



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 10:15 PM UTC

PDB ID : 6UWE / pdb_00006uwe
Title : Crystal structure of recombinant thiocyanate dehydrogenase from *Thioalkalivibrio paradoxus* saturated with copper
Authors : Shabalin, I.G.; Osipov, E.; Tikhonova, T.V.; Rakitina, T.V.; Boyko, K.M.; Popov, V.O.
Deposited on : 2019-11-05
Resolution : 1.60 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

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
Xtriage (Phenix) : 2.0
EDS : 3.0
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

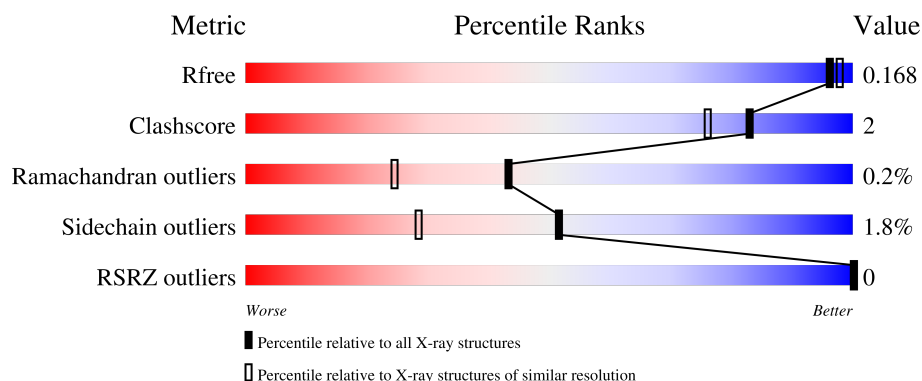
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

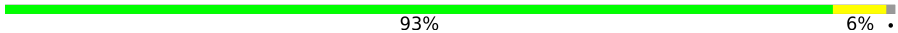
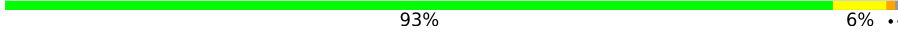
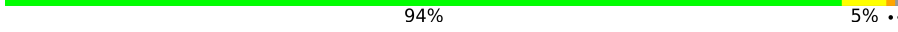
The reported resolution of this entry is 1.60 Å.

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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	471	 92% 6% ..
1	B	471	 93% 6% .
1	C	471	 93% 6% ..
1	D	471	 94% 5% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17147 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 thiocyanate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	467	Total	C	N	O	S	0	13	0
			3689	2363	610	696	20			
1	B	467	Total	C	N	O	S	0	14	0
			3692	2365	610	697	20			
1	C	467	Total	C	N	O	S	0	11	0
			3684	2355	615	694	20			
1	D	467	Total	C	N	O	S	0	11	0
			3683	2357	612	694	20			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	78	GLY	-	expression tag	UNP W0DP94
A	79	ALA	-	expression tag	UNP W0DP94
A	80	MET	-	expression tag	UNP W0DP94
A	81	GLY	-	expression tag	UNP W0DP94
B	78	GLY	-	expression tag	UNP W0DP94
B	79	ALA	-	expression tag	UNP W0DP94
B	80	MET	-	expression tag	UNP W0DP94
B	81	GLY	-	expression tag	UNP W0DP94
C	78	GLY	-	expression tag	UNP W0DP94
C	79	ALA	-	expression tag	UNP W0DP94
C	80	MET	-	expression tag	UNP W0DP94
C	81	GLY	-	expression tag	UNP W0DP94
D	78	GLY	-	expression tag	UNP W0DP94
D	79	ALA	-	expression tag	UNP W0DP94
D	80	MET	-	expression tag	UNP W0DP94
D	81	GLY	-	expression tag	UNP W0DP94

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	6	Total Cu 6 6	0	0
2	B	6	Total Cu 6 6	0	0
2	C	6	Total Cu 6 6	0	0
2	D	6	Total Cu 6 6	0	0

- Molecule 3 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total X 1 1	0	0
3	B	2	Total X 2 2	0	0
3	C	1	Total X 1 1	0	0
3	D	2	Total X 2 2	0	0

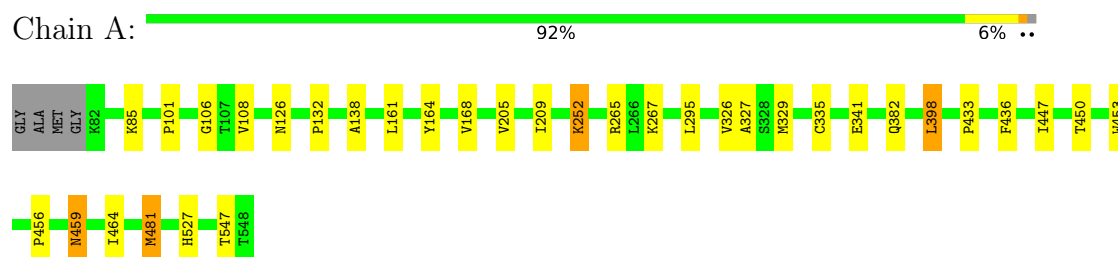
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	565	Total O 575 575	0	14
4	B	570	Total O 583 583	0	14
4	C	584	Total O 597 597	0	14
4	D	600	Total O 614 614	0	16

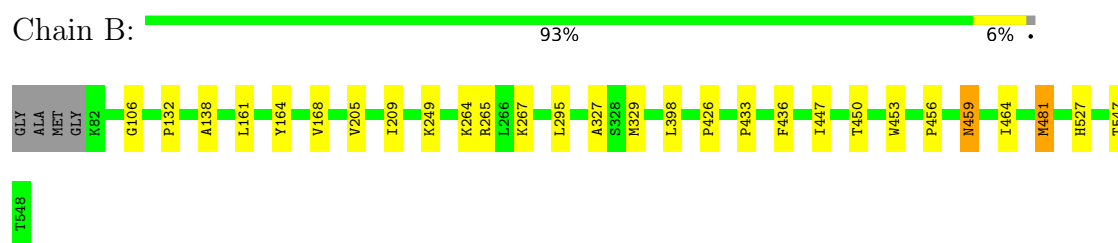
3 Residue-property plots

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.

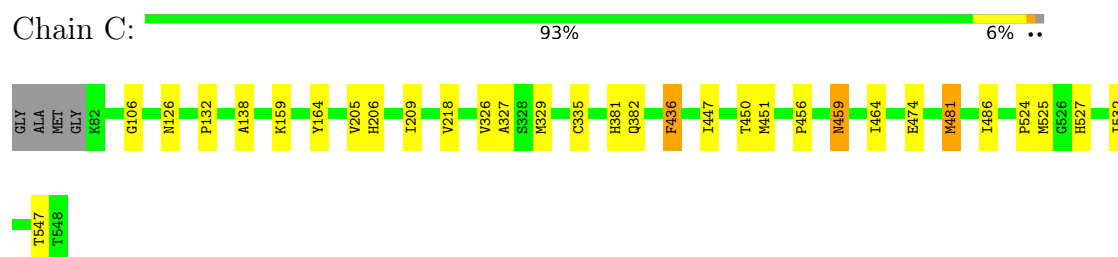
- Molecule 1: thiocyanate dehydrogenase



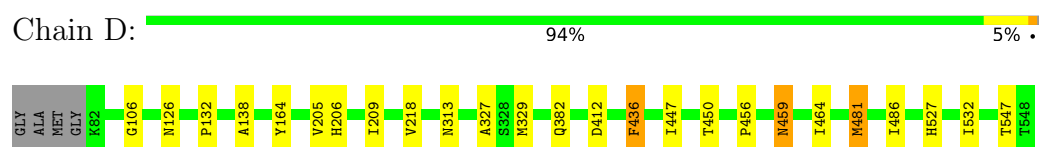
- Molecule 1: thiocyanate dehydrogenase



- Molecule 1: thiocyanate dehydrogenase



- Molecule 1: thiocyanate dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	90.42Å 163.15Å 90.63Å 90.00° 119.29° 90.00°	Depositor
Resolution (Å)	44.80 – 1.60 44.80 – 1.60	Depositor EDS
% Data completeness (in resolution range)	91.0 (44.80-1.60) 91.0 (44.80-1.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 1.59Å)	Xtriage
Refinement program	REFMAC 5.8.0257, Coot	Depositor
R, R_{free}	0.141 , 0.160 0.150 , 0.168	Depositor DCC
R_{free} test set	13464 reflections (4.32%)	wwPDB-VP
Wilson B-factor (Å ²)	13.3	Xtriage
Anisotropy	0.133	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 30.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.044 for -h-l,k,h 0.044 for l,k,-h-l 0.045 for h,-k,-h-l 0.044 for -h-l,-k,l 0.358 for l,-k,h	Xtriage
Reported twinning fraction	0.688 for H, K, L 0.312 for -L, -K, -H	Depositor
Outliers	0 of 276564 reflections	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	17147	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% 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: CU, UNX

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	0.96	0/3840	1.08	2/5237 (0.0%)
1	B	0.98	1/3850 (0.0%)	1.07	1/5251 (0.0%)
1	C	0.96	0/3829	1.08	1/5221 (0.0%)
1	D	0.96	0/3825	1.08	1/5217 (0.0%)
All	All	0.97	1/15344 (0.0%)	1.08	5/20926 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	426	PRO	C-O	-7.46	1.14	1.24

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	164	TYR	CB-CA-C	7.40	125.61	111.48
1	D	164	TYR	CB-CA-C	7.00	124.86	111.48
1	A	164	TYR	CB-CA-C	5.93	122.81	111.48
1	B	164	TYR	CB-CA-C	5.90	122.76	111.48
1	A	126	ASN	CA-CB-CG	5.39	117.99	112.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3689	0	3604	24	0
1	B	3692	0	3602	16	0
1	C	3684	0	3591	16	0
1	D	3683	0	3595	13	0
2	A	6	0	0	0	0
2	B	6	0	0	0	0
2	C	6	0	0	0	0
2	D	6	0	0	0	0
3	A	1	0	0	0	0
3	B	2	0	0	1	0
3	C	1	0	0	0	0
3	D	2	0	0	1	0
4	A	575	0	0	1	0
4	B	583	0	0	1	0
4	C	597	0	0	2	0
4	D	614	0	0	1	0
All	All	17147	0	14392	69	0

