



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 11, 2025 – 04:20 PM EST

PDB ID : 9OEV / pdb_00009oev
Title : HalA I151N with lysine, succinate, chloride, and vanadium(IV)-oxo
Authors : Kissman, E.N.; Chang, M.C.Y.
Deposited on : 2025-04-29
Resolution : 2.17 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

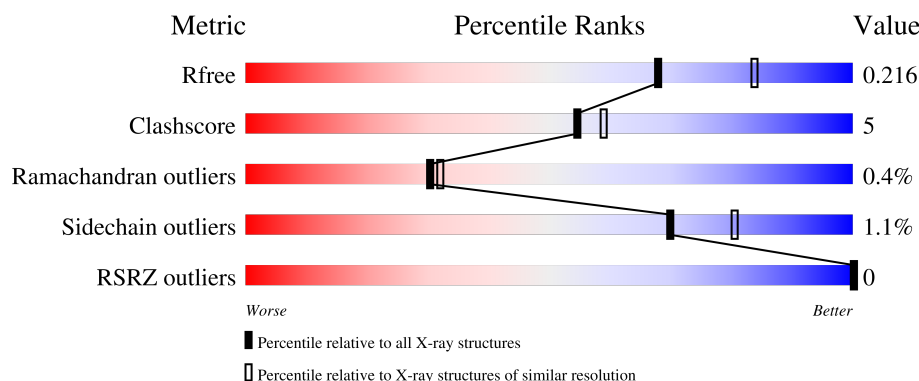
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 2.17 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}	164625	8336 (2.20-2.16)
Clashscore	180529	9404 (2.20-2.16)
Ramachandran outliers	177936	9297 (2.20-2.16)
Sidechain outliers	177891	9297 (2.20-2.16)
RSRZ outliers	164620	8337 (2.20-2.16)

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	258	
1	B	258	
1	C	258	
1	D	258	
1	E	258	

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Mol	Chain	Length	Quality of chain
1	F	258	 91% 7%
1	G	258	 87% 10%
1	H	258	 88% 10%

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	-	-	X	-
4	VVO	B	303	-	-	X	-
4	VVO	C	303	-	-	X	-
4	VVO	D	303	-	-	X	-
4	VVO	F	303	-	-	X	-
4	VVO	H	303	-	-	X	-
5	CL	B	304	-	-	X	-
5	CL	D	304	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 16283 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.

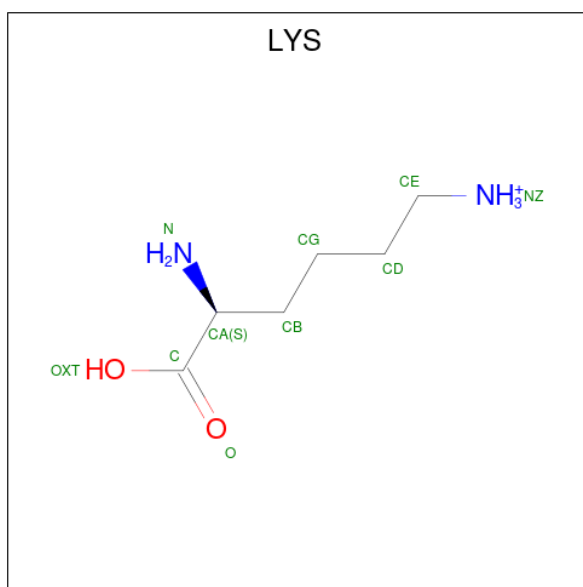
- Molecule 1 is a protein called Lysine halogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1968	1235	355	372	6			
1	B	253	Total	C	N	O	S	0	0	0
			1973	1240	360	367	6			
1	C	252	Total	C	N	O	S	0	1	0
			1969	1237	355	371	6			
1	D	253	Total	C	N	O	S	0	0	0
			1966	1236	354	370	6			
1	E	251	Total	C	N	O	S	0	0	0
			1957	1231	352	368	6			
1	F	253	Total	C	N	O	S	0	0	0
			1944	1222	350	366	6			
1	G	251	Total	C	N	O	S	0	0	0
			1941	1219	348	368	6			
1	H	253	Total	C	N	O	S	0	0	0
			1956	1231	354	365	6			

There are 8 discrepancies between the modelled and reference sequences:

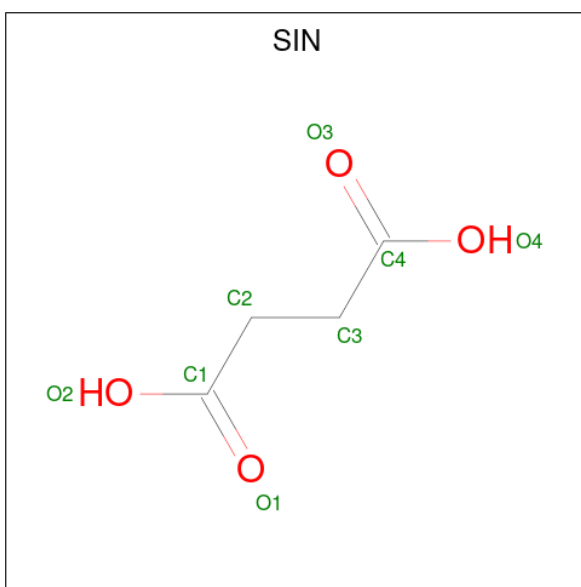
Chain	Residue	Modelled	Actual	Comment	Reference
A	151	ASN	ILE	engineered mutation	UNP A0A561WR11
B	151	ASN	ILE	engineered mutation	UNP A0A561WR11
C	151	ASN	ILE	engineered mutation	UNP A0A561WR11
D	151	ASN	ILE	engineered mutation	UNP A0A561WR11
E	151	ASN	ILE	engineered mutation	UNP A0A561WR11
F	151	ASN	ILE	engineered mutation	UNP A0A561WR11
G	151	ASN	ILE	engineered mutation	UNP A0A561WR11
H	151	ASN	ILE	engineered mutation	UNP A0A561WR11

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



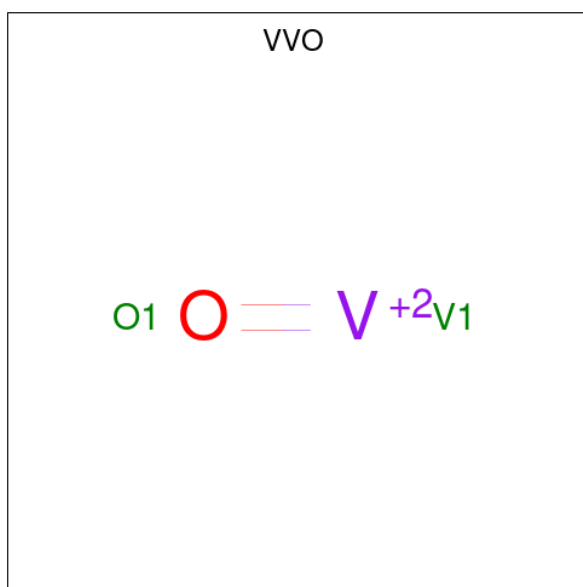
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	6	2	2		
2	B	1	Total	C	N	O	0	0
			10	6	2	2		
2	C	1	Total	C	N	O	0	0
			10	6	2	2		
2	D	1	Total	C	N	O	0	0
			10	6	2	2		
2	E	1	Total	C	N	O	0	0
			10	6	2	2		
2	F	1	Total	C	N	O	0	0
			10	6	2	2		
2	G	1	Total	C	N	O	0	0
			10	6	2	2		
2	H	1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

- Molecule 3 is SUCCINIC ACID (CCD ID: SIN) (formula: C₄H₆O₄) (labeled as "Ligand of Interest" by depositor).



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

- 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 2 1 1	0	0
4	B	1	Total O V 2 1 1	0	0
4	C	1	Total O V 2 1 1	0	0
4	D	1	Total O V 2 1 1	0	0
4	E	1	Total O V 2 1 1	0	0
4	F	1	Total O V 2 1 1	0	0
4	H	1	Total O V 2 1 1	0	0

- 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 1 1	0	0
5	B	1	Total Cl 1 1	0	0
5	C	1	Total Cl 1 1	0	0
5	D	1	Total Cl 1 1	0	0

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

- Molecule 6 is VANADIUM ION (CCD ID: V) (formula: V) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	G	1	Total 1	V 1	0	0

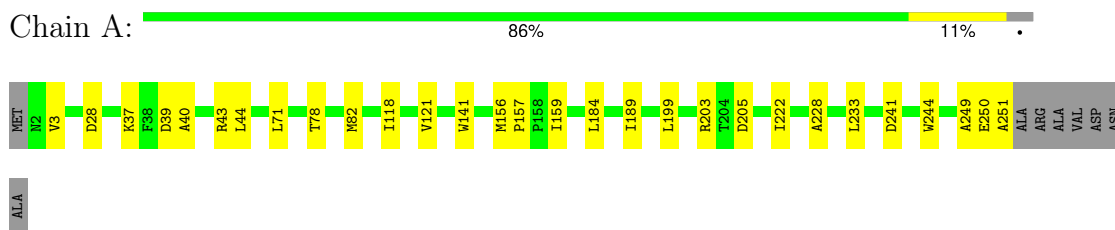
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	66	Total 66	O 66	0	0
7	B	55	Total 55	O 55	0	0
7	C	68	Total 68	O 68	0	0
7	D	60	Total 60	O 60	0	0
7	E	63	Total 63	O 63	0	0
7	F	48	Total 48	O 48	0	0
7	G	47	Total 47	O 47	0	0
7	H	36	Total 36	O 36	0	0

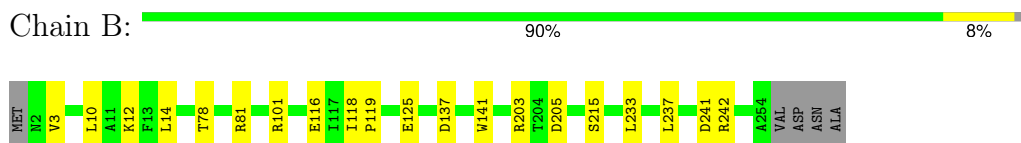
3 Residue-property plots

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

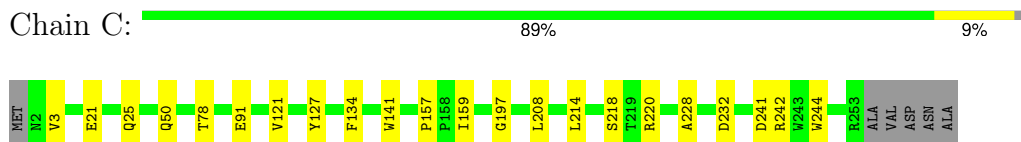
- Molecule 1: Lysine halogenase



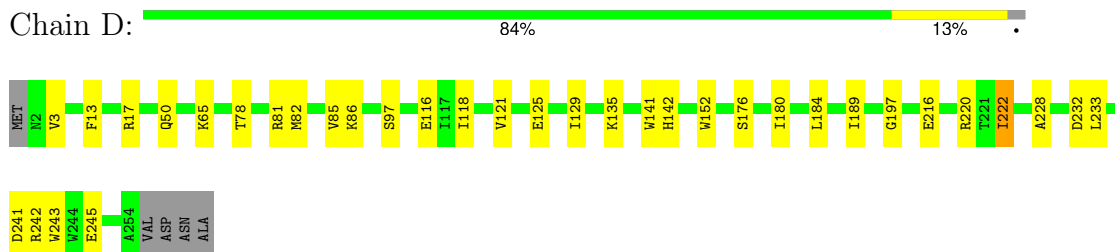
- Molecule 1: Lysine halogenase



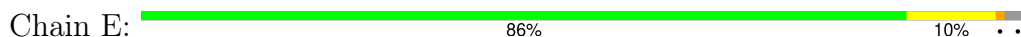
- Molecule 1: Lysine halogenase

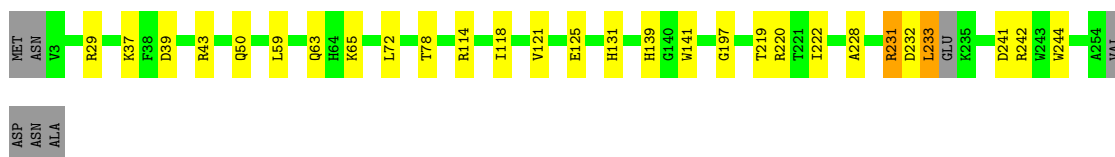


- Molecule 1: Lysine halogenase



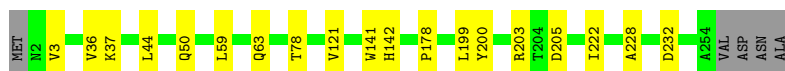
- Molecule 1: Lysine halogenase





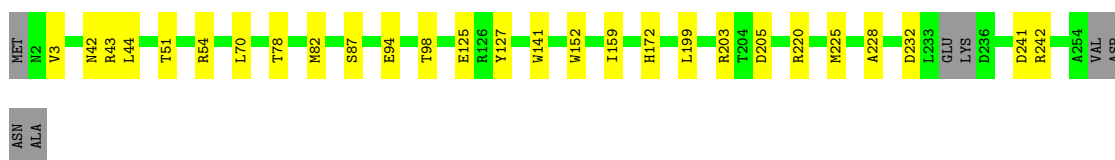
- Molecule 1: Lysine halogenase

Chain F: 91% 7% •



- Molecule 1: Lysine halogenase

Chain G: 87% 10% •



- Molecule 1: Lysine halogenase

Chain H: 88% 10% •



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	146.60Å 146.60Å 286.76Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	95.05 – 2.17 95.05 – 2.17	Depositor EDS
% Data completeness (in resolution range)	98.0 (95.05-2.17) 98.0 (95.05-2.17)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 2.16Å)	Xtriage
Refinement program	PHENIX 1.21rc1_5156	Depositor
R, R_{free}	0.189 , 0.215 0.191 , 0.216	Depositor DCC
R_{free} test set	6047 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	27.5	Xtriage
Anisotropy	0.683	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 12.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.408 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16283	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.15	0/2012	0.28	0/2740
1	B	0.10	0/2018	0.26	0/2750
1	C	0.09	0/2013	0.25	0/2744
1	D	0.10	0/2010	0.26	0/2740
1	E	0.19	0/2000	0.31	0/2724
1	F	0.08	0/1988	0.25	0/2714
1	G	0.10	0/1984	0.24	0/2706
1	H	0.13	0/2001	0.27	0/2730
All	All	0.12	0/16026	0.27	0/21848

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	E	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	231	ARG	Sidechain

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	1968	0	1870	16	0
1	B	1973	0	1873	12	0
1	C	1969	0	1859	14	0
1	D	1966	0	1859	23	0
1	E	1957	0	1856	17	0
1	F	1944	0	1818	10	0
1	G	1941	0	1813	16	0
1	H	1956	0	1841	17	0
2	A	10	0	12	1	0
2	B	10	0	12	0	0
2	C	10	0	12	0	0
2	D	10	0	12	3	0
2	E	10	0	12	3	0
2	F	10	0	12	0	0
2	G	10	0	12	1	0
2	H	10	0	12	2	0
3	A	8	0	4	1	0
3	B	8	0	4	0	0
3	C	8	0	4	1	0
3	D	8	0	4	1	0
3	E	8	0	4	1	0
3	F	8	0	4	1	0
3	G	8	0	4	1	0
3	H	8	0	4	3	0
4	A	2	0	0	3	0
4	B	2	0	0	2	0
4	C	2	0	0	2	0
4	D	2	0	0	2	0
4	E	2	0	0	1	0
4	F	2	0	0	3	0
4	H	2	0	0	3	0
5	A	1	0	0	1	0
5	B	1	0	0	2	0
5	C	1	0	0	1	0
5	D	1	0	0	2	0
5	E	1	0	0	0	0
5	F	1	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	1	0	0	1	0
6	G	1	0	0	0	0
7	A	66	0	0	0	0
7	B	55	0	0	1	0
7	C	68	0	0	1	0
7	D	60	0	0	5	0
7	E	63	0	0	3	0
7	F	48	0	0	1	0
7	G	47	0	0	5	0
7	H	36	0	0	2	0
All	All	16283	0	14917	143	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 5.

The worst 5 of 143 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:F:303:VVO:O1	5:F:304:CL:CL	2.10	1.06
4:C:303:VVO:O1	5:C:304:CL:CL	2.28	0.89
1:H:124:ASP:HB2	1:H:245:GLU:HG3	1.61	0.81
1:D:13:PHE:O	7:D:401:HOH:O	2.03	0.76
1:D:81:ARG:NH1	7:D:402:HOH:O	2.20	0.74

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	248/258 (96%)	236 (95%)	11 (4%)	1 (0%)	30 32
1	B	251/258 (97%)	239 (95%)	11 (4%)	1 (0%)	30 32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	251/258 (97%)	240 (96%)	10 (4%)	1 (0%)	30	32
1	D	251/258 (97%)	240 (96%)	10 (4%)	1 (0%)	30	32
1	E	247/258 (96%)	235 (95%)	12 (5%)	0	100	100
1	F	251/258 (97%)	241 (96%)	9 (4%)	1 (0%)	30	32
1	G	247/258 (96%)	235 (95%)	11 (4%)	1 (0%)	30	32
1	H	251/258 (97%)	240 (96%)	10 (4%)	1 (0%)	30	32
All	All	1997/2064 (97%)	1906 (95%)	84 (4%)	7 (0%)	30	32

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	VAL
1	B	3	VAL
1	F	3	VAL
1	G	3	VAL
1	C	3	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	206/229 (90%)	204 (99%)	2 (1%)	73	82
1	B	203/229 (89%)	202 (100%)	1 (0%)	86	93
1	C	203/229 (89%)	202 (100%)	1 (0%)	86	93
1	D	202/229 (88%)	199 (98%)	3 (2%)	60	72
1	E	202/229 (88%)	198 (98%)	4 (2%)	50	62
1	F	197/229 (86%)	194 (98%)	3 (2%)	60	72
1	G	198/229 (86%)	196 (99%)	2 (1%)	73	82
1	H	199/229 (87%)	199 (100%)	0	100	100
All	All	1610/1832 (88%)	1594 (99%)	16 (1%)	70	82

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	70	LEU
1	F	222	ILE
1	E	231	ARG
1	F	50	GLN
1	E	222	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	50	GLN
1	F	9	ASN
1	C	132	GLN
1	F	132	GLN
1	E	77	ASN

