



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 07:16 AM UTC

PDB ID : 8I07 / pdb_00008i07
Title : Crystal structure of Escherichia coli glyoxylate carboligase double mutant in complex with glycolaldehyde
Authors : Kim, J.H.; Kim, J.S.
Deposited on : 2023-01-10
Resolution : 1.99 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

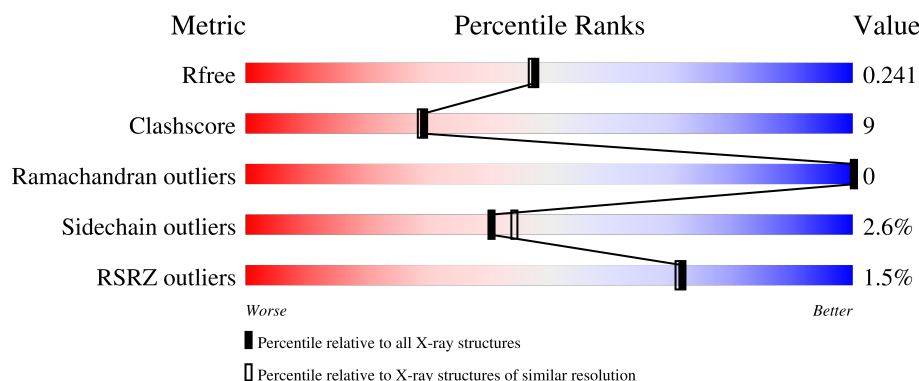
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	594	0% 89% 10% .
1	B	594	2% 88% 11% .
1	C	594	2% 85% 14% .
1	D	594	0% 87% 12% .
1	E	594	2% 81% 17% .

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Mol	Chain	Length	Quality of chain
1	F	594	 2% 83% 15%

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
6	UQ1	B	607	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 30838 atoms, of which 24 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 Glyoxylate carboligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	594	Total	C	N	O	S	0	0	0
			4540	2877	791	836	36			
1	B	594	Total	C	N	O	S	0	0	0
			4540	2877	791	836	36			
1	C	594	Total	C	N	O	S	0	0	0
			4540	2877	791	836	36			
1	D	594	Total	C	N	O	S	0	0	0
			4540	2877	791	836	36			
1	E	594	Total	C	N	O	S	0	0	0
			4540	2877	791	836	36			
1	F	594	Total	C	N	O	S	0	0	0
			4540	2877	791	836	36			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P0AEP7
A	283	GLN	ASN	engineered mutation	UNP P0AEP7
A	484	MET	ARG	engineered mutation	UNP P0AEP7
B	0	GLY	-	expression tag	UNP P0AEP7
B	283	GLN	ASN	engineered mutation	UNP P0AEP7
B	484	MET	ARG	engineered mutation	UNP P0AEP7
C	0	GLY	-	expression tag	UNP P0AEP7
C	283	GLN	ASN	engineered mutation	UNP P0AEP7
C	484	MET	ARG	engineered mutation	UNP P0AEP7
D	0	GLY	-	expression tag	UNP P0AEP7
D	283	GLN	ASN	engineered mutation	UNP P0AEP7
D	484	MET	ARG	engineered mutation	UNP P0AEP7
E	0	GLY	-	expression tag	UNP P0AEP7
E	283	GLN	ASN	engineered mutation	UNP P0AEP7
E	484	MET	ARG	engineered mutation	UNP P0AEP7
F	0	GLY	-	expression tag	UNP P0AEP7
F	283	GLN	ASN	engineered mutation	UNP P0AEP7

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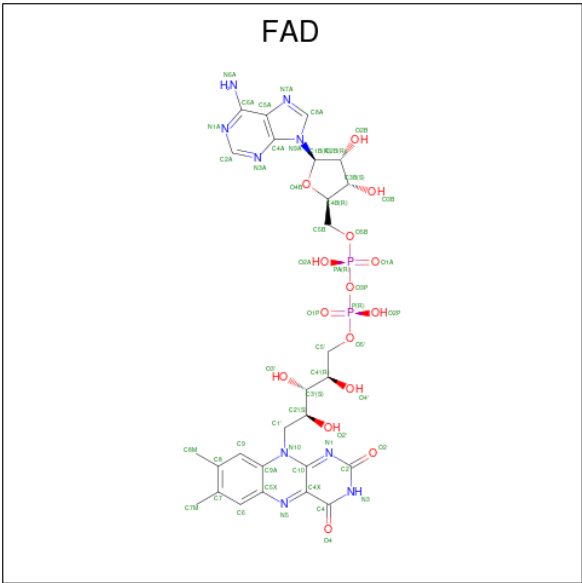
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Chain	Residue	Modelled	Actual	Comment	Reference
F	484	MET	ARG	engineered mutation	UNP P0AEP7

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mg 2 2	0	0
2	B	2	Total Mg 2 2	0	0
2	C	2	Total Mg 2 2	0	0
2	D	1	Total Mg 1 1	0	0
2	E	1	Total Mg 1 1	0	0
2	F	2	Total Mg 2 2	0	0

