Full wwPDB X-ray Structure Validation Report (i)

Aug 5, 2026 – 02:48 PM EDT

PDB ID	:	9OEU / pdb_00009oeu
Title	:	HalA with lysine, succinate, chloride, and vanadium(IV)-oxo at pH 7
Authors	:	Kissman, E.N.; Stone, E.A.; Chang, M.C.Y.
Deposited on	:	2025-04-29
Resolution	:	1.67 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 (i) 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 (i)) were used in the production of this report:

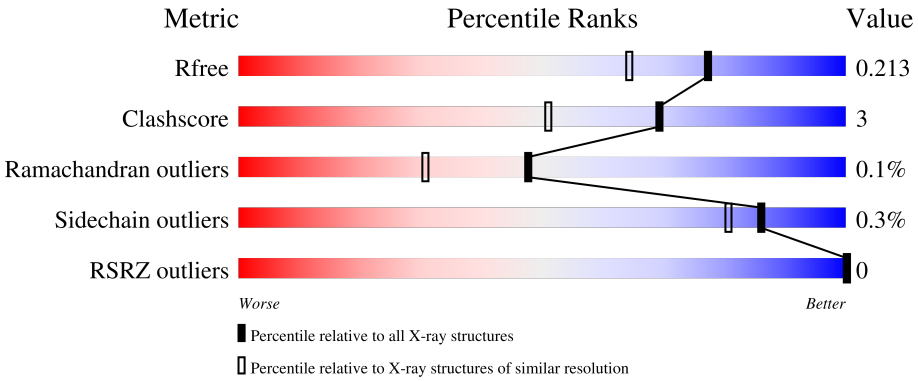
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.67 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	1054 (1.68-1.68)
Clashscore	190562	1078 (1.68-1.68)
Ramachandran outliers	187476	1068 (1.68-1.68)
Sidechain outliers	187428	1067 (1.68-1.68)
RSRZ outliers	180081	1055 (1.68-1.68)

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	258	94%
1	B	258	92% 6%
1	C	258	92% 5%
1	D	258	91% 5%
1	E	258	95%

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Mol	Chain	Length	Quality of chain
1	F	258	
1	G	258	
1	H	258	

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	VVO	A	303[A]	-	-	X	-
4	VVO	B	303[A]	-	-	X	-
4	VVO	B	303[B]	-	-	X	-
4	VVO	C	303[A]	-	-	X	-
4	VVO	C	303[B]	-	-	X	-
4	VVO	D	303[A]	-	-	X	-
4	VVO	E	303[A]	-	-	X	-
4	VVO	F	303[A]	-	-	X	-
4	VVO	F	303[B]	-	-	X	-
4	VVO	G	303[A]	-	-	X	-
4	VVO	G	303[B]	-	-	X	-
4	VVO	H	303[A]	-	-	X	-
5	CL	B	304[B]	-	-	X	-
5	CL	C	304[B]	-	-	X	-
5	CL	D	304[B]	-	-	X	-
5	CL	E	304[A]	-	-	X	-
5	CL	F	304[A]	-	-	X	-
5	CL	G	304[A]	-	-	X	-

2 Entry composition (i)

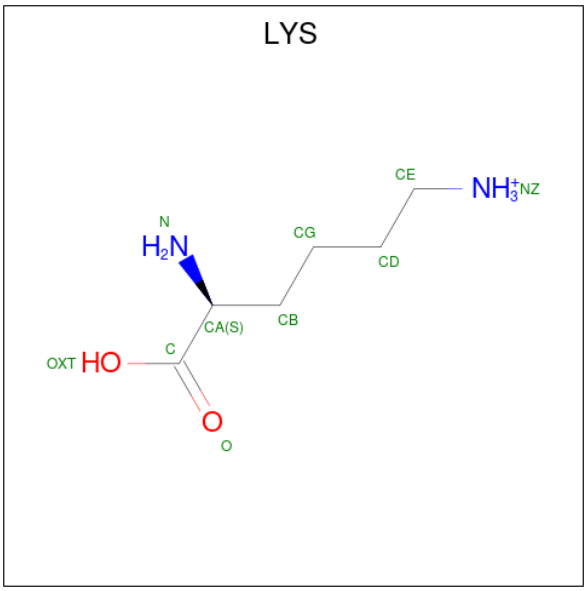
There are 6 unique types of molecules in this entry. The entry contains 16741 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Lysine halogenase.

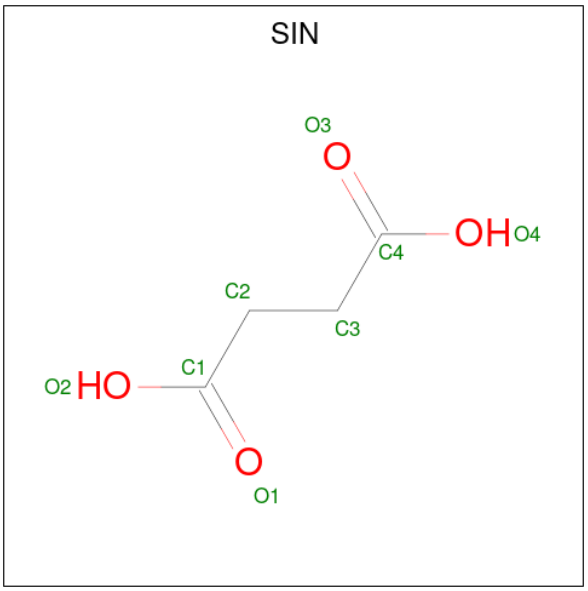
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	0	0	0
			1941	1222	350	363	6			
1	B	252	Total	C	N	O	S	0	0	0
			1958	1233	356	363	6			
1	C	251	Total	C	N	O	S	0	0	0
			1944	1228	350	360	6			
1	D	250	Total	C	N	O	S	0	0	0
			1919	1214	349	350	6			
1	E	250	Total	C	N	O	S	0	0	0
			1941	1220	351	364	6			
1	F	249	Total	C	N	O	S	0	0	0
			1909	1204	347	352	6			
1	G	248	Total	C	N	O	S	0	0	0
			1889	1194	345	344	6			
1	H	249	Total	C	N	O	S	0	0	0
			1912	1206	345	355	6			

- Molecule 2 is LYSINE (CCD ID: LYS) (formula: $C_6H_{15}N_2O_2$) (labeled as "Ligand of Interest" by depositor).



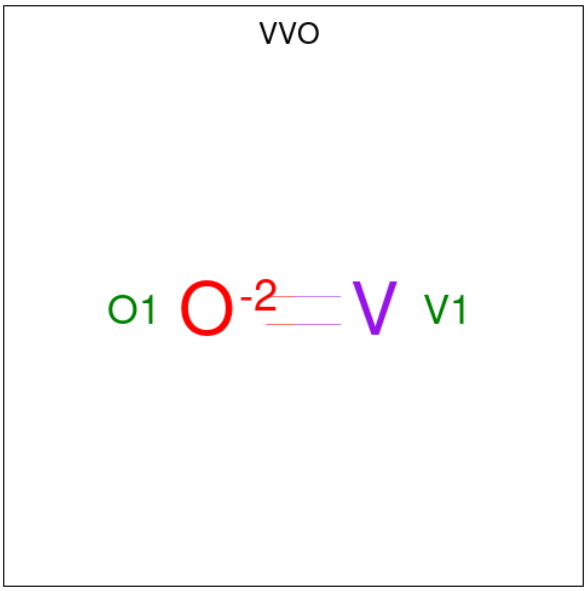
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O 10 6 2 2	0	0
2	B	1	Total C N O 10 6 2 2	0	0
2	C	1	Total C N O 10 6 2 2	0	0
2	D	1	Total C N O 10 6 2 2	0	0
2	E	1	Total C N O 10 6 2 2	0	0
2	F	1	Total C N O 10 6 2 2	0	0
2	G	1	Total C N O 10 6 2 2	0	0
2	H	1	Total C N O 10 6 2 2	0	0

- Molecule 3 is SUCCINIC ACID (CCD ID: SIN) (formula: $C_4H_6O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 8 4 4	0	0
3	B	1	Total C O 8 4 4	0	0
3	C	1	Total C O 8 4 4	0	0
3	D	1	Total C O 8 4 4	0	0
3	E	1	Total C O 8 4 4	0	0
3	F	1	Total C O 8 4 4	0	0
3	G	1	Total C O 8 4 4	0	0
3	H	1	Total C O 8 4 4	0	0

- Molecule 4 is oxovanadium(2+) (CCD ID: VVO) (formula: OV) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O V 4 2 2	0	1
4	B	1	Total O V 4 2 2	0	1
4	C	1	Total O V 4 2 2	0	1
4	D	1	Total O V 4 2 2	0	1
4	E	1	Total O V 4 2 2	0	1
4	F	1	Total O V 4 2 2	0	1
4	G	1	Total O V 4 2 2	0	1
4	H	1	Total O V 4 2 2	0	1

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	D	1	Total Cl 2 2	0	1
5	E	1	Total Cl 2 2	0	1
5	F	1	Total Cl 2 2	0	1
5	G	1	Total Cl 2 2	0	1
5	H	1	Total Cl 2 2	0	1

- Molecule 6 is water.

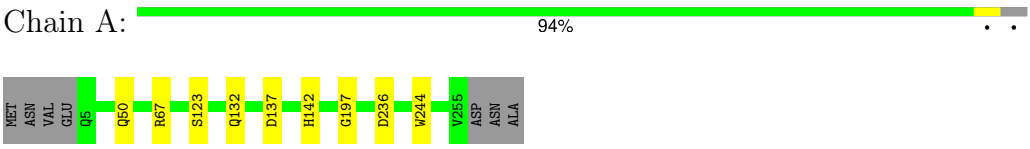
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	160	Total O 160 160	0	0
6	B	144	Total O 144 144	0	0
6	C	153	Total O 153 153	0	0
6	D	146	Total O 146 146	0	0
6	E	157	Total O 157 157	0	0
6	F	152	Total O 152 152	0	0
6	G	112	Total O 112 112	0	0
6	H	112	Total O 112 112	0	0

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.

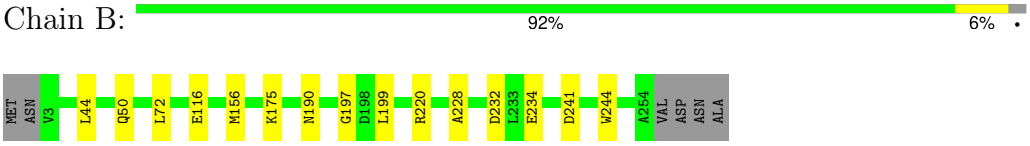
• Molecule 1: Lysine halogenase

Chain A:



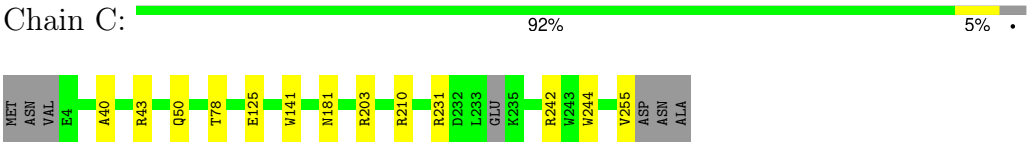
• Molecule 1: Lysine halogenase

Chain B:



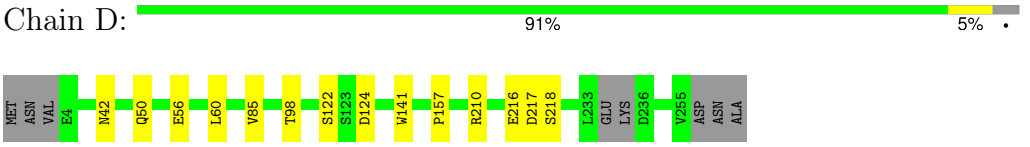
• Molecule 1: Lysine halogenase

Chain C:



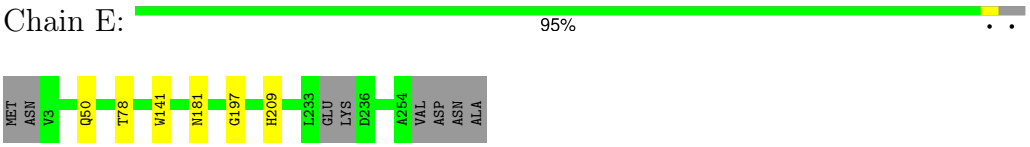
• Molecule 1: Lysine halogenase

Chain D:



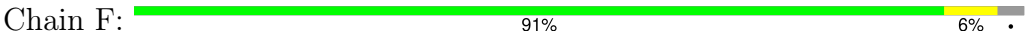
• Molecule 1: Lysine halogenase

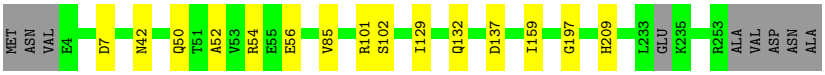
Chain E:



• Molecule 1: Lysine halogenase

Chain F:

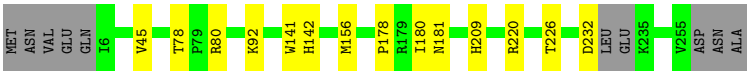




• Molecule 1: Lysine halogenase

Chain G:





• Molecule 1: Lysine halogenase

Chain H:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	147.32Å 147.32Å 286.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	95.61 – 1.67 95.61 – 1.67	Depositor EDS
% Data completeness (in resolution range)	100.0 (95.61-1.67) 100.0 (95.61-1.67)	Depositor EDS
R_{merge}	0.29	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.55 (at 1.67Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.185 , 0.213 0.186 , 0.213	Depositor DCC
R_{free} test set	13540 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	19.3	Xtriage
Anisotropy	0.400	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 24.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.24$	Xtriage
Estimated twinning fraction	0.198 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	16741	wwPDB-VP
Average B, all atoms (Å^2)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.59% of the height of the origin peak. No significant pseudotranslation is detected.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, SIN, VVO

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	0.20	0/1985	0.40	0/2708
1	B	0.17	0/2002	0.38	0/2728
1	C	0.18	0/1987	0.40	0/2707
1	D	0.18	0/1962	0.39	0/2677
1	E	0.17	0/1985	0.37	0/2706
1	F	0.18	0/1953	0.38	0/2664
1	G	0.16	0/1933	0.37	0/2639
1	H	0.18	0/1955	0.36	0/2669
All	All	0.18	0/15762	0.38	0/21498

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1941	0	1832	10	0
1	B	1958	0	1862	11	0
1	C	1944	0	1849	7	0
1	D	1919	0	1825	9	0
1	E	1941	0	1827	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1909	0	1782	11	0
1	G	1889	0	1770	9	0
1	H	1912	0	1792	12	0
2	A	10	0	12	3	0
2	B	10	0	12	2	0
2	C	10	0	12	2	0
2	D	10	0	12	1	0
2	E	10	0	12	1	0
2	F	10	0	12	1	0
2	G	10	0	12	0	0
2	H	10	0	12	2	0
3	A	8	0	4	0	0
3	B	8	0	4	0	0
3	C	8	0	4	0	0
3	D	8	0	4	0	0
3	E	8	0	4	0	0
3	F	8	0	4	0	0
3	G	8	0	4	0	0
3	H	8	0	4	0	0
4	A	4	0	0	3	0
4	B	4	0	0	4	0
4	C	4	0	0	4	0
4	D	4	0	0	3	0
4	E	4	0	0	3	0
4	F	4	0	0	4	0
4	G	4	0	0	5	0
4	H	4	0	0	3	0
5	A	2	0	0	1	0
5	B	2	0	0	3	0
5	C	2	0	0	3	0
5	D	2	0	0	3	0
5	E	2	0	0	3	0
5	F	2	0	0	3	0
5	G	2	0	0	3	0
5	H	2	0	0	2	0
6	A	160	0	0	3	0
6	B	144	0	0	4	0
6	C	153	0	0	0	0
6	D	146	0	0	5	0
6	E	157	0	0	1	0
6	F	152	0	0	3	0
6	G	112	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	H	112	0	0	3	0
All	All	16741	0	14667	105	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.

All (105) 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)
4:H:303[A]:VVO:O1	5:H:304[A]:CL:CL	2.22	0.95
4:F:303[A]:VVO:O1	5:F:304[A]:CL:CL	2.44	0.73
1:H:32:ARG:NH2	6:H:401:HOH:O	2.22	0.72
4:D:303[A]:VVO:O1	5:D:304[A]:CL:CL	2.46	0.70
1:H:29:ARG:NH1	6:H:401:HOH:O	2.27	0.67
1:B:175:LYS:O	6:B:401:HOH:O	2.14	0.66
1:G:181:ASN:HB3	1:H:159:ILE:HG22	1.77	0.66
2:B:301:LYS:HG2	5:B:304[B]:CL:CL	2.37	0.62
1:D:157:PRO:HB3	1:D:218:SER:HB3	1.81	0.62
2:C:301:LYS:HG2	5:C:304[B]:CL:CL	2.38	0.61
1:D:98:THR:O	6:D:401:HOH:O	2.16	0.61
4:C:303[A]:VVO:V1	4:C:303[A]:VVO:O1	1.58	0.60
4:F:303[B]:VVO:V1	4:F:303[B]:VVO:O1	1.57	0.60
4:D:303[B]:VVO:V1	4:D:303[B]:VVO:O1	1.58	0.60
4:A:303[A]:VVO:V1	4:A:303[A]:VVO:O1	1.58	0.60
4:B:303[A]:VVO:V1	4:B:303[A]:VVO:O1	1.58	0.60
4:E:303[A]:VVO:V1	4:E:303[A]:VVO:O1	1.58	0.60
4:D:303[A]:VVO:O1	4:D:303[A]:VVO:V1	1.58	0.60
4:E:303[B]:VVO:O1	4:E:303[B]:VVO:V1	1.58	0.60
4:H:303[B]:VVO:V1	4:H:303[B]:VVO:O1	1.58	0.60
4:G:303[B]:VVO:V1	4:G:303[B]:VVO:O1	1.58	0.60
4:F:303[A]:VVO:O1	4:F:303[A]:VVO:V1	1.58	0.59
4:B:303[B]:VVO:V1	4:B:303[B]:VVO:O1	1.58	0.59
1:F:101:ARG:NH2	6:F:405:HOH:O	2.34	0.59
4:A:303[B]:VVO:O1	4:A:303[B]:VVO:V1	1.58	0.59
2:H:301:LYS:HG2	5:H:304[B]:CL:CL	2.39	0.59
4:G:303[A]:VVO:O1	4:G:303[A]:VVO:V1	1.59	0.58
2:F:301:LYS:HG2	5:F:304[B]:CL:CL	2.40	0.58
4:C:303[B]:VVO:V1	4:C:303[B]:VVO:O1	1.58	0.58
4:H:303[A]:VVO:O1	4:H:303[A]:VVO:V1	1.58	0.57
4:B:303[A]:VVO:O1	5:B:304[A]:CL:CL	2.59	0.57
1:H:203:ARG:NH1	6:H:405:HOH:O	2.33	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:304[B]:CL:CL	6:D:461:HOH:O	2.50	0.55
4:C:303[A]:VVO:O1	5:C:304[A]:CL:CL	2.62	0.55
4:C:303[B]:VVO:O1	5:C:304[B]:CL:CL	2.62	0.55
1:G:78:THR:HG21	1:G:141:TRP:HB2	1.89	0.55
1:A:236:ASP:OD1	6:A:401:HOH:O	2.18	0.54
1:A:142:HIS:NE2	4:A:303[A]:VVO:O1	2.40	0.54
4:B:303[B]:VVO:O1	5:B:304[B]:CL:CL	2.63	0.54
1:F:132:GLN:HB3	1:F:137:ASP:HB3	1.89	0.54
1:G:92:LYS:NZ	6:G:409:HOH:O	2.43	0.52
1:A:123:SER:O	6:A:402:HOH:O	2.19	0.52
1:D:56:GLU:OE2	6:D:402:HOH:O	2.18	0.51
1:H:97:SER:HB2	1:H:101:ARG:HH12	1.75	0.51
2:E:301:LYS:HG2	5:E:304[B]:CL:CL	2.48	0.51
1:G:45:VAL:O	6:G:401:HOH:O	2.19	0.51
2:A:301:LYS:HG2	5:A:304[B]:CL:CL	2.48	0.51
1:A:132:GLN:HB3	1:A:137:ASP:HB3	1.92	0.51
1:F:42:ASN:ND2	6:F:411:HOH:O	2.44	0.50
1:B:244:TRP:CZ3	2:B:301:LYS:HB2	2.46	0.50
1:H:228:ALA:HB1	1:H:232:ASP:HB2	1.93	0.49
1:B:234:GLU:N	6:B:411:HOH:O	2.45	0.48
1:G:209:HIS:CE1	5:G:304[A]:CL:CL	3.02	0.48
1:E:78:THR:HG21	1:E:141:TRP:HB2	1.94	0.48
2:D:301:LYS:HG2	5:D:304[B]:CL:CL	2.51	0.48
1:E:50:GLN:OE1	1:E:197:GLY:HA2	2.13	0.48
4:G:303[B]:VVO:O1	5:G:304[B]:CL:CL	2.69	0.48
1:D:50:GLN:OE1	6:D:403:HOH:O	2.20	0.47
1:H:132:GLN:HB3	1:H:137:ASP:HB3	1.95	0.47
1:F:209:HIS:NE2	4:F:303[B]:VVO:O1	2.48	0.47
1:E:181:ASN:ND2	6:E:410:HOH:O	2.48	0.46
1:D:60:LEU:HB3	1:D:85:VAL:HG11	1.97	0.46
1:F:52:ALA:O	1:F:56:GLU:HG2	2.16	0.46
4:G:303[A]:VVO:O1	5:G:304[A]:CL:CL	2.71	0.46
1:G:156:MET:HE1	1:G:220:ARG:CZ	2.46	0.46
1:A:50:GLN:HE22	1:A:197:GLY:HA2	1.81	0.45
1:C:125:GLU:OE1	1:C:242:ARG:NH2	2.48	0.45
1:H:67:ARG:NH2	1:H:137:ASP:OD1	2.46	0.45
1:B:50:GLN:NE2	1:B:197:GLY:HA2	2.32	0.45
1:F:50:GLN:OE1	1:F:197:GLY:HA2	2.16	0.45
1:F:7:ASP:OD1	1:F:102:SER:OG	2.32	0.45
1:H:78:THR:HG21	1:H:141:TRP:HB2	1.97	0.45
1:B:228:ALA:HB1	1:B:232:ASP:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:GLN:NE2	6:A:412:HOH:O	2.50	0.44
1:C:181:ASN:HB3	1:F:159:ILE:HG22	2.00	0.44
1:A:50:GLN:NE2	1:A:197:GLY:HA2	2.33	0.43
1:A:67:ARG:NH2	1:A:137:ASP:OD1	2.39	0.43
1:F:85:VAL:HB	1:F:129:ILE:HB	2.01	0.43
1:A:244:TRP:CZ3	2:A:301:LYS:HB2	2.54	0.43
4:E:303[A]:VVO:O1	5:E:304[A]:CL:CL	2.74	0.43
1:G:178:PRO:HB2	1:G:180:ILE:HG13	2.00	0.43
1:C:244:TRP:CZ3	2:C:301:LYS:HB2	2.54	0.43
1:H:156:MET:HE1	1:H:220:ARG:CZ	2.49	0.43
1:E:209:HIS:HE1	5:E:304[A]:CL:CL	2.33	0.42
1:B:156:MET:HE1	1:B:220:ARG:CZ	2.49	0.42
1:D:122:SER:OG	1:D:124:ASP:OD1	2.35	0.42
1:C:203:ARG:NH2	1:C:231:ARG:NH1	2.67	0.42
1:B:72:LEU:HD11	1:B:241:ASP:HB2	2.01	0.42
1:C:78:THR:HG21	1:C:141:TRP:HB2	2.01	0.42
1:D:141:TRP:HA	1:D:210:ARG:HB3	2.01	0.42
1:F:54:ARG:HD3	6:F:428:HOH:O	2.20	0.41
1:G:80:ARG:NH2	1:G:142:HIS:HB3	2.35	0.41
1:B:116:GLU:OE2	6:B:402:HOH:O	2.22	0.41
1:A:142:HIS:CD2	2:A:301:LYS:HA	2.56	0.41
1:F:209:HIS:CE1	5:F:304[A]:CL:CL	3.10	0.41
1:B:44:LEU:HD23	1:B:199:LEU:HD22	2.03	0.41
1:C:40:ALA:HA	1:C:43:ARG:NE	2.36	0.41
1:D:42:ASN:OD1	6:D:404:HOH:O	2.22	0.41
1:G:142:HIS:NE2	4:G:303[A]:VVO:O1	2.54	0.41
1:C:141:TRP:HA	1:C:210:ARG:HB3	2.03	0.41
1:B:190:ASN:HB3	6:B:529:HOH:O	2.21	0.40
1:H:152:TRP:HB2	1:H:223:LEU:HB3	2.03	0.40
1:D:216:GLU:O	1:D:218:SER:N	2.54	0.40
1:H:244:TRP:CZ3	2:H:301:LYS:HB2	2.57	0.40
1:B:50:GLN:HE22	1:B:197:GLY:HA2	1.86	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	249/258 (96%)	243 (98%)	6 (2%)	0	100	100
1	B	250/258 (97%)	242 (97%)	8 (3%)	0	100	100
1	C	247/258 (96%)	242 (98%)	5 (2%)	0	100	100
1	D	246/258 (95%)	238 (97%)	7 (3%)	1 (0%)	30	13
1	E	246/258 (95%)	239 (97%)	7 (3%)	0	100	100
1	F	245/258 (95%)	240 (98%)	5 (2%)	0	100	100
1	G	244/258 (95%)	238 (98%)	6 (2%)	0	100	100
1	H	245/258 (95%)	237 (97%)	8 (3%)	0	100	100
All	All	1972/2064 (96%)	1919 (97%)	52 (3%)	1 (0%)	48	31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	217	ASP

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	198/229 (86%)	198 (100%)	0	100	100
1	B	200/229 (87%)	200 (100%)	0	100	100
1	C	198/229 (86%)	196 (99%)	2 (1%)	68	52
1	D	194/229 (85%)	194 (100%)	0	100	100
1	E	199/229 (87%)	199 (100%)	0	100	100
1	F	190/229 (83%)	190 (100%)	0	100	100
1	G	187/229 (82%)	185 (99%)	2 (1%)	65	47
1	H	192/229 (84%)	191 (100%)	1 (0%)	81	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1558/1832 (85%)	1553 (100%)	5 (0%)	86 81

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	50	GLN
1	C	255	VAL
1	G	226	THR
1	G	232	ASP
1	H	50	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	50	GLN
1	A	64	HIS
1	A	132	GLN
1	B	9	ASN
1	B	50	GLN
1	C	63	GLN
1	C	132	GLN
1	C	161	HIS
1	C	240	ASN
1	D	9	ASN
1	D	132	GLN
1	E	132	GLN
1	E	181	ASN
1	F	25	GLN
1	F	132	GLN
1	F	161	HIS
1	G	50	GLN
1	G	132	GLN
1	G	246	ASN
1	H	63	GLN
1	H	64	HIS
1	H	170	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 48 ligands modelled in this entry, 16 are monoatomic - leaving 32 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	$\#\|Z\| > 2$
4	VVO	G	303[A]	3,1	0,1,1	-	-	-		
2	LYS	H	301	-	8,9,9	0.81	1 (12%)	7,10,10	1.06	1 (14%)
2	LYS	G	301	-	8,9,9	0.85	1 (12%)	7,10,10	1.11	1 (14%)
4	VVO	D	303[A]	3,1	0,1,1	-	-	-		
4	VVO	E	303[B]	3,1	0,1,1	-	-	-		
2	LYS	E	301	-	8,9,9	0.83	1 (12%)	7,10,10	1.13	1 (14%)
3	SIN	C	302	4	7,7,7	1.21	0	8,8,8	1.43	1 (12%)
3	SIN	D	302	4	7,7,7	1.13	0	8,8,8	1.52	0
4	VVO	A	303[A]	3,1	0,1,1	-	-	-		
4	VVO	B	303[A]	3,1	0,1,1	-	-	-		
4	VVO	G	303[B]	3,1	0,1,1	-	-	-		
4	VVO	H	303[A]	3,1	0,1,1	-	-	-		
2	LYS	F	301	-	8,9,9	0.84	1 (12%)	7,10,10	1.04	1 (14%)
4	VVO	A	303[B]	3,1	0,1,1	-	-	-		
4	VVO	D	303[B]	3,1	0,1,1	-	-	-		
2	LYS	A	301	-	8,9,9	0.81	1 (12%)	7,10,10	1.09	1 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	VVO	B	303[B]	3,1	0,1,1	-	-	-		
3	SIN	E	302	4	7,7,7	1.20	0	8,8,8	1.44	0
4	VVO	H	303[B]	3,1	0,1,1	-	-	-		
3	SIN	H	302	4	7,7,7	1.21	0	8,8,8	1.41	0
4	VVO	C	303[A]	3,1	0,1,1	-	-	-		
4	VVO	F	303[A]	3,1	0,1,1	-	-	-		
3	SIN	G	302	4	7,7,7	1.18	0	8,8,8	1.54	2 (25%)
3	SIN	B	302	4	7,7,7	1.20	0	8,8,8	1.46	0
2	LYS	C	301	-	8,9,9	0.81	1 (12%)	7,10,10	1.10	1 (14%)
4	VVO	C	303[B]	3,1	0,1,1	-	-	-		
2	LYS	B	301	-	8,9,9	0.81	1 (12%)	7,10,10	1.05	1 (14%)
2	LYS	D	301	-	8,9,9	0.83	1 (12%)	7,10,10	1.04	1 (14%)
4	VVO	F	303[B]	3,1	0,1,1	-	-	-		
3	SIN	F	302	4	7,7,7	1.12	0	8,8,8	1.59	1 (12%)
3	SIN	A	302	4	7,7,7	1.20	0	8,8,8	1.44	0
4	VVO	E	303[A]	3,1	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
2	LYS	C	301	-	-	3/9/9/9	-
3	SIN	E	302	4	-	3/5/5/5	-
2	LYS	H	301	-	-	1/9/9/9	-
2	LYS	B	301	-	-	1/9/9/9	-
2	LYS	D	301	-	-	1/9/9/9	-
2	LYS	F	301	-	-	2/9/9/9	-
2	LYS	G	301	-	-	2/9/9/9	-
3	SIN	F	302	4	-	2/5/5/5	-
3	SIN	H	302	4	-	2/5/5/5	-
2	LYS	A	301	-	-	0/9/9/9	-
3	SIN	A	302	4	-	2/5/5/5	-
3	SIN	G	302	4	-	3/5/5/5	-
2	LYS	E	301	-	-	1/9/9/9	-
3	SIN	C	302	4	-	2/5/5/5	-
3	SIN	D	302	4	-	2/5/5/5	-
3	SIN	B	302	4	-	3/5/5/5	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	301	LYS	OXT-C	-2.31	1.23	1.30
2	F	301	LYS	OXT-C	-2.24	1.23	1.30
2	D	301	LYS	OXT-C	-2.21	1.23	1.30
2	E	301	LYS	OXT-C	-2.19	1.23	1.30
2	A	301	LYS	OXT-C	-2.18	1.23	1.30
2	B	301	LYS	OXT-C	-2.15	1.23	1.30
2	H	301	LYS	OXT-C	-2.15	1.23	1.30
2	C	301	LYS	OXT-C	-2.13	1.23	1.30

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	301	LYS	OXT-C-O	-2.74	117.87	124.08
2	H	301	LYS	OXT-C-O	-2.67	118.02	124.08
2	C	301	LYS	OXT-C-O	-2.67	118.03	124.08
2	D	301	LYS	OXT-C-O	-2.60	118.17	124.08
2	E	301	LYS	OXT-C-O	-2.59	118.21	124.08
2	F	301	LYS	OXT-C-O	-2.59	118.21	124.08
2	G	301	LYS	OXT-C-O	-2.52	118.36	124.08
2	B	301	LYS	OXT-C-O	-2.52	118.37	124.08
3	F	302	SIN	O2-C1-C2	2.21	120.98	114.00
3	C	302	SIN	O4-C4-C3	2.06	120.51	114.00
3	G	302	SIN	O2-C1-C2	2.04	120.43	114.00
3	G	302	SIN	O4-C4-C3	2.00	120.33	114.00

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	302	SIN	C1-C2-C3-C4
2	F	301	LYS	CG-CD-CE-NZ
2	G	301	LYS	OXT-C-CA-CB
2	G	301	LYS	O-C-CA-CB
2	C	301	LYS	O-C-CA-CB
3	H	302	SIN	O1-C1-C2-C3
3	A	302	SIN	C2-C3-C4-O4
2	H	301	LYS	CG-CD-CE-NZ
2	E	301	LYS	O-C-CA-N
2	F	301	LYS	O-C-CA-N
2	C	301	LYS	OXT-C-CA-CB
3	G	302	SIN	C2-C3-C4-O3

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Mol	Chain	Res	Type	Atoms
3	H	302	SIN	O2-C1-C2-C3
3	G	302	SIN	C2-C3-C4-O4
3	A	302	SIN	C2-C3-C4-O3
3	C	302	SIN	C2-C3-C4-O4
3	C	302	SIN	C2-C3-C4-O3
3	G	302	SIN	C1-C2-C3-C4
3	F	302	SIN	C2-C3-C4-O3
3	D	302	SIN	C2-C3-C4-O3
3	D	302	SIN	C2-C3-C4-O4
3	F	302	SIN	C2-C3-C4-O4
3	B	302	SIN	C2-C3-C4-O4
2	C	301	LYS	CG-CD-CE-NZ
2	D	301	LYS	CG-CD-CE-NZ
3	B	302	SIN	C2-C3-C4-O3
3	E	302	SIN	C2-C3-C4-O4
3	E	302	SIN	C2-C3-C4-O3
3	B	302	SIN	C1-C2-C3-C4
2	B	301	LYS	O-C-CA-CB

There are no ring outliers.

