WORLDWIDE PDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 11, 2022 – 09:12 pm GMT

PDB ID	:	7PU0
Title	:	Crystal Structure of Two-Domain Laccase mutant H165A/M199G from Streptomyces griseoflavus
Authors	:	Gabdulkhakov, A.; Tishchenko, S.; Kolyadenko, I.
Deposited on	:	2021-09-28
Resolution	:	2.20 Å(reported)

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

|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.24
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.24

1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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.
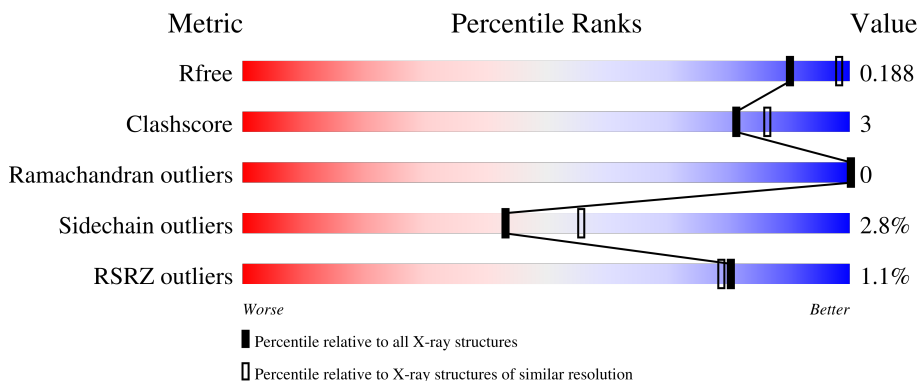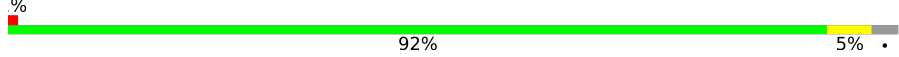

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 <=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	283	
1	B	283	
1	C	283	
1	D	283	
1	E	283	

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Mol	Chain	Length	Quality of chain
1	F	283	

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 13327 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 Two-domain laccase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	280	Total	C	N	O	S	0	2	0
			2157	1342	392	412	11			
1	B	278	Total	C	N	O	S	0	1	0
			2132	1328	391	402	11			
1	C	275	Total	C	N	O	S	0	0	0
			2101	1310	384	396	11			
1	D	278	Total	C	N	O	S	0	2	0
			2139	1332	390	406	11			
1	E	278	Total	C	N	O	S	0	1	0
			2128	1327	388	402	11			
1	F	275	Total	C	N	O	S	0	0	0
			2101	1310	384	396	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	165	ALA	HIS	engineered mutation	UNP A0A0M4FJ81
A	199	GLY	MET	engineered mutation	UNP A0A0M4FJ81
B	165	ALA	HIS	engineered mutation	UNP A0A0M4FJ81
B	199	GLY	MET	engineered mutation	UNP A0A0M4FJ81
C	165	ALA	HIS	engineered mutation	UNP A0A0M4FJ81
C	199	GLY	MET	engineered mutation	UNP A0A0M4FJ81
D	165	ALA	HIS	engineered mutation	UNP A0A0M4FJ81
D	199	GLY	MET	engineered mutation	UNP A0A0M4FJ81
E	165	ALA	HIS	engineered mutation	UNP A0A0M4FJ81
E	199	GLY	MET	engineered mutation	UNP A0A0M4FJ81
F	165	ALA	HIS	engineered mutation	UNP A0A0M4FJ81
F	199	GLY	MET	engineered mutation	UNP A0A0M4FJ81

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total 5	Cu 5	0	0
2	B	3	Total 3	Cu 3	0	0
2	C	4	Total 4	Cu 4	0	0
2	D	4	Total 4	Cu 4	0	0
2	E	4	Total 4	Cu 4	0	0
2	F	4	Total 4	Cu 4	0	0
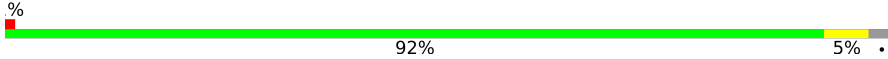
- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	90	Total 90	O 90	0	0
4	B	94	Total 94	O 94	0	0
4	C	93	Total 93	O 93	0	0
4	D	98	Total 98	O 98	0	0
4	E	83	Total 83	O 83	0	0
4	F	85	Total 85	O 85	0	0

3 Residue-property plots ⓘ

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: Two-domain laccase

Chain A:

- Molecule 1: Two-domain laccase

Chain B:

- Molecule 1: Two-domain laccase

Chain C:

- Molecule 1: Two-domain laccase

Chain D:

- Molecule 1: Two-domain laccase

Chain E:

• Molecule 1: Two-domain laccase

Chain F:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	76.23Å 94.59Å 120.87Å 90.00° 91.39° 90.00°	Depositor
Resolution (Å)	24.74 – 2.20 24.74 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.1 (24.74-2.20) 98.1 (24.74-2.20)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.63 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.8.0230, PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.157 , 0.189 0.160 , 0.188	Depositor DCC
R_{free} test set	3332 reflections (3.90%)	wwPDB-VP
Wilson B-factor (Å^2)	22.2	Xtriage
Anisotropy	0.200	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< |L| > = 0.52, < L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.017 for h,-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	13327	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, CU

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	0.38	0/2218	0.63	0/3014
1	B	0.39	0/2193	0.64	0/2979
1	C	0.38	0/2161	0.64	0/2935
1	D	0.38	0/2200	0.64	0/2990
1	E	0.36	0/2189	0.63	0/2975
1	F	0.38	0/2161	0.63	0/2935
All	All	0.38	0/13122	0.63	0/17828

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2157	0	2018	11	0
1	B	2132	0	2005	12	0
1	C	2101	0	1977	12	0
1	D	2139	0	2006	15	0
1	E	2128	0	2001	13	0
1	F	2101	0	1977	7	0
2	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	3	0	0	0	0
2	C	4	0	0	0	0
2	D	4	0	0	0	0
2	E	4	0	0	0	0
2	F	4	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	90	0	0	1	0
4	B	94	0	0	0	0
4	C	93	0	0	1	0
4	D	98	0	0	0	0
4	E	83	0	0	2	0
4	F	85	0	0	1	0
All	All	13327	0	11984	65	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 3.

The worst 5 of 65 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:294:HIS:HA	1:A:297:MET:HE2	1.72	0.71
1:A:45:ALA:HB2	1:A:183:LYS:HD2	1.72	0.71
1:C:50:ARG:NH1	1:C:86:ASP:OD2	2.27	0.68
1:E:124:GLU:HG3	1:E:125:PRO:HD2	1.76	0.67
1:D:289:CYS:HB2	1:D:299:MET:HE2	1.76	0.67

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	280/283 (99%)	272 (97%)	8 (3%)	0	100	100
1	B	277/283 (98%)	271 (98%)	6 (2%)	0	100	100
1	C	273/283 (96%)	268 (98%)	5 (2%)	0	100	100
1	D	278/283 (98%)	274 (99%)	4 (1%)	0	100	100
1	E	277/283 (98%)	274 (99%)	3 (1%)	0	100	100
1	F	273/283 (96%)	269 (98%)	4 (2%)	0	100	100
All	All	1658/1698 (98%)	1628 (98%)	30 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	221/221 (100%)	210 (95%)	11 (5%)	24	30
1	B	218/221 (99%)	210 (96%)	8 (4%)	34	43
1	C	215/221 (97%)	210 (98%)	5 (2%)	50	63
1	D	219/221 (99%)	215 (98%)	4 (2%)	59	72
1	E	218/221 (99%)	213 (98%)	5 (2%)	50	63
1	F	215/221 (97%)	211 (98%)	4 (2%)	57	71
All	All	1306/1326 (98%)	1269 (97%)	37 (3%)	43	56

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	51	ARG
1	F	240	ARG
1	E	121	SER
1	E	297	MET
1	B	118	GLN

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 26 ligands modelled in this entry, 26 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 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(Å²)	Q<0.9
1	A	280/283 (98%)	-0.68	3 (1%)	80	79	14, 22, 40, 70	3 (1%)
1	B	278/283 (98%)	-0.73	5 (1%)	68	66	13, 20, 41, 90	4 (1%)
1	C	275/283 (97%)	-0.74	1 (0%)	92	91	14, 22, 38, 48	2 (0%)
1	D	278/283 (98%)	-0.72	5 (1%)	68	66	14, 22, 43, 113	2 (0%)
1	E	278/283 (98%)	-0.55	2 (0%)	87	86	14, 25, 46, 69	3 (1%)
1	F	275/283 (97%)	-0.64	2 (0%)	87	86	15, 25, 42, 55	4 (1%)
All	All	1664/1698 (97%)	-0.68	18 (1%)	80	79	13, 23, 41, 113	18 (1%)

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	40	ALA	8.0
1	D	40	ALA	5.5
1	E	40	ALA	5.4
1	D	316	ASP	4.8
1	A	318	GLN	4.5