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 31 ligands modelled in this entry, 8 are monoatomic - leaving 23 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SIN	C	302	4	7,7,7	1.13	0	8,8,8	1.53	0
2	LYS	E	301	-	8,9,9	0.84	1 (12%)	7,10,10	1.00	1 (14%)
3	SIN	B	302	4	7,7,7	1.18	0	8,8,8	1.44	0
3	SIN	D	302	4	7,7,7	1.14	0	8,8,8	1.47	0
3	SIN	G	302	6	7,7,7	1.18	0	8,8,8	1.47	0
4	VVO	B	303	1,3	0,1,1	-	-	-		
4	VVO	C	303	1,3	0,1,1	-	-	-		
3	SIN	E	302	4	7,7,7	1.15	0	8,8,8	1.45	0
2	LYS	C	301	-	8,9,9	0.84	1 (12%)	7,10,10	1.03	1 (14%)
2	LYS	B	301	-	8,9,9	0.84	1 (12%)	7,10,10	1.05	1 (14%)
2	LYS	G	301	-	8,9,9	0.83	1 (12%)	7,10,10	1.06	1 (14%)
4	VVO	E	303	5,1,3	0,1,1	-	-	-		
4	VVO	F	303	1,3	0,1,1	-	-	-		
2	LYS	D	301	-	8,9,9	0.82	1 (12%)	7,10,10	1.03	1 (14%)
2	LYS	A	301	-	8,9,9	0.86	1 (12%)	7,10,10	1.04	1 (14%)
3	SIN	F	302	4	7,7,7	1.17	0	8,8,8	1.45	1 (12%)
3	SIN	H	302	4	7,7,7	1.19	0	8,8,8	1.45	0
4	VVO	D	303	1,3	0,1,1	-	-	-		
3	SIN	A	302	4	7,7,7	1.14	0	8,8,8	1.52	0
4	VVO	H	303	1,3	0,1,1	-	-	-		
2	LYS	F	301	-	8,9,9	0.84	1 (12%)	7,10,10	1.03	1 (14%)
4	VVO	A	303	1,3	0,1,1	-	-	-		
2	LYS	H	301	-	8,9,9	0.84	1 (12%)	7,10,10	1.10	1 (14%)

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	B	301	-	-	2/9/9/9	-
2	LYS	F	301	-	-	2/9/9/9	-
3	SIN	C	302	4	-	4/5/5/5	-
3	SIN	F	302	4	-	3/5/5/5	-
2	LYS	E	301	-	-	1/9/9/9	-
2	LYS	G	301	-	-	0/9/9/9	-
2	LYS	H	301	-	-	2/9/9/9	-
3	SIN	B	302	4	-	4/5/5/5	-
3	SIN	D	302	4	-	5/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SIN	E	302	4	-	2/5/5/5	-
3	SIN	H	302	4	-	3/5/5/5	-
2	LYS	D	301	-	-	3/9/9/9	-
3	SIN	G	302	6	-	4/5/5/5	-
2	LYS	A	301	-	-	1/9/9/9	-
3	SIN	A	302	4	-	4/5/5/5	-
2	LYS	C	301	-	-	3/9/9/9	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	LYS	OXT-C	-2.27	1.23	1.30
2	C	301	LYS	OXT-C	-2.23	1.23	1.30
2	B	301	LYS	OXT-C	-2.22	1.23	1.30
2	E	301	LYS	OXT-C	-2.22	1.23	1.30
2	F	301	LYS	OXT-C	-2.22	1.23	1.30

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	301	LYS	OXT-C-O	-2.77	117.79	124.08
2	A	301	LYS	OXT-C-O	-2.68	117.99	124.08
2	B	301	LYS	OXT-C-O	-2.68	118.00	124.08
2	G	301	LYS	OXT-C-O	-2.65	118.06	124.08
2	D	301	LYS	OXT-C-O	-2.63	118.11	124.08

There are no chirality outliers.

5 of 43 torsion outliers are listed below:

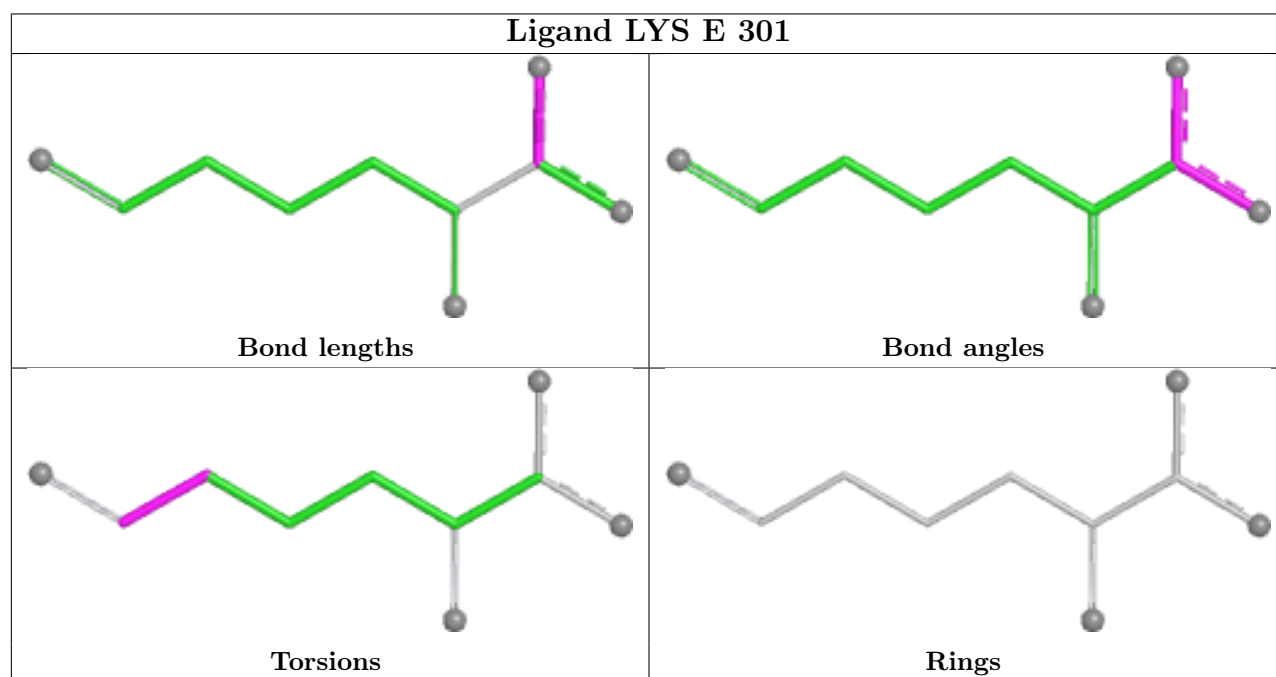
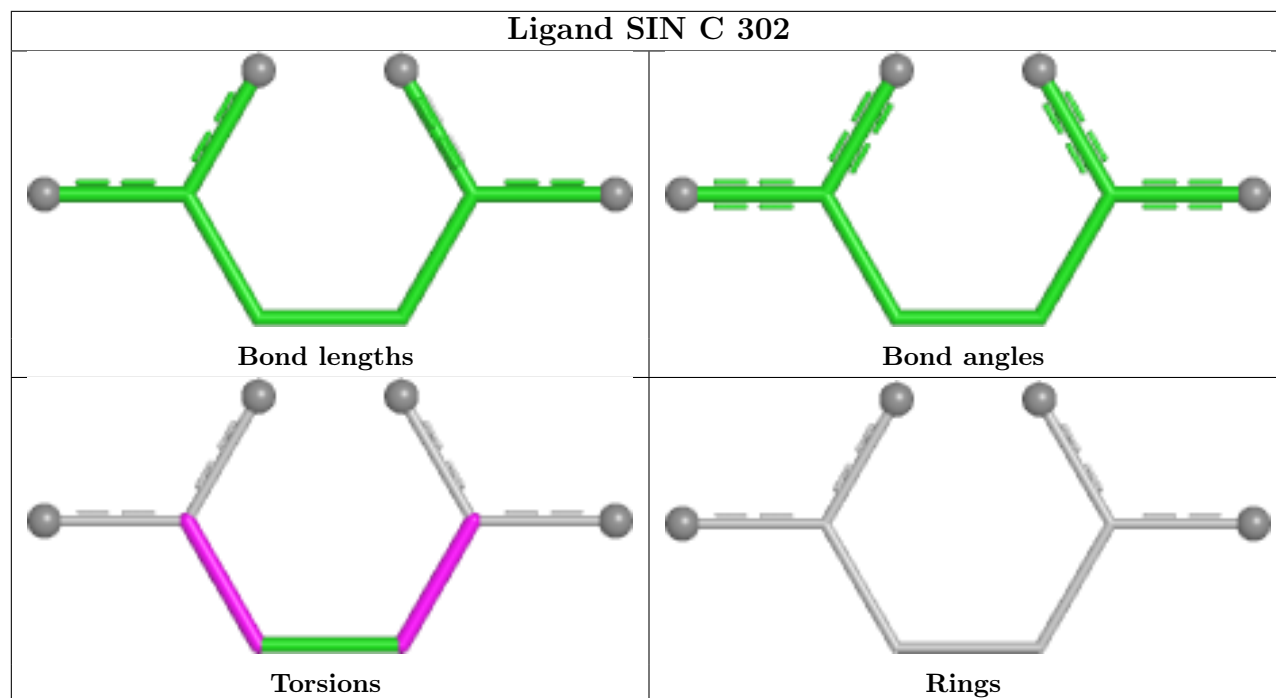
Mol	Chain	Res	Type	Atoms
3	H	302	SIN	C1-C2-C3-C4
2	D	301	LYS	CE-CD-CG-CB
2	A	301	LYS	CE-CD-CG-CB
2	F	301	LYS	CG-CD-CE-NZ
2	E	301	LYS	CG-CD-CE-NZ

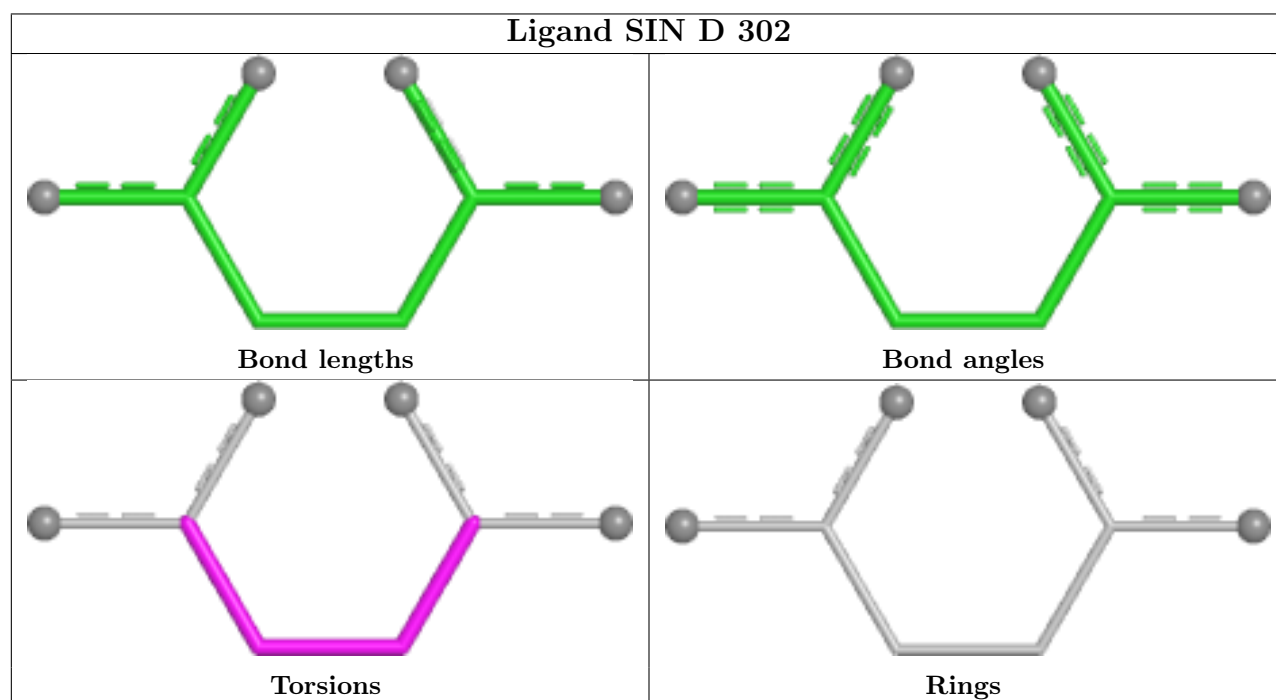
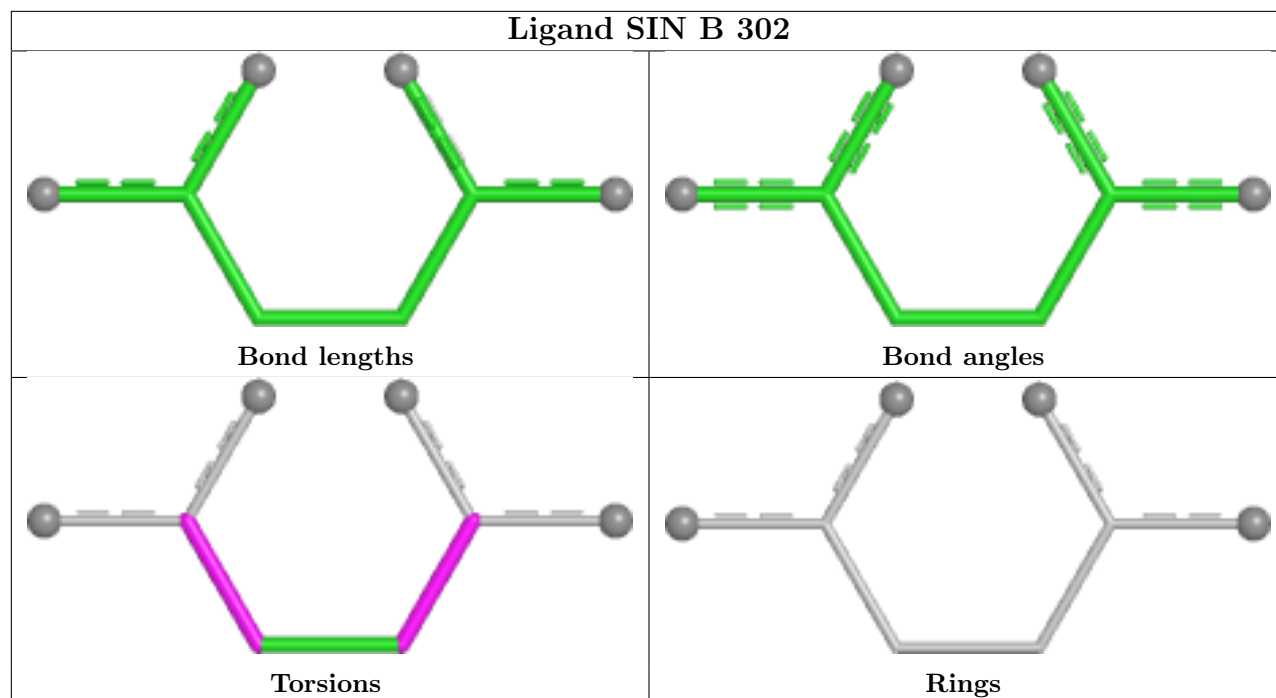
There are no ring outliers.


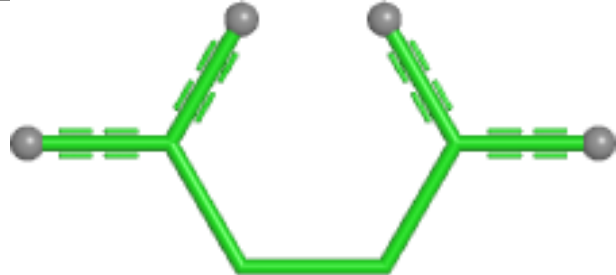
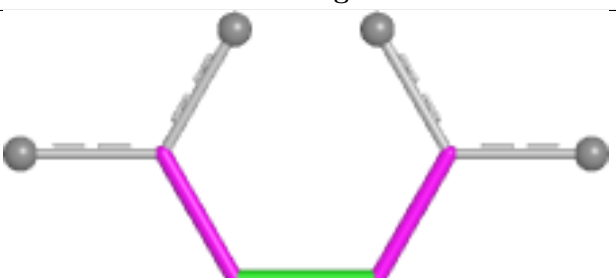
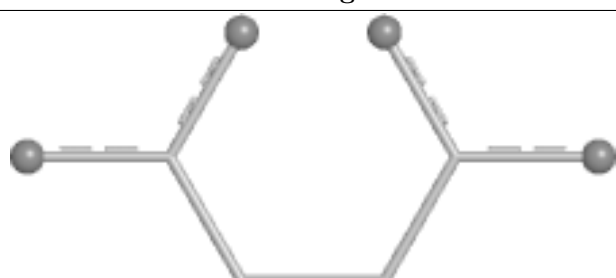
19 monomers are involved in 33 short contacts:





Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	302	SIN	1	0
2	E	301	LYS	3	0
3	D	302	SIN	1	0
3	G	302	SIN	1	0
4	B	303	VVO	2	0
4	C	303	VVO	2	0
3	E	302	SIN	1	0
2	G	301	LYS	1	0
4	E	303	VVO	1	0
4	F	303	VVO	3	0
2	D	301	LYS	3	0
2	A	301	LYS	1	0
3	F	302	SIN	1	0
3	H	302	SIN	3	0
4	D	303	VVO	2	0
3	A	302	SIN	1	0
4	H	303	VVO	3	0
4	A	303	VVO	3	0
2	H	301	LYS	2	0



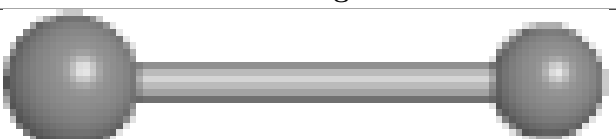
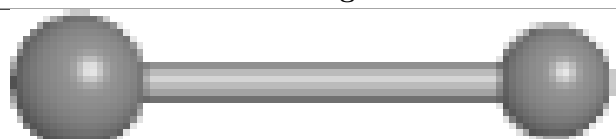
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