23 monomers are involved in 41 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	303[A]	VVO	3	0
2	H	301	LYS	2	0
4	D	303[A]	VVO	2	0
4	E	303[B]	VVO	1	0
2	E	301	LYS	1	0
4	A	303[A]	VVO	2	0
4	B	303[A]	VVO	2	0
4	G	303[B]	VVO	2	0
4	H	303[A]	VVO	2	0
2	F	301	LYS	1	0
4	A	303[B]	VVO	1	0
4	D	303[B]	VVO	1	0
2	A	301	LYS	3	0
4	B	303[B]	VVO	2	0
4	H	303[B]	VVO	1	0
4	C	303[A]	VVO	2	0
4	F	303[A]	VVO	2	0
2	C	301	LYS	2	0
4	C	303[B]	VVO	2	0

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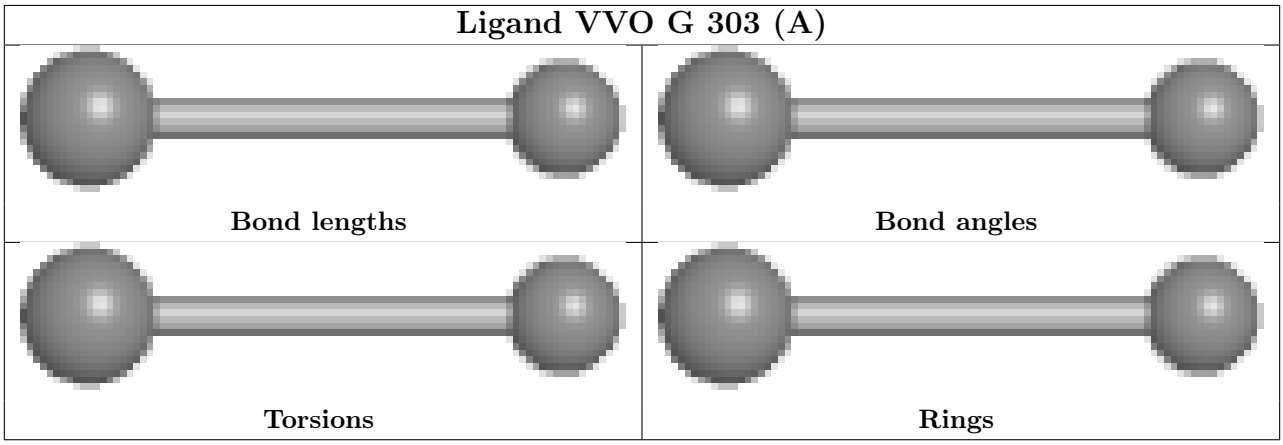
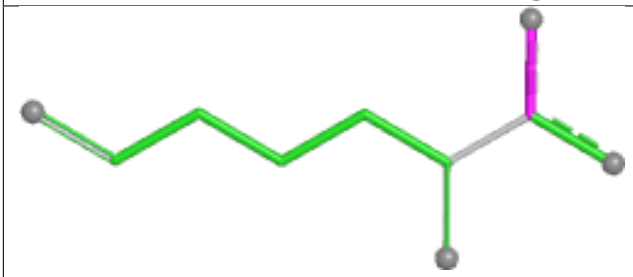
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	LYS	2	0
2	D	301	LYS	1	0
4	F	303[B]	VVO	2	0
4	E	303[A]	VVO	2	0

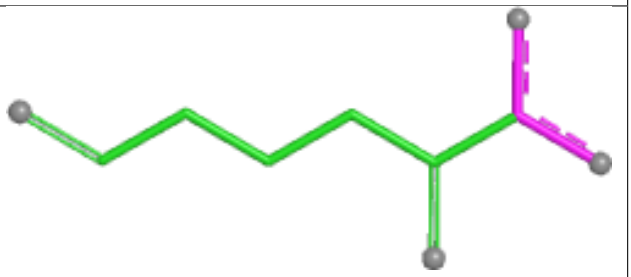
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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 LYS H 301



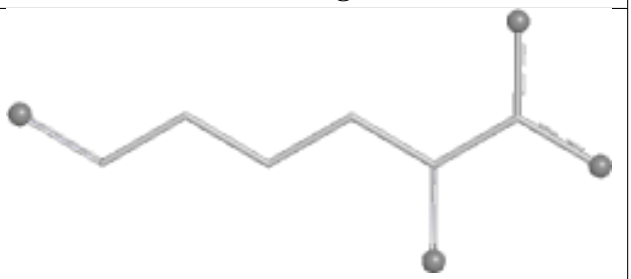
Bond lengths



Bond angles

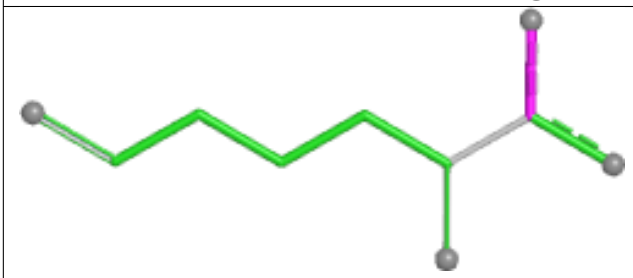


Torsions

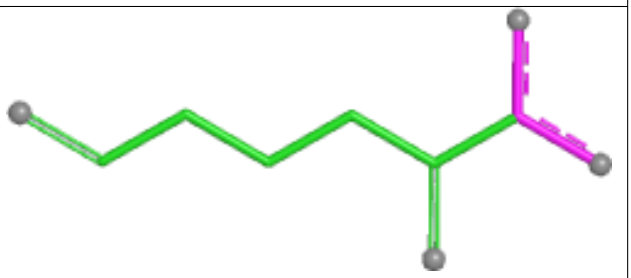


Rings

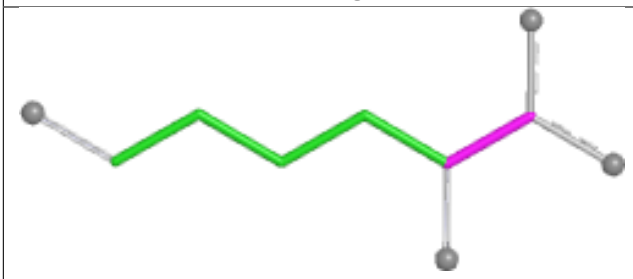
Ligand LYS G 301



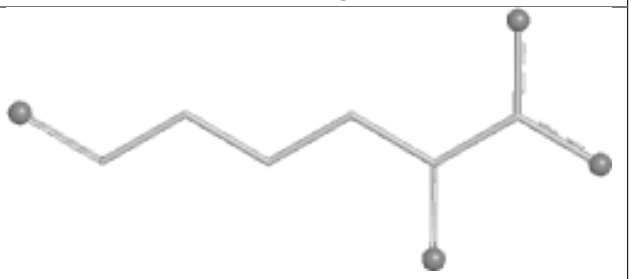
Bond lengths



Bond angles

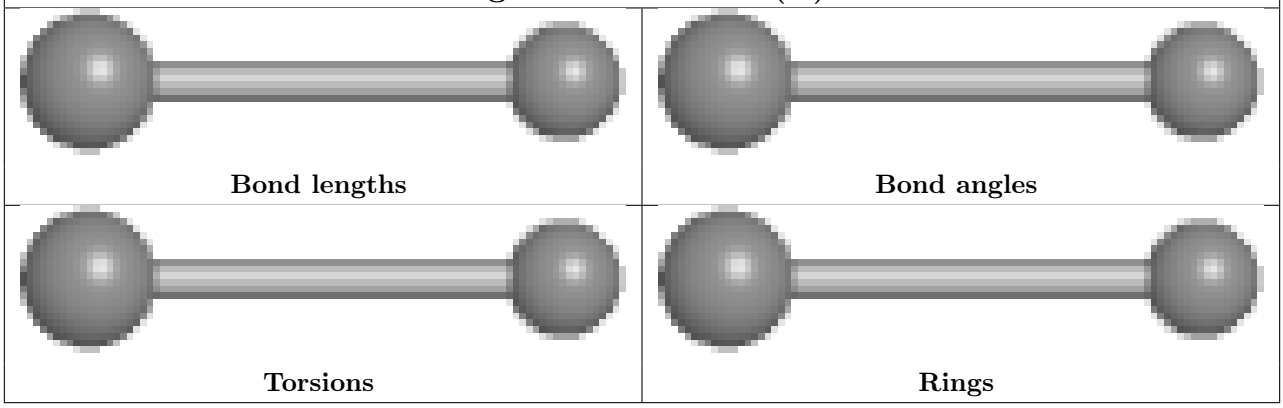


Torsions

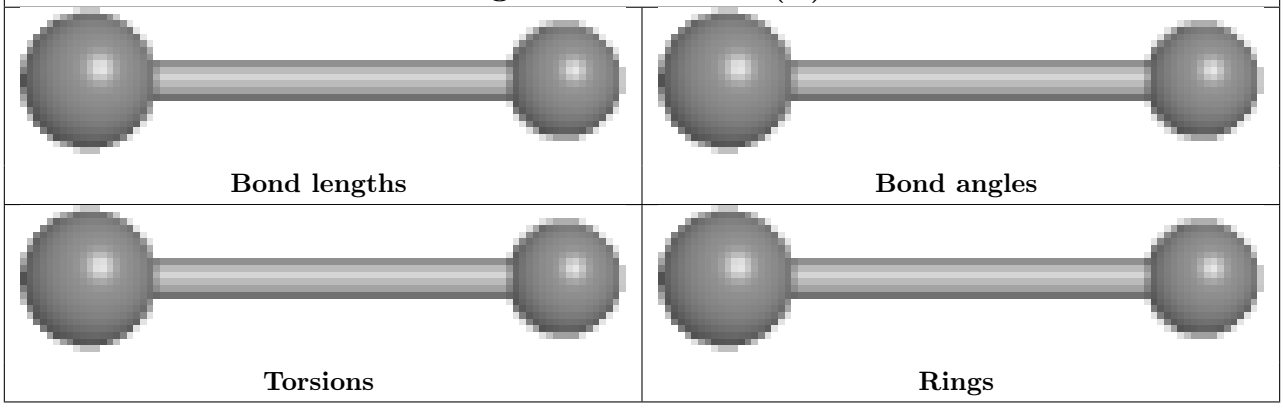


Rings

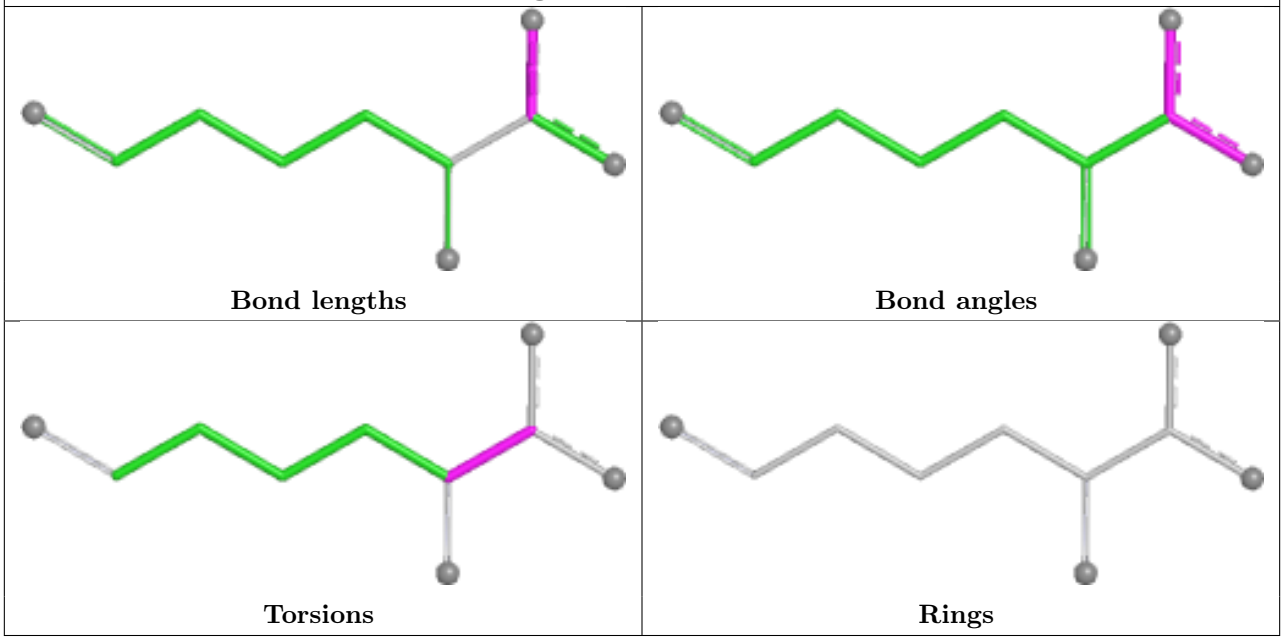
Ligand VVO D 303 (A)



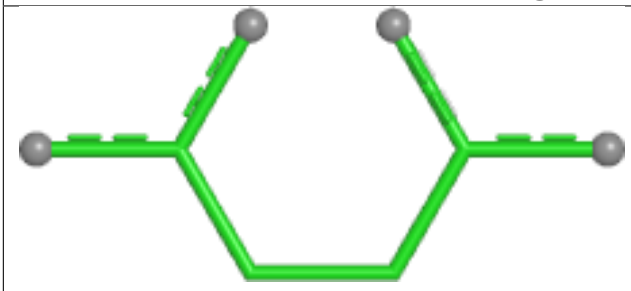
Ligand VVO E 303 (B)



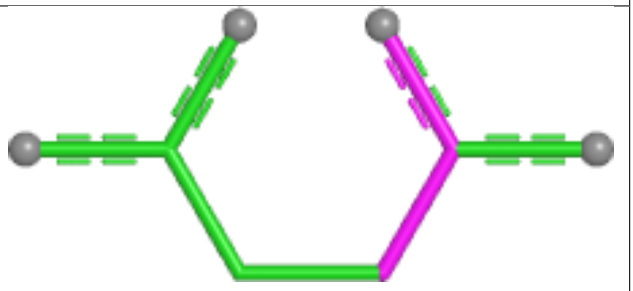
Ligand LYS E 301



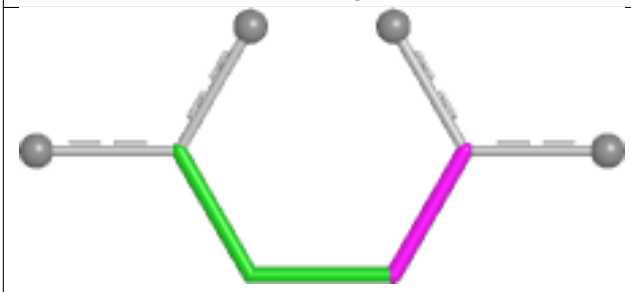
Ligand SIN C 302



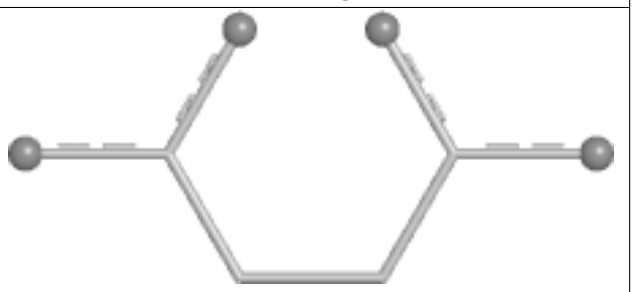
Bond lengths



Bond angles

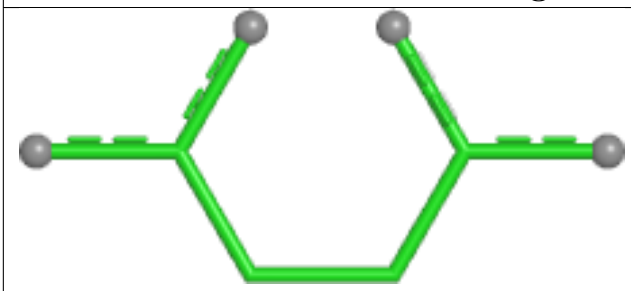


Torsions



Rings

Ligand SIN D 302



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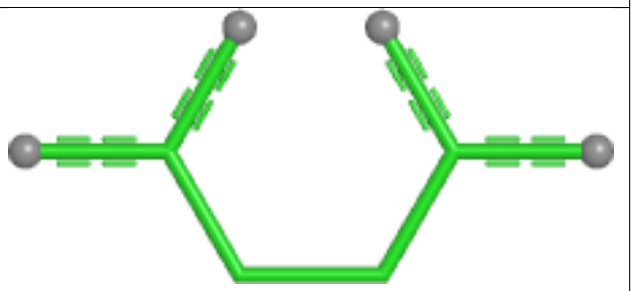
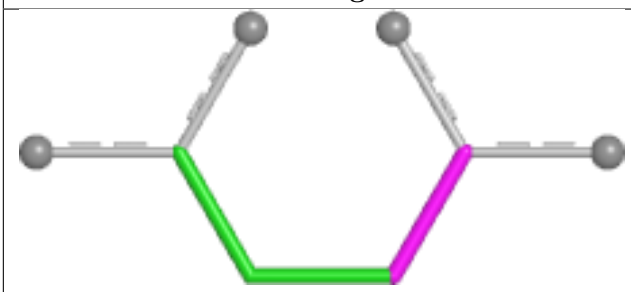


Bond angles



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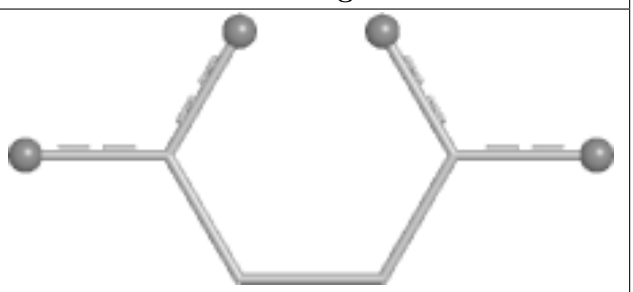
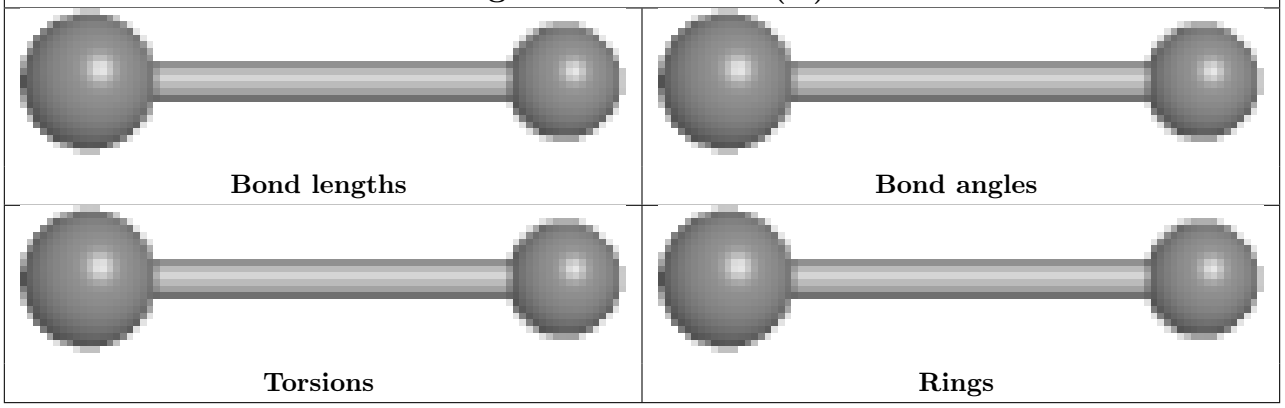
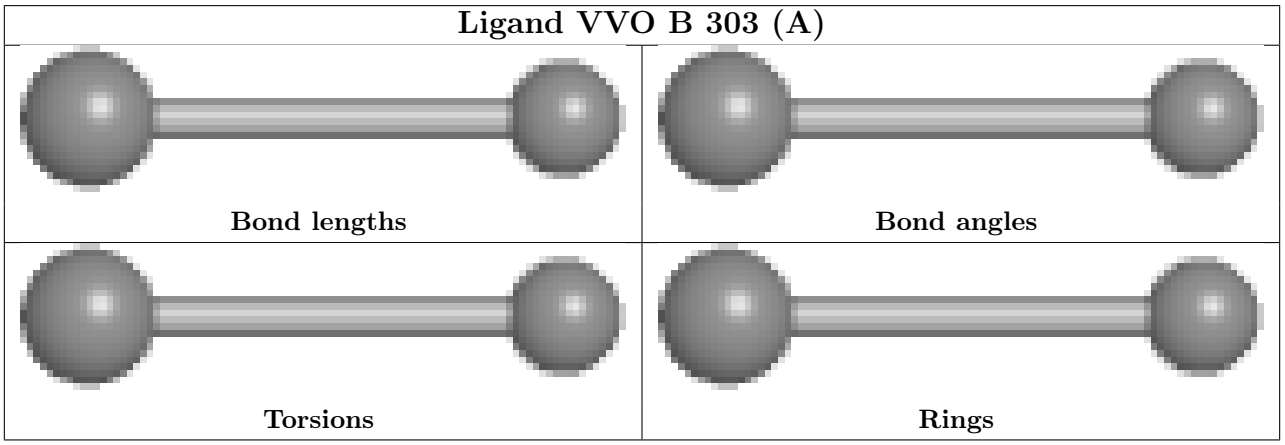


Rings

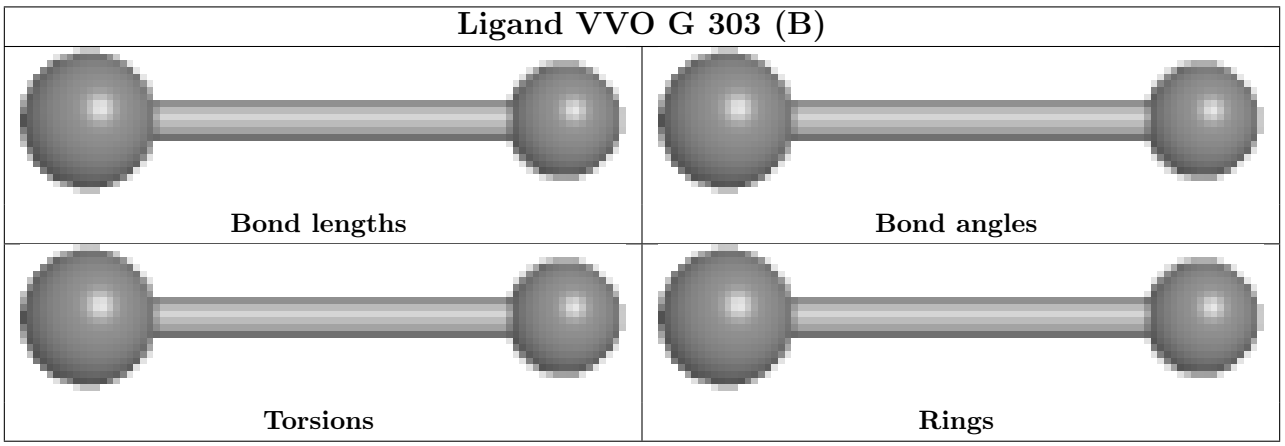
Ligand VVO A 303 (A)



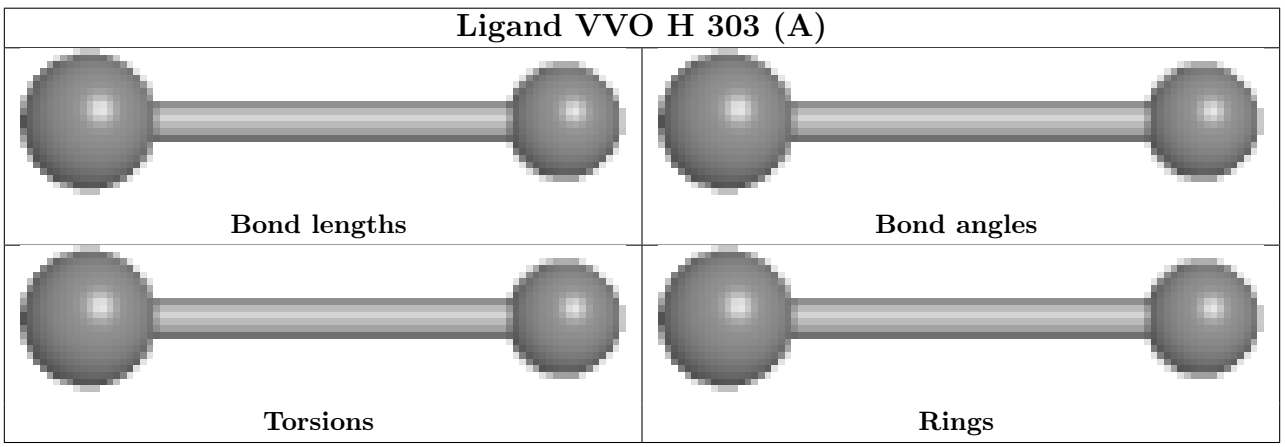
Ligand VVO B 303 (A)



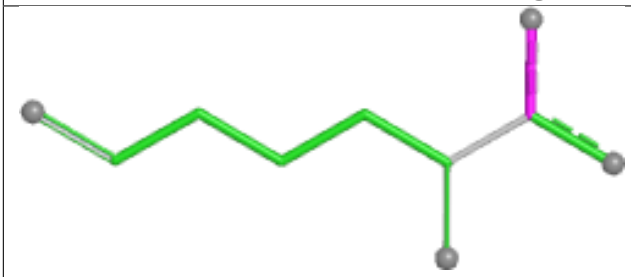
Ligand VVO G 303 (B)



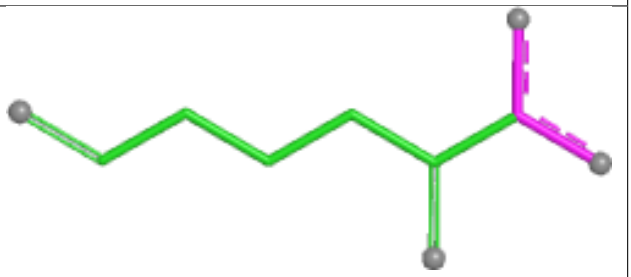
Ligand VVO H 303 (A)



