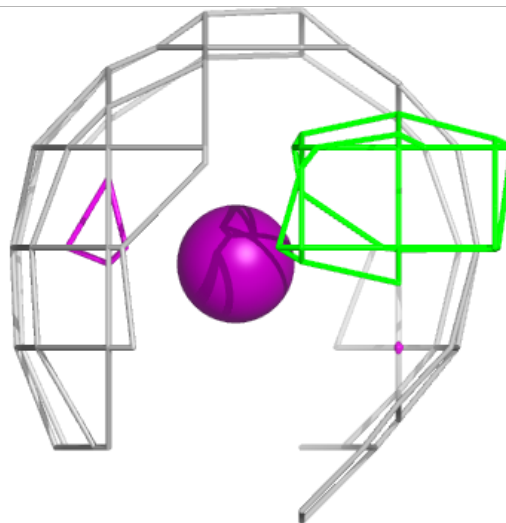
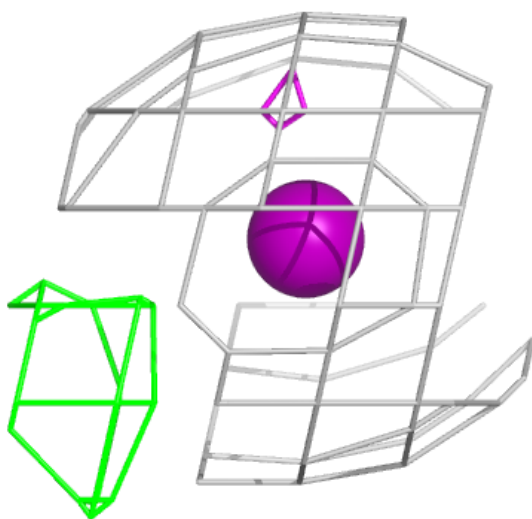
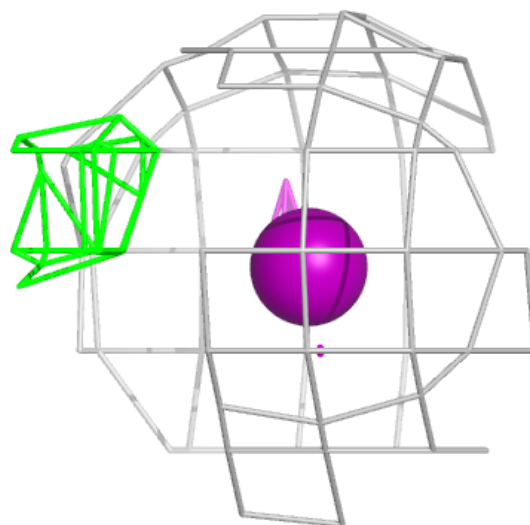
**Electron density around IOD A 627:**

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



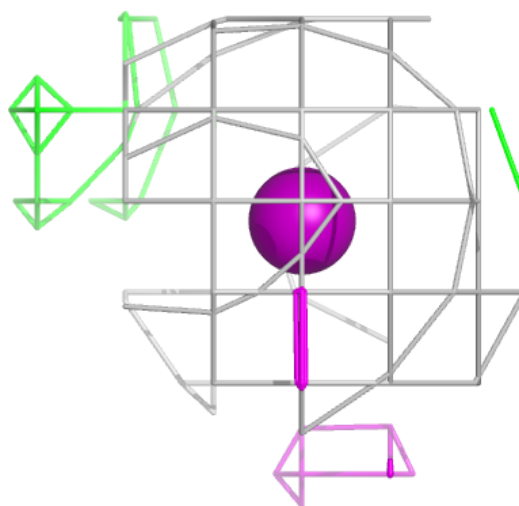
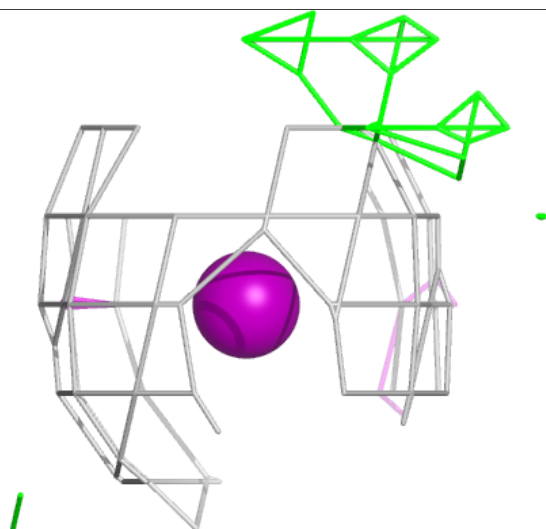
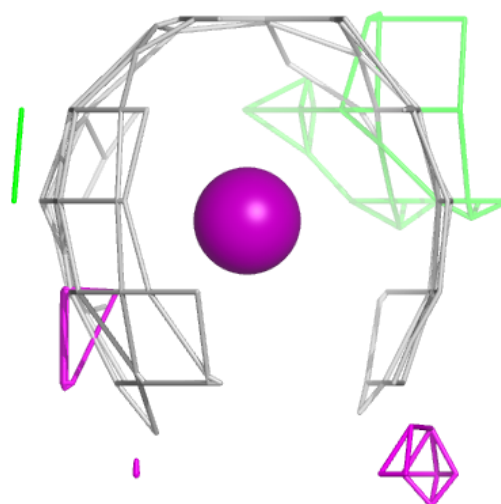
**Electron density around IOD A 628:**