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

All (69) 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:295:LEU:HG	1:A:398[A]:LEU:HD22	1.59	0.82
1:C:451:MET:HG3	1:C:474:GLU:OE1	1.84	0.78
1:A:161:LEU:HG	1:A:168[B]:VAL:HG11	1.73	0.69
1:A:295:LEU:HG	1:A:398[A]:LEU:CD2	2.22	0.69
1:B:161:LEU:HG	1:B:168[A]:VAL:HG11	1.76	0.66
1:B:168[A]:VAL:HG13	1:C:126:ASN:O	1.98	0.63
1:B:295:LEU:HG	1:B:398[A]:LEU:HD23	1.82	0.61
1:B:327:ALA:HB1	1:B:329[B]:MET:HE1	1.82	0.60
1:A:295:LEU:CD1	1:A:398[A]:LEU:HD21	2.36	0.55
1:B:161:LEU:CD2	1:B:168[A]:VAL:HG11	2.37	0.55
1:D:327:ALA:HB1	1:D:329[B]:MET:HE1	1.88	0.54
1:A:161:LEU:CG	1:A:168[B]:VAL:HG11	2.37	0.54
1:A:168[B]:VAL:HG13	1:D:126:ASN:O	2.08	0.54
1:D:313:ASN:HD22	1:D:329[B]:MET:HE3	1.72	0.54
1:A:106:GLY:HA2	1:A:132:PRO:O	2.10	0.52
1:B:161:LEU:CG	1:B:168[A]:VAL:HG11	2.38	0.52
1:A:161:LEU:CD2	1:A:168[B]:VAL:HG11	2.39	0.52
1:C:106:GLY:HA2	1:C:132:PRO:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:313:ASN:HD22	1:D:329[B]:MET:CE	2.23	0.51
1:B:106:GLY:HA2	1:B:132:PRO:O	2.11	0.51
1:D:106:GLY:HA2	1:D:132:PRO:O	2.10	0.50
1:A:295:LEU:CG	1:A:398[A]:LEU:CD2	2.91	0.49
1:A:327:ALA:CB	1:A:329[B]:MET:HE1	2.43	0.48
1:D:447:ILE:HG23	1:D:464:ILE:HB	1.97	0.47
1:B:265:ARG:HD2	1:B:267:LYS:HE2	1.96	0.47
1:A:327:ALA:HB1	1:A:329[B]:MET:HE1	1.95	0.47
1:C:382:GLN:HG3	1:C:436:PHE:C	2.40	0.46
1:C:447:ILE:HG23	1:C:464:ILE:HB	1.98	0.46
1:C:524:PRO:C	1:C:525[B]:MET:HG3	2.41	0.45
1:A:295:LEU:HD11	1:A:398[A]:LEU:HD21	1.98	0.45
1:A:265:ARG:HD2	1:A:267:LYS:HE2	1.97	0.45
1:D:382:GLN:HG3	1:D:436:PHE:C	2.42	0.45
1:A:447:ILE:HG23	1:A:464:ILE:HB	1.99	0.45
1:B:264:LYS:HG2	4:B:1066:HOH:O	2.17	0.44
1:B:327:ALA:CB	1:B:329[B]:MET:HE1	2.46	0.44
1:C:381:HIS:HB3	4:C:853:HOH:O	2.17	0.44
3:D:607:UNX:UNK	3:D:608:UNX:UNK	1.60	0.44
1:C:450:THR:CG2	1:C:481:MET:HG2	2.48	0.44
1:A:382:GLN:HG3	1:A:436:PHE:C	2.44	0.43
1:B:447:ILE:HG23	1:B:464:ILE:HB	1.99	0.43
1:B:138:ALA:HB1	1:B:209:ILE:HG12	2.00	0.43
1:D:138:ALA:HB1	1:D:209:ILE:HG12	2.01	0.43
1:C:459:ASN:N	1:C:459:ASN:HD22	2.17	0.43
1:A:138:ALA:HB1	1:A:209:ILE:HG12	2.01	0.43
1:A:252:LYS:NZ	4:A:703:HOH:O	2.37	0.43
1:C:159:LYS:NZ	4:C:713:HOH:O	2.50	0.43
1:B:459:ASN:HD22	1:B:459:ASN:N	2.17	0.42
1:B:433:PRO:HD3	1:B:453:TRP:CZ2	2.54	0.42
1:D:450:THR:CG2	1:D:481:MET:HG2	2.49	0.42
1:C:138:ALA:HB1	1:C:209:ILE:HG12	2.00	0.42
1:C:486:ILE:C	1:C:532[A]:ILE:HD12	2.44	0.42
1:A:450:THR:HB	1:A:481:MET:HG2	2.01	0.42
1:C:327:ALA:HB3	1:C:329[B]:MET:HE1	2.01	0.42
1:A:459:ASN:HD22	1:A:459:ASN:N	2.18	0.41
1:C:326:VAL:CG1	1:C:335:CYS:HB3	2.50	0.41
1:A:326:VAL:CG1	1:A:335:CYS:HB3	2.50	0.41
1:A:450:THR:CG2	1:A:481:MET:HG2	2.50	0.41
1:D:206:HIS:O	1:D:218:VAL:HA	2.21	0.41
1:A:101:PRO:HA	1:A:108[B]:VAL:HG12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:486:ILE:C	1:D:532[A]:ILE:HD12	2.46	0.41
1:A:433:PRO:HD3	1:A:453:TRP:CZ2	2.56	0.41
1:D:459:ASN:N	1:D:459:ASN:HD22	2.19	0.41
1:D:412:ASP:CB	4:D:1162:HOH:O	2.69	0.41
1:C:206:HIS:O	1:C:218:VAL:HA	2.20	0.40
1:B:450:THR:CG2	1:B:481:MET:HG2	2.51	0.40
3:B:607:UNX:UNK	3:B:608:UNX:UNK	1.65	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	478/471 (102%)	451 (94%)	26 (5%)	1 (0%)	43	24
1	B	479/471 (102%)	453 (95%)	25 (5%)	1 (0%)	43	24
1	C	476/471 (101%)	447 (94%)	28 (6%)	1 (0%)	43	24
1	D	476/471 (101%)	451 (95%)	24 (5%)	1 (0%)	43	24
All	All	1909/1884 (101%)	1802 (94%)	103 (5%)	4 (0%)	43	24

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	205	VAL
1	B	205	VAL
1	C	205	VAL
1	D	205	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	404/393 (103%)	394 (98%)	10 (2%)	42	18
1	B	405/393 (103%)	398 (98%)	7 (2%)	53	30
1	C	402/393 (102%)	396 (98%)	6 (2%)	57	35
1	D	402/393 (102%)	396 (98%)	6 (2%)	57	35
All	All	1613/1572 (103%)	1584 (98%)	29 (2%)	51	28

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	LYS
1	A	252	LYS
1	A	341	GLU
1	A	398[A]	LEU
1	A	398[B]	LEU
1	A	456	PRO
1	A	459	ASN
1	A	481	MET
1	A	527	HIS
1	A	547	THR
1	B	249	LYS
1	B	436	PHE
1	B	456	PRO
1	B	459	ASN
1	B	481	MET
1	B	527	HIS
1	B	547	THR
1	C	436	PHE
1	C	456	PRO
1	C	459	ASN
1	C	481	MET
1	C	527	HIS
1	C	547	THR
1	D	436	PHE

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Mol	Chain	Res	Type
1	D	456	PRO
1	D	459	ASN
1	D	481	MET
1	D	527	HIS
1	D	547	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	GLN
1	A	190	ASN
1	A	390	GLN
1	A	434	ASN
1	B	360	GLN
1	B	434	ASN
1	B	530	ASN
1	C	342	ASN
1	C	360	GLN
1	C	390	GLN
1	C	434	ASN
1	D	313	ASN
1	D	360	GLN
1	D	390	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 30 ligands modelled in this entry, 24 are monoatomic and 6 are unknown - 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 [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	467/471 (99%)	-1.40	0 100 100	5, 14, 27, 54	13 (2%)
1	B	467/471 (99%)	-1.42	0 100 100	5, 14, 26, 49	14 (2%)
1	C	467/471 (99%)	-1.39	0 100 100	5, 14, 24, 52	11 (2%)
1	D	467/471 (99%)	-1.42	0 100 100	5, 13, 23, 48	11 (2%)
All	All	1868/1884 (99%)	-1.41	0 100 100	5, 14, 25, 54	49 (2%)

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	B	605	1/1	0.95	0.11	61,61,61,61	1
3	UNX	C	607	1/1	0.98	0.11	32,32,32,32	0
2	CU	A	605	1/1	0.99	0.05	41,41,41,41	1
2	CU	B	606	1/1	0.99	0.03	36,36,36,36	1

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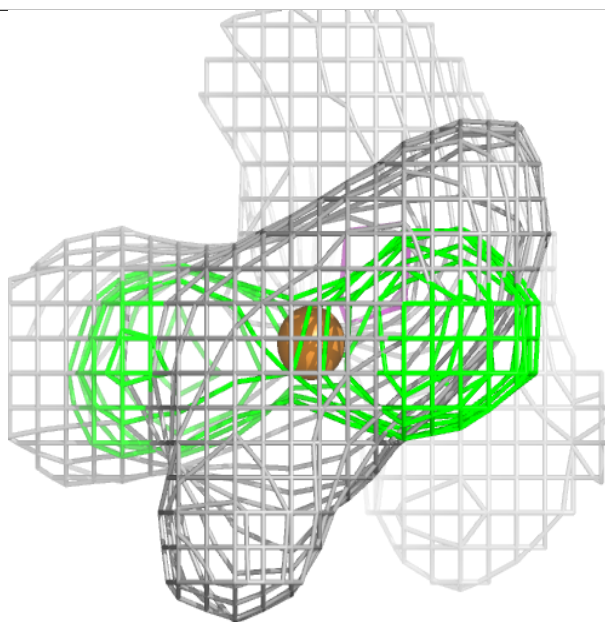
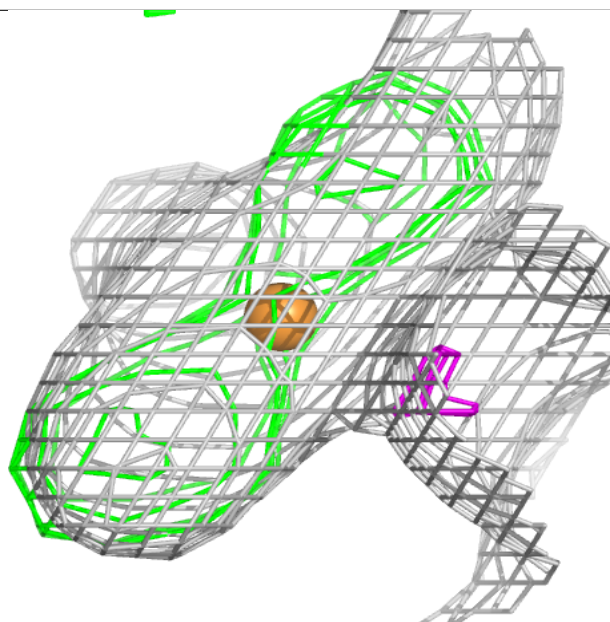
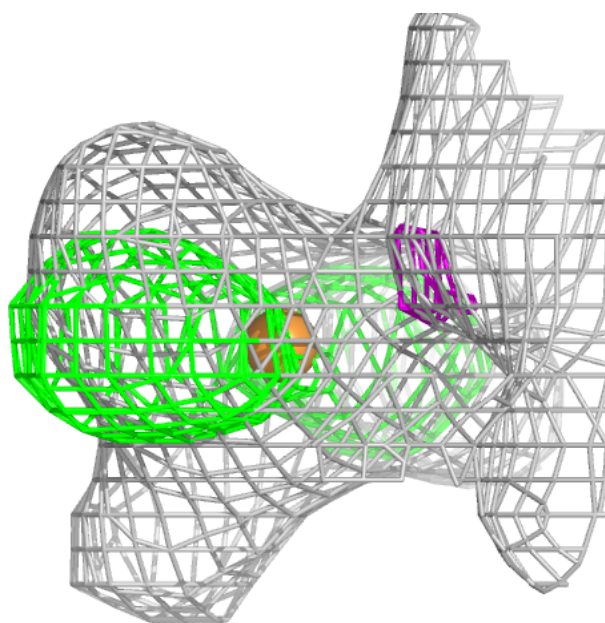
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	UNX	A	607	1/1	0.99	0.07	27,27,27,27	0
3	UNX	B	607	1/1	0.99	0.06	26,26,26,26	0
3	UNX	B	608	1/1	0.99	0.06	33,33,33,33	0
2	CU	A	606	1/1	0.99	0.04	37,37,37,37	1
2	CU	B	603	1/1	1.00	0.01	12,12,12,12	0
2	CU	B	604	1/1	1.00	0.01	21,21,21,21	1
2	CU	A	603	1/1	1.00	0.01	13,13,13,13	0
2	CU	A	604	1/1	1.00	0.02	25,25,25,25	1
2	CU	C	601	1/1	1.00	0.02	15,15,15,15	0
2	CU	C	602	1/1	1.00	0.01	13,13,13,13	0
2	CU	C	603	1/1	1.00	0.01	13,13,13,13	0
2	CU	C	604	1/1	1.00	0.02	24,24,24,24	1
2	CU	C	605	1/1	1.00	0.04	29,29,29,29	1
2	CU	C	606	1/1	1.00	0.01	30,30,30,30	1
2	CU	D	601	1/1	1.00	0.02	13,13,13,13	0
2	CU	D	602	1/1	1.00	0.01	11,11,11,11	0
2	CU	D	603	1/1	1.00	0.01	13,13,13,13	0
2	CU	D	604	1/1	1.00	0.01	25,25,25,25	1
2	CU	D	605	1/1	1.00	0.03	28,28,28,28	1
2	CU	D	606	1/1	1.00	0.05	36,36,36,36	1
2	CU	A	601	1/1	1.00	0.02	13,13,13,13	0
2	CU	A	602	1/1	1.00	0.01	11,11,11,11	0
2	CU	B	601	1/1	1.00	0.01	13,13,13,13	0
2	CU	B	602	1/1	1.00	0.01	10,10,10,10	0
3	UNX	D	607	1/1	1.00	0.03	26,26,26,26	0
3	UNX	D	608	1/1	1.00	0.04	30,30,30,30	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.