Ligand LYS F 301



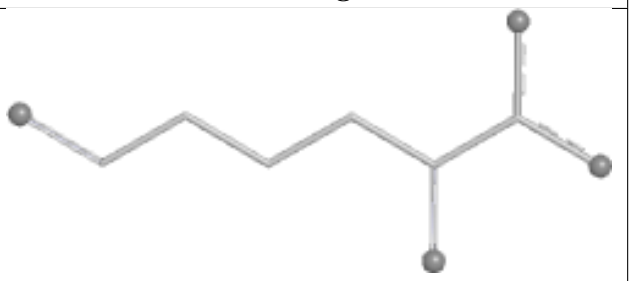
Bond lengths



Bond angles

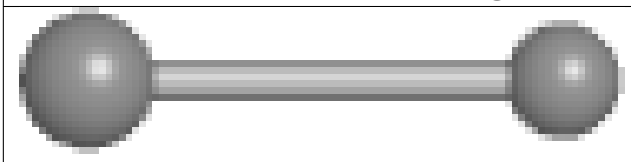


Torsions

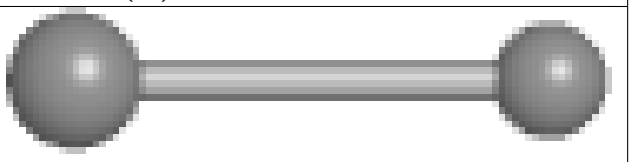


Rings

Ligand VVO A 303 (B)



Bond lengths



Bond angles



Torsions



Rings

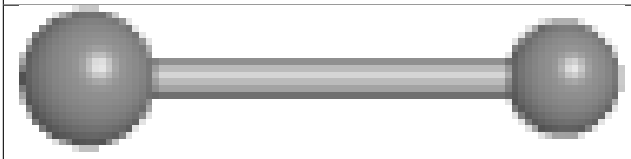
Ligand VVO D 303 (B)



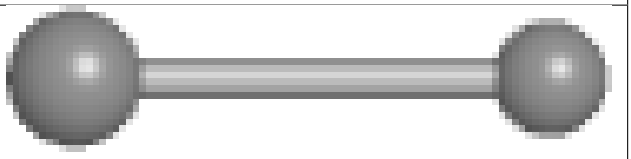
Bond lengths



Bond angles

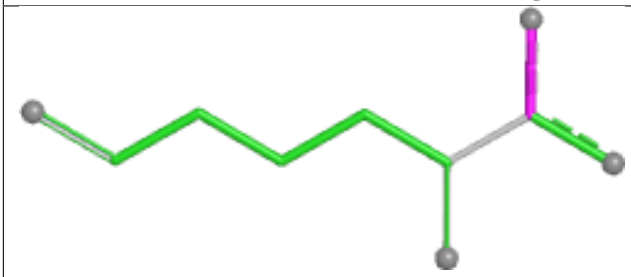


Torsions



Rings

Ligand LYS A 301



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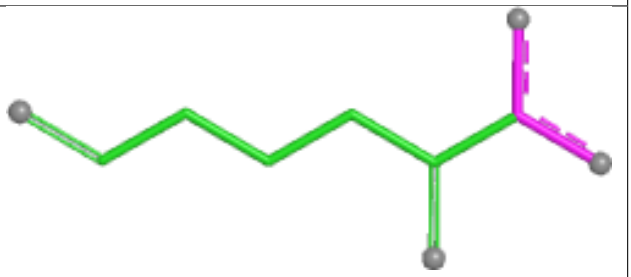
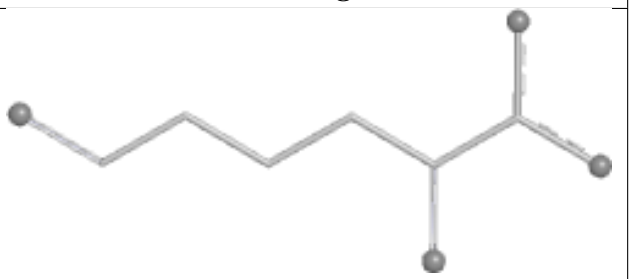


Bond angles

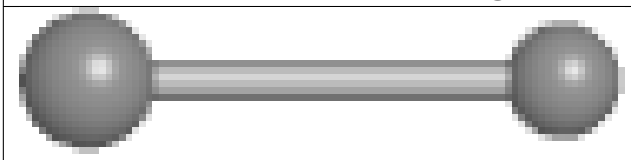


Torsions

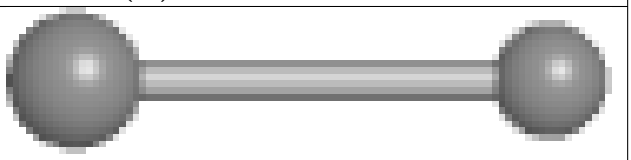


Rings

Ligand VVO B 303 (B)



Bond lengths



Bond angles

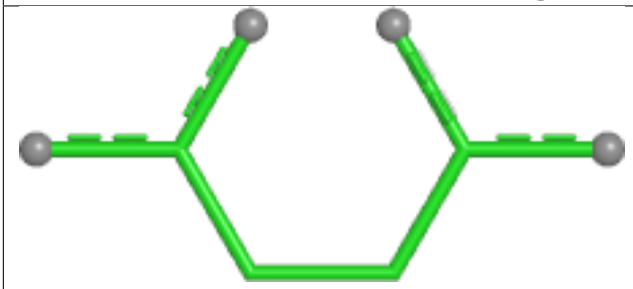


Torsions



Rings

Ligand SIN E 302



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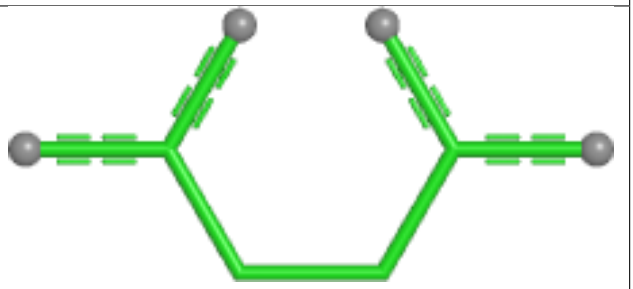
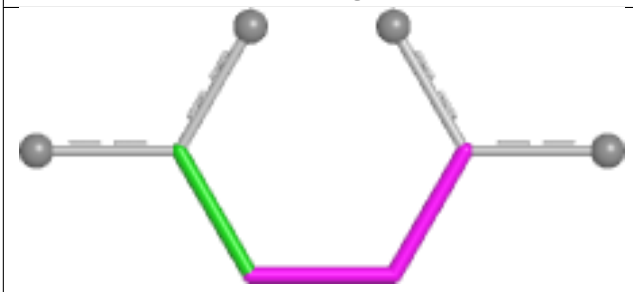
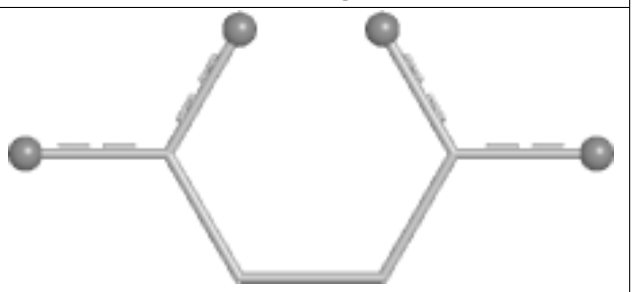


Bond angles

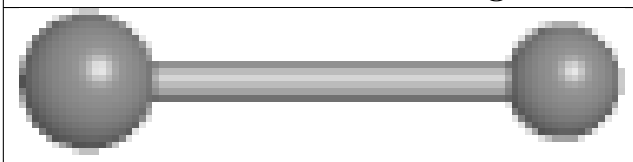


Torsions

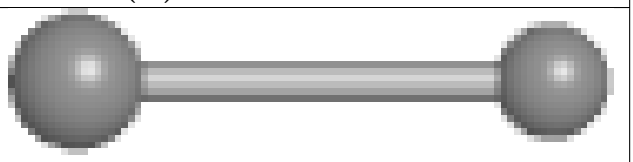


Rings

Ligand VVO H 303 (B)



Bond lengths



Bond angles

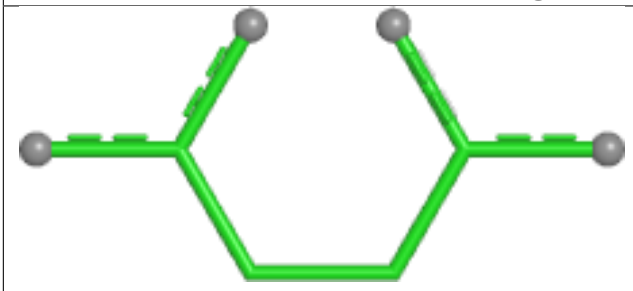


Torsions

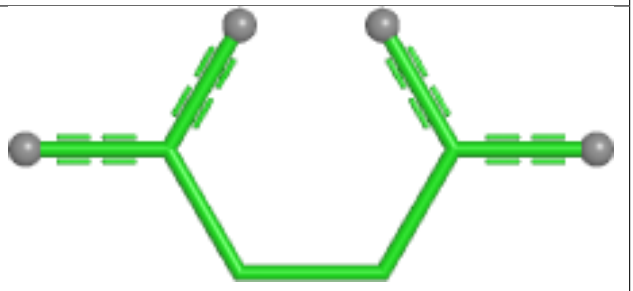


Rings

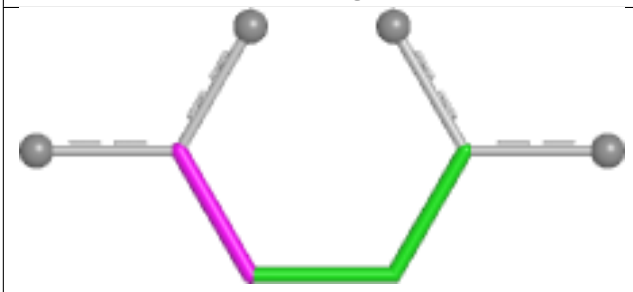
Ligand SIN H 302



Bond lengths



Bond angles



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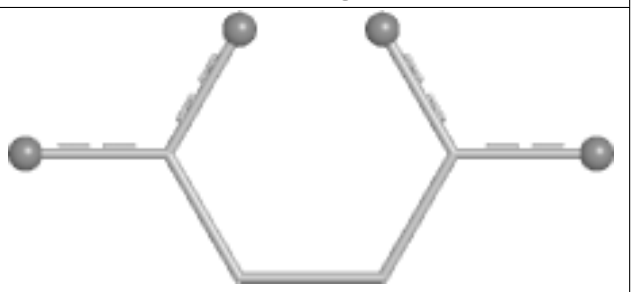
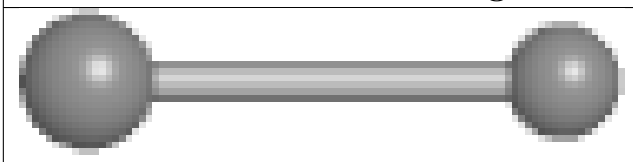


Rings

Ligand VVO C 303 (A)



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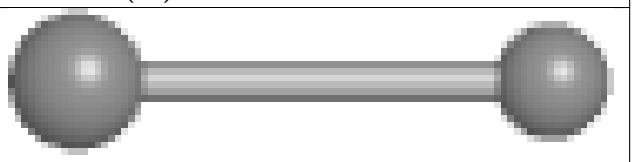


Bond angles



Torsions



Rings

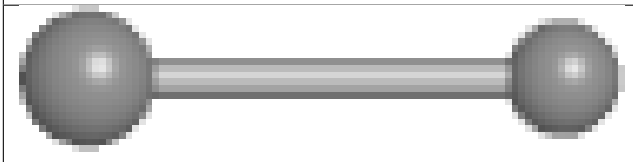
Ligand VVO F 303 (A)



Bond lengths



Bond angles



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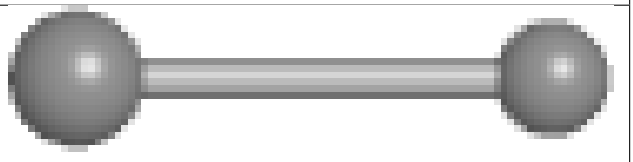
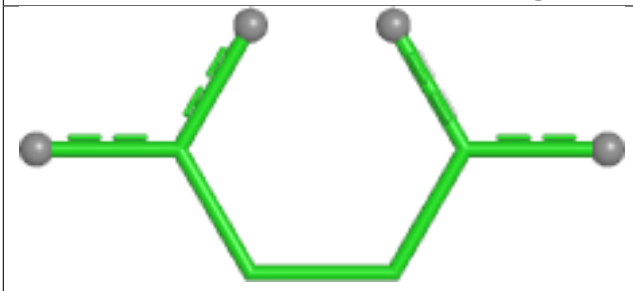
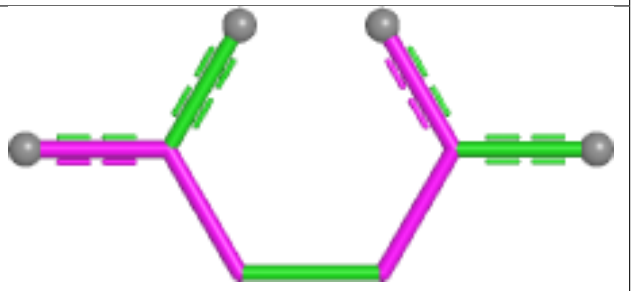


Rings

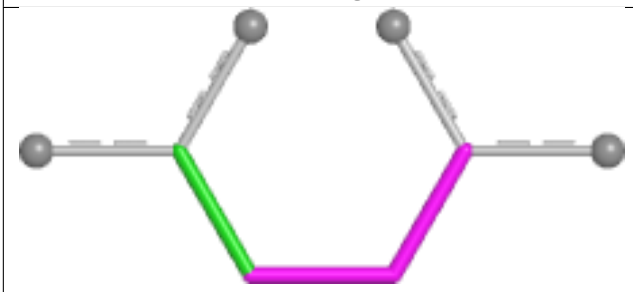
Ligand SIN G 302



Bond lengths



Bond angles



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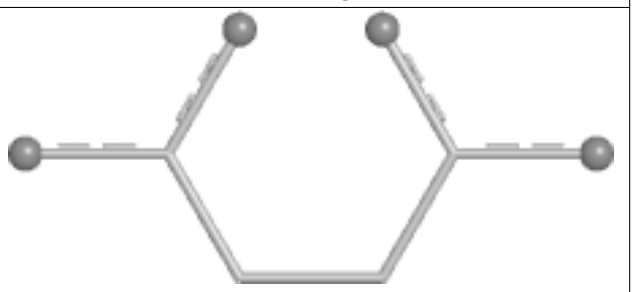
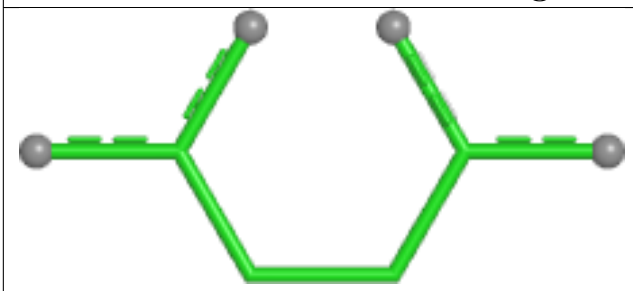
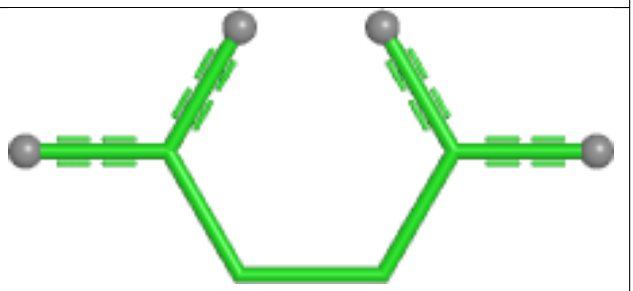


Rings

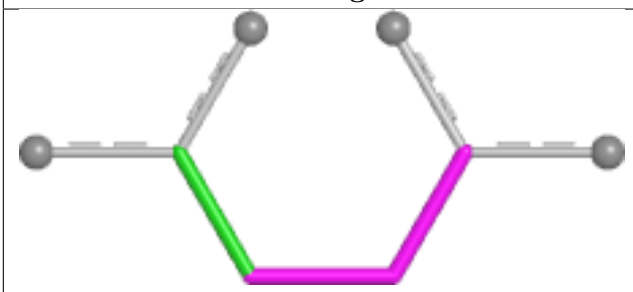
Ligand SIN B 302



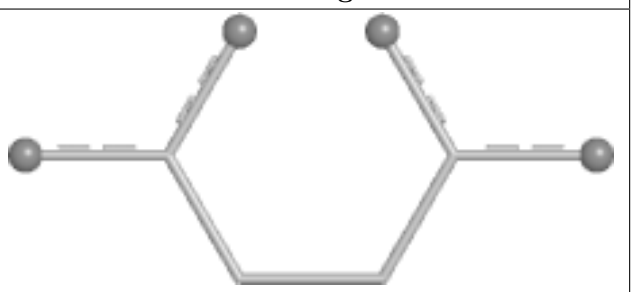
Bond lengths



Bond angles

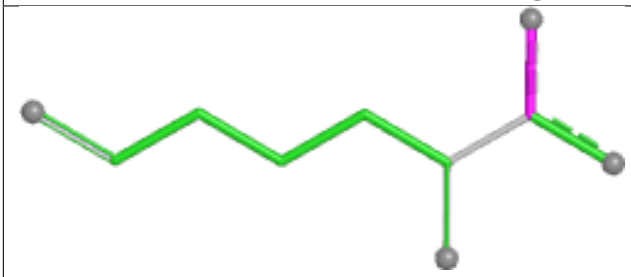


Torsions



Rings

Ligand LYS C 301



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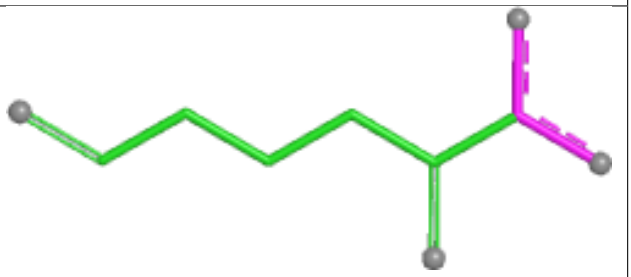
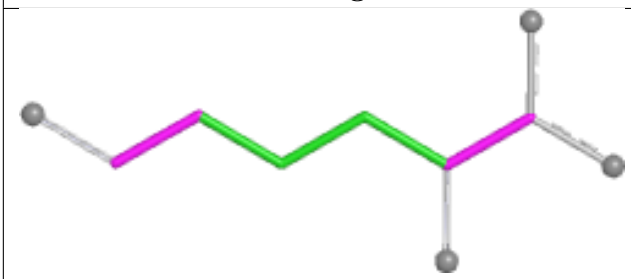


Bond angles



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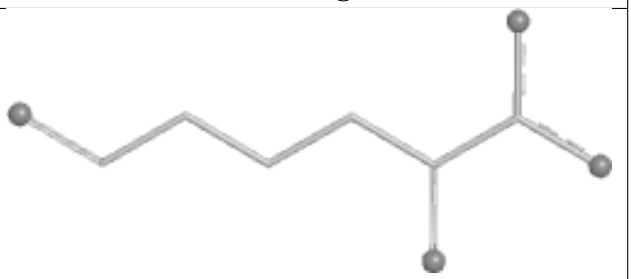
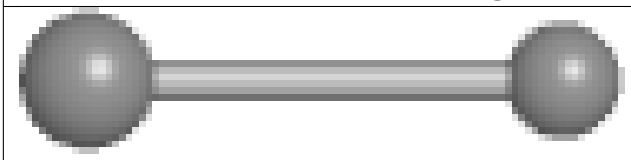
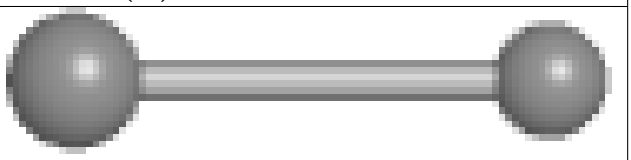


Rings

Ligand VVO C 303 (B)



Bond lengths



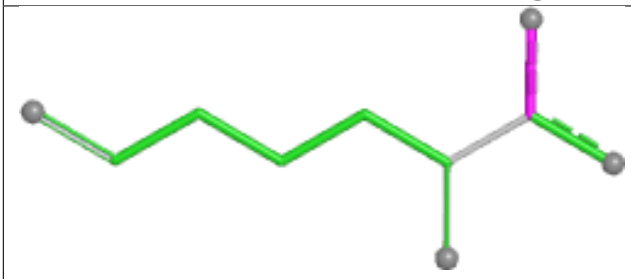
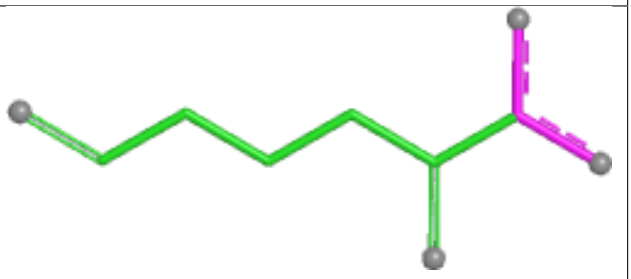
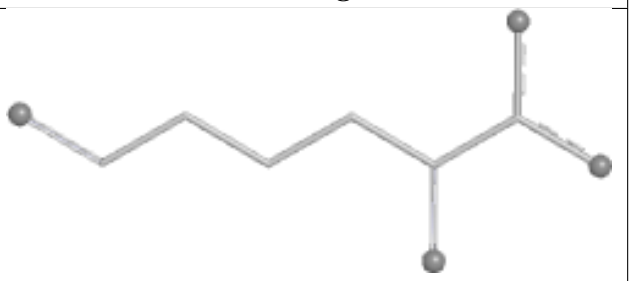
Bond angles

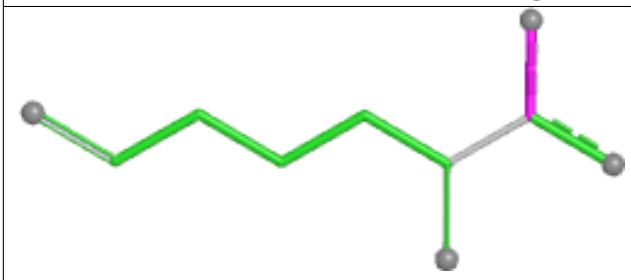
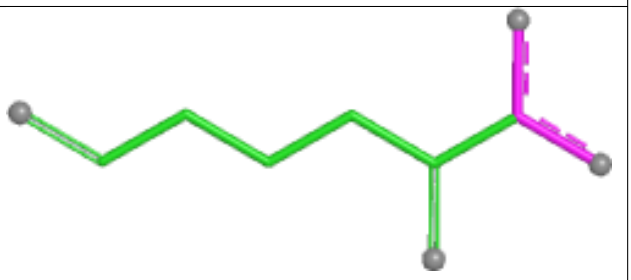
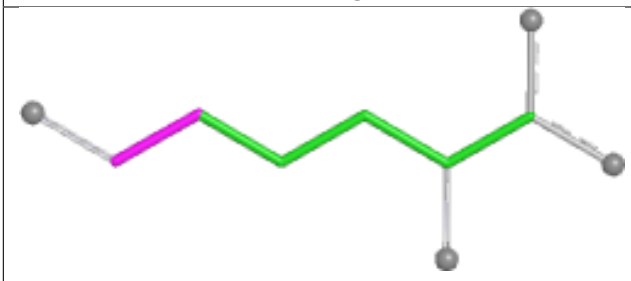
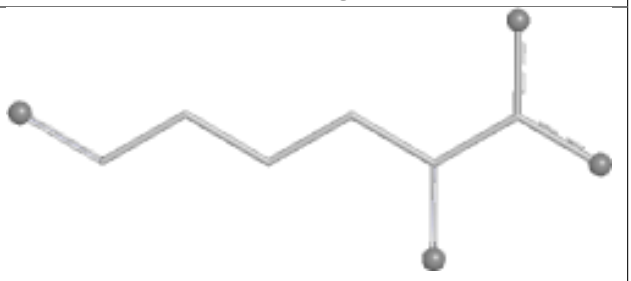


Torsions

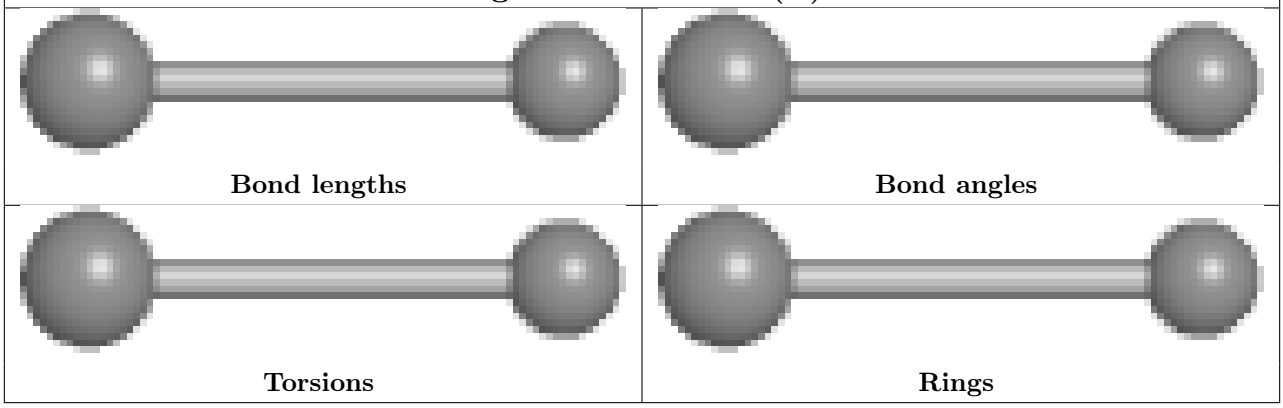


Rings

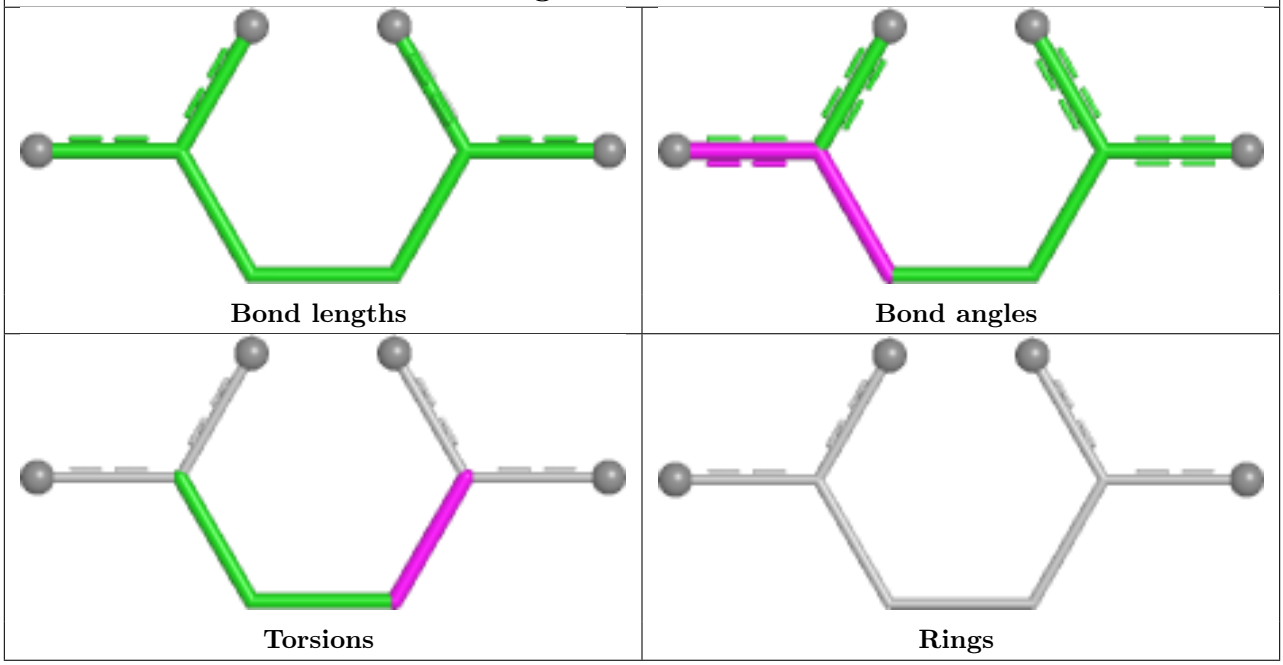
Ligand LYS B 301	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LYS D 301	
 Bond lengths	 Bond angles
 Torsions	 Rings

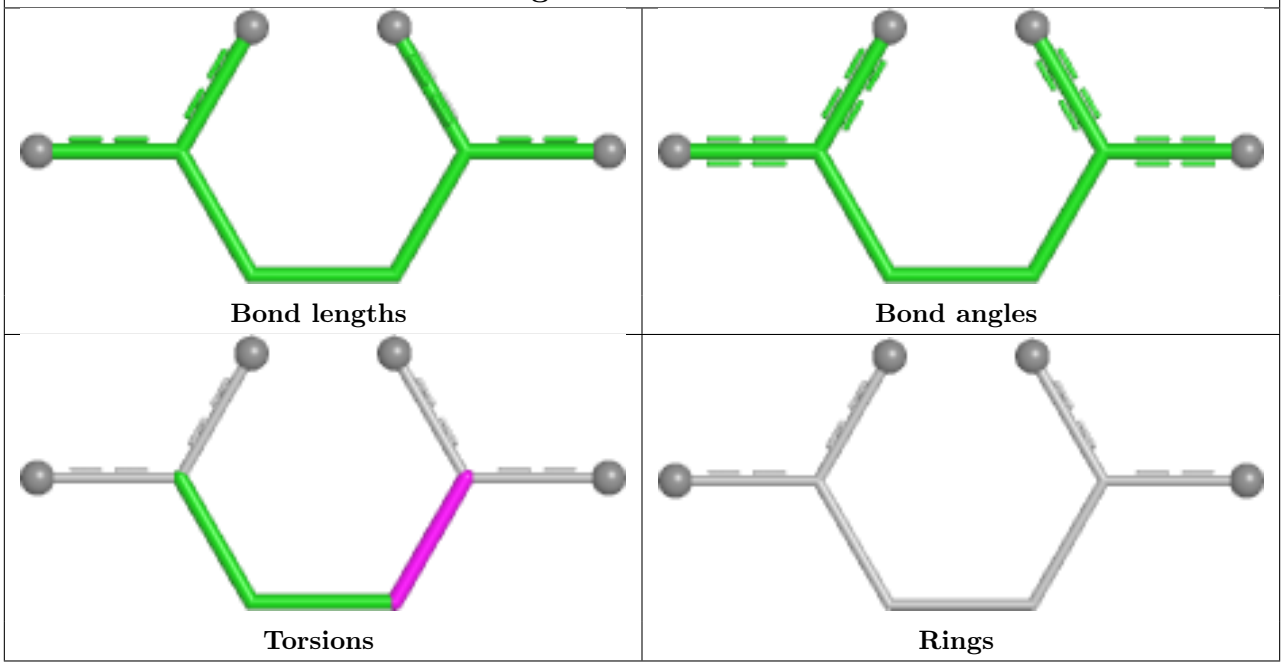
Ligand VVO F 303 (B)



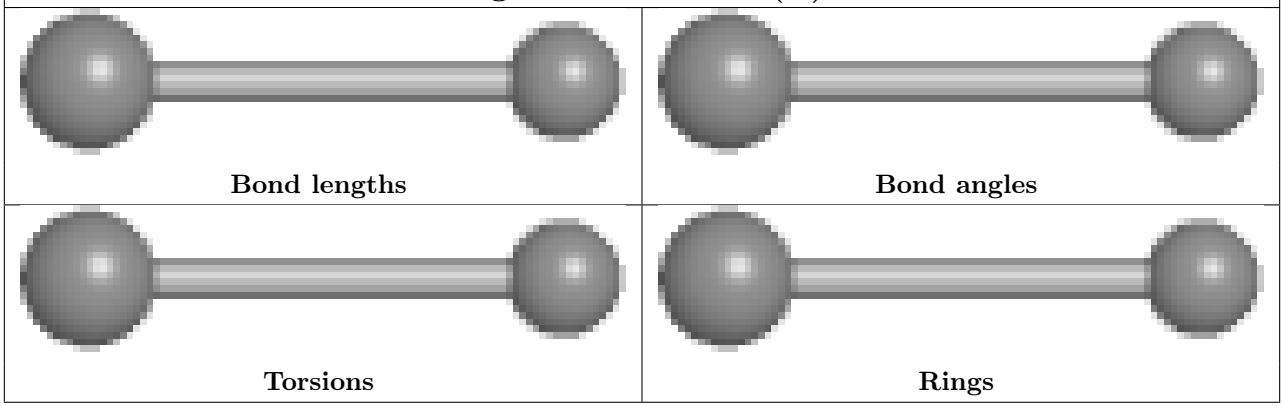
Ligand SIN F 302



Ligand SIN A 302



Ligand VVO E 303 (A)



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	251/258 (97%)	-1.14	0	100	100	10, 15, 24, 42	0
1	B	252/258 (97%)	-1.08	0	100	100	11, 17, 26, 38	0
1	C	251/258 (97%)	-1.06	0	100	100	12, 18, 27, 32	0
1	D	250/258 (96%)	-1.07	0	100	100	12, 18, 26, 36	0
1	E	250/258 (96%)	-1.07	0	100	100	13, 18, 26, 44	0
1	F	249/258 (96%)	-1.08	0	100	100	12, 18, 25, 40	0
1	G	248/258 (96%)	-0.95	0	100	100	13, 21, 30, 36	0
1	H	249/258 (96%)	-0.93	0	100	100	14, 21, 31, 43	0
All	All	2000/2064 (96%)	-1.05	0	100	100	10, 18, 28, 44	0

There are no RSRZ outliers to report.