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



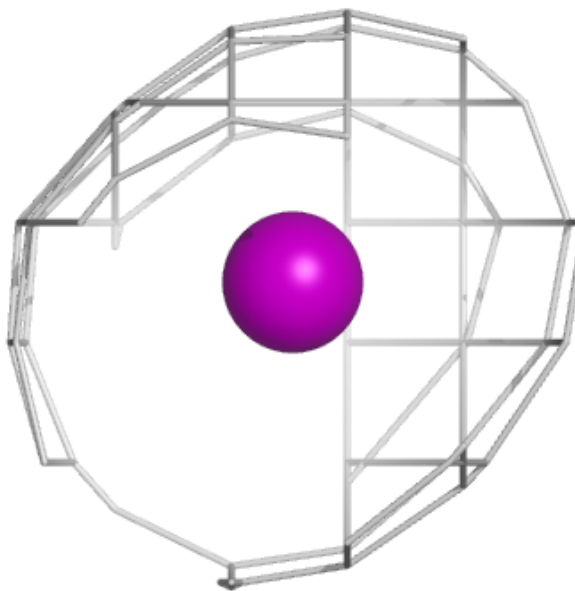
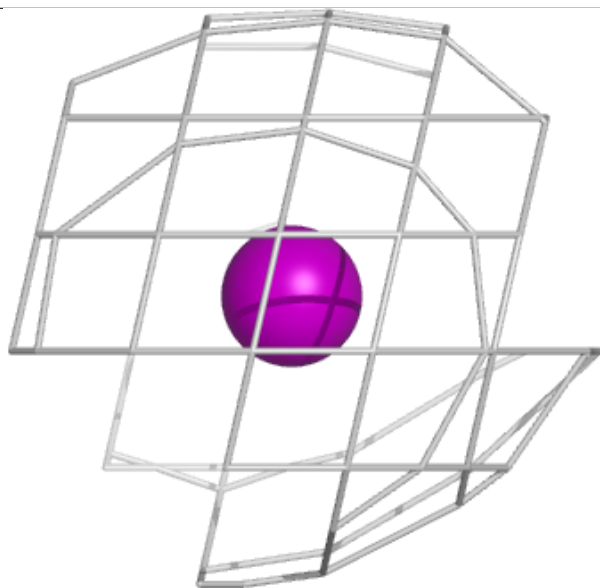
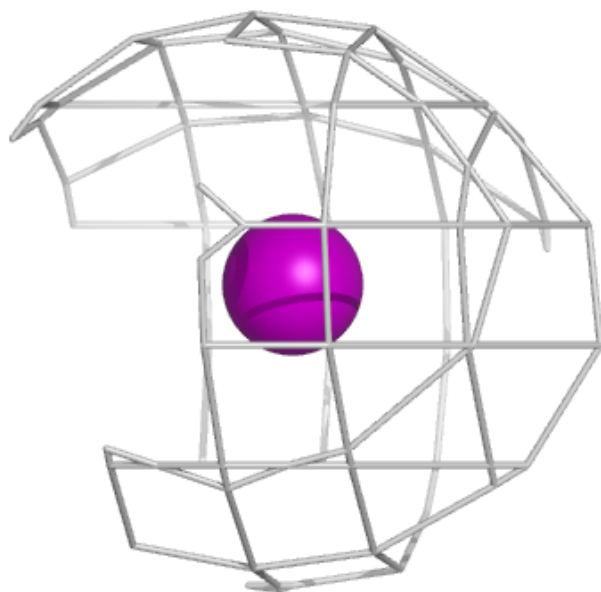
**Electron density around IOD A 629:**