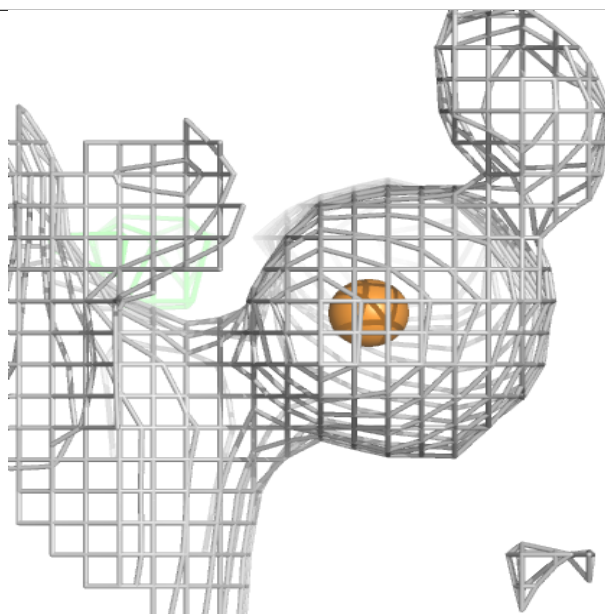
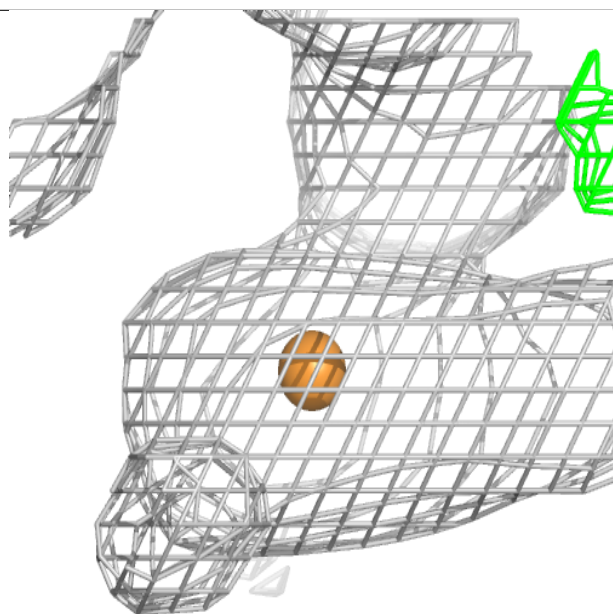
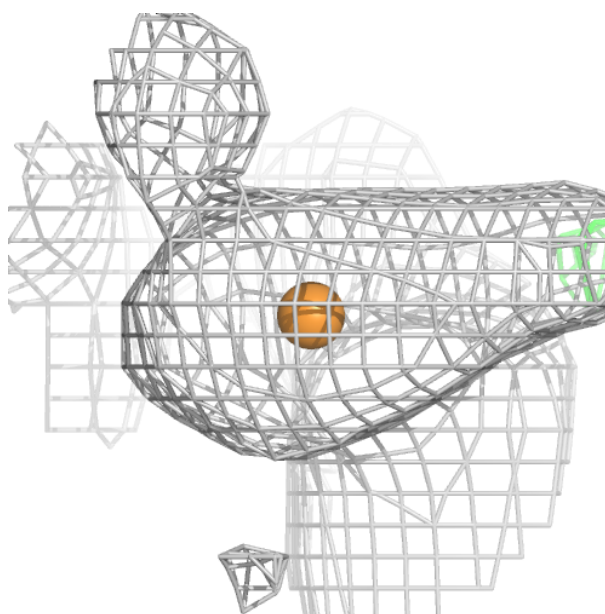
Electron density around CU B 605:

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



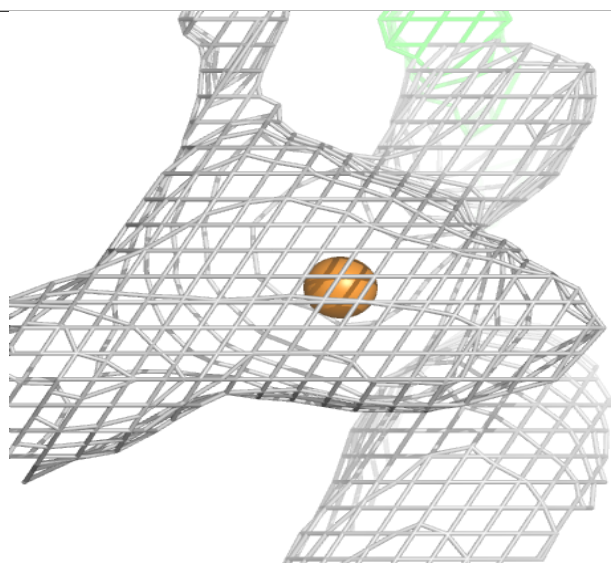
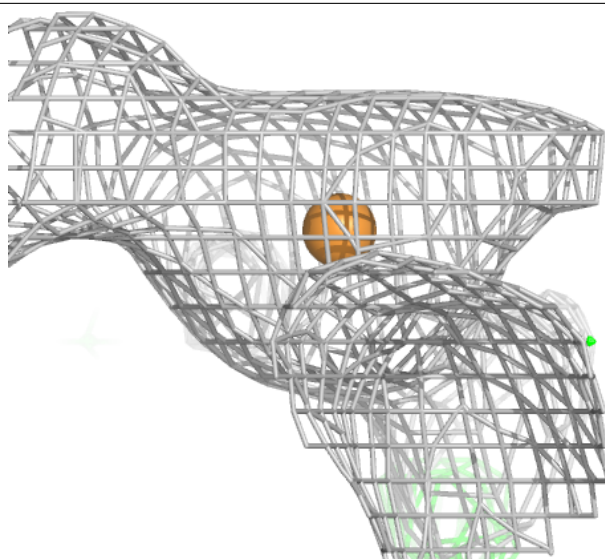
Electron density around CU A 605:

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



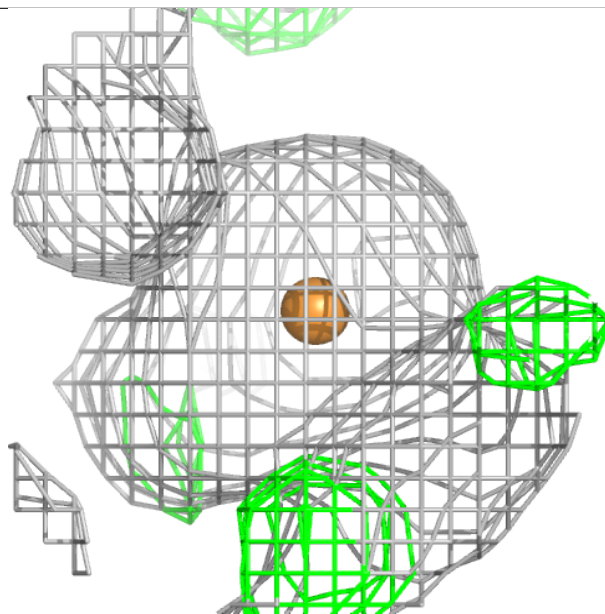
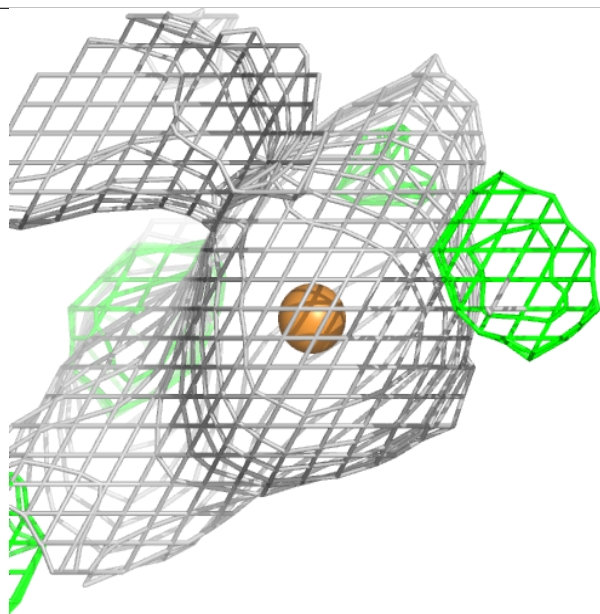
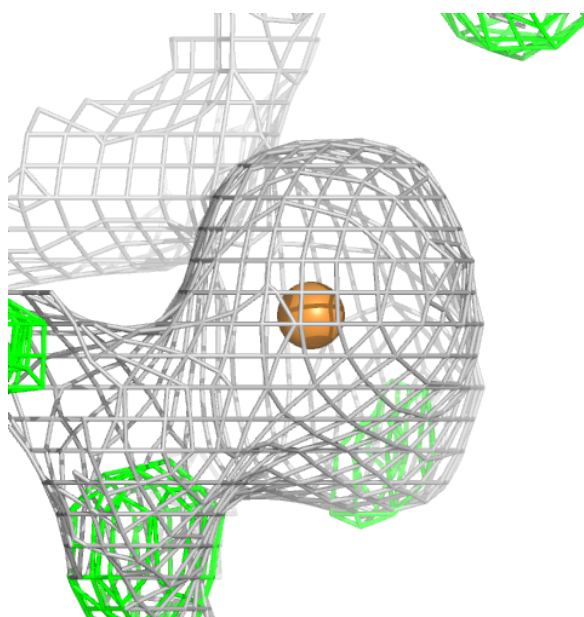
Electron density around CU B 606:

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and green (positive)



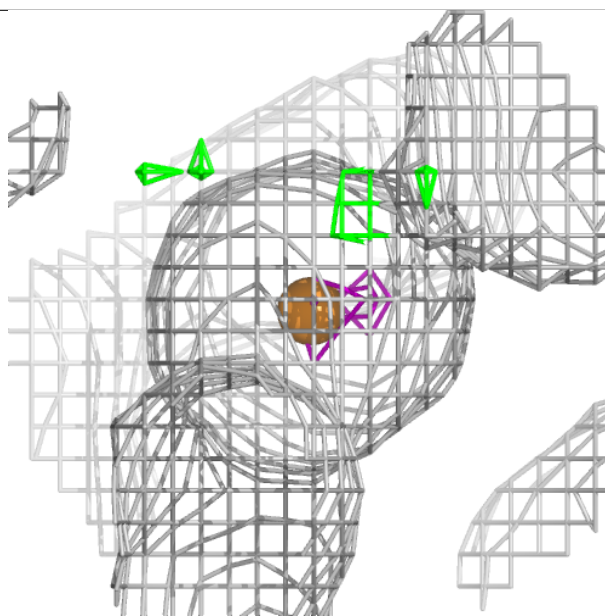
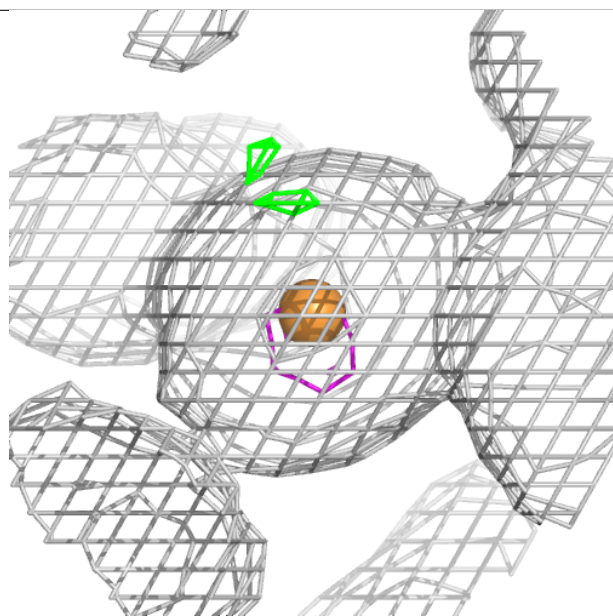
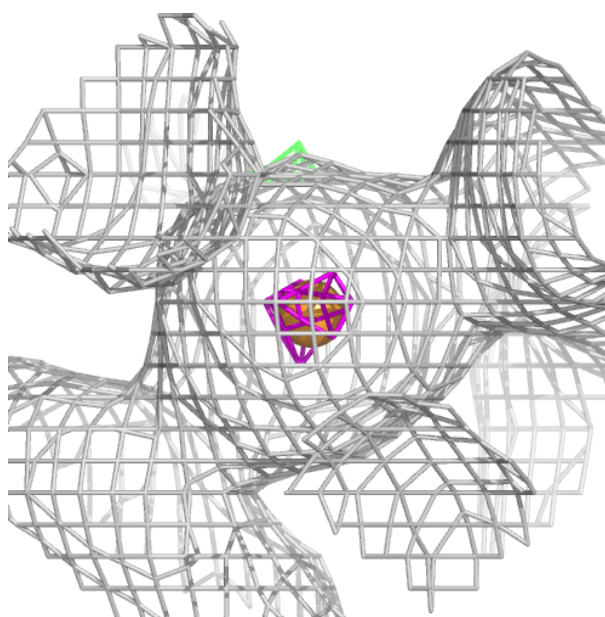
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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



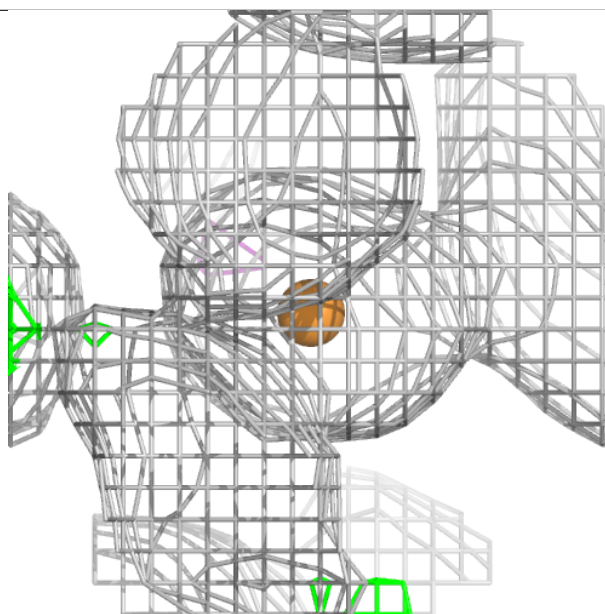
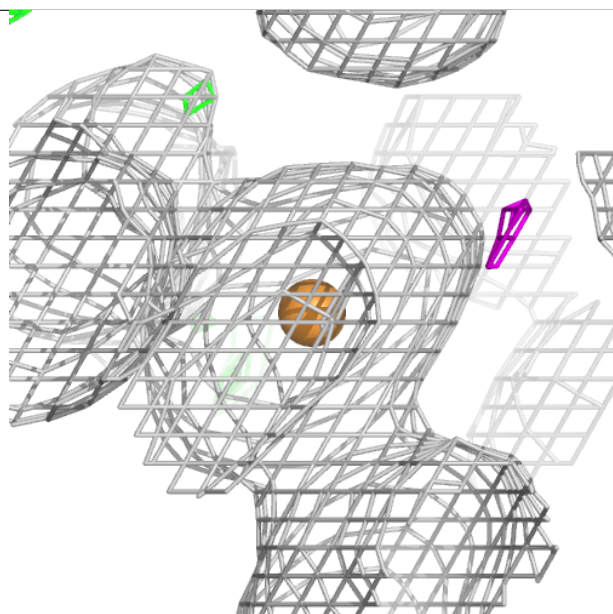
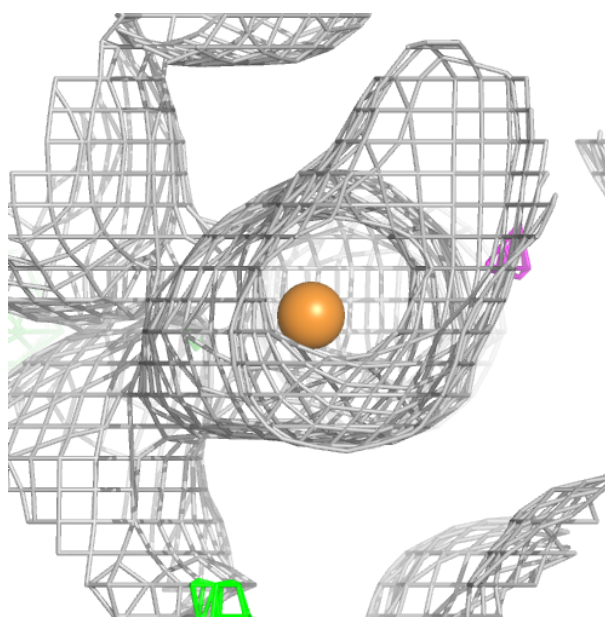
Electron density around CU B 603:

