



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 03:23 AM UTC

PDB ID : 9KU6 / pdb_00009ku6
Title : Crystal structure of the complex of lactoperoxidase with nitric oxide at 1.72 Å resolution
Authors : Maurya, A.; Sharma, P.; Sharma, S.; Singh, T.P.
Deposited on : 2024-12-03
Resolution : 1.72 Å(reported)

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

We welcome your comments at 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>.

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

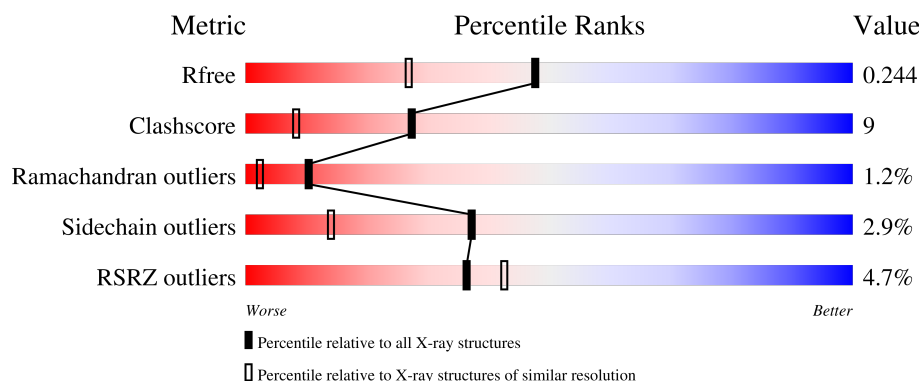
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.72 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	1039 (1.72-1.72)
Clashscore	190562	1049 (1.72-1.72)
Ramachandran outliers	187476	1041 (1.72-1.72)
Sidechain outliers	187428	1041 (1.72-1.72)
RSRZ outliers	180081	1039 (1.72-1.72)

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 ≥ 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	5% 84% 14% .
2	C	2	100%

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
4	IOD	A	644	-	-	X	-
4	IOD	A	650	-	-	X	-
4	IOD	A	651	-	-	X	-
5	SCN	A	622	-	-	X	-
5	SCN	A	629	-	-	X	-
7	NO2	A	637	-	-	X	-
8	NO	A	635	-	-	X	-

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 5522 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.

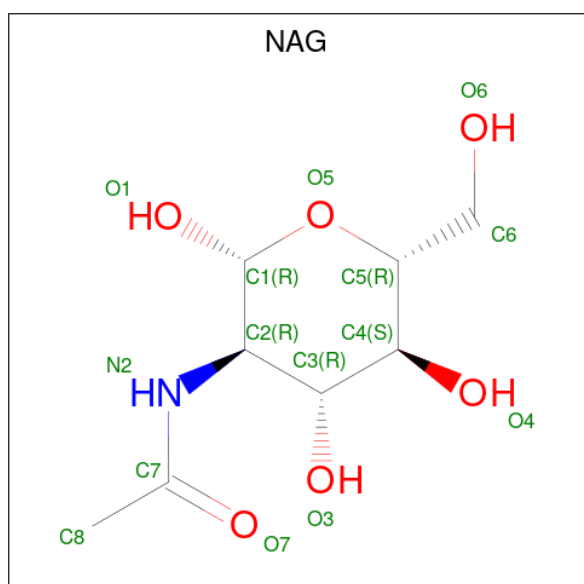
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	595	4792	3050	849	866	27	0	3	0

- 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
			Total	C	N	O			
2	C	2	28	16	2	10	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆) (labeled as "Ligand of Interest" by depositor).

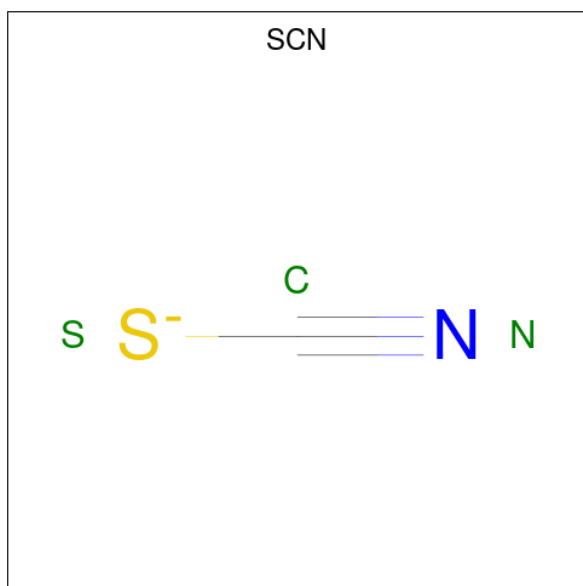


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is IODIDE ION (CCD ID: IOD) (formula: I) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	24	Total	I	0	0
			24	24		

- Molecule 5 is THIOCYANATE ION (CCD ID: SCN) (formula: CNS) (labeled as "Ligand of Interest" by depositor).



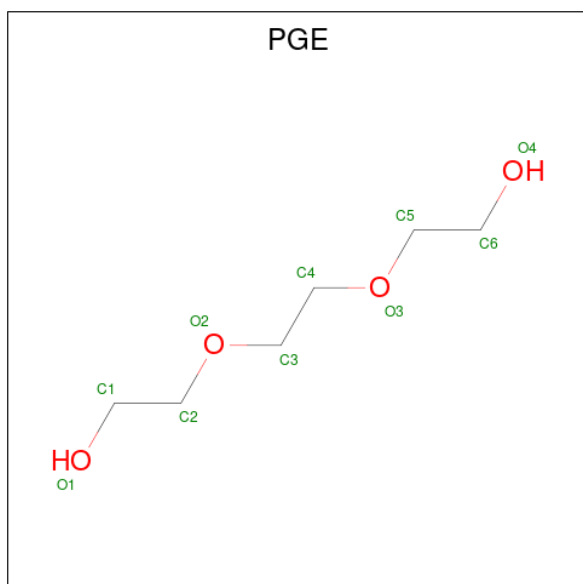
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	S	0	0
			3	1	1	1		
5	A	1	Total	C	N	S	0	0
			3	1	1	1		
5	A	1	Total	C	N	S	0	0
			3	1	1	1		
5	A	1	Total	C	N	S	0	0
			3	1	1	1		
5	A	1	Total	C	N	S	0	0
			3	1	1	1		

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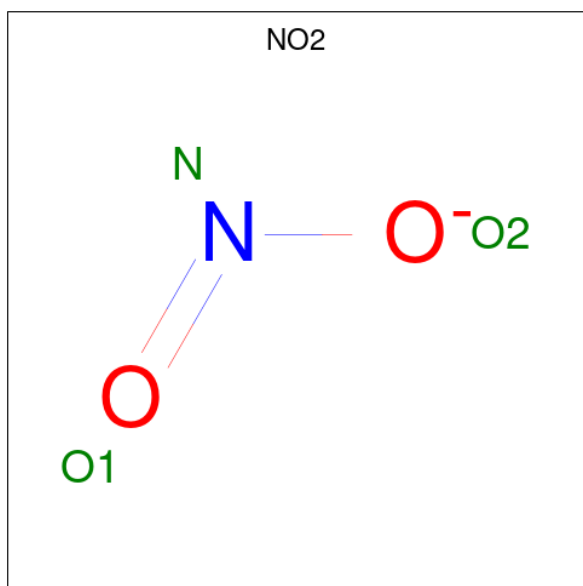
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	S	0	0
			3	1	1	1		
5	A	1	Total	C	N	S	0	0
			3	1	1	1		
5	A	1	Total	C	N	S	0	0
			3	1	1	1		
5	A	1	Total	C	N	S	0	0
			3	1	1	1		
5	A	1	Total	C	N	S	0	0
			3	1	1	1		
5	A	1	Total	C	N	S	0	0
			3	1	1	1		
5	A	1	Total	C	N	S	0	0
			3	1	1	1		
5	A	1	Total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

- Molecule 6 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$) (labeled as "Ligand of Interest" by depositor).



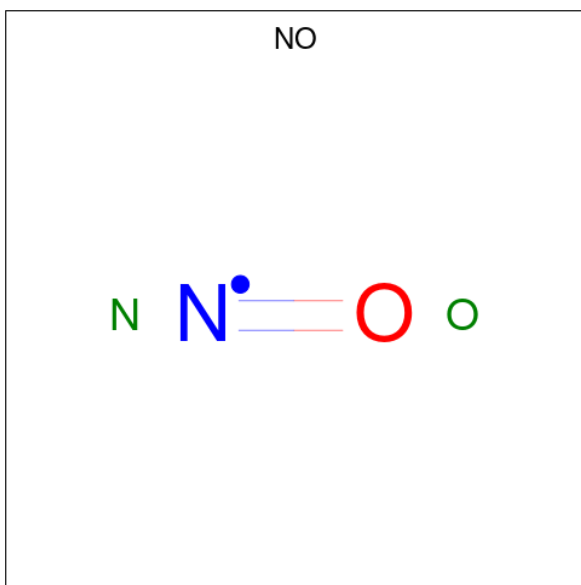
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 7 is NITRITE ION (CCD ID: NO₂) (formula: NO₂) (labeled as "Ligand of Interest" by depositor).



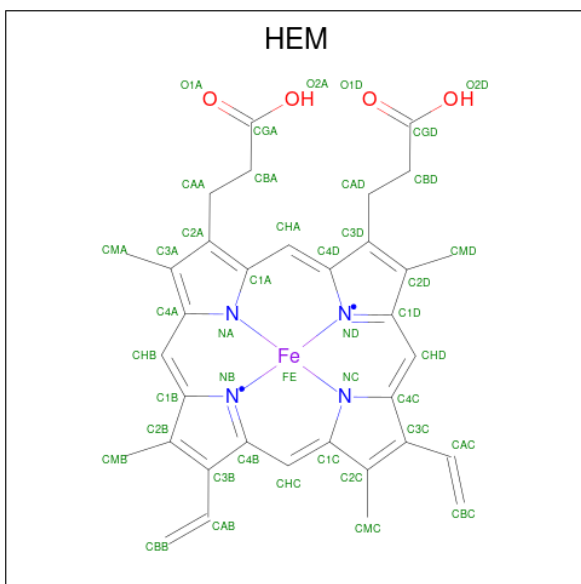
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	N	O	0	0
			3	1	2		
7	A	1	Total	N	O	0	0
			3	1	2		

- Molecule 8 is NITRIC OXIDE (CCD ID: NO) (formula: NO) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 9 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 10 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

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

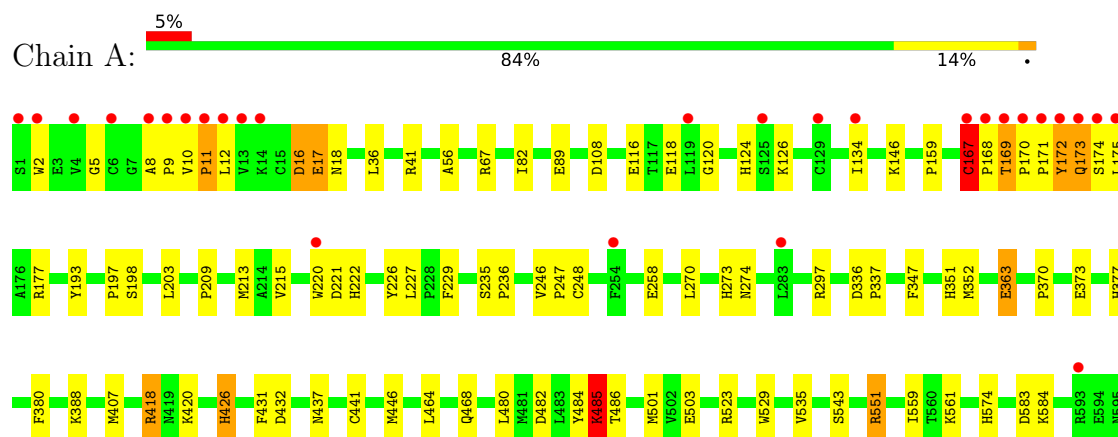
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	521	Total 521	O 521	0	0

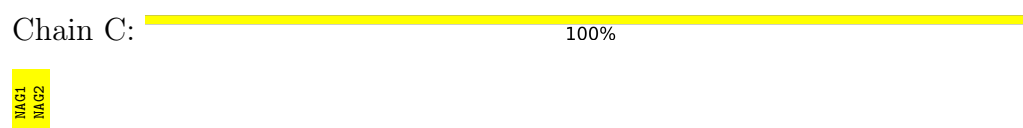
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 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, α , β , γ	54.02Å 80.41Å 75.84Å 90.00° 103.12° 90.00°	Depositor
Resolution (Å)	73.86 – 1.72 73.86 – 1.72	Depositor EDS
% Data completeness (in resolution range)	99.0 (73.86-1.72) 99.0 (73.86-1.72)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 1.72Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.186 , 0.235 0.196 , 0.244	Depositor DCC
R_{free} test set	1320 reflections (1.97%)	wwPDB-VP
Wilson B-factor (Å ²)	36.0	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 57.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5522	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: NO2, CA, PGE, HEM, NO, SCN, NAG, IOD, CSD

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	0.58	0/4913	1.10	12/6667 (0.2%)

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

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	418	ARG	CB-CA-C	7.41	123.45	110.85
1	A	167	CYS	CB-CA-C	7.06	124.07	110.17
1	A	485	LYS	CB-CA-C	-6.57	100.60	110.06
1	A	426	HIS	CB-CA-C	6.05	119.55	109.38
1	A	363	GLU	CB-CG-CD	5.96	122.73	112.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	551	ARG	Sidechain
1	A	67	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4792	0	4703	71	0
2	C	28	0	25	1	0
3	A	42	0	39	0	0
4	A	24	0	0	16	0
5	A	51	0	0	6	0
6	A	10	0	14	3	0
7	A	6	0	0	2	0
8	A	4	0	0	6	0
9	A	43	0	30	16	0
10	A	1	0	0	0	0
11	A	521	0	0	14	0
All	All	5522	0	4811	88	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 9.

The worst 5 of 88 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:108:ASP:OD2	9:A:639:HEM:CMD	1.67	1.40
1:A:258:GLU:OE2	9:A:639:HEM:CMB	1.72	1.37
5:A:621:SCN:N	11:A:701:HOH:O	1.66	1.28
1:A:258:GLU:OE2	9:A:639:HEM:HMB1	0.91	1.09
1:A:235:SER:OG	4:A:651:IOD:I	2.49	1.00

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%)	20 (3%)	7 (1%)	10	2

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	CYS
1	A	11	PRO
1	A	56	ALA
1	A	169	THR
1	A	10	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	519/517 (100%)	504 (97%)	15 (3%)	37	14

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	172	TYR
1	A	543	SER
1	A	173	GLN
1	A	574	HIS
1	A	485	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	556	ASN
1	A	565	HIS
1	A	568	GLN
1	A	322	GLN

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Mol	Chain	Res	Type
1	A	329	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CSD	A	441[B]	1	4,7,8	0.63	0	1,8,10	1.03	0
1	CSD	A	441[A]	1	4,7,8	0.76	0	1,8,10	1.26	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
1	CSD	A	441[B]	1	-	1/2/6/8	-
1	CSD	A	441[A]	1	-	1/2/6/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	441[B]	CSD	N-CA-CB-SG
1	A	441[A]	CSD	CA-CB-SG-OD1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	441[A]	CSD	1	0

5.5 Carbohydrates

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	C	1	1,2	14,14,15	0.51	0	17,19,21	0.85	0
2	NAG	C	2	2	14,14,15	0.53	0	17,19,21	0.91	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	NAG	C	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C8-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2
2	C	1	NAG	O5-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6

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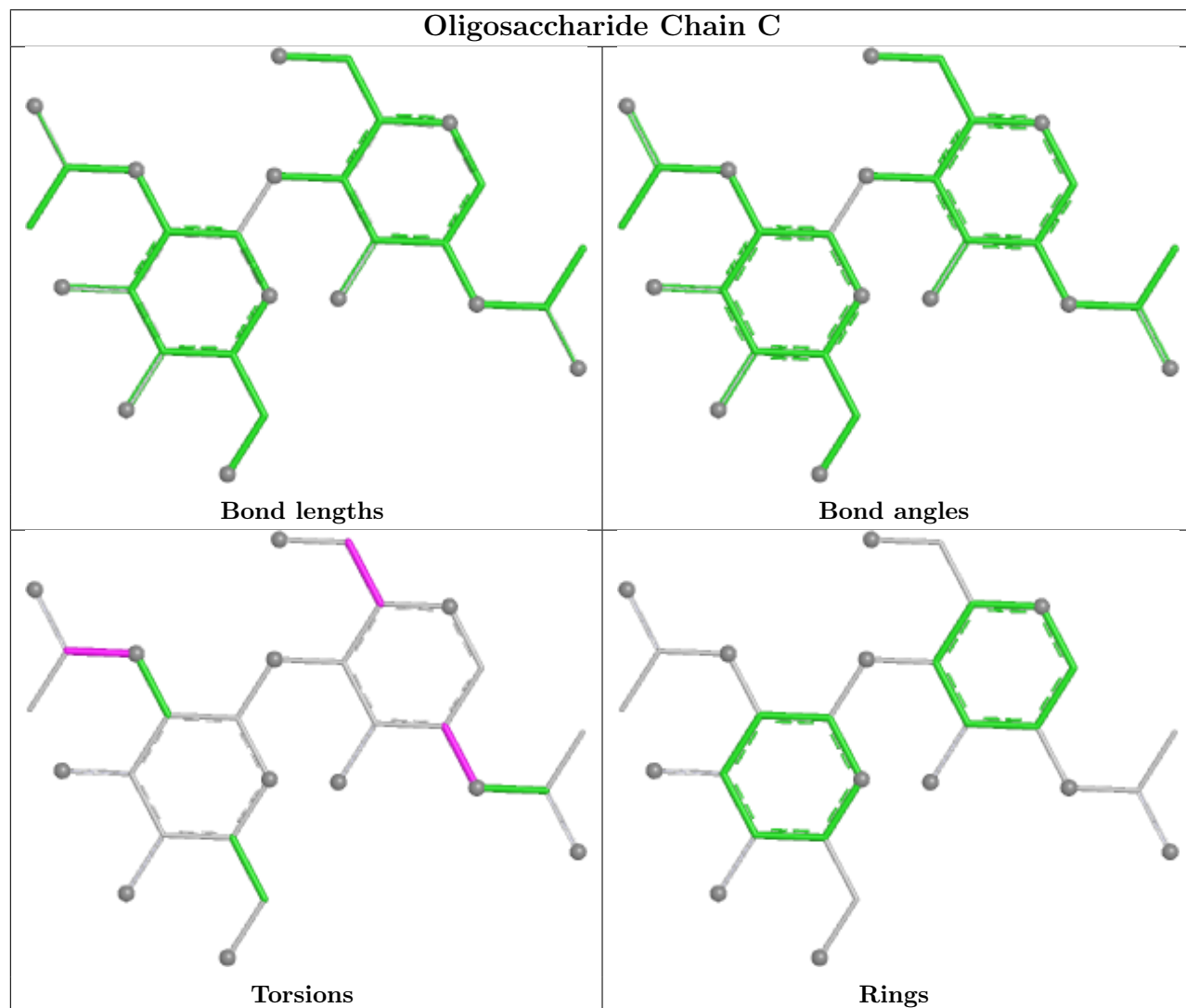
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	C1-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	1	0
2	C	1	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 oligosaccharide.



5.6 Ligand geometry

Of 51 ligands modelled in this entry, 25 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$
3	NAG	A	638	1	14,14,15	0.54	0	17,19,21	1.55	2 (11%)
5	SCN	A	616	-	1,2,2	0.13	0	0,1,1	-	-
8	NO	A	635	-	0,1,1	-	-	-	-	-
5	SCN	A	628	4	1,2,2	0.80	0	0,1,1	-	-
5	SCN	A	633	-	1,2,2	0.42	0	0,1,1	-	-
6	PGE	A	632	-	9,9,9	0.19	0	8,8,8	0.24	0
5	SCN	A	626	-	1,2,2	0.06	0	0,1,1	-	-
5	SCN	A	624	-	1,2,2	0.37	0	0,1,1	-	-
5	SCN	A	627	-	1,2,2	0.28	0	0,1,1	-	-
5	SCN	A	625	-	1,2,2	0.02	0	0,1,1	-	-
5	SCN	A	629	-	1,2,2	0.53	0	0,1,1	-	-
3	NAG	A	615	1	14,14,15	0.41	0	17,19,21	1.05	1 (5%)
5	SCN	A	621	-	1,2,2	0.20	0	0,1,1	-	-
7	NO2	A	637	4	1,2,2	0.99	0	0,1,1	-	-
5	SCN	A	618	-	1,2,2	1.26	0	0,1,1	-	-
3	NAG	A	601	1	14,14,15	0.46	0	17,19,21	0.89	1 (5%)
5	SCN	A	630	4	1,2,2	0.66	0	0,1,1	-	-
5	SCN	A	631	-	1,2,2	0.96	0	0,1,1	-	-
5	SCN	A	623	-	1,2,2	0.65	0	0,1,1	-	-
5	SCN	A	619	-	1,2,2	1.46	0	0,1,1	-	-
5	SCN	A	620	-	1,2,2	0.06	0	0,1,1	-	-
5	SCN	A	617	-	1,2,2	1.07	0	0,1,1	-	-
5	SCN	A	622	-	1,2,2	0.52	0	0,1,1	-	-
9	HEM	A	639	1	50,50,50	1.64	7 (14%)	67,82,82	1.57	14 (20%)
7	NO2	A	634	-	1,2,2	0.59	0	0,1,1	-	-
8	NO	A	636	-	0,1,1	-	-	-	-	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	615	1	-	2/6/23/26	0/1/1/1
3	NAG	A	638	1	-	2/6/23/26	0/1/1/1
6	PGE	A	632	-	-	4/7/7/7	-
3	NAG	A	601	1	-	2/6/23/26	0/1/1/1
9	HEM	A	639	1	-	4/14/54/54	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	639	HEM	FE-NB	5.29	2.11	1.94
9	A	639	HEM	FE-NC	4.90	2.11	1.95
9	A	639	HEM	C1B-NB	-3.60	1.34	1.40
9	A	639	HEM	C4D-ND	-3.07	1.34	1.40
9	A	639	HEM	FE-NA	2.88	2.04	1.95

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	638	NAG	C1-O5-C5	5.15	119.09	112.19
9	A	639	HEM	C1B-NB-C4B	4.34	110.35	105.21
9	A	639	HEM	CMD-C2D-C1D	4.11	131.45	125.03
9	A	639	HEM	CHC-C4B-NB	3.54	128.23	124.42
9	A	639	HEM	CAD-C3D-C4D	3.22	130.31	124.70

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	638	NAG	C8-C7-N2-C2
3	A	601	NAG	O5-C5-C6-O6
6	A	632	PGE	C6-C5-O3-C4
3	A	601	NAG	C4-C5-C6-O6
6	A	632	PGE	O1-C1-C2-O2

There are no ring outliers.