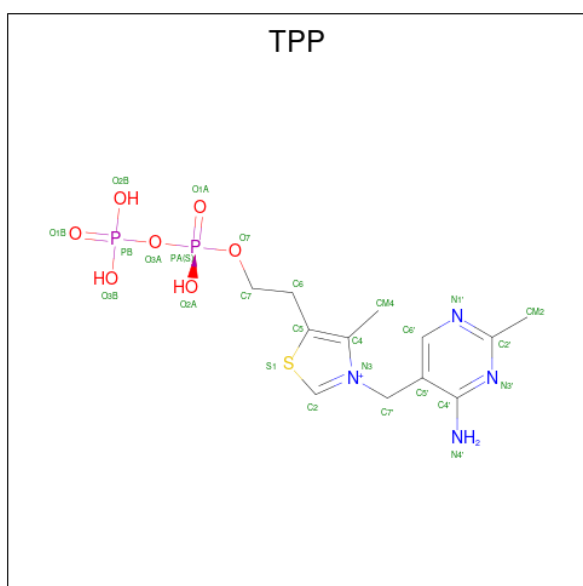
- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂) (labeled as "Ligand of Interest" by depositor).



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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	E	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	F	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

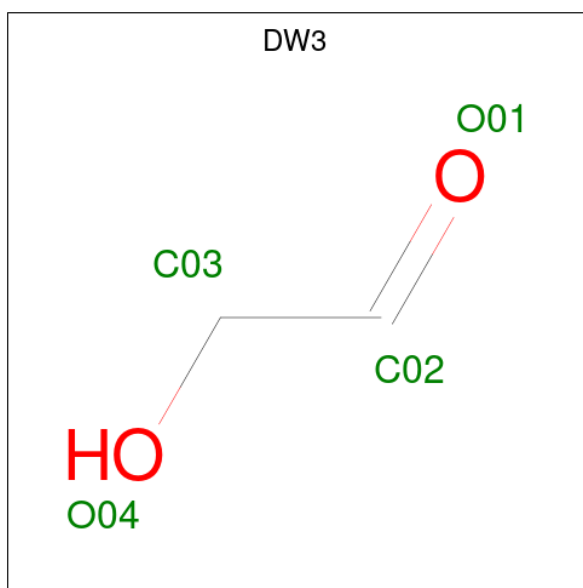
- Molecule 4 is THIAMINE DIPHOSPHATE (CCD ID: TPP) (formula: $C_{12}H_{19}N_4O_7P_2S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
4	B	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
4	C	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
4	D	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
4	E	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
4	F	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		

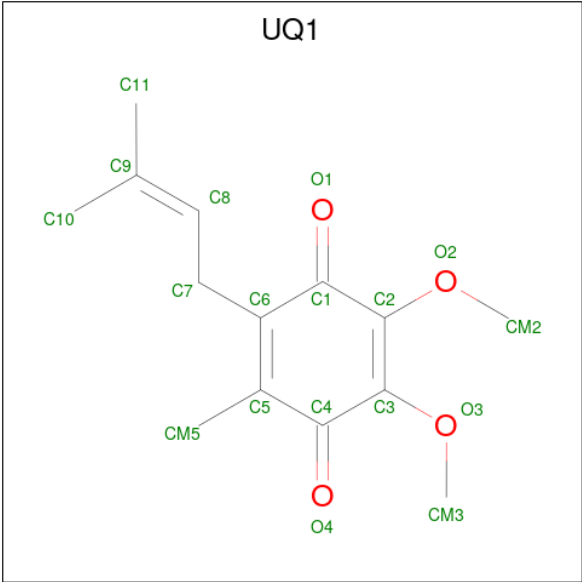
- Molecule 5 is 2-oxidanylethanal (CCD ID: DW3) (formula: $C_2H_4O_2$) (labeled as "Ligand of

Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			8	2	4	2		
5	B	1	Total	C	H	O	0	0
			8	2	4	2		
5	C	1	Total	C	H	O	0	0
			8	2	4	2		
5	C	1	Total	C	H	O	0	0
			8	2	4	2		
5	D	1	Total	C	H	O	0	0
			8	2	4	2		
5	D	1	Total	C	H	O	0	0
			8	2	4	2		

- Molecule 6 is UBIQUINONE-1 (CCD ID: UQ1) (formula: $C_{14}H_{18}O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			13	9	4		
6	A	1	Total	C	O	0	0
			13	9	4		
6	B	1	Total	C	O	0	0
			13	9	4		
6	B	1	Total	C	O	0	0
			13	9	4		
6	C	1	Total	C	O	0	0
			13	9	4		
6	C	1	Total	C	O	0	0
			13	9	4		
6	D	1	Total	C	O	0	0
			13	9	4		
6	D	1	Total	C	O	0	0
			13	9	4		
6	E	1	Total	C	O	0	0
			13	9	4		
6	E	1	Total	C	O	0	0
			13	9	4		
6	F	1	Total	C	O	0	0
			13	9	4		
6	F	1	Total	C	O	0	0
			13	9	4		