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

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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(Å^2)	Q<0.9
2	CU	D	403	1/1	0.86	0.43	139,139,139,139	1
2	CU	C	404	1/1	0.93	0.38	62,62,62,62	1
2	CU	A	403	1/1	0.93	0.50	117,117,117,117	1
2	CU	A	405	1/1	0.94	0.52	147,147,147,147	1
2	CU	F	404	1/1	0.94	0.40	76,76,76,76	1
2	CU	E	403	1/1	0.95	0.40	121,121,121,121	1
3	NA	D	405	1/1	0.95	0.24	46,46,46,46	0
3	NA	C	405	1/1	0.96	0.33	41,41,41,41	0
2	CU	B	403	1/1	0.97	0.11	29,29,29,29	1
2	CU	E	402	1/1	0.98	0.07	31,31,31,31	1
2	CU	A	404	1/1	0.98	0.06	33,33,33,33	1
2	CU	E	404	1/1	0.98	0.09	32,32,32,32	1
2	CU	B	402	1/1	0.99	0.03	31,31,31,31	1
2	CU	D	402	1/1	0.99	0.05	35,35,35,35	1
2	CU	F	401	1/1	0.99	0.07	28,28,28,28	1
2	CU	F	403	1/1	0.99	0.05	32,32,32,32	1
2	CU	A	402	1/1	0.99	0.09	35,35,35,35	1
2	CU	D	404	1/1	0.99	0.12	27,27,27,27	1
2	CU	C	401	1/1	0.99	0.07	32,32,32,32	1
2	CU	A	401	1/1	1.00	0.04	18,18,18,18	1