9 monomers are involved in 28 short contacts:

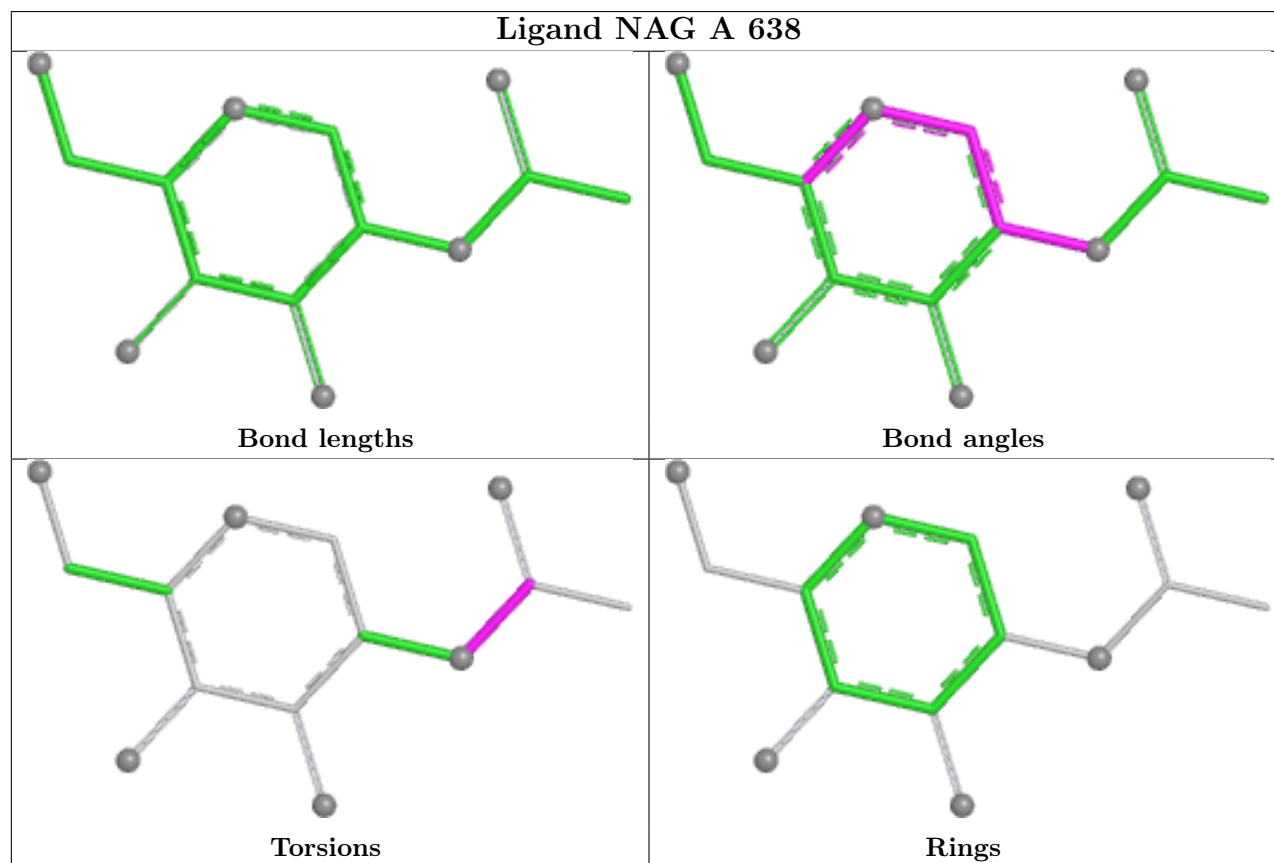
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	635	NO	5	0
6	A	632	PGE	3	0
5	A	629	SCN	2	0

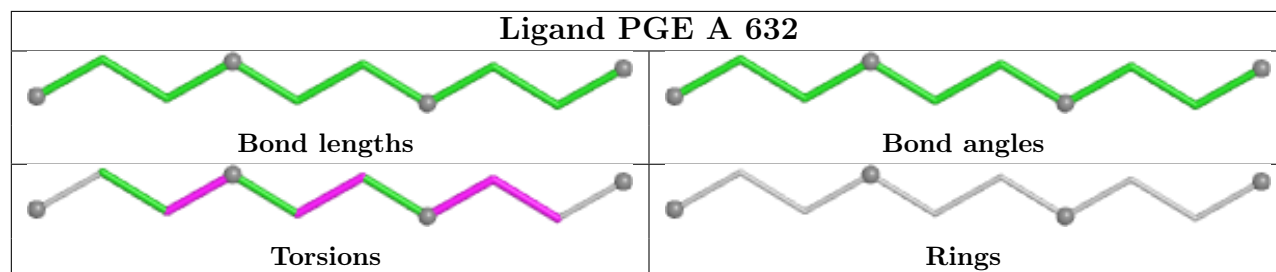
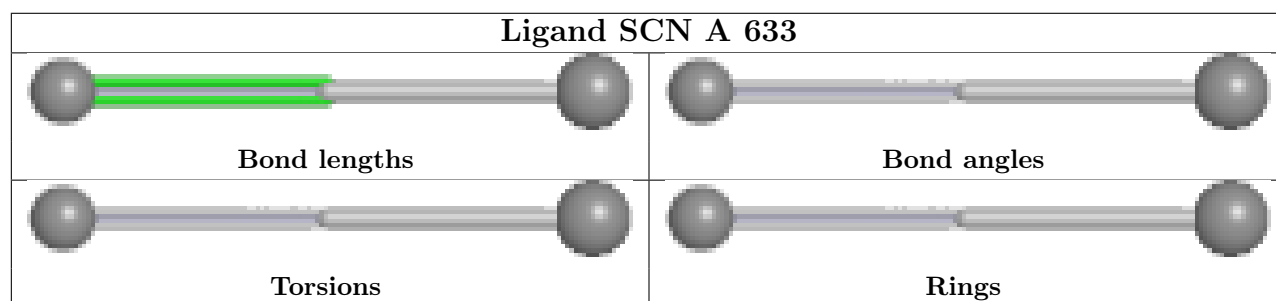
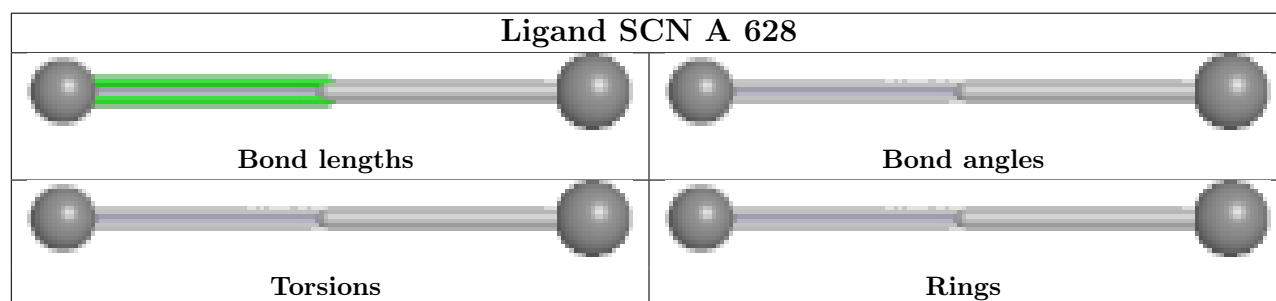
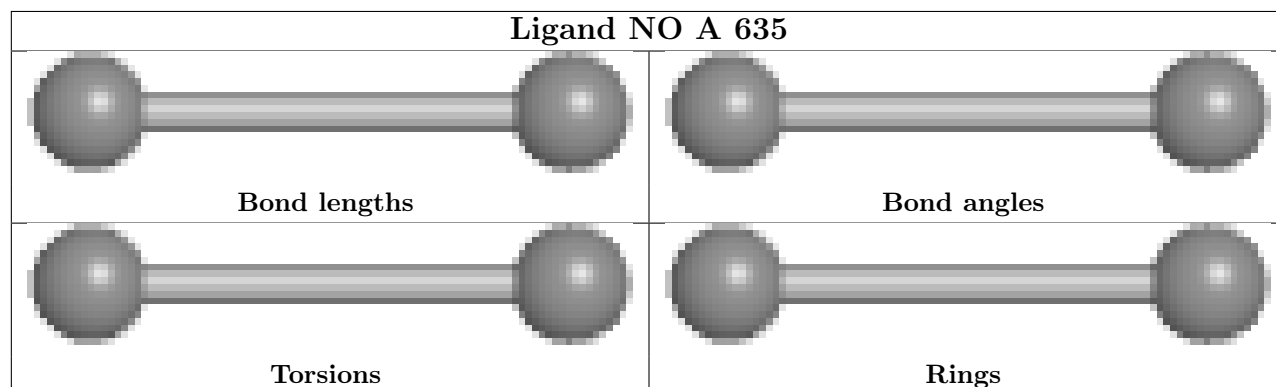
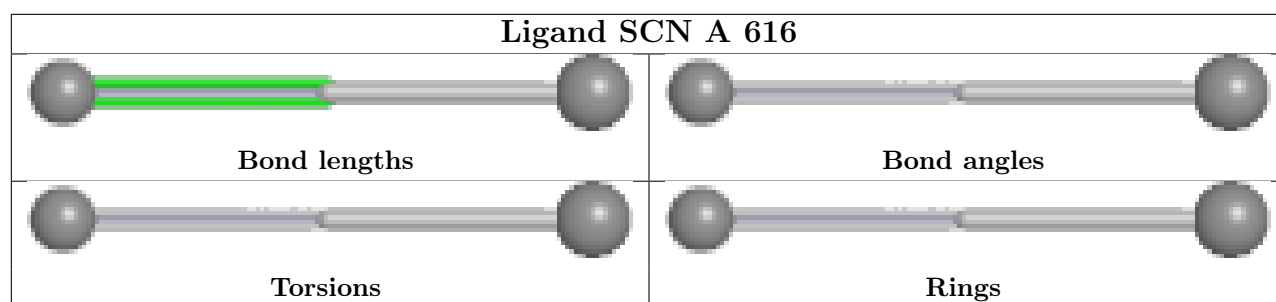
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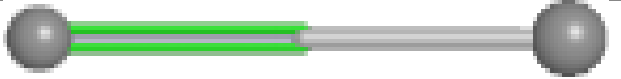
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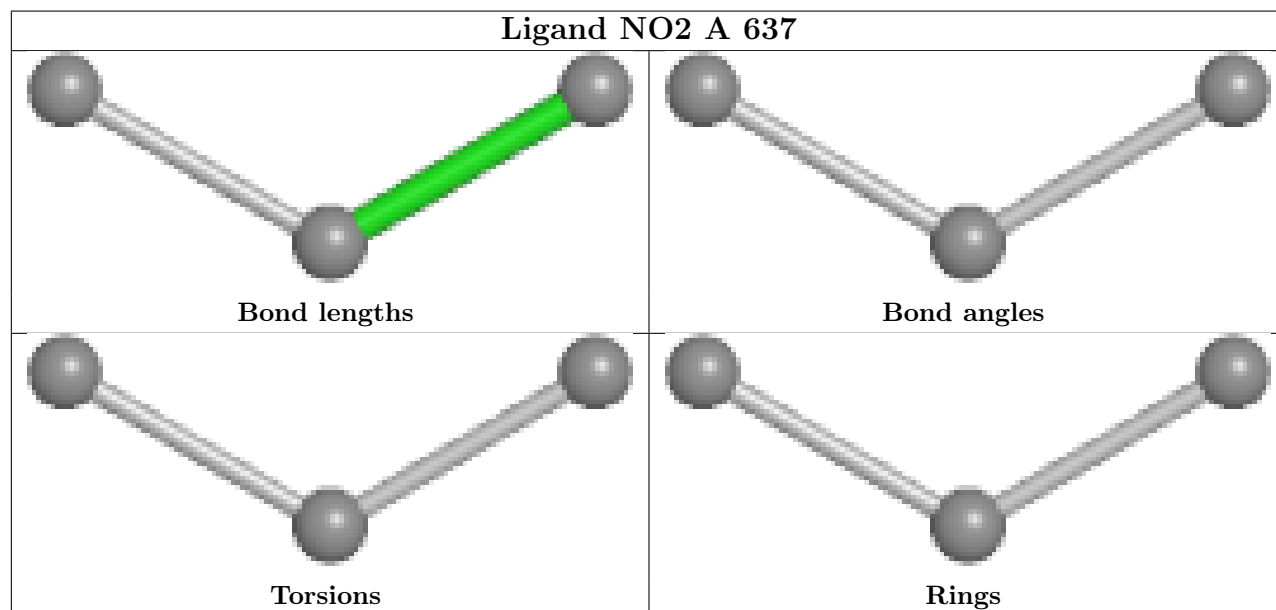
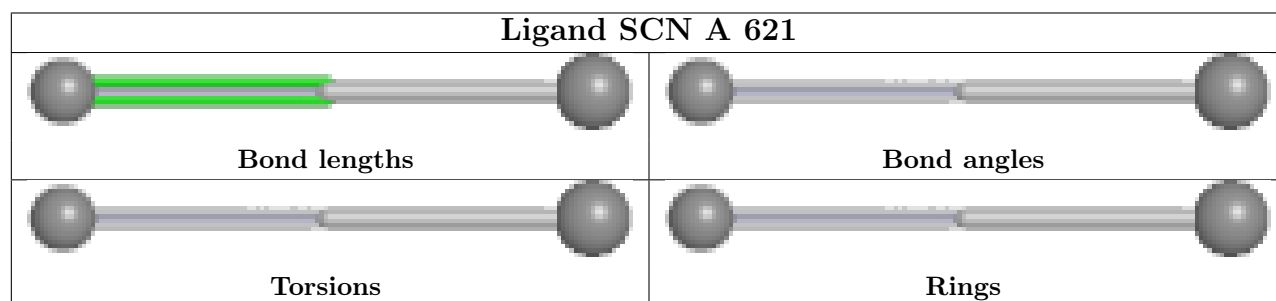
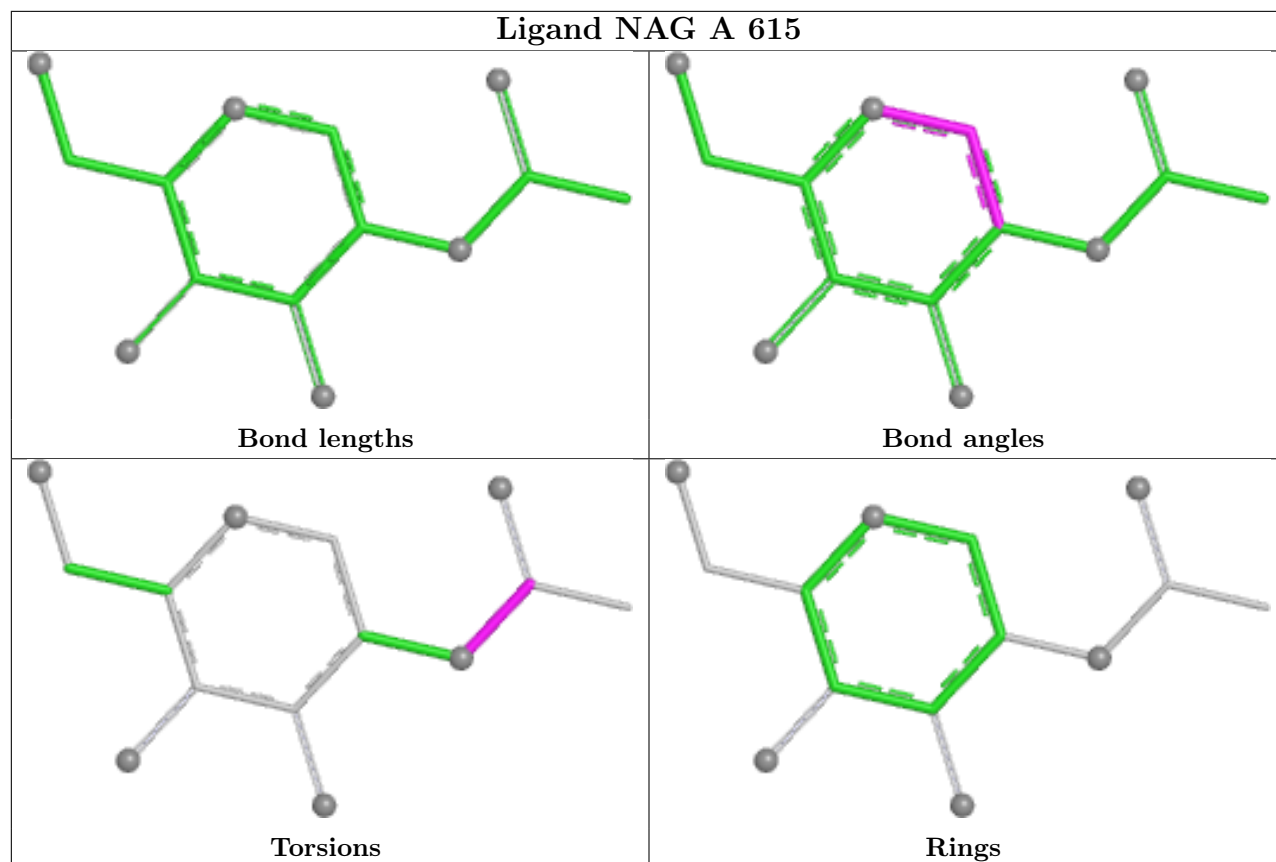
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	621	SCN	1	0
7	A	637	NO2	2	0
5	A	620	SCN	1	0
5	A	622	SCN	2	0
9	A	639	HEM	16	0
8	A	636	NO	1	0

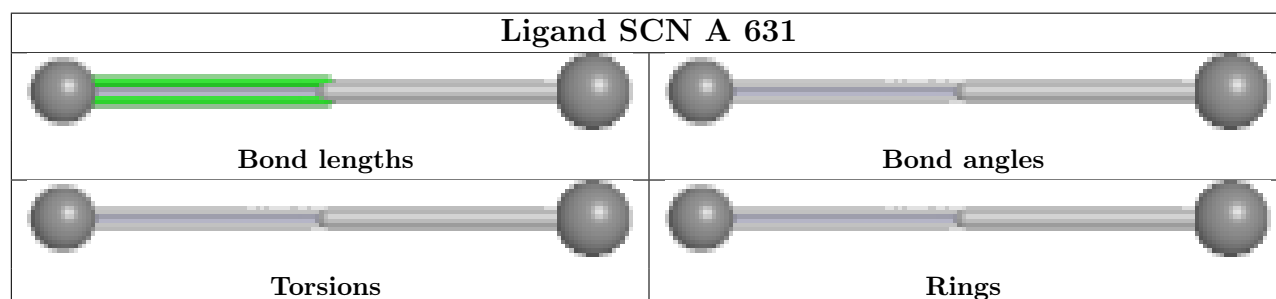
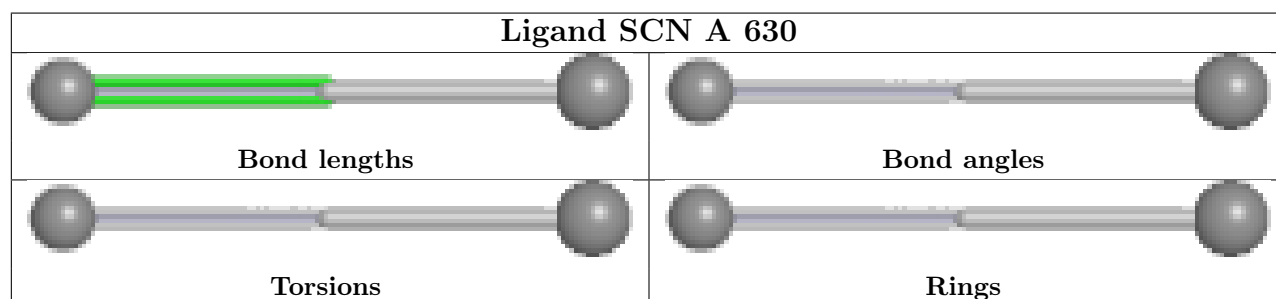
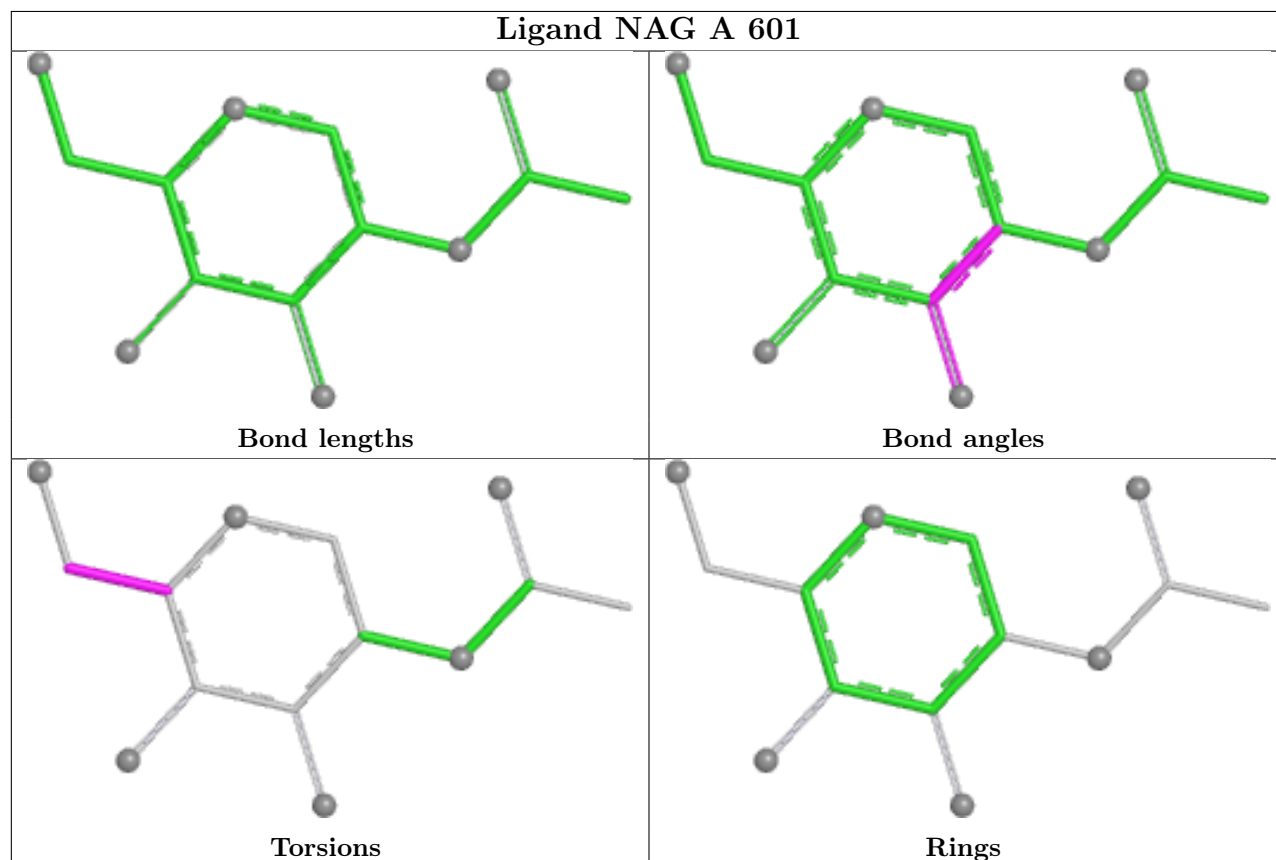
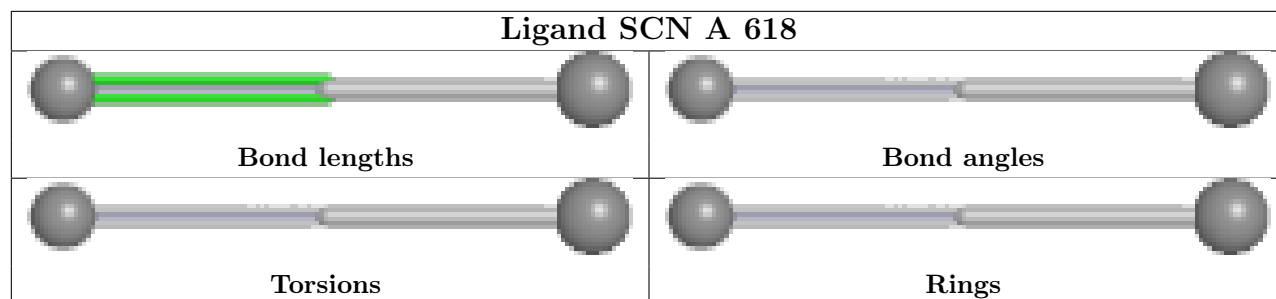
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

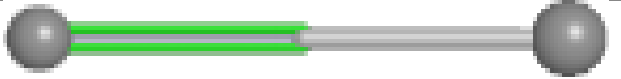


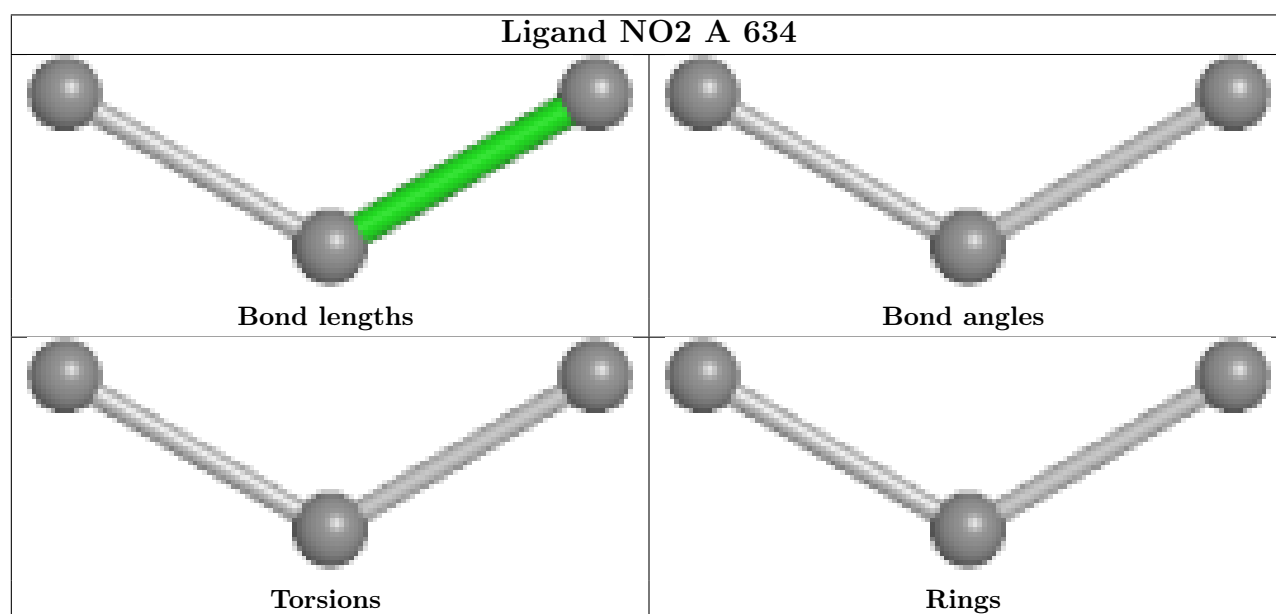
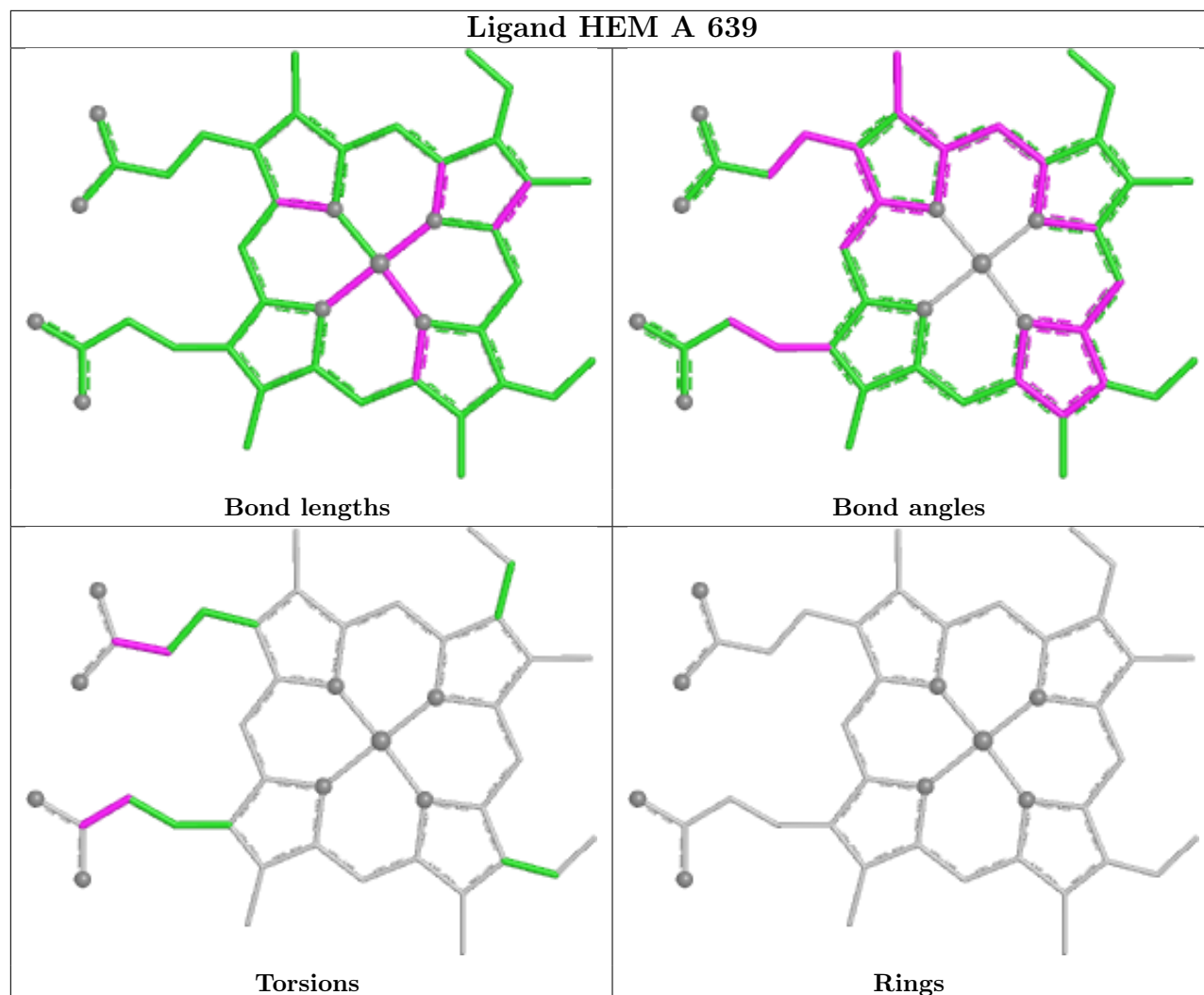