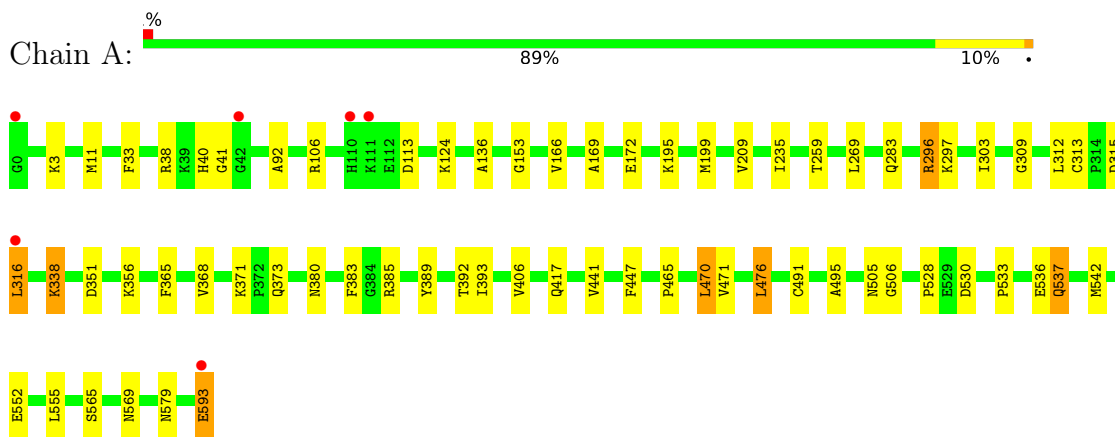
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	639	Total 639	O 639	0	0
7	B	581	Total 581	O 581	0	0
7	C	445	Total 445	O 445	0	0
7	D	433	Total 433	O 433	0	0
7	E	409	Total 409	O 409	0	0
7	F	403	Total 403	O 403	0	0

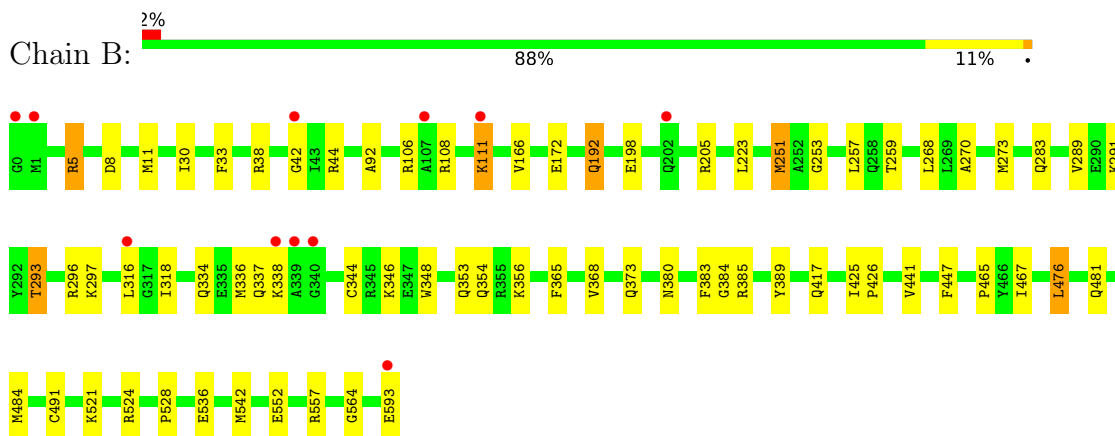
3 Residue-property plots

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.

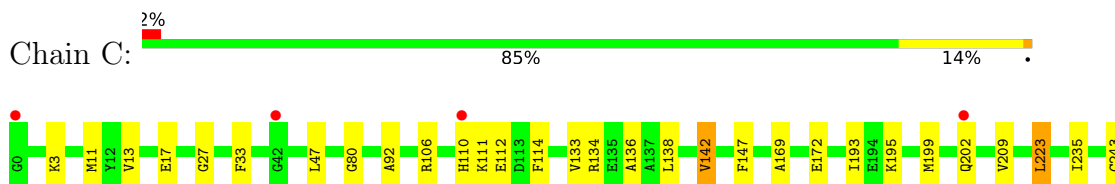
• Molecule 1: Glyoxylate carboligase

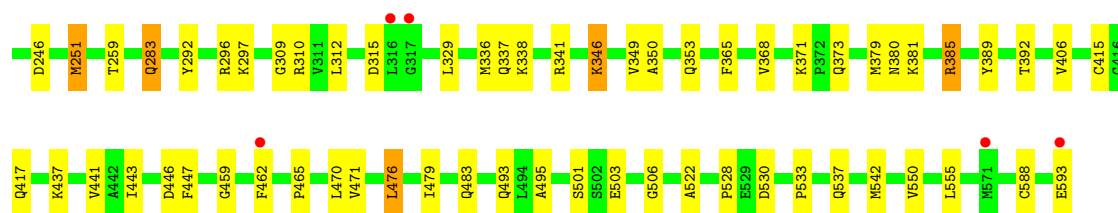


• Molecule 1: Glyoxylate carboligase

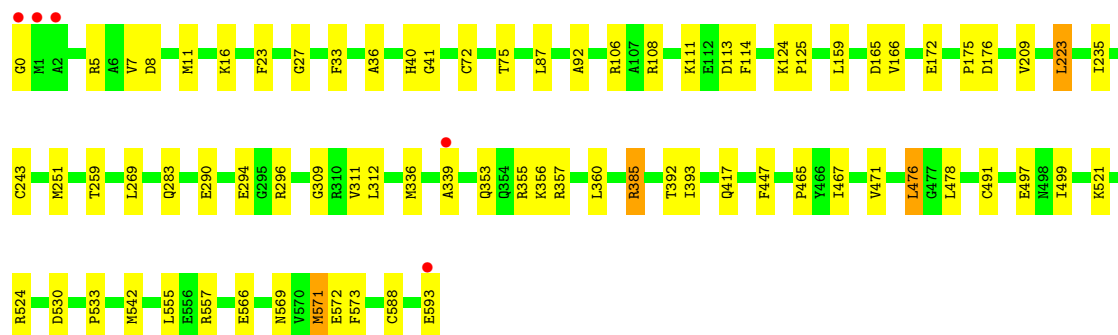
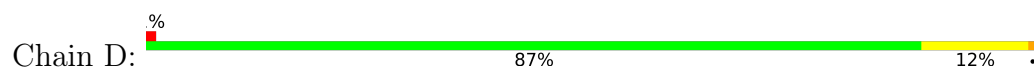