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 oligosaccharides in this entry.

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
5	CL	D	304[A]	1/1	0.96	0.07	22,22,22,22	1
5	CL	D	304[B]	1/1	0.96	0.07	28,28,28,28	1
2	LYS	D	301	10/10	0.97	0.05	17,18,20,23	0
2	LYS	H	301	10/10	0.97	0.05	16,21,24,25	0
2	LYS	F	301	10/10	0.98	0.04	15,16,18,19	0
2	LYS	G	301	10/10	0.98	0.05	18,20,22,24	0
2	LYS	C	301	10/10	0.98	0.04	14,17,19,19	0
2	LYS	A	301	10/10	0.98	0.04	14,15,16,18	0
2	LYS	E	301	10/10	0.98	0.04	17,18,20,21	0
5	CL	E	304[A]	1/1	0.98	0.19	29,29,29,29	1
5	CL	E	304[B]	1/1	0.98	0.19	23,23,23,23	1
5	CL	G	304[A]	1/1	0.98	0.14	23,23,23,23	1
5	CL	G	304[B]	1/1	0.98	0.14	21,21,21,21	1
5	CL	H	304[A]	1/1	0.98	0.10	26,26,26,26	1
5	CL	H	304[B]	1/1	0.98	0.10	33,33,33,33	1
4	VVO	F	303[A]	2/2	0.99	0.04	16,16,16,17	2
4	VVO	F	303[B]	2/2	0.99	0.04	16,16,16,16	2
4	VVO	H	303[A]	2/2	0.99	0.04	21,21,21,22	2
4	VVO	H	303[B]	2/2	0.99	0.04	20,20,20,21	2
5	CL	B	304[A]	1/1	0.99	0.07	23,23,23,23	1
5	CL	B	304[B]	1/1	0.99	0.07	26,26,26,26	1
5	CL	C	304[A]	1/1	0.99	0.16	32,32,32,32	1
5	CL	C	304[B]	1/1	0.99	0.16	27,27,27,27	1
2	LYS	B	301	10/10	0.99	0.03	16,16,17,18	0
3	SIN	A	302	8/8	0.99	0.03	11,14,16,17	0
3	SIN	C	302	8/8	0.99	0.03	15,17,19,19	0
3	SIN	D	302	8/8	0.99	0.03	15,15,17,18	0
5	CL	F	304[A]	1/1	0.99	0.05	17,17,17,17	1
5	CL	F	304[B]	1/1	0.99	0.05	22,22,22,22	1
3	SIN	E	302	8/8	0.99	0.03	16,17,20,22	0
3	SIN	F	302	8/8	0.99	0.03	13,15,18,18	0
3	SIN	G	302	8/8	0.99	0.03	17,18,21,22	0
3	SIN	H	302	8/8	0.99	0.04	16,18,20,22	0
5	CL	A	304[B]	1/1	1.00	0.02	21,21,21,21	1
4	VVO	B	303[B]	2/2	1.00	0.03	17,17,17,17	2
4	VVO	C	303[A]	2/2	1.00	0.02	17,17,17,19	2
4	VVO	C	303[B]	2/2	1.00	0.02	18,18,18,19	2
4	VVO	D	303[A]	2/2	1.00	0.04	17,17,17,18	2
4	VVO	D	303[B]	2/2	1.00	0.04	17,17,17,17	2
4	VVO	E	303[A]	2/2	1.00	0.03	19,19,19,19	2
4	VVO	E	303[B]	2/2	1.00	0.03	17,17,17,19	2
3	SIN	B	302	8/8	1.00	0.03	15,17,19,19	0
4	VVO	A	303[A]	2/2	1.00	0.03	15,15,15,17	2

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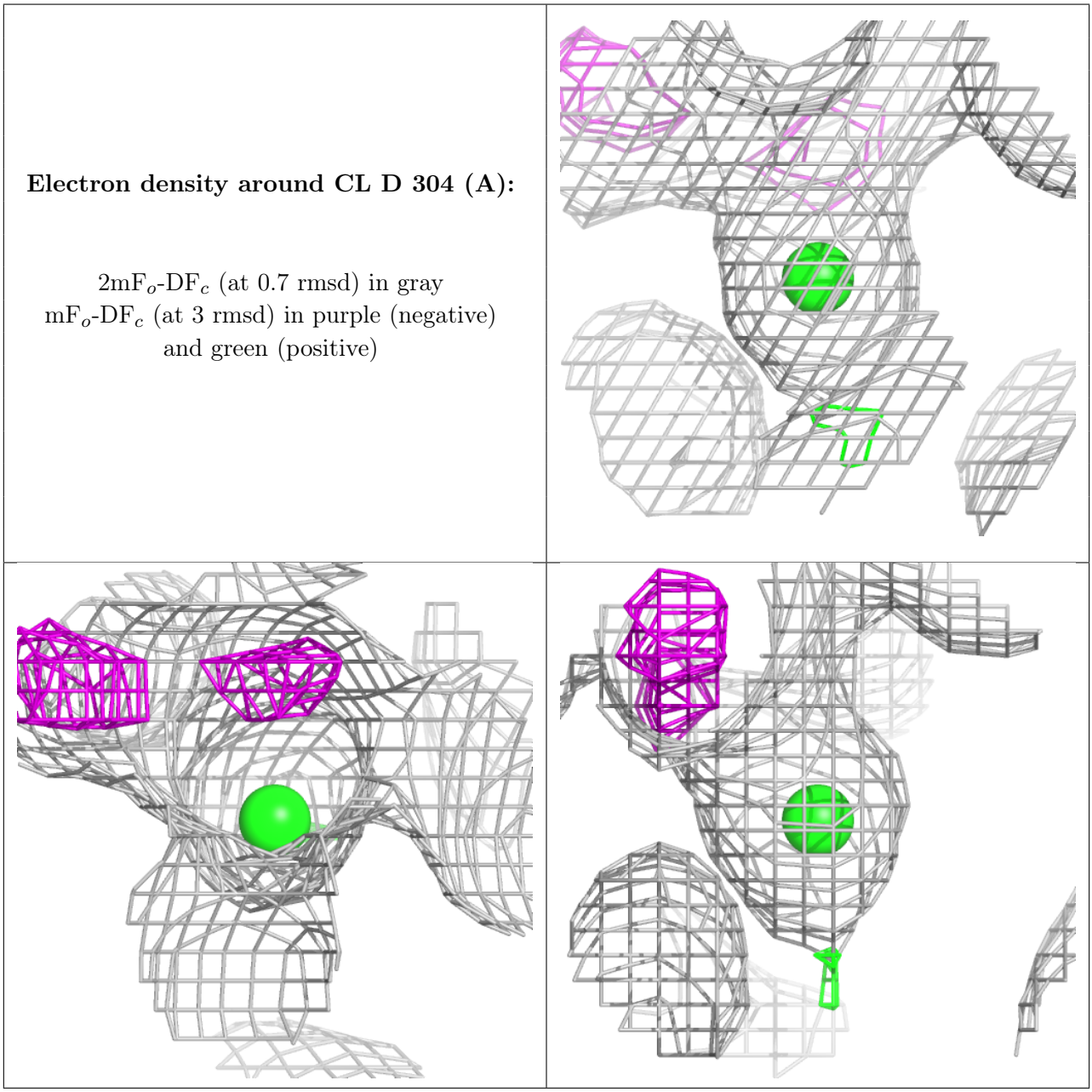
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	VVO	G	303[A]	2/2	1.00	0.02	19,19,19,22	2
4	VVO	G	303[B]	2/2	1.00	0.02	19,19,19,22	2
4	VVO	A	303[B]	2/2	1.00	0.03	12,12,12,15	2
4	VVO	B	303[A]	2/2	1.00	0.03	18,18,18,19	2
5	CL	A	304[A]	1/1	1.00	0.02	14,14,14,14	1

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.

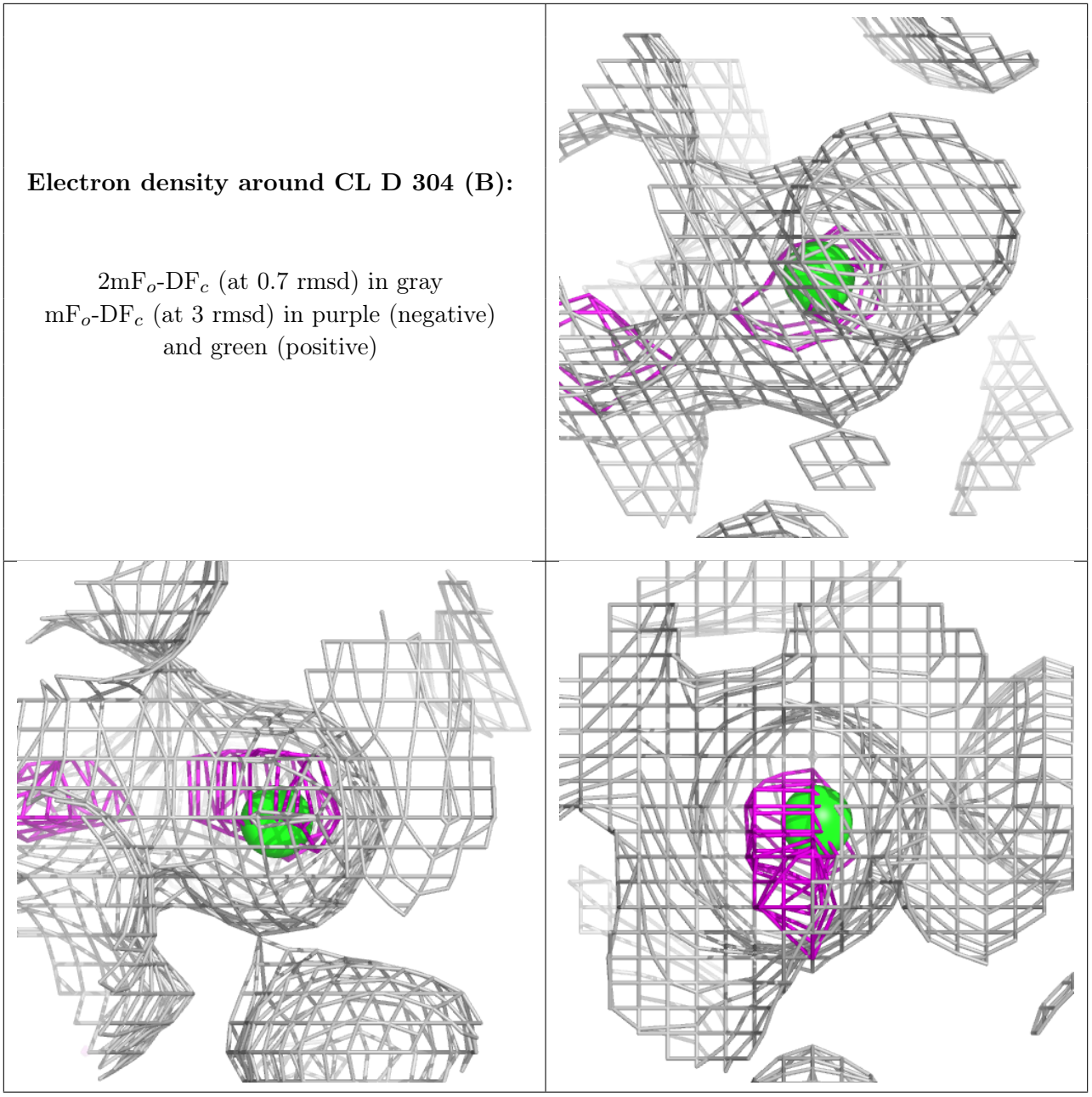
Electron density around CL D 304 (A):

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



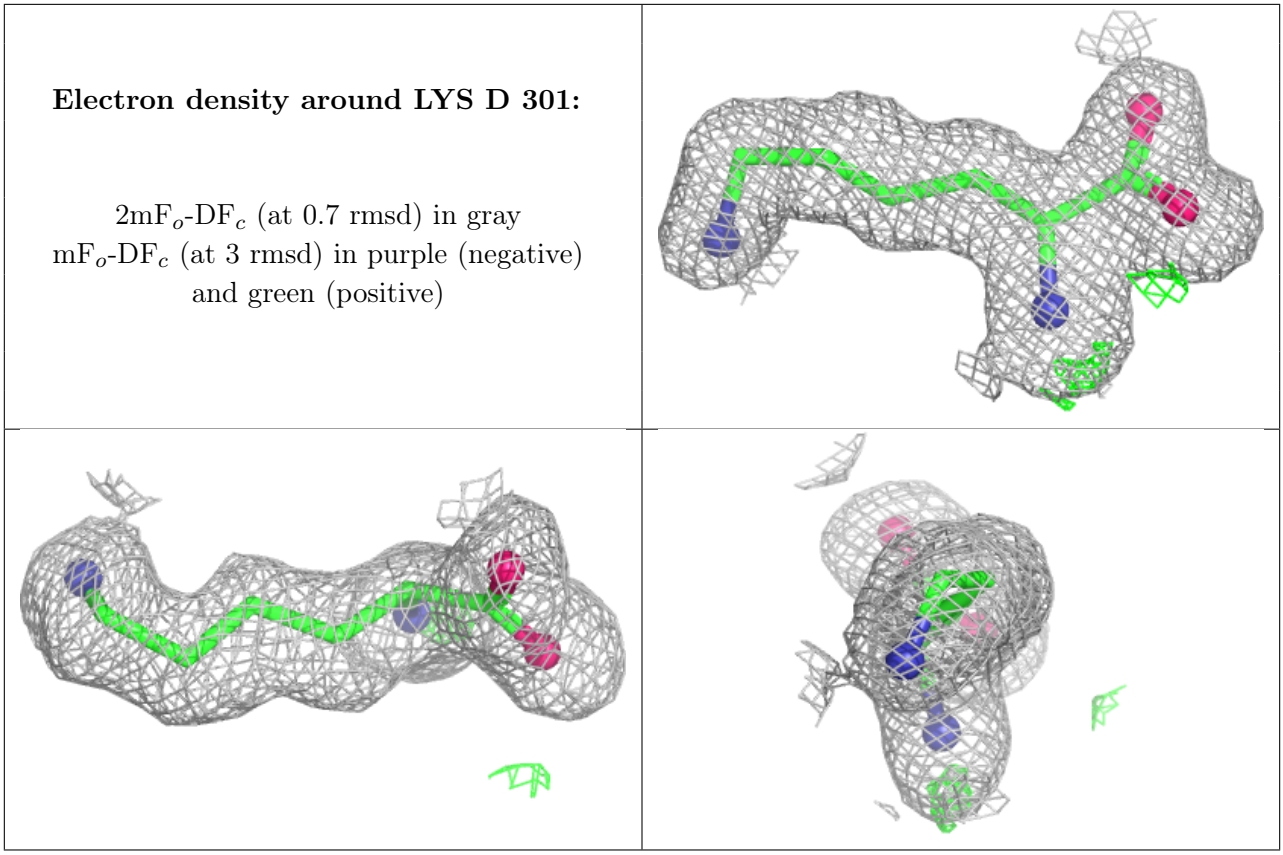
Electron density around CL D 304 (B):

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



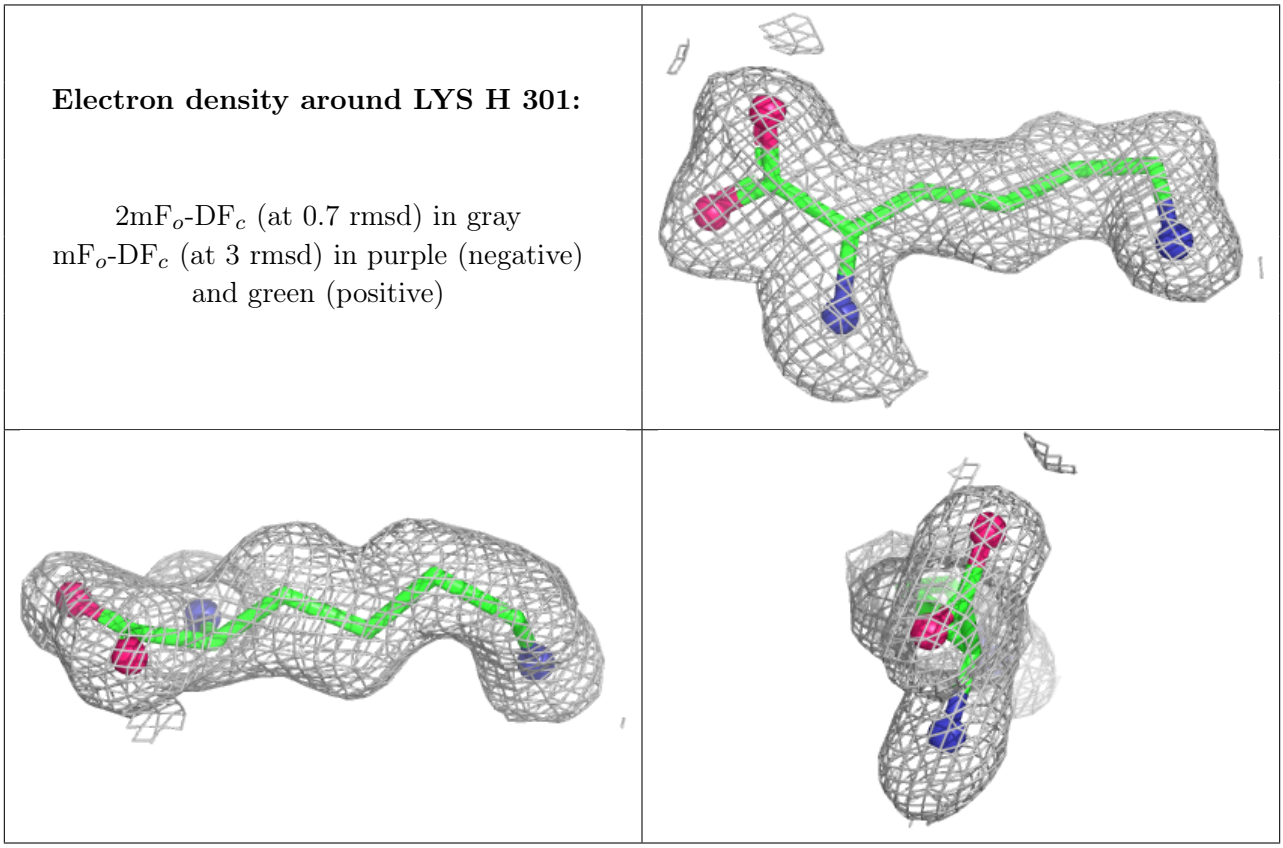
Electron density around LYS D 301:

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



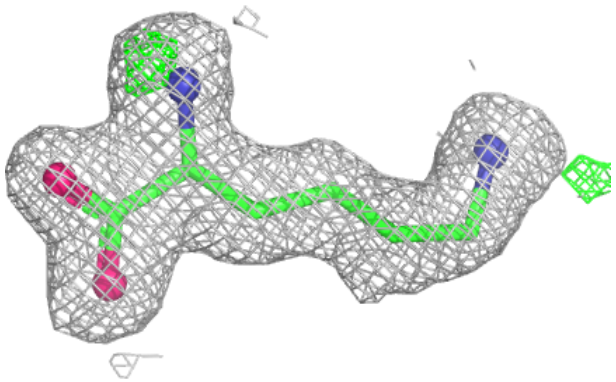
Electron density around LYS H 301:

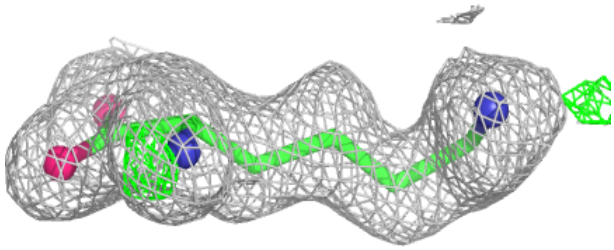
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

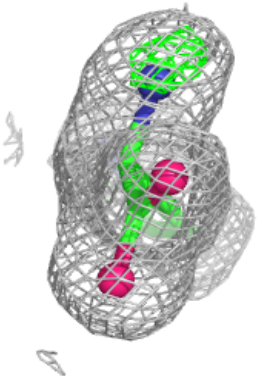


Electron density around LYS F 301:

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

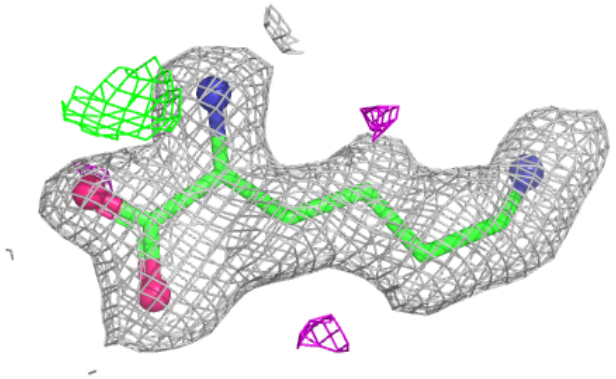


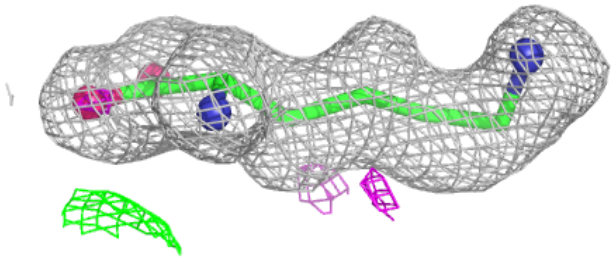


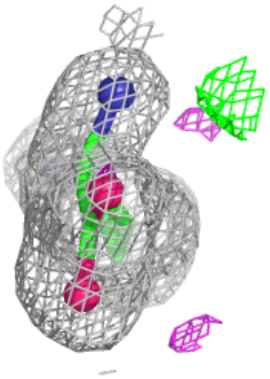


Electron density around LYS G 301:

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

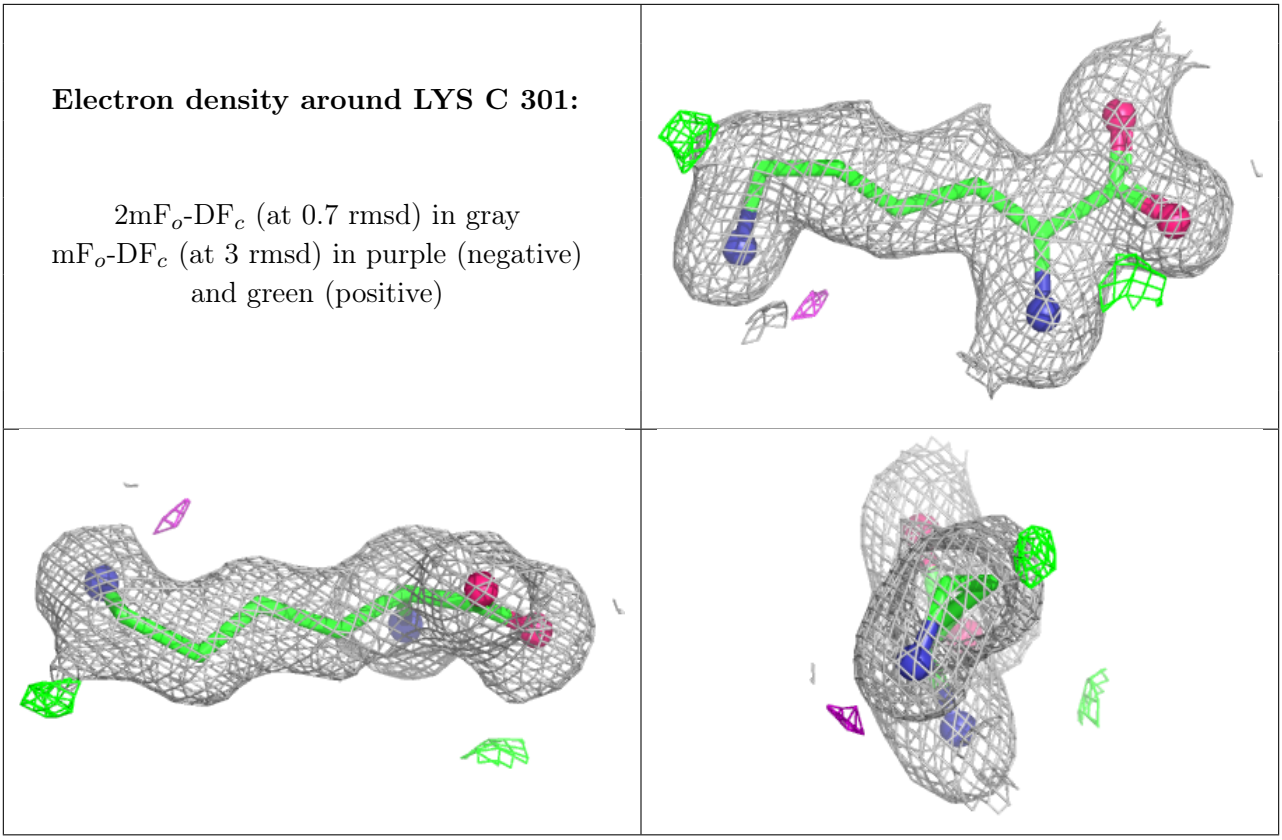






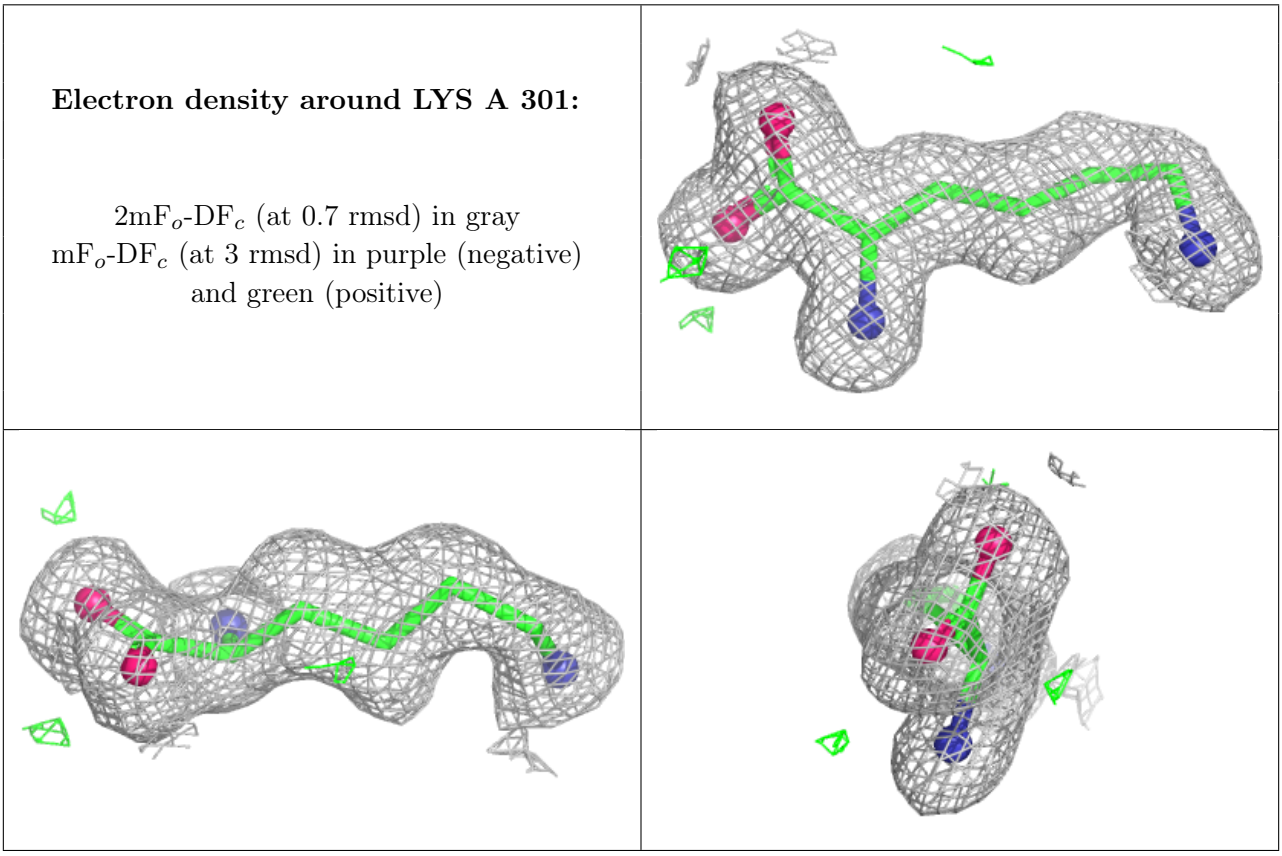
Electron density around LYS C 301:

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



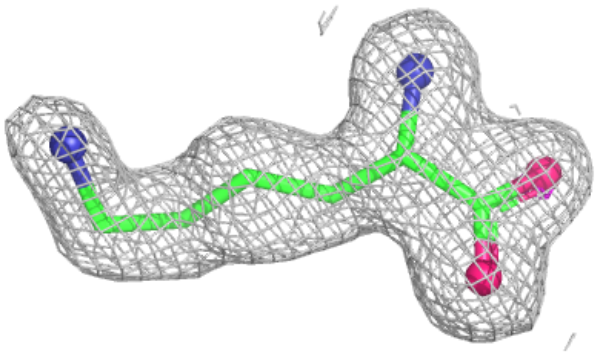
Electron density around LYS A 301:

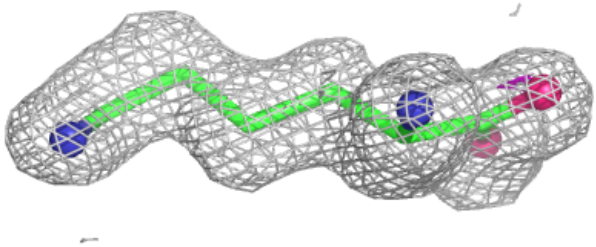
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

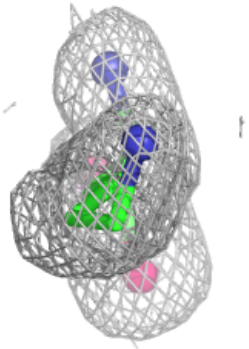


Electron density around LYS E 301:

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

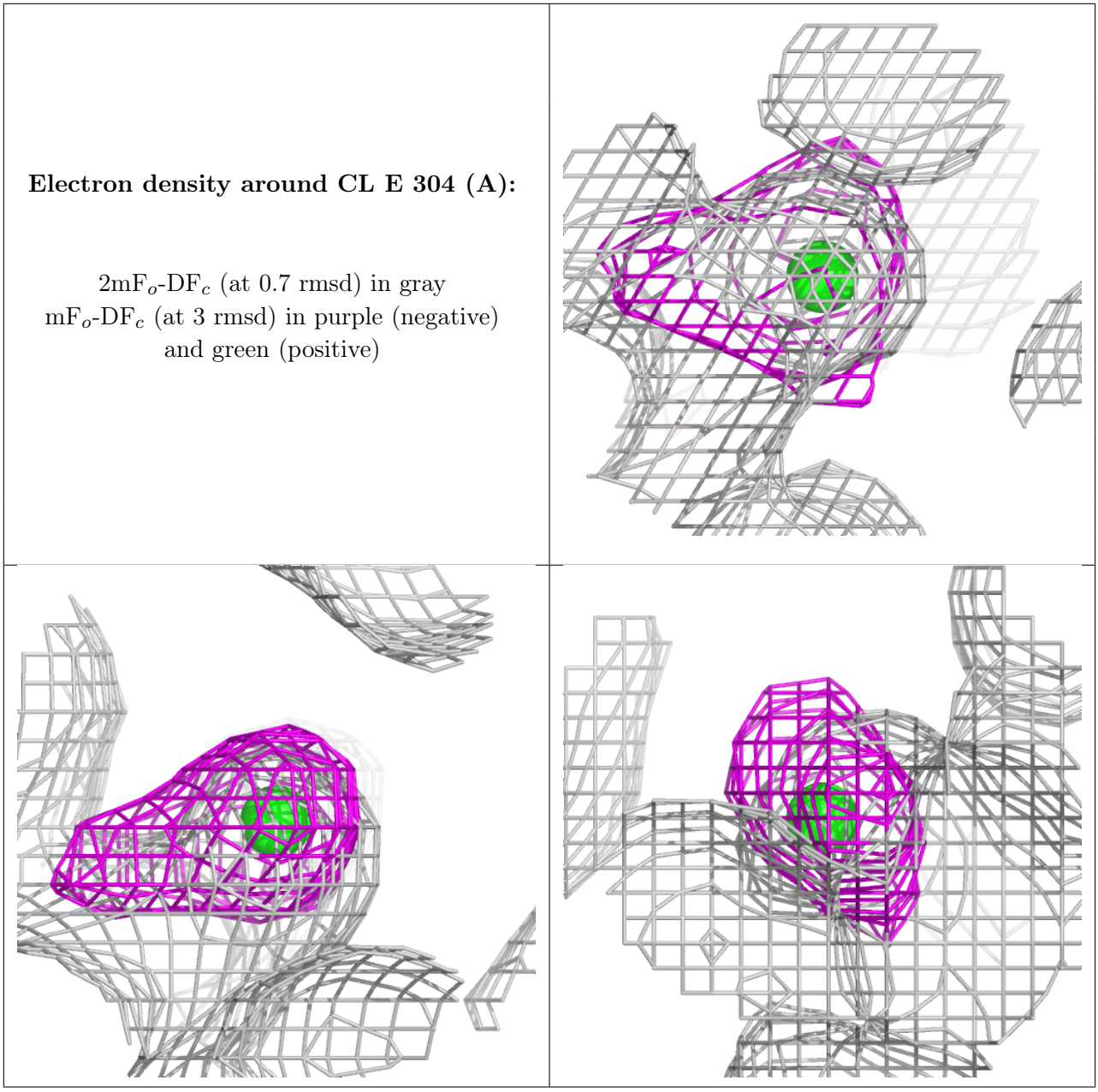






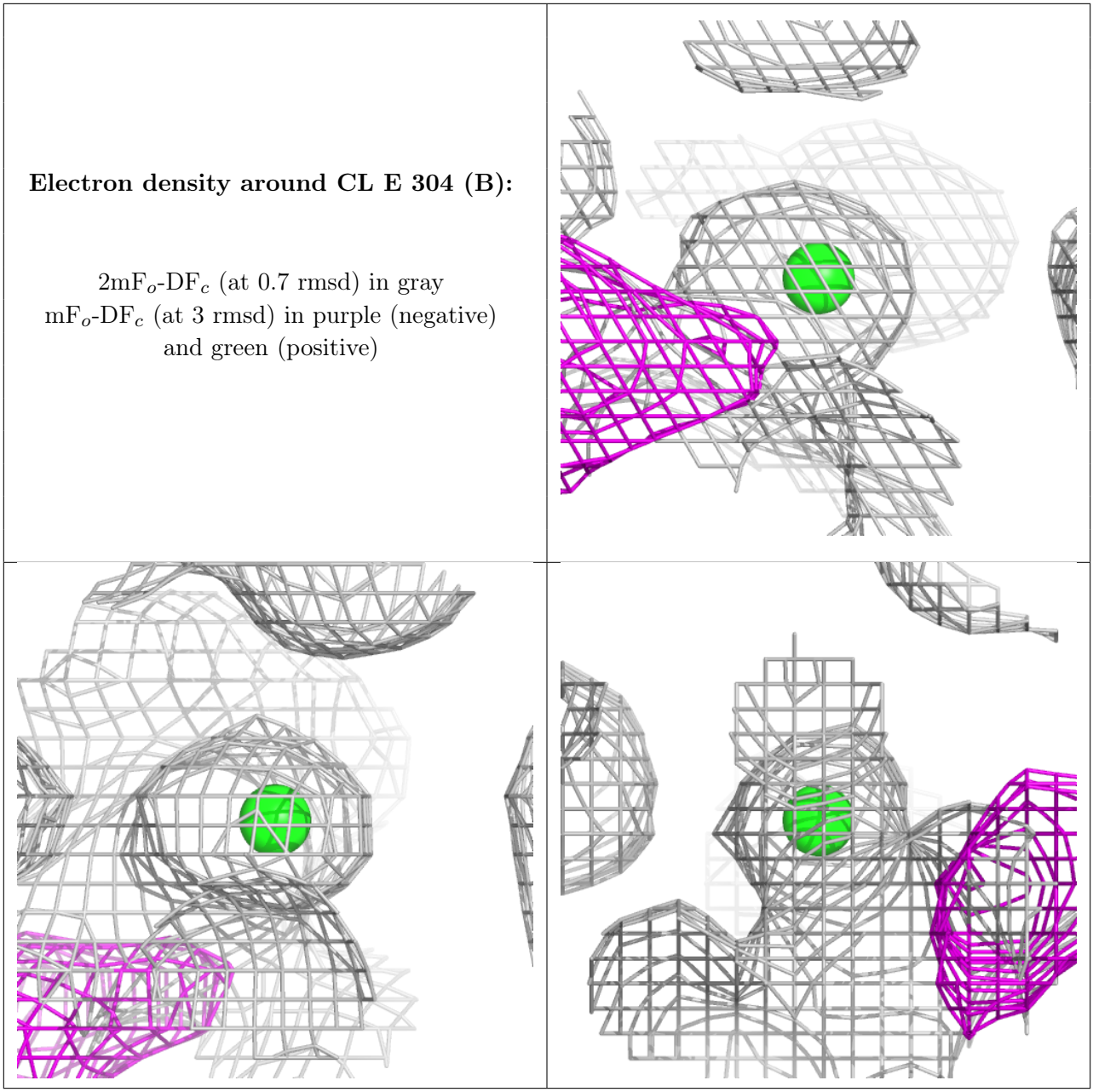
Electron density around CL E 304 (A):

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



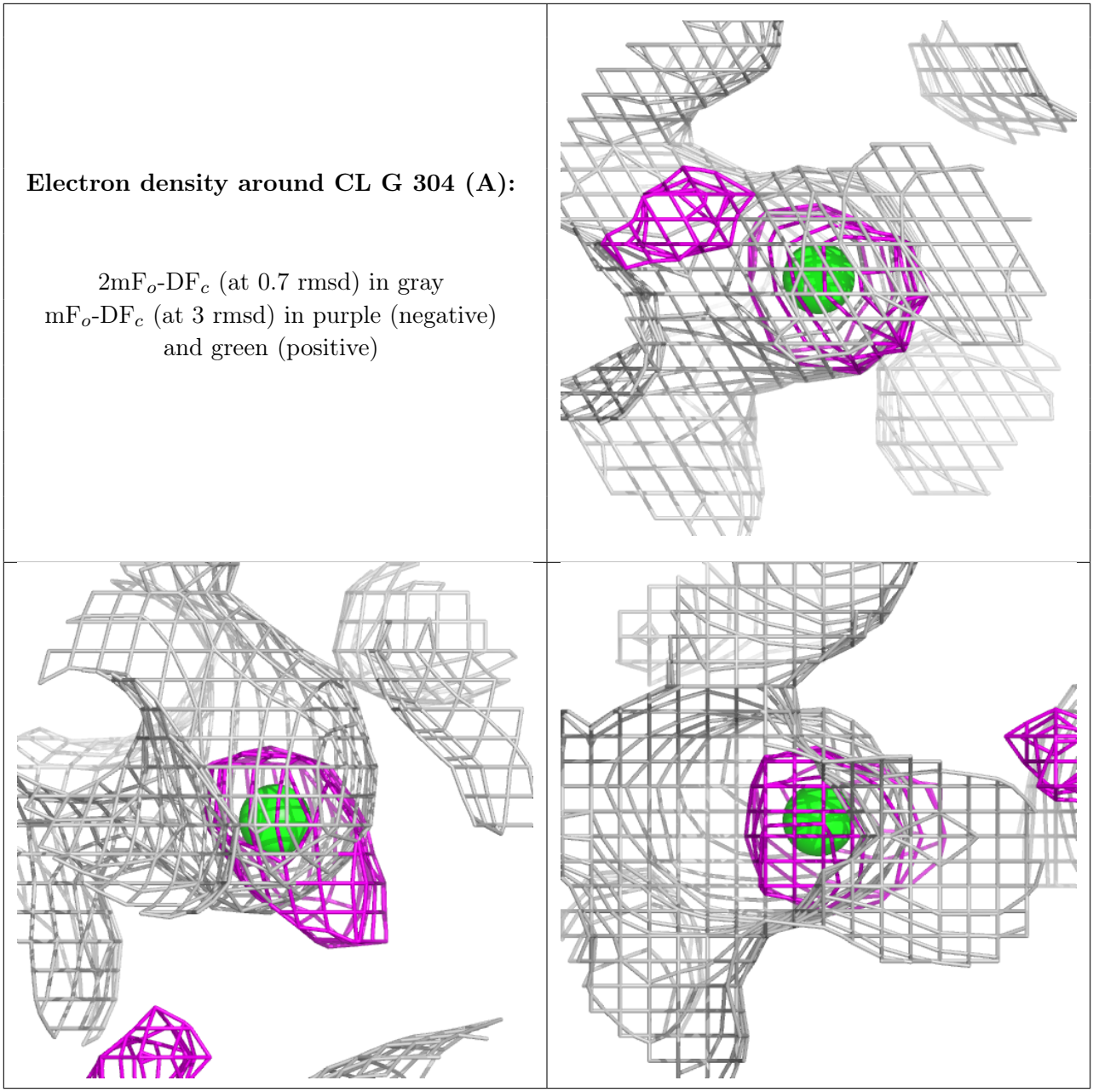
Electron density around CL E 304 (B):

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



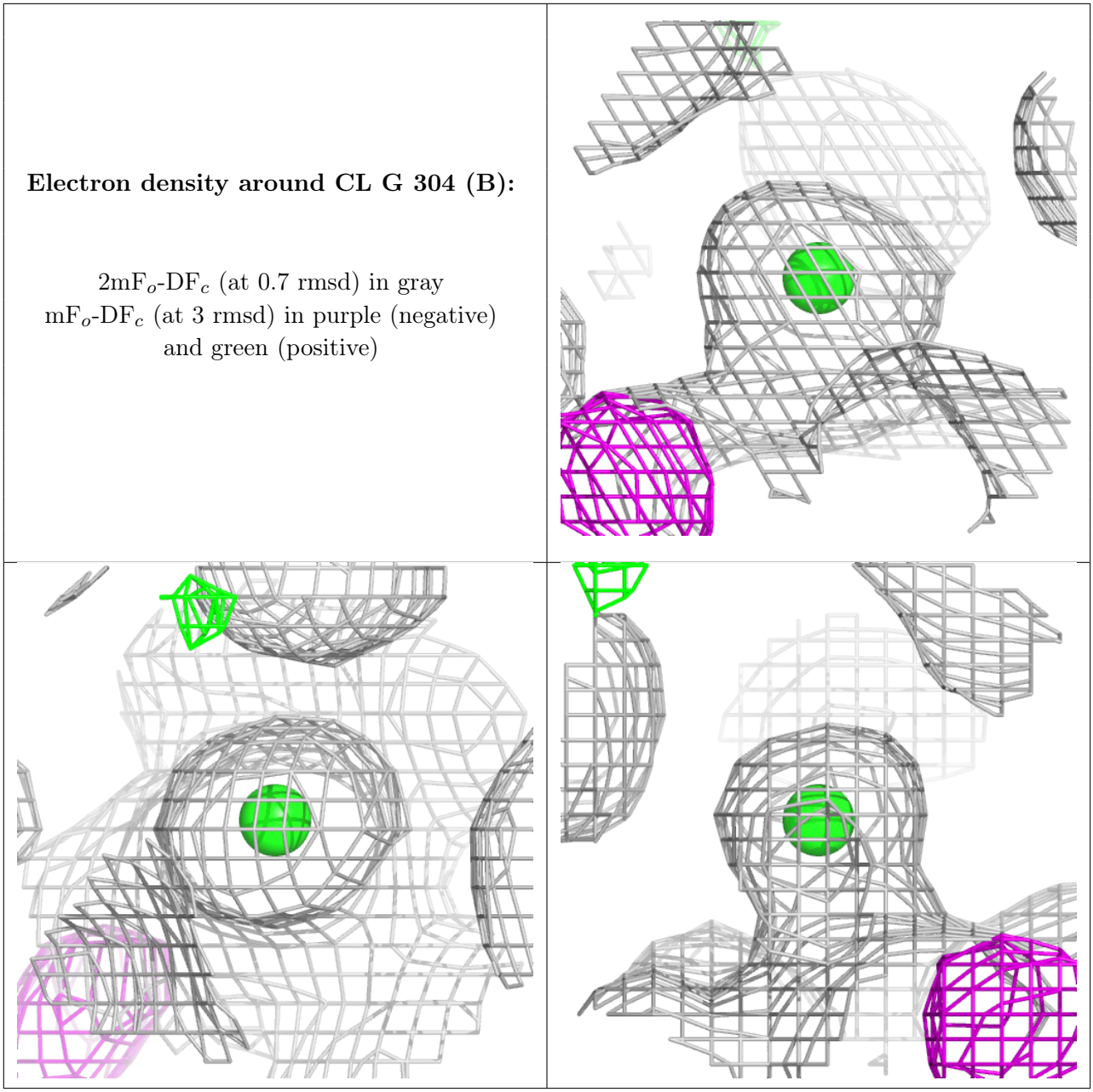
Electron density around CL G 304 (A):

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



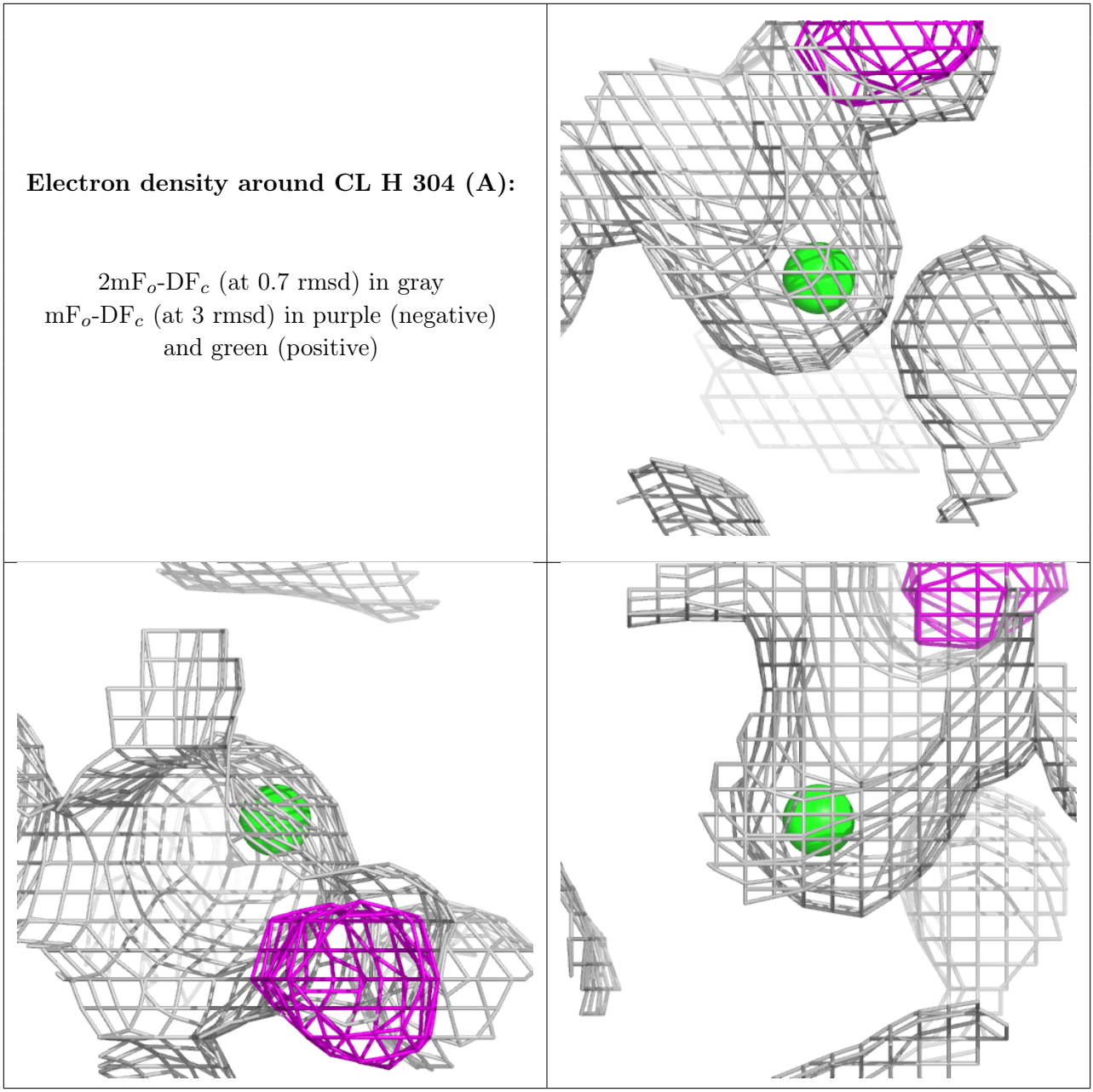
Electron density around CL G 304 (B):

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



Electron density around CL H 304 (A):

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



Electron density around CL H 304 (B):

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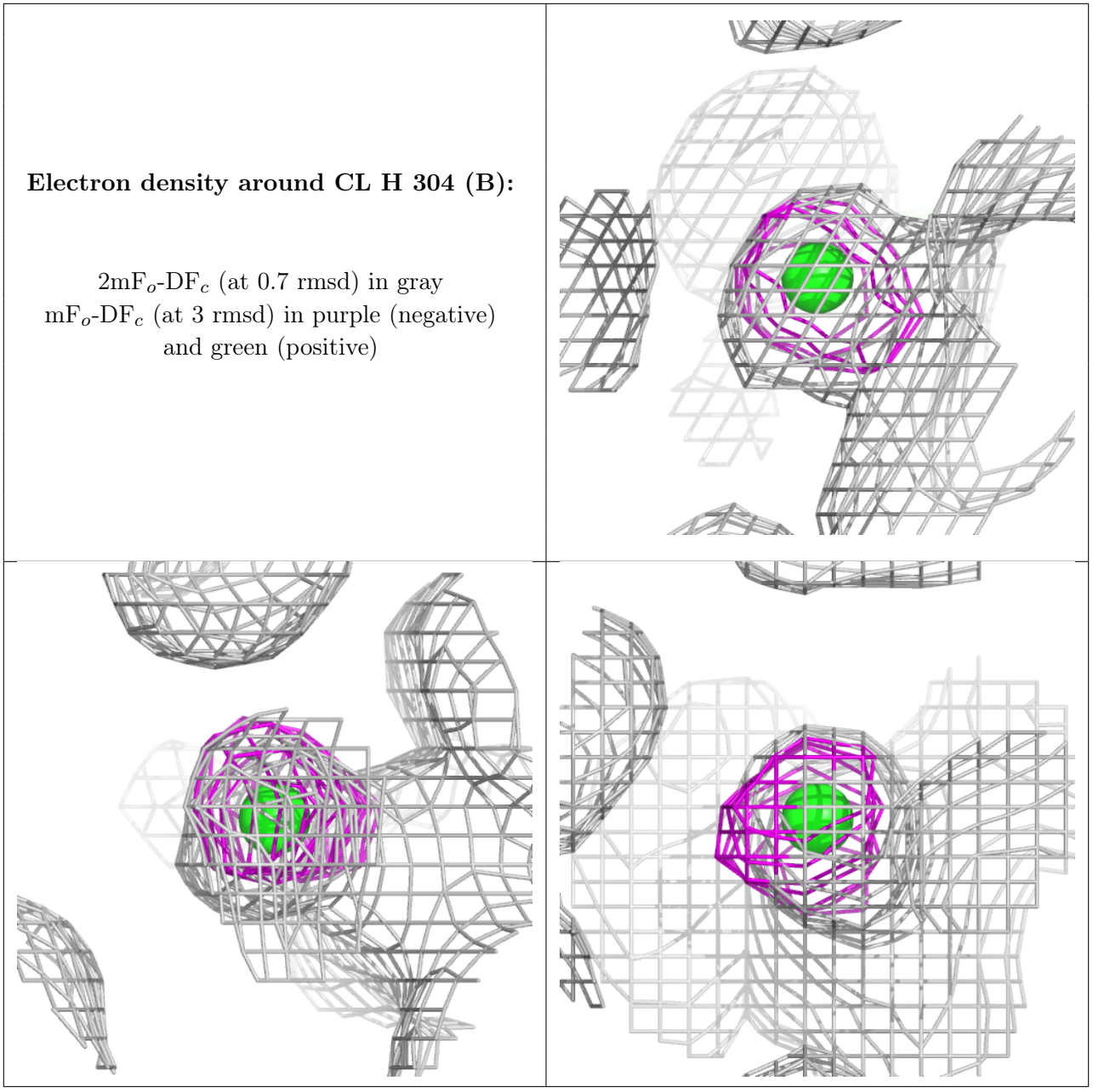
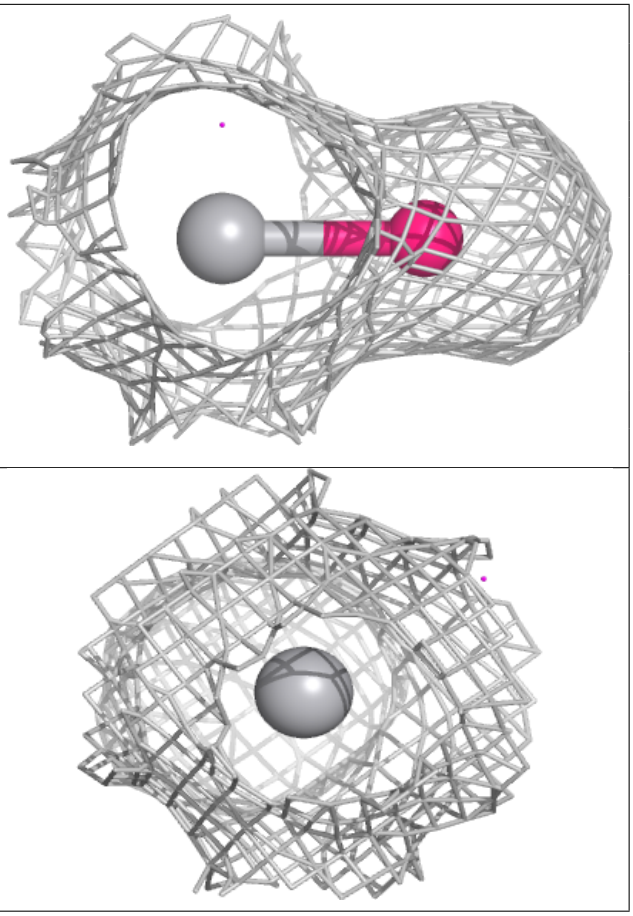
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



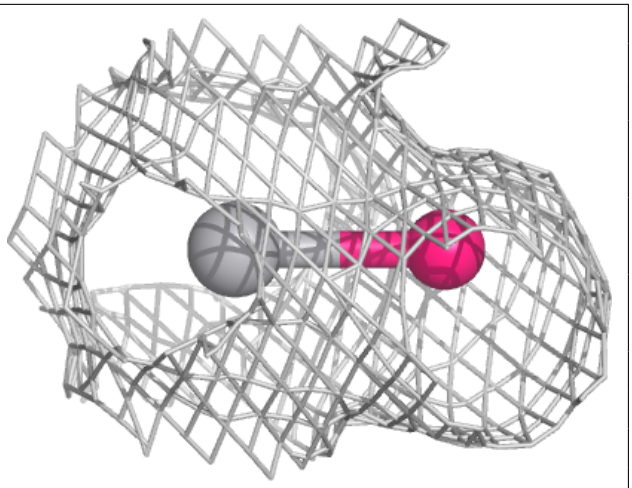
Electron density around VVO F 303 (A):

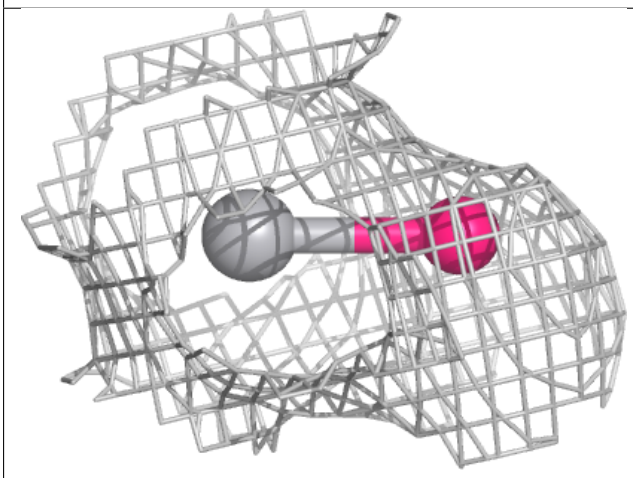
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