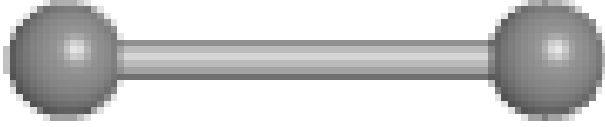
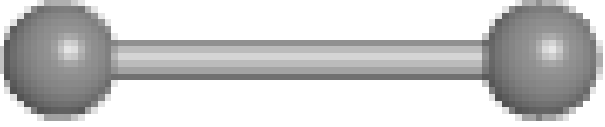
Ligand SCN A 626			
			
Bond lengths			
			
			Bond angles
			
Torsions			
			
			Rings
Ligand SCN A 624			
			
Bond lengths			
			
			Bond angles
			
Torsions			
			
			Rings
Ligand SCN A 627			
			
Bond lengths			
			
			Bond angles
			
Torsions			
			
			Rings
Ligand SCN A 625			
			
Bond lengths			
			
			Bond angles
			
Torsions			
			
			Rings
Ligand SCN A 629			
			
Bond lengths			
			
			Bond angles
			
Torsions			
			
			Rings





Ligand SCN A 623			
			
Bond lengths			
			
			Bond angles
			
Torsions			
			
			Rings
Ligand SCN A 619			
			
Bond lengths			
			
			Bond angles
			
Torsions			
			
			Rings
Ligand SCN A 620			
			
Bond lengths			
			
			Bond angles
			
Torsions			
			
			Rings
Ligand SCN A 617			
			
Bond lengths			
			
			Bond angles
			
Torsions			
			
			Rings
Ligand SCN A 622			
			
Bond lengths			
			
			Bond angles
			
Torsions			
			
			Rings



Ligand NO A 636	
 Bond lengths	 Bond angles
 Torsions	 Rings

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th 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 ²)	Q<0.9
1	A	594/595 (99%)	0.42	28 (4%)	36 42	26, 45, 114, 204	2 (0%)

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	12	LEU	5.3
1	A	10	VAL	5.3
1	A	173	GLN	5.2
1	A	119	LEU	3.9
1	A	8	ALA	3.9

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, 95th 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 ²)	Q<0.9
1	CSD	A	441[A]	8/9	0.95	0.12	35,41,58,59	8
1	CSD	A	441[B]	8/9	0.95	0.12	28,29,32,33	8

6.3 Carbohydrates [i](#)

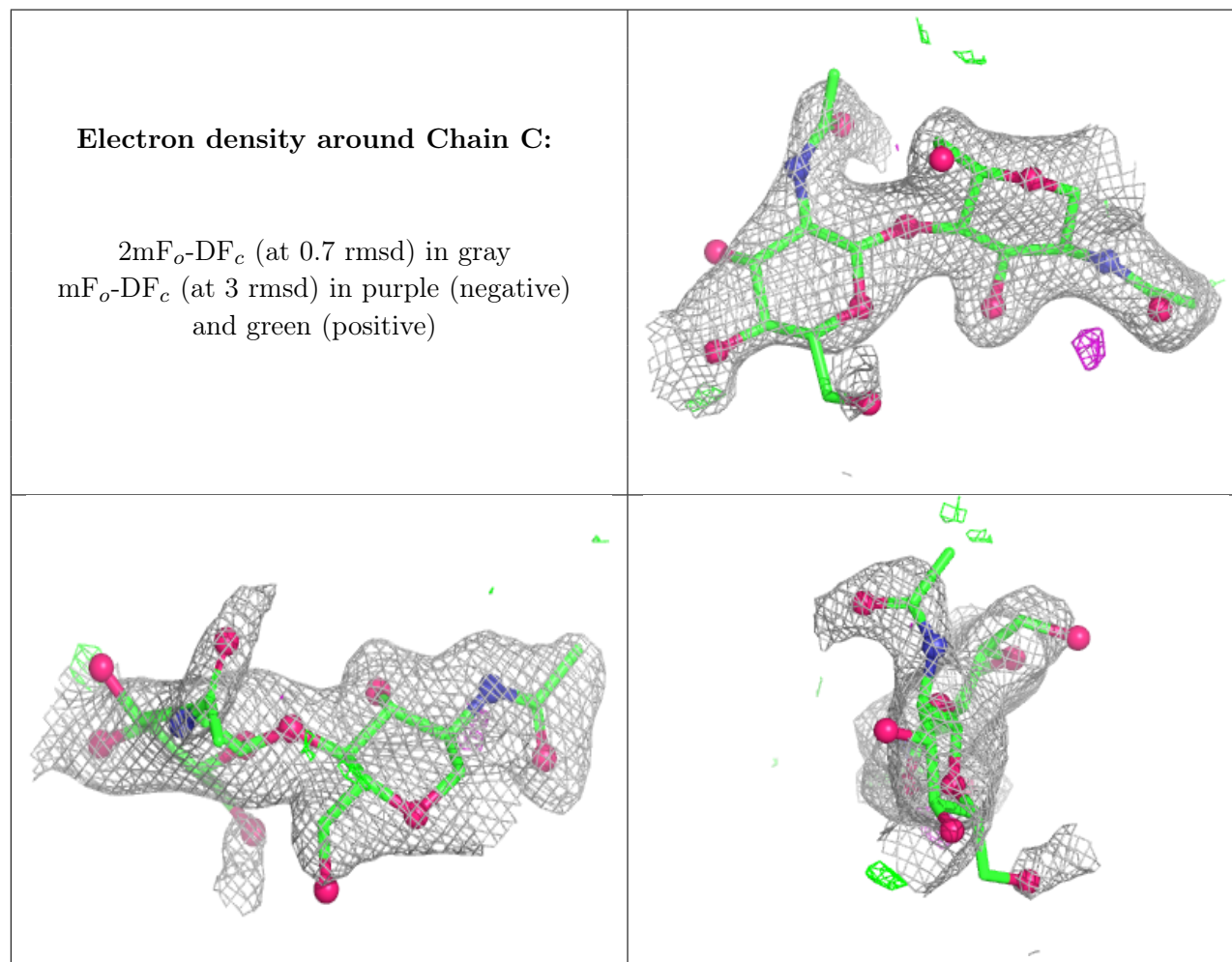
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	C	1	14/15	-	-	41,49,58,73	0
2	NAG	C	2	14/15	-	-	63,84,92,98	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 ⓘ

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, 95th 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	638	14/15	0.71	0.13	76,89,94,96	0

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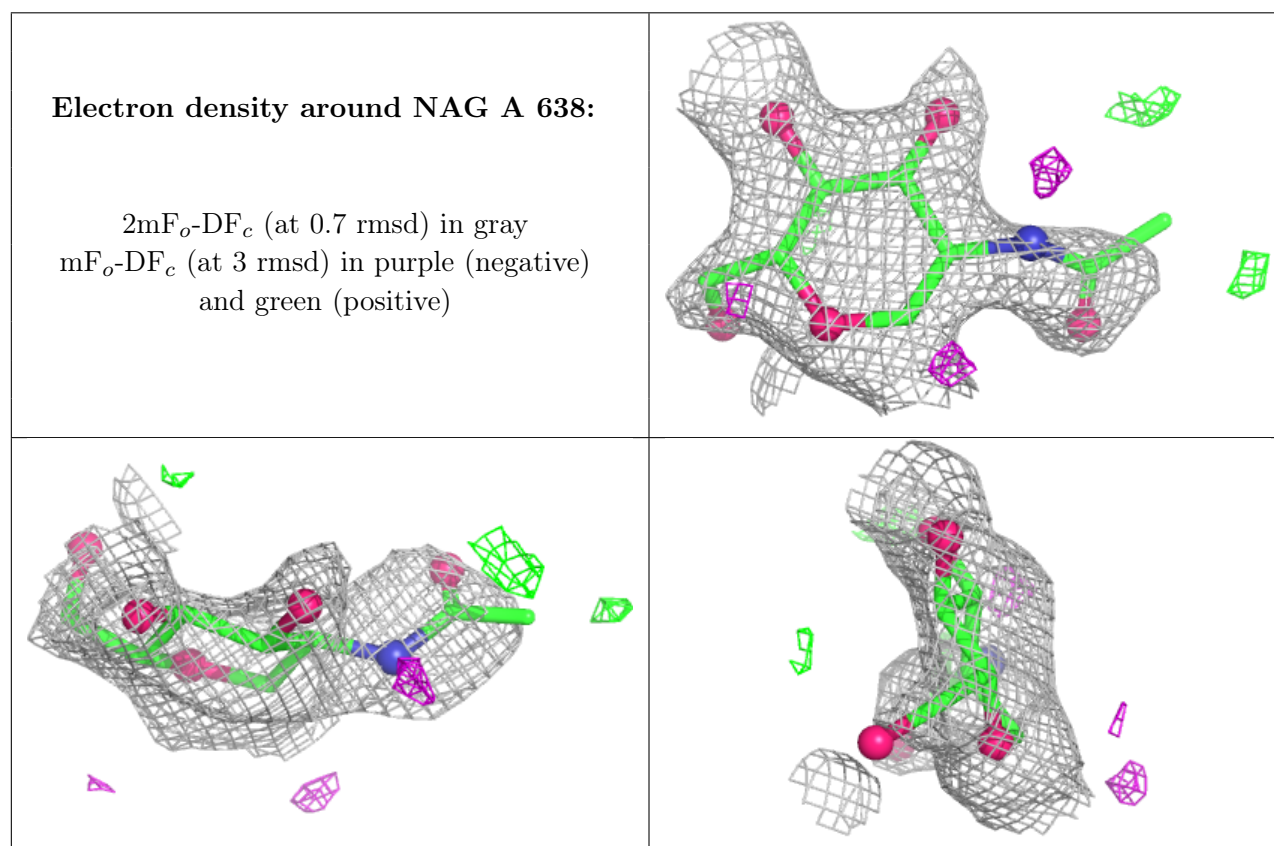
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	A	601	14/15	0.84	0.10	66,76,88,90	0
5	SCN	A	630	3/3	0.88	0.11	63,63,75,76	3
3	NAG	A	615	14/15	0.90	0.10	52,68,73,80	0
4	IOD	A	650	1/1	0.91	0.10	73,73,73,73	1
4	IOD	A	645	1/1	0.91	0.11	73,73,73,73	1
5	SCN	A	633	3/3	0.91	0.10	65,65,65,69	0
7	NO2	A	637	3/3	0.91	0.09	43,43,44,45	0
5	SCN	A	629	3/3	0.92	0.10	23,23,24,29	3
6	PGE	A	632	10/10	0.92	0.10	60,61,67,72	0
5	SCN	A	626	3/3	0.92	0.09	36,36,48,60	0
8	NO	A	635	2/2	0.92	0.12	37,37,37,45	2
5	SCN	A	619	3/3	0.94	0.08	19,19,23,40	3
4	IOD	A	609	1/1	0.94	0.09	70,70,70,70	1
4	IOD	A	643	1/1	0.94	0.09	62,62,62,62	1
4	IOD	A	651	1/1	0.94	0.08	61,61,61,61	1
5	SCN	A	617	3/3	0.95	0.07	31,31,32,32	3
5	SCN	A	627	3/3	0.95	0.08	50,50,53,66	0
5	SCN	A	628	3/3	0.95	0.10	30,30,46,55	3
5	SCN	A	622	3/3	0.96	0.05	20,20,23,30	3
5	SCN	A	623	3/3	0.96	0.10	41,41,47,57	0
5	SCN	A	625	3/3	0.96	0.06	25,25,27,40	3
4	IOD	A	644	1/1	0.96	0.07	51,51,51,51	1
4	IOD	A	610	1/1	0.96	0.12	59,59,59,59	1
4	IOD	A	607	1/1	0.96	0.06	65,65,65,65	1
8	NO	A	636	2/2	0.96	0.07	40,40,40,48	0
5	SCN	A	616	3/3	0.97	0.06	32,32,38,43	3
4	IOD	A	648	1/1	0.97	0.06	60,60,60,60	1
5	SCN	A	618	3/3	0.97	0.07	43,43,45,50	0
4	IOD	A	614	1/1	0.97	0.07	51,51,51,51	1
5	SCN	A	620	3/3	0.97	0.06	27,27,27,30	3
4	IOD	A	606	1/1	0.97	0.08	91,91,91,91	1
5	SCN	A	624	3/3	0.98	0.07	39,39,43,52	0
5	SCN	A	631	3/3	0.98	0.05	20,20,20,25	3
4	IOD	A	642	1/1	0.98	0.08	66,66,66,66	1
4	IOD	A	647	1/1	0.98	0.07	58,58,58,58	1
7	NO2	A	634	3/3	0.98	0.04	30,30,31,31	3
5	SCN	A	621	3/3	0.98	0.10	30,30,32,32	3
4	IOD	A	608	1/1	0.98	0.05	59,59,59,59	1
4	IOD	A	603	1/1	0.98	0.04	53,53,53,53	1
9	HEM	A	639	43/43	0.98	0.05	26,31,35,38	0
4	IOD	A	612	1/1	0.99	0.03	41,41,41,41	1
4	IOD	A	605	1/1	0.99	0.04	39,39,39,39	1

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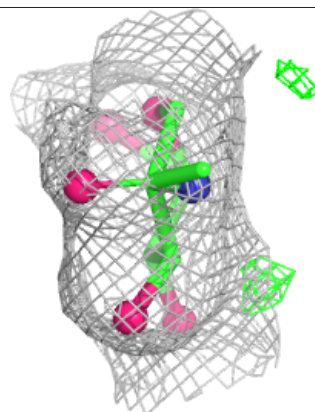
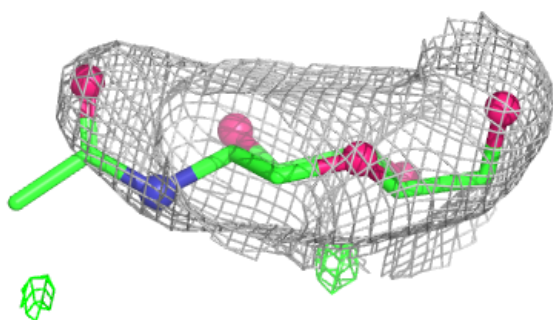
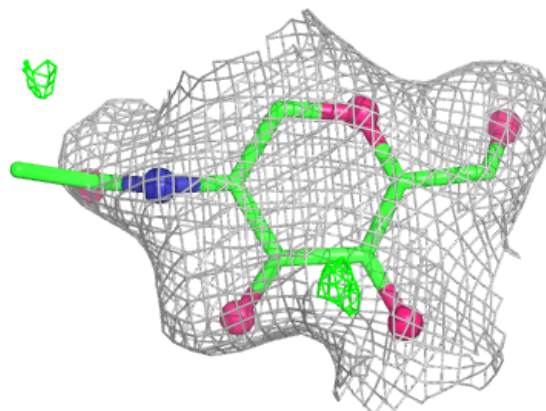
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	IOD	A	646	1/1	0.99	0.06	49,49,49,49	1
4	IOD	A	604	1/1	0.99	0.04	45,45,45,45	1
4	IOD	A	611	1/1	0.99	0.03	47,47,47,47	1
4	IOD	A	641	1/1	1.00	0.01	27,27,27,27	1
4	IOD	A	613	1/1	1.00	0.04	48,48,48,48	1
4	IOD	A	649	1/1	1.00	0.05	41,41,41,41	1
4	IOD	A	602	1/1	1.00	0.05	32,32,32,32	1
10	CA	A	640	1/1	1.00	0.02	34,34,34,34	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.

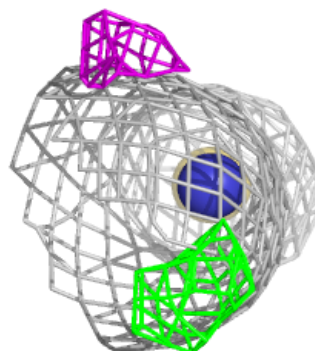
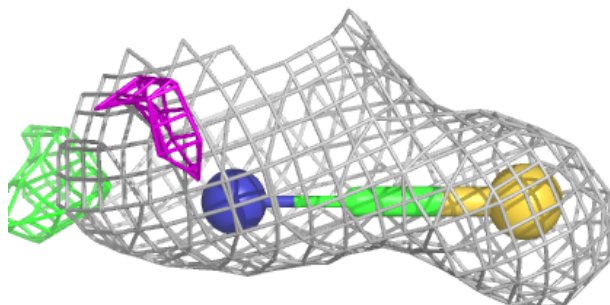
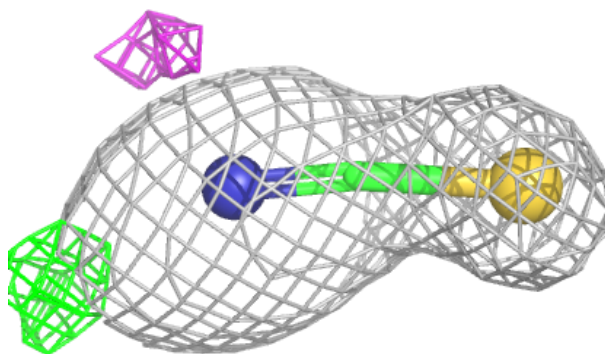


Electron density around NAG A 601:

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

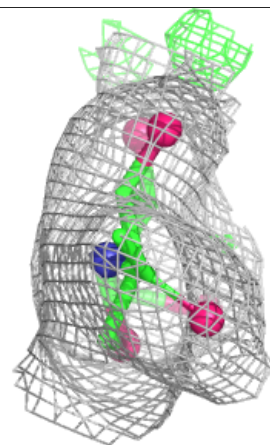
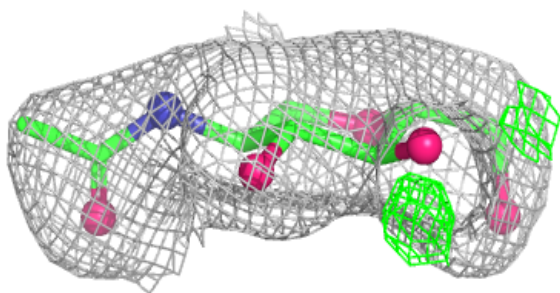
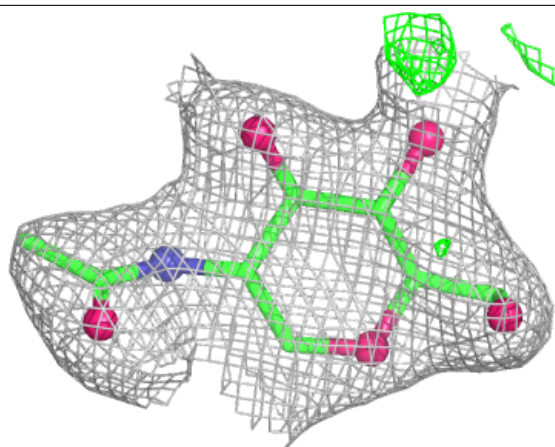
**Electron density around SCN A 630:**

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and green (positive)



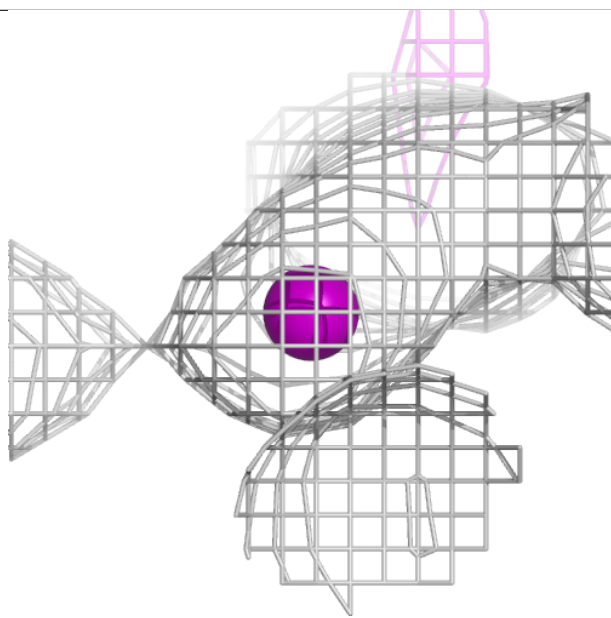
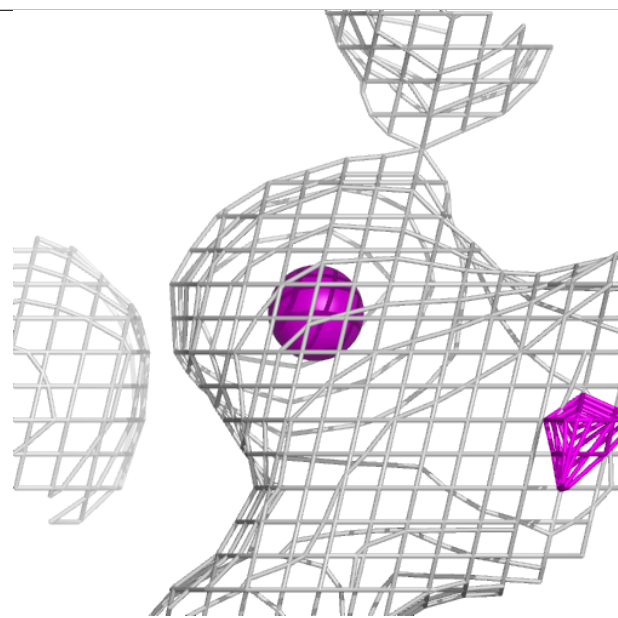
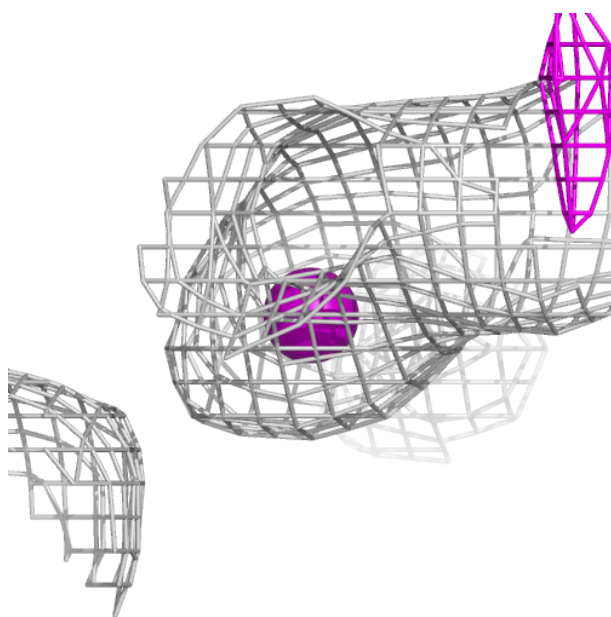
Electron density around NAG A 615:

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and green (positive)