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



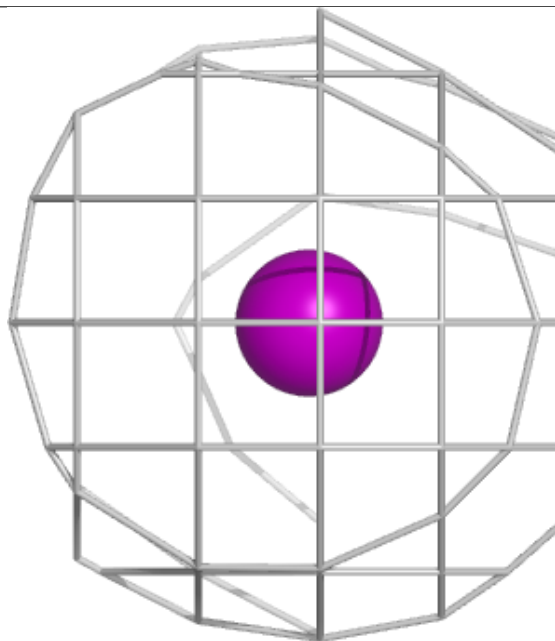
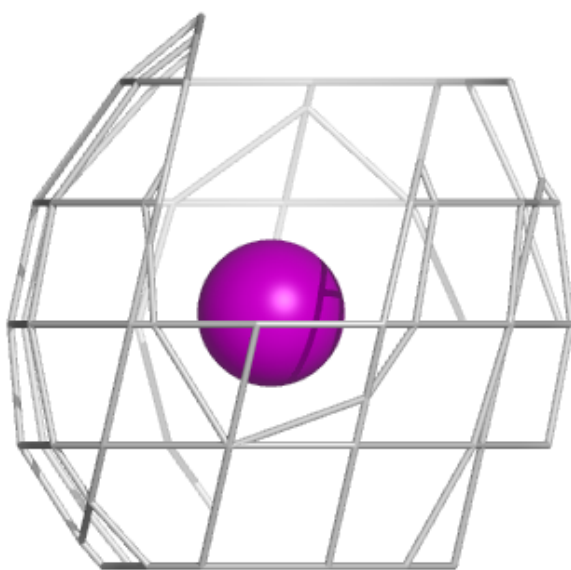
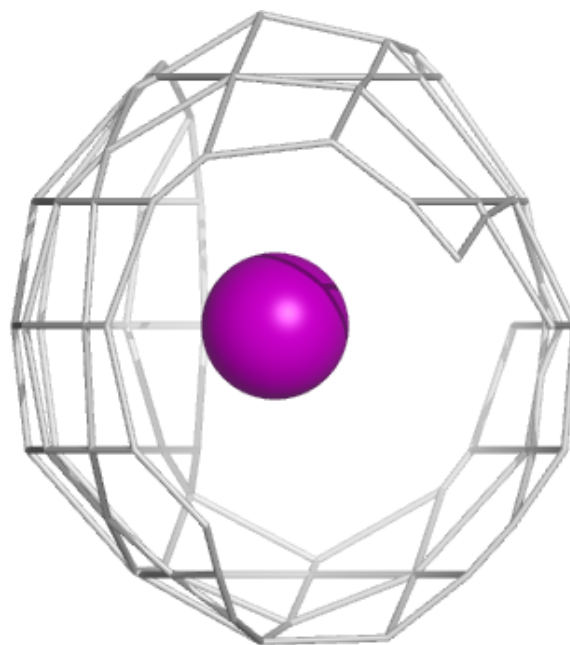
**Electron density around IOD A 631:**

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



**Electron density around IOD A 632:**

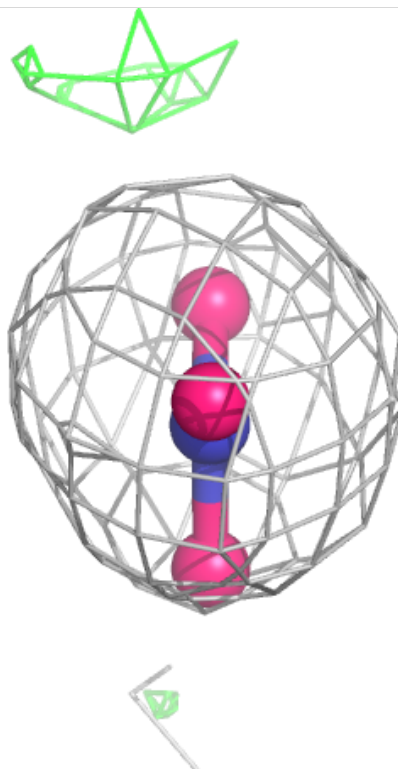
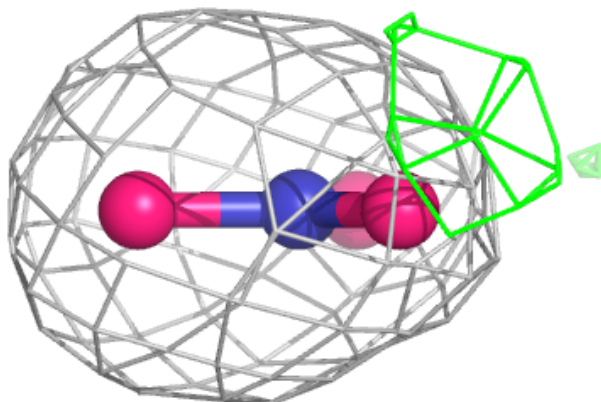
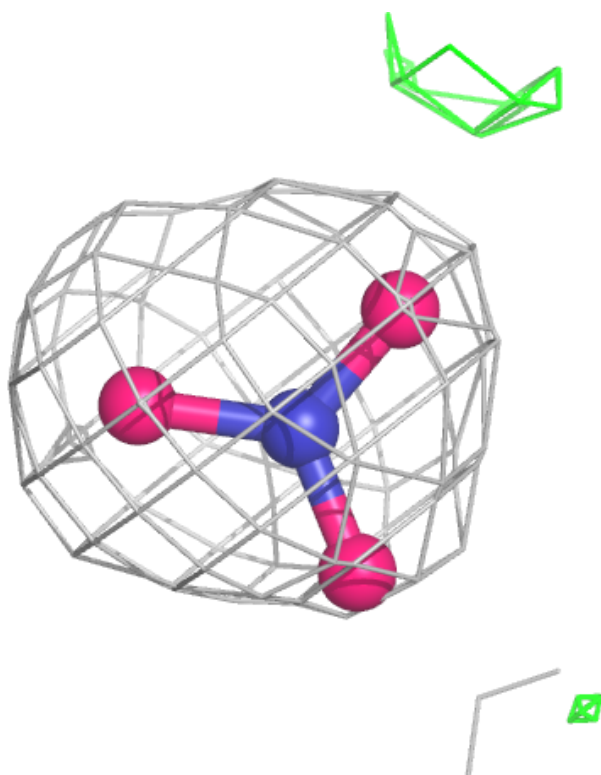
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