• Molecule 1: Glyoxylate carboligase

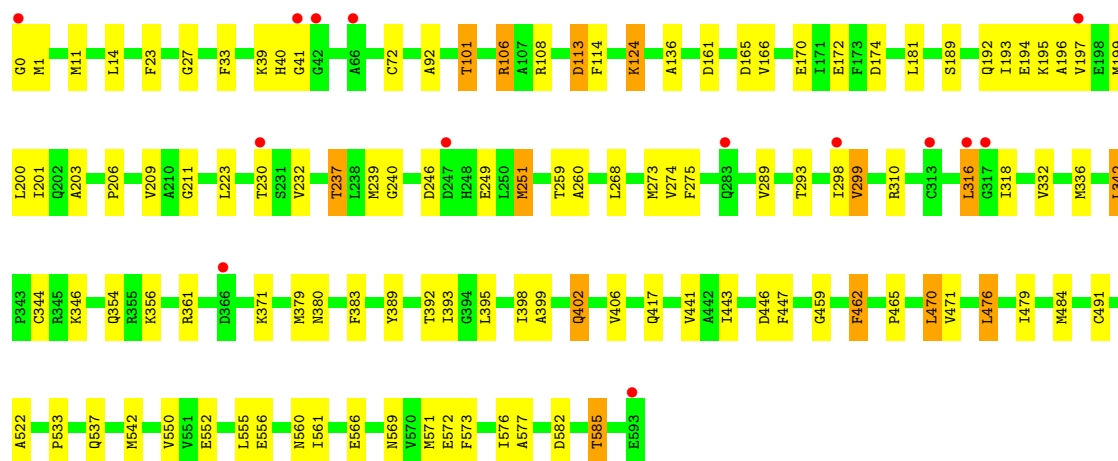
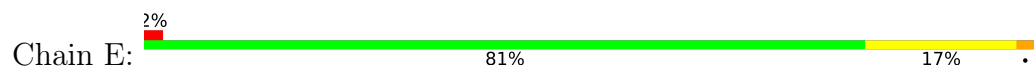




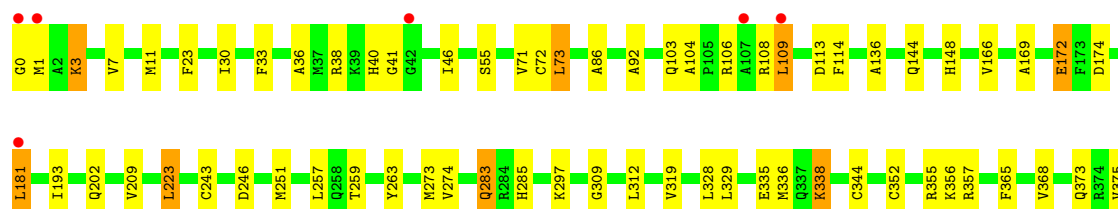
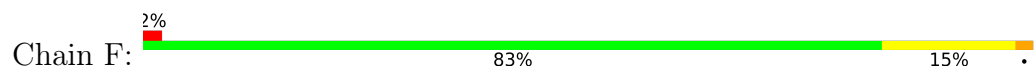
• Molecule 1: Glyoxylate carboligase

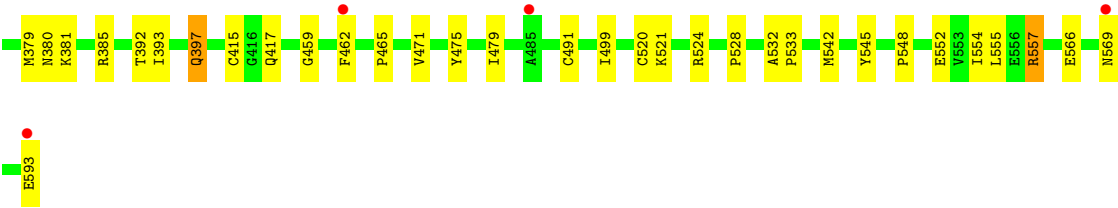


• Molecule 1: Glyoxylate carboligase



• Molecule 1: Glyoxylate carboligase





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	189.30Å 189.30Å 246.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.89 – 1.99 49.89 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.4 (49.89-1.99) 99.3 (49.89-1.99)	Depositor EDS
R_{merge}	1.00	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 1.98Å)	Xtriage
Refinement program	PHENIX v2.0	Depositor
R, R_{free}	0.208 , 0.242 0.208 , 0.241	Depositor DCC
R_{free} test set	10000 reflections (3.29%)	wwPDB-VP
Wilson B-factor (Å ²)	26.0	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 34.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.55$, $\langle L^2 \rangle = 0.39$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	30838	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 65.65 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.8555e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, FAD, TPP, UQ1, DW3