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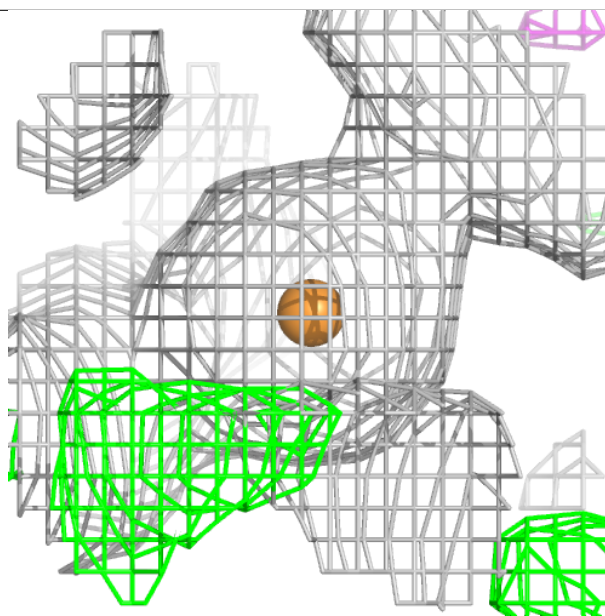
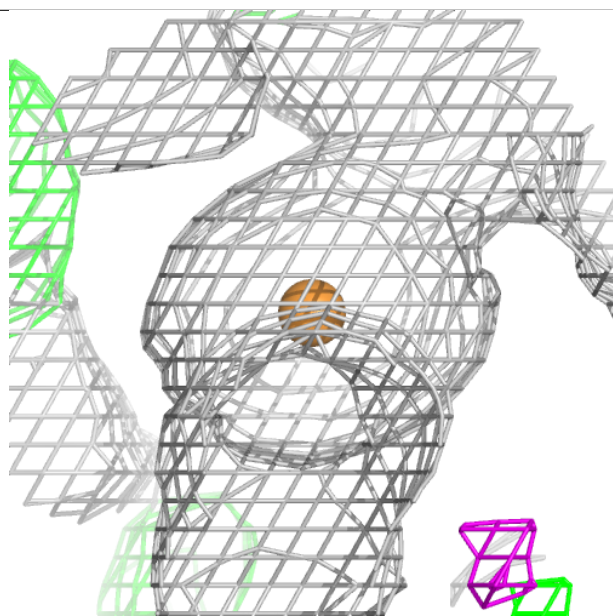
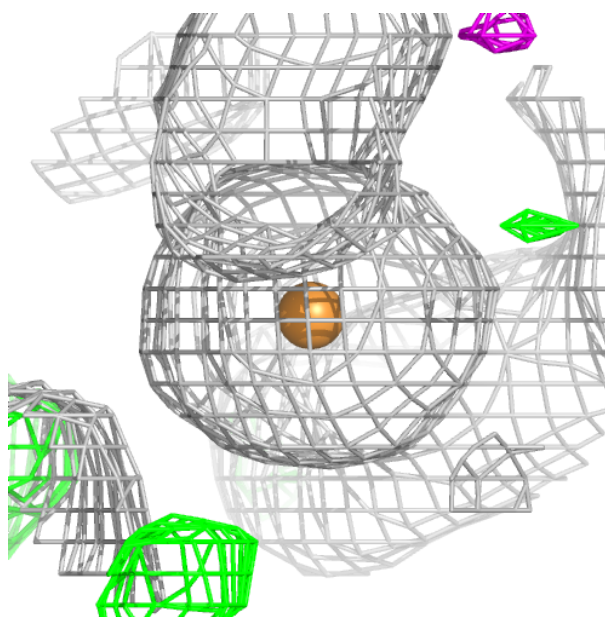
Electron density around CU B 604:

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and green (positive)



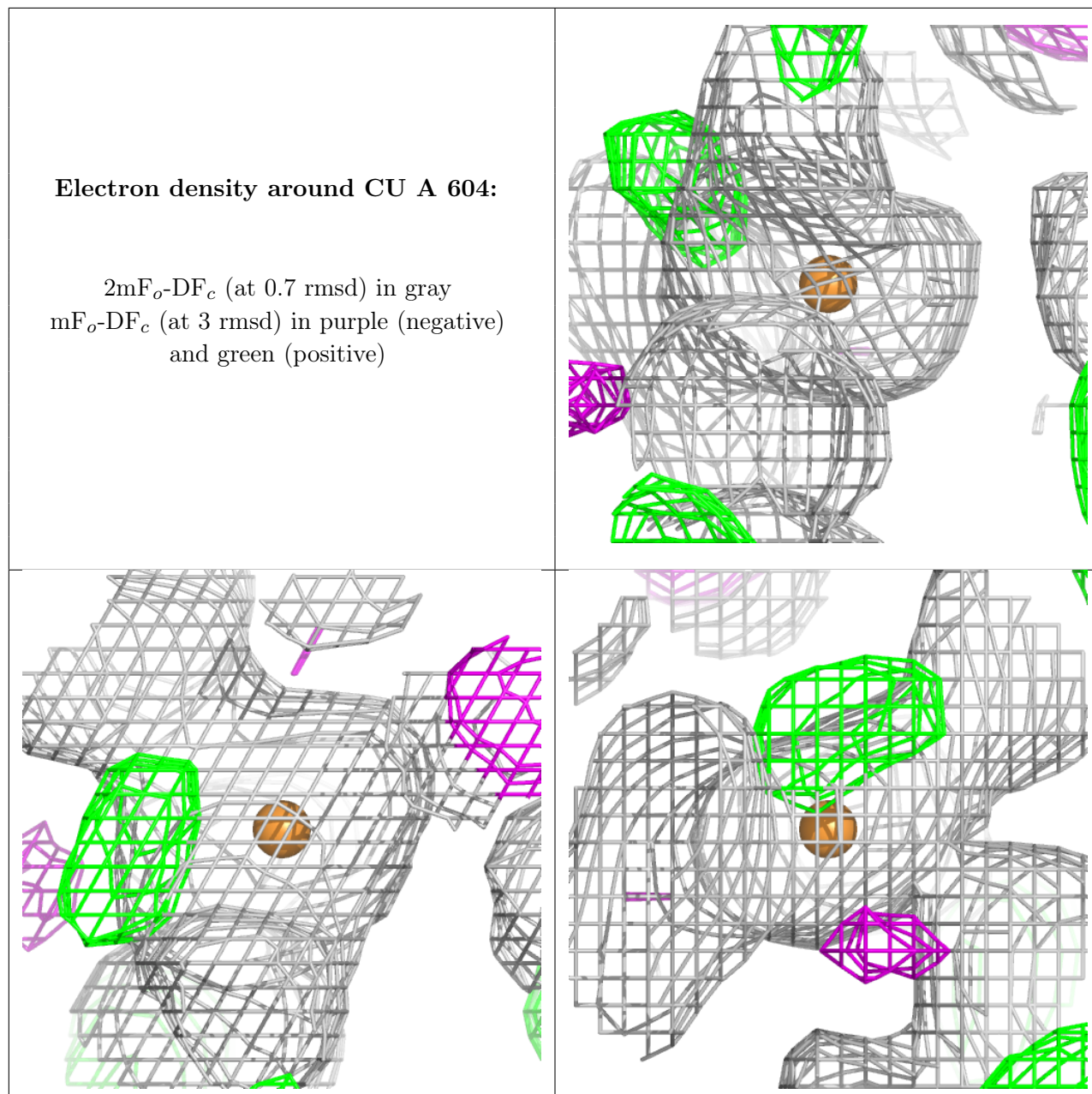
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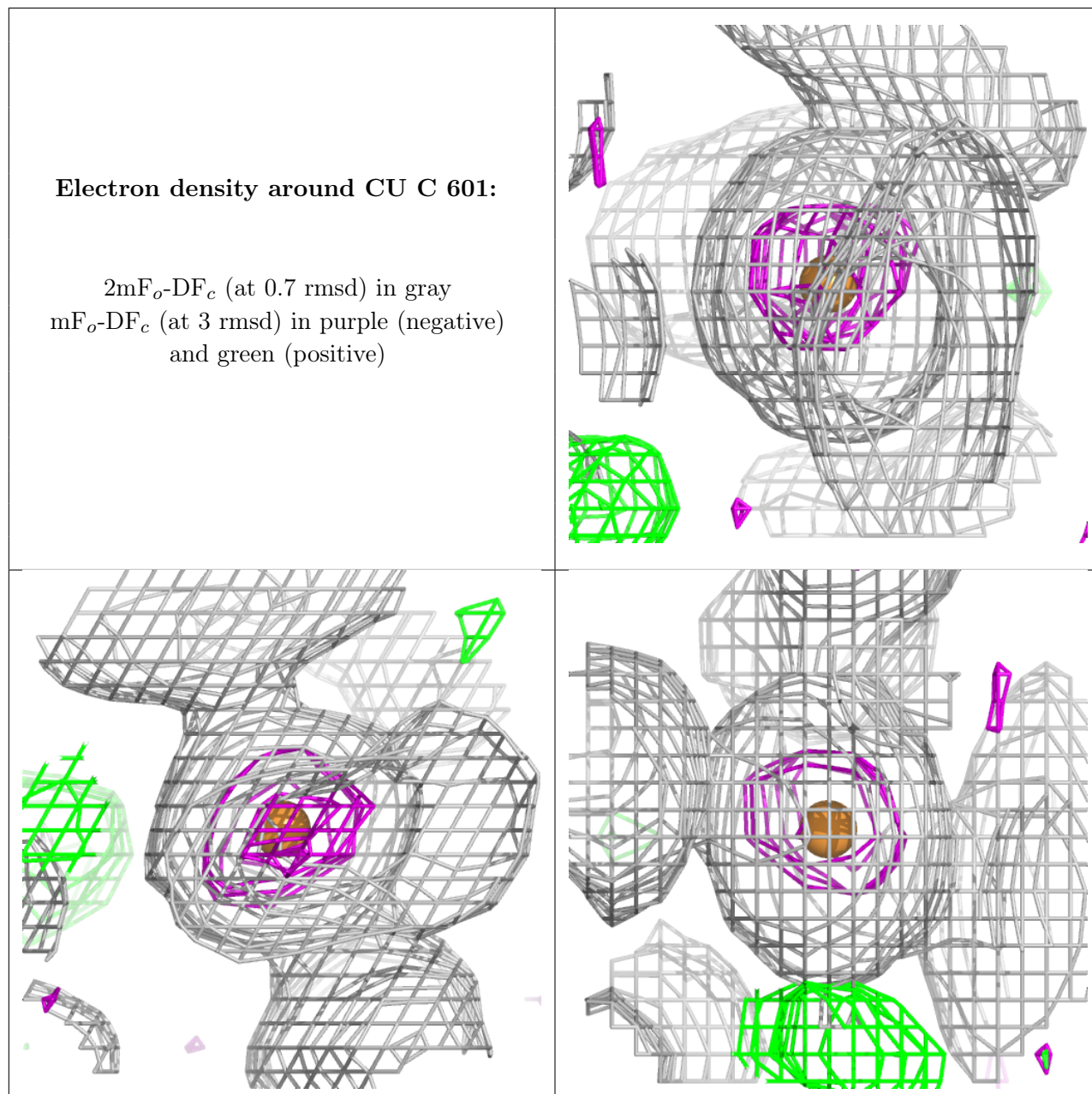
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and green (positive)