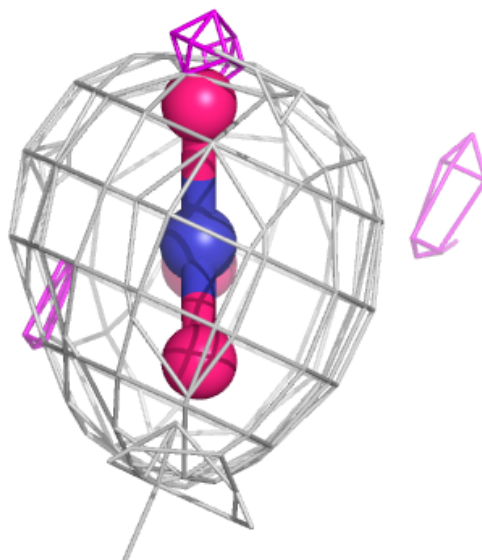
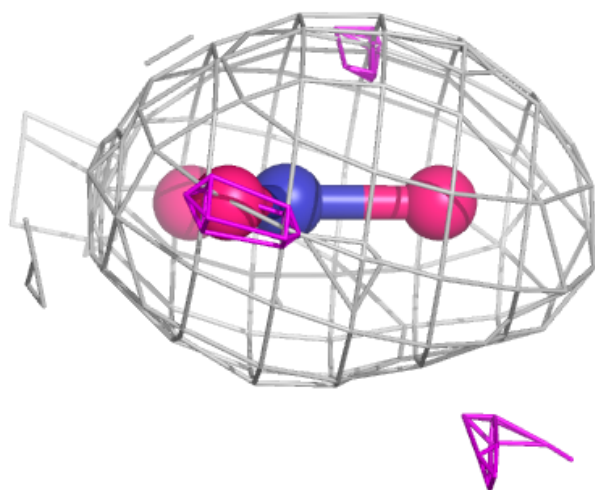
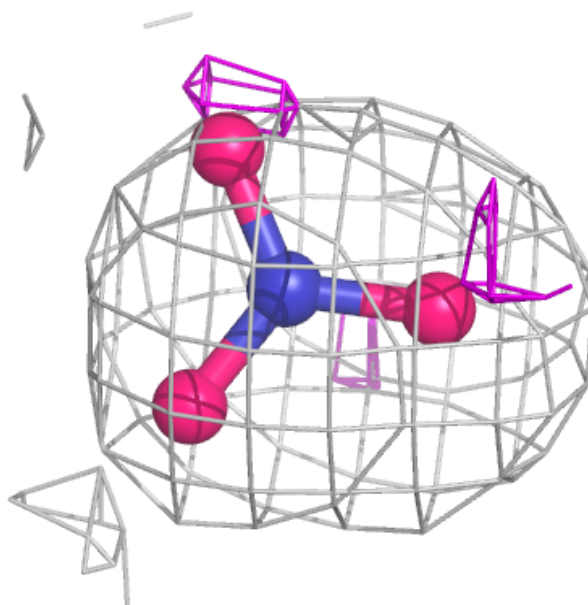
**Electron density around NO3 A 618:**

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



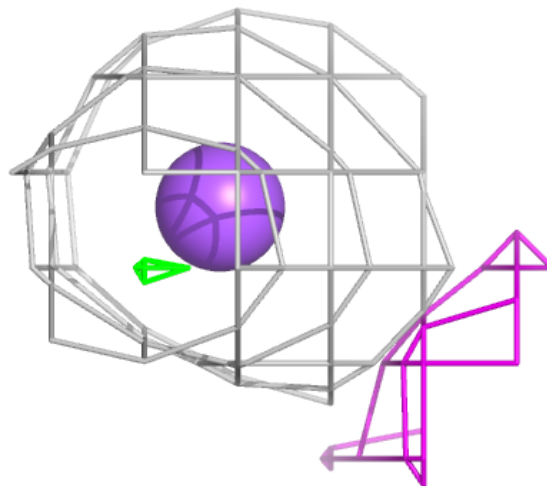
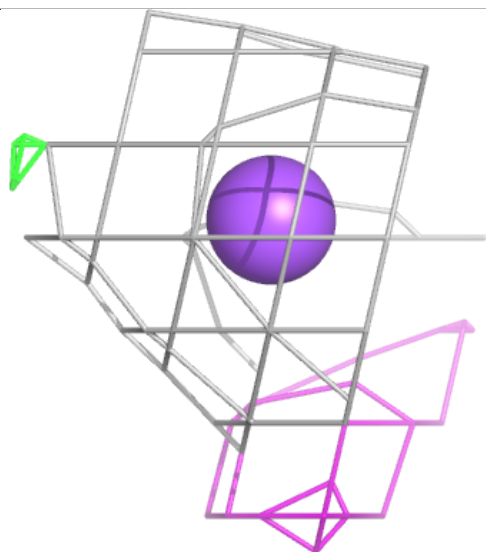
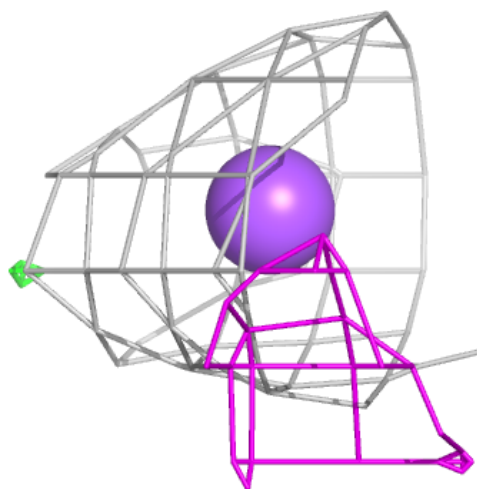
**Electron density around NO3 A 619:**