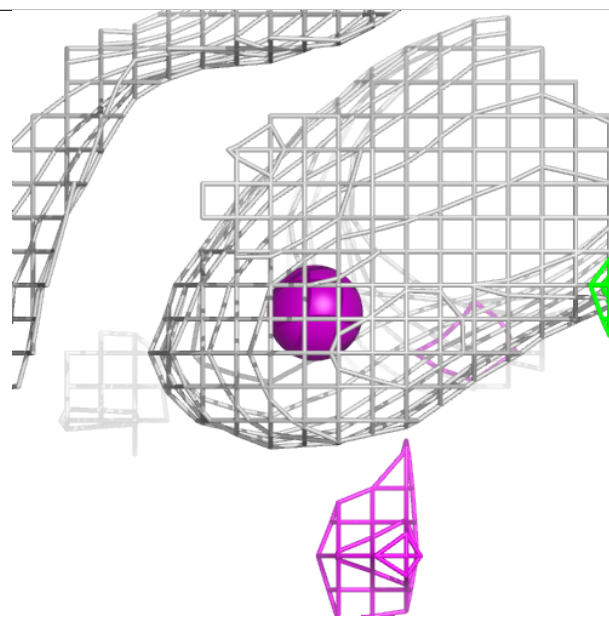
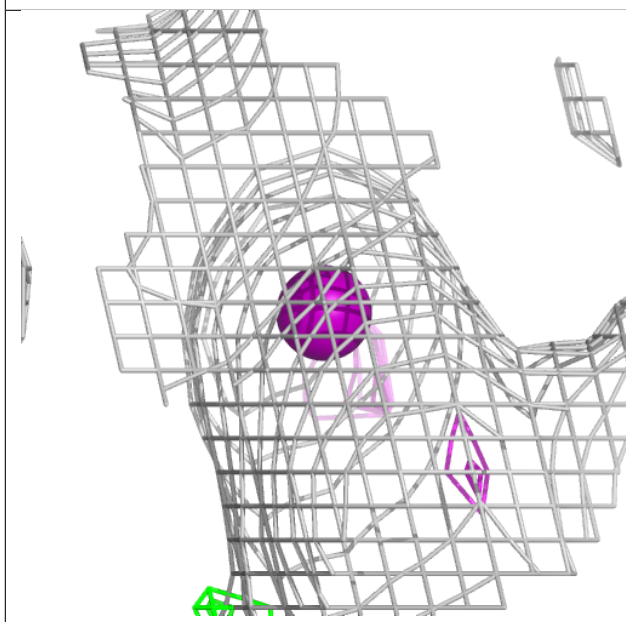
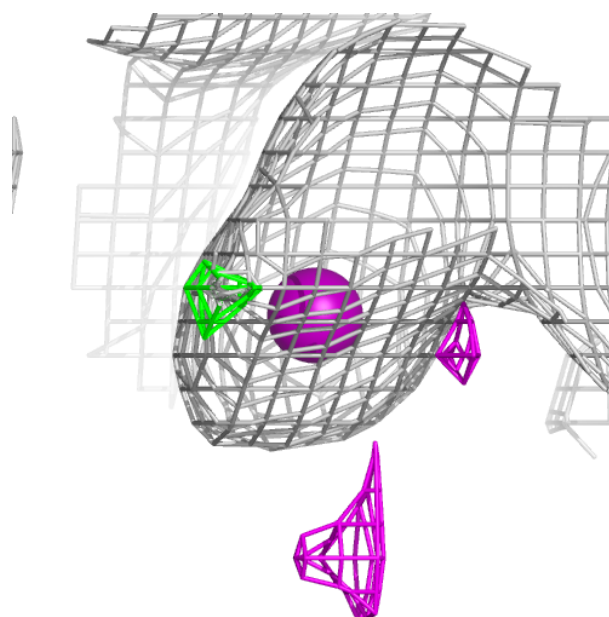
Electron density around IOD A 650:

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



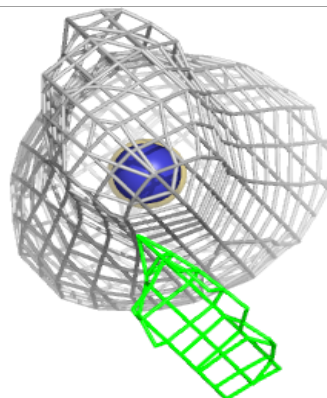
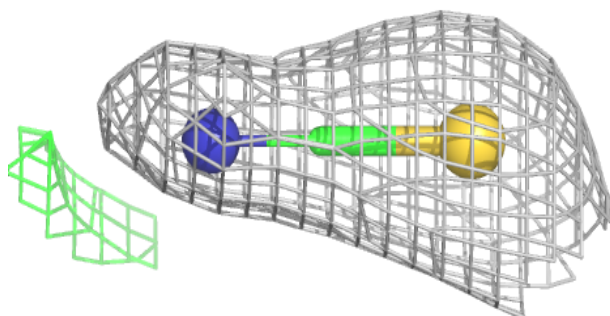
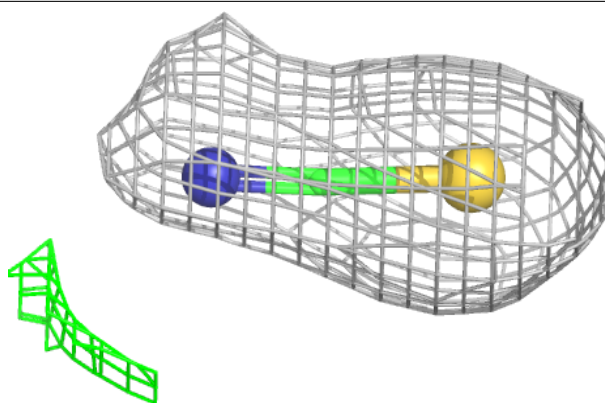
Electron density around IOD A 645:

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

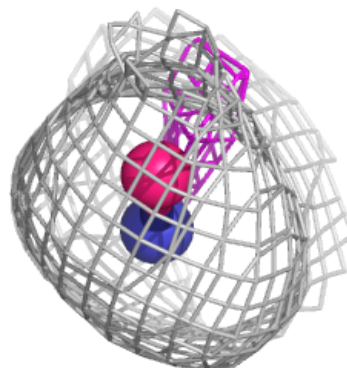
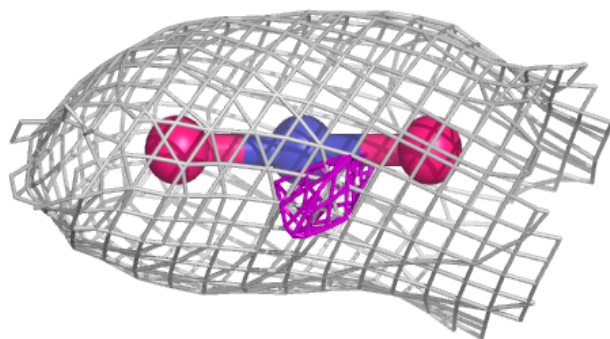
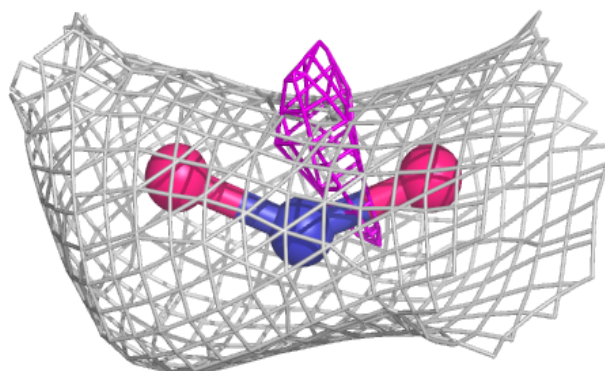


Electron density around SCN A 633:

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

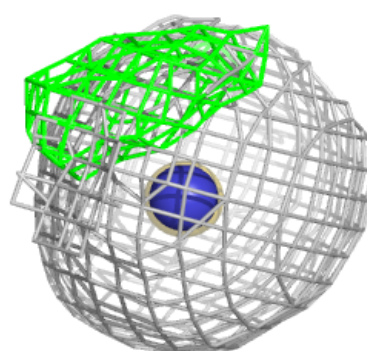
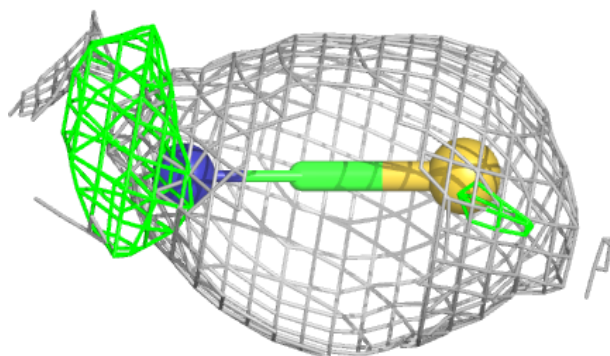
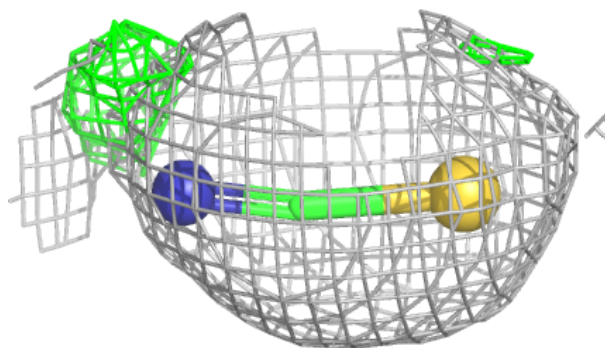
**Electron density around NO2 A 637:**

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

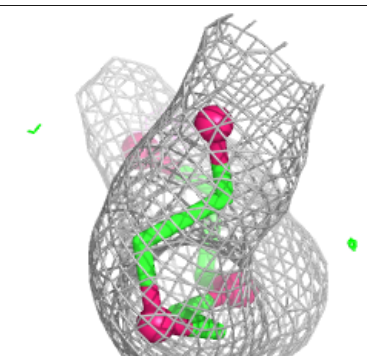
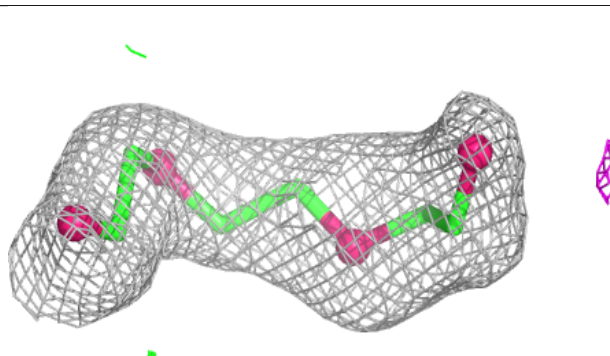
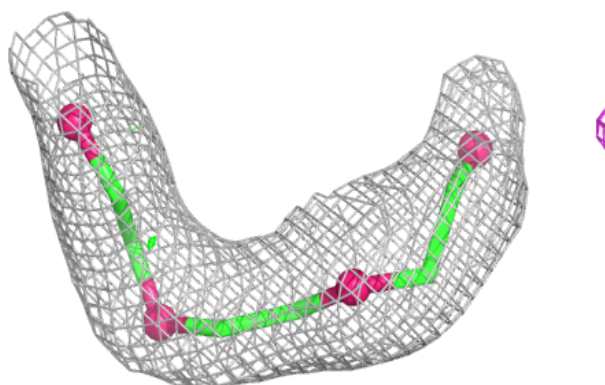


Electron density around SCN A 629:

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

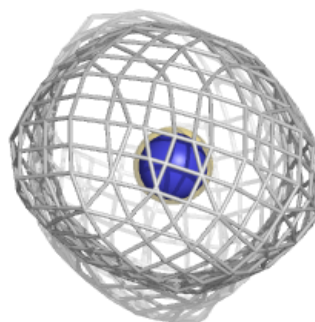
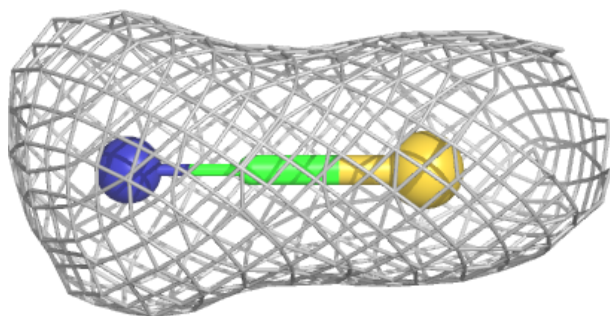
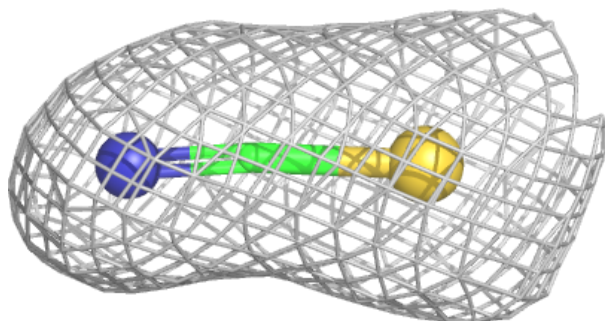
**Electron density around PGE A 632:**

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

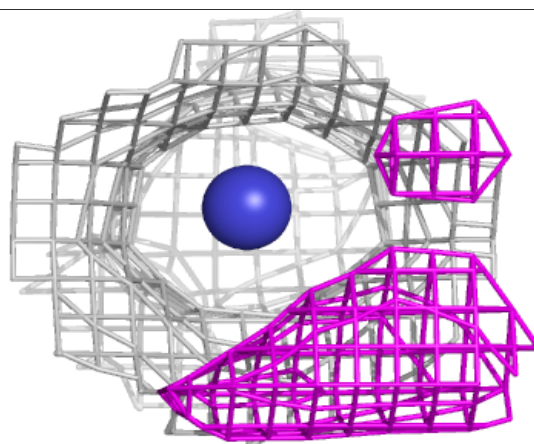
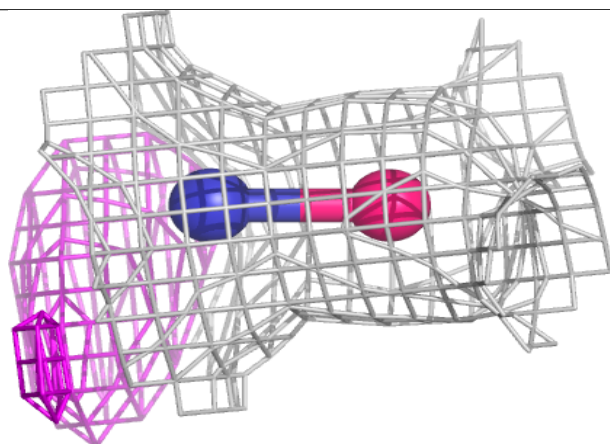
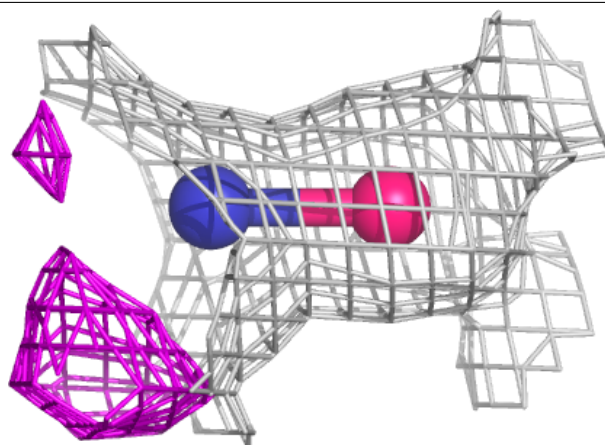


Electron density around SCN A 626:

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

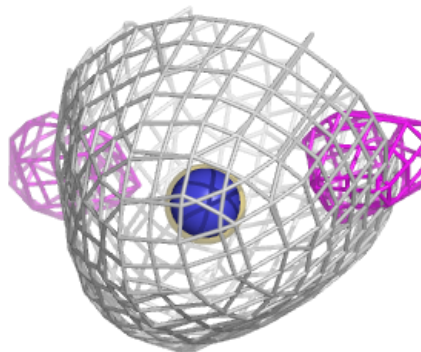
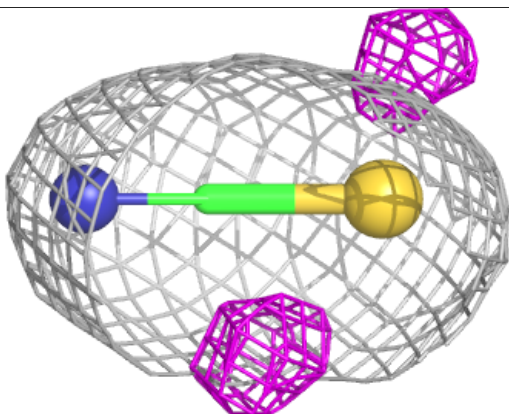
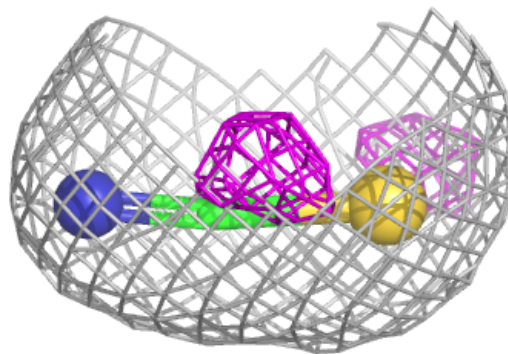
**Electron density around NO A 635:**

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



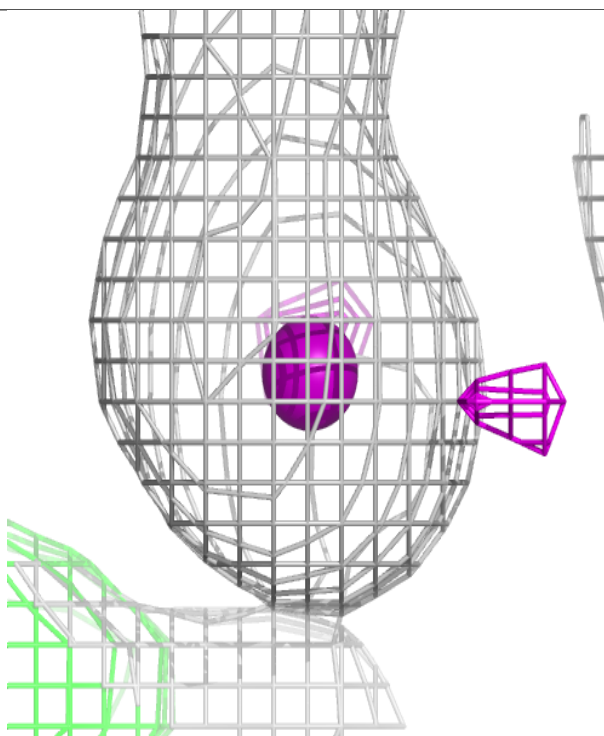
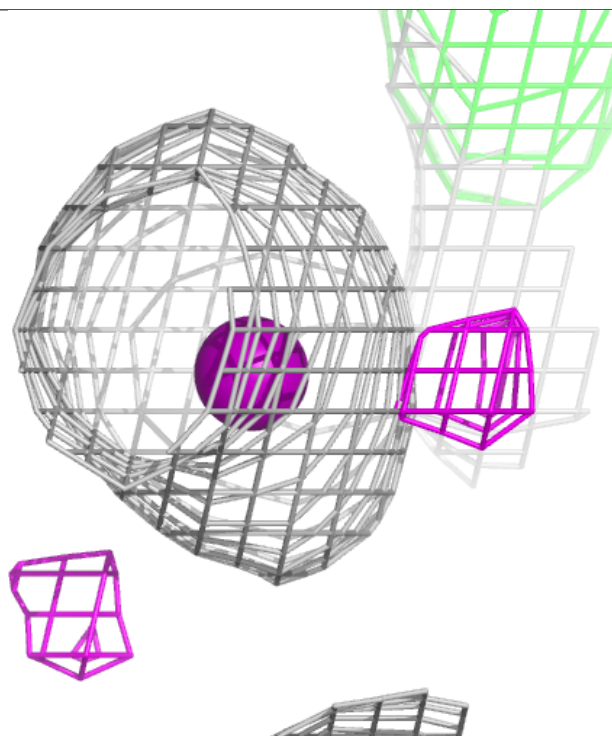
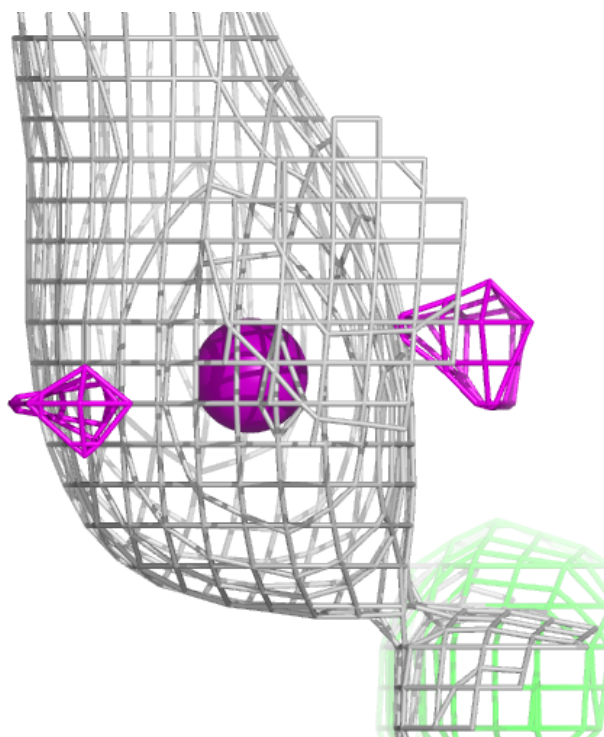
Electron density around SCN A 619:

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



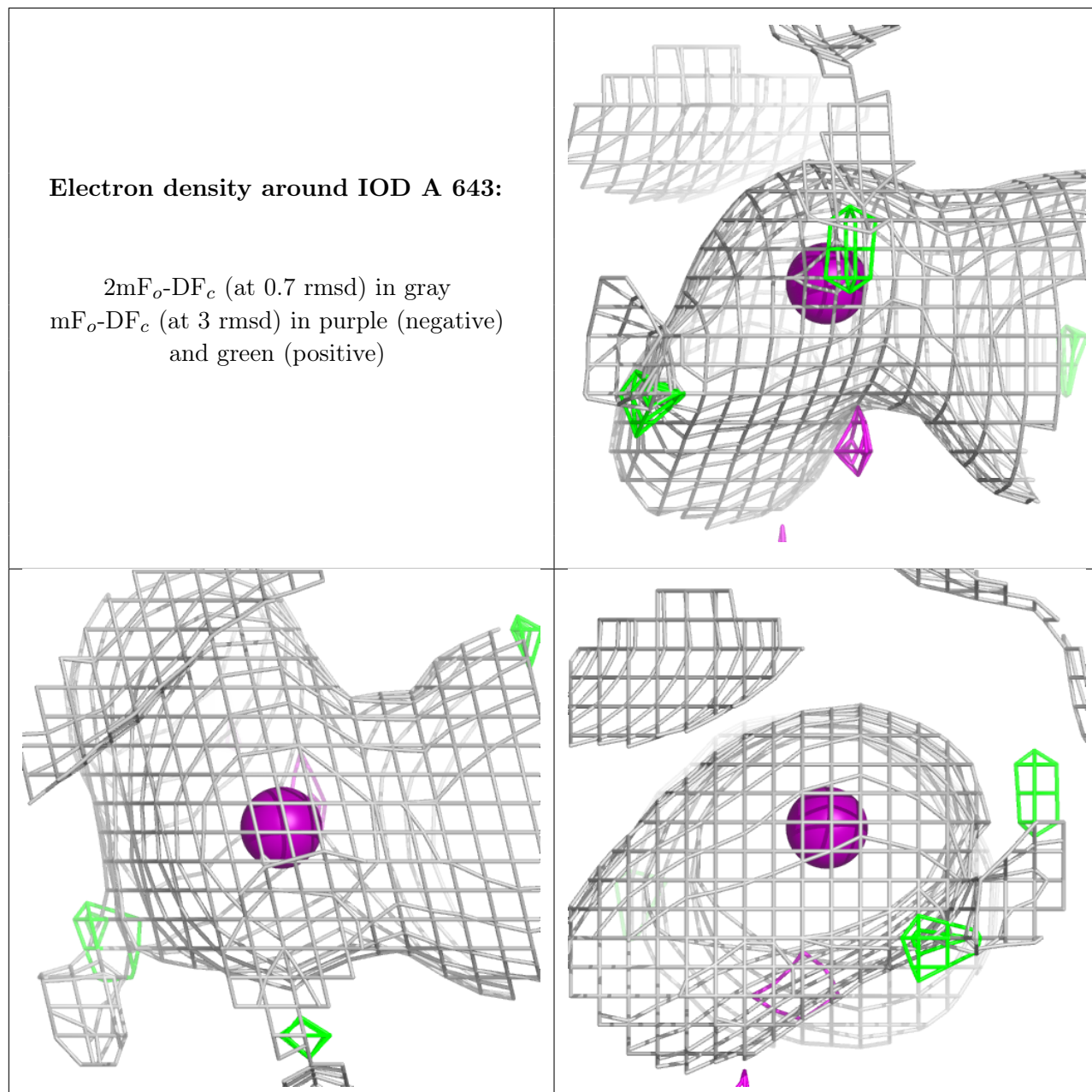
Electron density around IOD A 609:

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



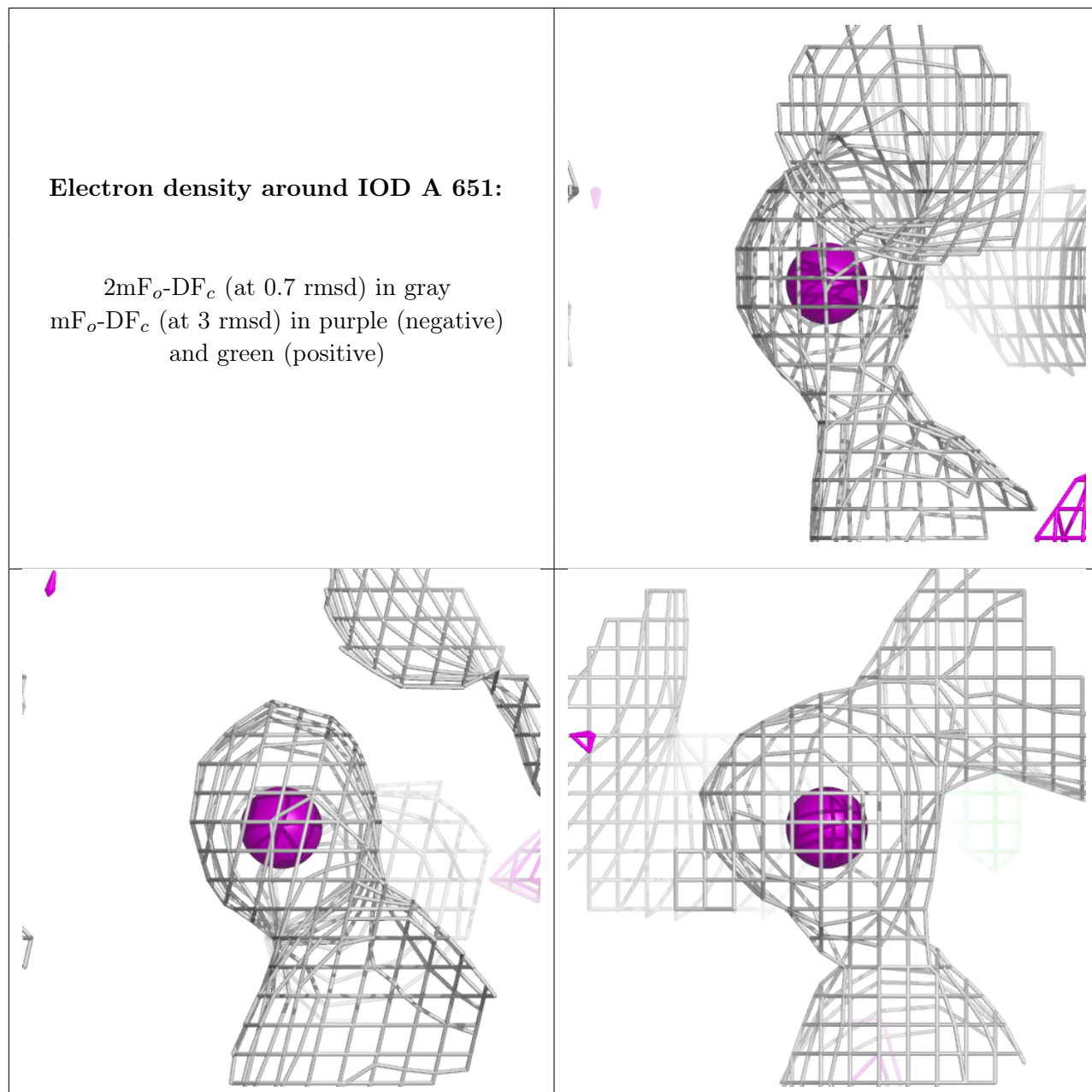
Electron density around IOD A 643:

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



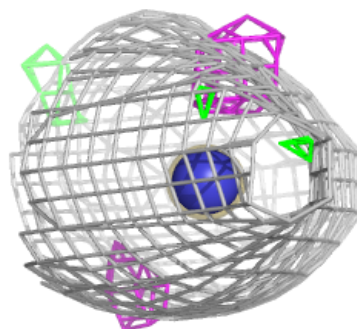
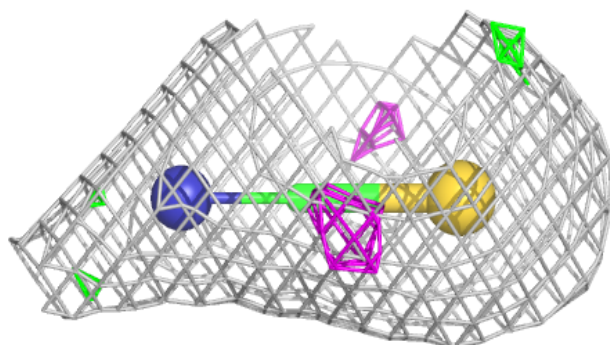
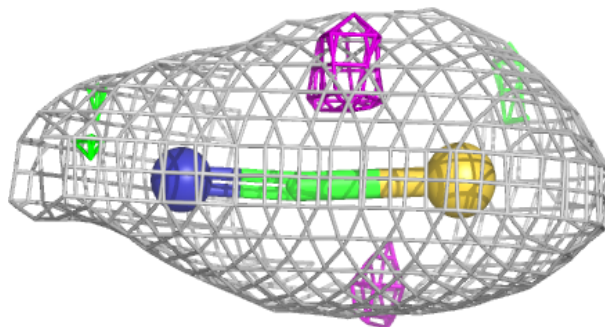
Electron density around IOD A 651:

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

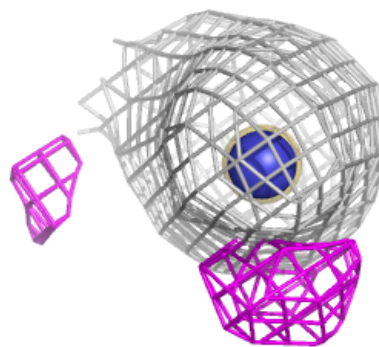
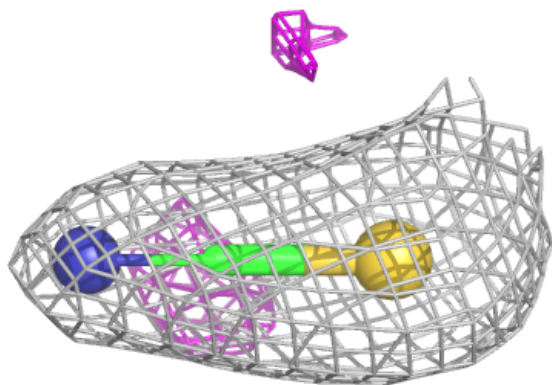
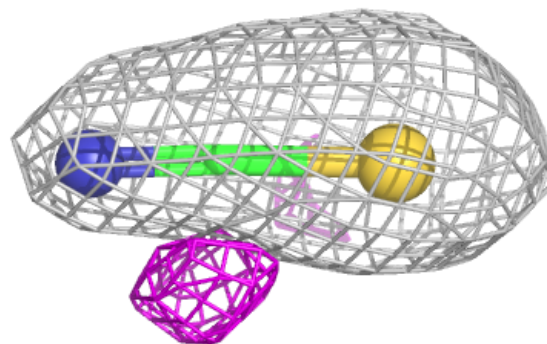


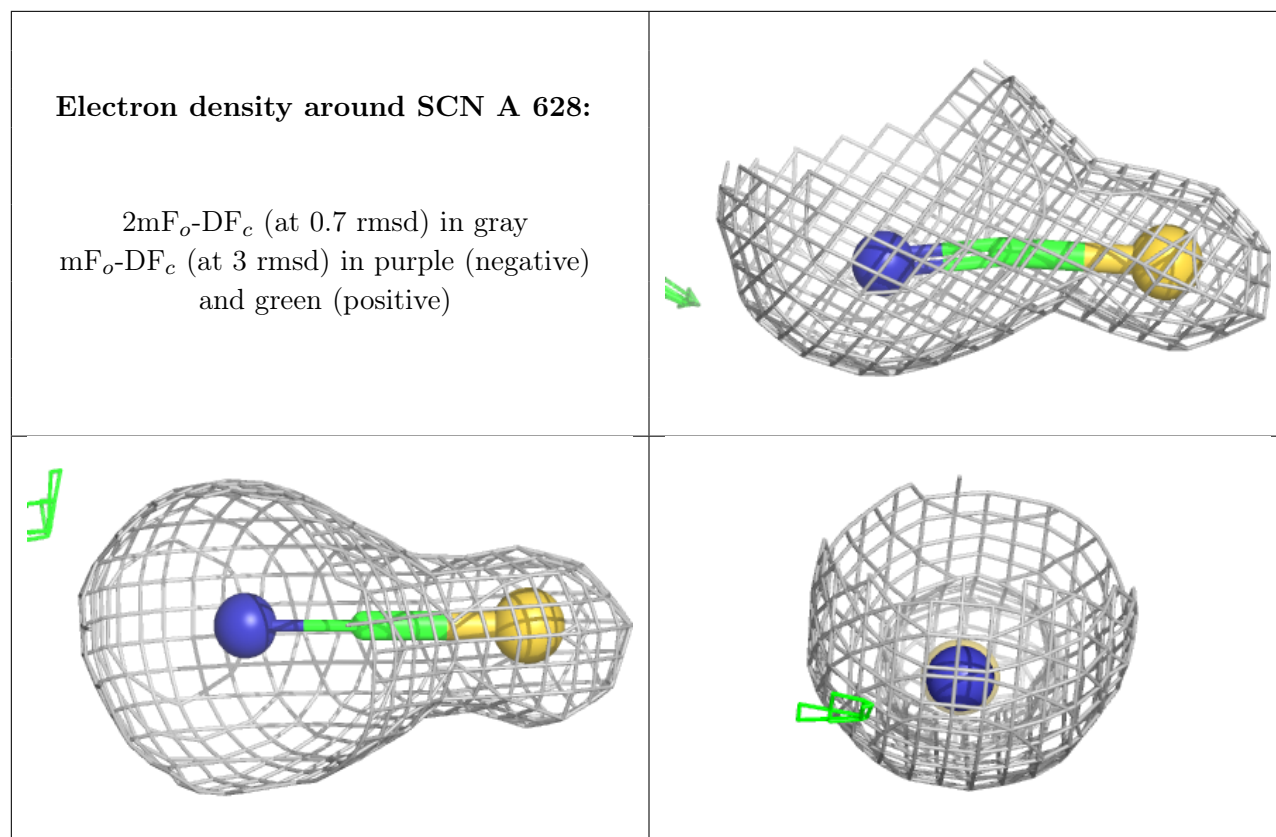
Electron density around SCN A 617:

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

**Electron density around SCN A 627:**

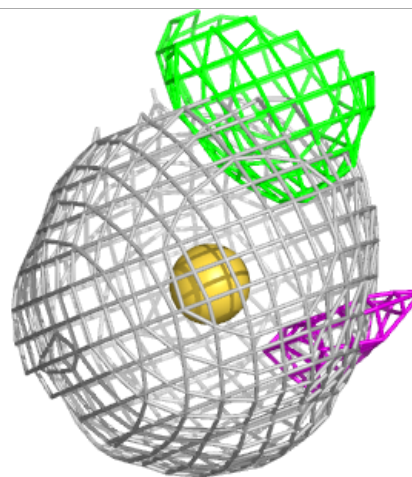
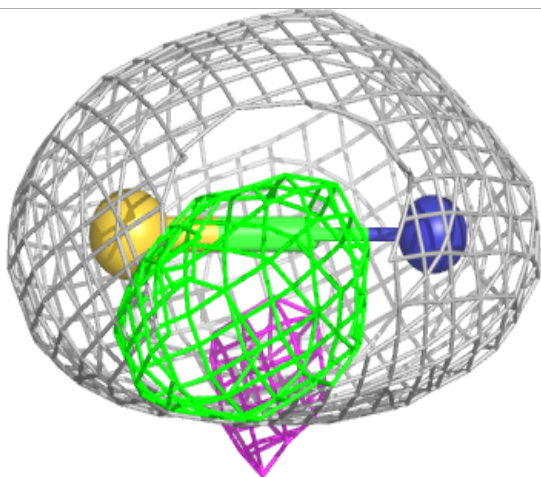
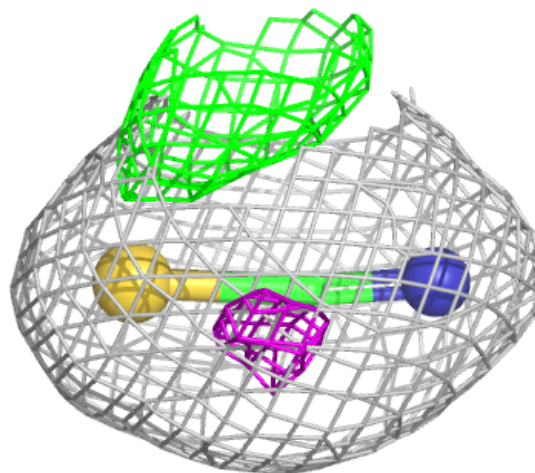
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





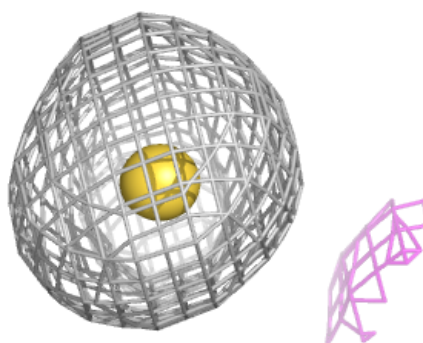
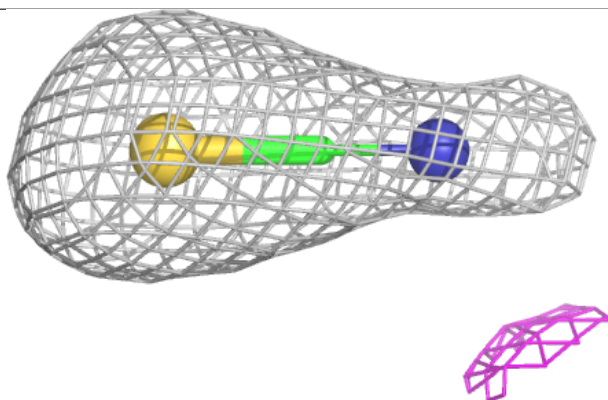
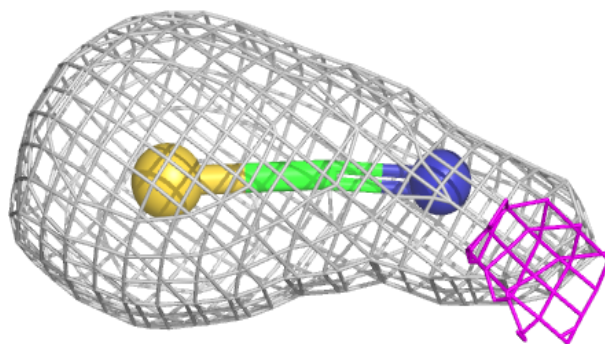
Electron density around SCN A 622:

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

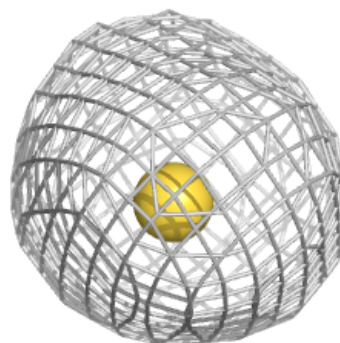
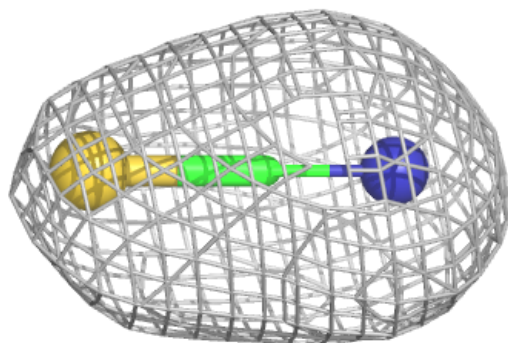
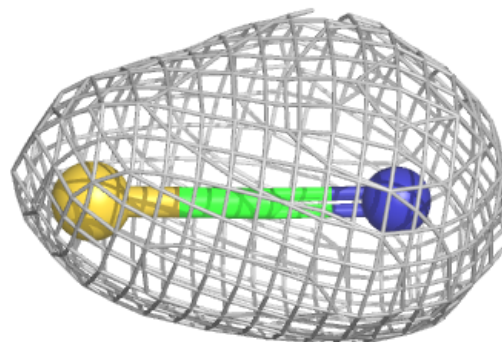


Electron density around SCN A 623:

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

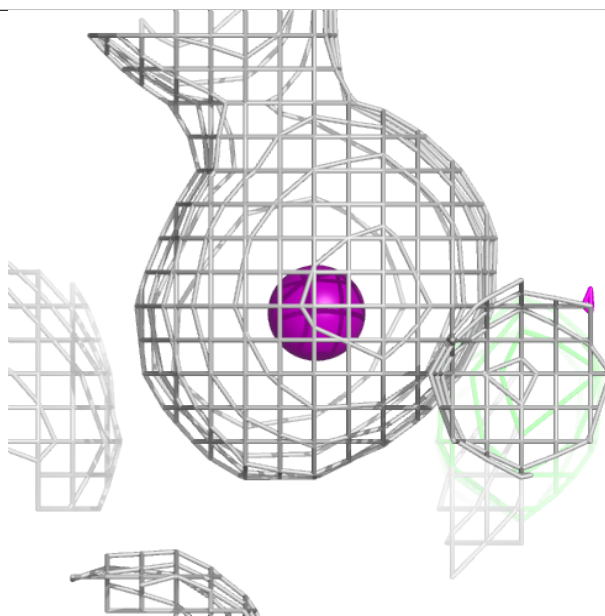
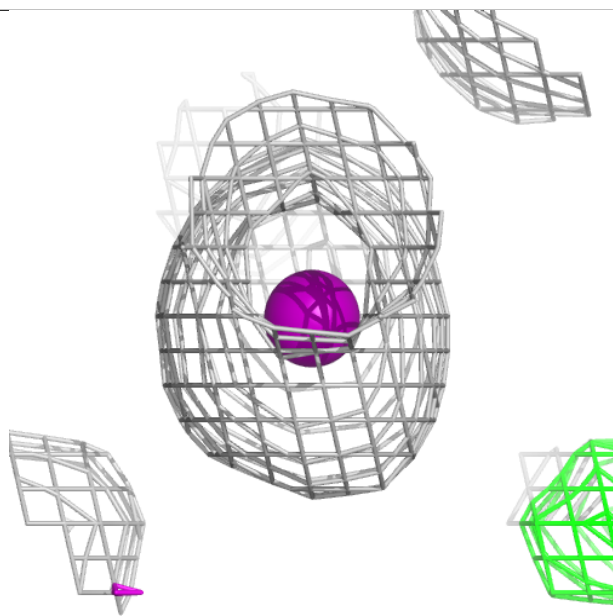
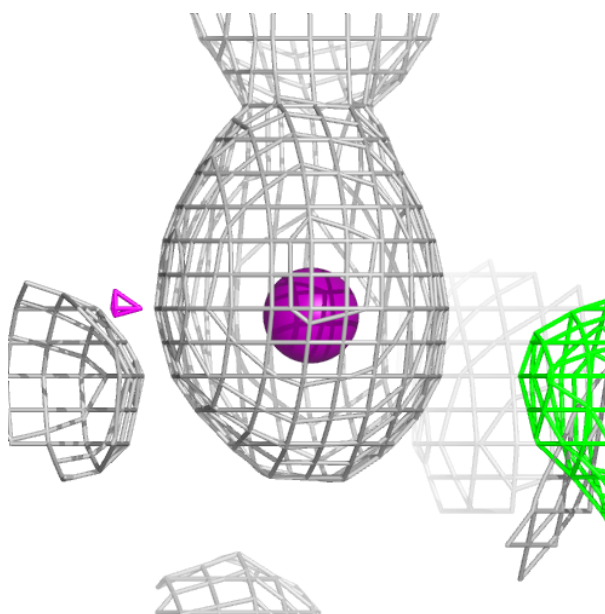
**Electron density around SCN A 625:**

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



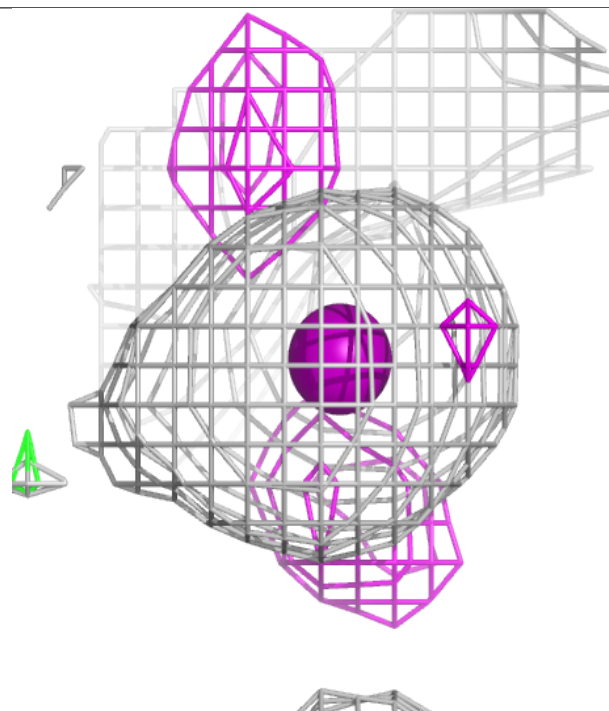
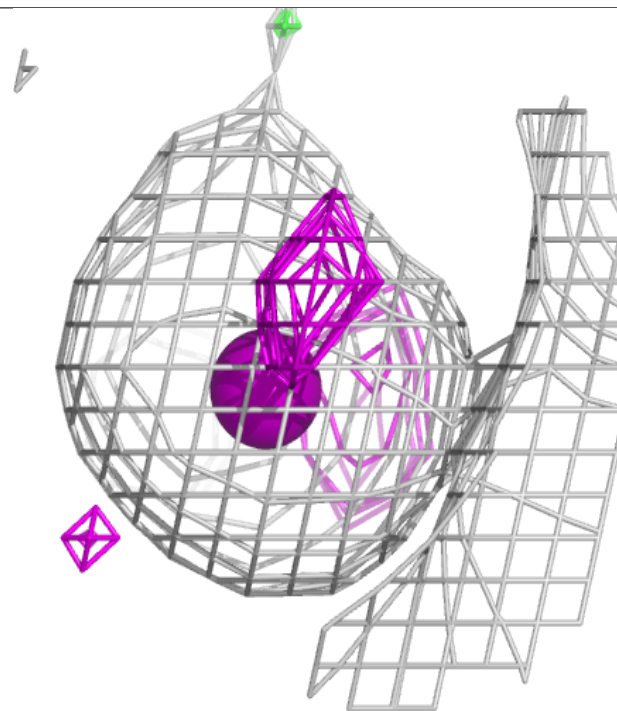
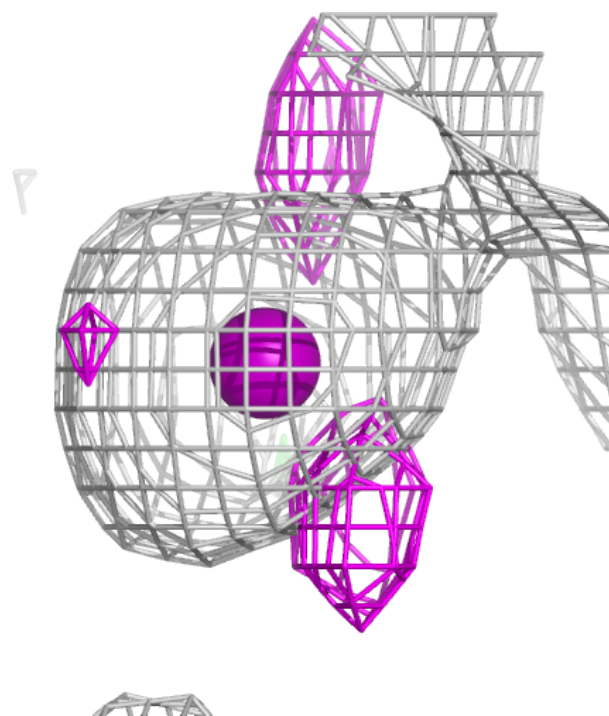
Electron density around IOD A 644:

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



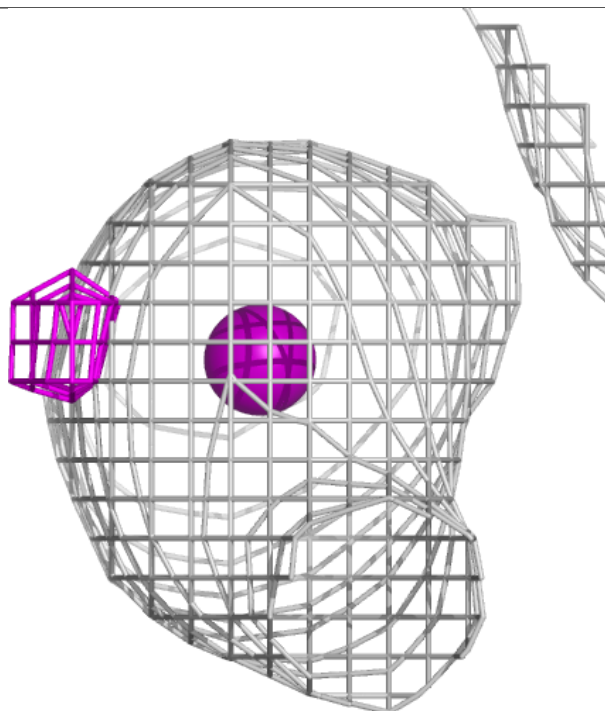
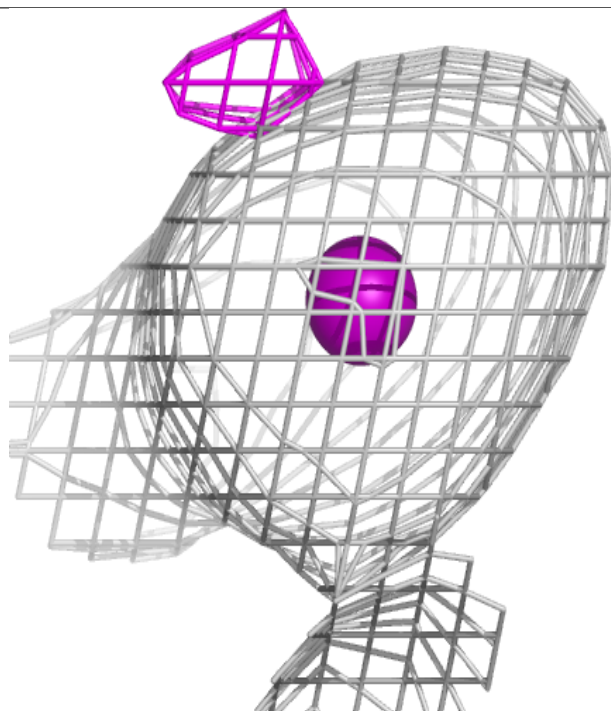
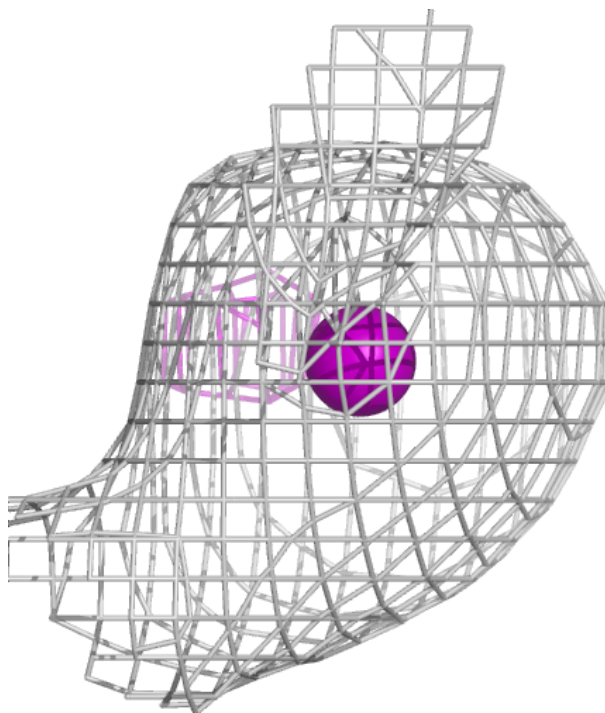
Electron density around IOD A 610:

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



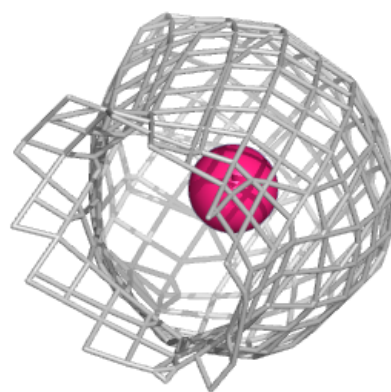
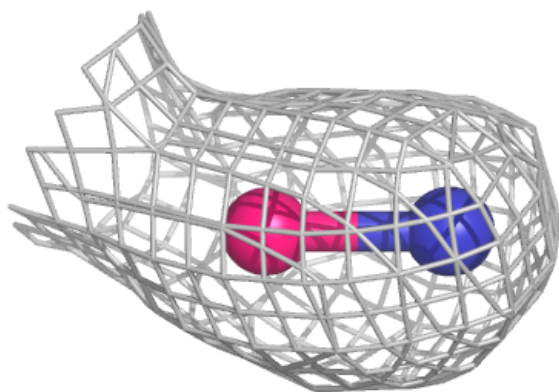
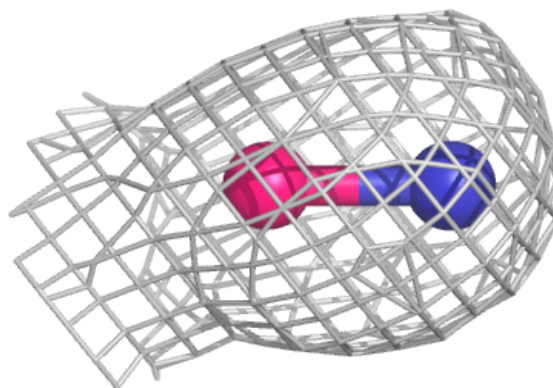
Electron density around IOD A 607:

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

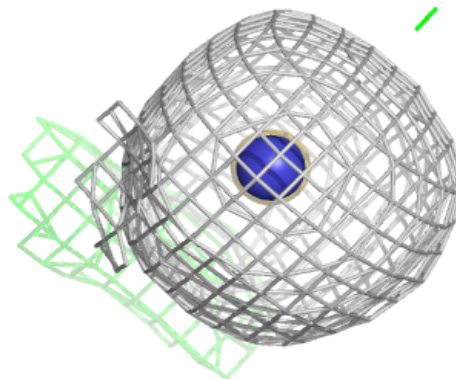
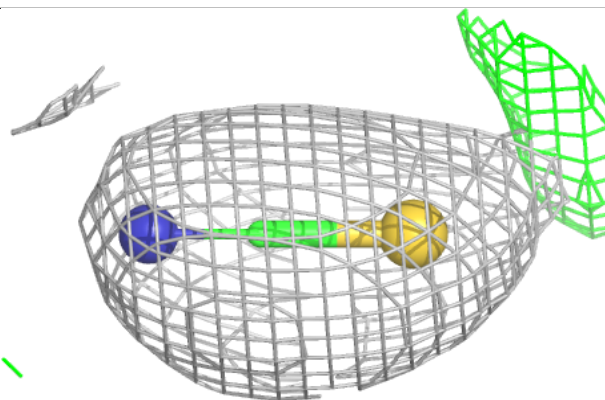
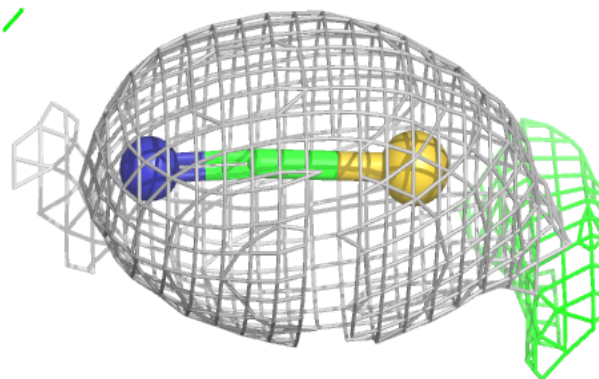


Electron density around NO A 636:

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

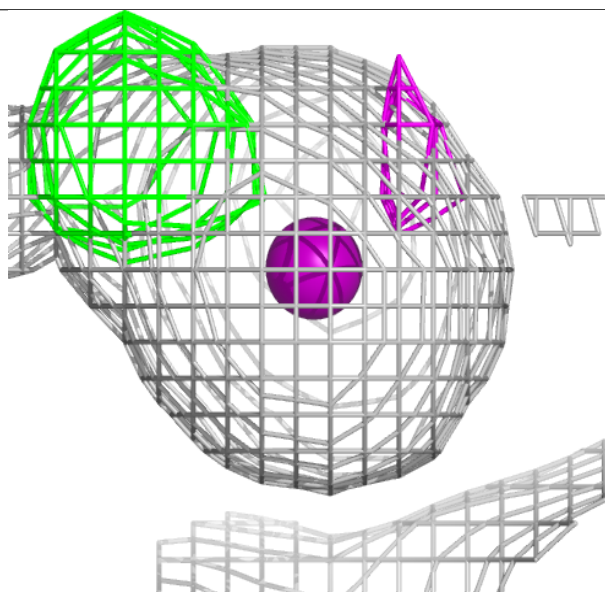
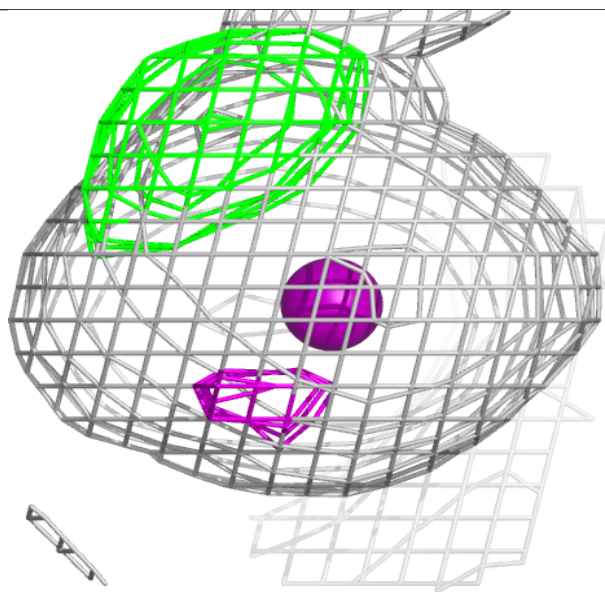
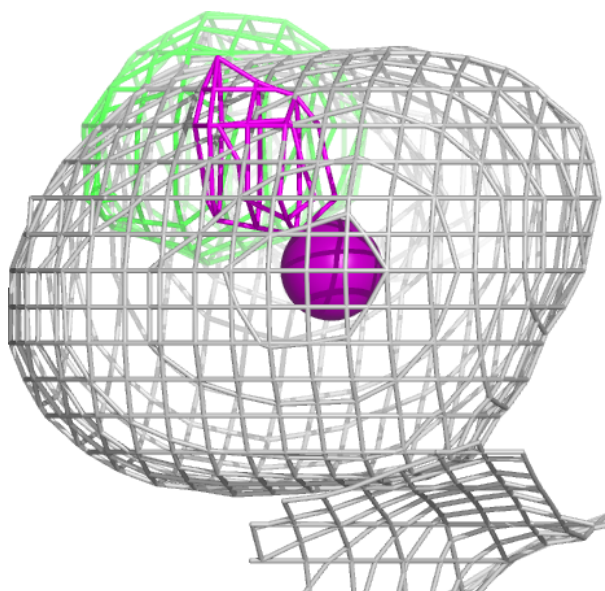
**Electron density around SCN A 616:**

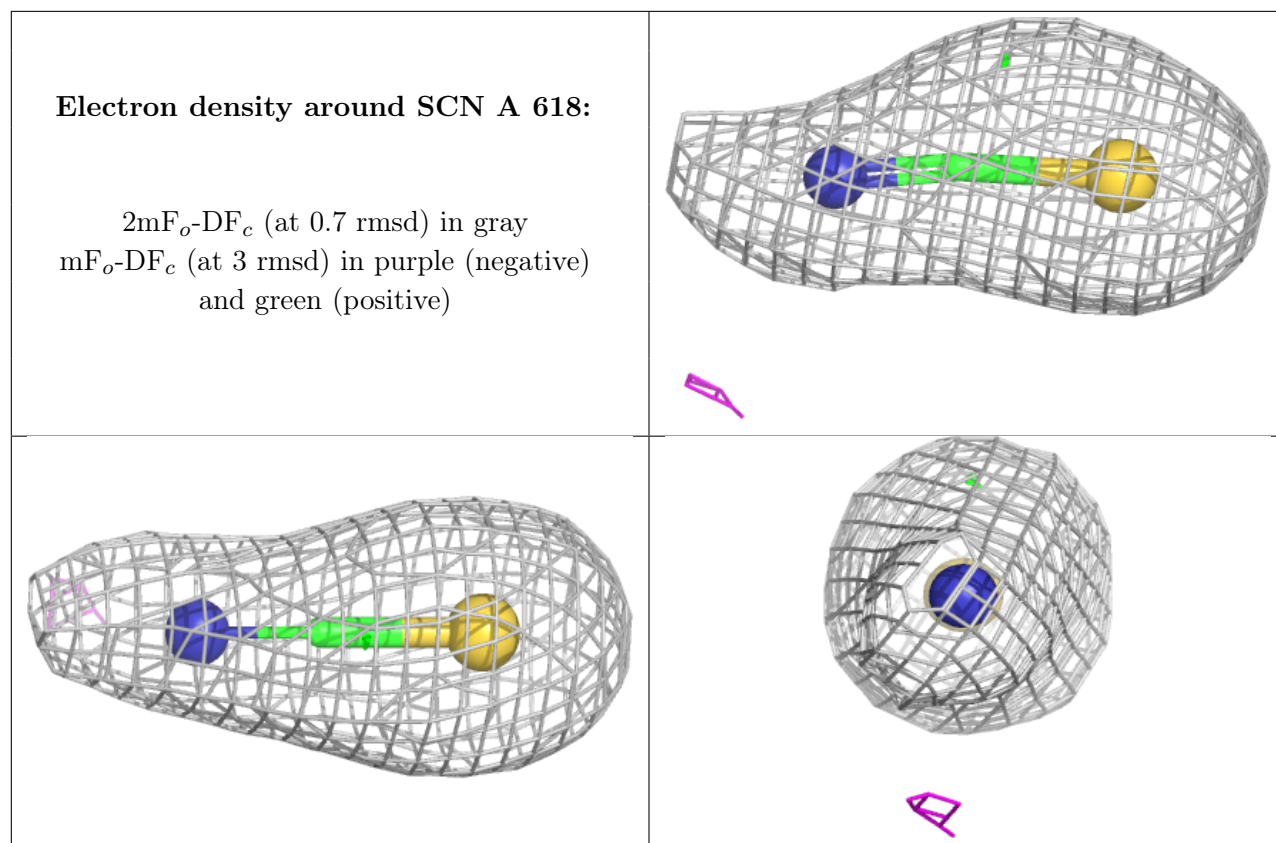
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around IOD A 648:

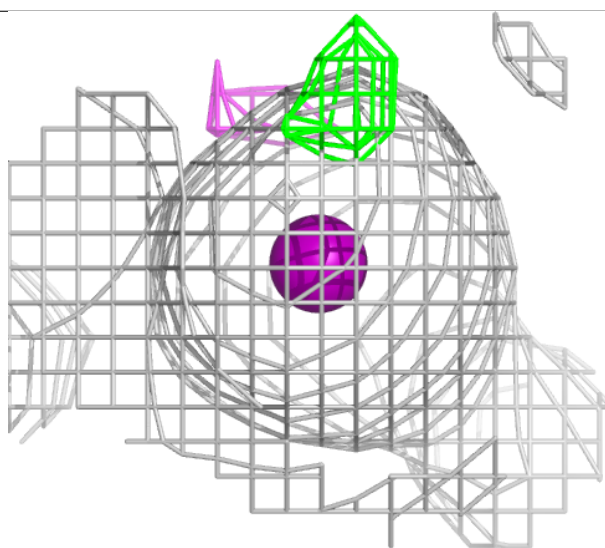
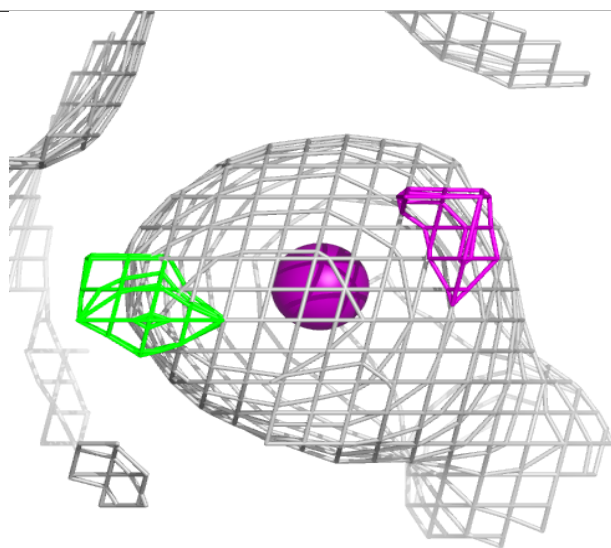
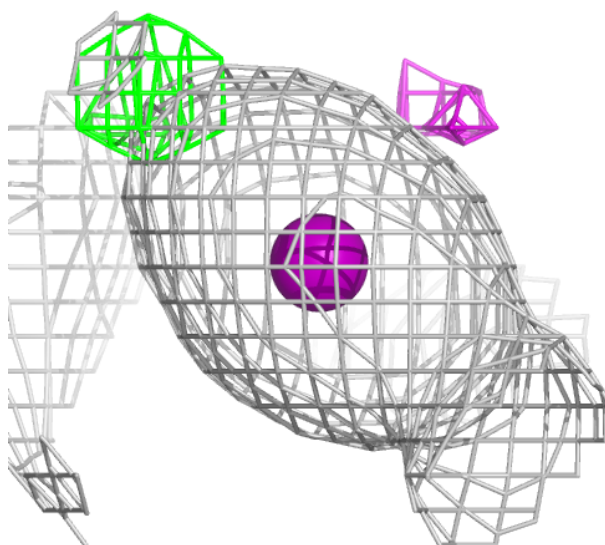
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





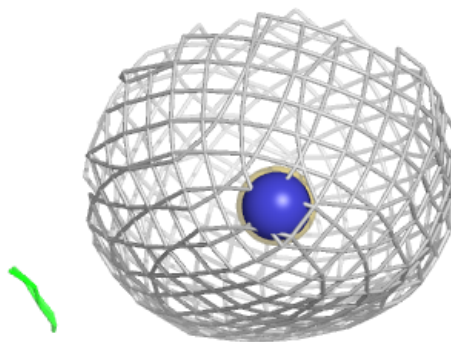
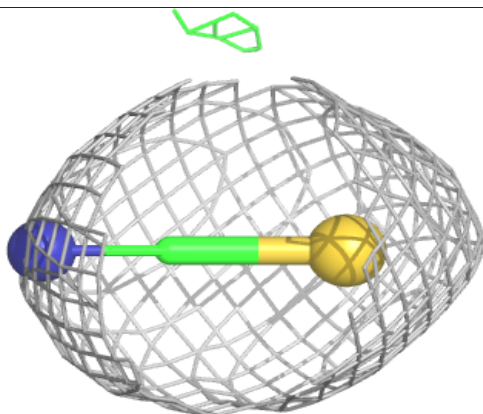
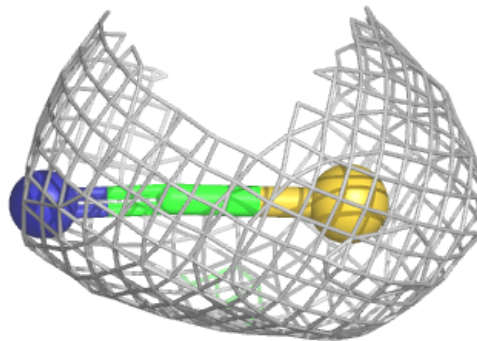
Electron density around IOD A 614:

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



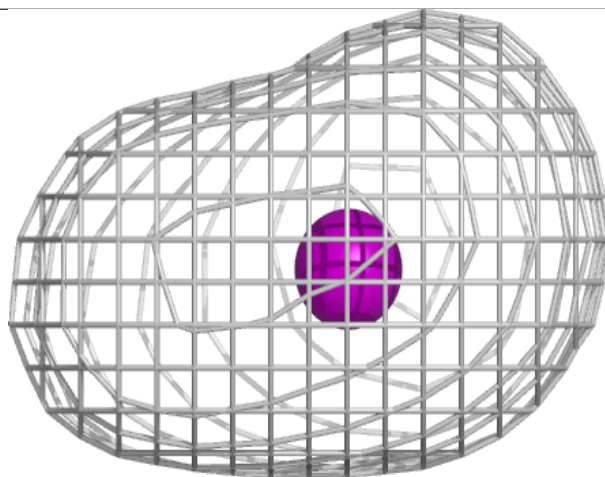
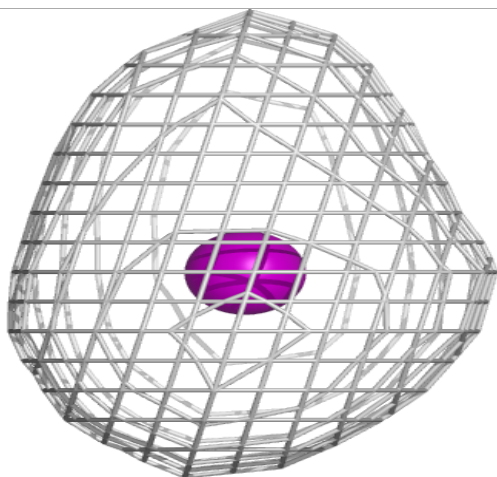
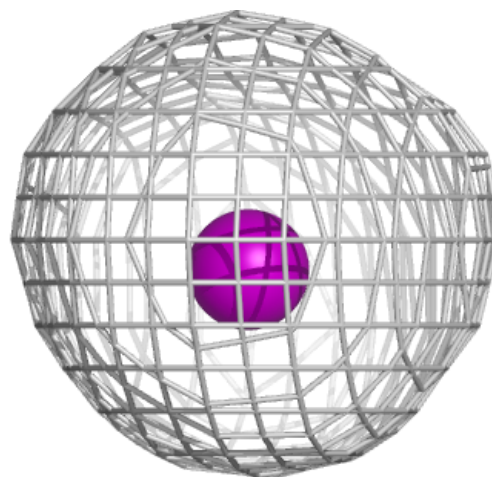
Electron density around SCN A 620:

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



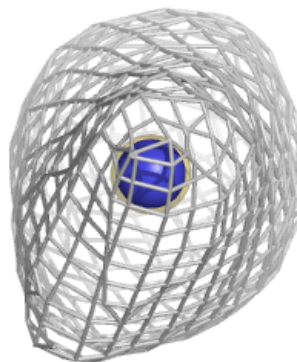
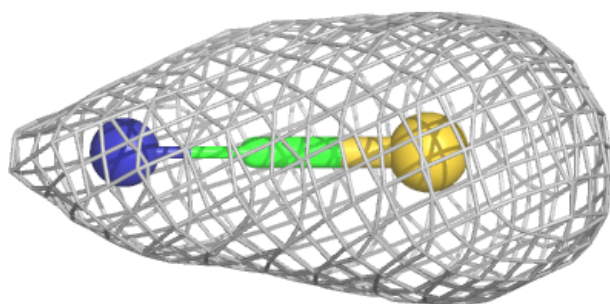
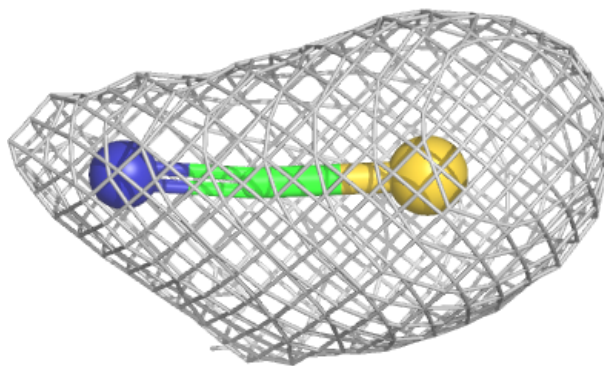
Electron density around IOD A 606:

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



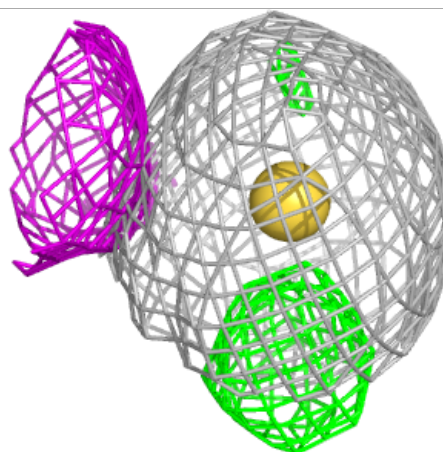
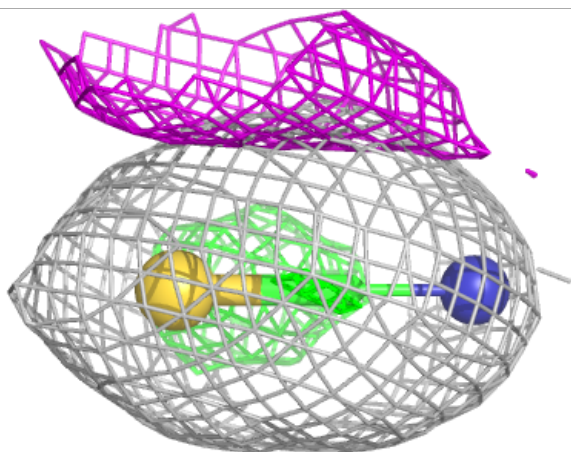
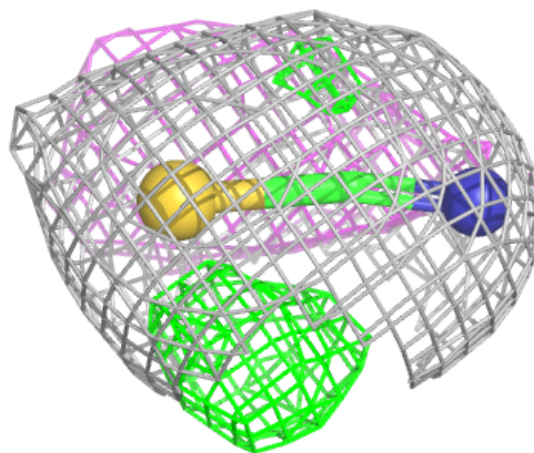
Electron density around SCN A 624:

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



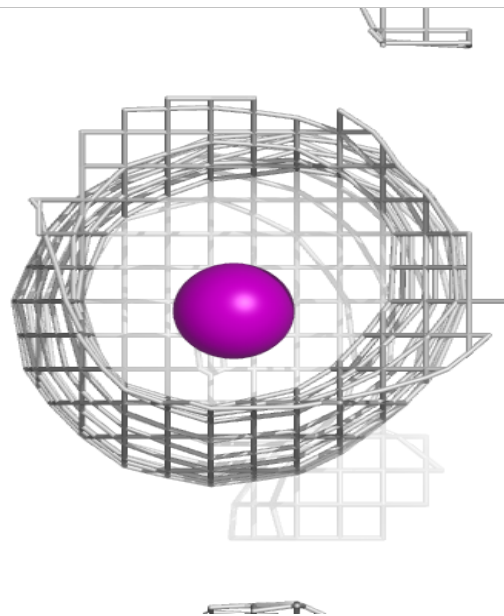
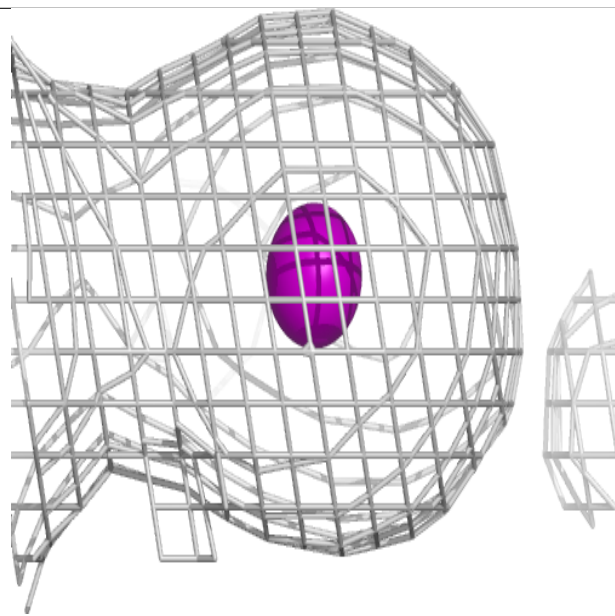
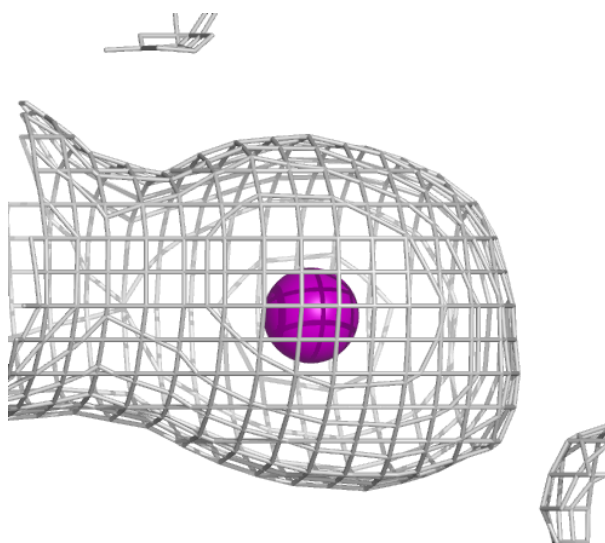
Electron density around SCN A 631:

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



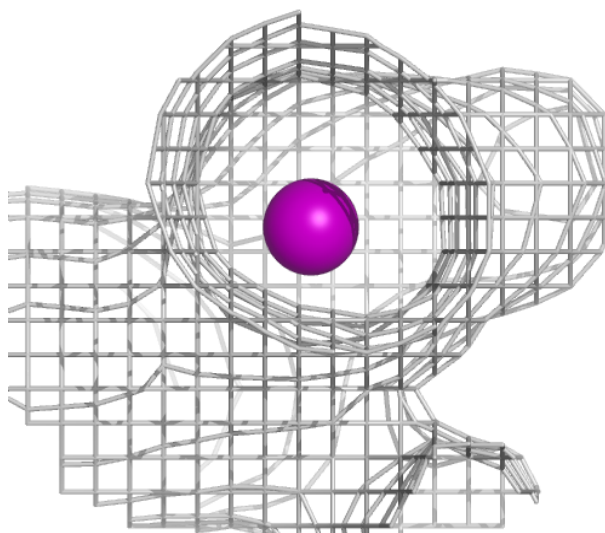
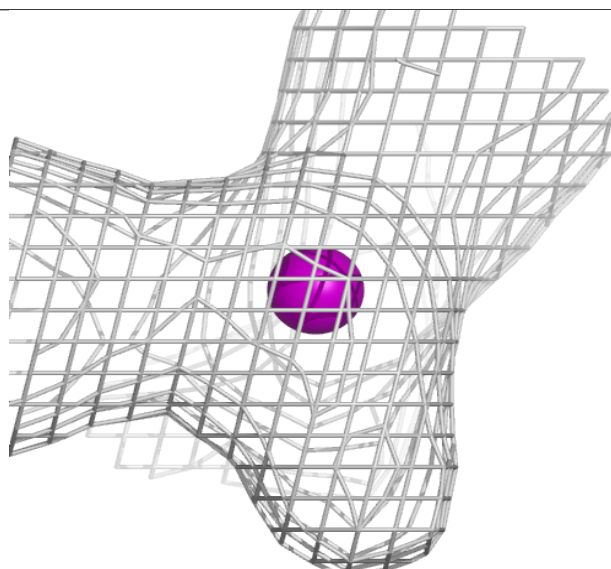
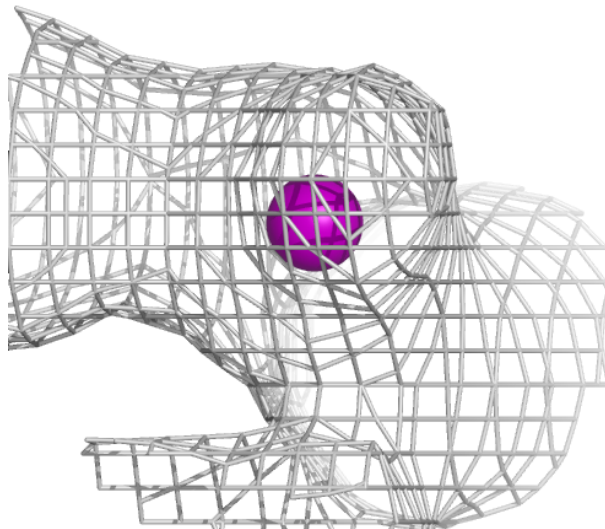
Electron density around IOD A 642:

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



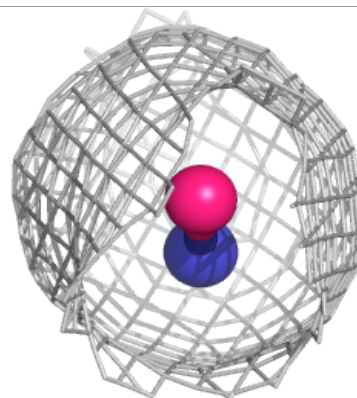
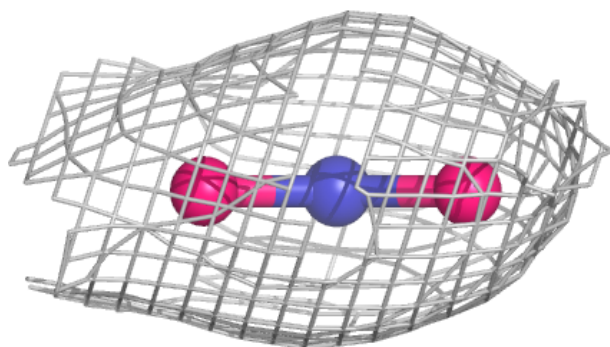
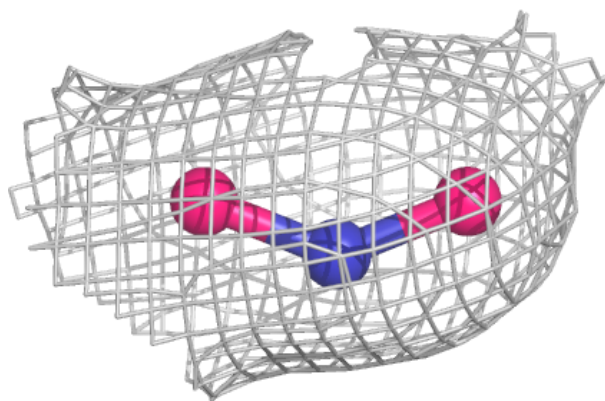
Electron density around IOD A 647:

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

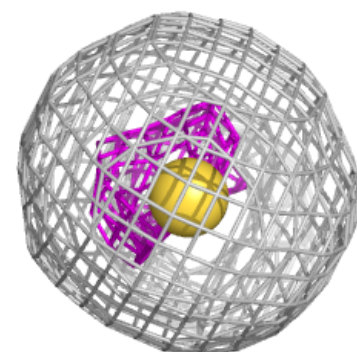
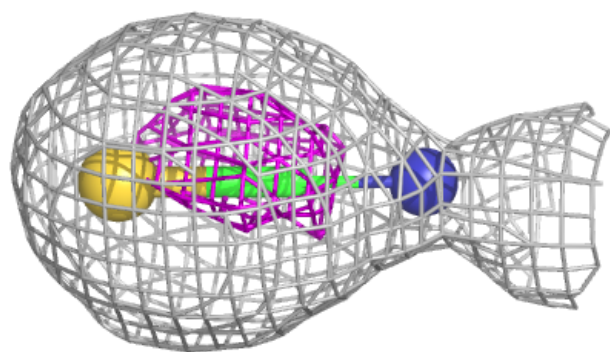
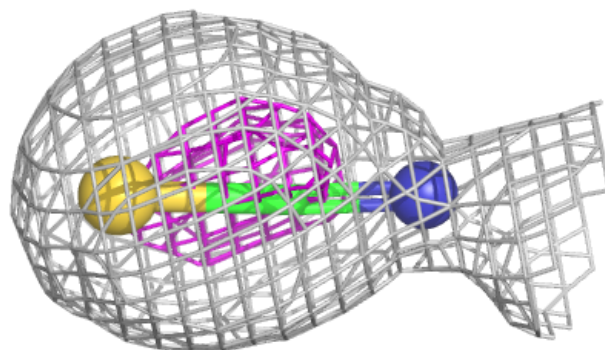


Electron density around NO2 A 634:

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

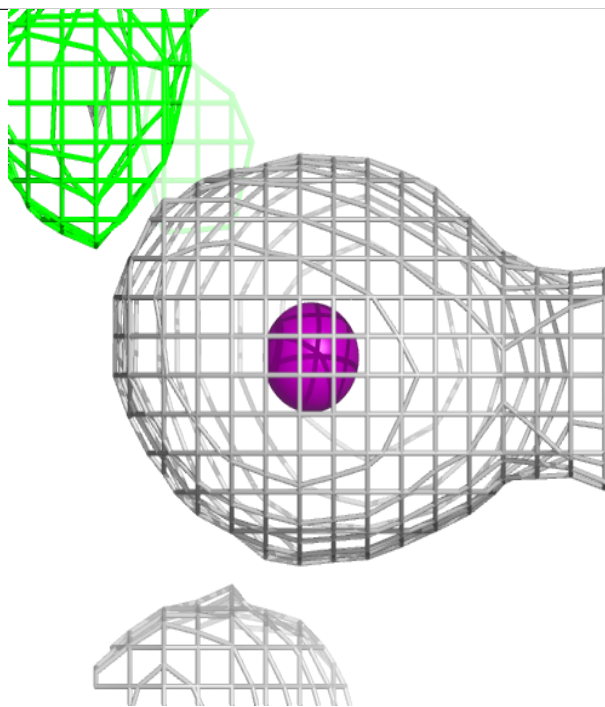
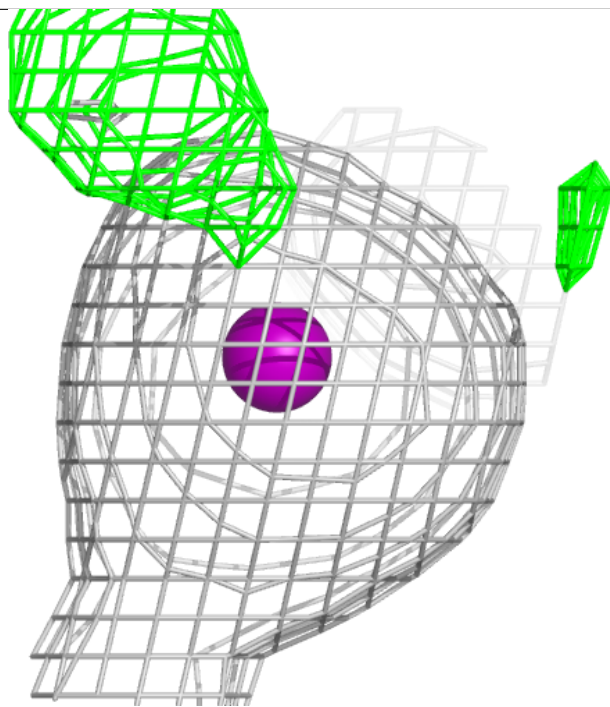
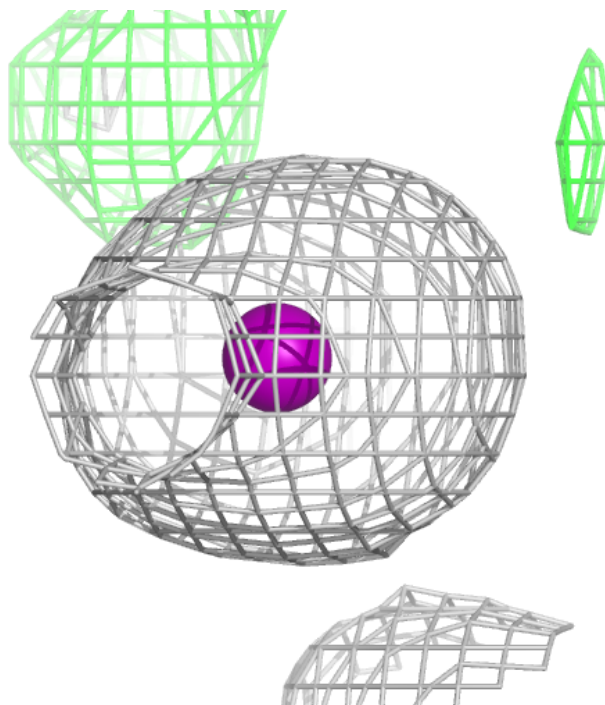
**Electron density around SCN A 621:**

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



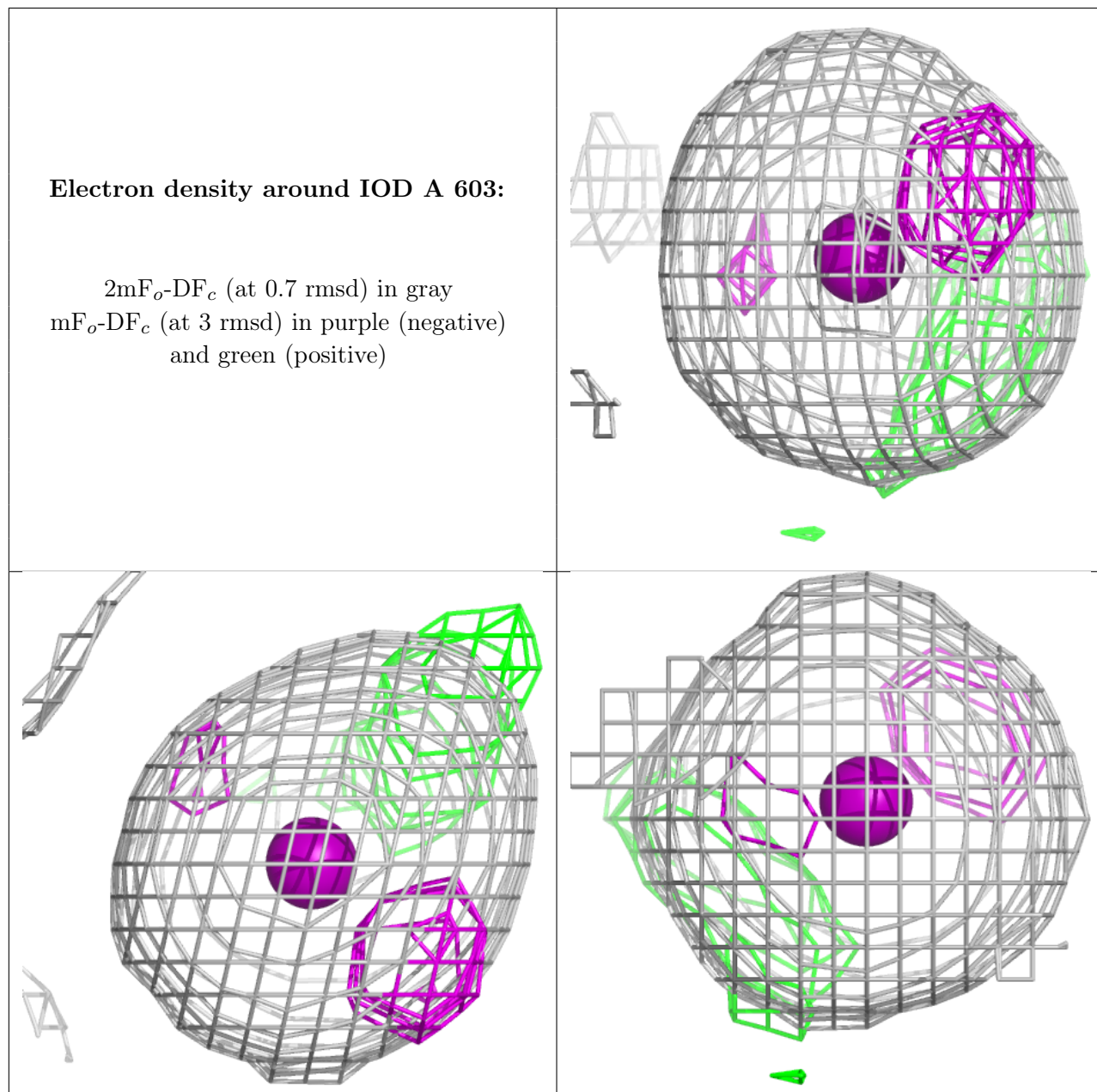
Electron density around IOD A 608:

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



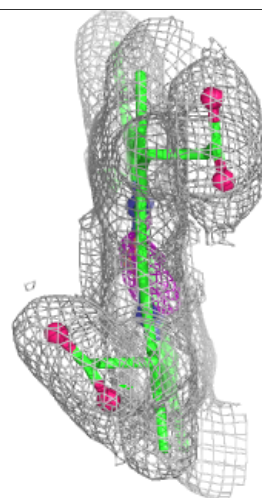
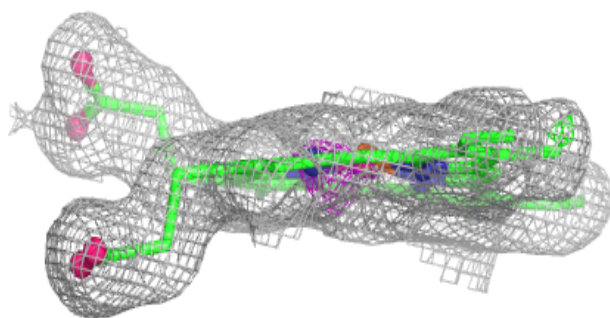
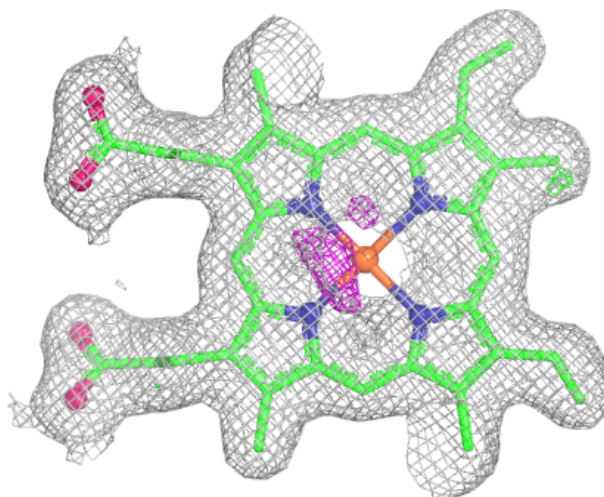
Electron density around IOD A 603:

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



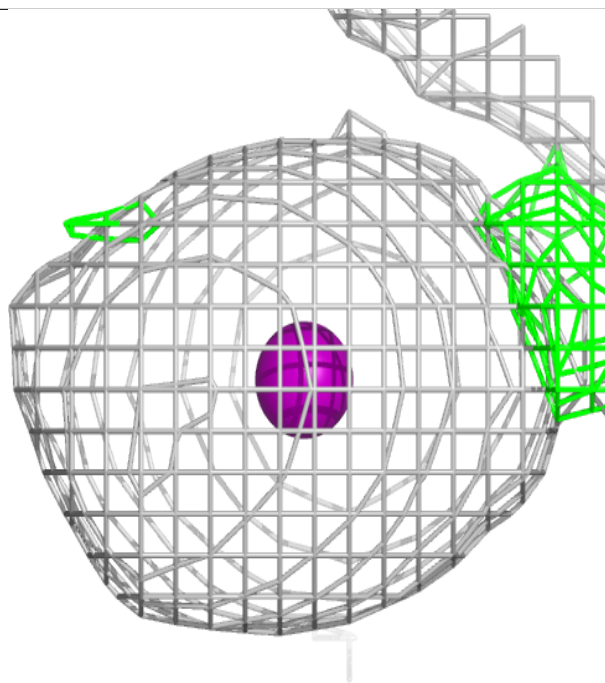
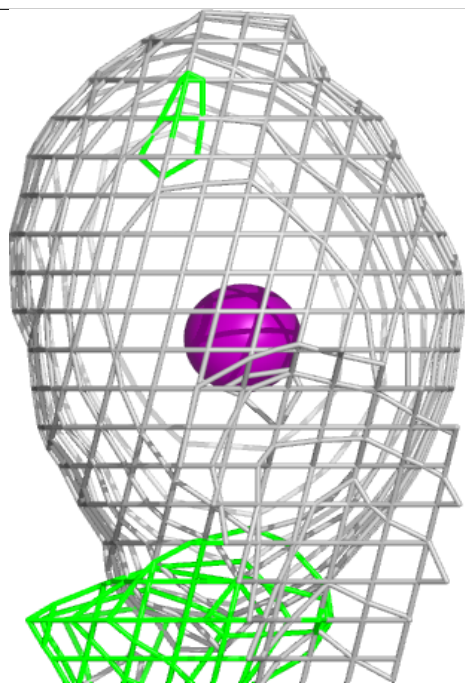
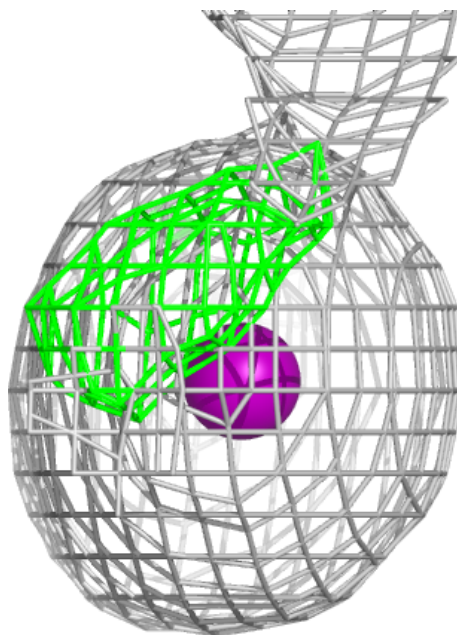
Electron density around HEM A 639:

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



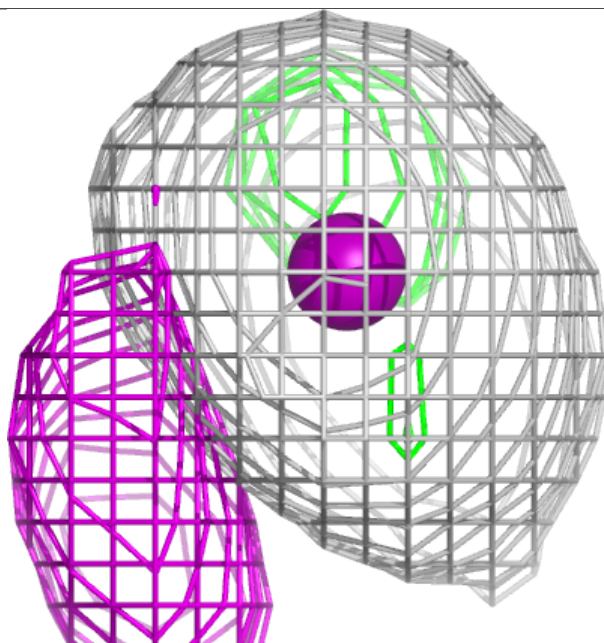
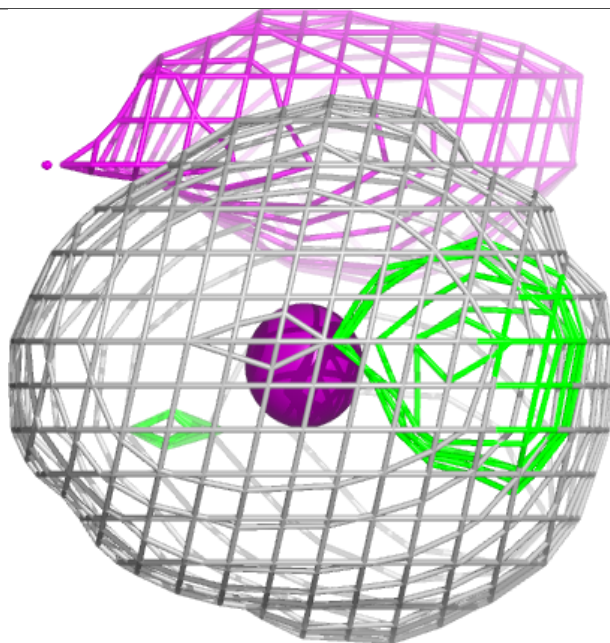
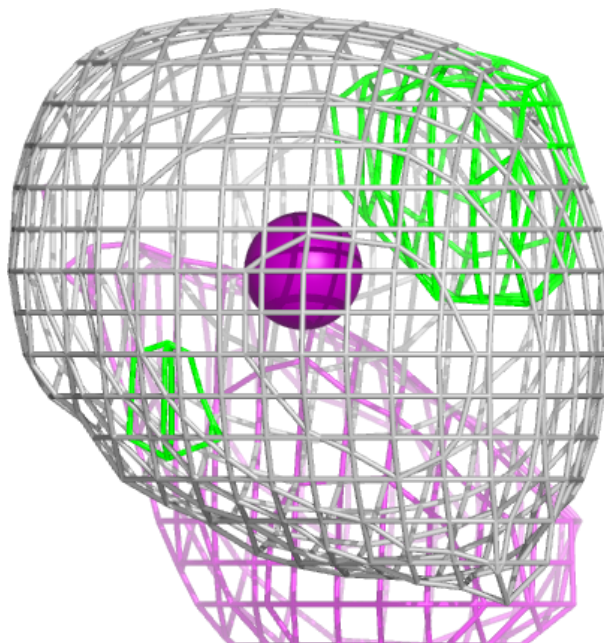
Electron density around IOD A 612:

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



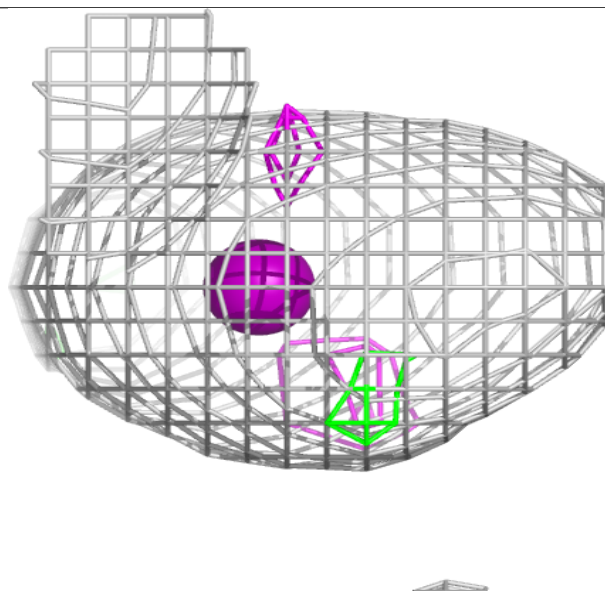
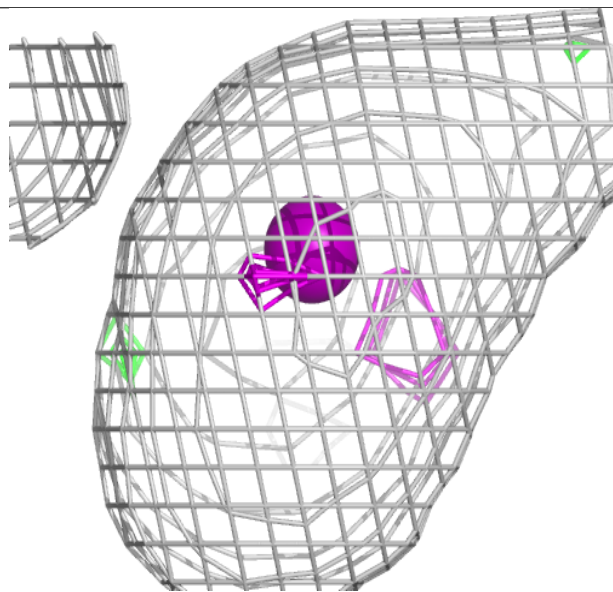
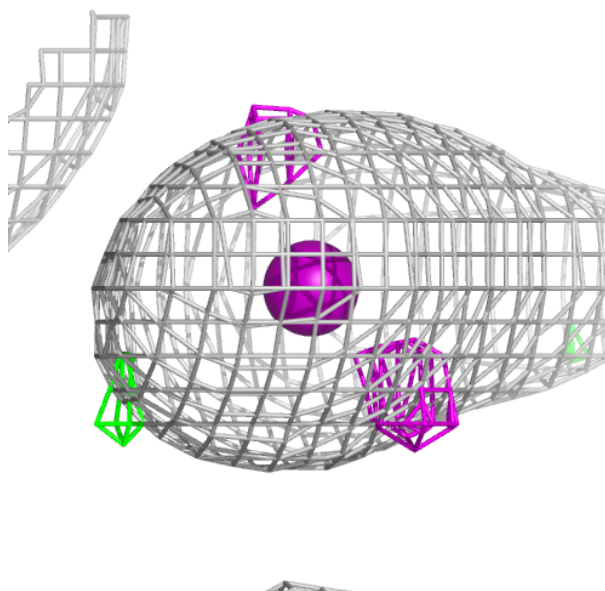
Electron density around IOD A 605:

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



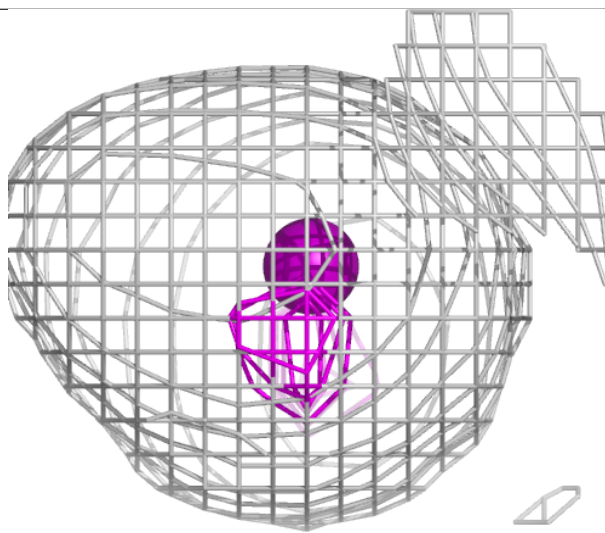
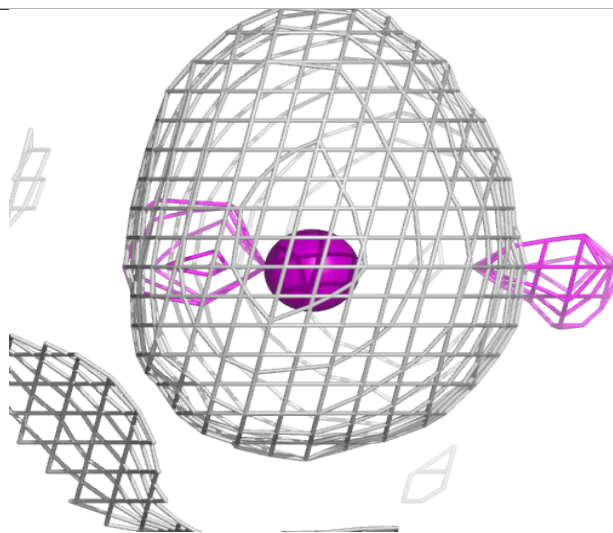
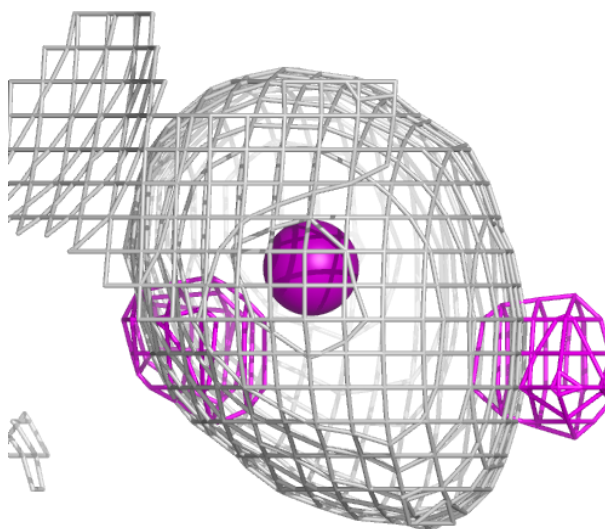
Electron density around IOD A 646:

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



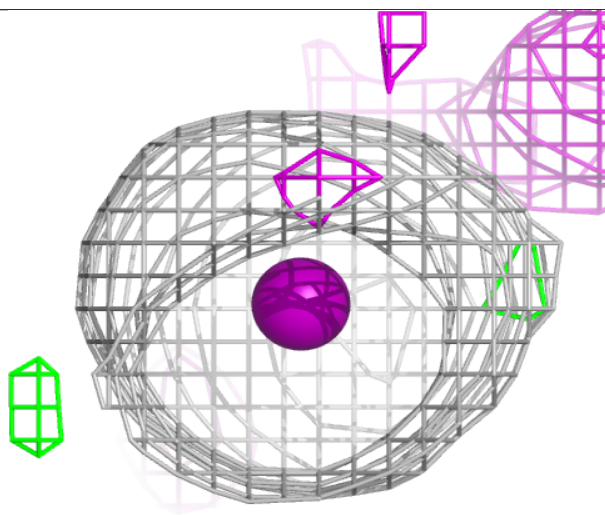
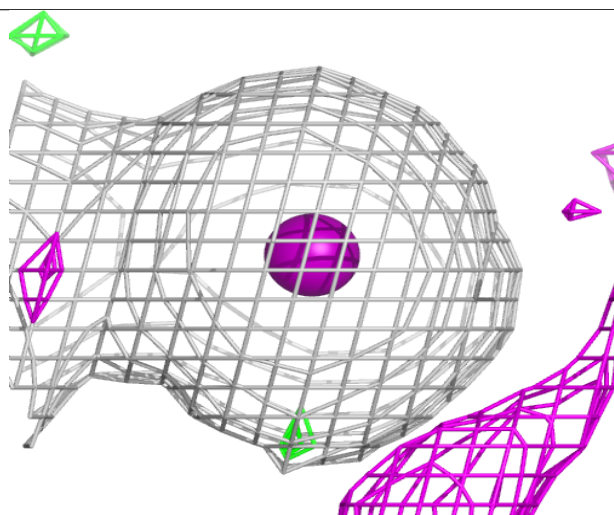
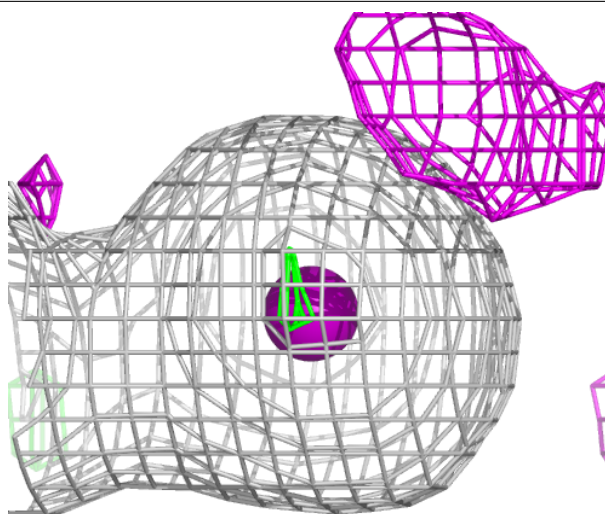
Electron density around IOD A 604:

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



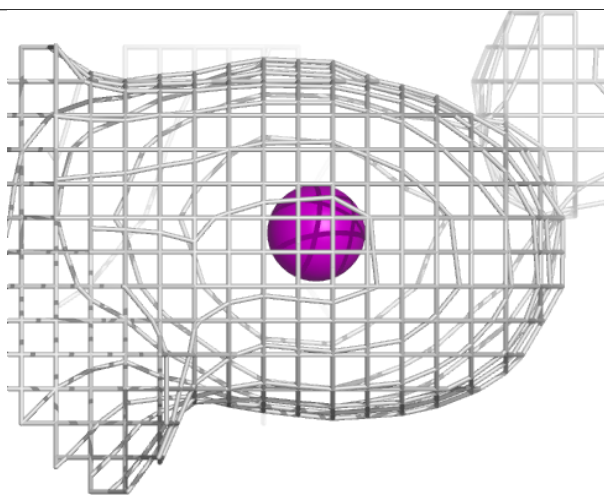
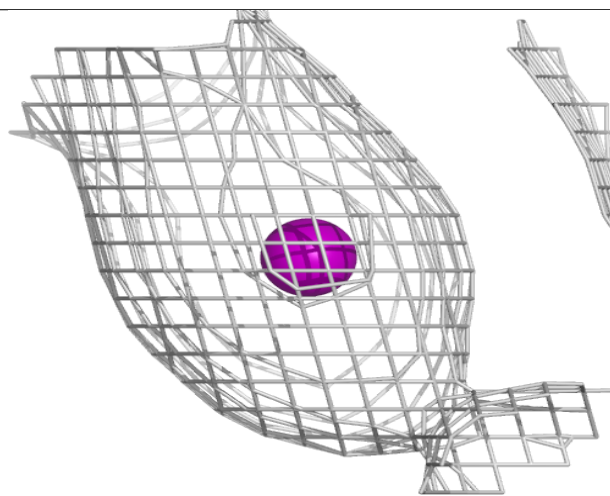
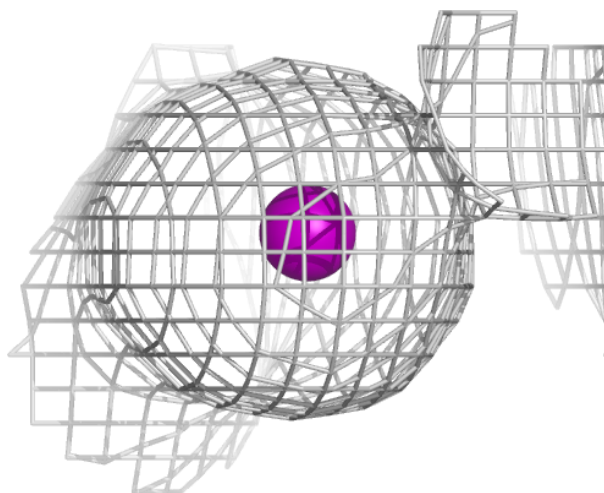
Electron density around IOD A 611:

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



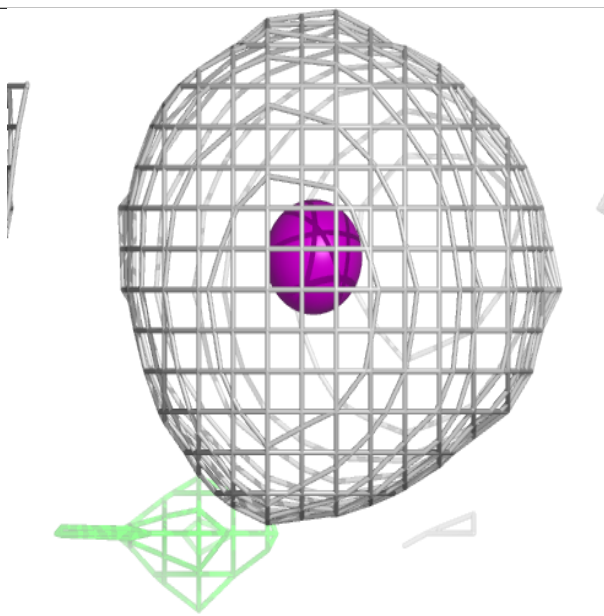
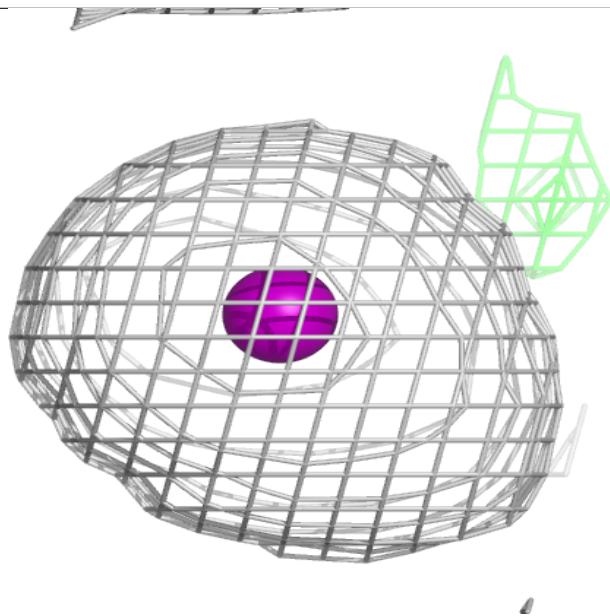
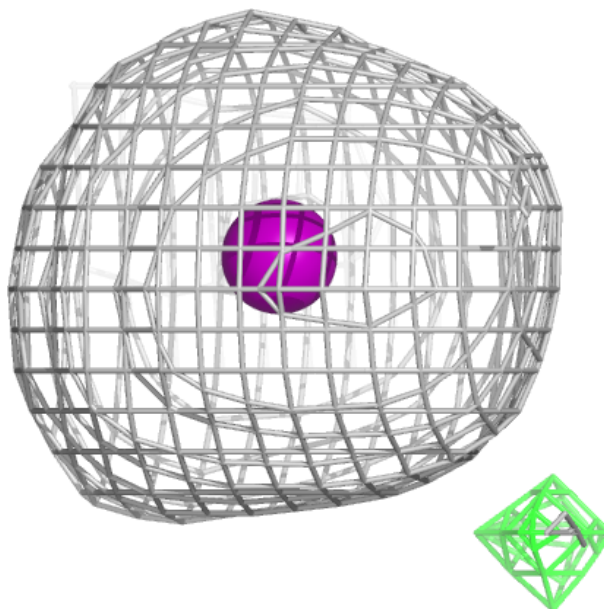
Electron density around IOD A 641:

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



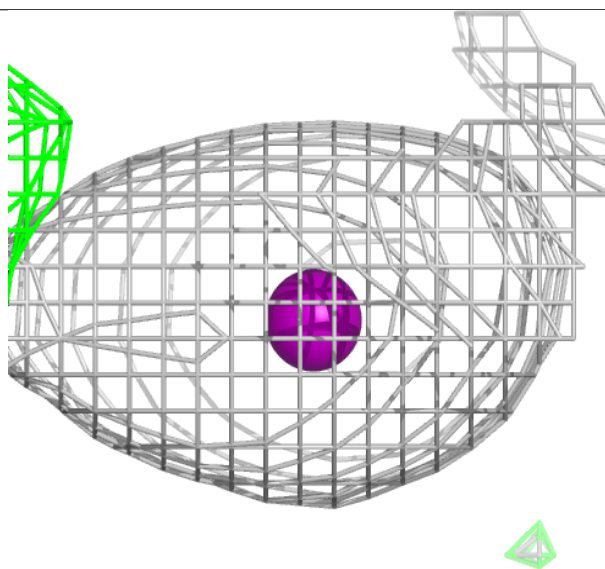
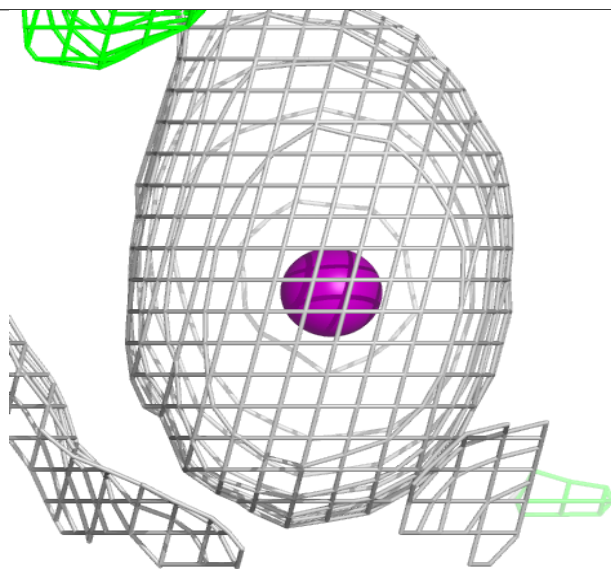
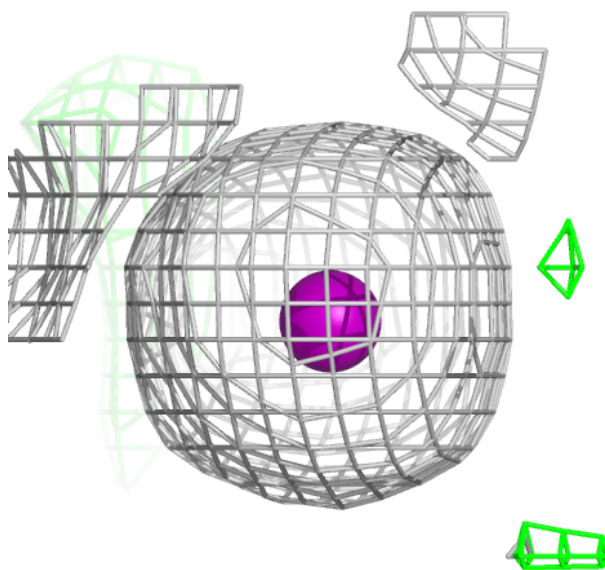
Electron density around IOD A 613:

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



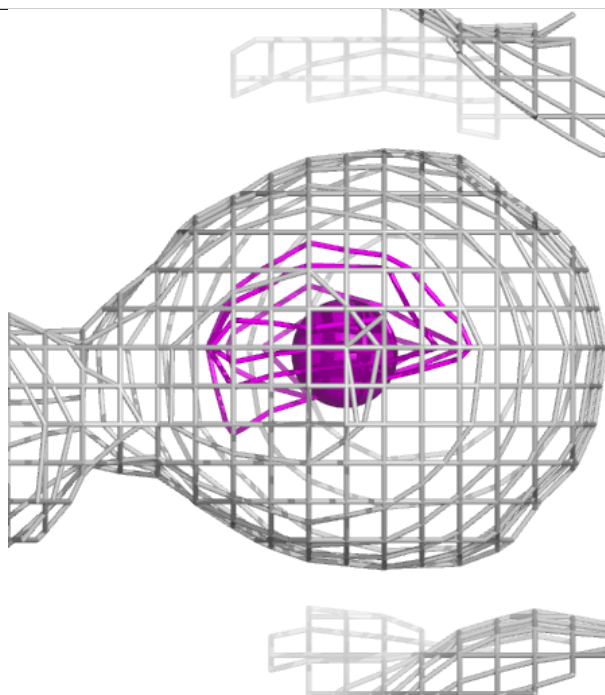
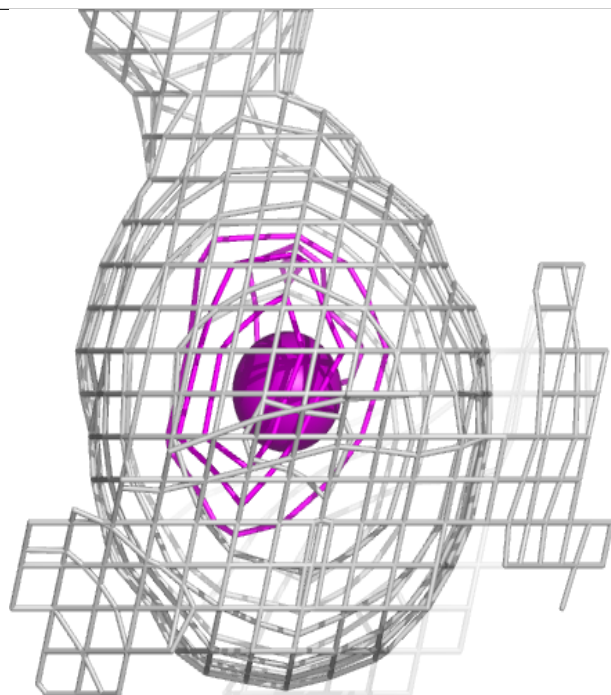
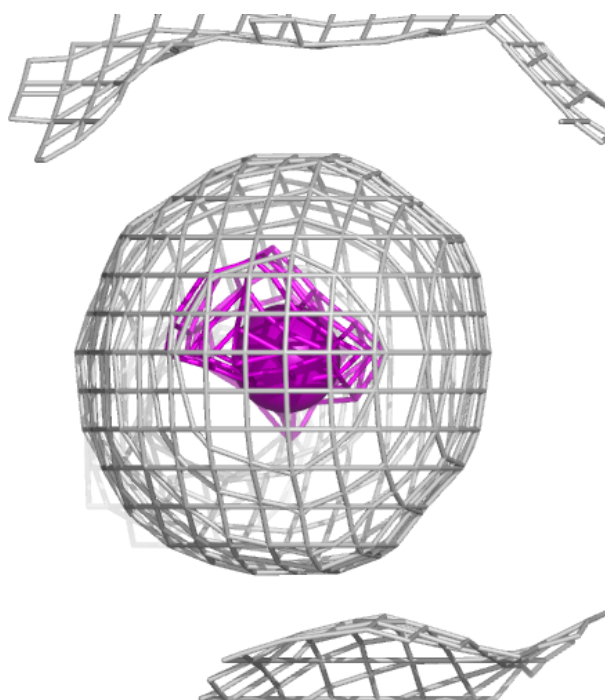
Electron density around IOD A 649:

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



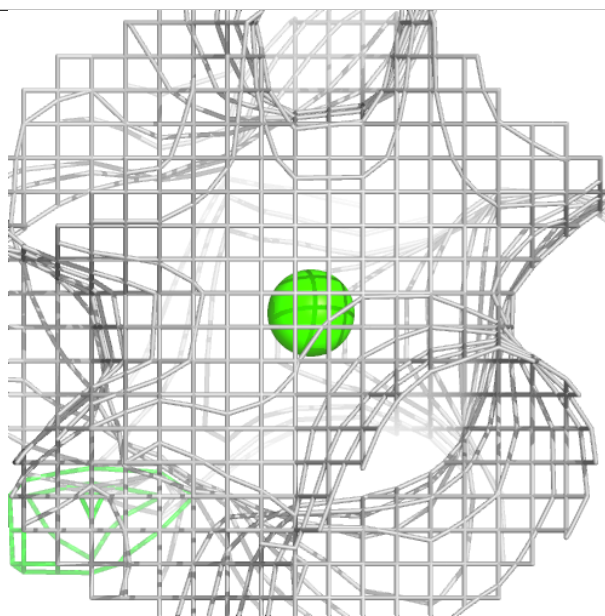
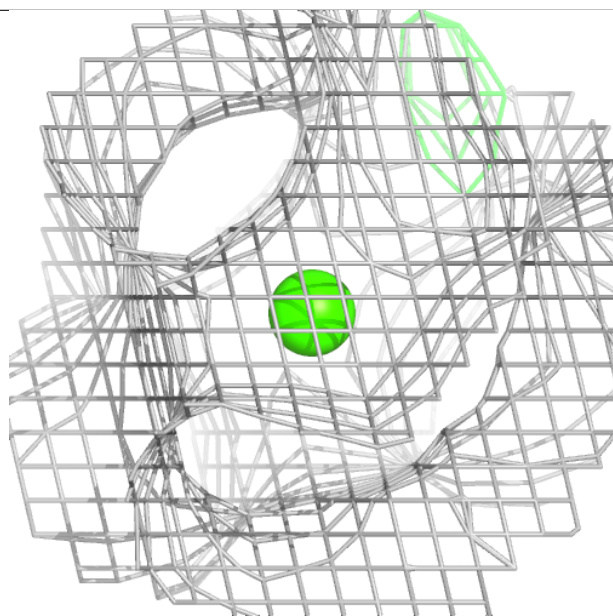
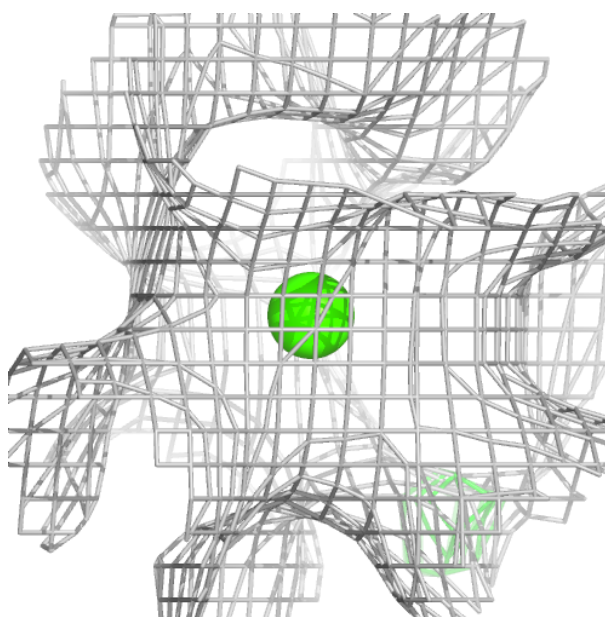
Electron density around IOD A 602:

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



Electron density around CA A 640:

$2mF_o-DF_c$ (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.