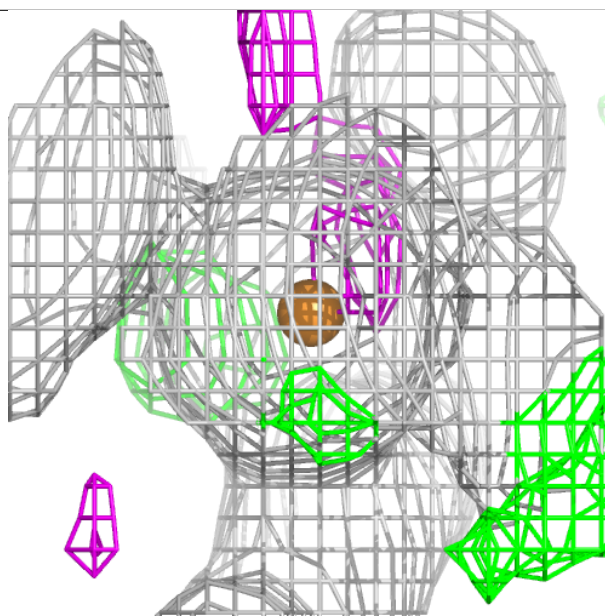
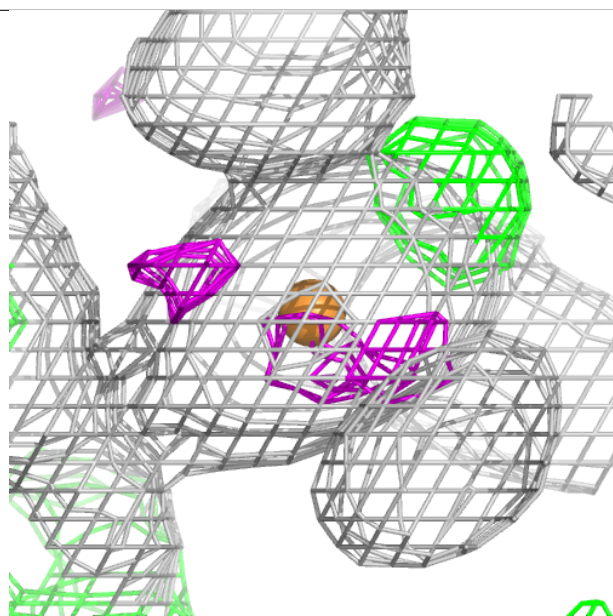
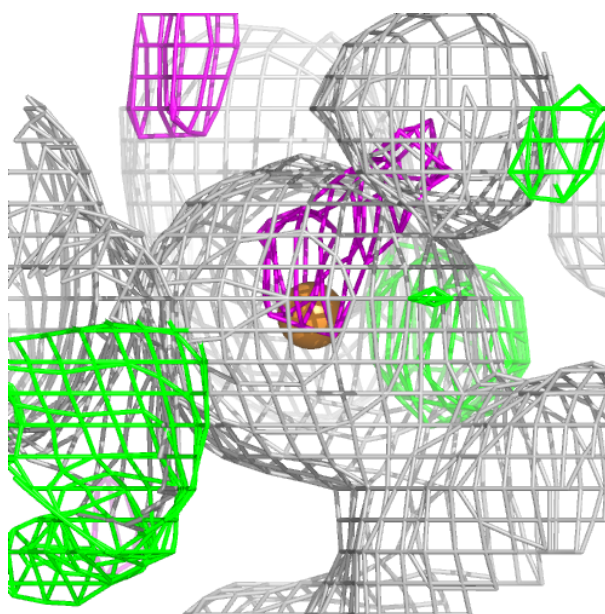
Electron density around CU C 601:

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and green (positive)



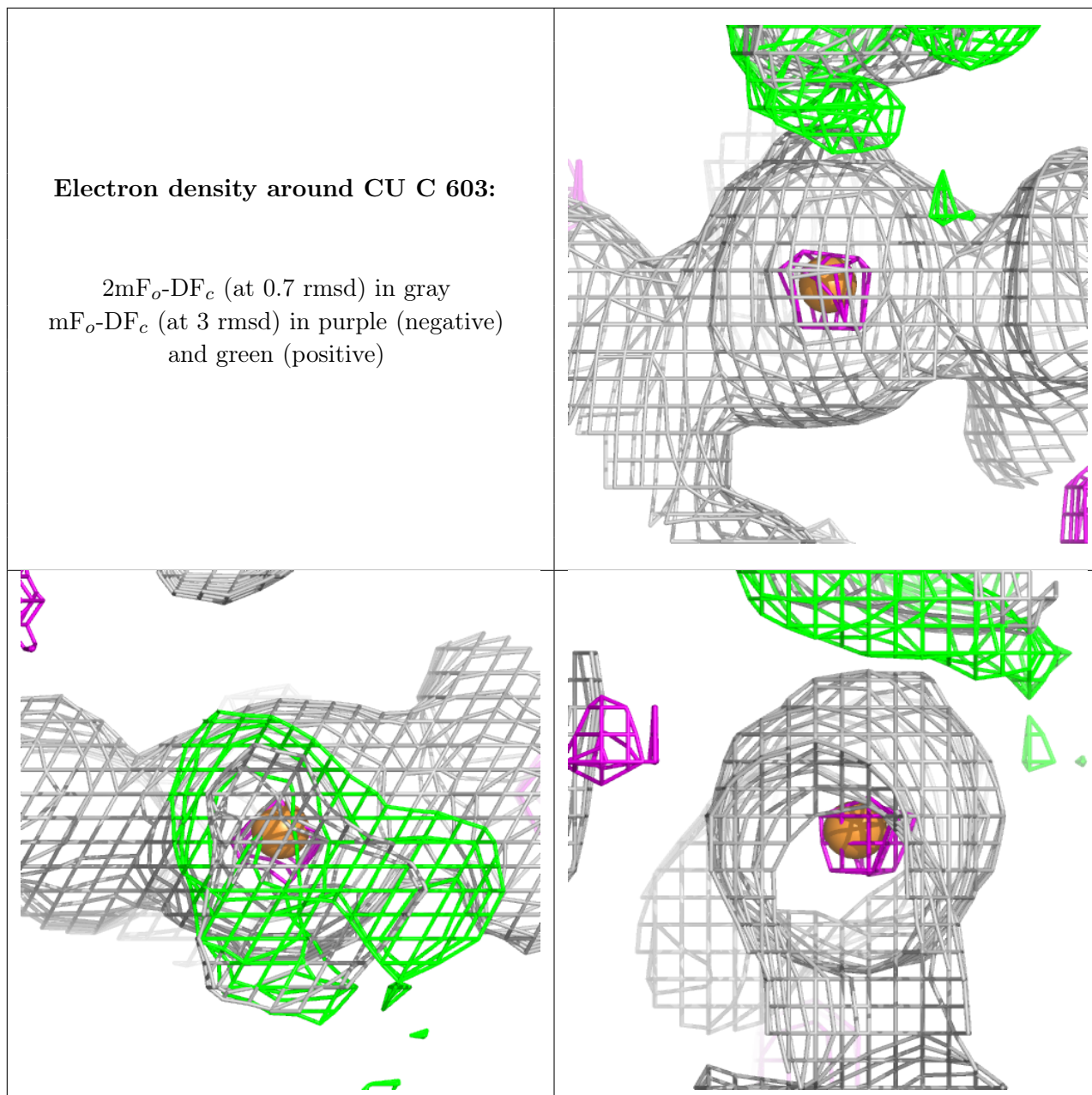
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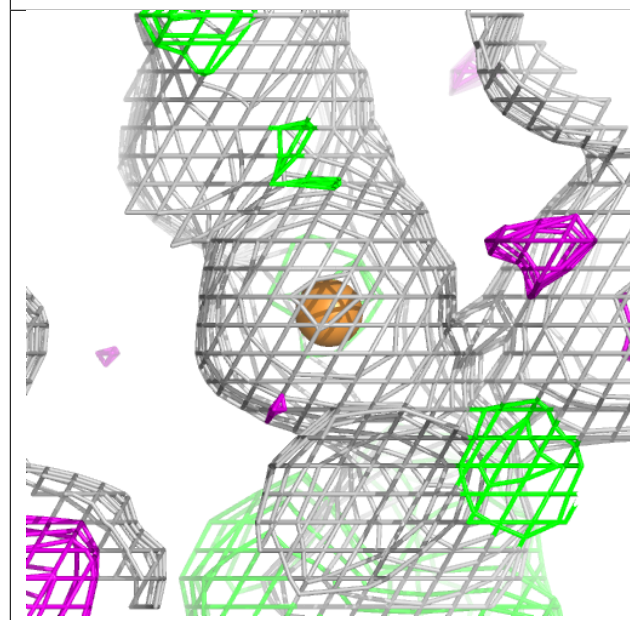
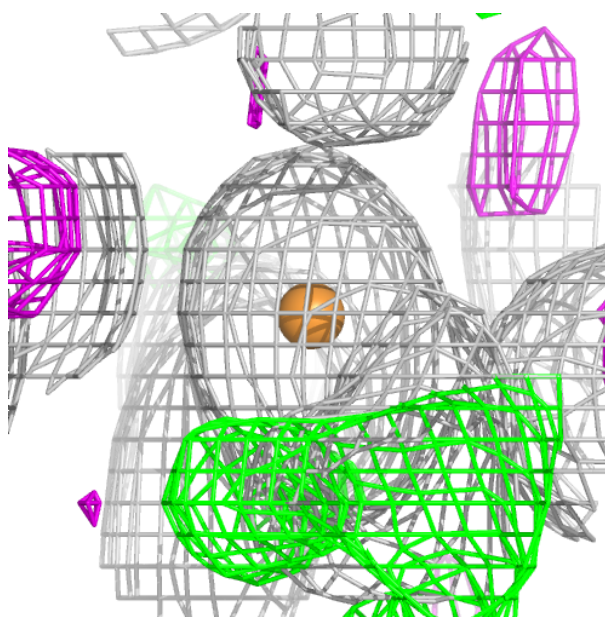
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and green (positive)



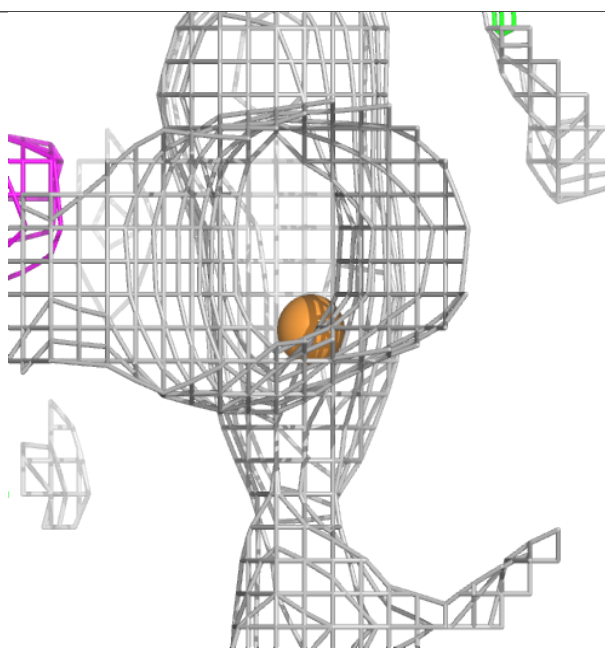
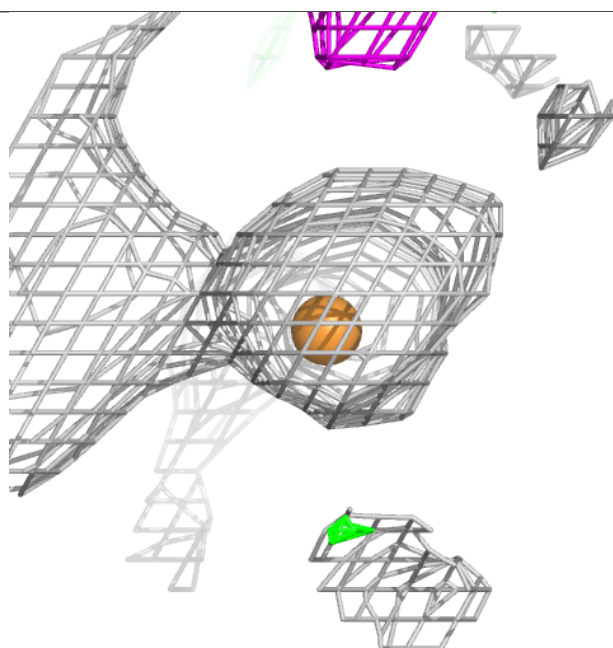
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and green (positive)