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



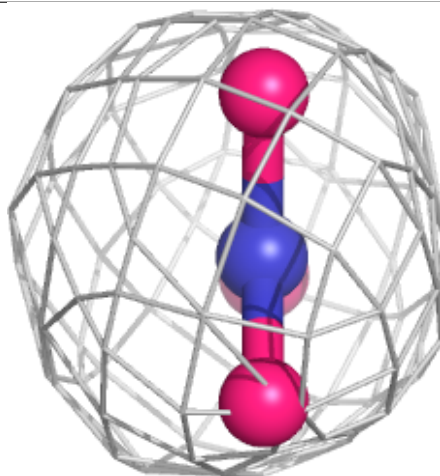
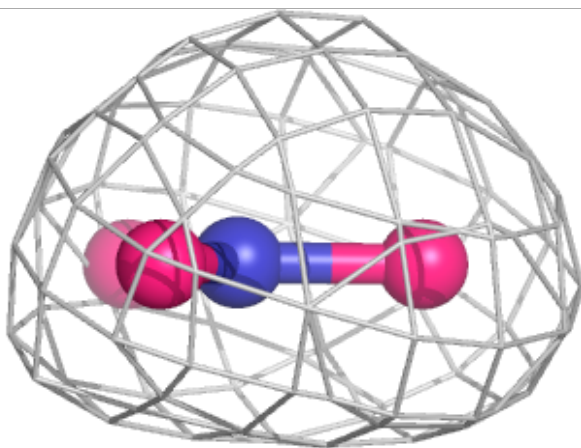
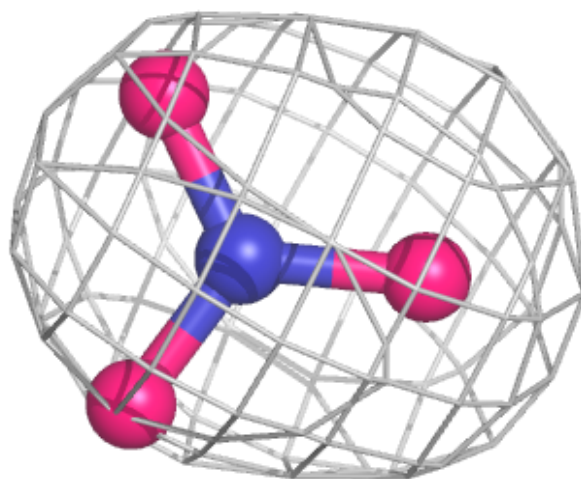
**Electron density around NA A 635:**

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



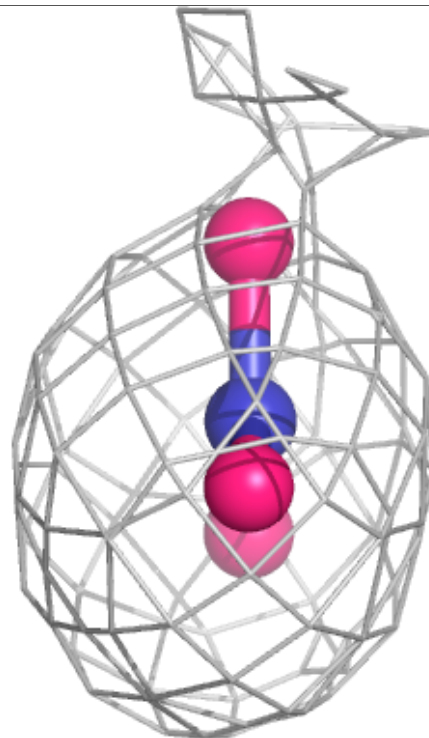
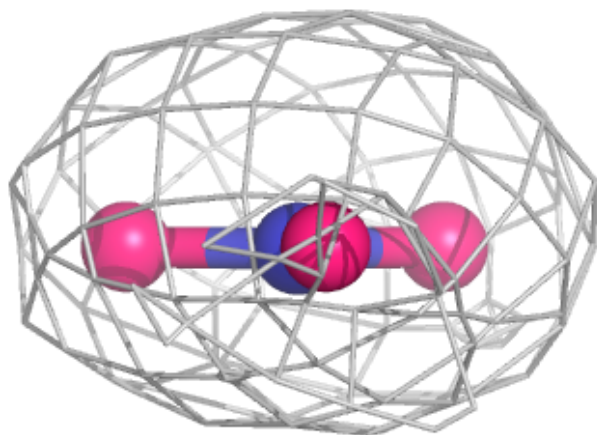
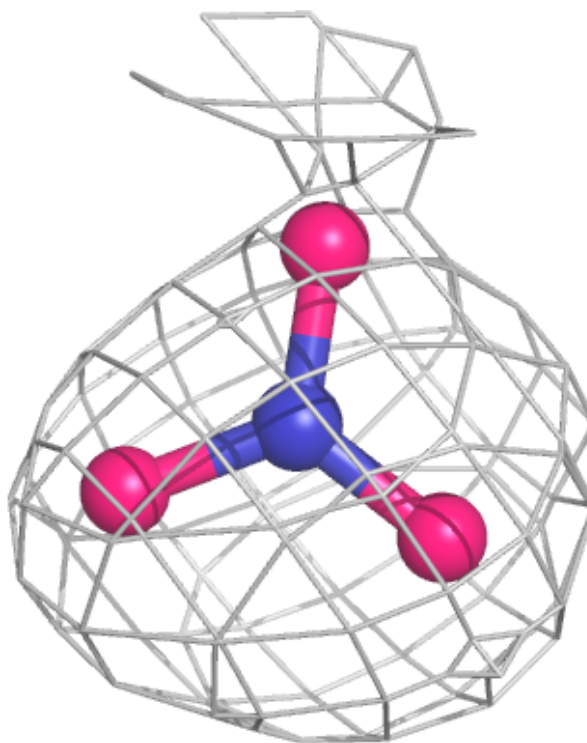
**Electron density around NO3 A 607:**