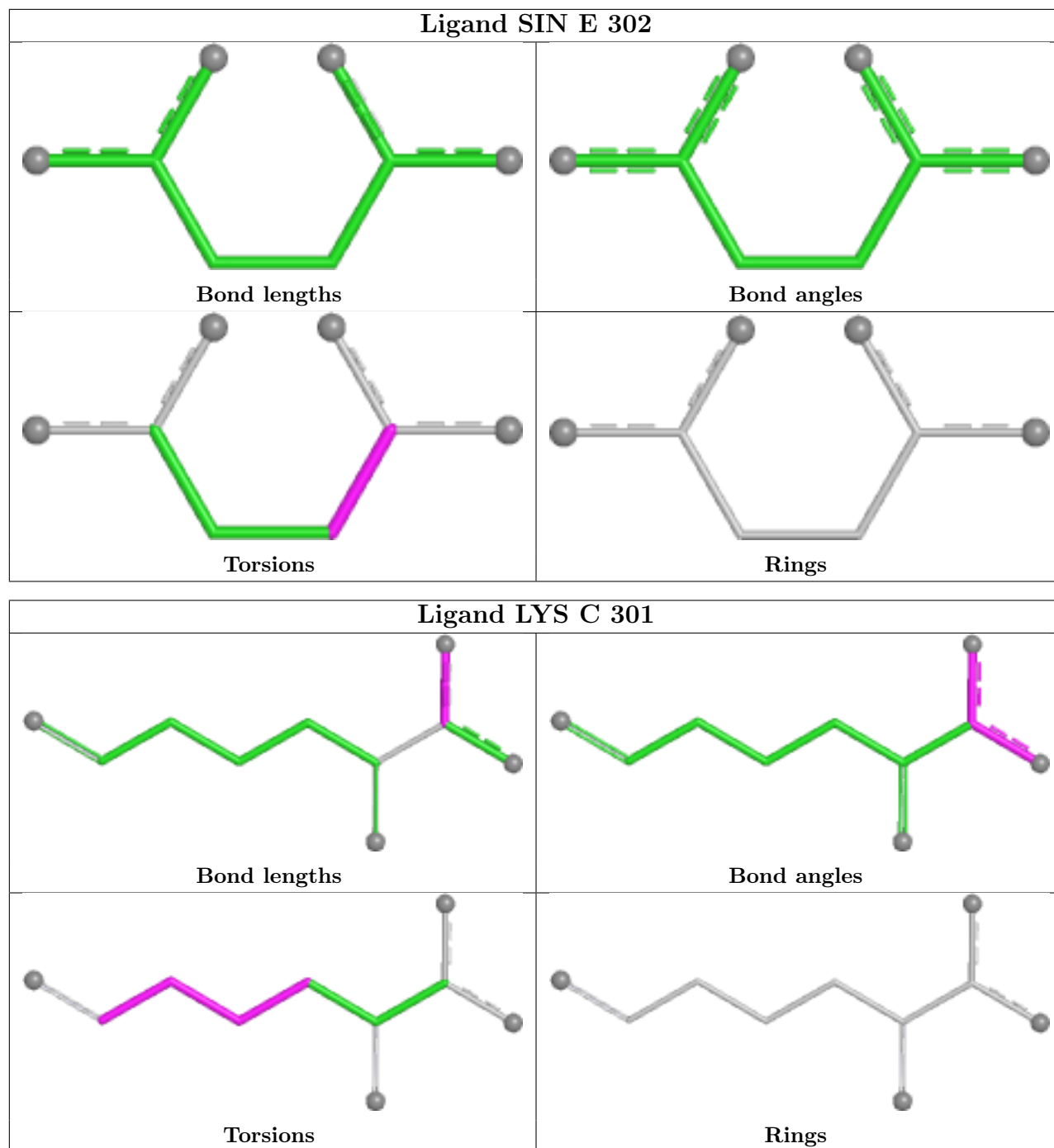




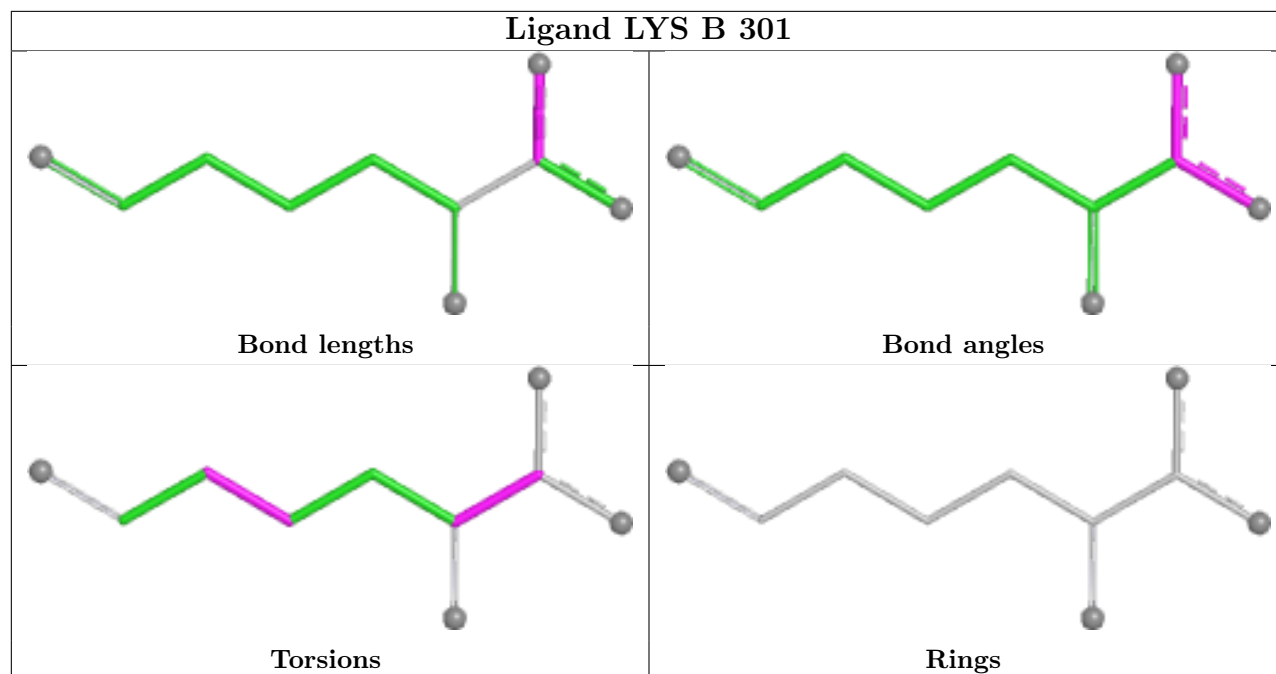
Ligand SIN G 302	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand VVO B 303	
	
Bond lengths	Bond angles
	
Torsions	Rings

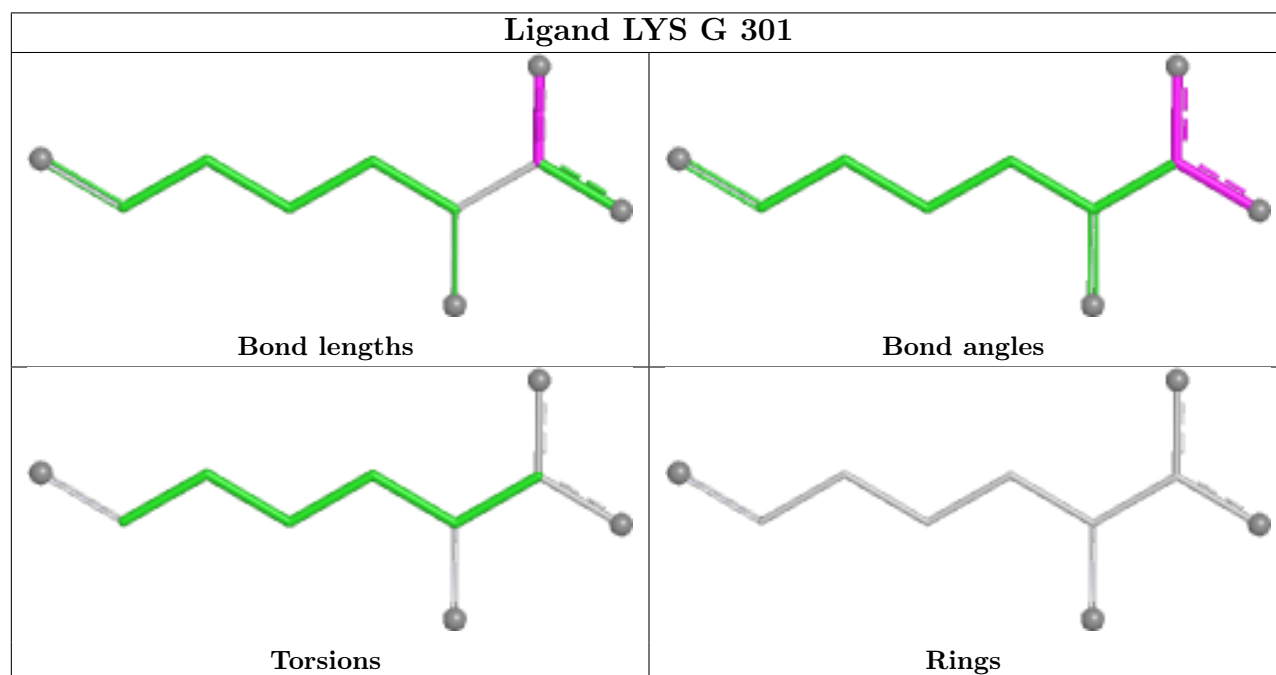
Ligand VVO C 303	
	
Bond lengths	Bond angles
	
Torsions	Rings

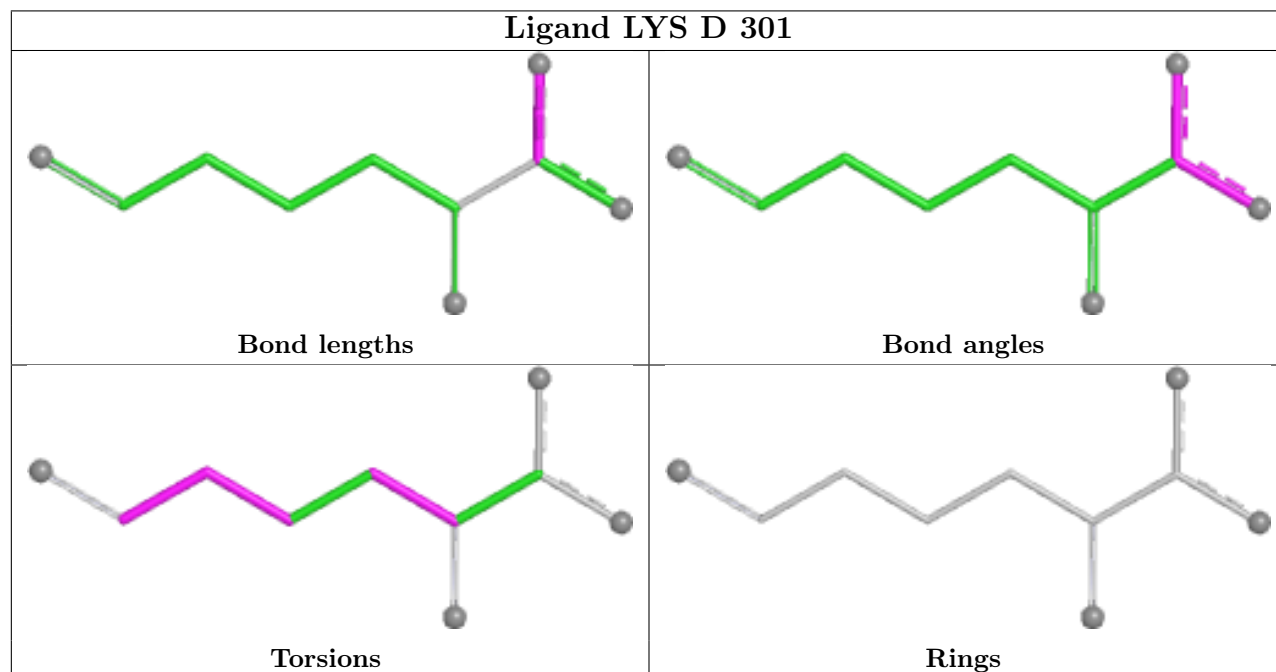
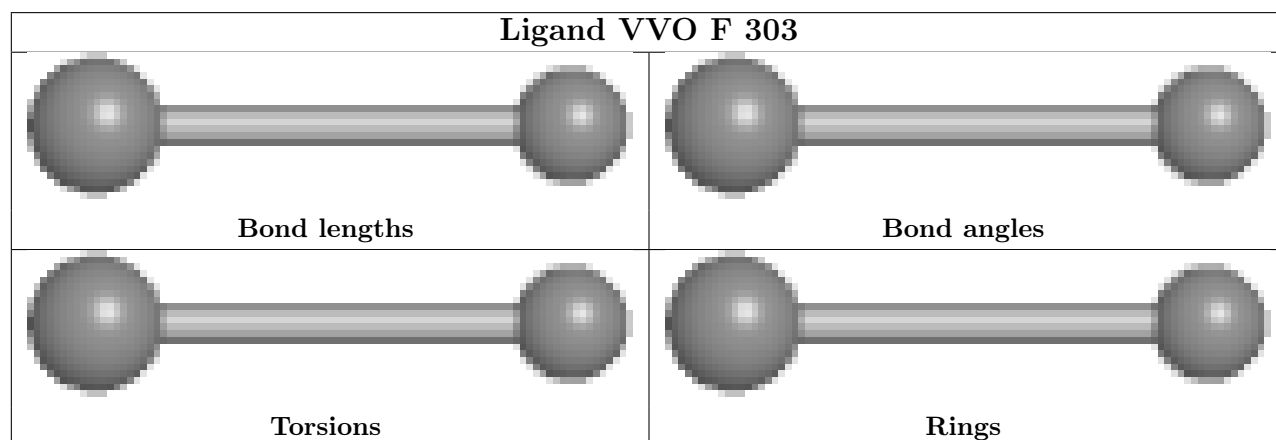
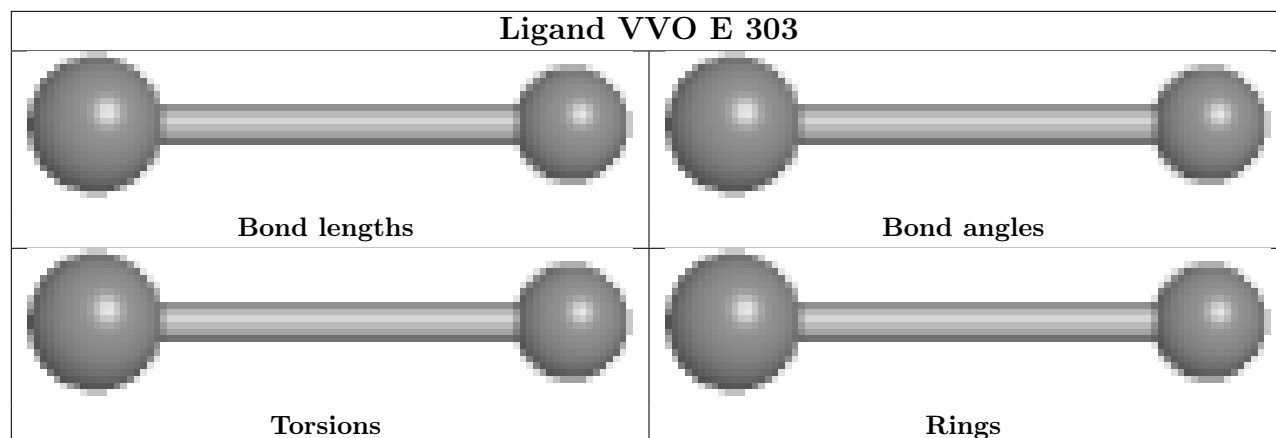


Ligand LYS B 301

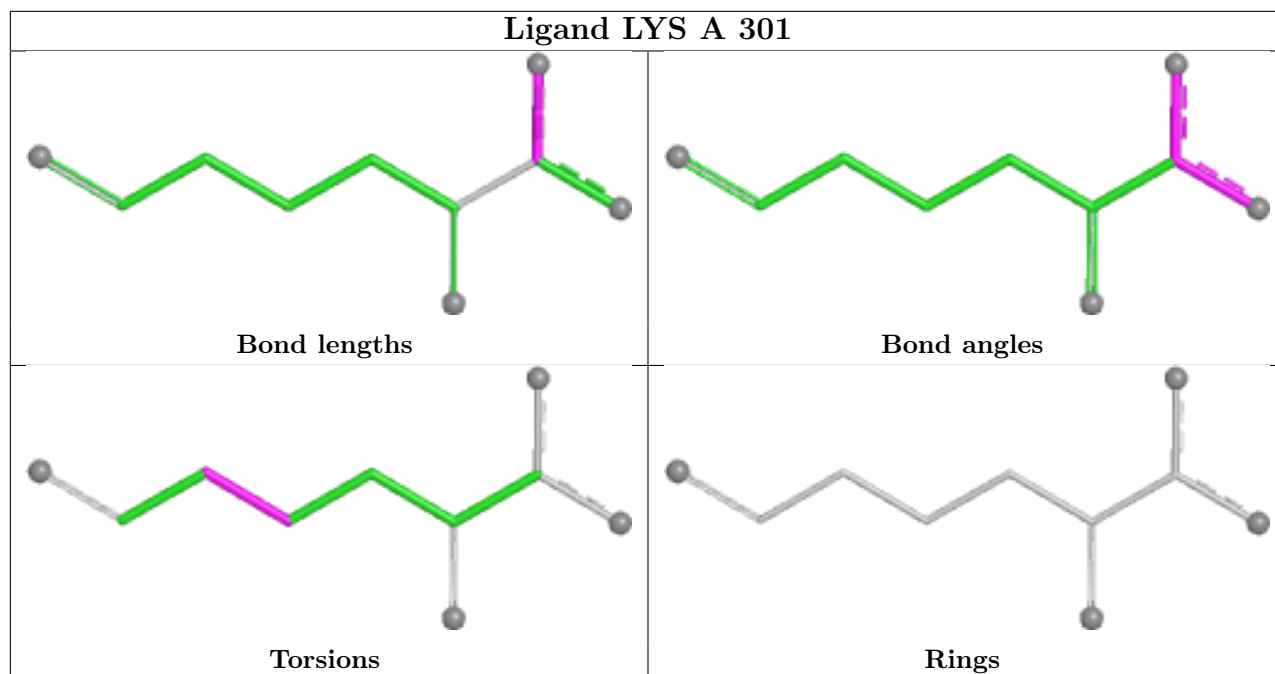


Ligand LYS G 301

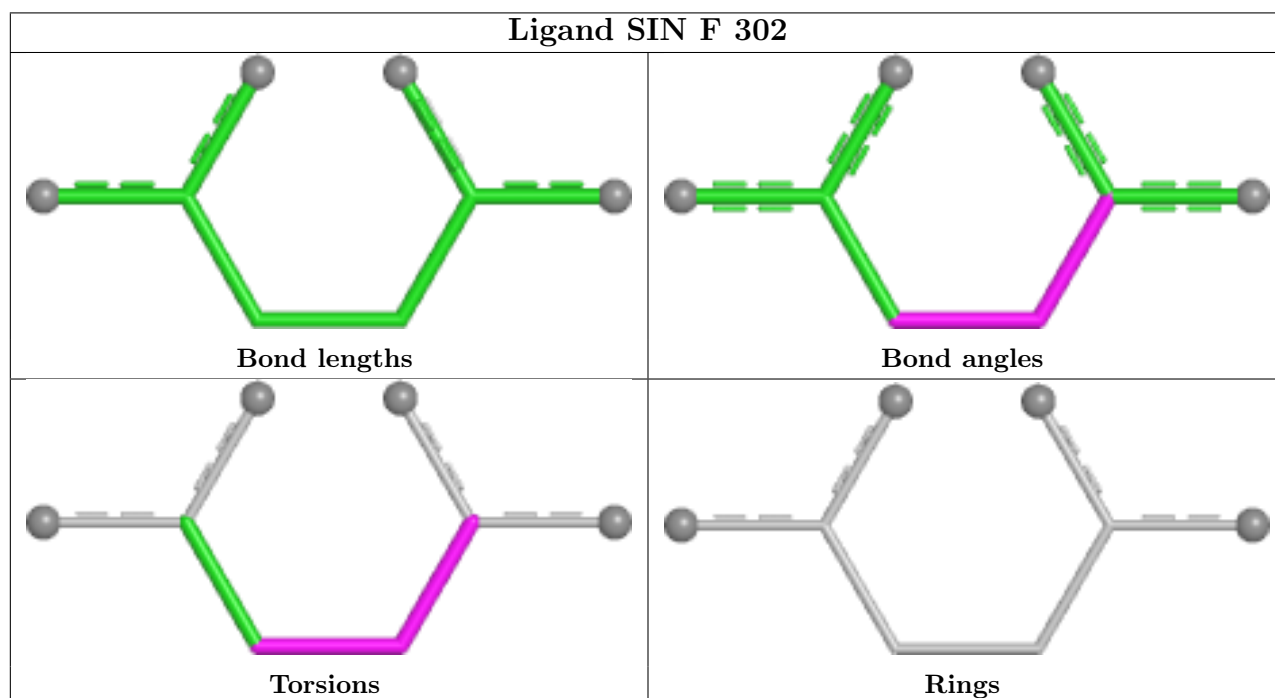



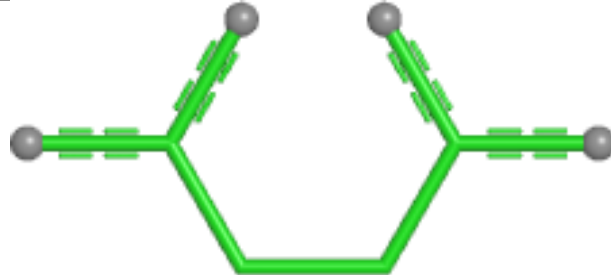
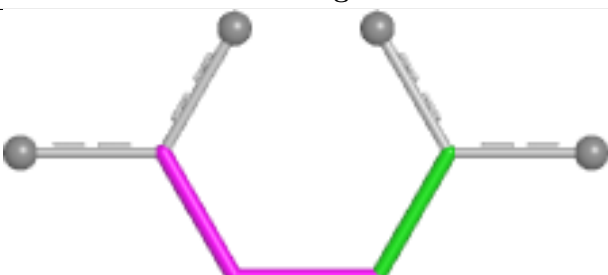
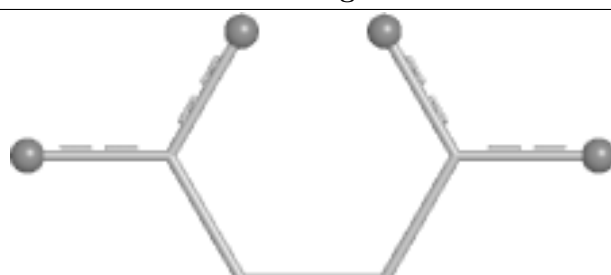