2	CU	C	402	1/1	1.00	0.03	17,17,17,17	0
2	CU	F	402	1/1	1.00	0.03	22,22,22,22	1
2	CU	C	403	1/1	1.00	0.05	27,27,27,27	1
2	CU	E	401	1/1	1.00	0.04	21,21,21,21	0
2	CU	B	401	1/1	1.00	0.02	18,18,18,18	1
2	CU	D	401	1/1	1.00	0.03	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 CU D 403:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
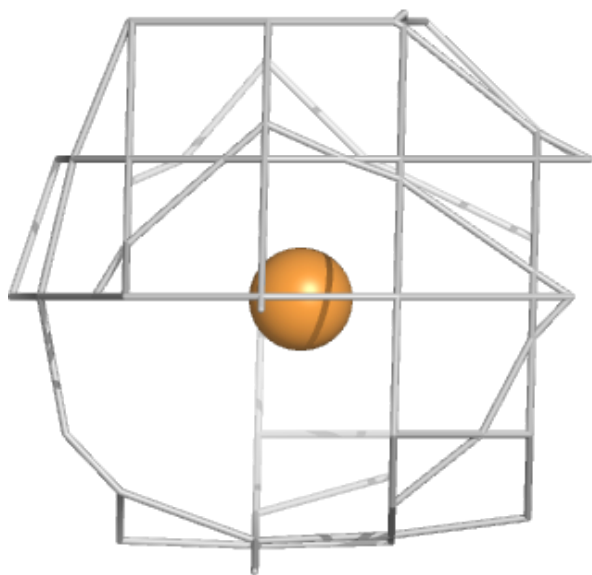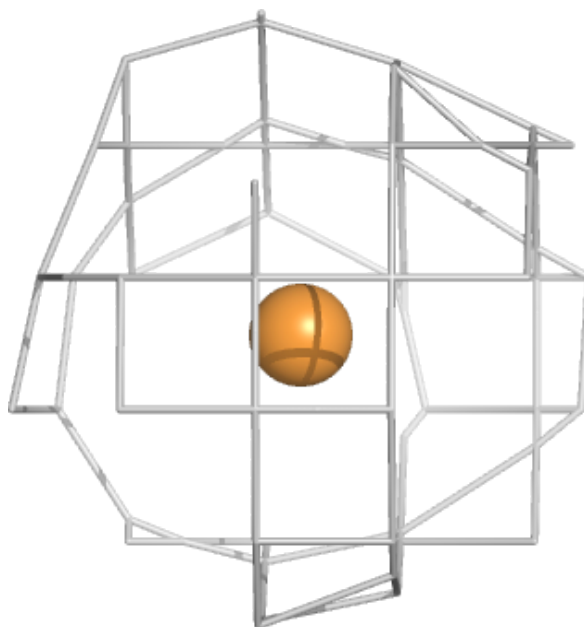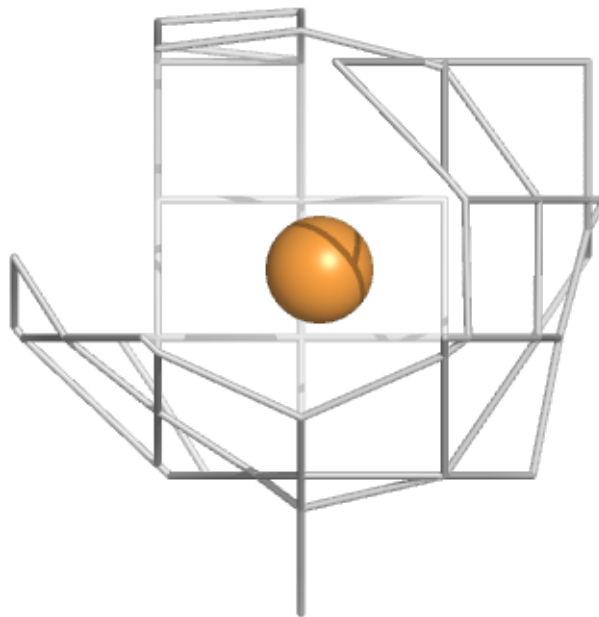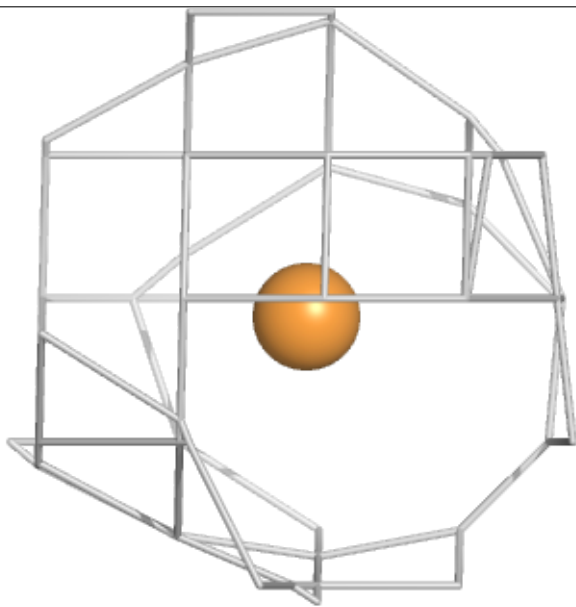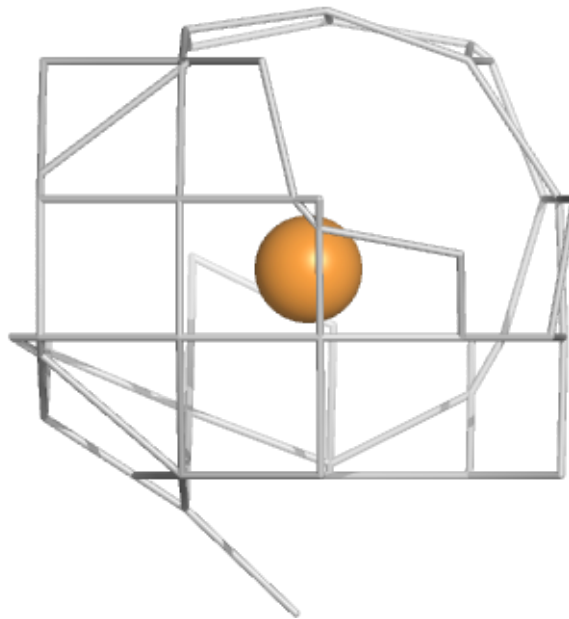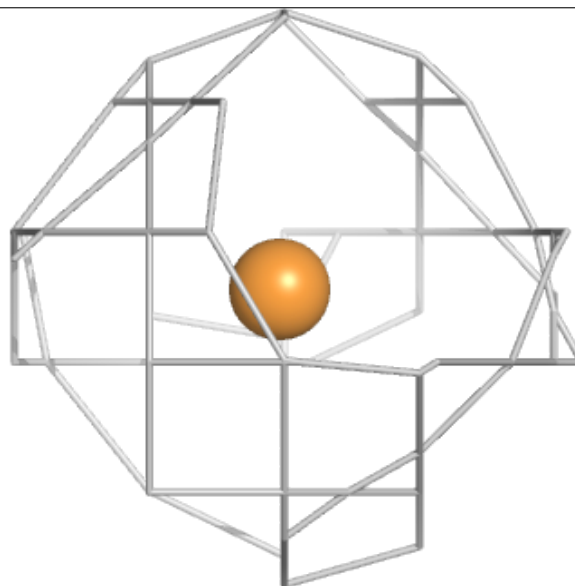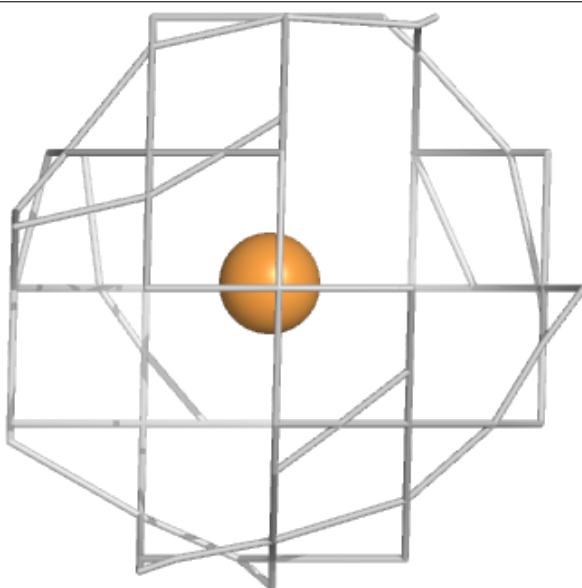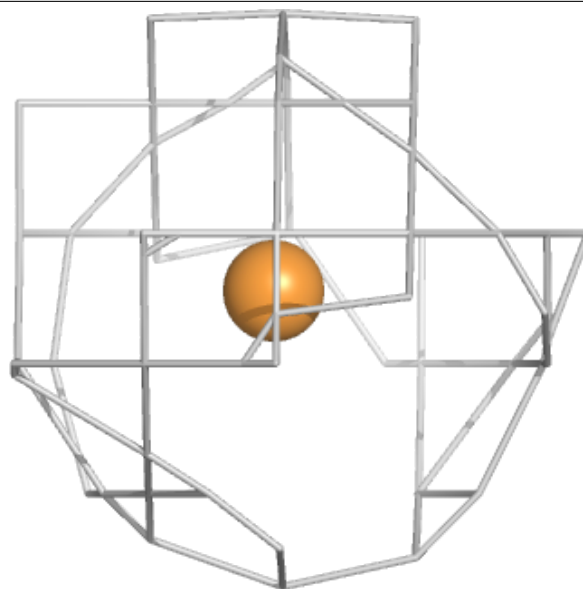and green (positive)
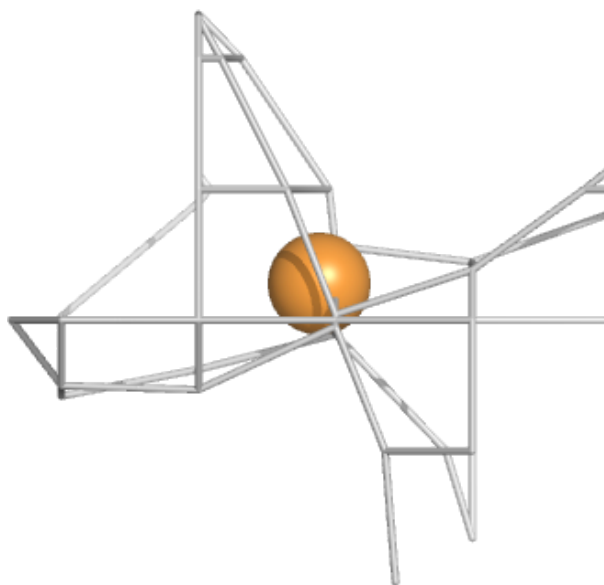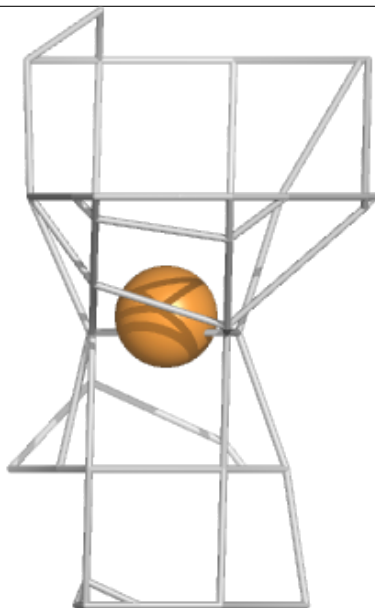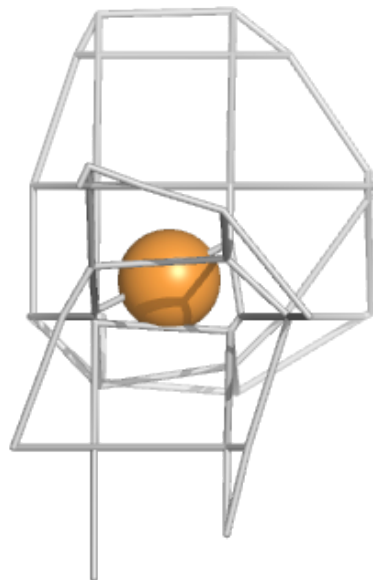
Electron density around CU C 404:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