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



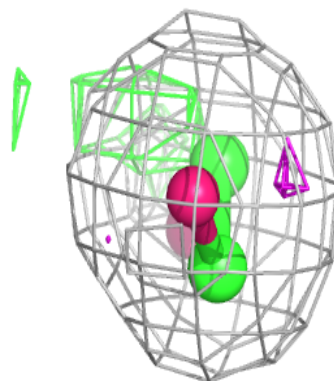
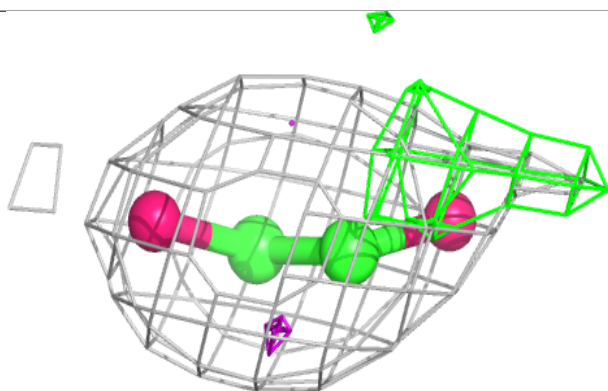
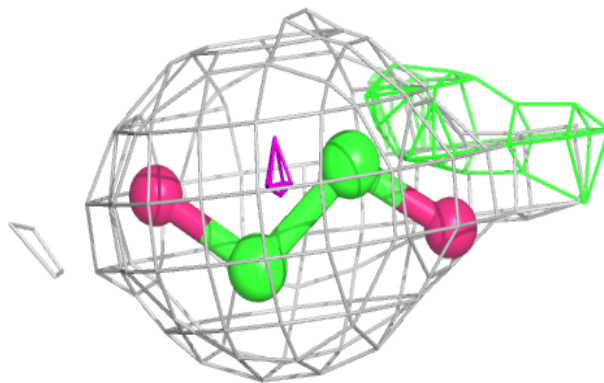
**Electron density around NO3 A 616:**

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

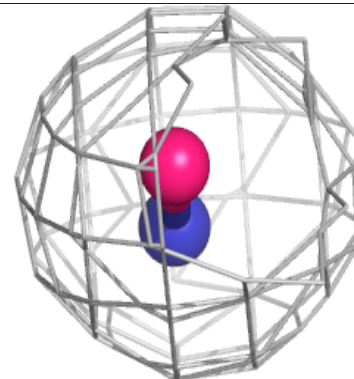
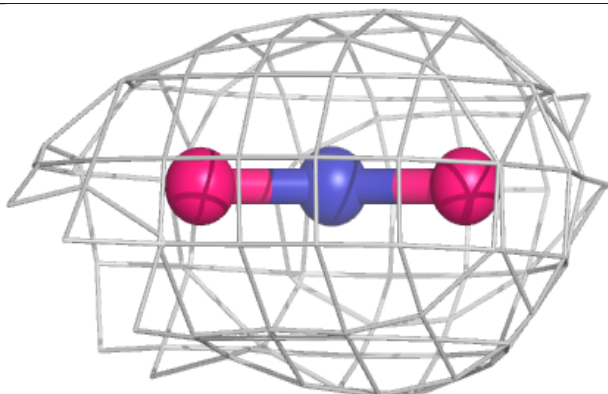
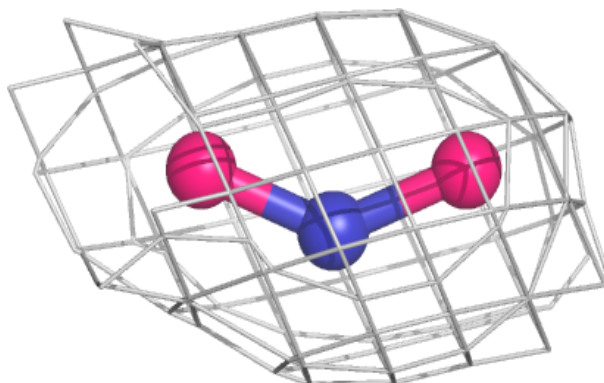