Ligand LYS A 301


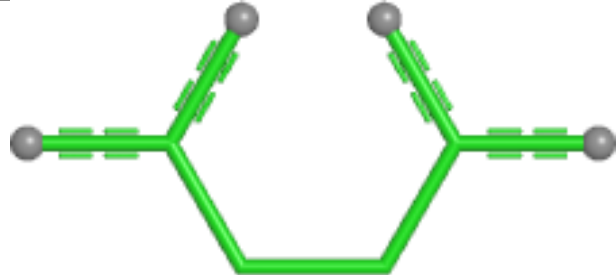
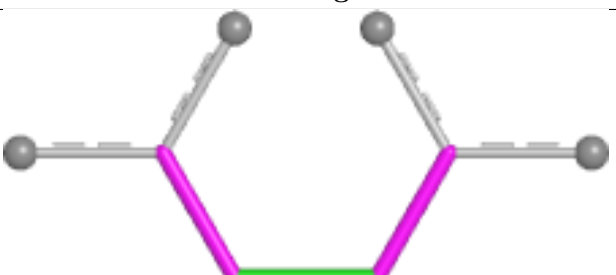
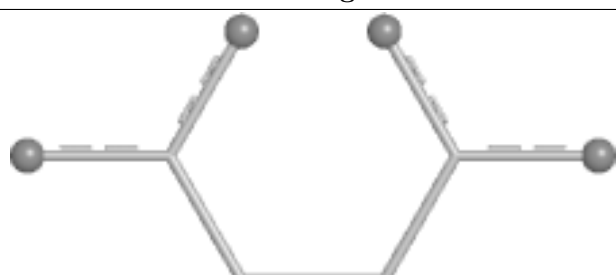






Ligand SIN F 302

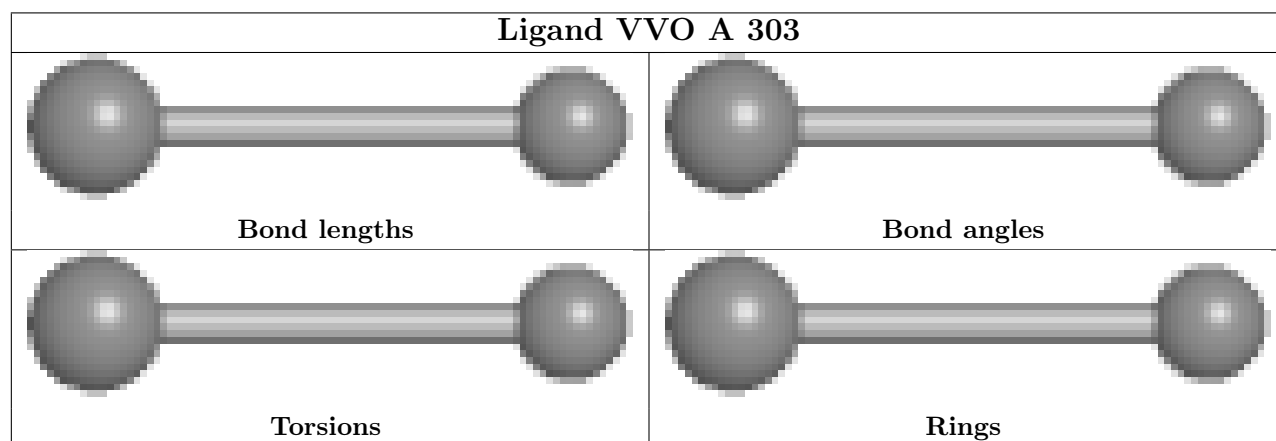
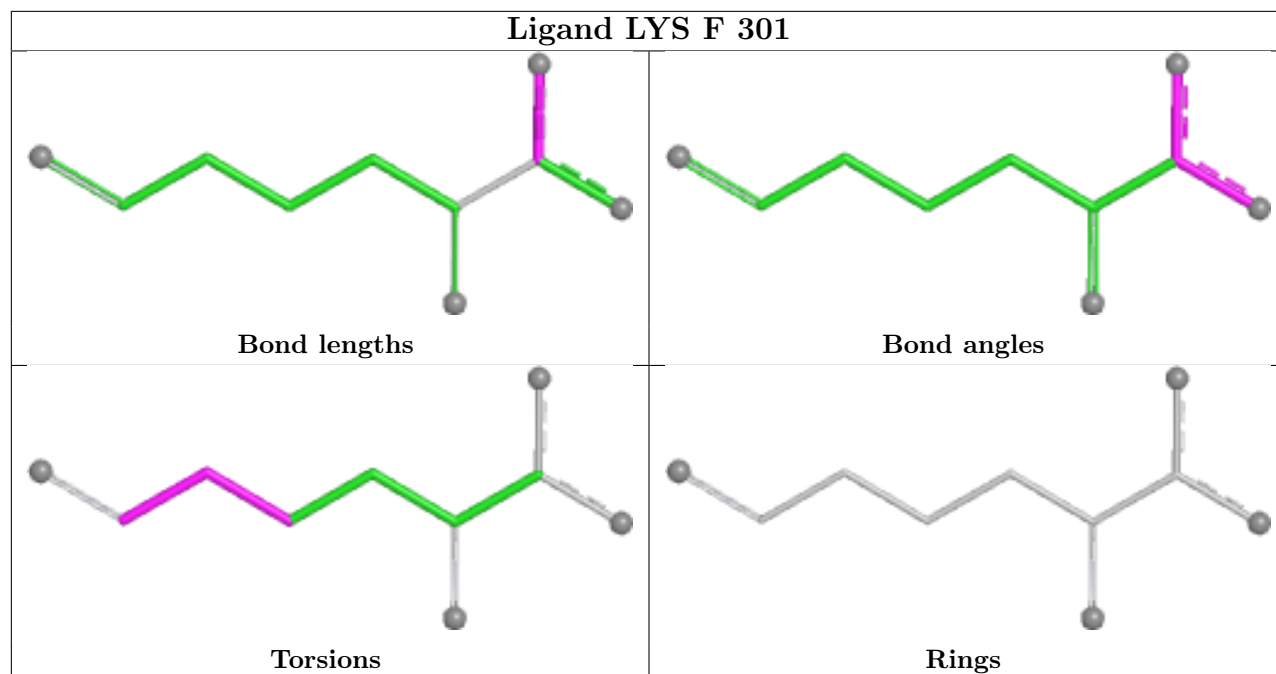


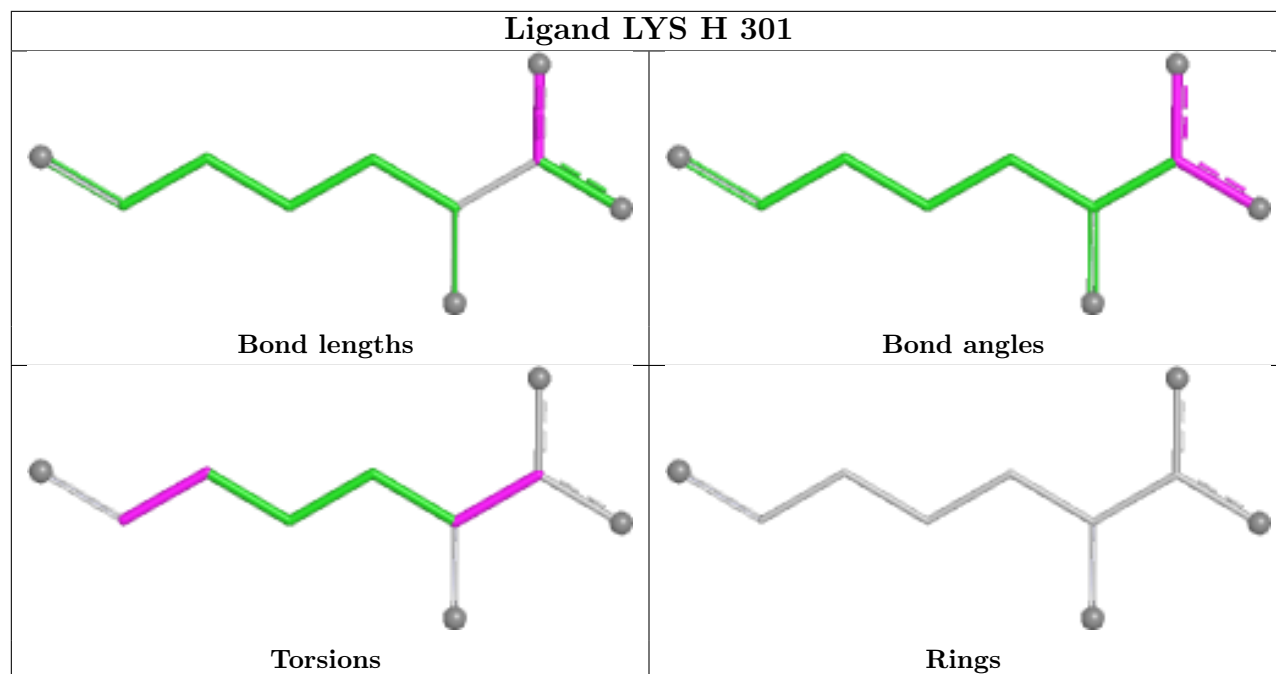
Ligand SIN H 302	
	Bond lengths
	Bond angles
	Torsions
	Rings

Ligand VVO D 303	
	Bond lengths
	Bond angles
	Torsions
	Rings

Ligand SIN A 302	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand VVO H 303	
	
Bond lengths	Bond angles
	
Torsions	Rings





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	250/258 (96%)	-1.51	0 100 100	14, 24, 35, 59	0
1	B	253/258 (98%)	-1.50	0 100 100	15, 26, 37, 57	0
1	C	252/258 (97%)	-1.50	0 100 100	11, 27, 39, 58	1 (0%)
1	D	253/258 (98%)	-1.48	0 100 100	14, 26, 36, 59	0
1	E	251/258 (97%)	-1.51	0 100 100	14, 27, 37, 49	0
1	F	253/258 (98%)	-1.48	0 100 100	17, 27, 37, 62	0
1	G	251/258 (97%)	-1.42	0 100 100	18, 31, 44, 60	0
1	H	253/258 (98%)	-1.35	0 100 100	21, 34, 47, 63	0
All	All	2016/2064 (97%)	-1.47	0 100 100	11, 27, 42, 63	1 (0%)

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](#)

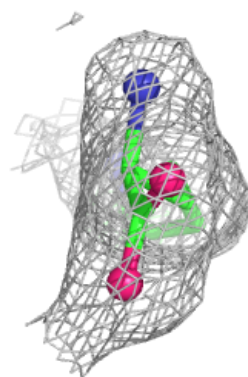
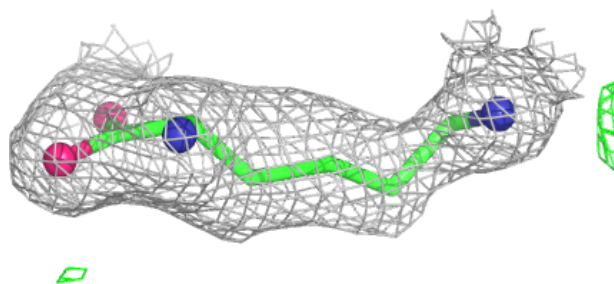
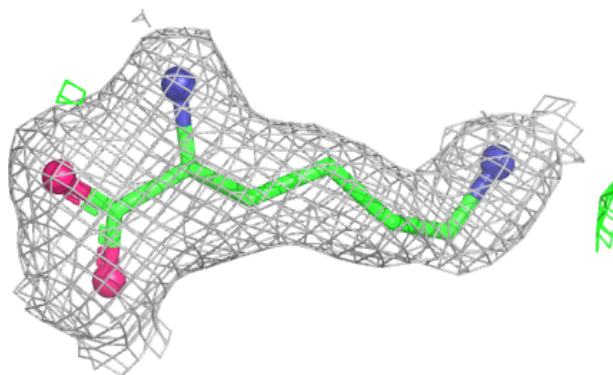
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	LYS	A	301	10/10	0.99	0.04	23,30,32,35	0
2	LYS	B	301	10/10	0.99	0.03	22,24,28,31	0
2	LYS	C	301	10/10	0.99	0.03	25,30,35,40	0
2	LYS	D	301	10/10	0.99	0.03	17,26,31,31	0
2	LYS	E	301	10/10	0.99	0.05	21,26,30,32	0
2	LYS	F	301	10/10	0.99	0.03	22,30,35,37	0
2	LYS	G	301	10/10	0.99	0.03	27,30,36,39	0
2	LYS	H	301	10/10	0.99	0.04	24,34,42,42	0
3	SIN	A	302	8/8	0.99	0.02	15,23,24,25	0
3	SIN	B	302	8/8	0.99	0.03	20,23,28,29	0
3	SIN	C	302	8/8	0.99	0.03	20,24,26,29	0
3	SIN	E	302	8/8	0.99	0.03	20,22,25,28	0
3	SIN	F	302	8/8	0.99	0.04	28,29,31,33	0
3	SIN	G	302	8/8	0.99	0.03	23,29,30,33	0
3	SIN	H	302	8/8	0.99	0.03	27,32,34,36	0
5	CL	A	304	1/1	0.99	0.08	26,26,26,26	1
5	CL	B	304	1/1	0.99	0.04	26,26,26,26	1
5	CL	C	304	1/1	0.99	0.03	25,25,25,25	1
5	CL	D	304	1/1	0.99	0.07	29,29,29,29	0
5	CL	E	304	1/1	0.99	0.08	27,27,27,27	1
5	CL	F	304	1/1	0.99	0.03	36,36,36,36	0
5	CL	G	304	1/1	0.99	0.03	34,34,34,34	0
4	VVO	H	303	2/2	1.00	0.02	30,30,30,33	0
3	SIN	D	302	8/8	1.00	0.03	20,24,30,31	0
4	VVO	A	303	2/2	1.00	0.01	18,18,18,23	0
4	VVO	B	303	2/2	1.00	0.01	23,23,23,23	0
4	VVO	C	303	2/2	1.00	0.02	22,22,22,23	0
4	VVO	D	303	2/2	1.00	0.01	23,23,23,24	0
4	VVO	E	303	2/2	1.00	0.02	18,18,18,18	0
4	VVO	F	303	2/2	1.00	0.01	29,29,29,35	0
6	V	G	303	1/1	1.00	0.01	28,28,28,28	0

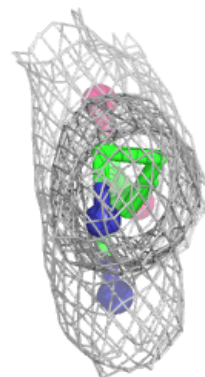
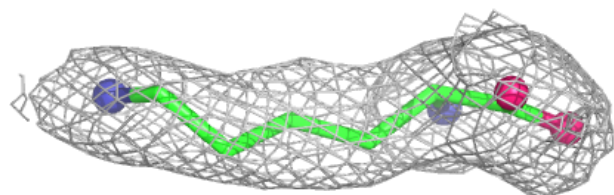
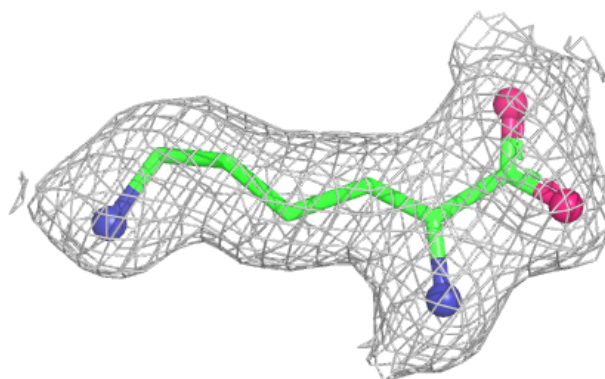
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 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)