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	0.34	0/4632	0.54	0/6286
1	B	0.33	0/4632	0.55	0/6286
1	C	0.29	0/4632	0.50	0/6286
1	D	0.28	0/4632	0.49	0/6286
1	E	0.28	0/4632	0.51	2/6286 (0.0%)
1	F	0.27	0/4632	0.49	0/6286
All	All	0.30	0/27792	0.51	2/37716 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	2
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	462	PHE	CA-C-N	-5.25	115.00	122.77
1	E	462	PHE	C-N-CA	-5.25	115.00	122.77

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	296	ARG	Sidechain
1	B	296	ARG	Sidechain
1	B	42	GLY	Peptide

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	4540	0	4546	49	0
1	B	4540	0	4546	68	0
1	C	4540	0	4546	75	0
1	D	4540	0	4546	69	0
1	E	4540	0	4546	118	0
1	F	4540	0	4546	93	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	2	0	0	0	0
3	A	53	0	31	1	0
3	B	53	0	31	1	0
3	C	53	0	31	3	0
3	D	53	0	31	5	0
3	E	53	0	31	6	0
3	F	53	0	31	6	0
4	A	26	0	16	0	0
4	B	26	0	16	0	0
4	C	26	0	16	0	0
4	D	26	0	16	1	0
4	E	26	0	16	0	0
4	F	26	0	16	0	0
5	A	4	4	0	0	0
5	B	4	4	0	0	0
5	C	8	8	0	0	0
5	D	8	8	0	0	0
6	A	26	0	18	4	0
6	B	26	0	18	11	0
6	C	26	0	15	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	26	0	18	7	0
6	E	26	0	17	6	0
6	F	26	0	18	5	0
7	A	639	0	0	11	0
7	B	581	0	0	17	0
7	C	445	0	0	10	0
7	D	433	0	0	7	0
7	E	409	0	0	12	0
7	F	403	0	0	10	0
All	All	30814	24	27662	478	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 478 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:467:ILE:HG13	1:D:542:MET:HE1	1.28	1.13
1:B:467:ILE:HG13	1:B:542:MET:HE1	1.25	1.12
1:B:251:MET:SD	7:B:1129:HOH:O	2.07	1.12
1:B:251:MET:HE3	1:B:253:GLY:N	1.69	1.05
1:B:353:GLN:HG2	6:B:606:UQ1:HM21	1.39	1.05

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	592/594 (100%)	581 (98%)	11 (2%)	0	100	100
1	B	592/594 (100%)	582 (98%)	10 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	592/594 (100%)	583 (98%)	9 (2%)	0	100	100
1	D	592/594 (100%)	579 (98%)	13 (2%)	0	100	100
1	E	592/594 (100%)	583 (98%)	9 (2%)	0	100	100
1	F	592/594 (100%)	584 (99%)	8 (1%)	0	100	100
All	All	3552/3564 (100%)	3492 (98%)	60 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	475/475 (100%)	465 (98%)	10 (2%)	47	52
1	B	475/475 (100%)	464 (98%)	11 (2%)	44	49
1	C	475/475 (100%)	465 (98%)	10 (2%)	47	52
1	D	475/475 (100%)	467 (98%)	8 (2%)	53	60
1	E	475/475 (100%)	456 (96%)	19 (4%)	28	27
1	F	475/475 (100%)	460 (97%)	15 (3%)	34	35
All	All	2850/2850 (100%)	2777 (97%)	73 (3%)	40	44

5 of 73 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	585	THR
1	F	475	TYR
1	F	46	ILE
1	F	223	LEU
1	C	283	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	202	GLN
1	F	537	GLN
1	C	167	GLN
1	D	115	GLN
1	D	167	GLN