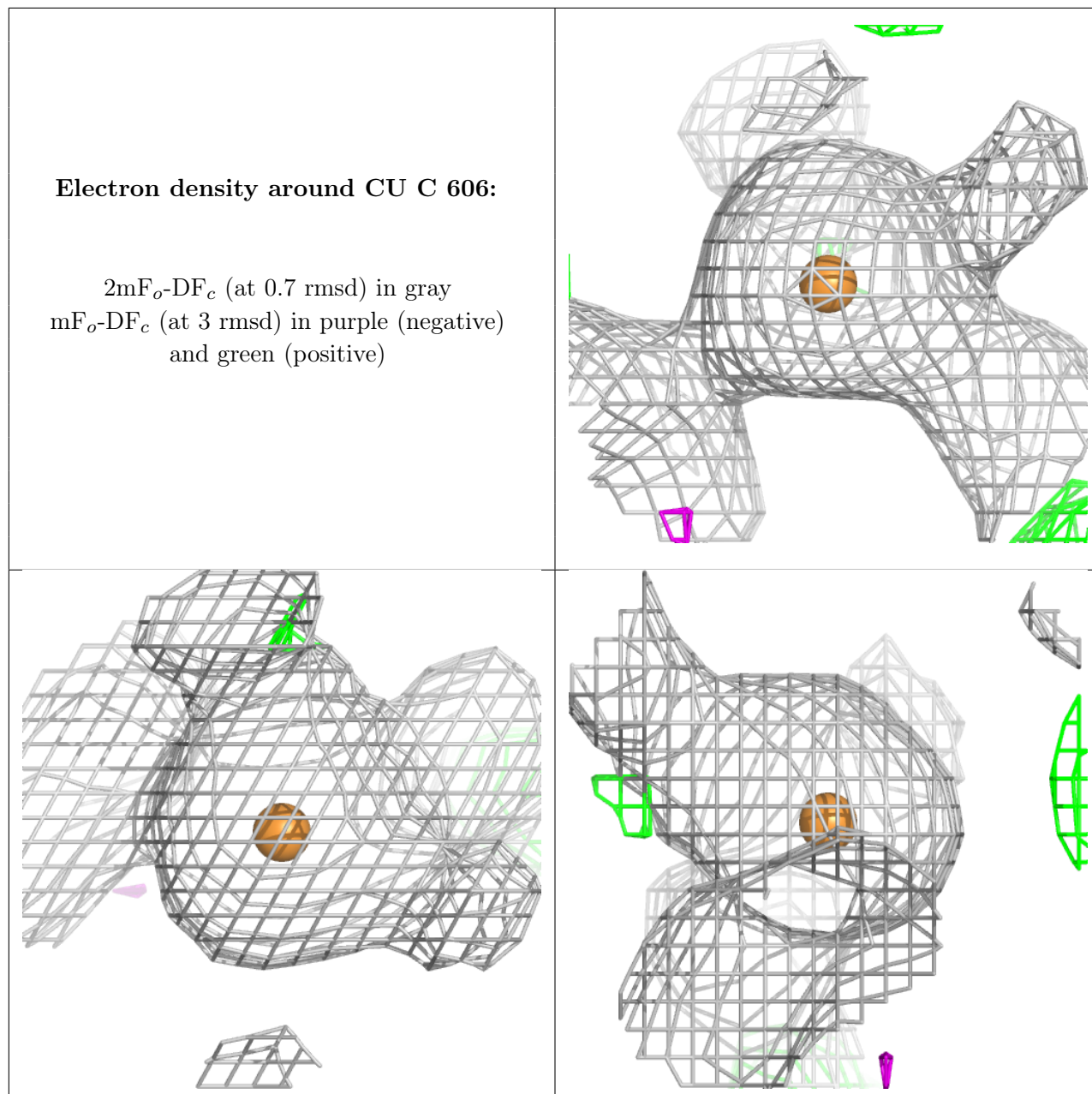
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and green (positive)



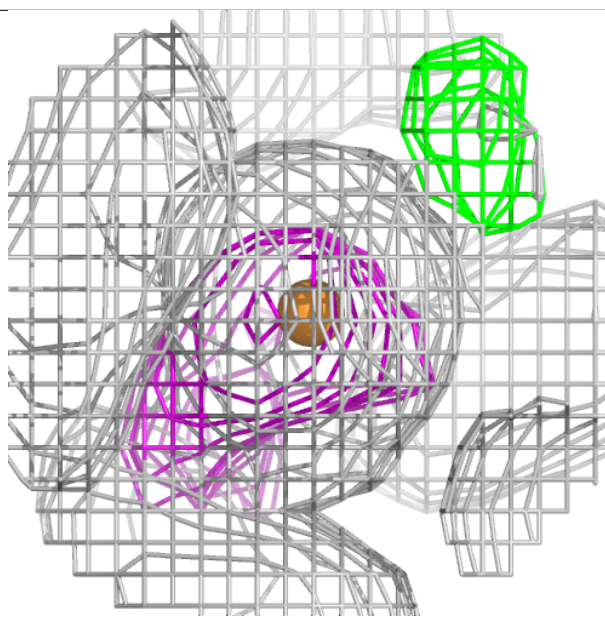
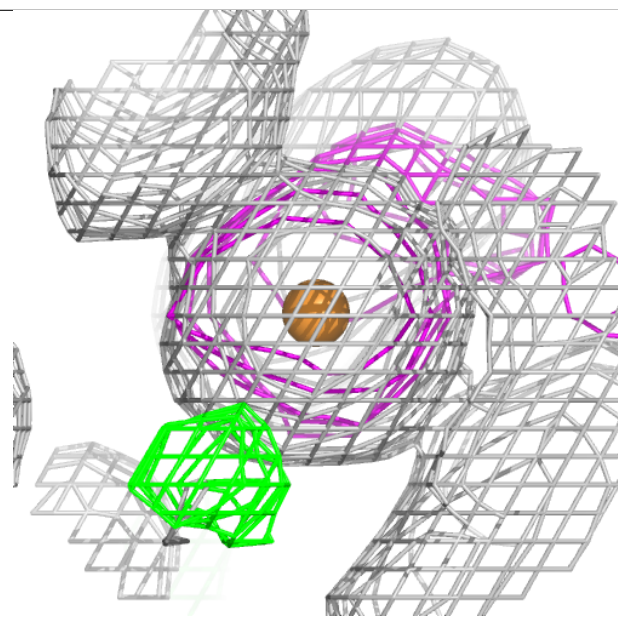
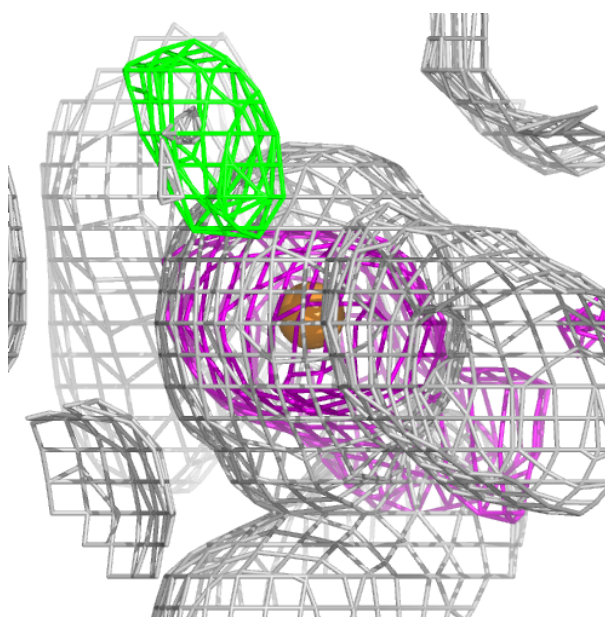
Electron density around CU C 606:

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and green (positive)



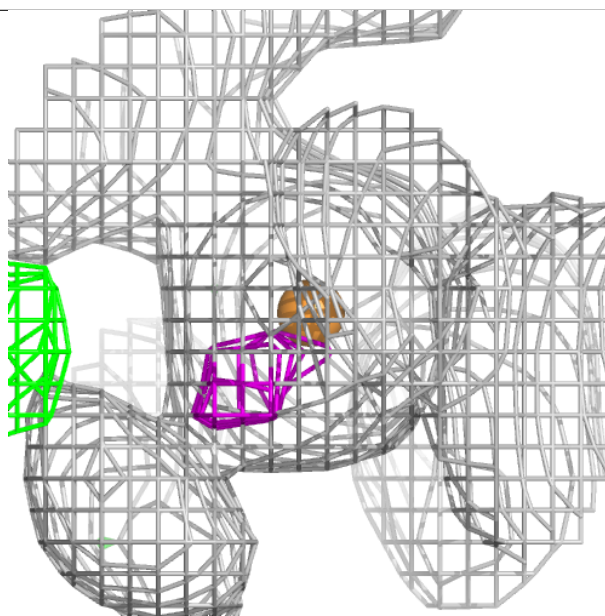
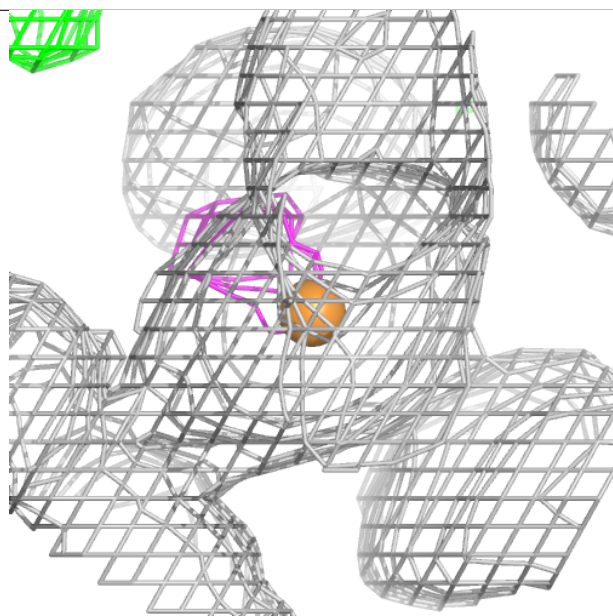
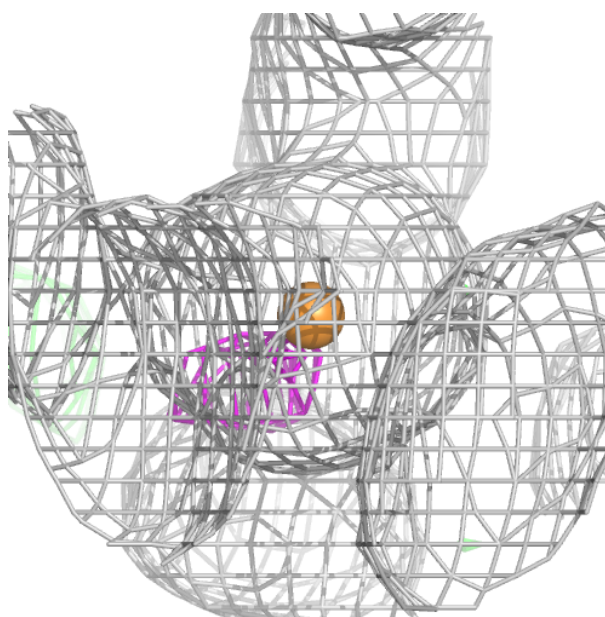
Electron density around CU D 601:

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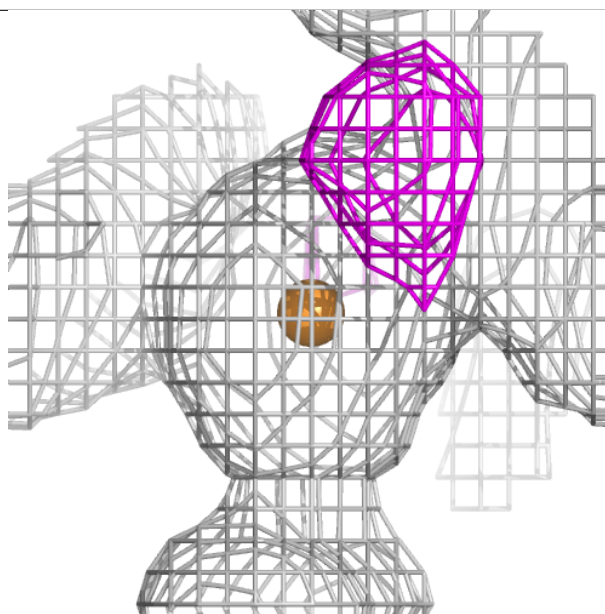
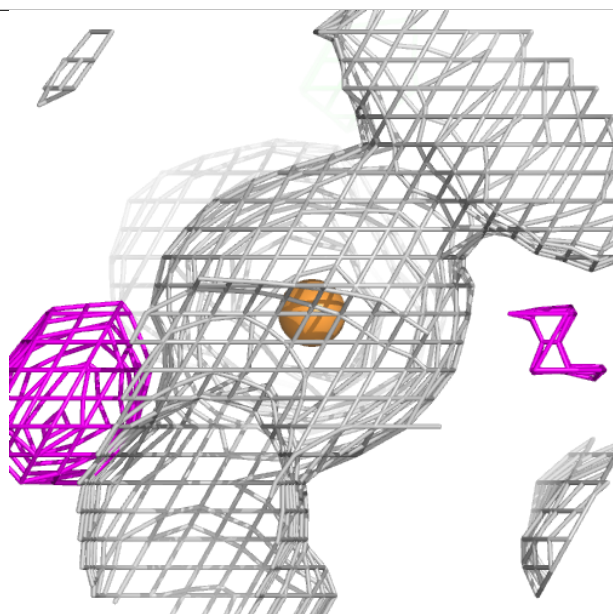
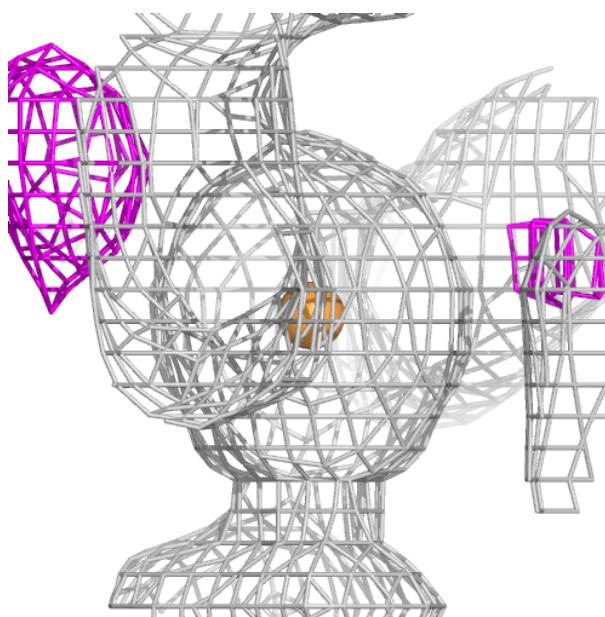
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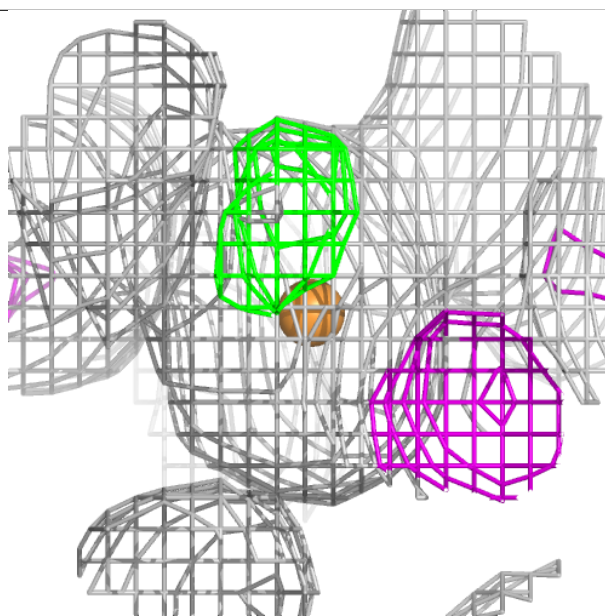
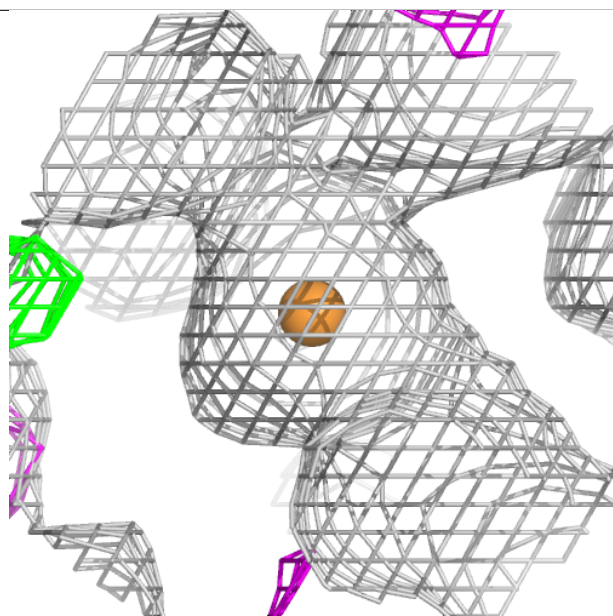
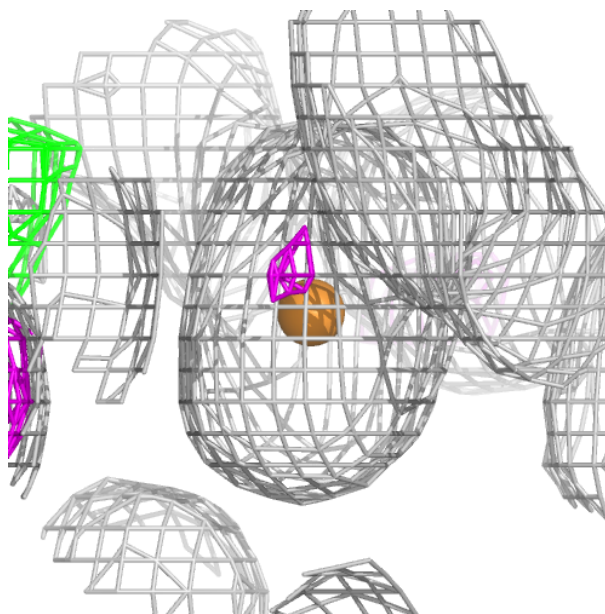
Electron density around CU D 603:

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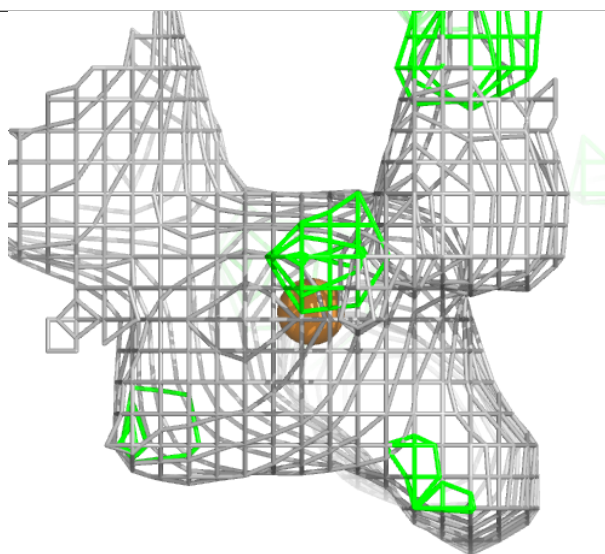
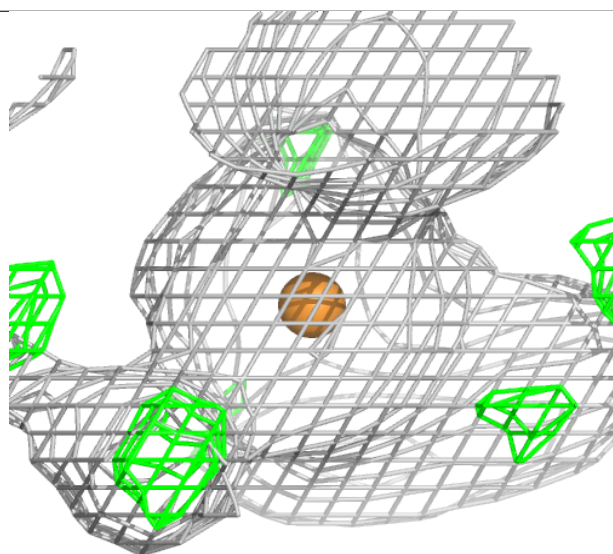
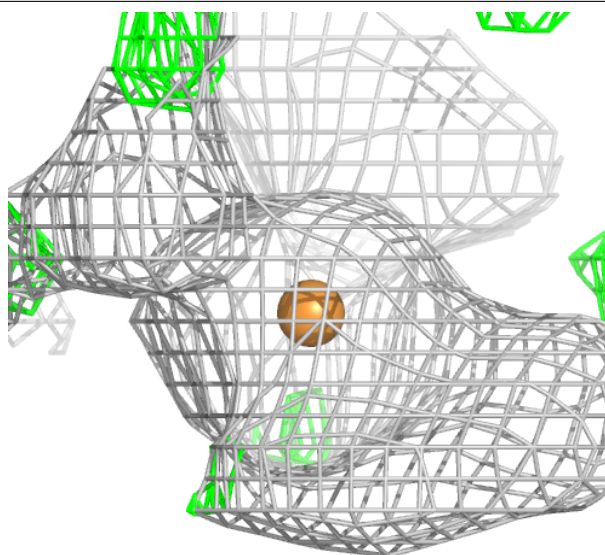
Electron density around CU D 604:

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and green (positive)



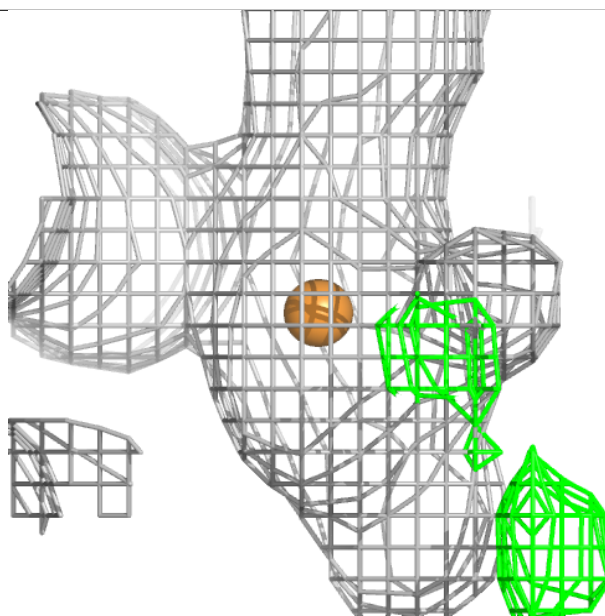
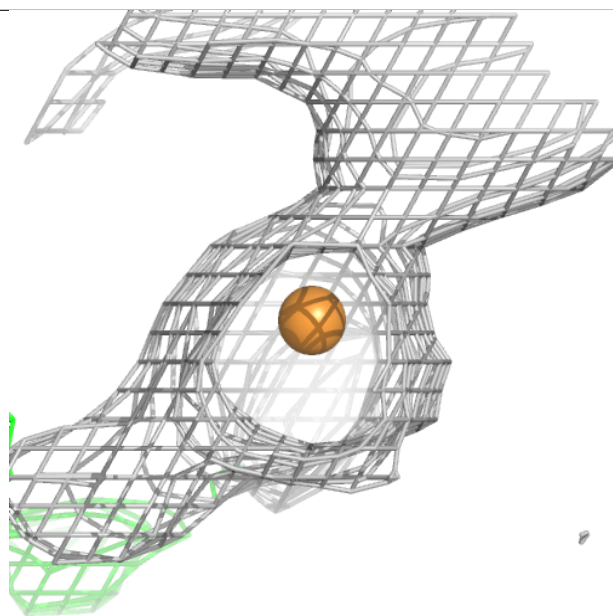
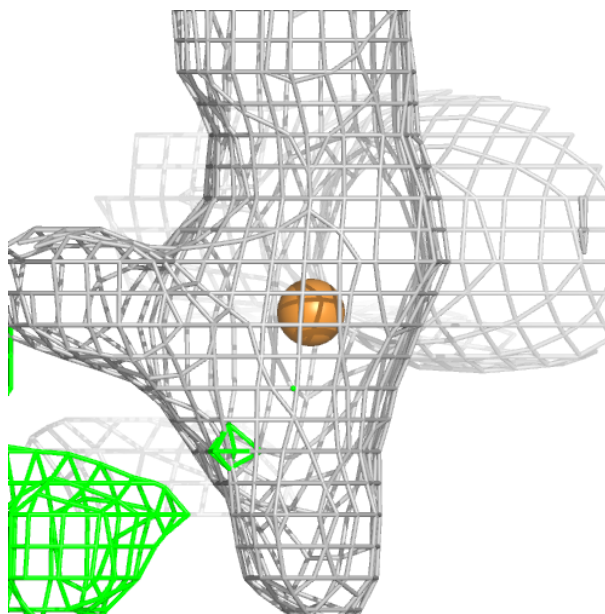
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and green (positive)