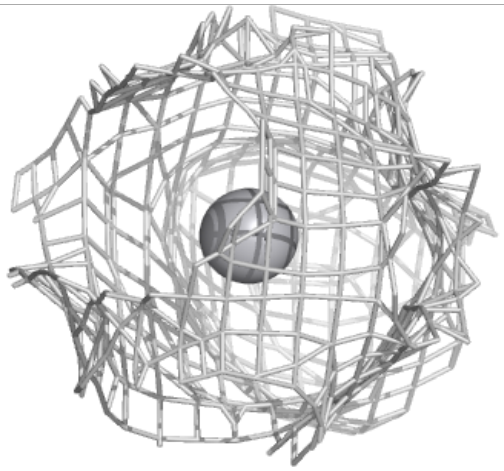


Electron density around VVO F 303 (B):

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

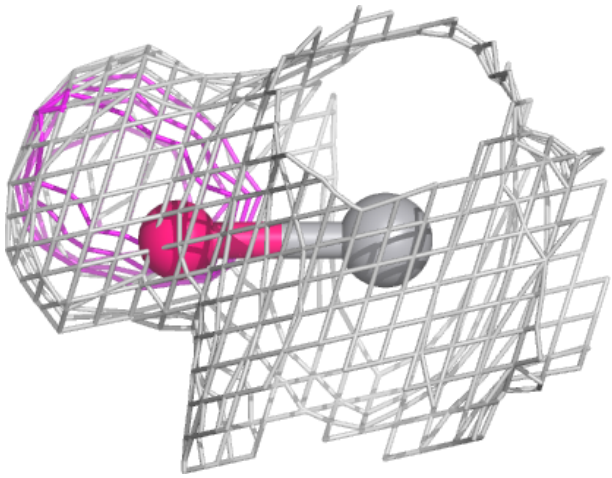


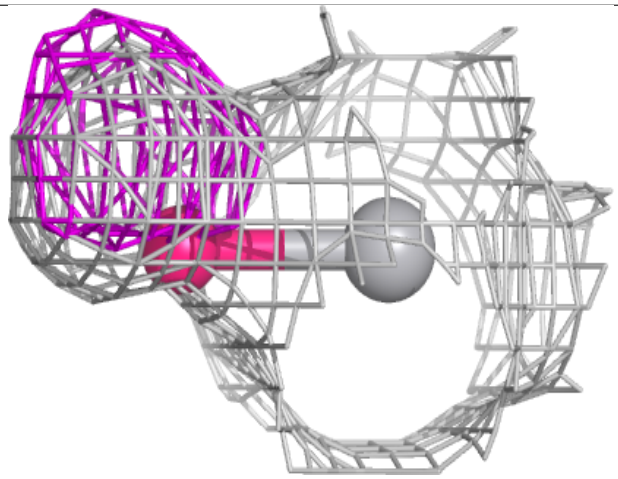


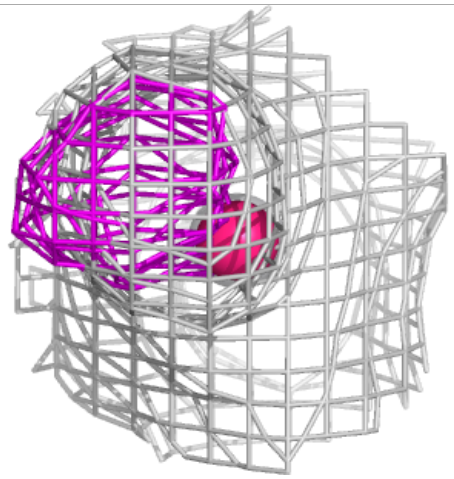


Electron density around VVO H 303 (A):

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

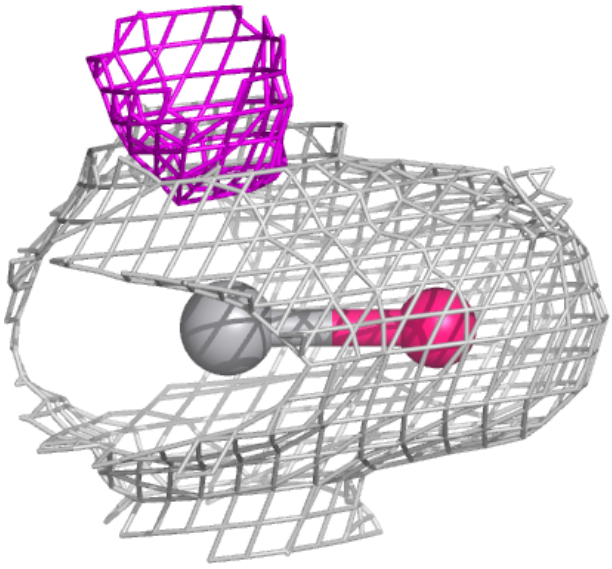


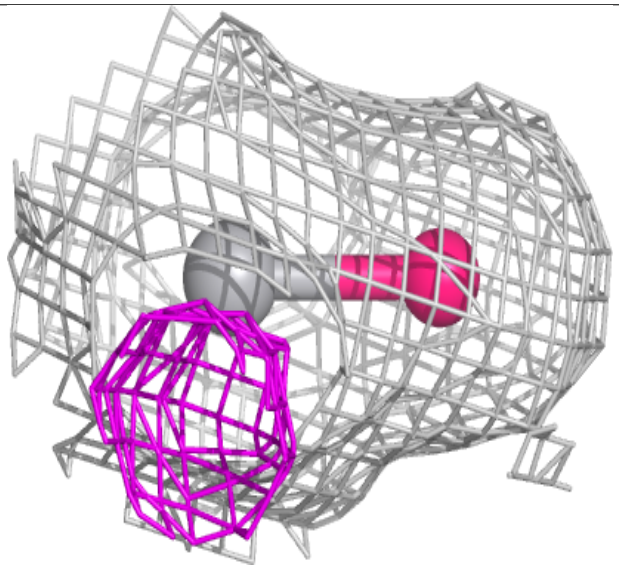


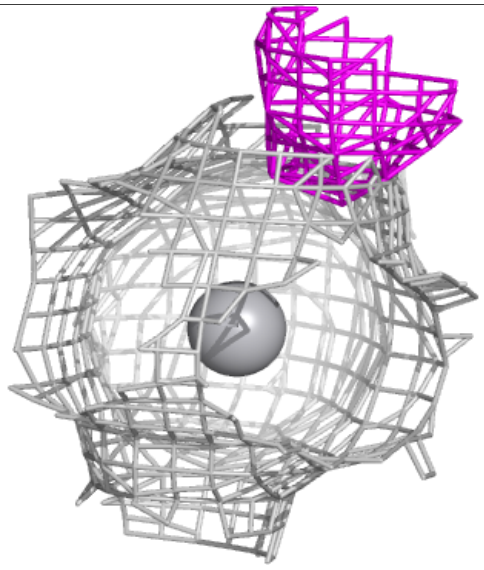


Electron density around VVO H 303 (B):

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

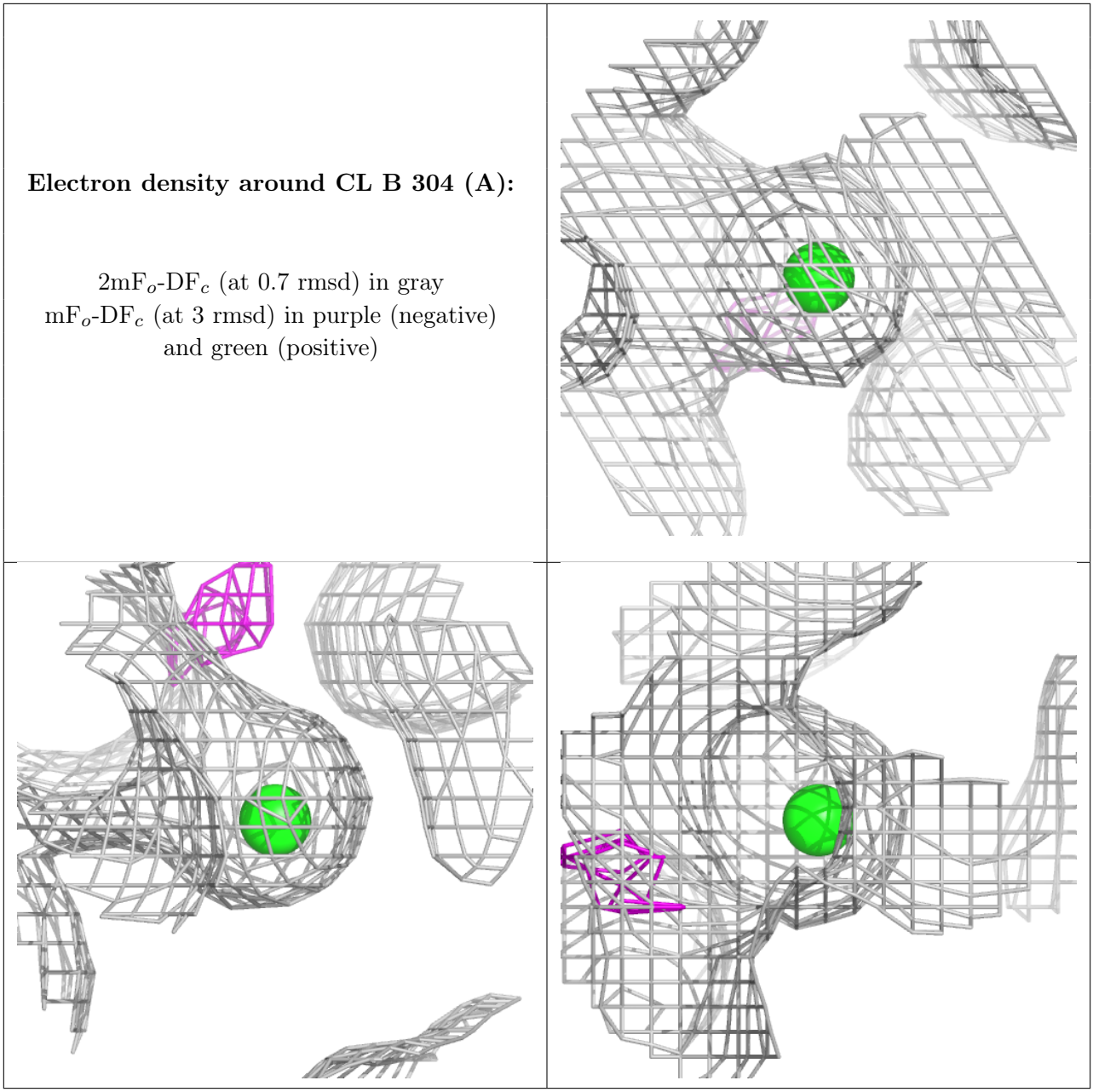






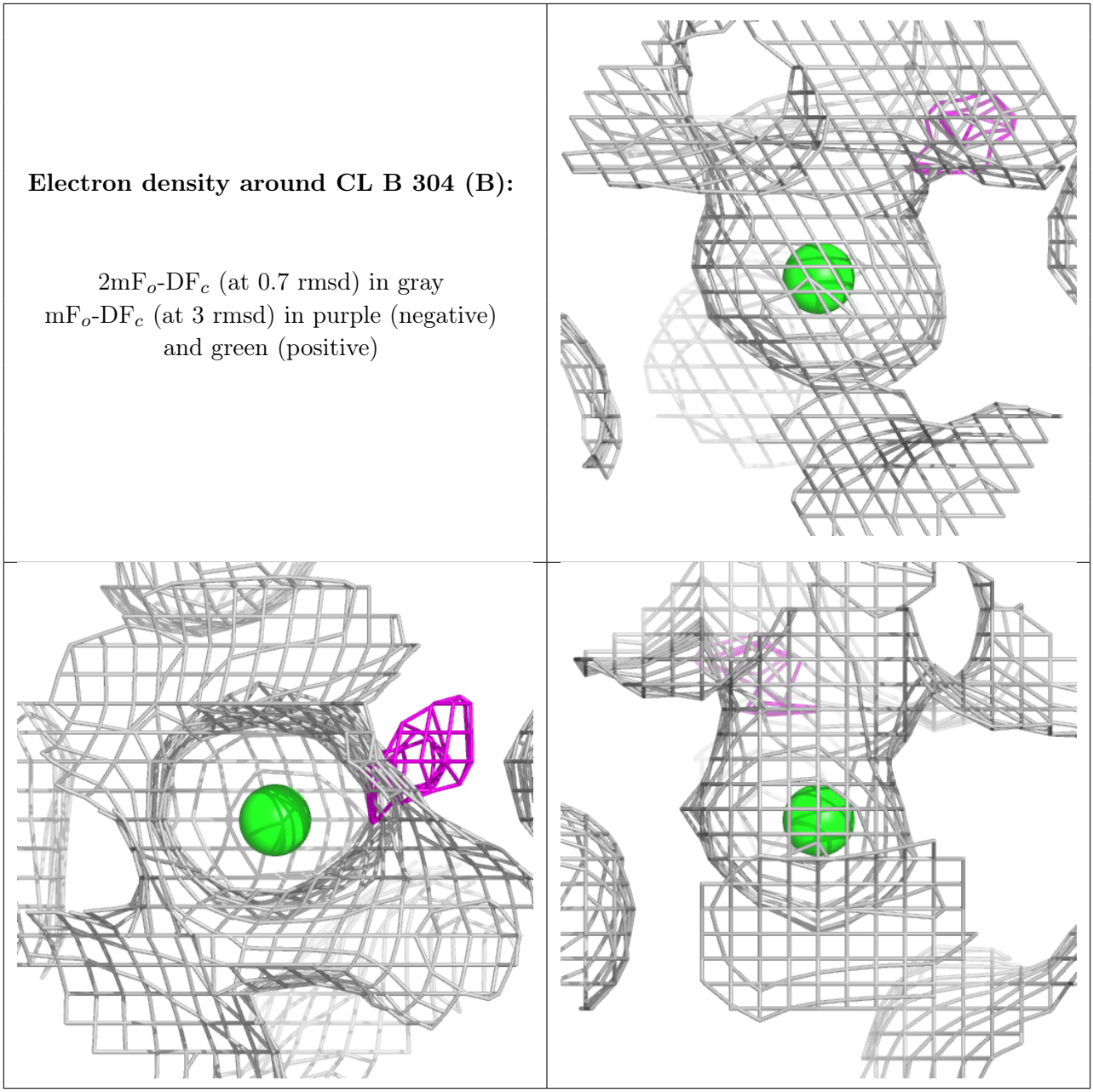
Electron density around CL B 304 (A):

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



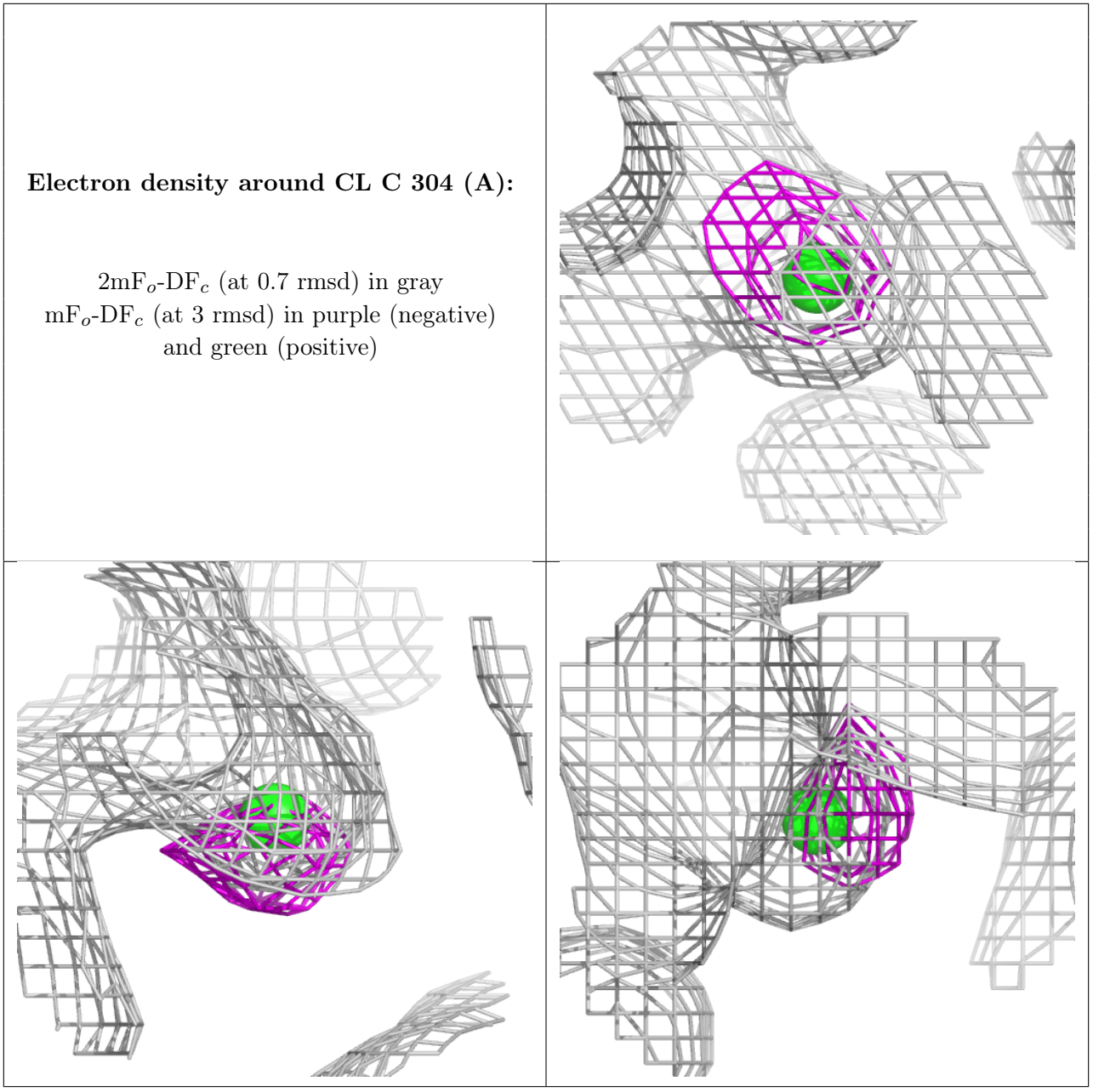
Electron density around CL B 304 (B):

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



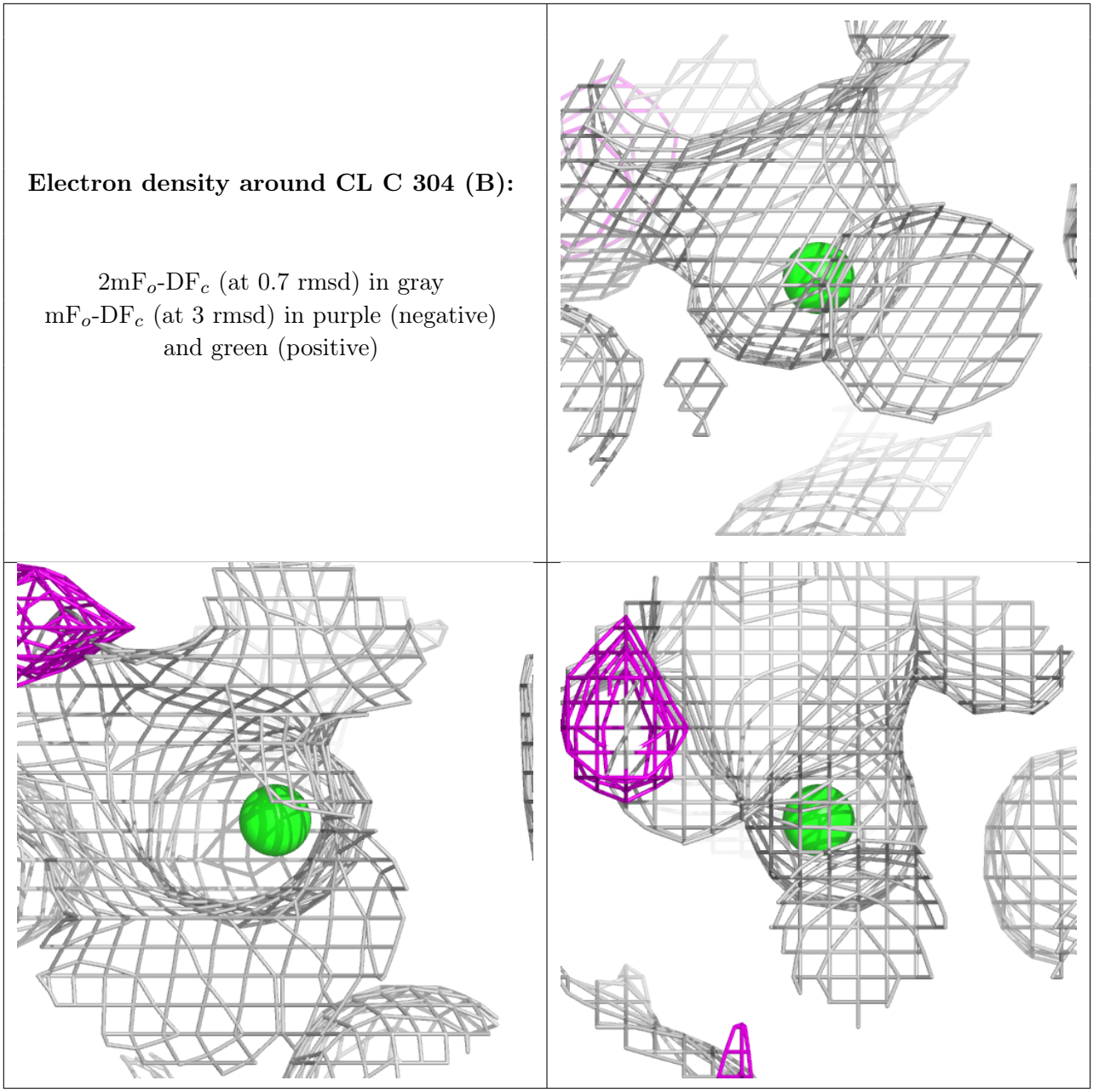
Electron density around CL C 304 (A):

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



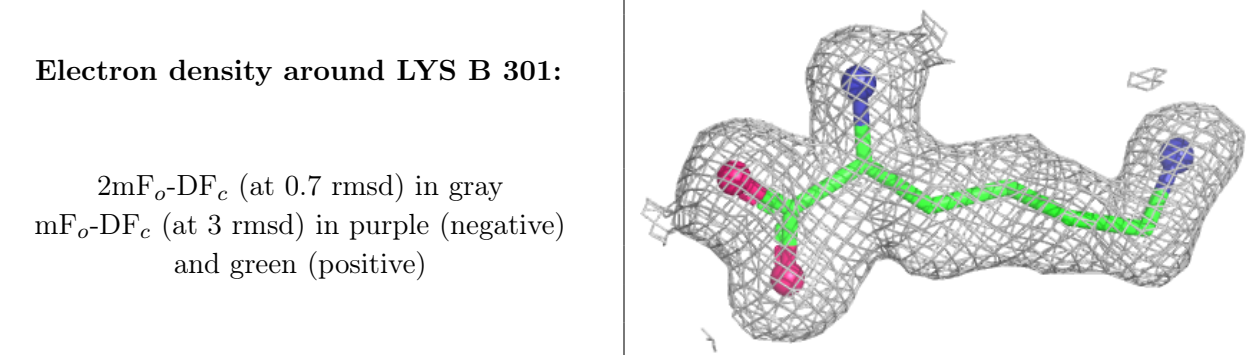
Electron density around CL C 304 (B):

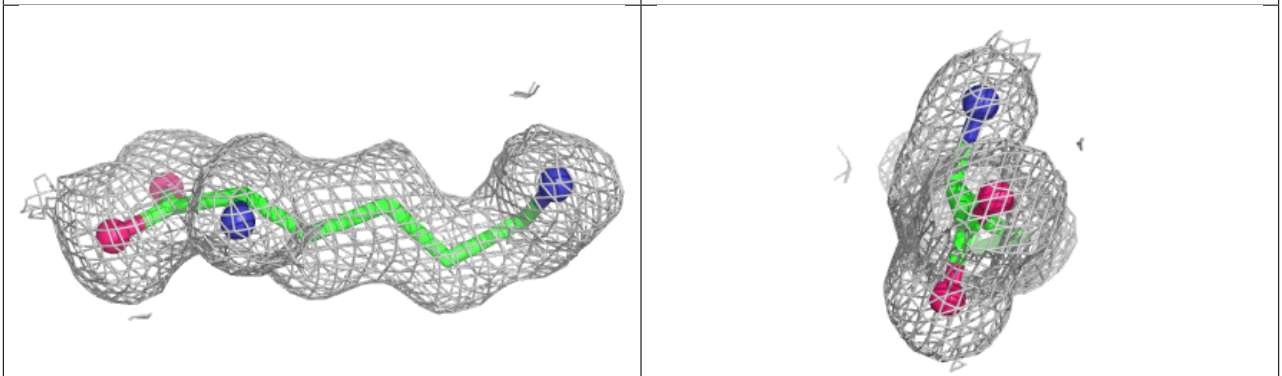
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around LYS B 301:

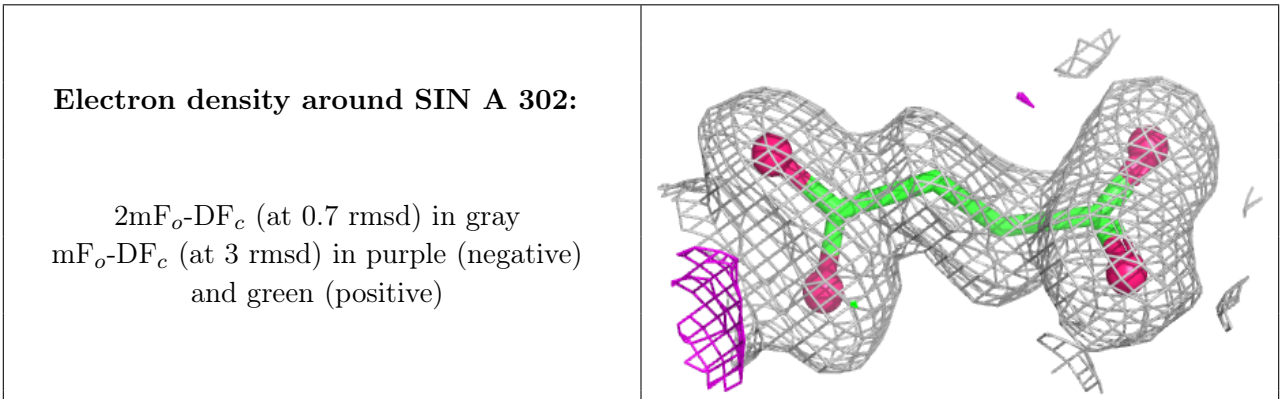
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

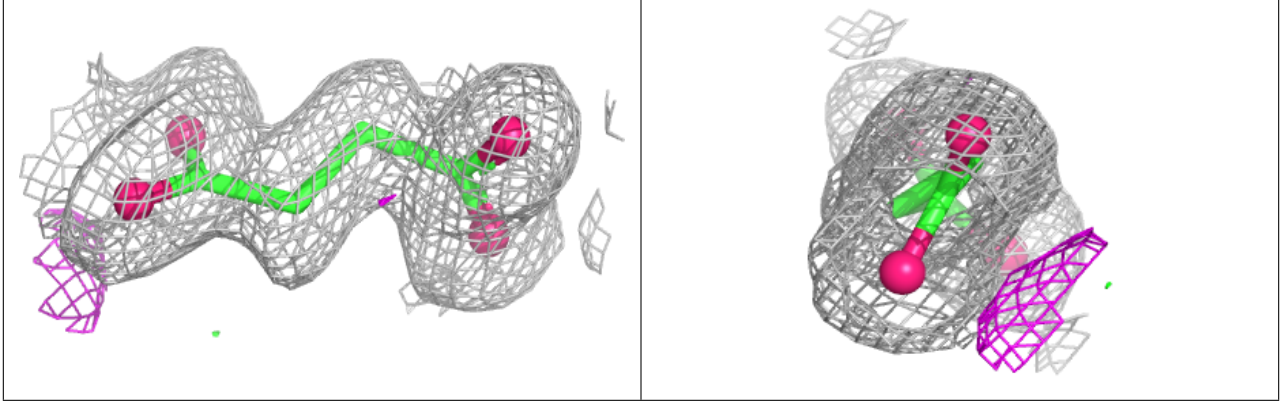




Electron density around SIN A 302:

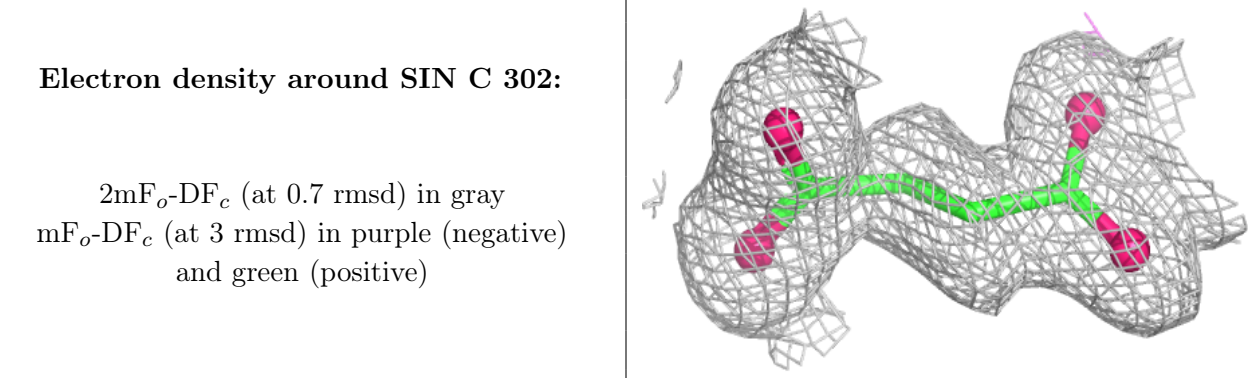
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