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 40 ligands modelled in this entry, 10 are monoatomic - leaving 30 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$
6	UQ1	B	607	-	13,13,18	3.62	7 (53%)	16,18,25	1.55	1 (6%)
6	UQ1	C	608	-	13,13,18	3.62	6 (46%)	16,18,25	1.45	1 (6%)
6	UQ1	E	605	-	13,13,18	3.51	8 (61%)	16,18,25	1.17	1 (6%)
6	UQ1	F	605	-	13,13,18	3.64	7 (53%)	16,18,25	1.55	1 (6%)
6	UQ1	F	606	-	13,13,18	3.45	8 (61%)	16,18,25	1.10	1 (6%)
3	FAD	D	602	-	58,58,58	0.41	0	85,89,89	0.59	1 (1%)
5	DW3	C	604	-	3,3,3	0.62	0	2,2,2	1.19	0
5	DW3	B	605	-	3,3,3	0.68	0	2,2,2	1.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	UQ1	C	607	-	13,13,18	3.46	6 (46%)	16,18,25	1.16	1 (6%)
6	UQ1	D	607	-	13,13,18	3.58	7 (53%)	16,18,25	1.61	1 (6%)
4	TPP	F	604	2	26,27,27	0.58	0	38,40,40	0.53	0
4	TPP	C	603	2	26,27,27	0.52	0	38,40,40	0.53	0
5	DW3	D	605	-	3,3,3	0.62	0	2,2,2	1.25	0
6	UQ1	A	606	-	13,13,18	3.52	6 (46%)	16,18,25	1.16	1 (6%)
4	TPP	A	604	2	26,27,27	0.55	0	38,40,40	0.53	0
6	UQ1	A	607	-	13,13,18	3.65	5 (38%)	16,18,25	1.61	1 (6%)
6	UQ1	E	604	-	13,13,18	3.60	7 (53%)	16,18,25	1.33	1 (6%)
6	UQ1	D	606	-	13,13,18	3.54	5 (38%)	16,18,25	1.14	0
3	FAD	F	603	-	58,58,58	0.46	0	85,89,89	0.59	1 (1%)
3	FAD	E	602	-	58,58,58	0.47	1 (1%)	85,89,89	0.58	0
4	TPP	D	603	2	26,27,27	0.58	0	38,40,40	0.52	0
5	DW3	D	604	-	3,3,3	0.65	0	2,2,2	1.02	0
3	FAD	C	602	-	58,58,58	0.38	0	85,89,89	0.62	2 (2%)
6	UQ1	B	606	-	13,13,18	3.44	5 (38%)	16,18,25	1.38	2 (12%)
5	DW3	A	605	-	3,3,3	0.68	0	2,2,2	1.12	0
4	TPP	E	603	2	26,27,27	0.65	1 (3%)	38,40,40	0.52	0
5	DW3	C	605	-	3,3,3	0.64	0	2,2,2	1.25	0
3	FAD	B	603	-	58,58,58	0.57	1 (1%)	85,89,89	0.66	1 (1%)
3	FAD	A	603	-	58,58,58	0.49	1 (1%)	85,89,89	0.68	2 (2%)
4	TPP	B	604	2	26,27,27	0.46	0	38,40,40	0.56	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	UQ1	B	607	-	-	1/4/24/33	0/1/1/1
6	UQ1	C	608	-	-	1/4/24/33	0/1/1/1
6	UQ1	E	605	-	-	1/4/24/33	0/1/1/1
6	UQ1	F	605	-	-	0/4/24/33	0/1/1/1
6	UQ1	F	606	-	-	1/4/24/33	0/1/1/1
3	FAD	D	602	-	-	7/34/50/50	0/6/6/6
5	DW3	C	604	-	-	0/0/1/1	-
5	DW3	B	605	-	-	0/0/1/1	-
6	UQ1	C	607	-	-	0/4/24/33	0/1/1/1
6	UQ1	D	607	-	-	0/4/24/33	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	TPP	F	604	2	-	1/17/17/17	0/2/2/2
4	TPP	C	603	2	-	1/17/17/17	0/2/2/2
5	DW3	D	605	-	-	0/0/1/1	-
6	UQ1	A	606	-	-	2/4/24/33	0/1/1/1
4	TPP	A	604	2	-	1/17/17/17	0/2/2/2
6	UQ1	A	607	-	-	1/4/24/33	0/1/1/1
6	UQ1	E	604	-	-	0/4/24/33	0/1/1/1
6	UQ1	D	606	-	-	0/4/24/33	0/1/1/1
3	FAD	F	603	-	-	9/34/50/50	0/6/6/6
3	FAD	E	602	-	-	12/34/50/50	0/6/6/6
4	TPP	D	603	2	-	2/17/17/17	0/2/2/2
5	DW3	D	604	-	-	0/0/1/1	-
3	FAD	C	602	-	-	8/34/50/50	0/6/6/6
6	UQ1	B	606	-	-	1/4/24/33	0/1/1/1
5	DW3	A	605	-	-	0/0/1/1	-
4	TPP	E	603	2	-	3/17/17/17	0/2/2/2
5	DW3	C	605	-	-	0/0/1/1	-
3	FAD	B	603	-	-	7/34/50/50	0/6/6/6
3	FAD	A	603	-	-	7/34/50/50	0/6/6/6
4	TPP	B	604	2	-	2/17/17/17	0/2/2/2

The worst 5 of 81 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	606	UQ1	C6-C5	9.24	1.53	1.35
6	A	607	UQ1	C6-C5	9.11	1.53	1.35
6	E	604	UQ1	C6-C5	9.02	1.53	1.35
6	A	606	UQ1	C6-C5	9.02	1.53	1.35
6	F	606	UQ1	C6-C5	9.01	1.53	1.35

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	607	UQ1	CM5-C5-C4	5.54	121.22	117.41
6	F	605	UQ1	CM5-C5-C4	5.20	120.98	117.41
6	B	607	UQ1	CM5-C5-C4	5.15	120.95	117.41
6	D	607	UQ1	CM5-C5-C4	5.15	120.95	117.41
6	C	608	UQ1	CM5-C5-C4	4.85	120.75	117.41

There are no chirality outliers.

5 of 68 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	603	FAD	C5B-O5B-PA-O1A
3	A	603	FAD	C5B-O5B-PA-O3P
3	B	603	FAD	C5B-O5B-PA-O1A
3	B	603	FAD	C5B-O5B-PA-O3P
3	C	602	FAD	C5B-O5B-PA-O1A

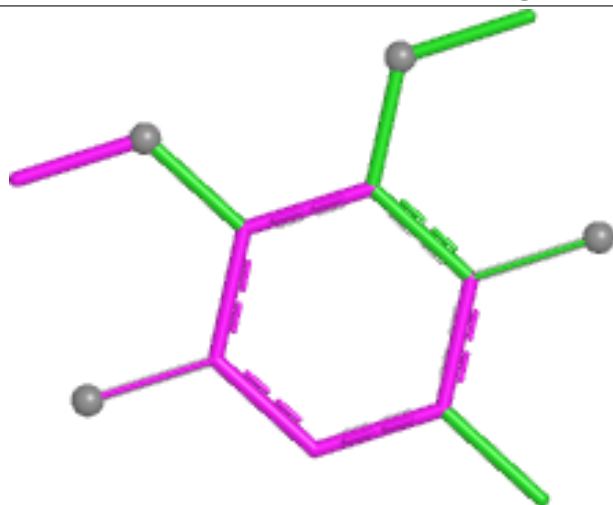
There are no ring outliers.