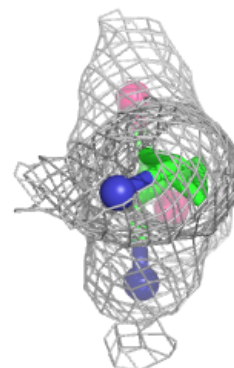
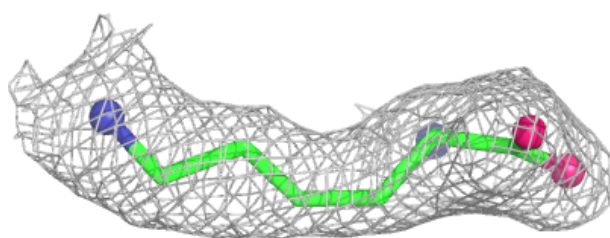
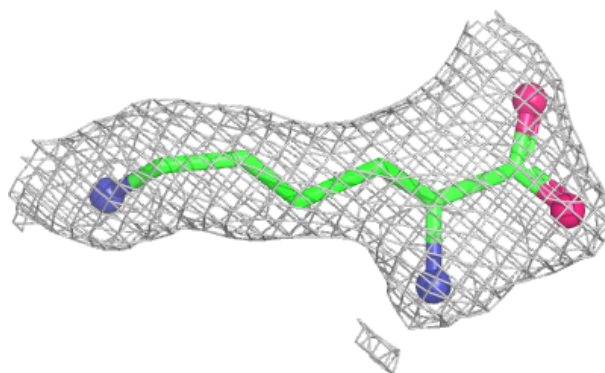
**Electron density around LYS B 301:**

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

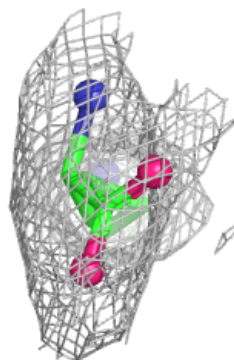
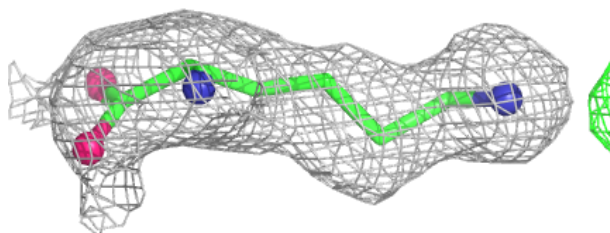
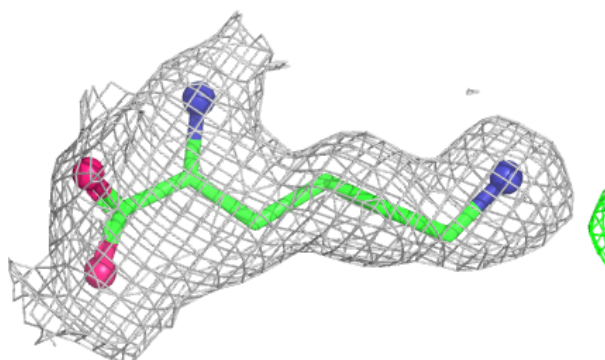


Electron density around LYS C 301:

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and green (positive)

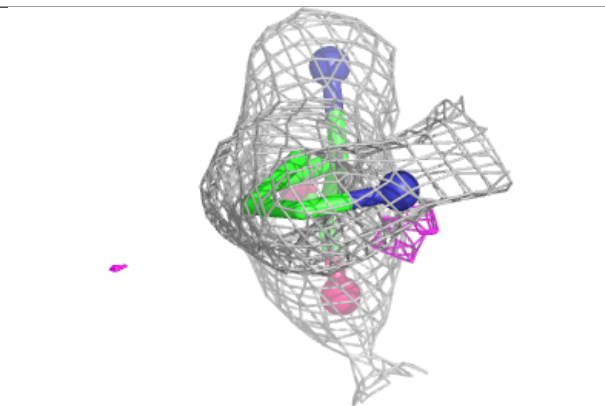
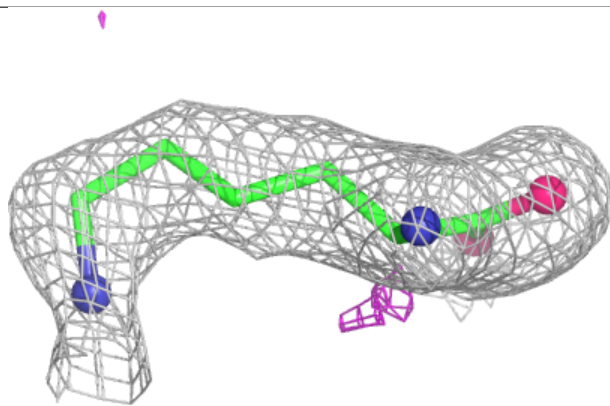
**Electron density around LYS D 301:**

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and green (positive)

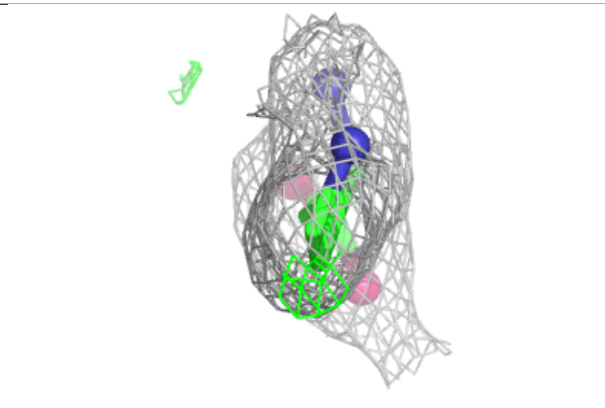
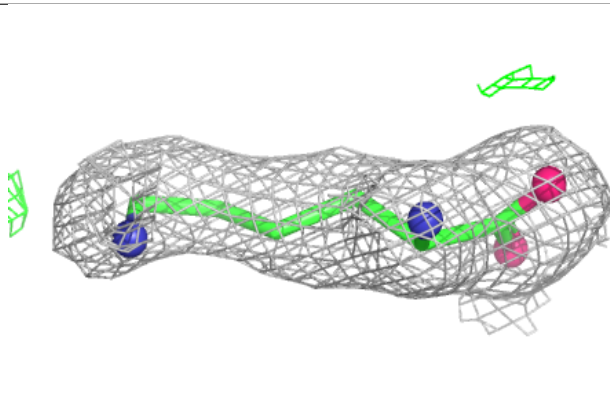
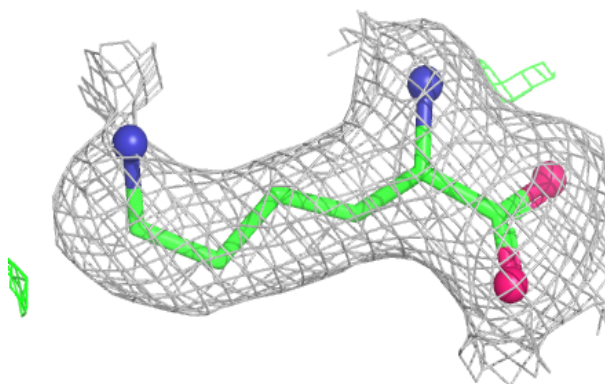


Electron density around LYS E 301:

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and green (positive)

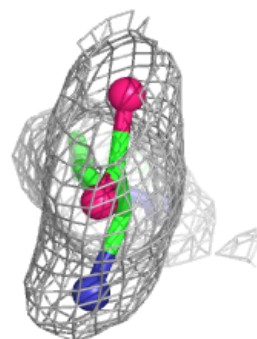
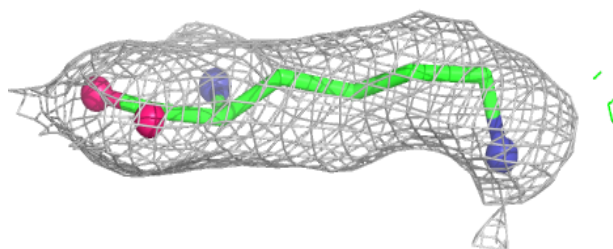
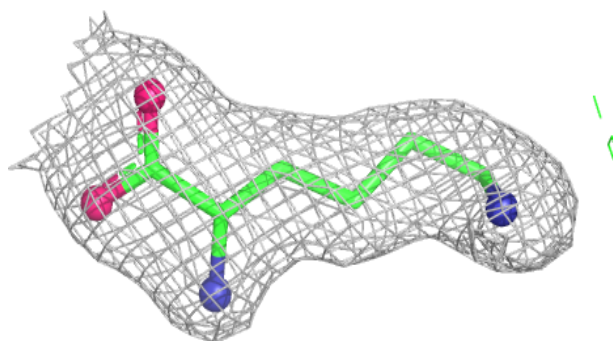
**Electron density around LYS F 301:**

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

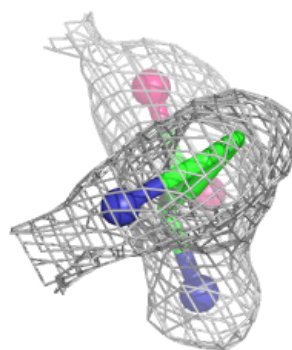
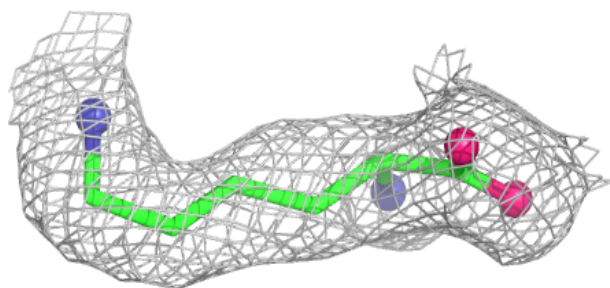
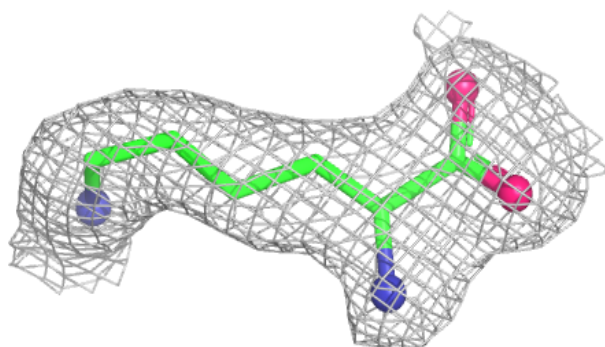


Electron density around LYS G 301:

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

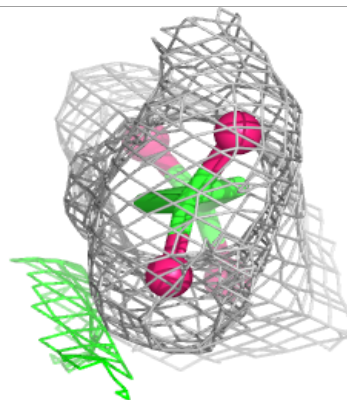
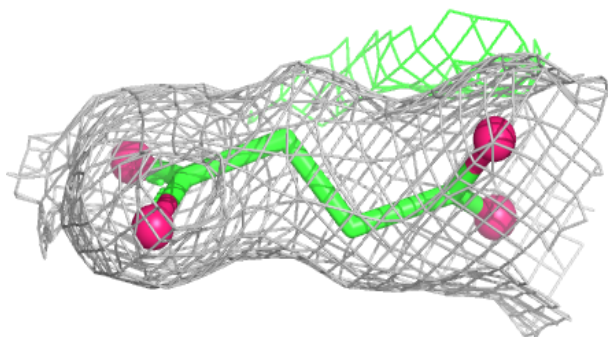
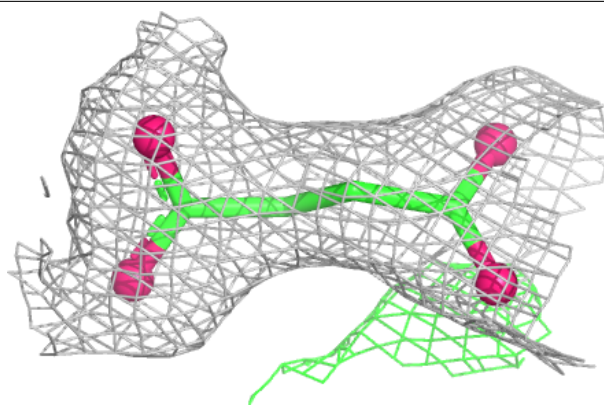
**Electron density around LYS H 301:**

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

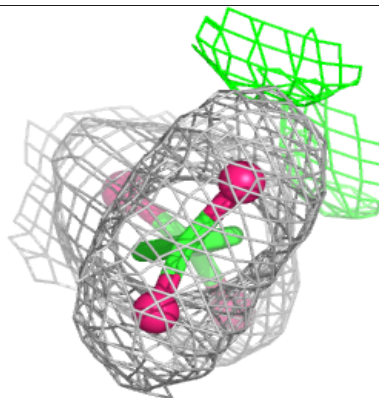
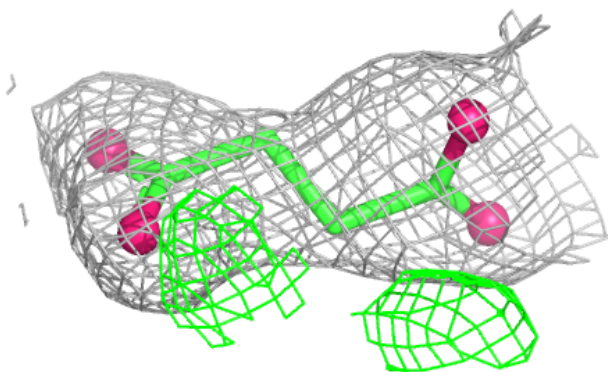
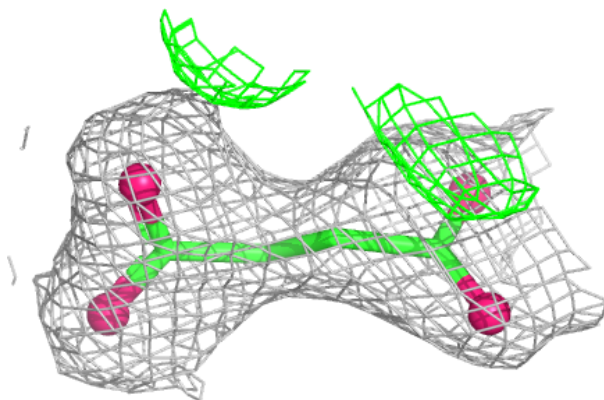


Electron density around SIN A 302:

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

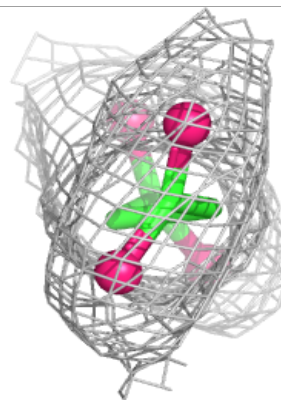
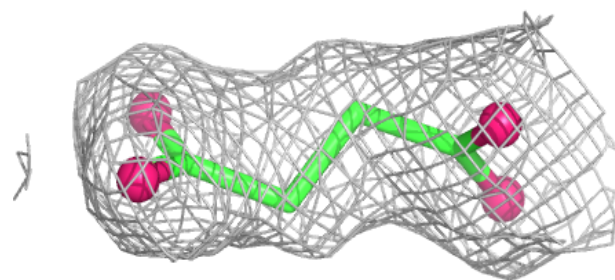
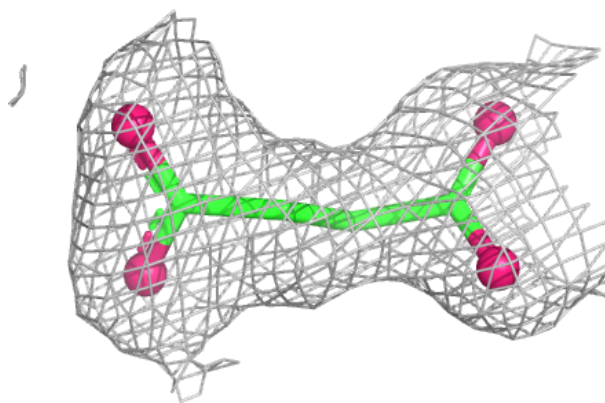
**Electron density around SIN B 302:**

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

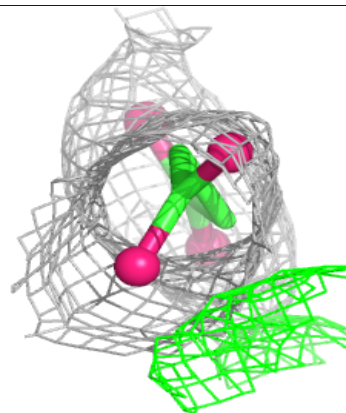
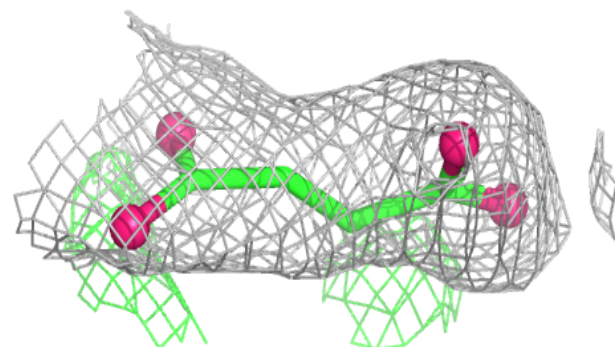
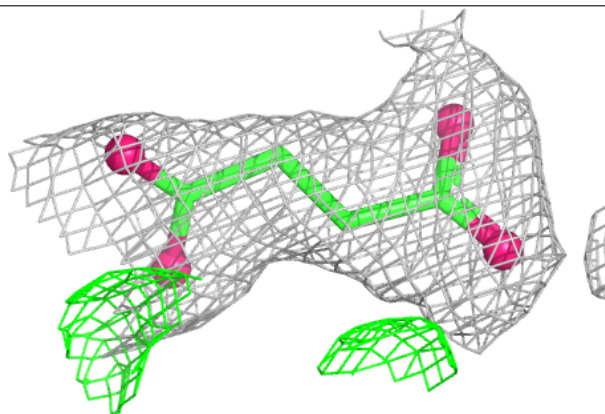


Electron density around SIN C 302:

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

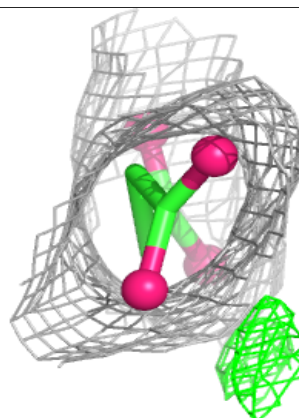
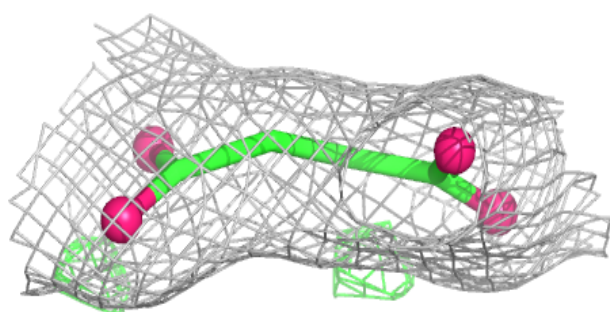
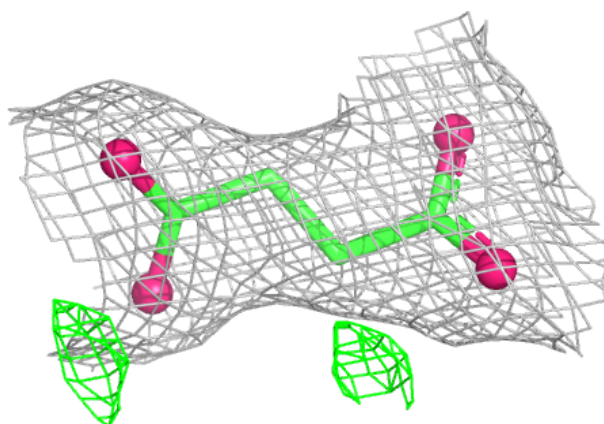
**Electron density around SIN E 302:**