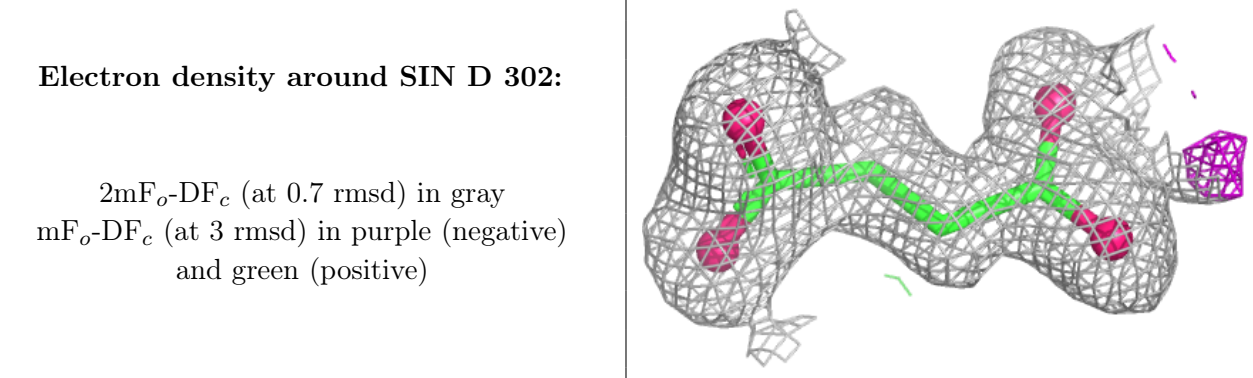
Electron density around SIN C 302:

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



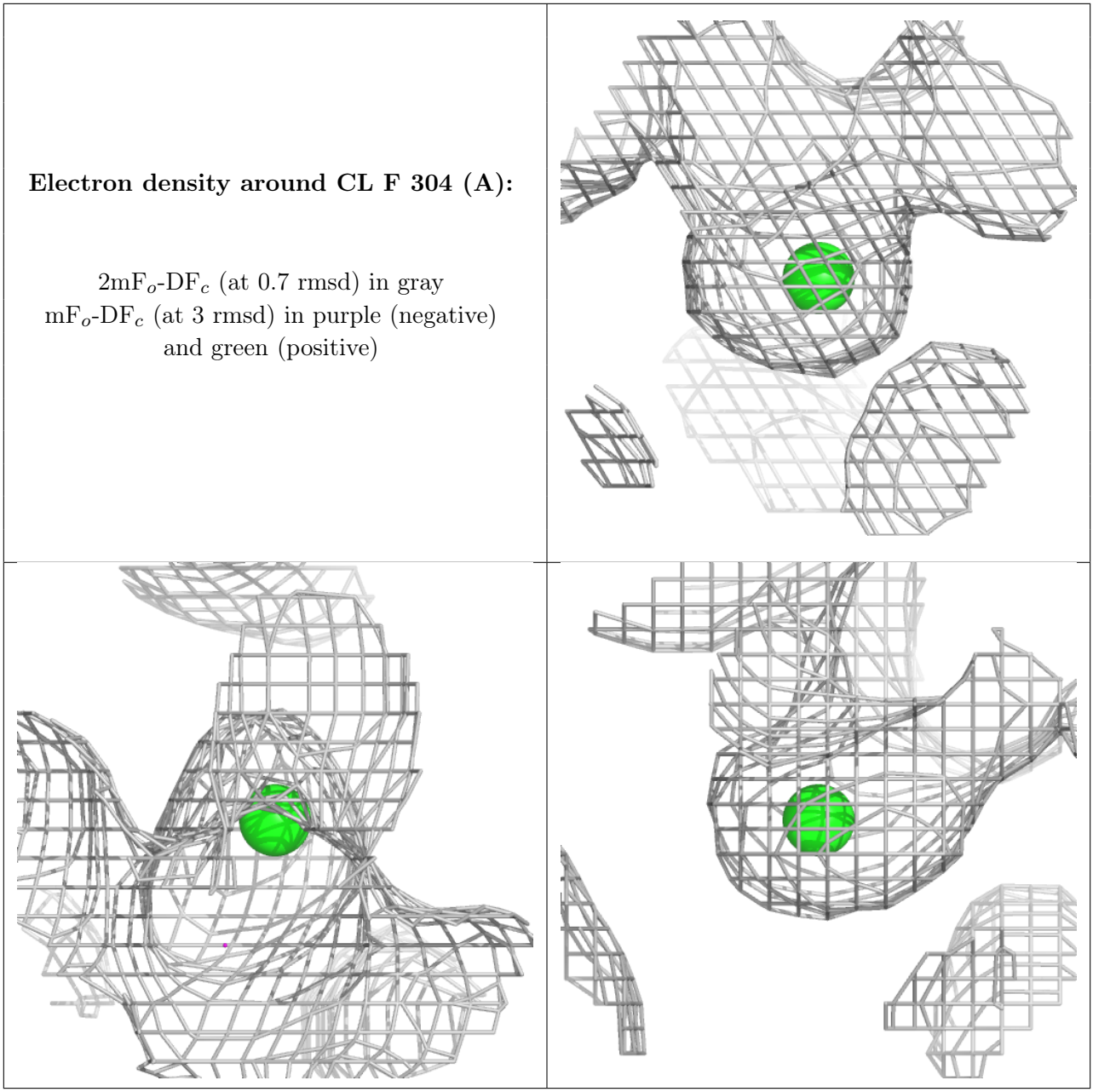
Electron density around SIN D 302:

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



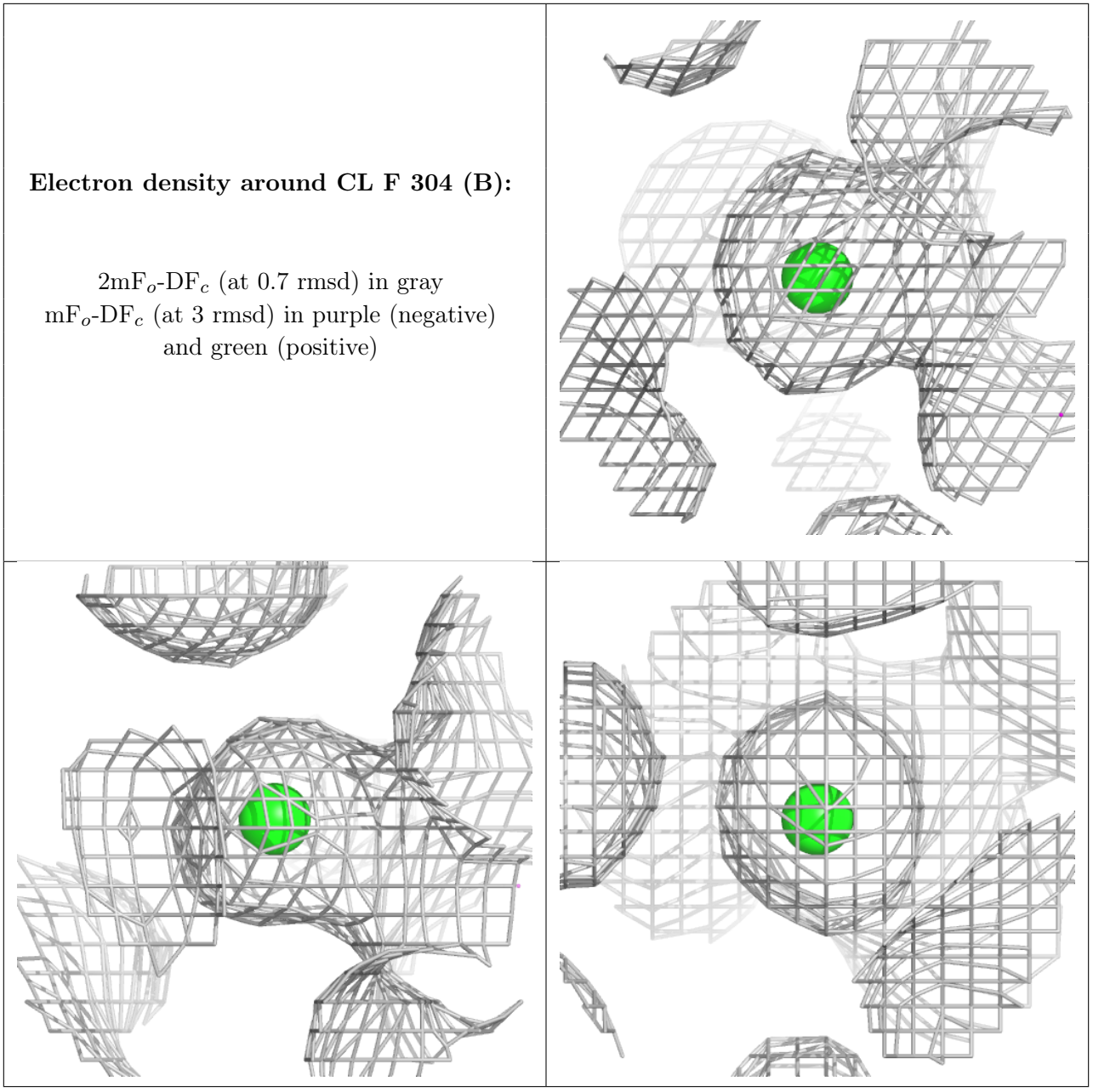
Electron density around CL F 304 (A):

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



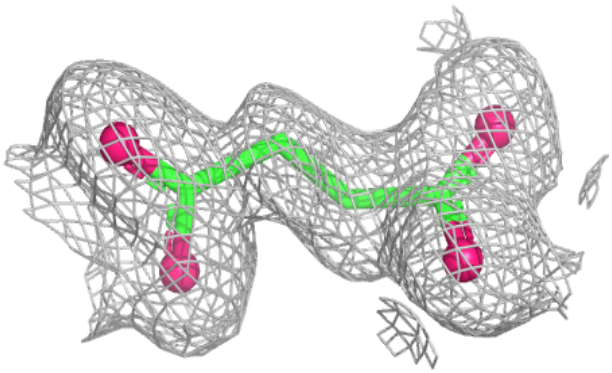
Electron density around CL F 304 (B):

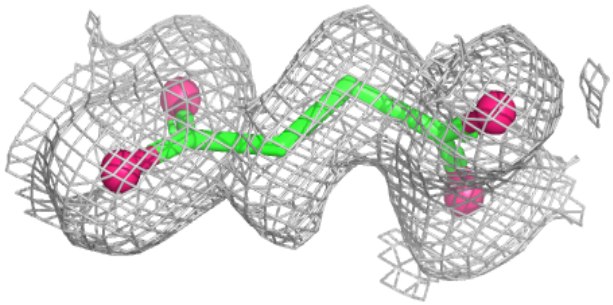
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

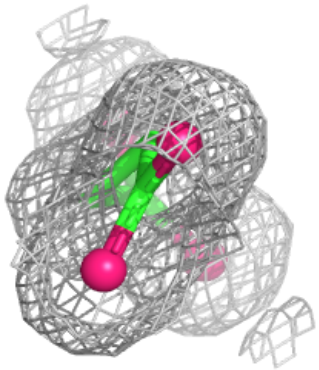


Electron density around SIN E 302:

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

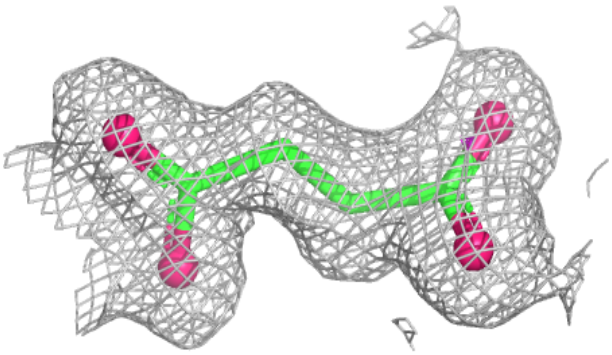


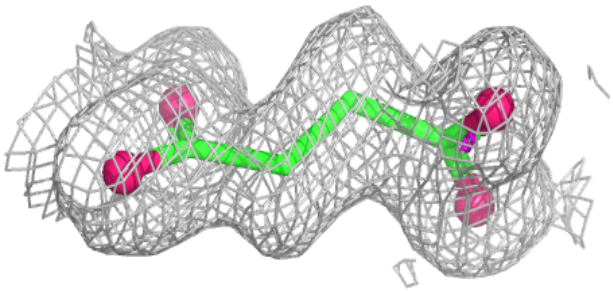


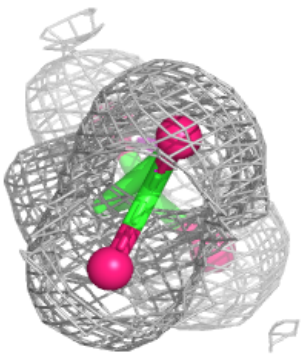


Electron density around SIN F 302:

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

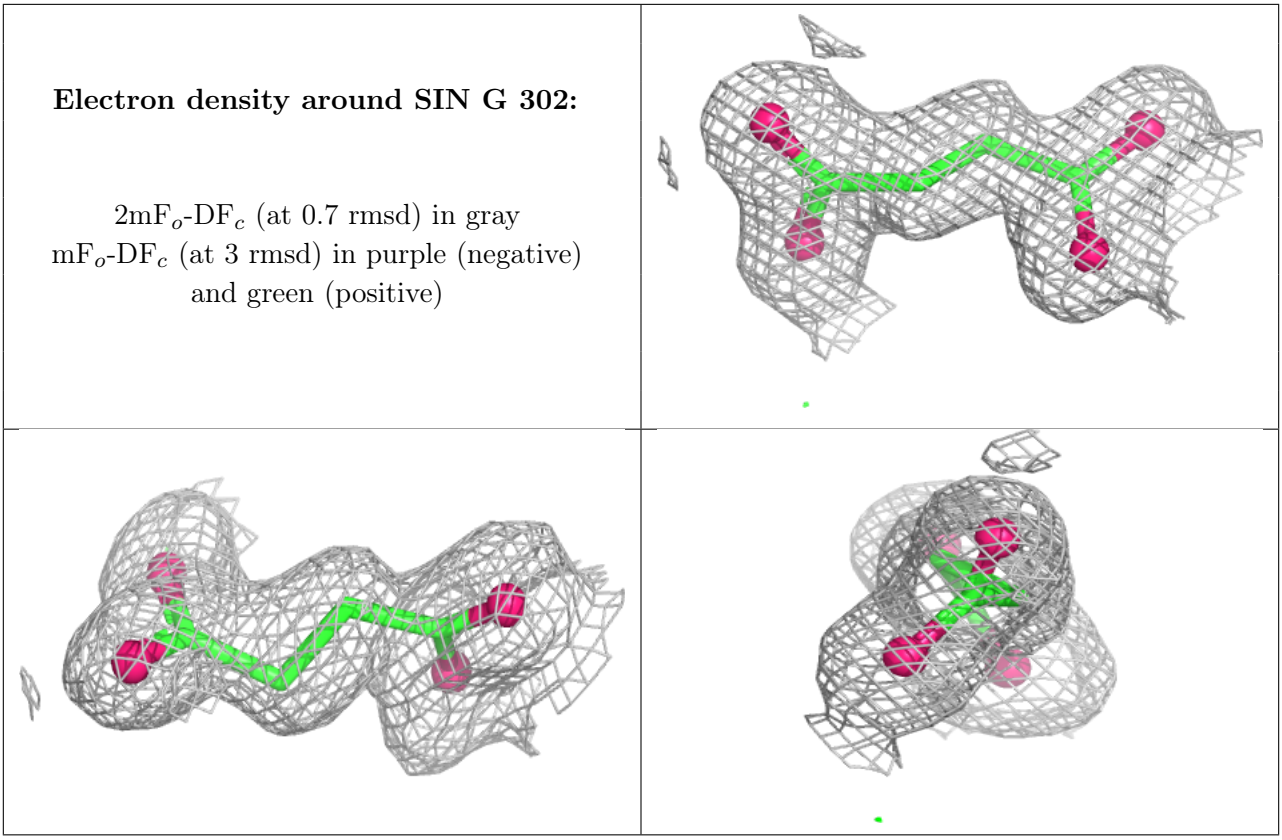






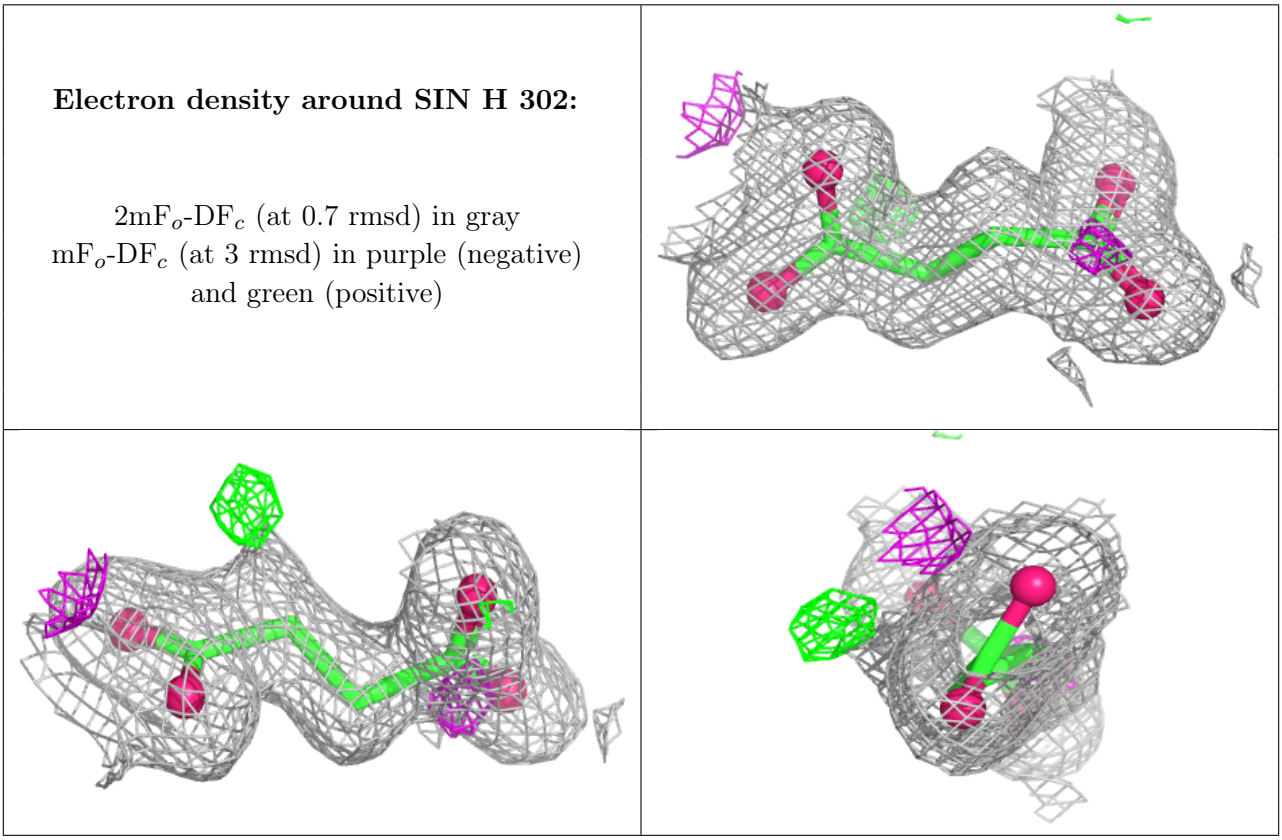
Electron density around SIN G 302:

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



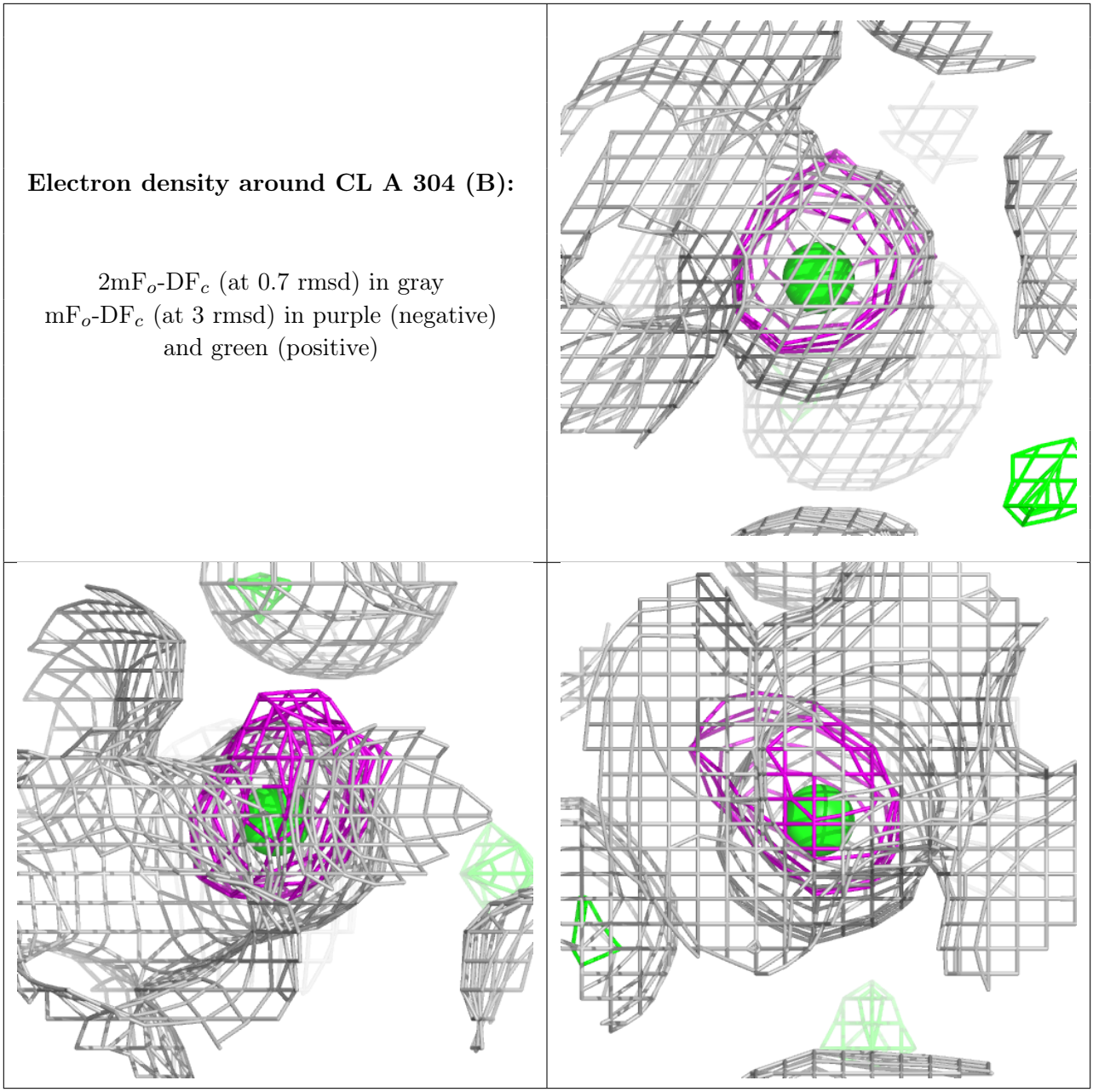
Electron density around SIN H 302:

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



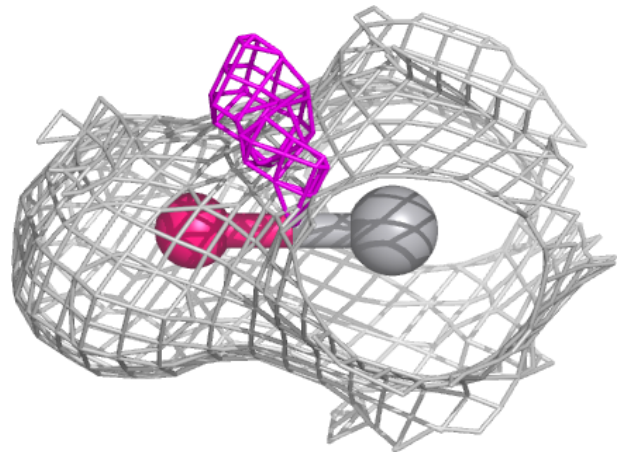
Electron density around CL A 304 (B):

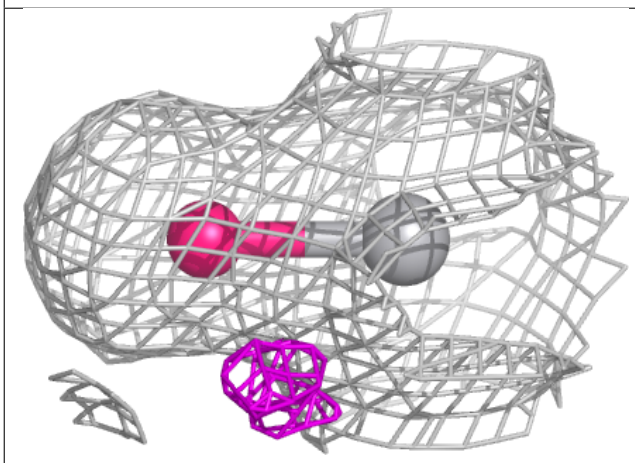
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

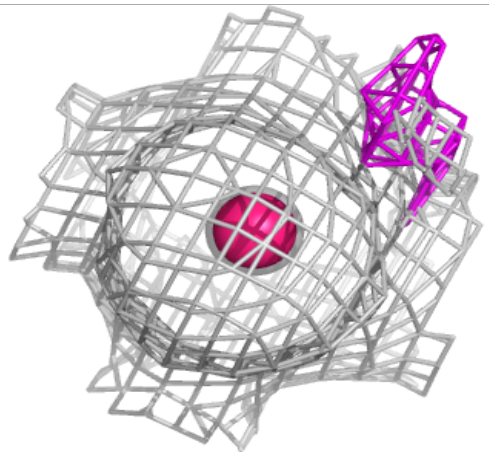


Electron density around VVO B 303 (B):

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

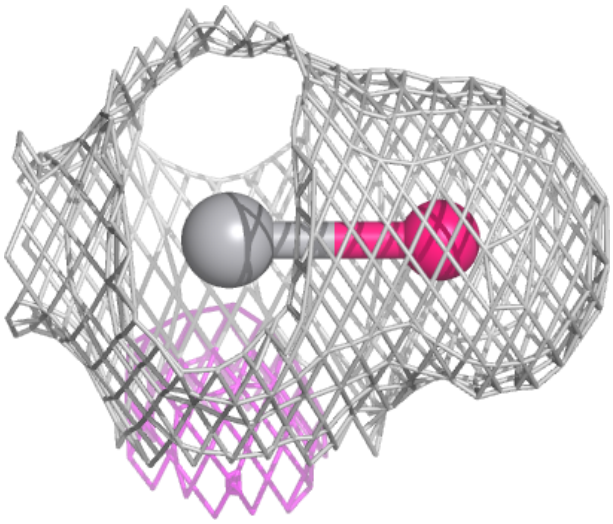


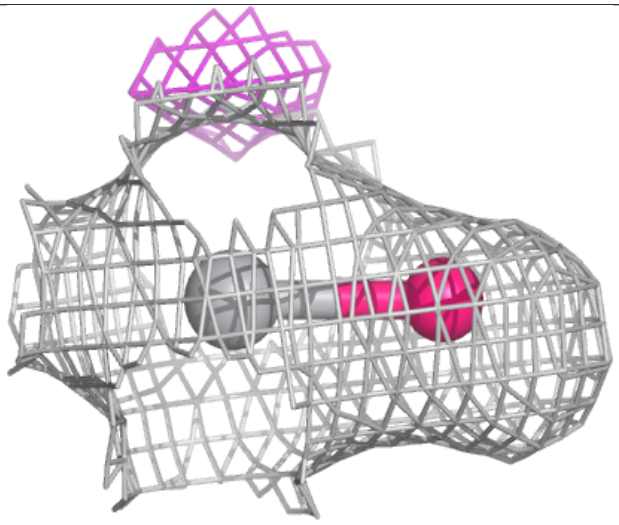


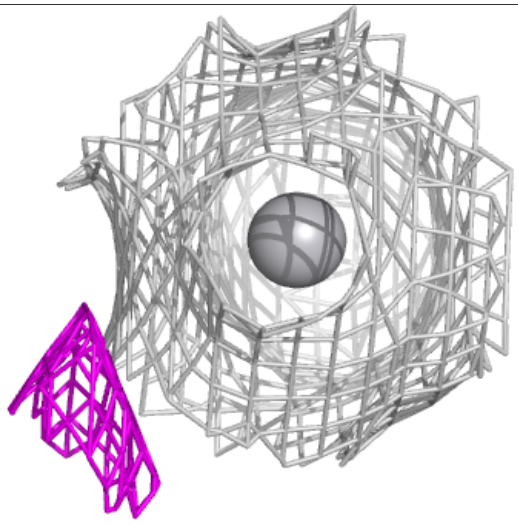


Electron density around VVO C 303 (A):

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

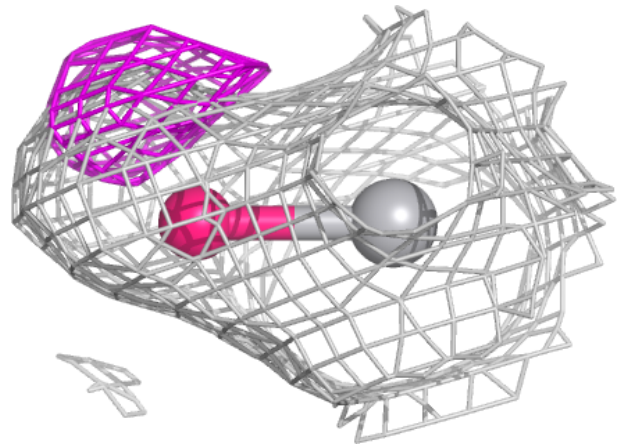


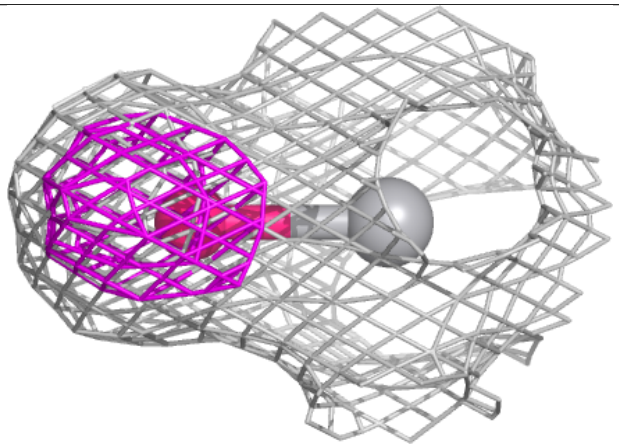


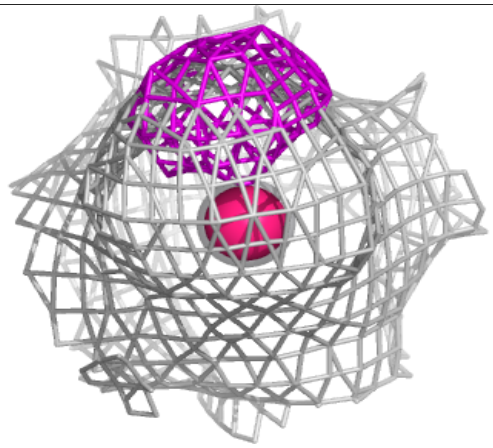


Electron density around VVO C 303 (B):