19 monomers are involved in 61 short contacts:

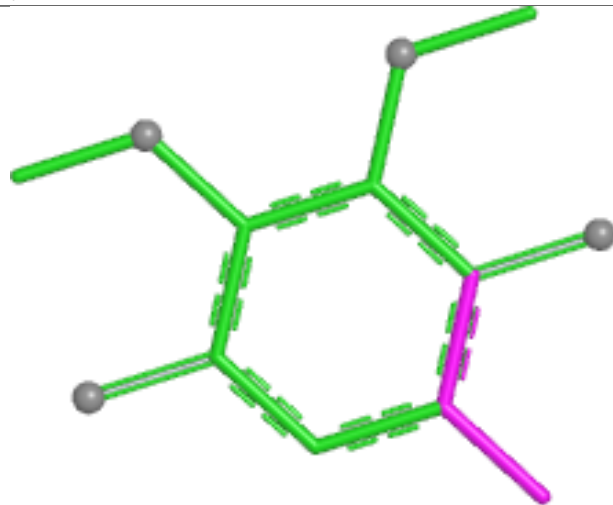
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	607	UQ1	8	0
6	C	608	UQ1	4	0
6	E	605	UQ1	1	0
6	F	605	UQ1	4	0
6	F	606	UQ1	1	0
3	D	602	FAD	5	0
6	C	607	UQ1	1	0
6	D	607	UQ1	3	0
6	A	606	UQ1	2	0
6	A	607	UQ1	2	0
6	E	604	UQ1	5	0
6	D	606	UQ1	4	0
3	F	603	FAD	6	0
3	E	602	FAD	6	0
4	D	603	TPP	1	0
3	C	602	FAD	3	0
6	B	606	UQ1	3	0
3	B	603	FAD	1	0
3	A	603	FAD	1	0