**Electron density around EDO A 622:**

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

**Electron density around NO2 A 605:**

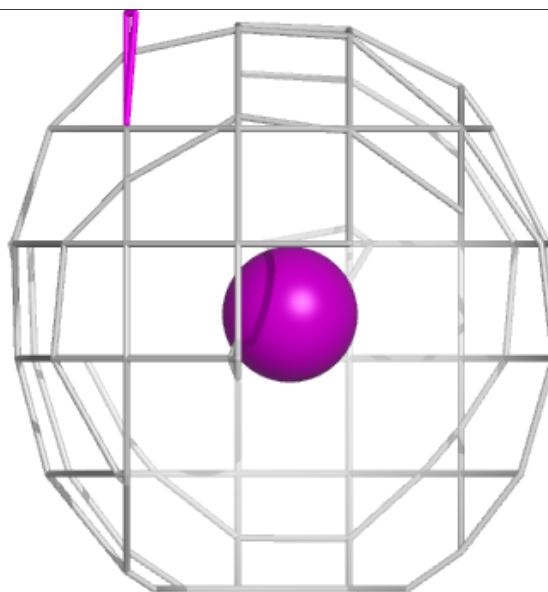
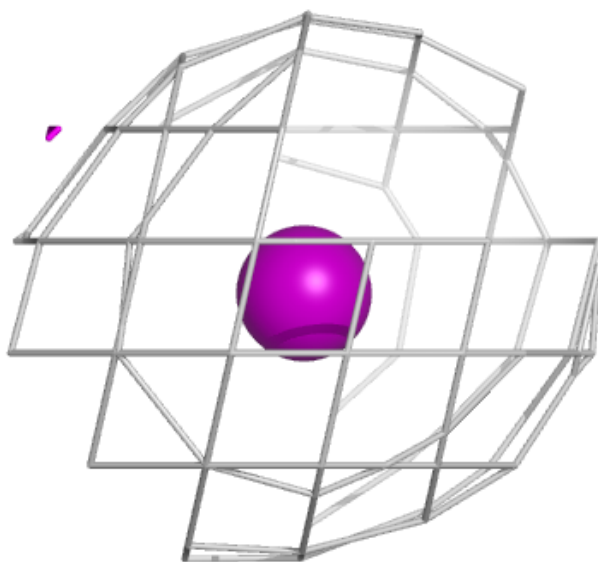
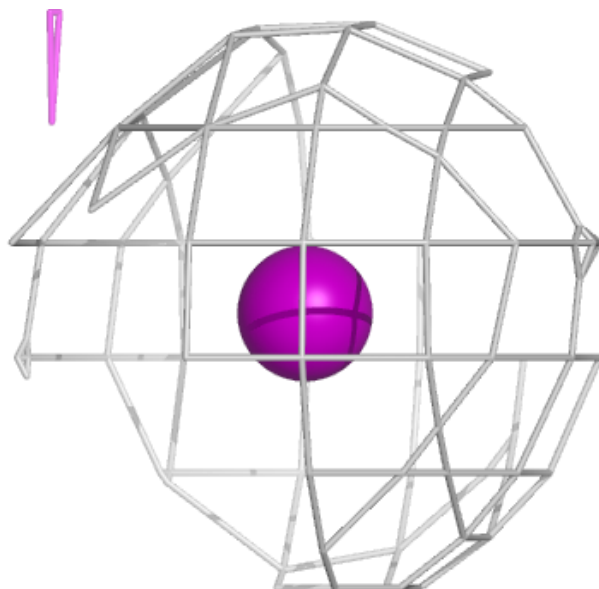
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