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

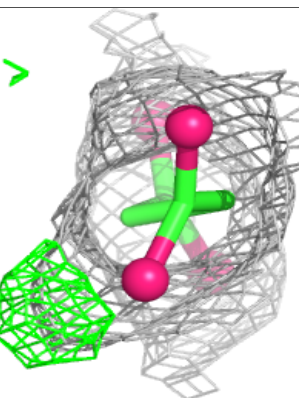
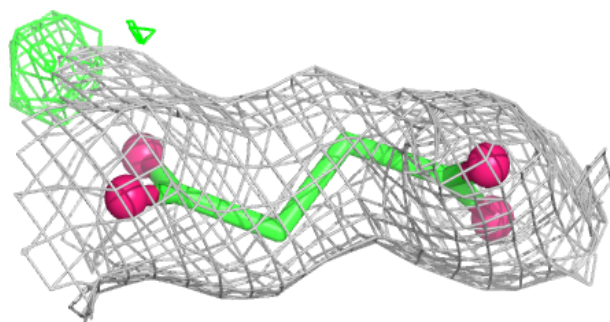
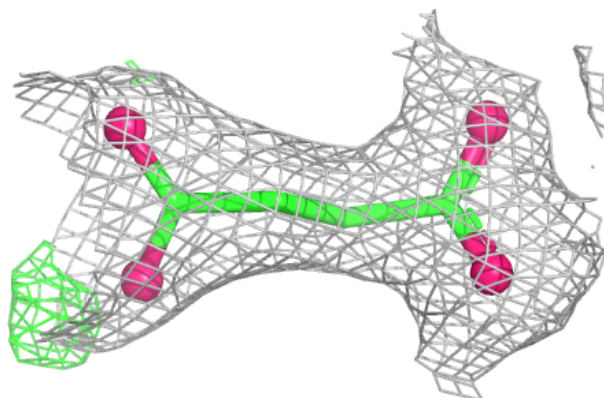


Electron density around SIN F 302:

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

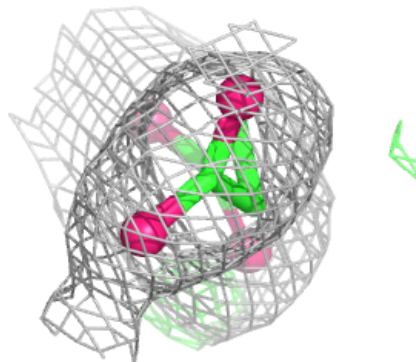
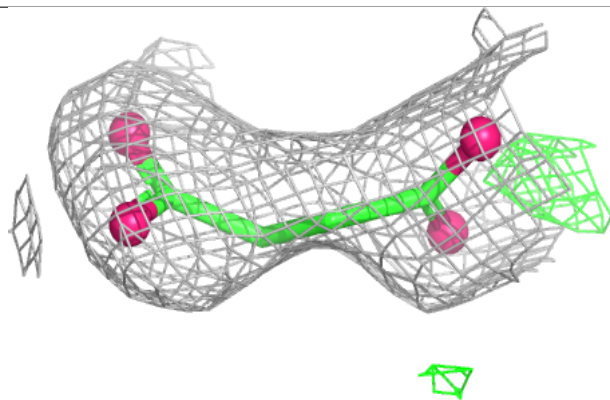
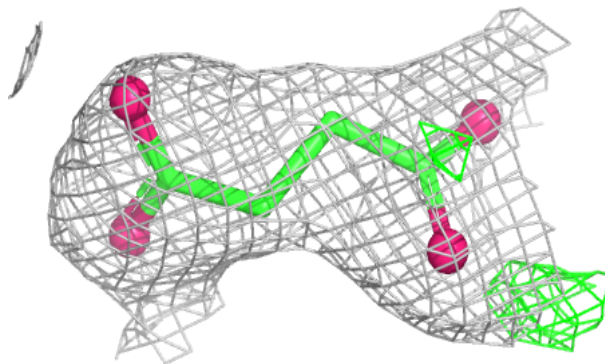
**Electron density around SIN G 302:**

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



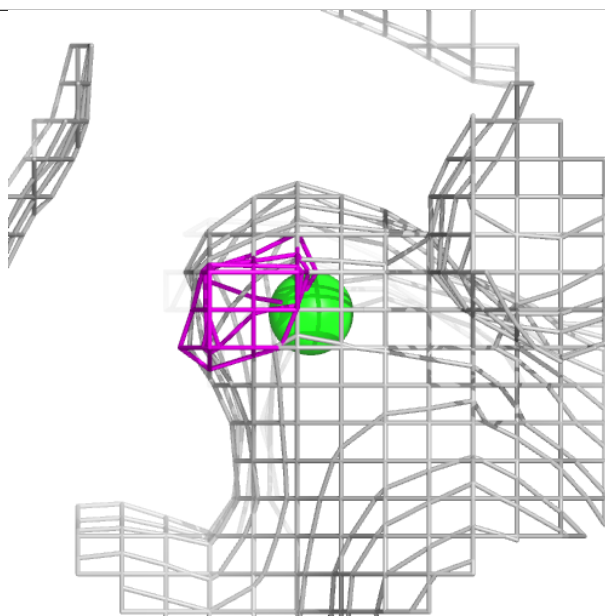
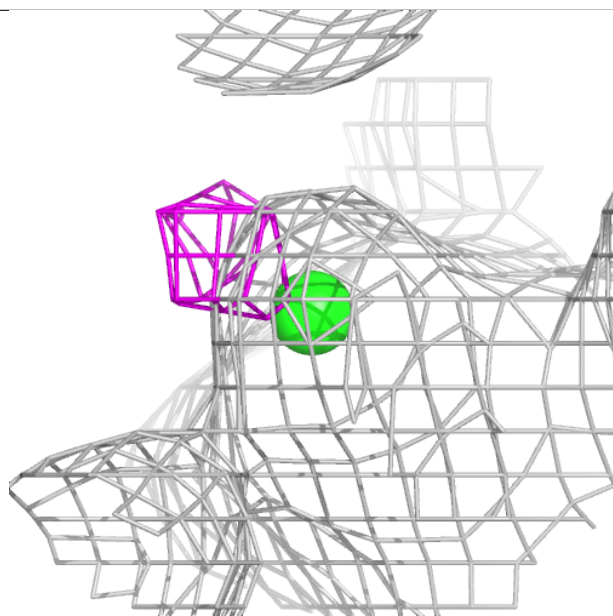
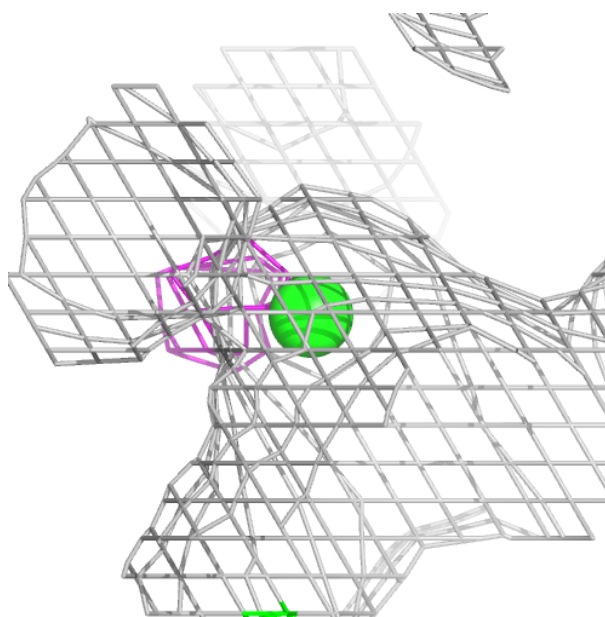
Electron density around SIN H 302:

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



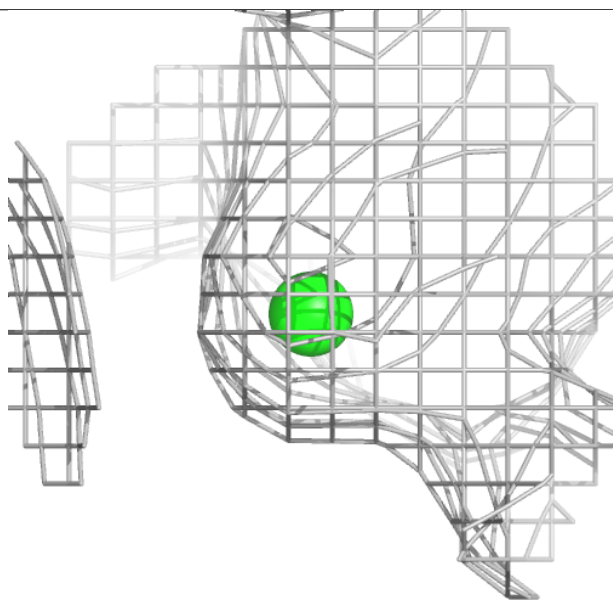
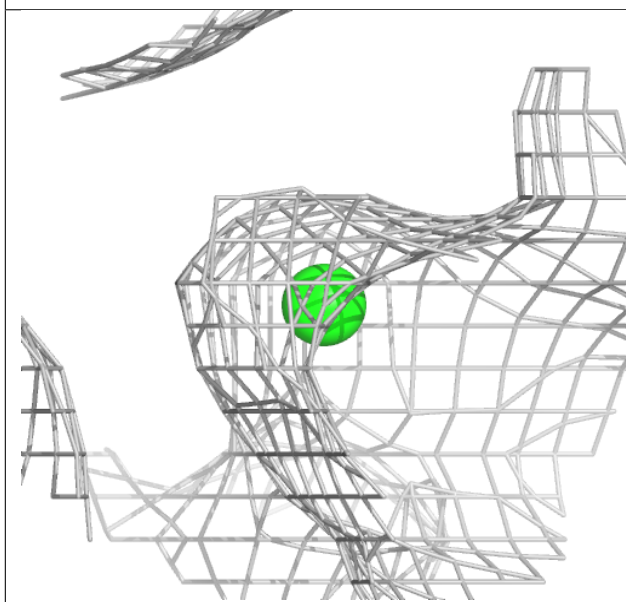
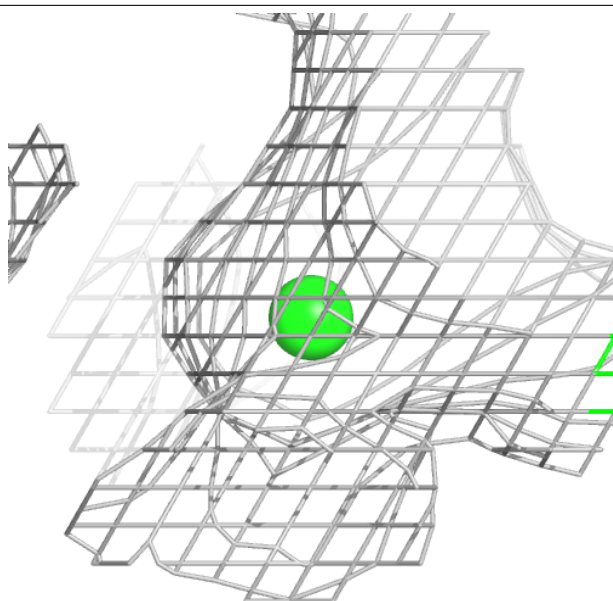
Electron density around CL A 304:

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



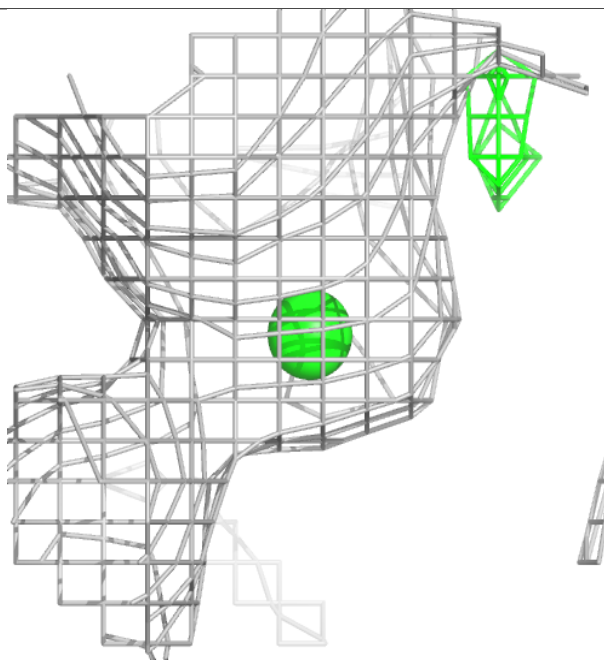
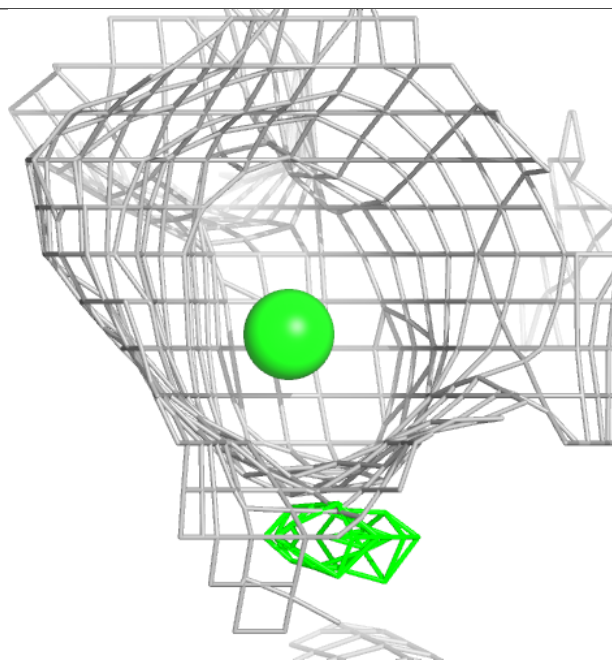
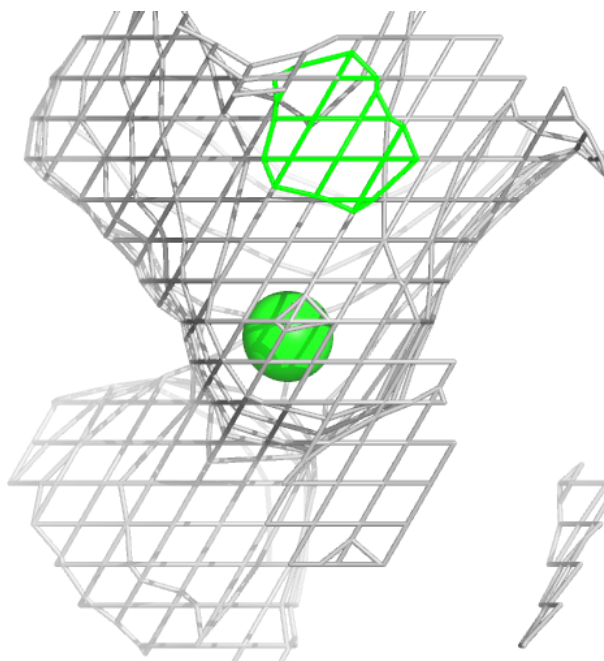
Electron density around CL B 304:

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



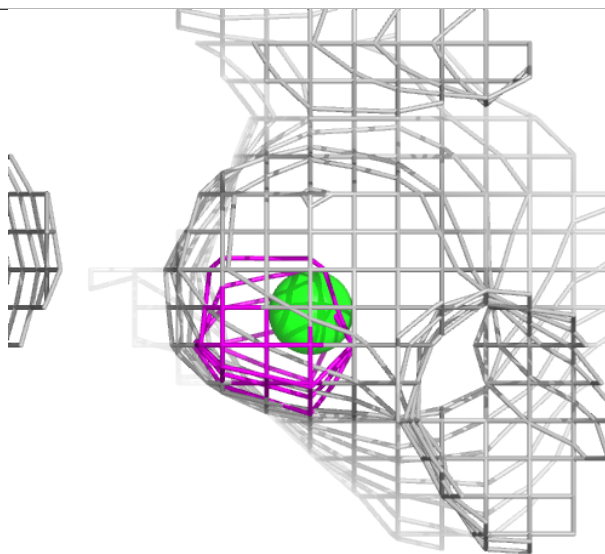
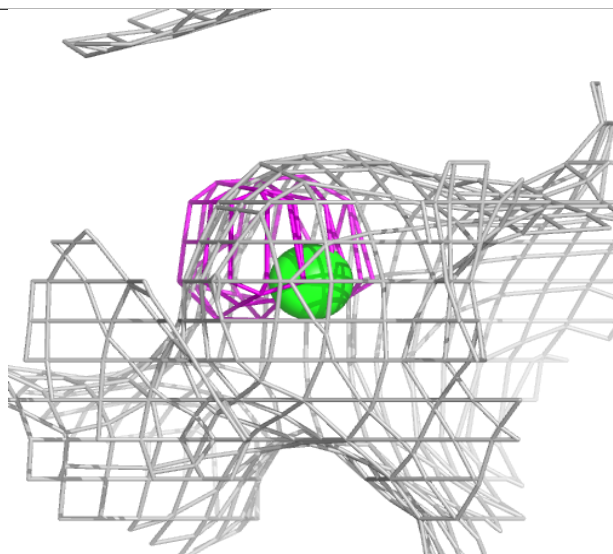
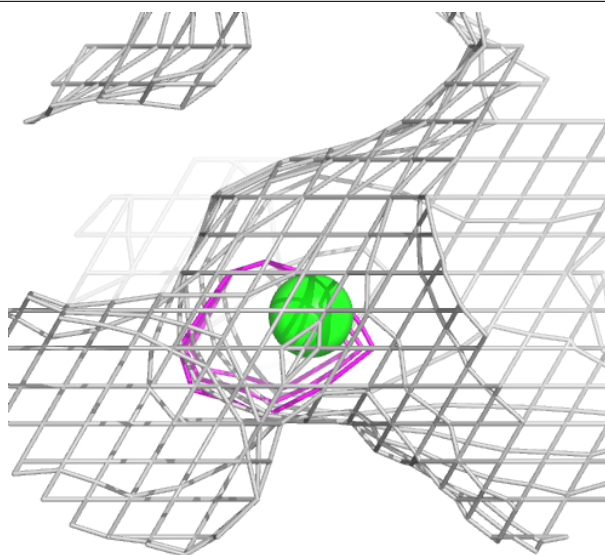
Electron density around CL C 304:

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



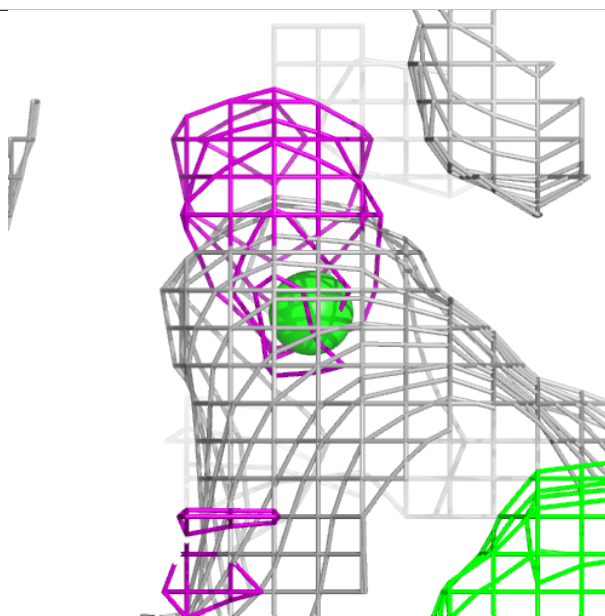
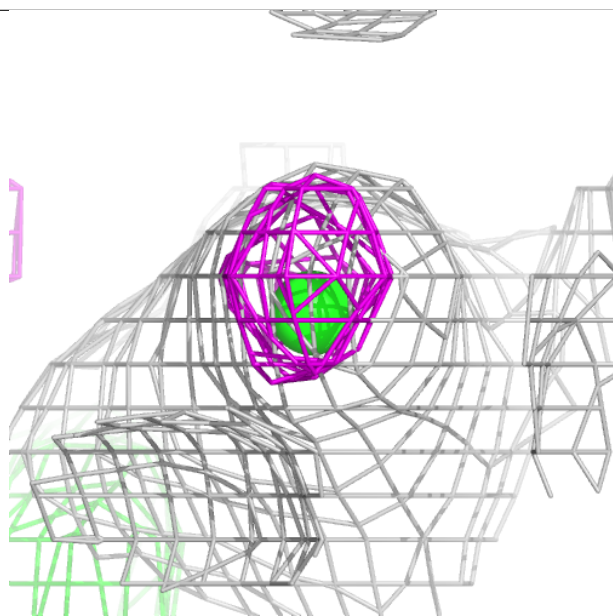
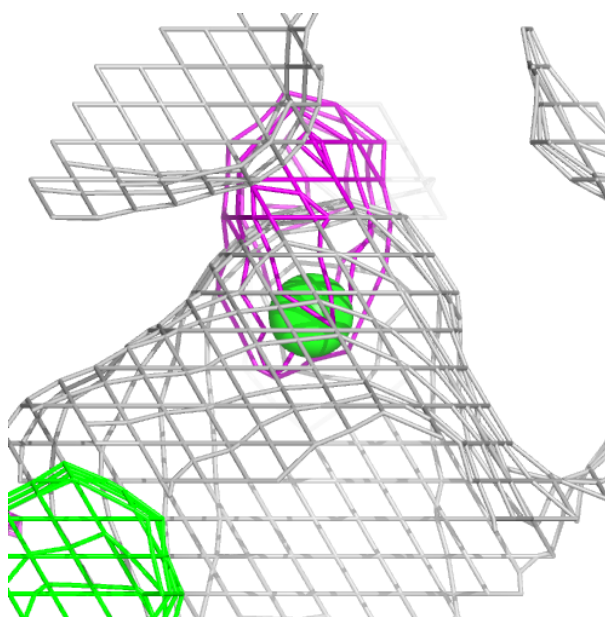
Electron density around CL D 304:

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



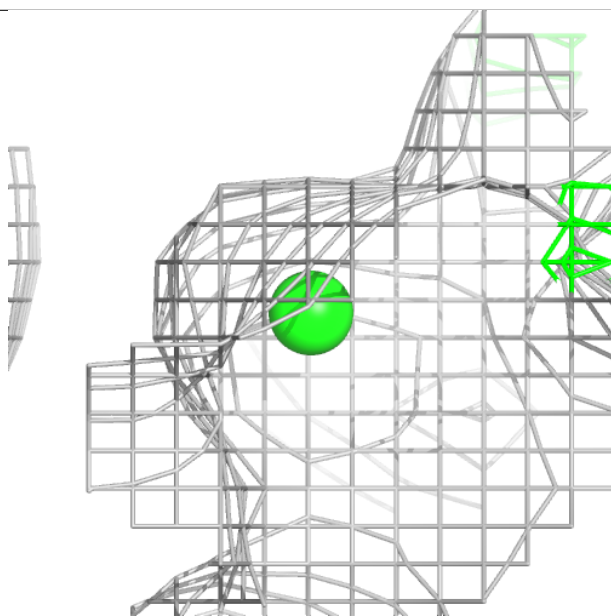
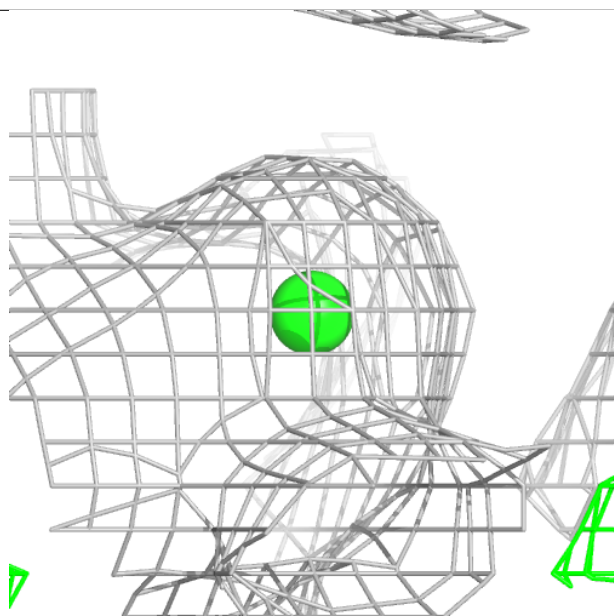
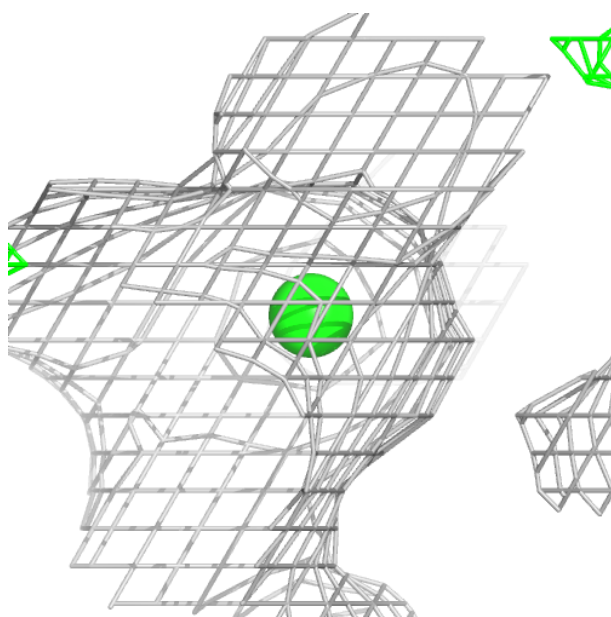
Electron density around CL E 304:

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



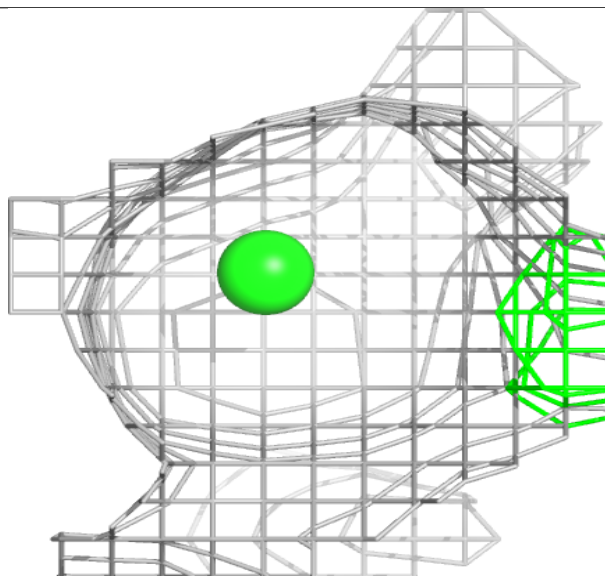
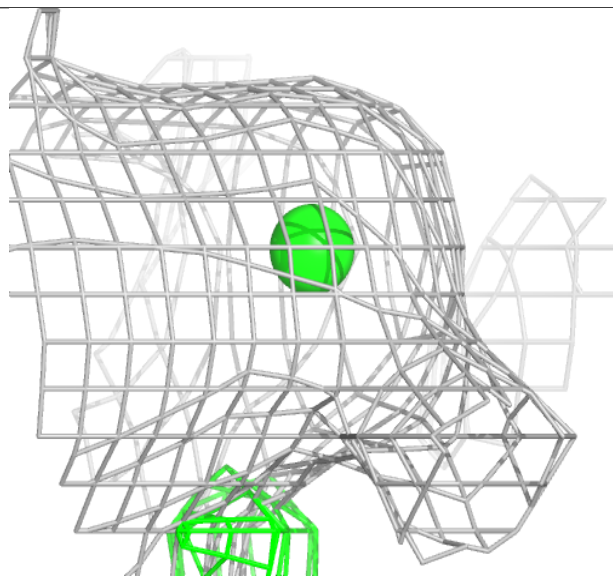
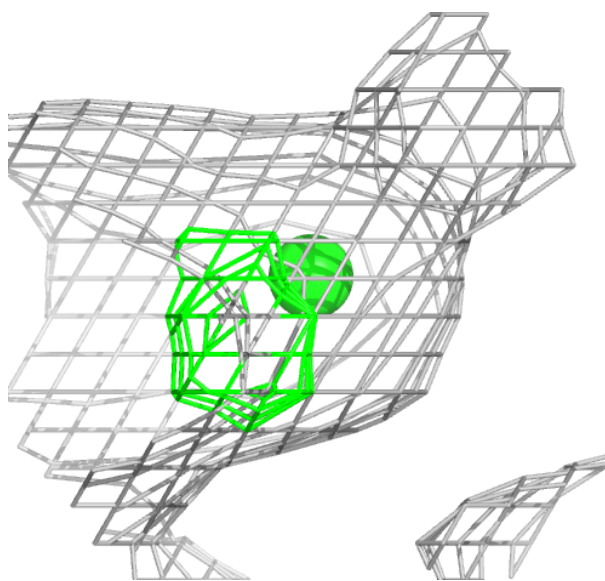
Electron density around CL F 304:

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



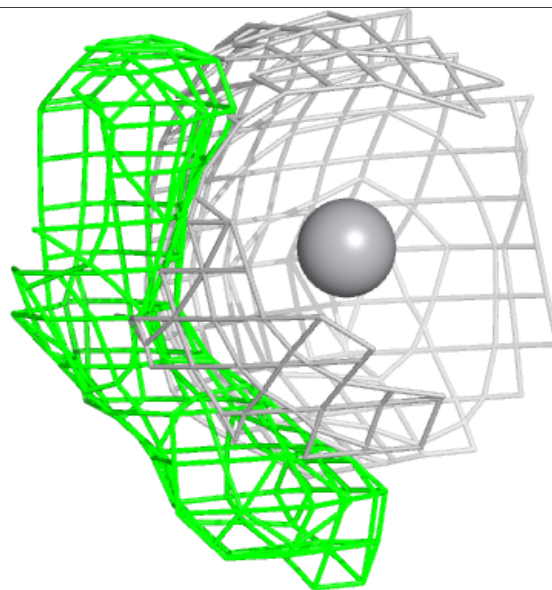
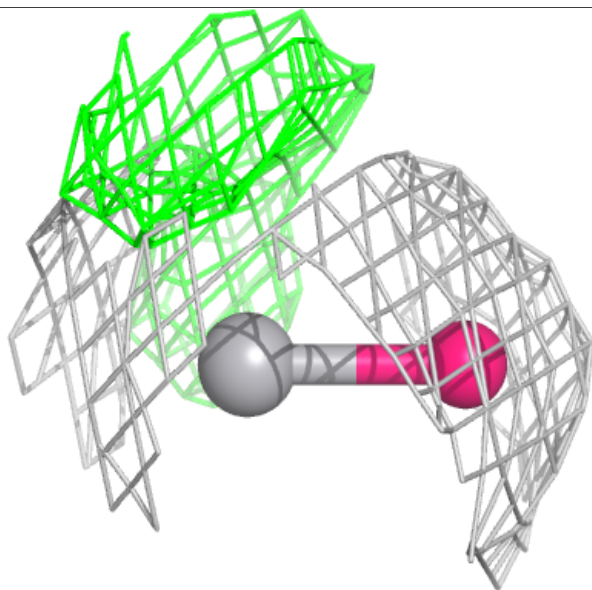
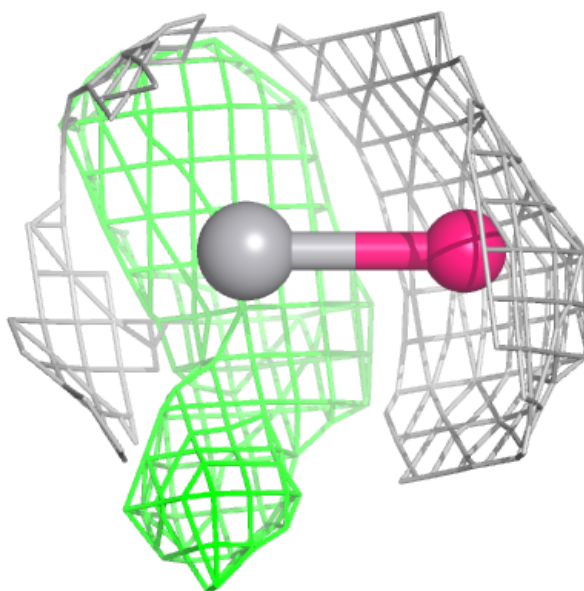
Electron density around CL G 304:

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



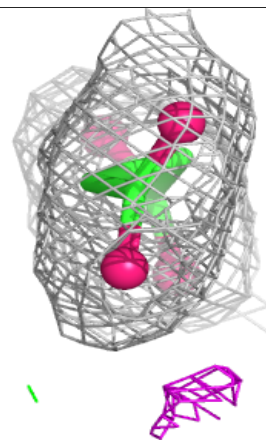
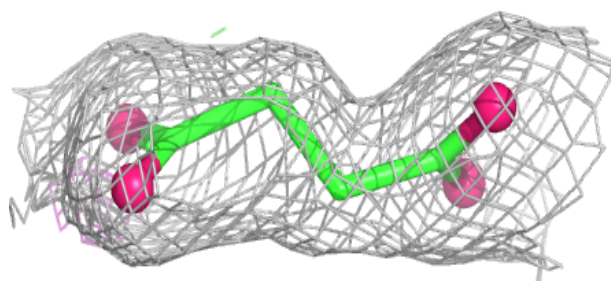
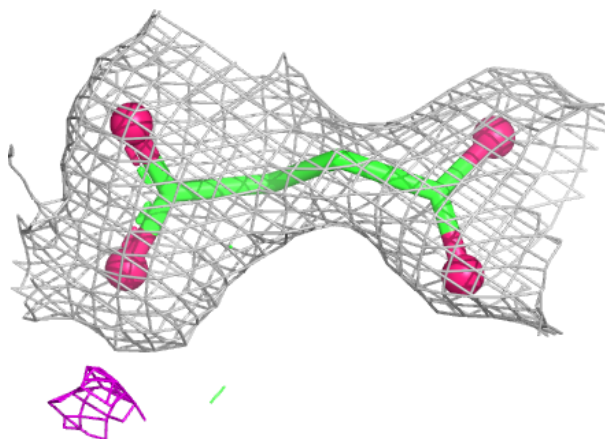
Electron density around VVO H 303:

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



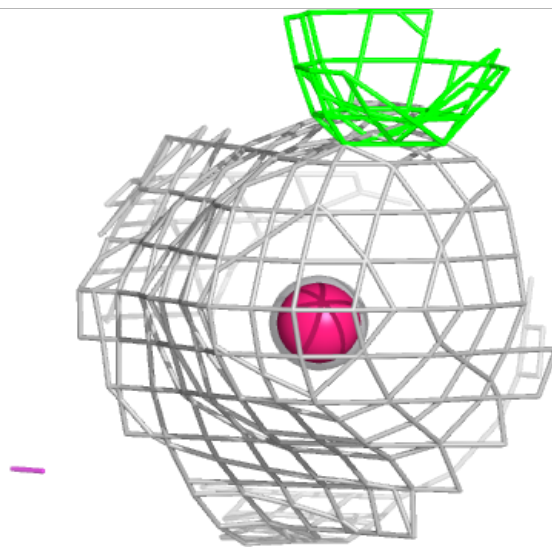
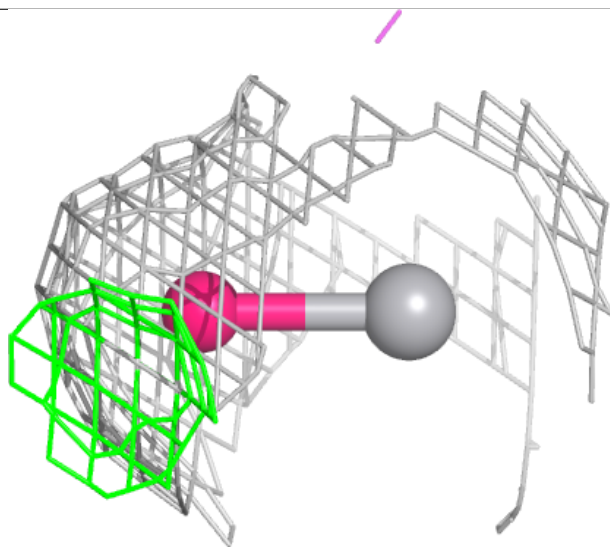
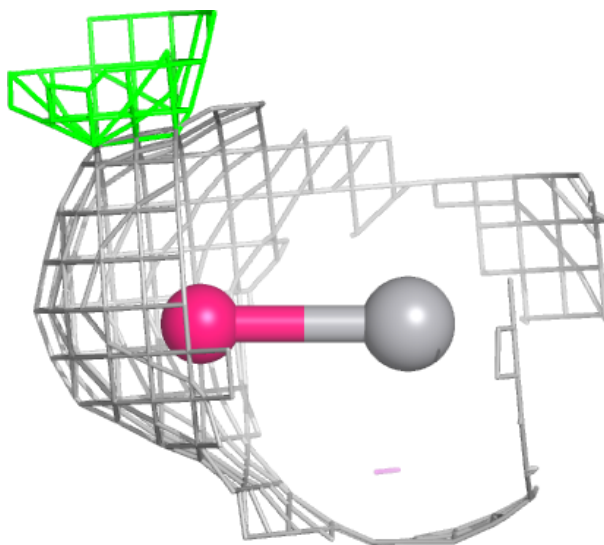
Electron density around SIN D 302:

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



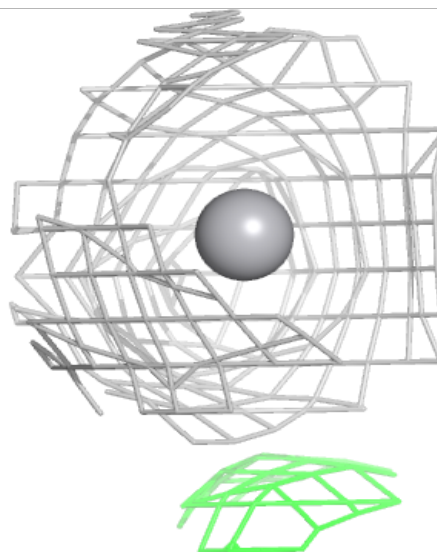
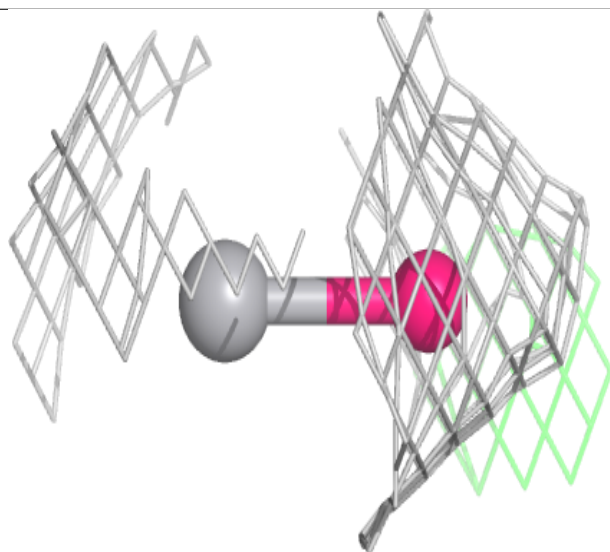
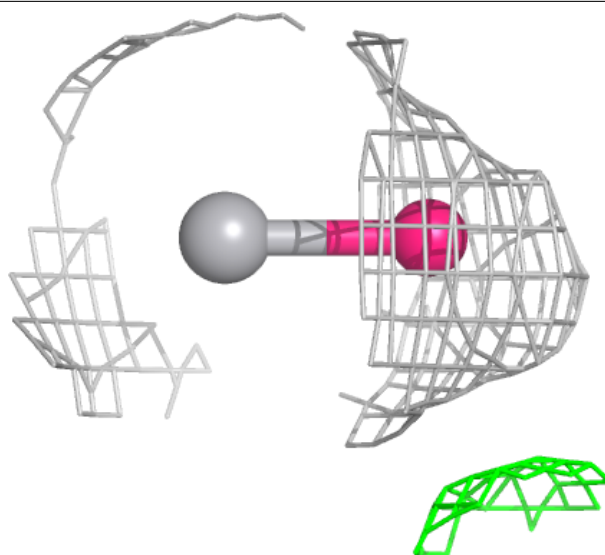
Electron density around VVO A 303:

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



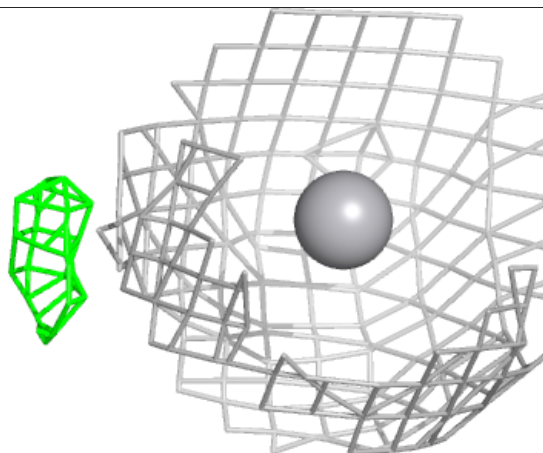
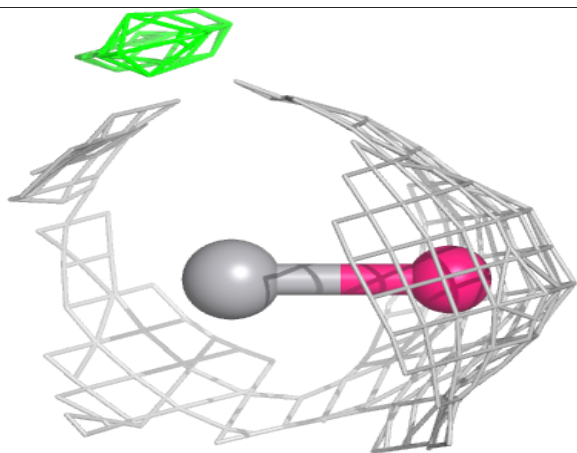
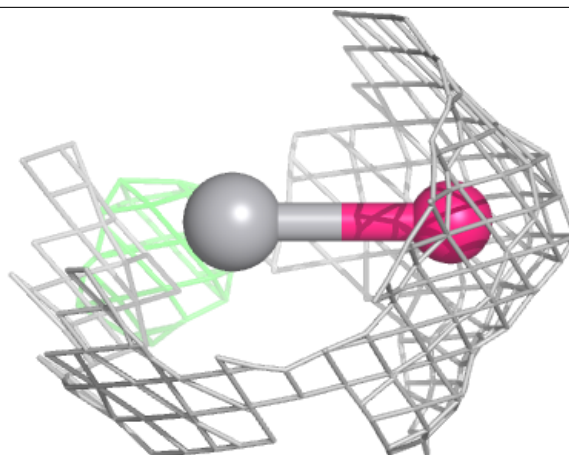
Electron density around VVO B 303:

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



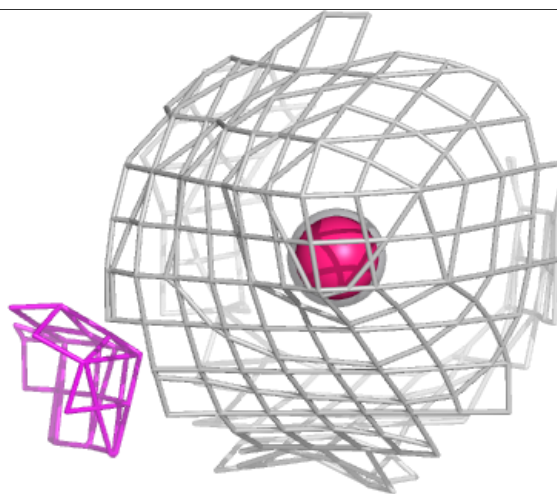
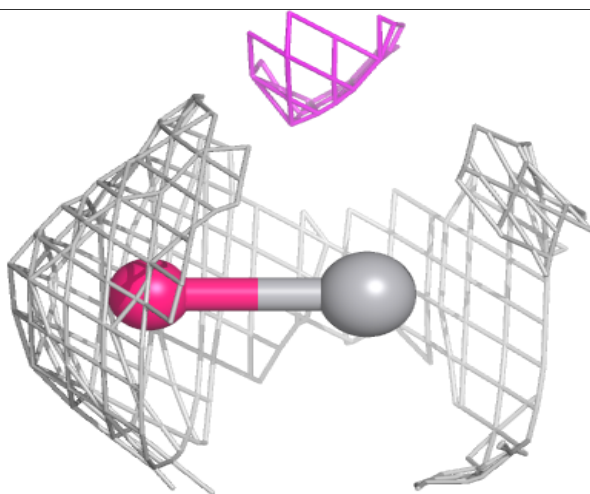
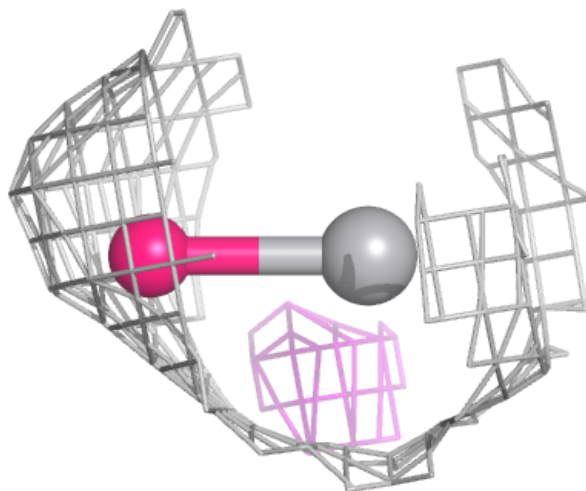
Electron density around VVO C 303:

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



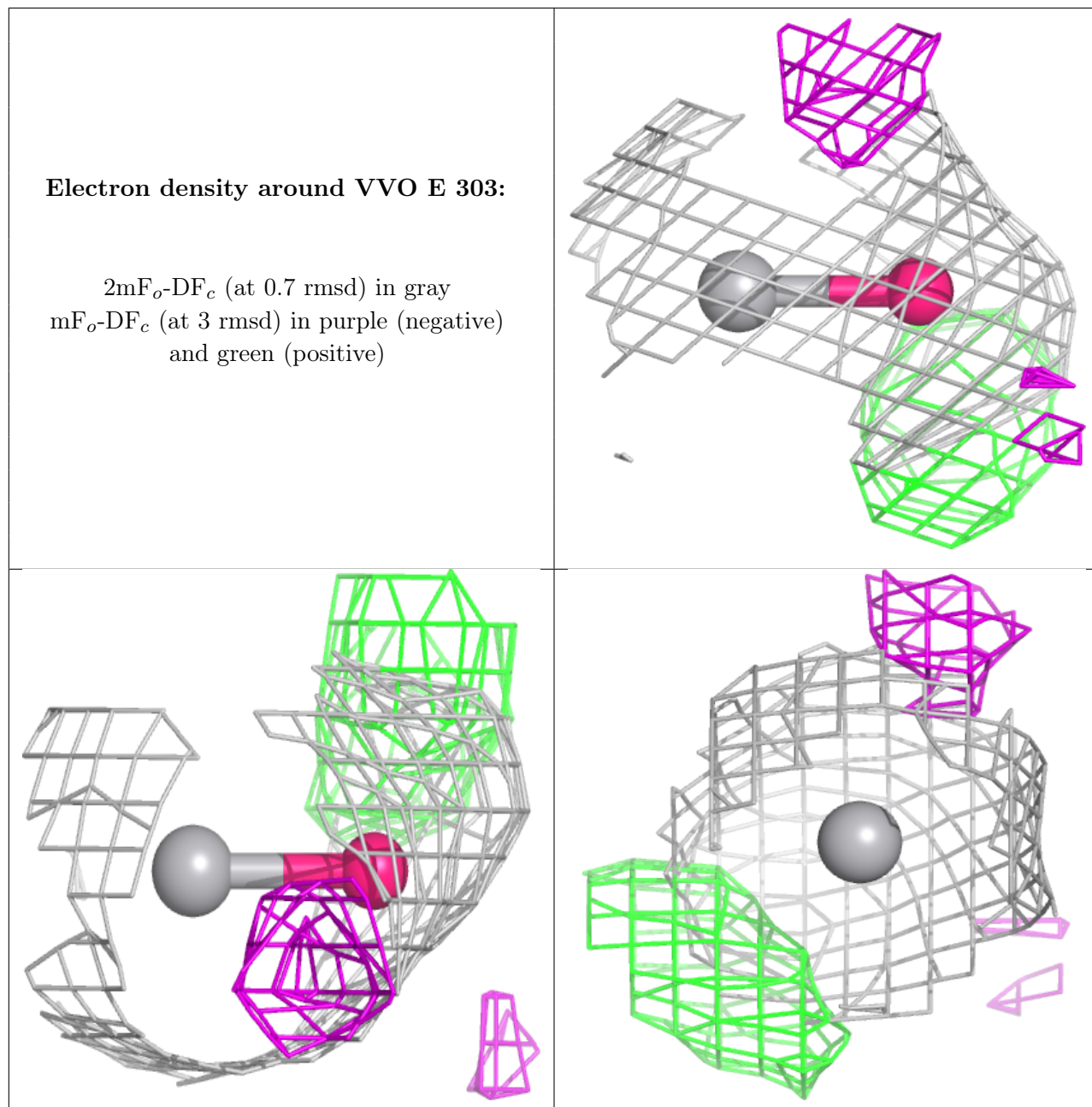
Electron density around VVO D 303:

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



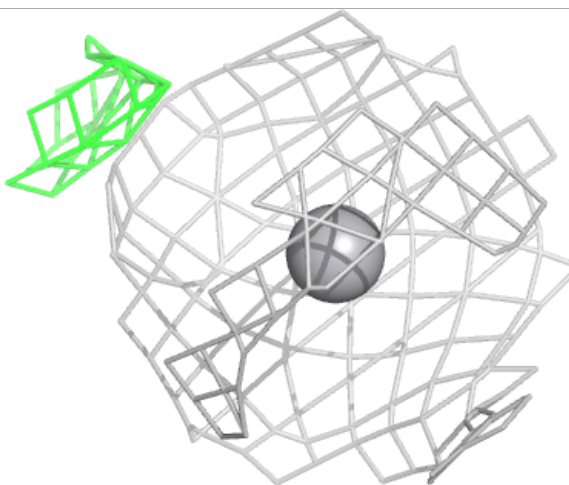
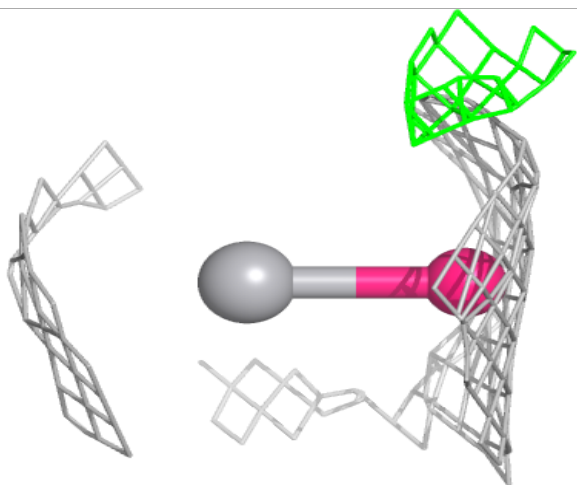
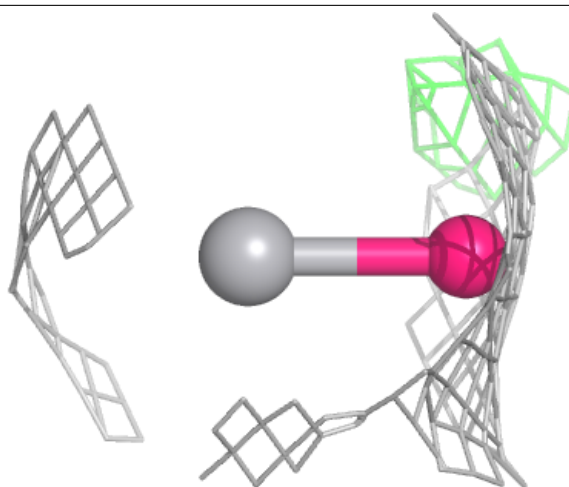
Electron density around VVO E 303:

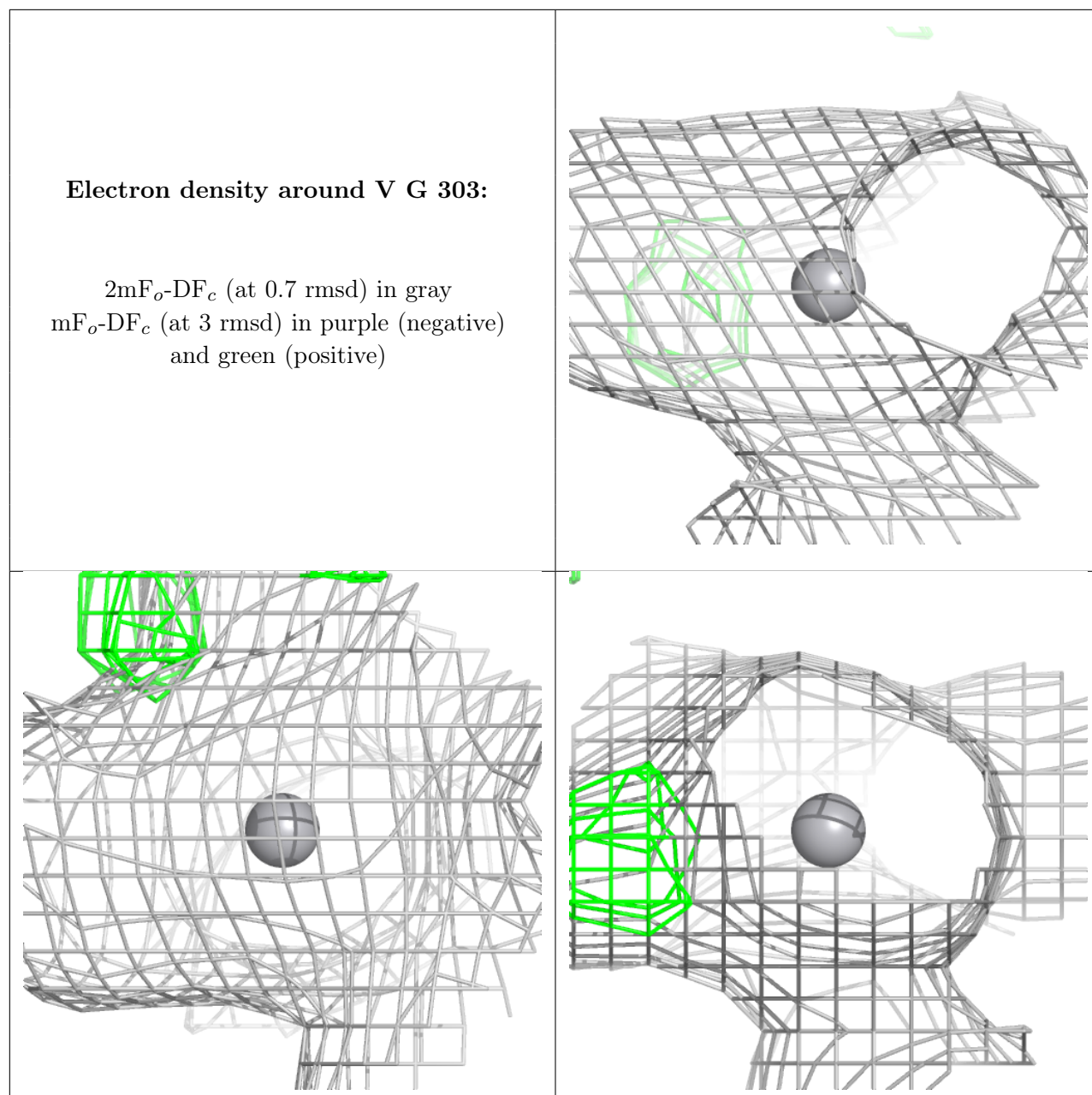
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around VVO F 303:

$2mF_o-DF_c$ (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.