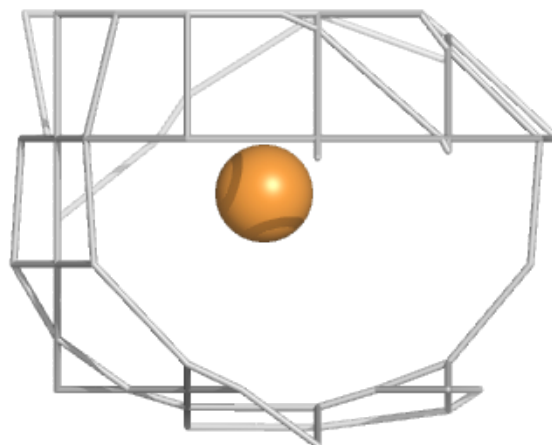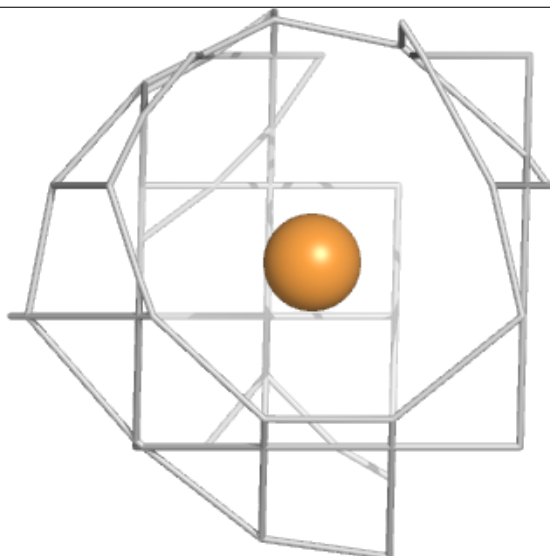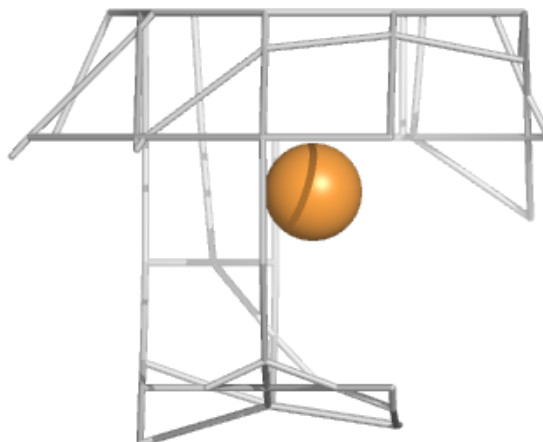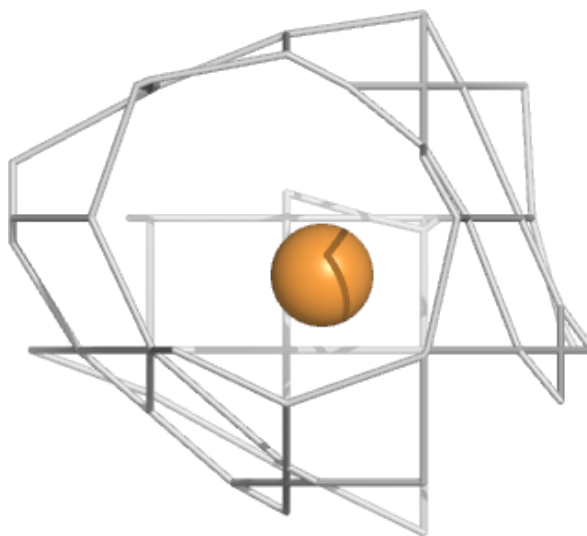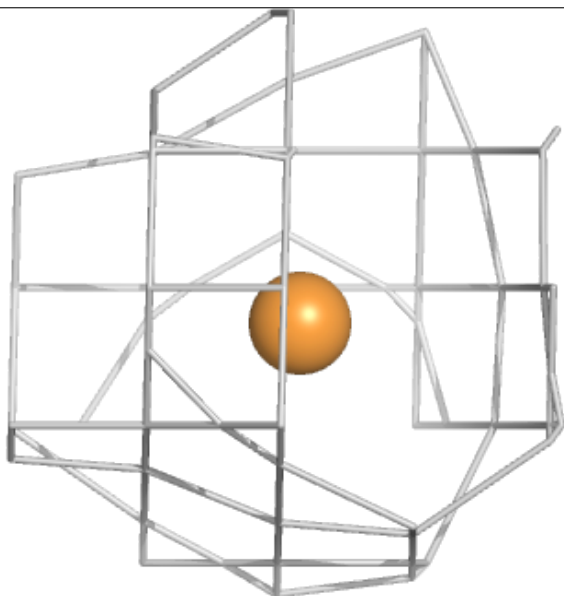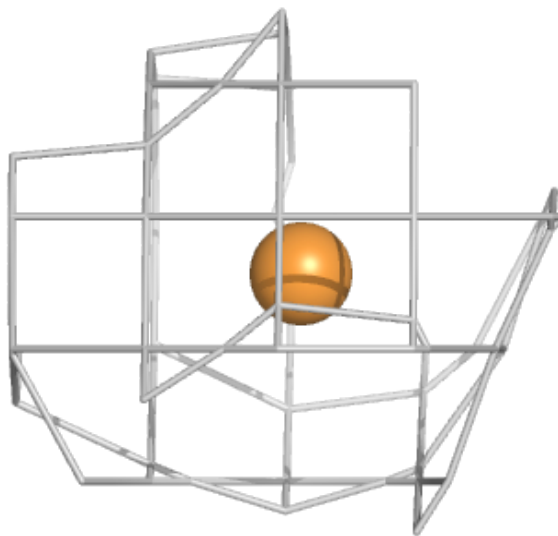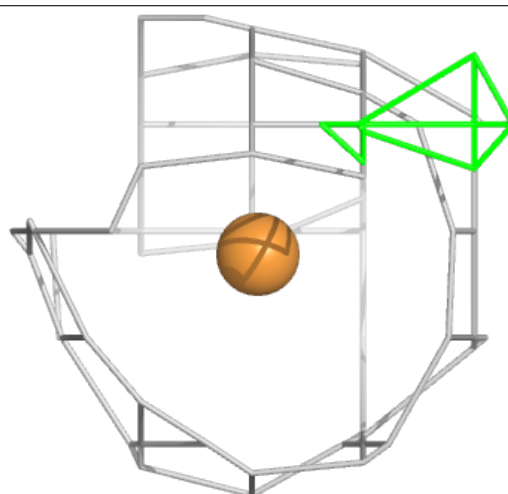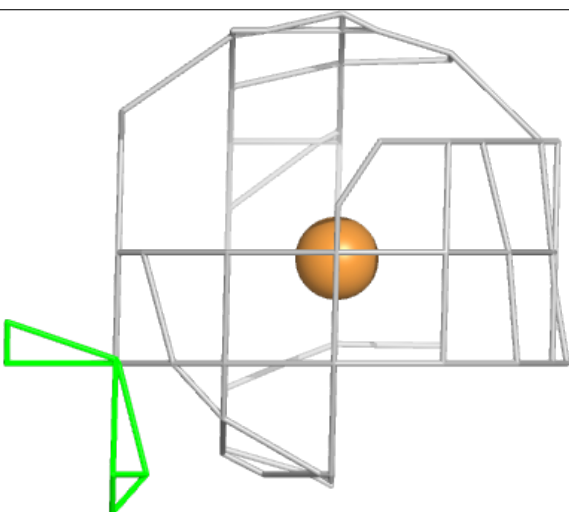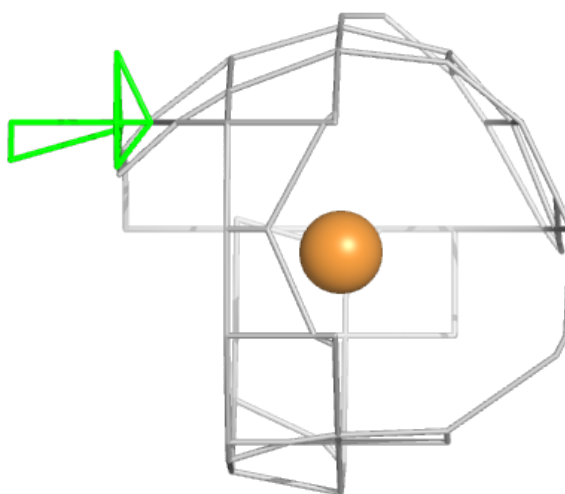mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
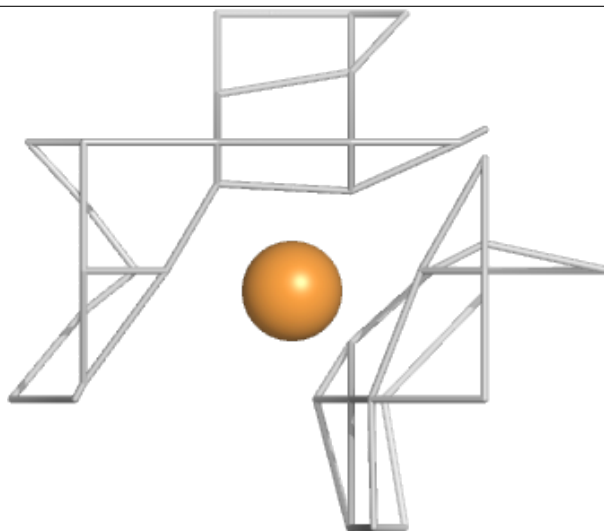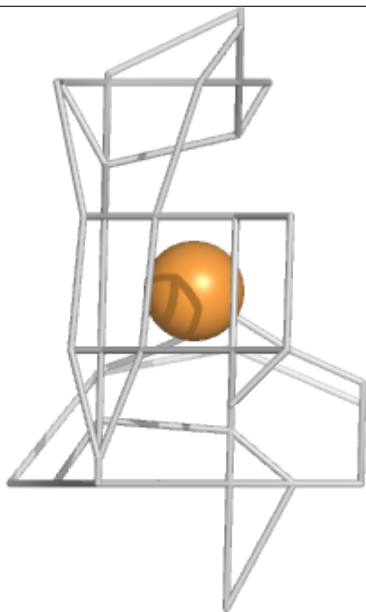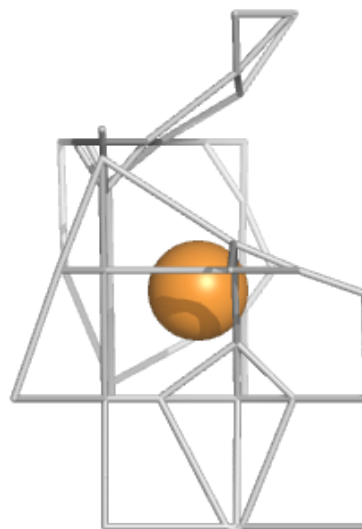
Electron density around CU A 403:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
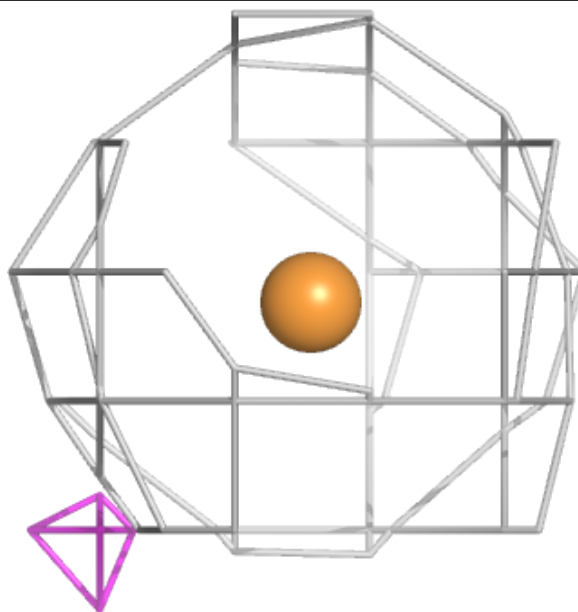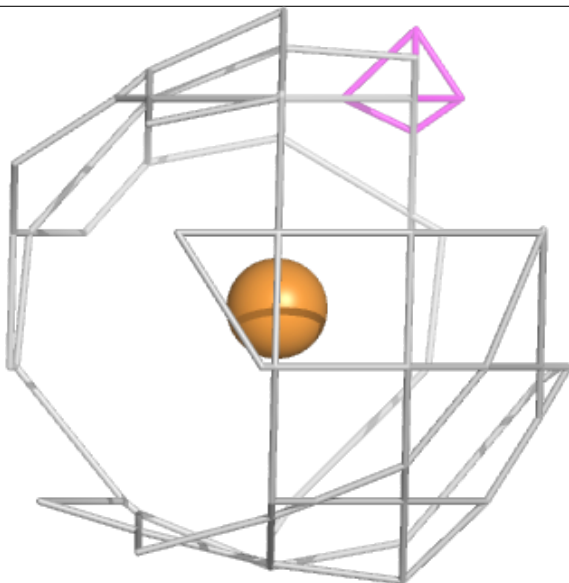and green (positive)
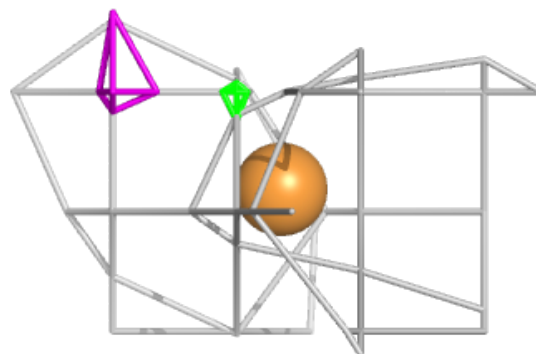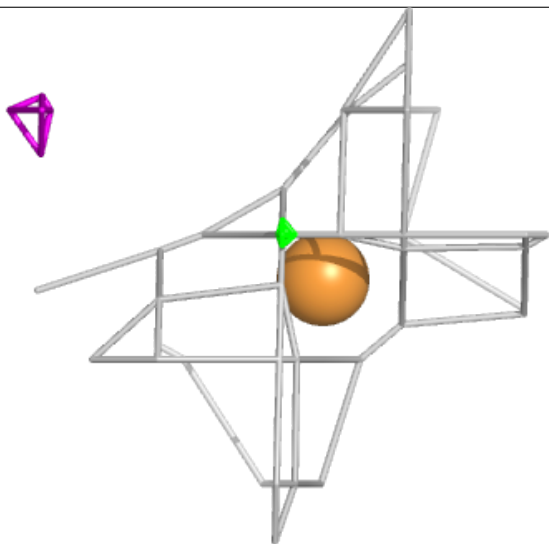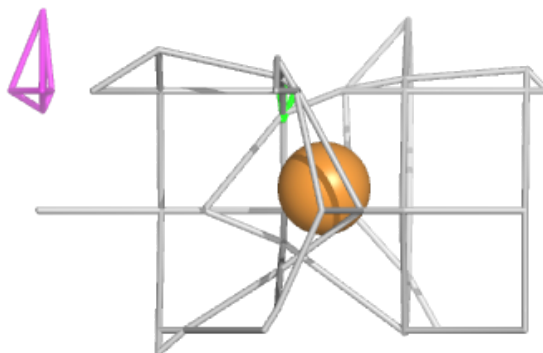
Electron density around CU A 405:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
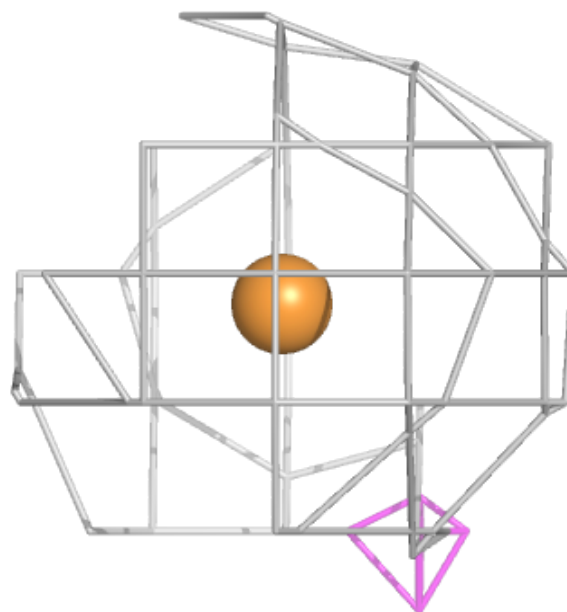and green (positive)
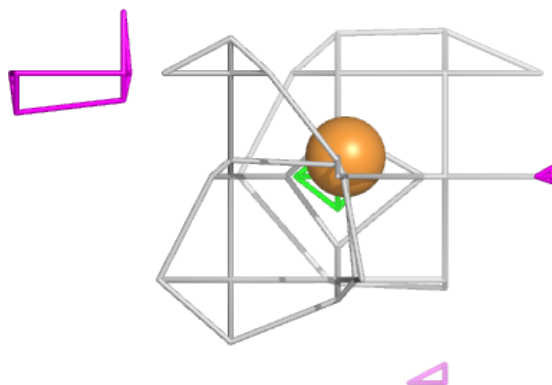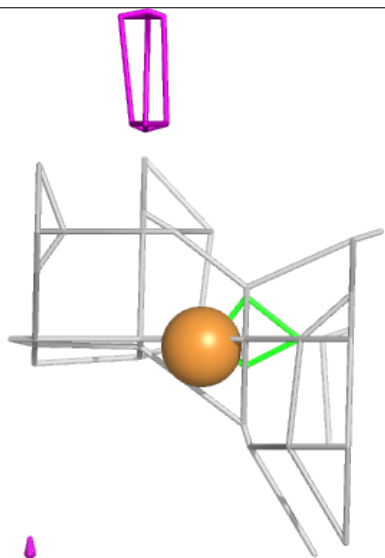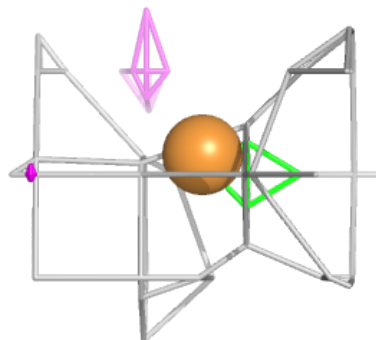