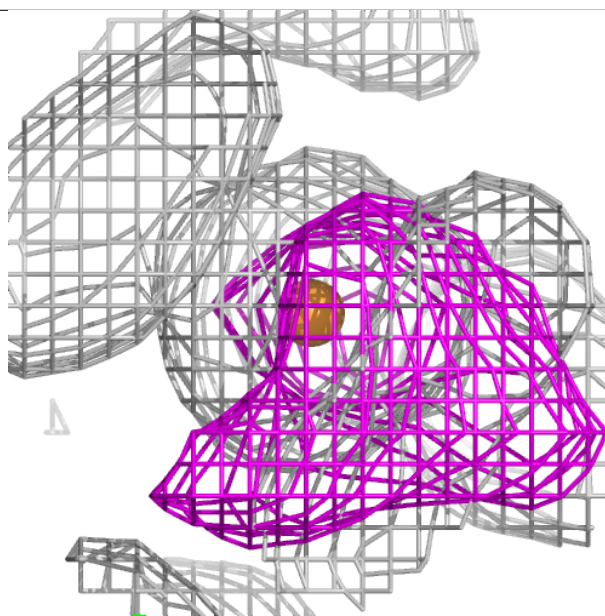
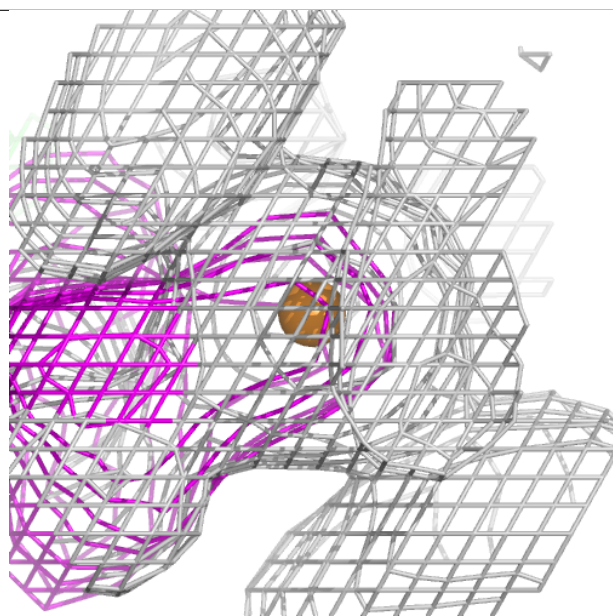
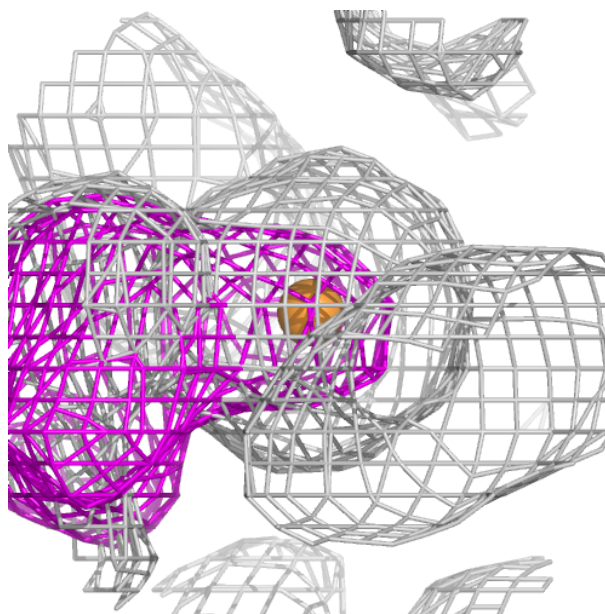
Electron density around CU D 606:

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and green (positive)



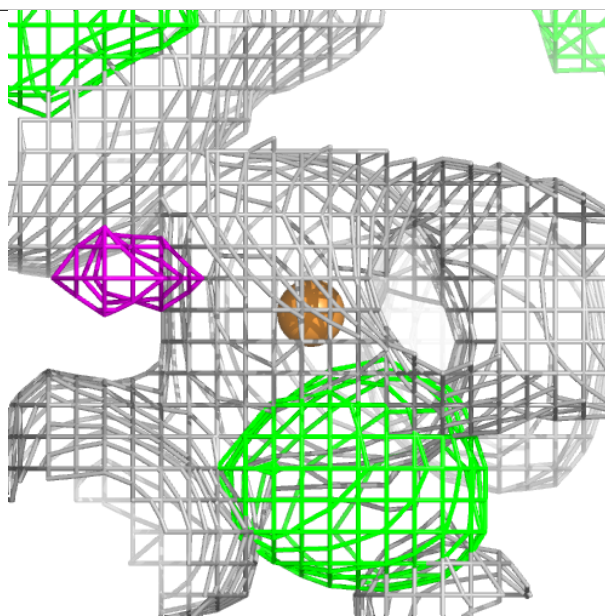
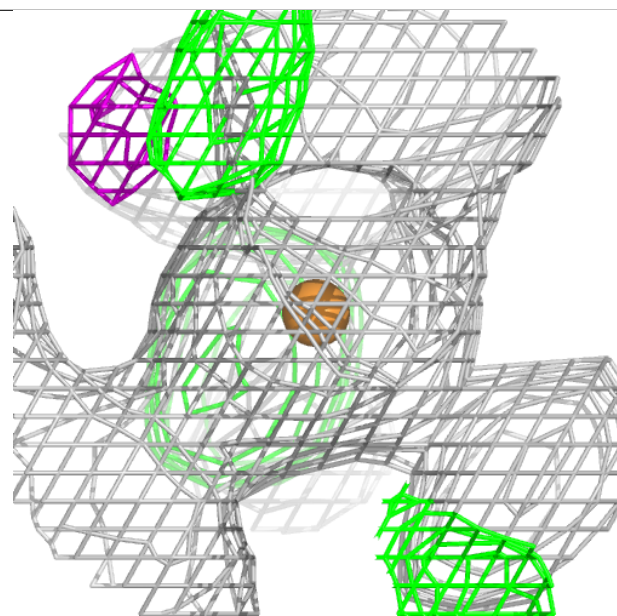
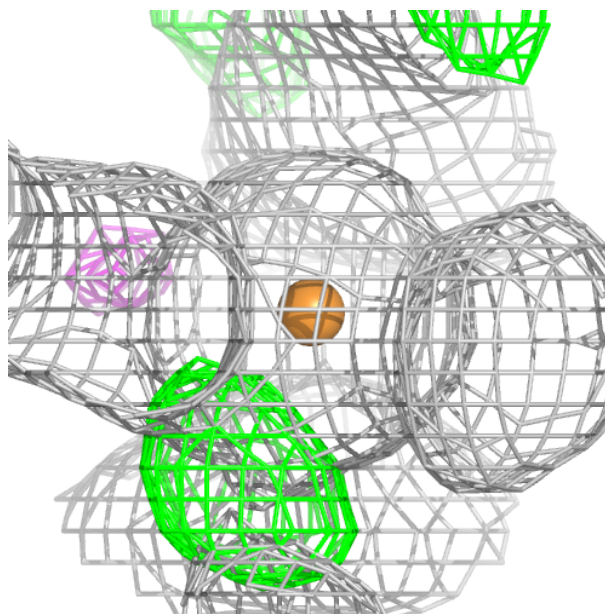
Electron density around CU A 601:

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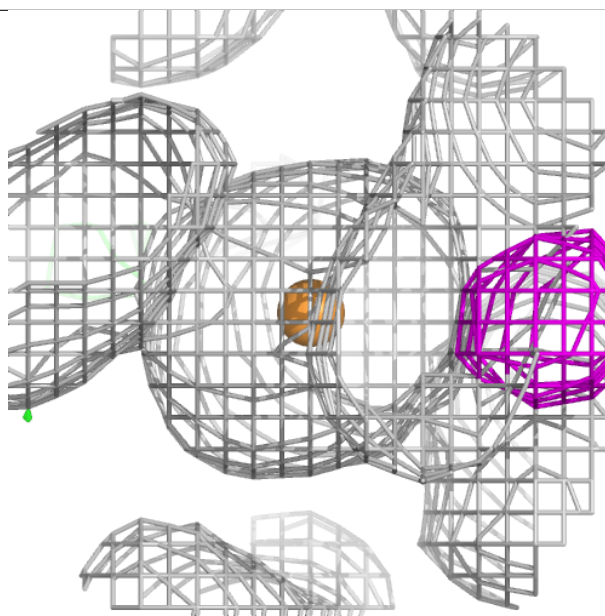
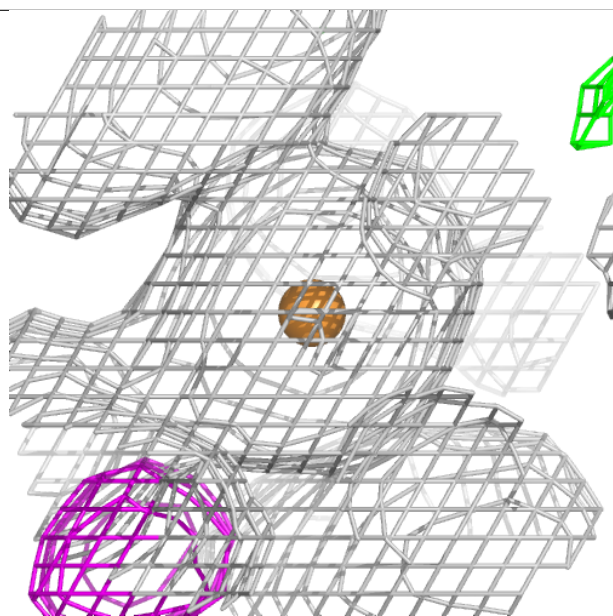
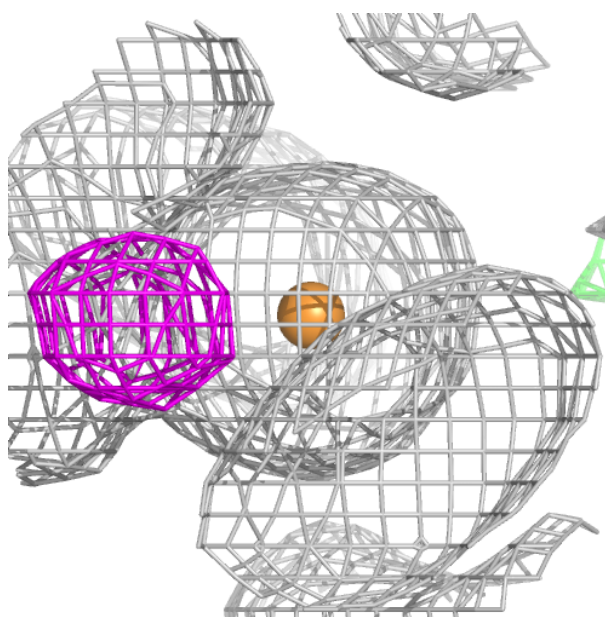
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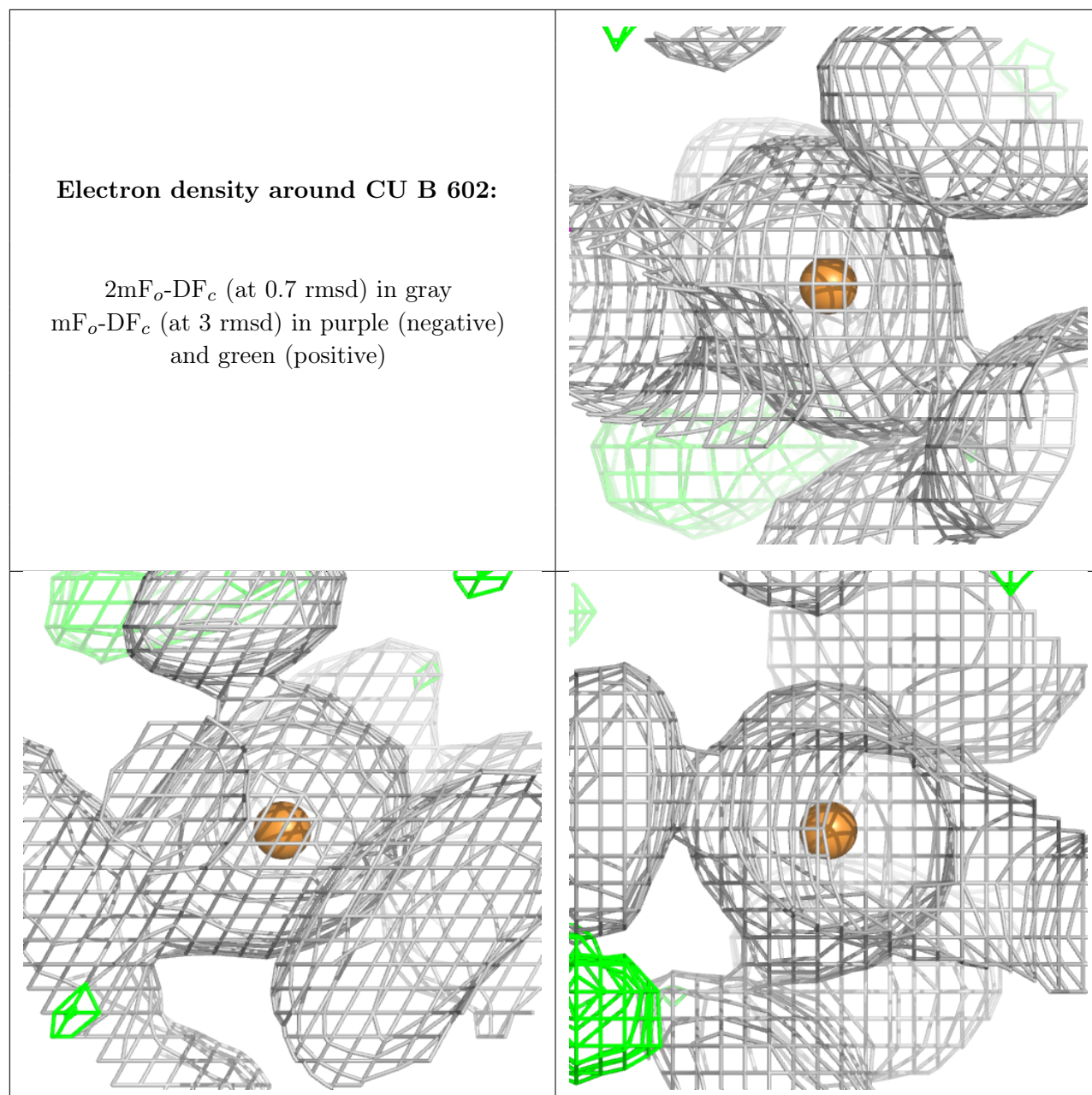
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around CU B 601:

$2mF_o-DF_c$ (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.