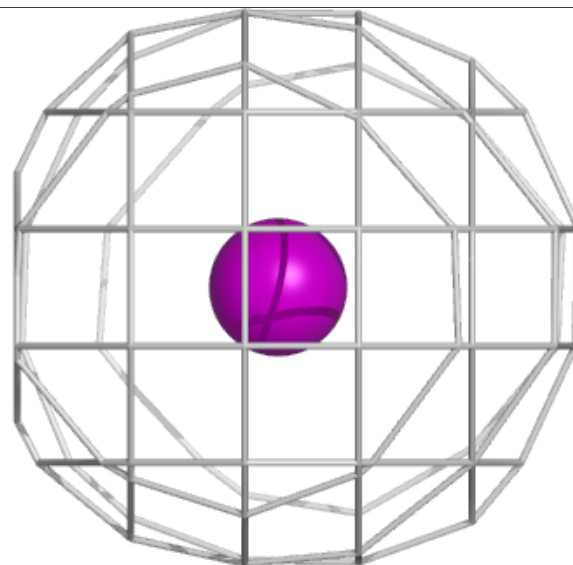
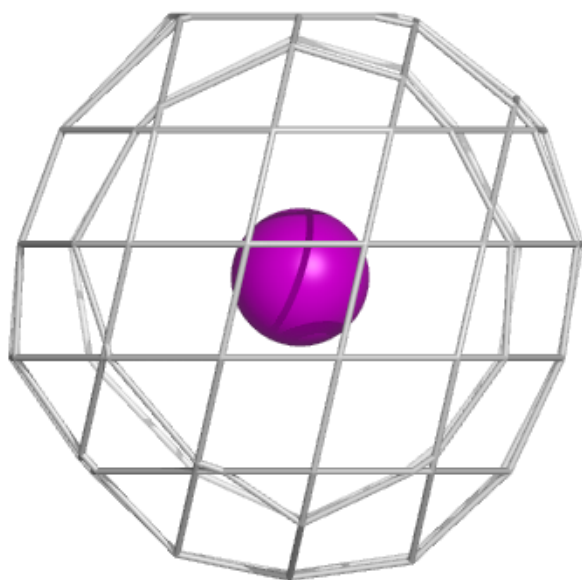
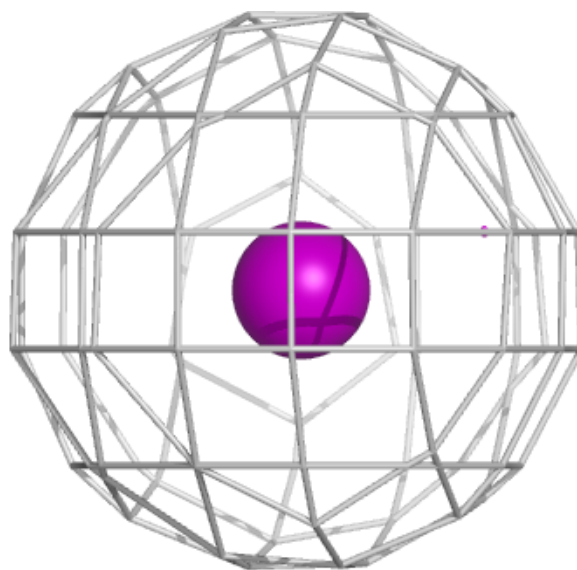
**Electron density around IOD A 630:**

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



**Electron density around IOD A 626:**

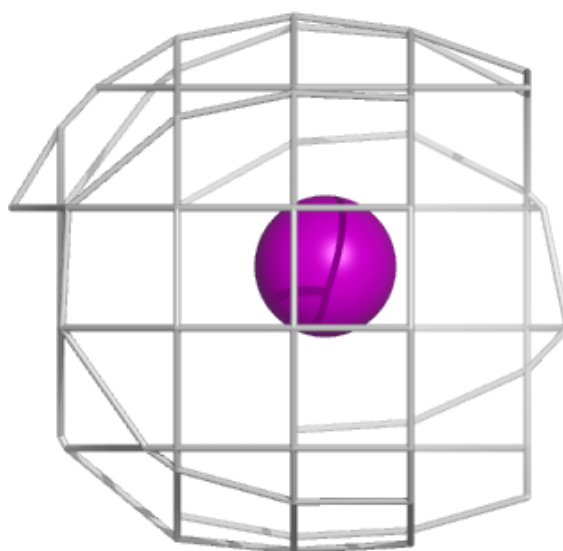
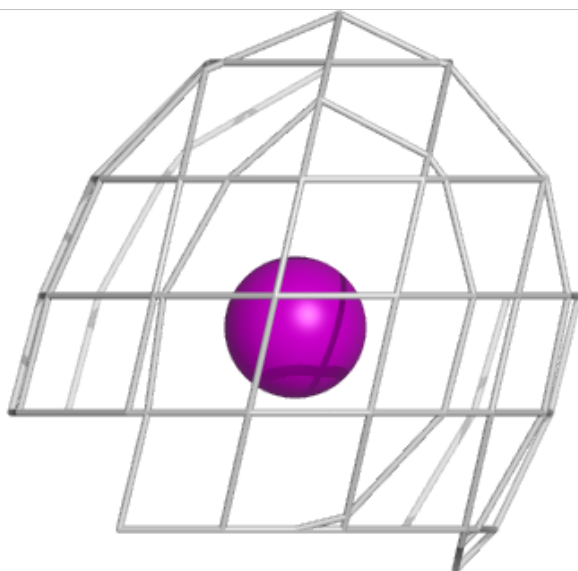
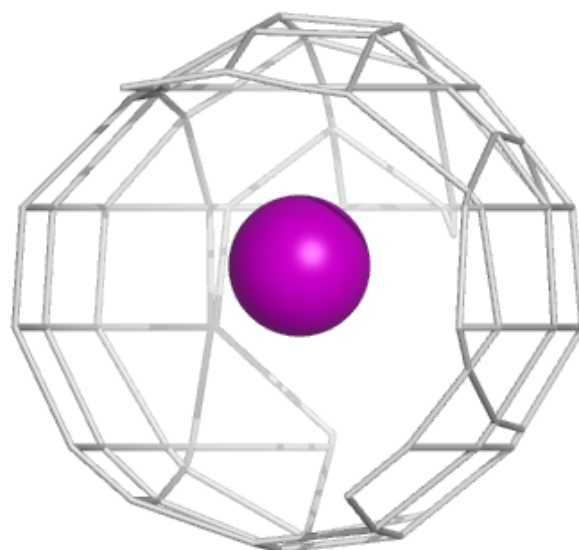
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around IOD A 623:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.