Electron density around CU F 404:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
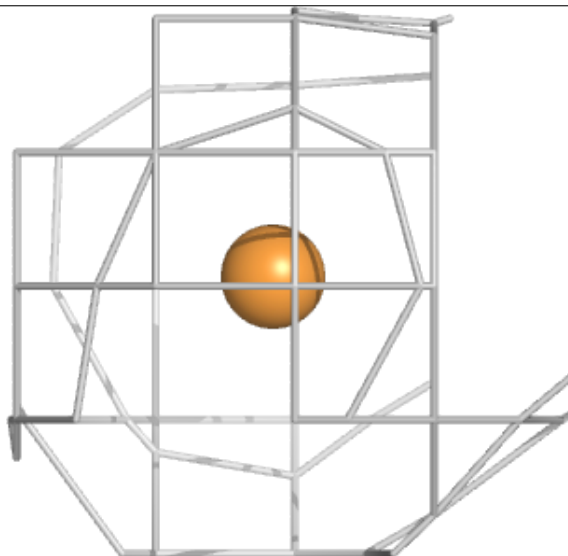and green (positive)
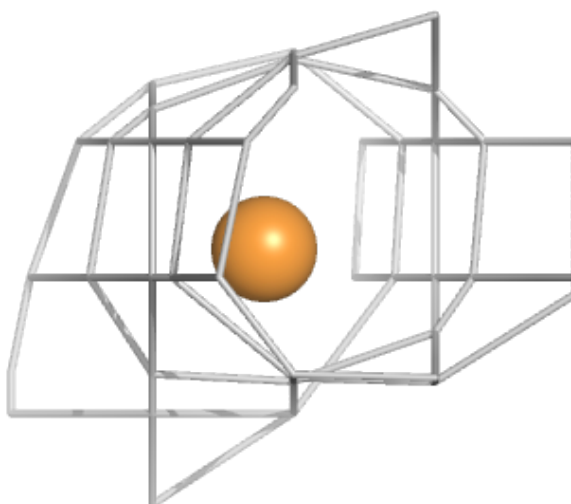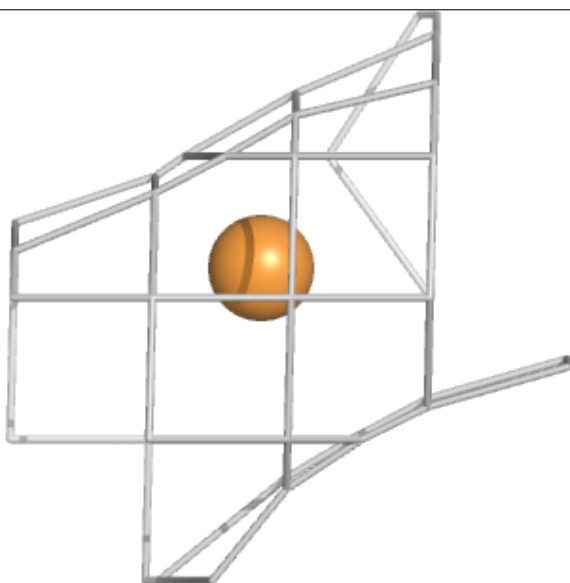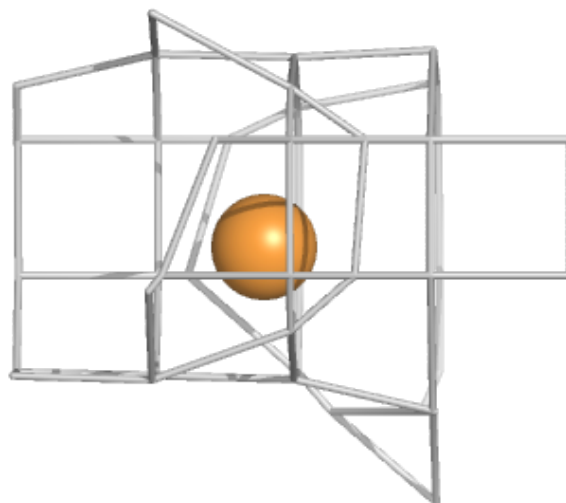
Electron density around CU E 403:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
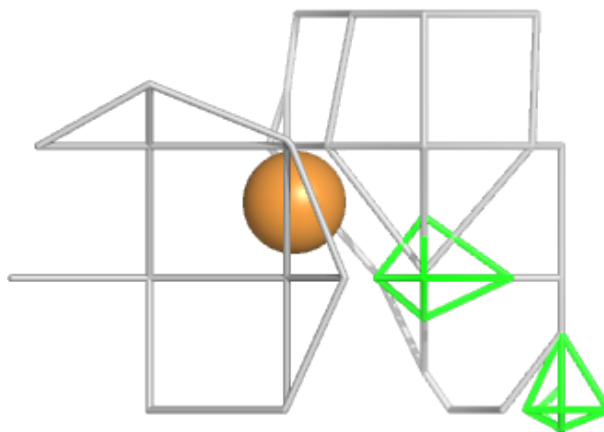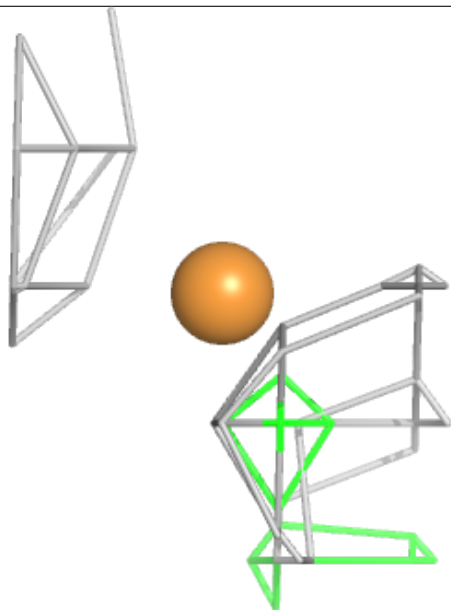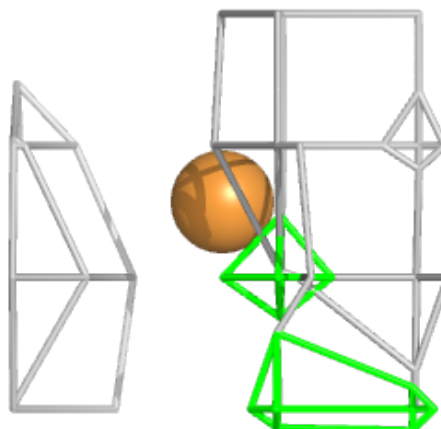
Electron density around CU B 403:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
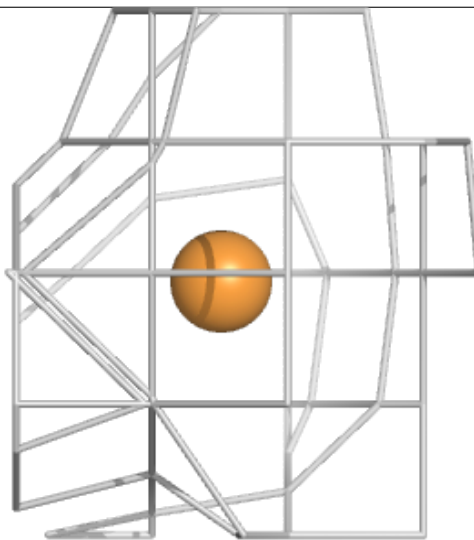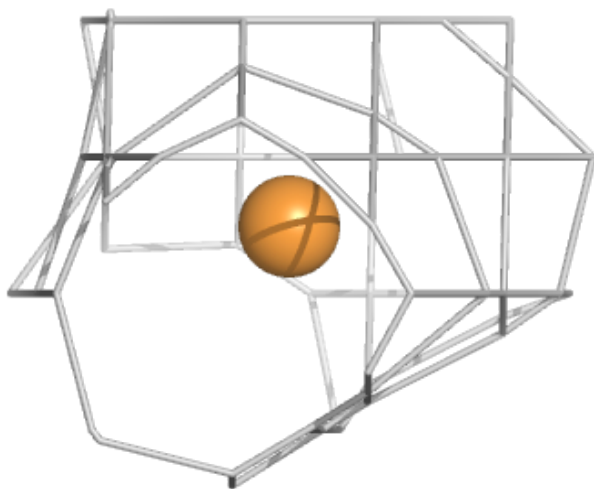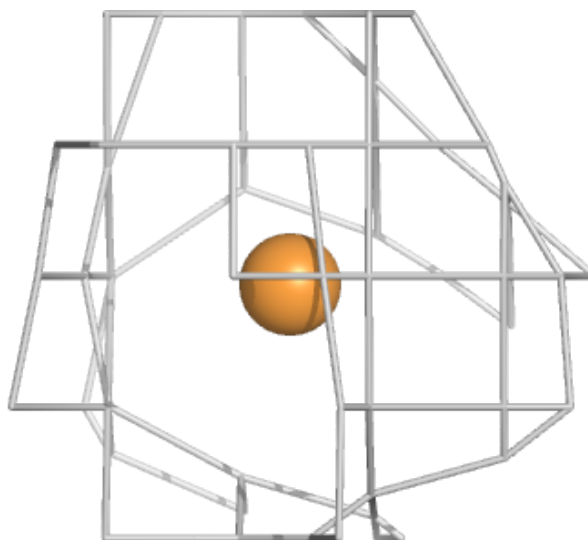
Electron density around CU E 402:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
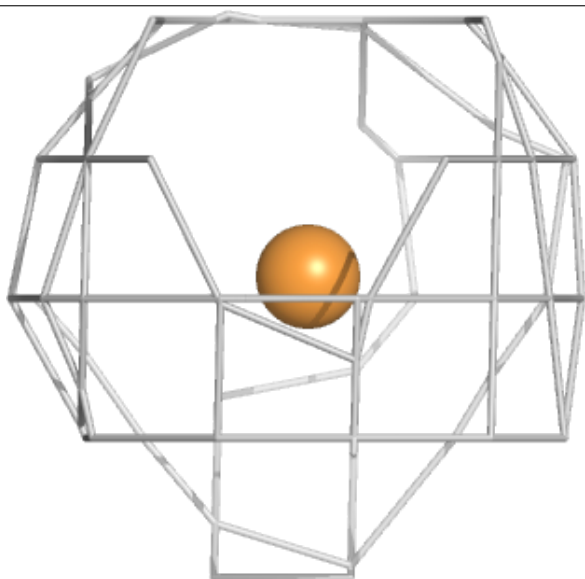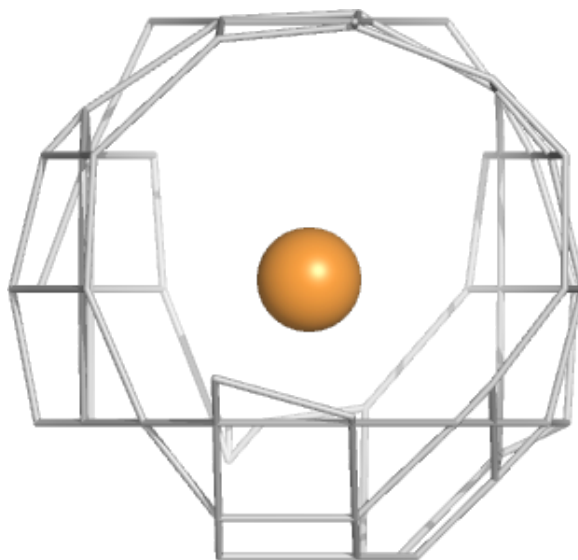and green (positive)
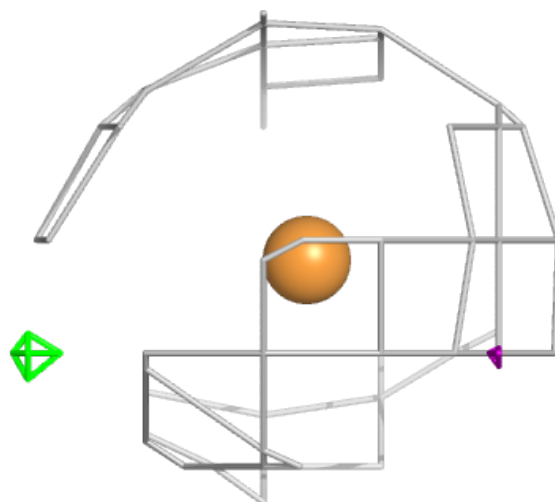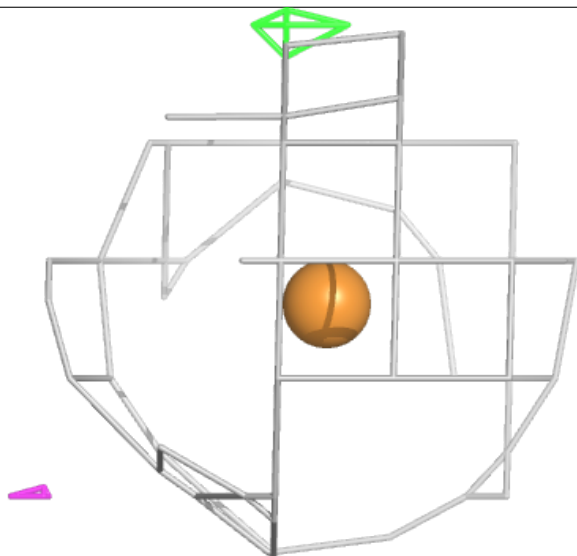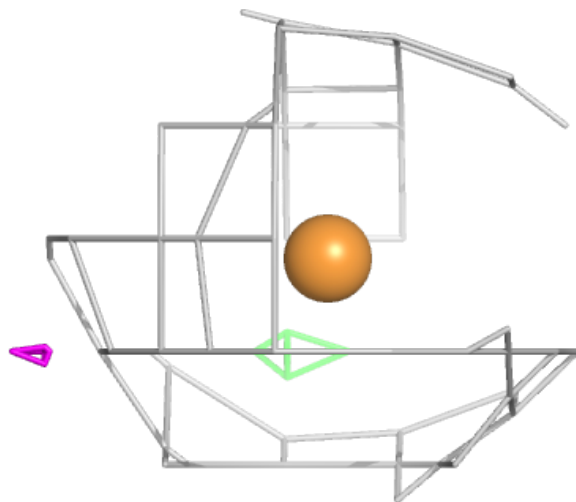