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

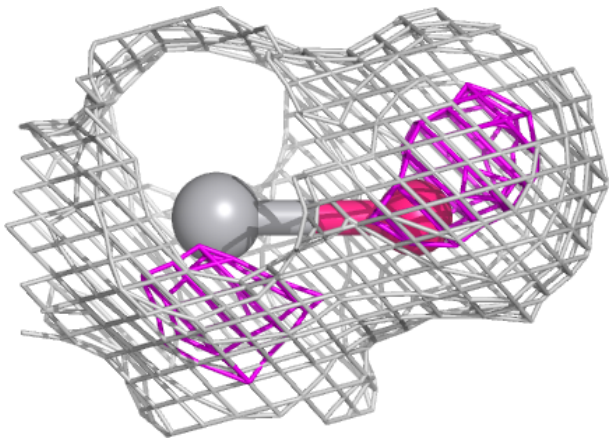


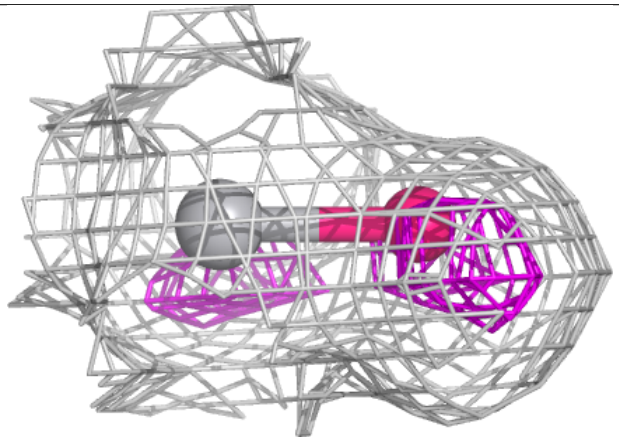


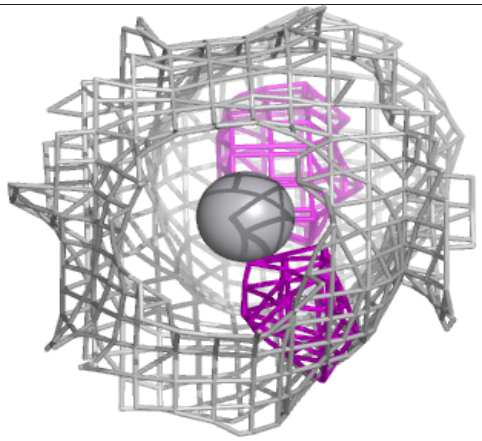


Electron density around VVO D 303 (A):

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

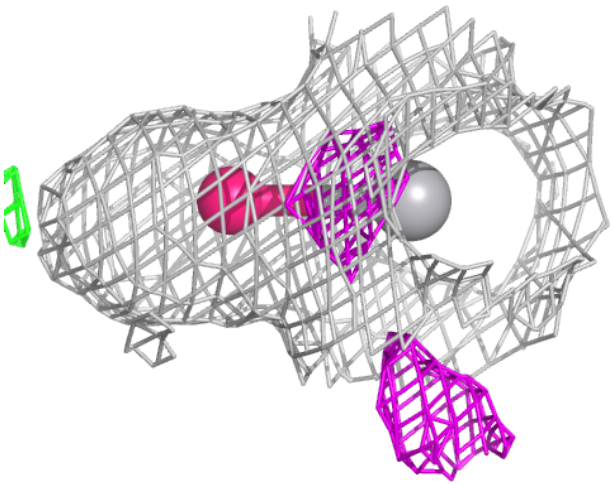


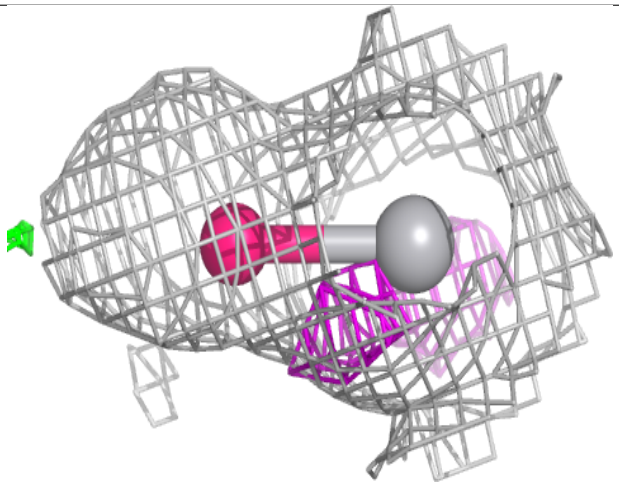


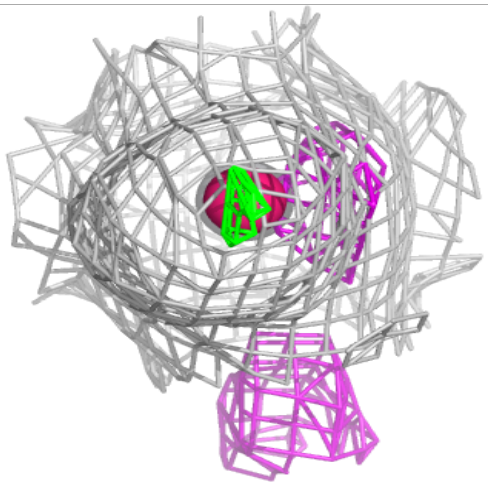


Electron density around VVO D 303 (B):

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

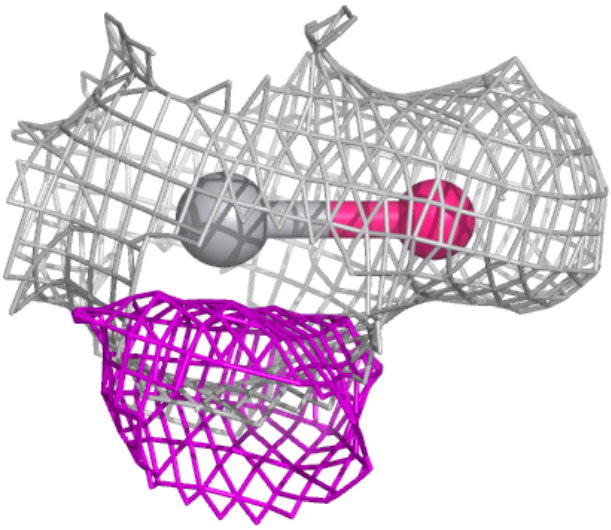


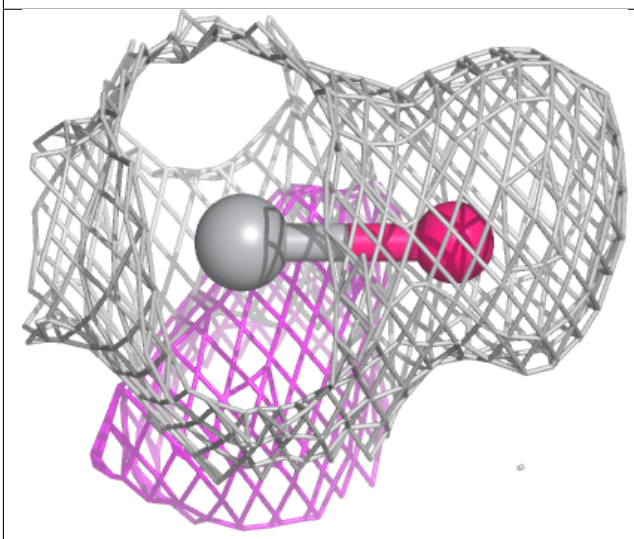


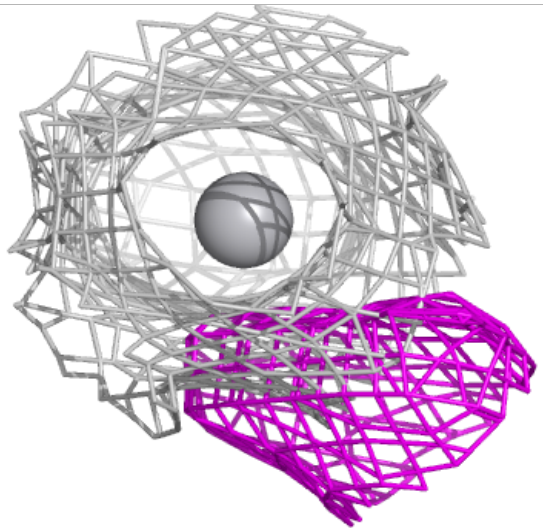


Electron density around VVO E 303 (A):

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

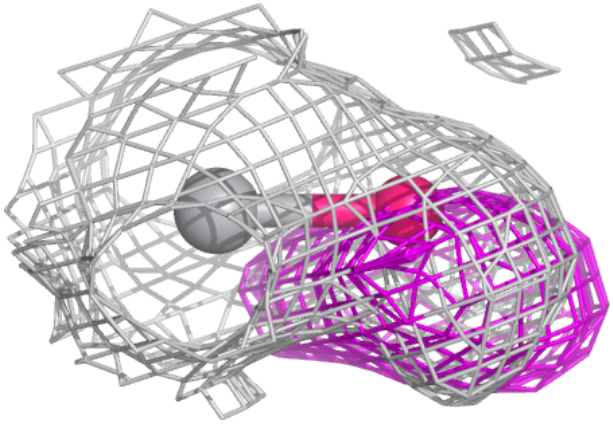


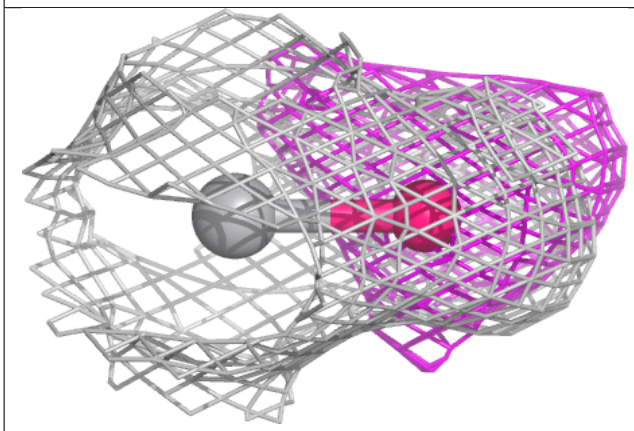


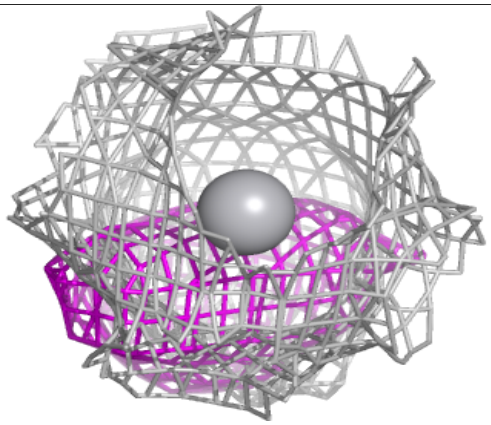


Electron density around VVO E 303 (B):

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

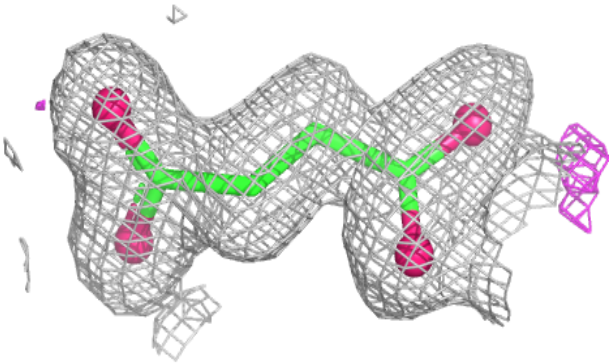


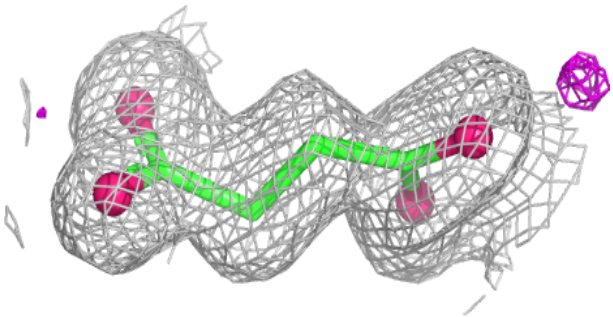


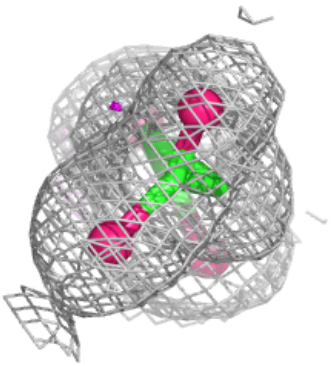


Electron density around SIN B 302:

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

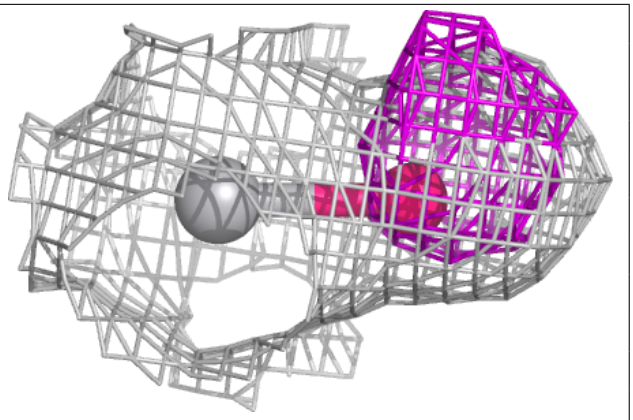


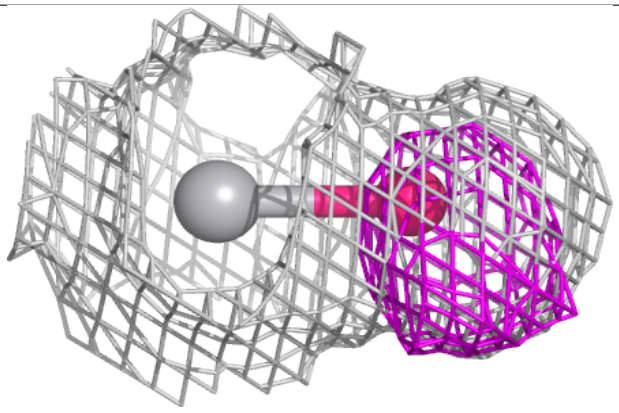


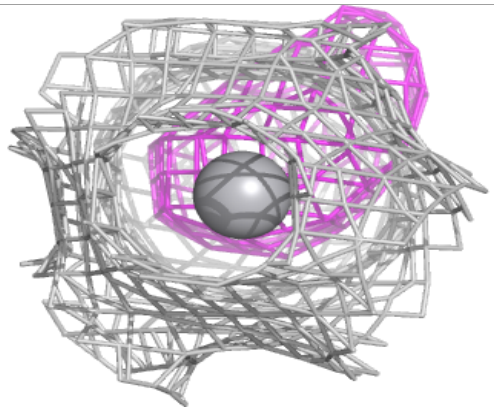


Electron density around VVO A 303 (A):

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

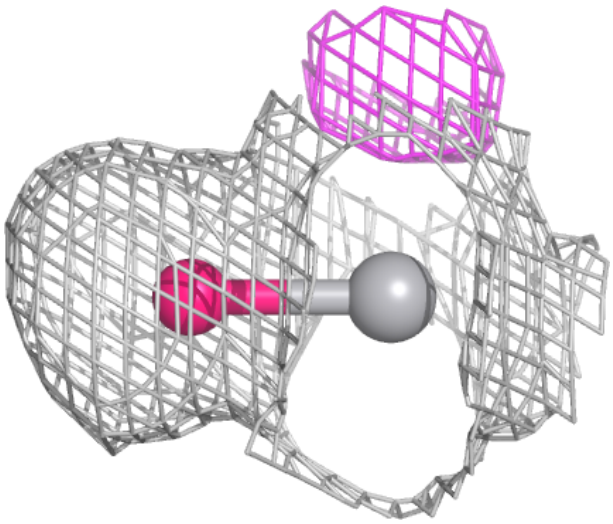


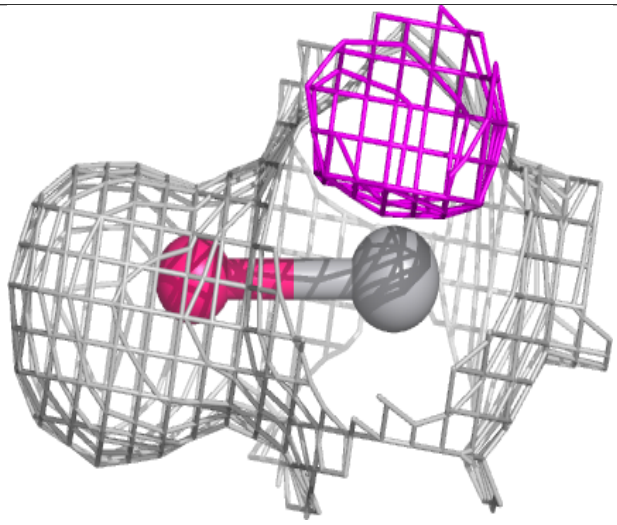


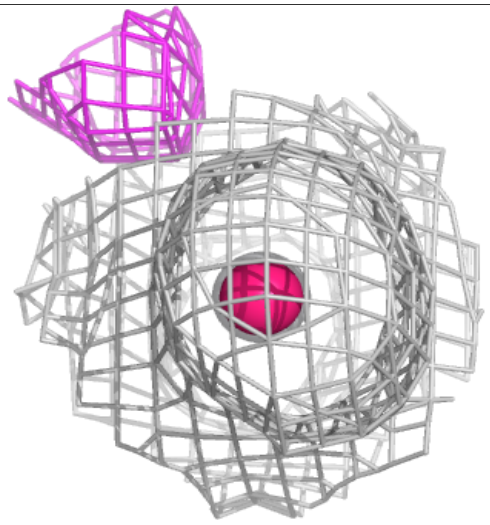


Electron density around VVO G 303 (A):

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

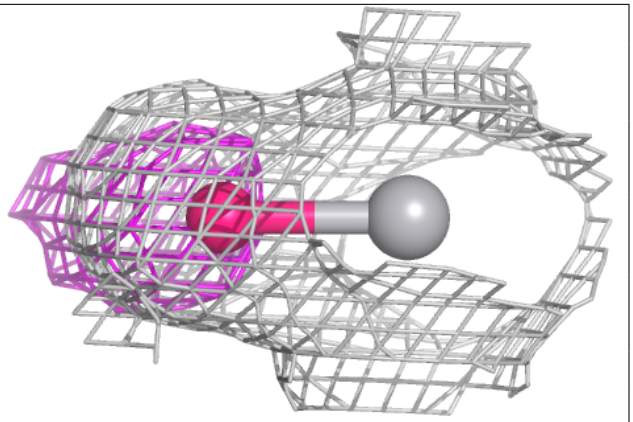


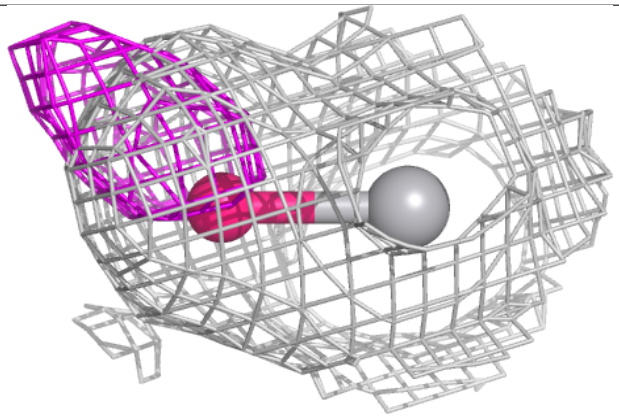


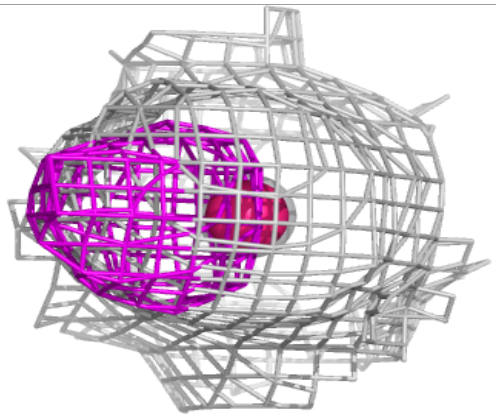


Electron density around VVO G 303 (B):

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

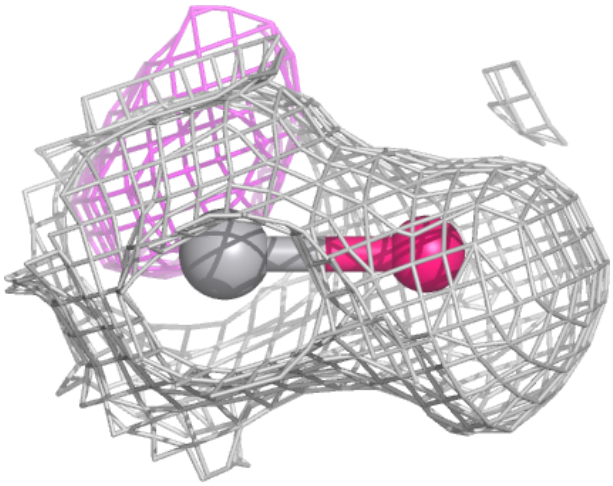


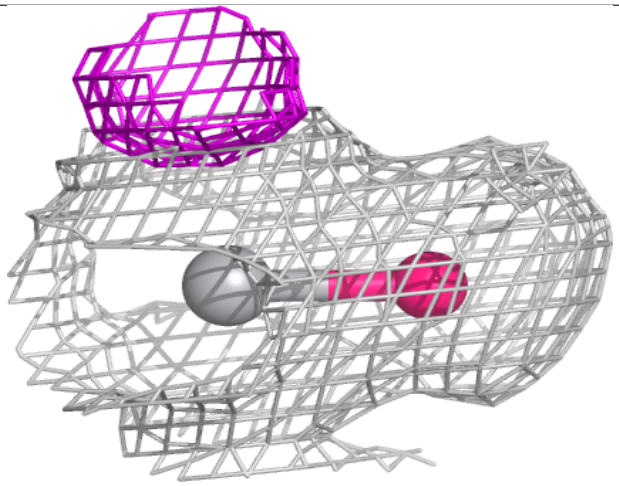


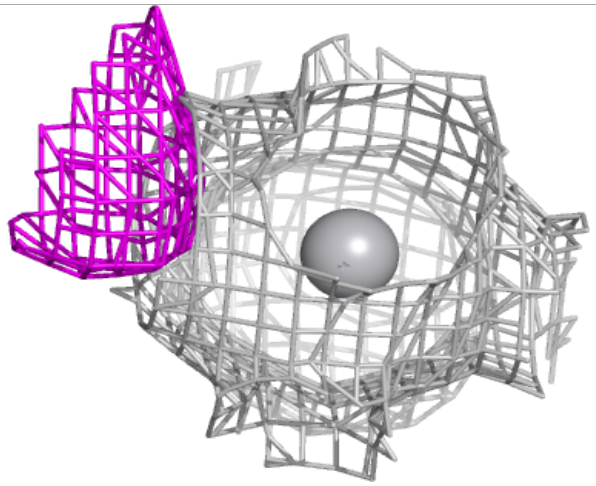


Electron density around VVO A 303 (B):

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

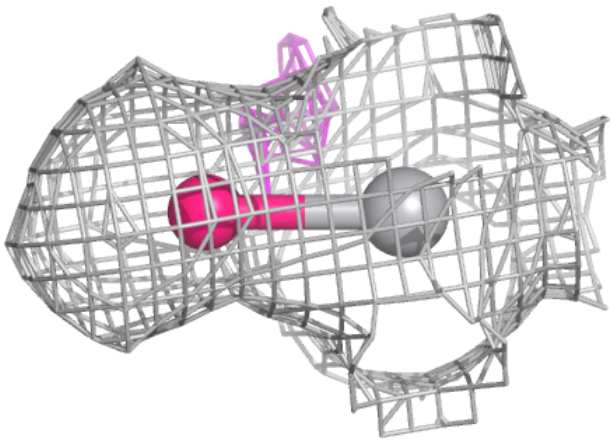


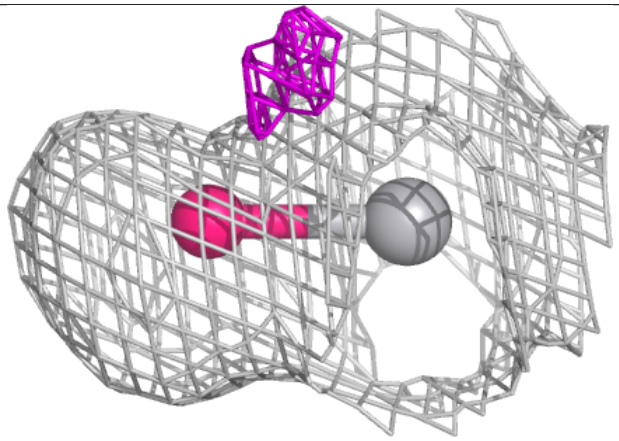


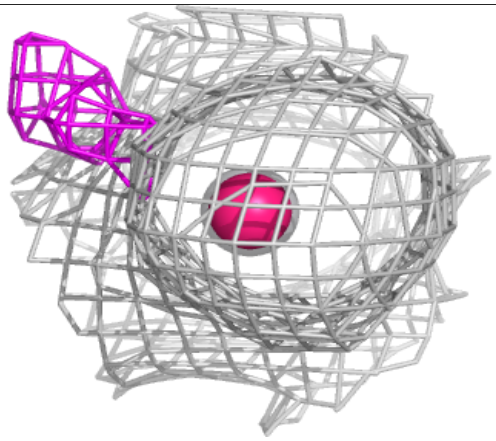


Electron density around VVO B 303 (A):

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

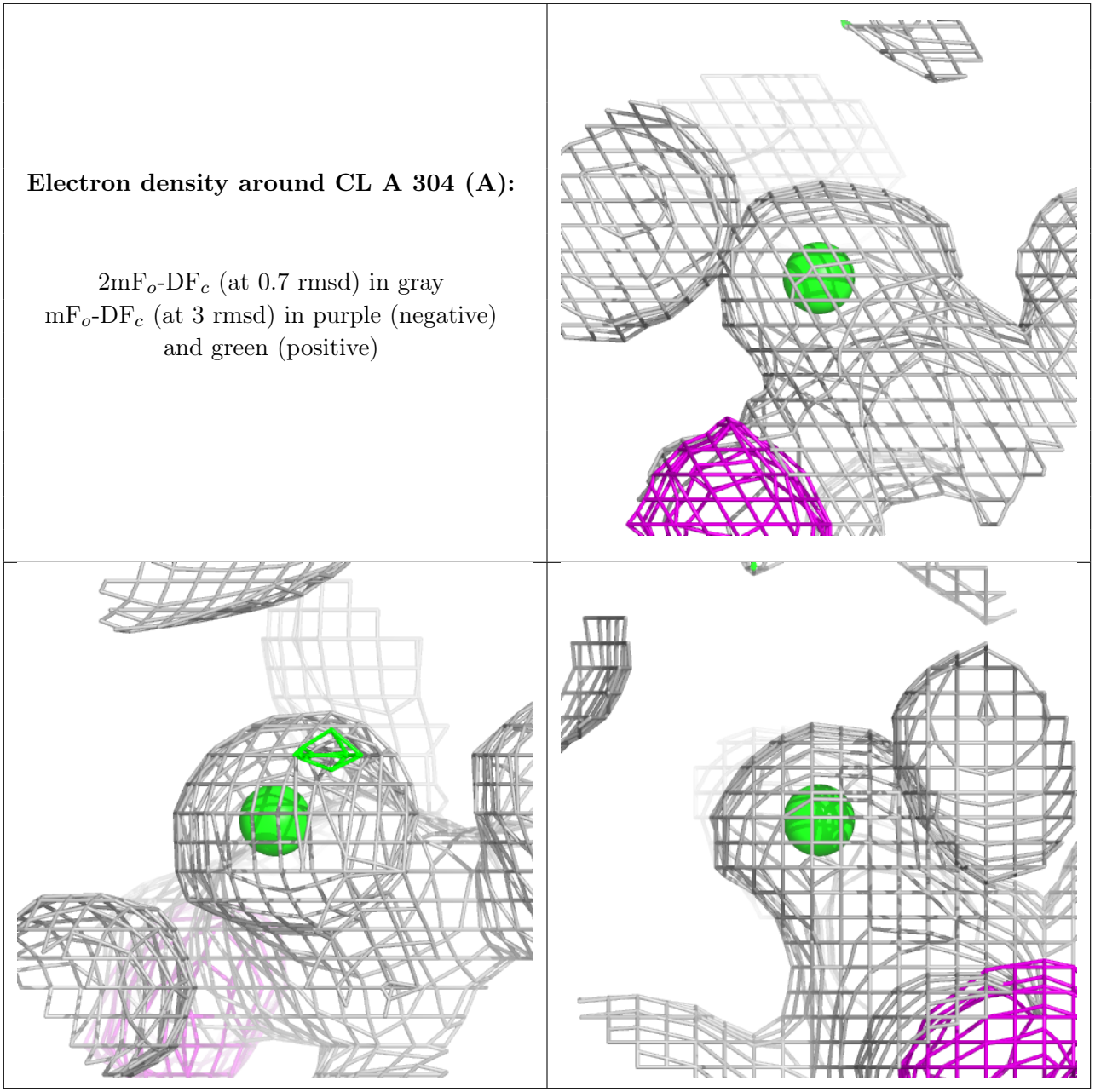






Electron density around CL A 304 (A):

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



6.5 Other polymers (i)

There are no such residues in this entry.