Electron density around CU A 404:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
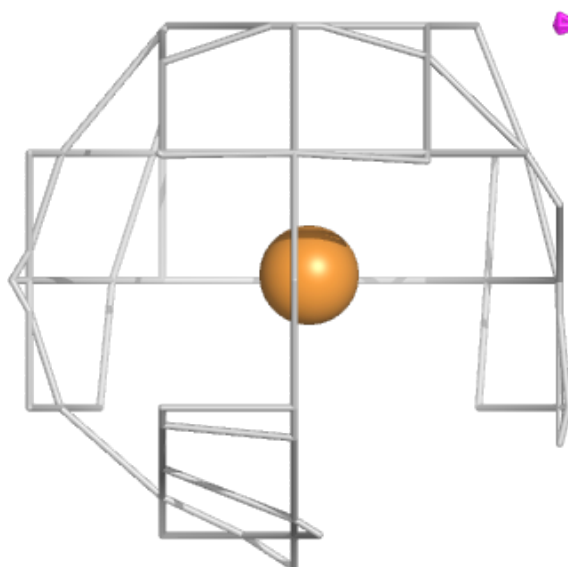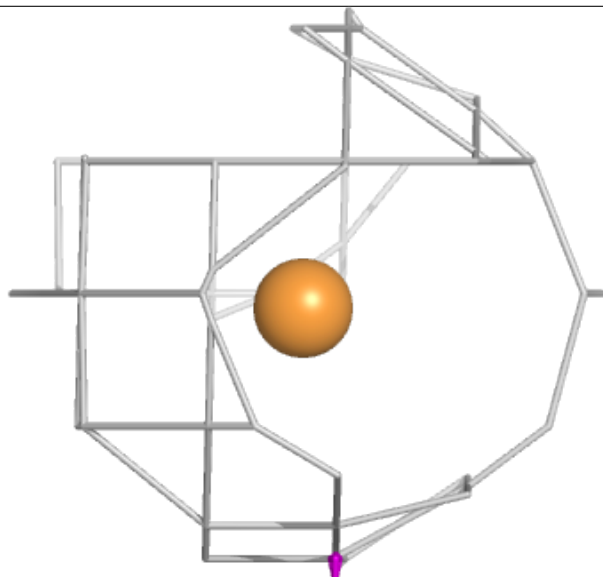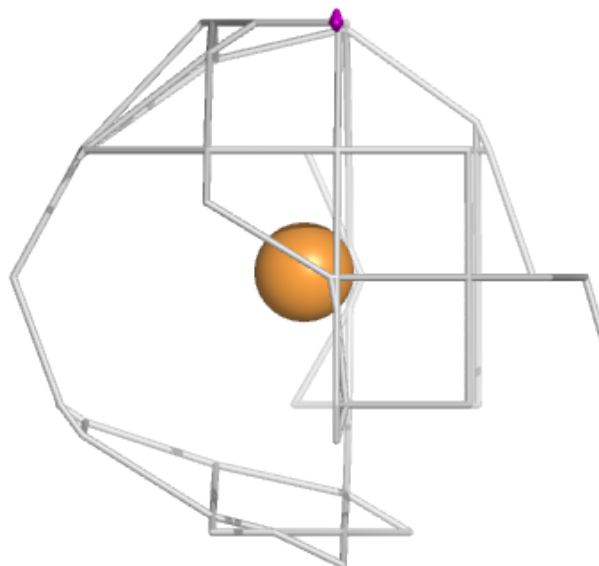
Electron density around CU E 404:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
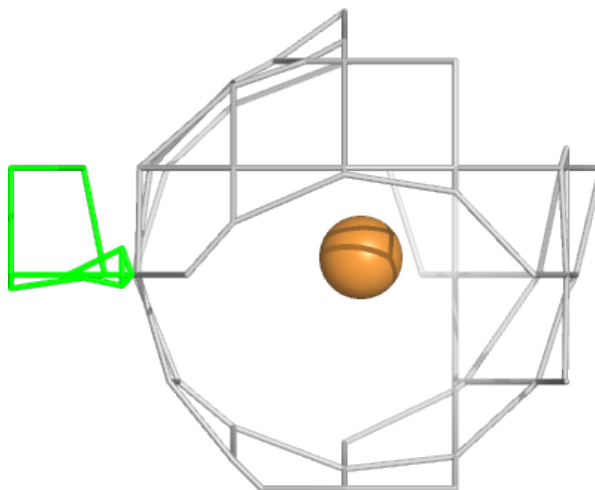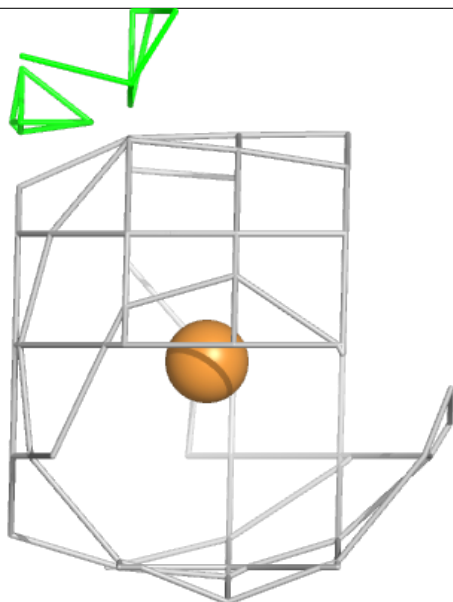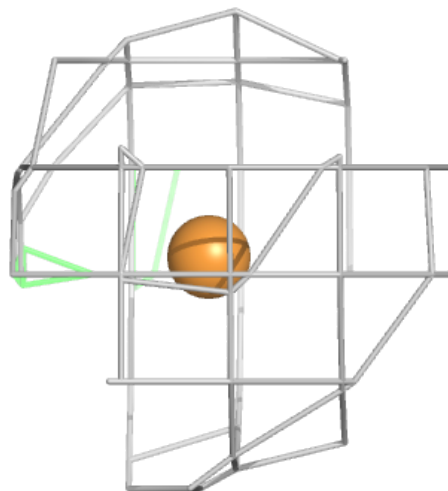and green (positive)
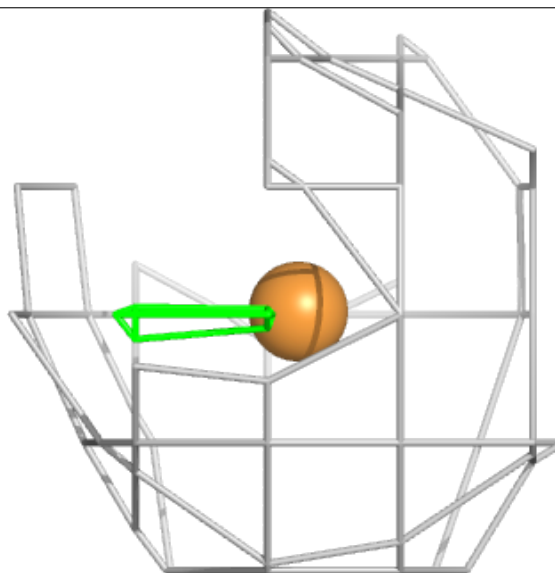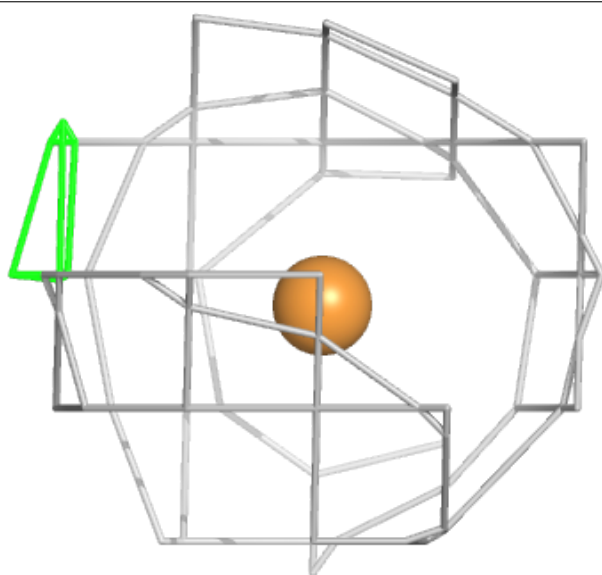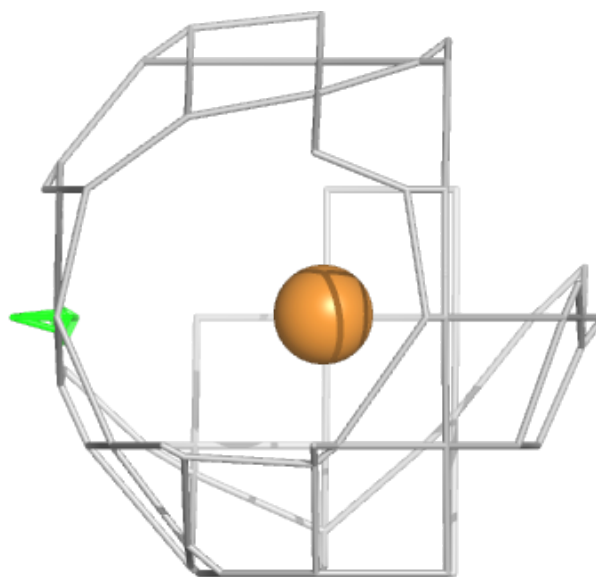
Electron density around CU B 402:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
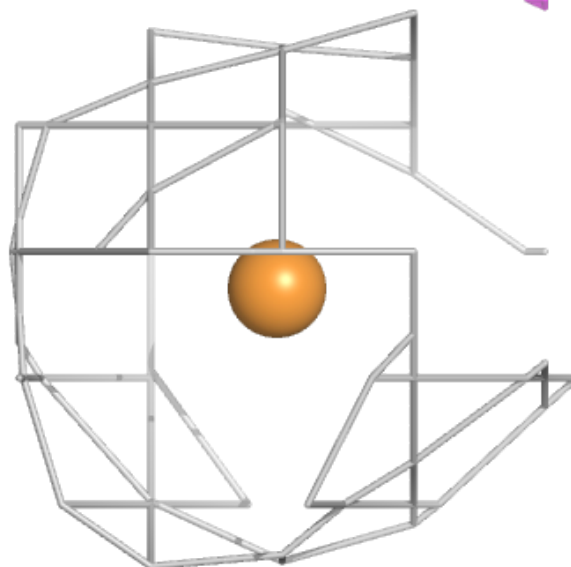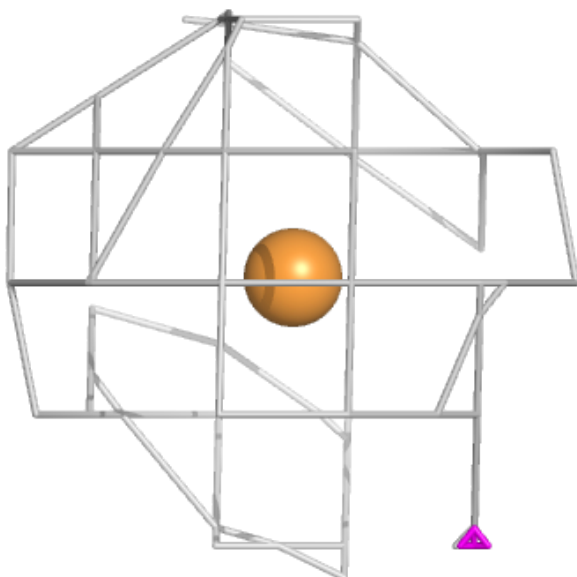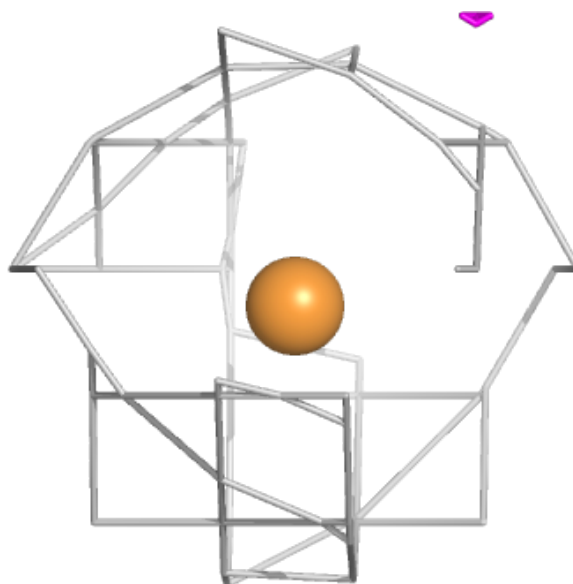
Electron density around CU D 402:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
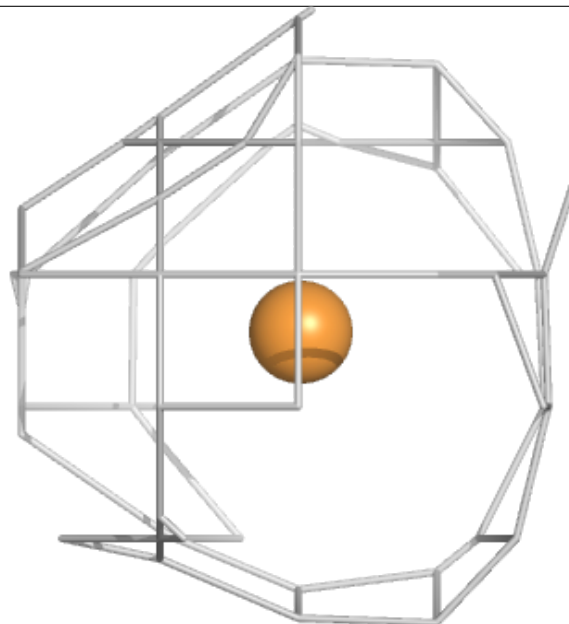
Electron density around CU F 401:

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

Electron density around CU F 403:

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

Electron density around CU A 402:

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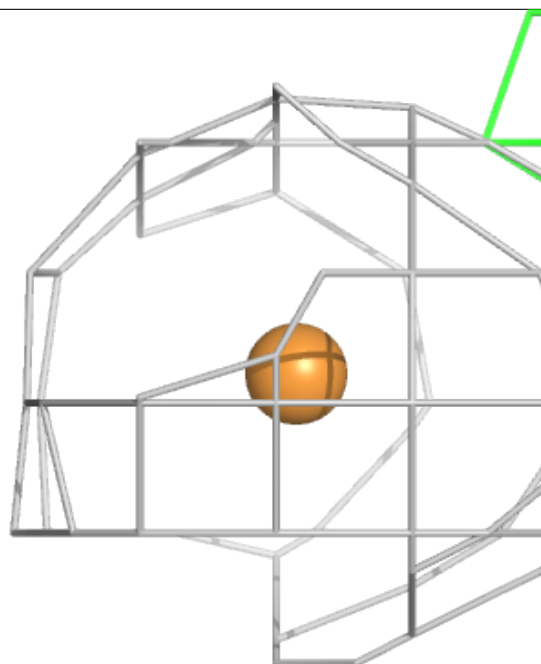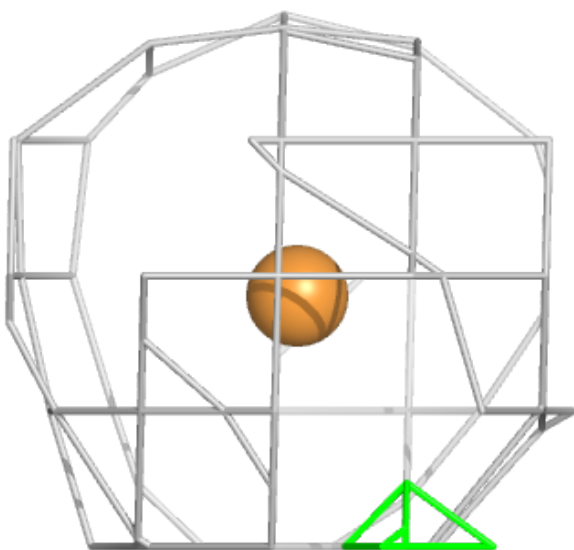$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
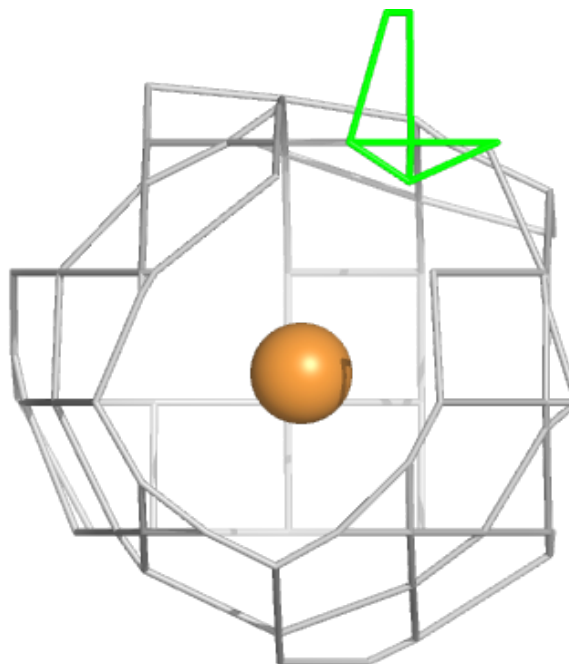and green (positive)

Electron density around CU D 404:

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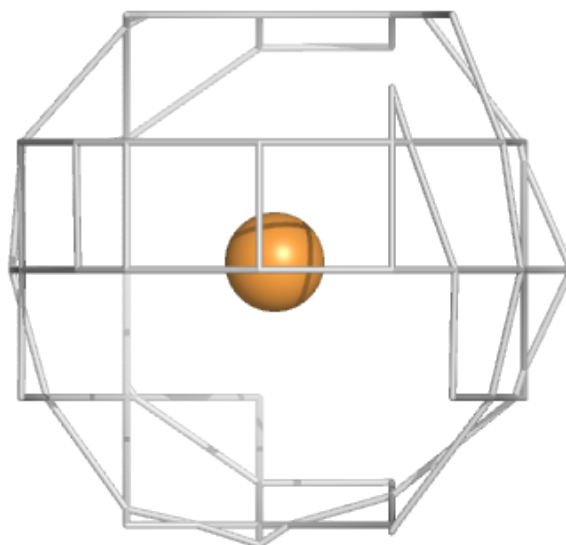and green (positive)

Electron density around CU C 401:

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

Electron density around CU A 401:

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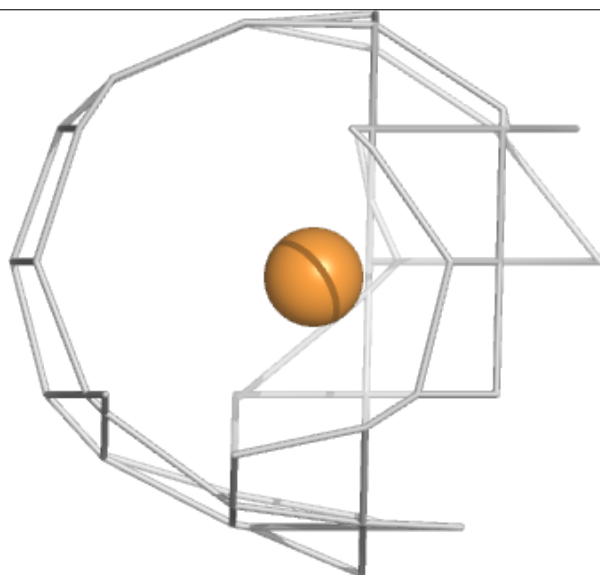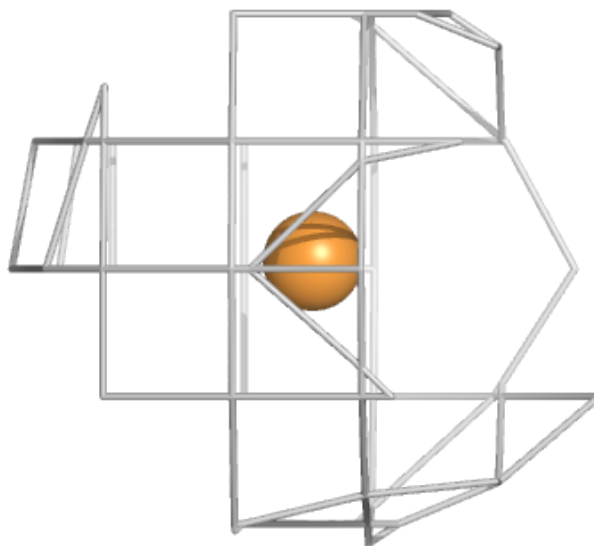and green (positive)

Electron density around CU C 402:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
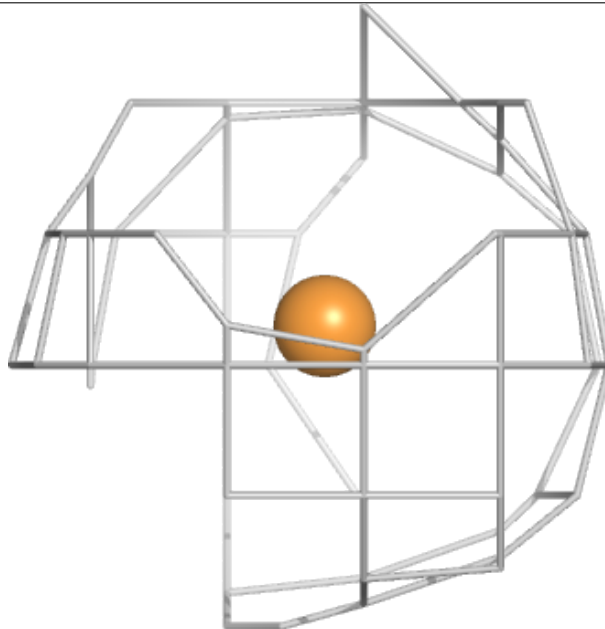and green (positive)

Electron density around CU F 402:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
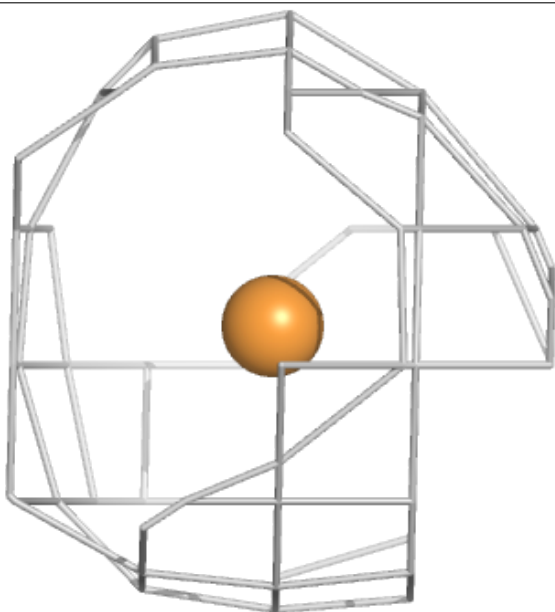
Electron density around CU C 403:

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

Electron density around CU E 401:

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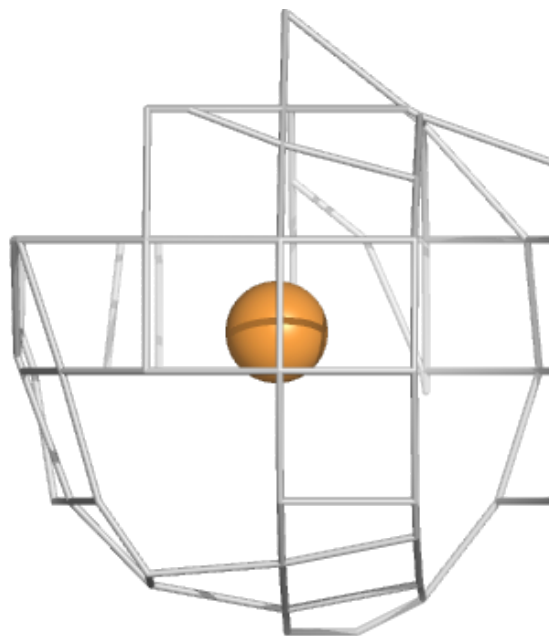and green (positive)

Electron density around CU B 401:
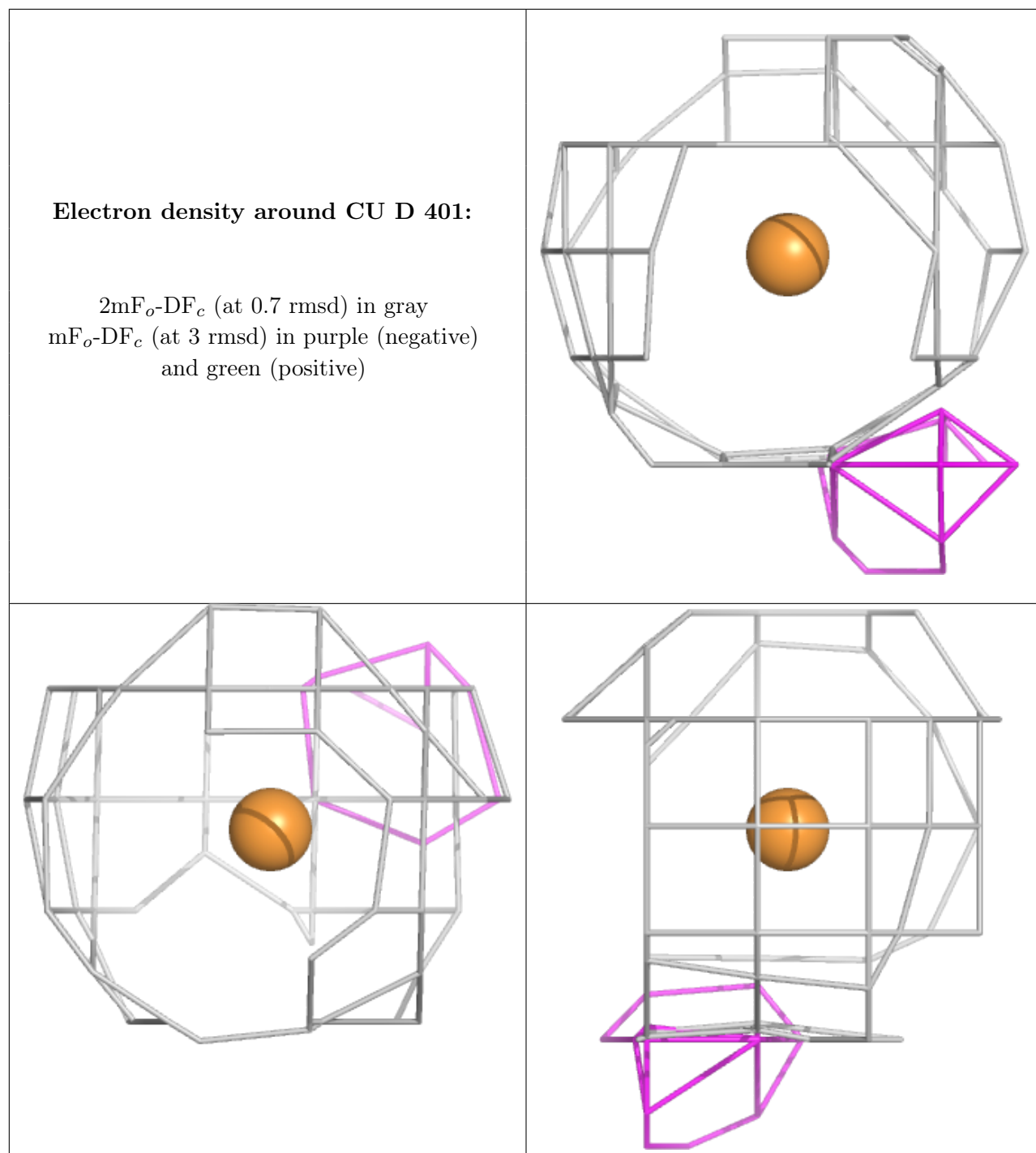
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around CU D 401:

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

6.5 Other polymers ⓘ

There are no such residues in this entry.