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

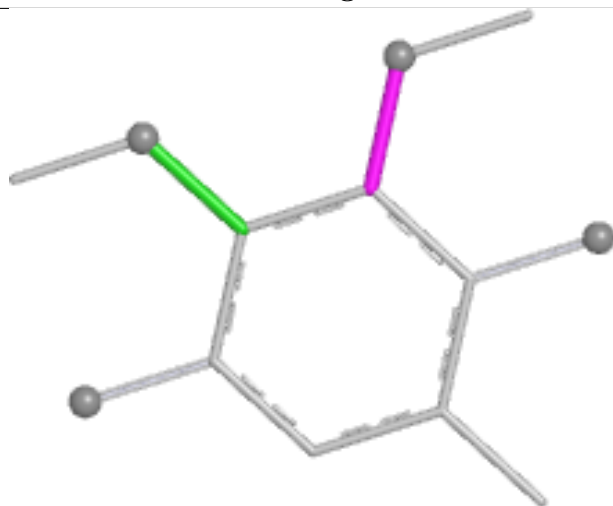
Ligand UQ1 B 607



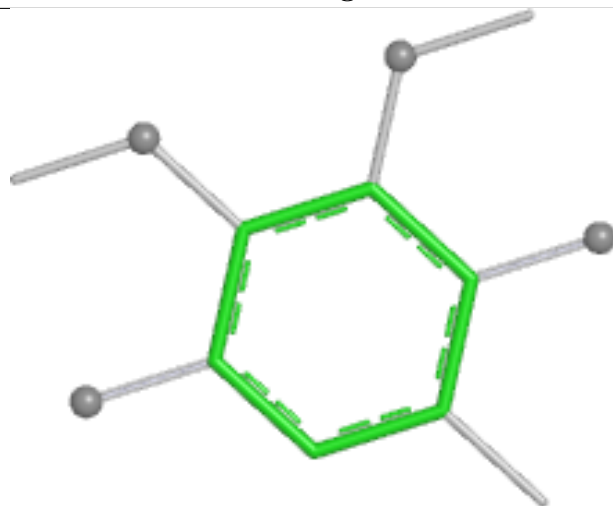
Bond lengths



Bond angles

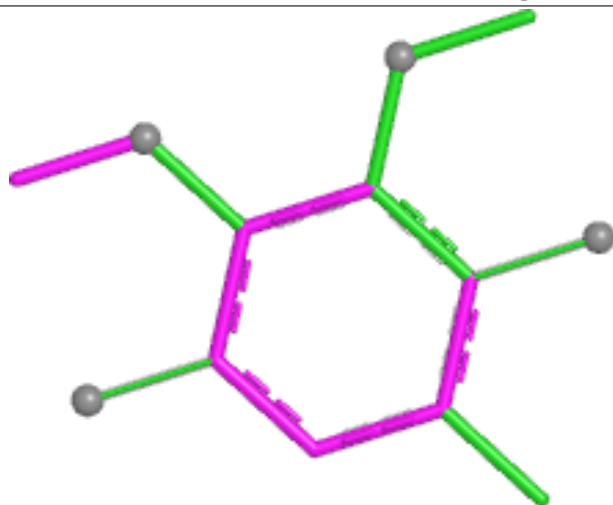


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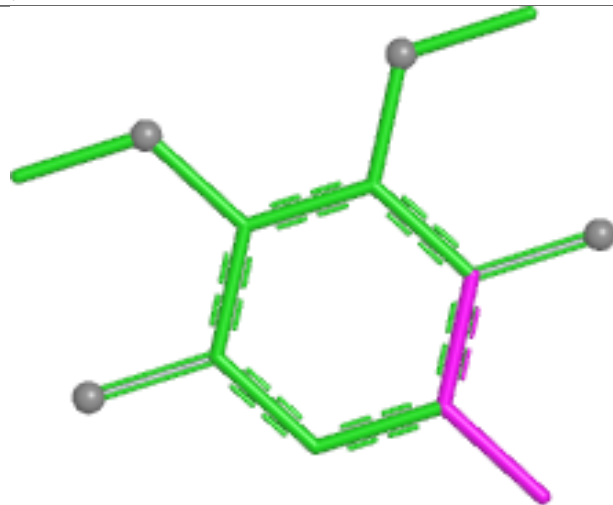


Rings

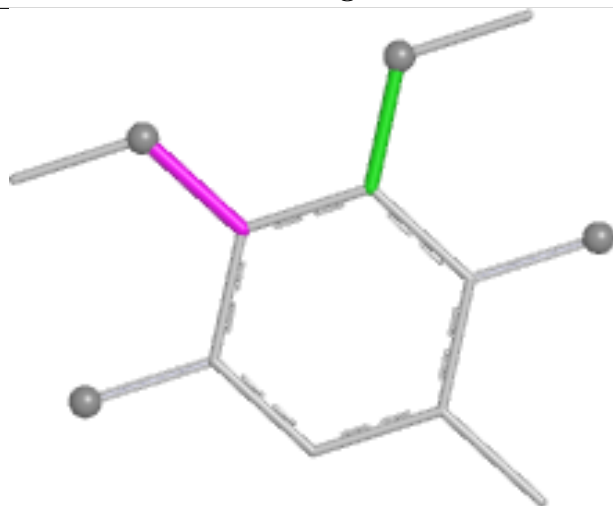
Ligand UQ1 C 608



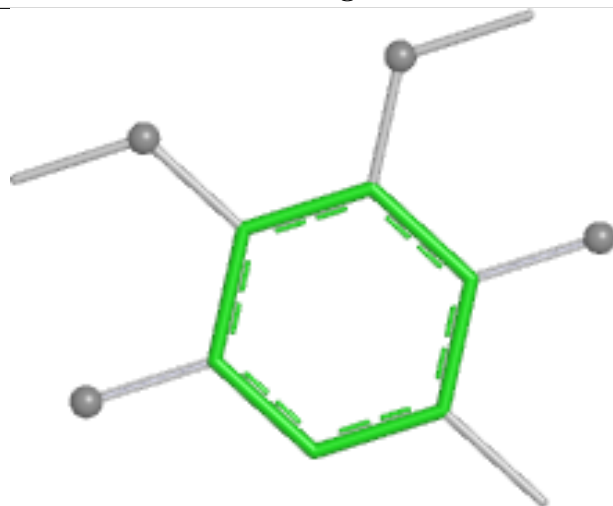
Bond lengths



Bond angles

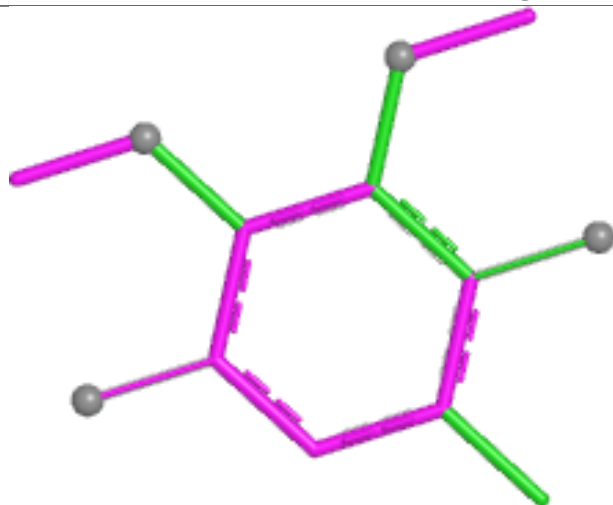


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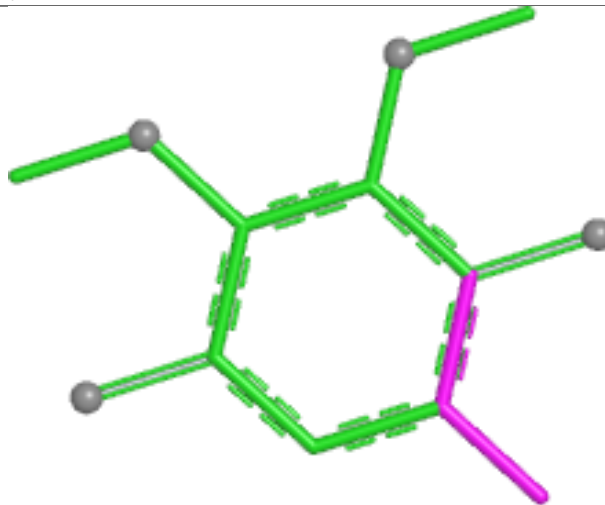


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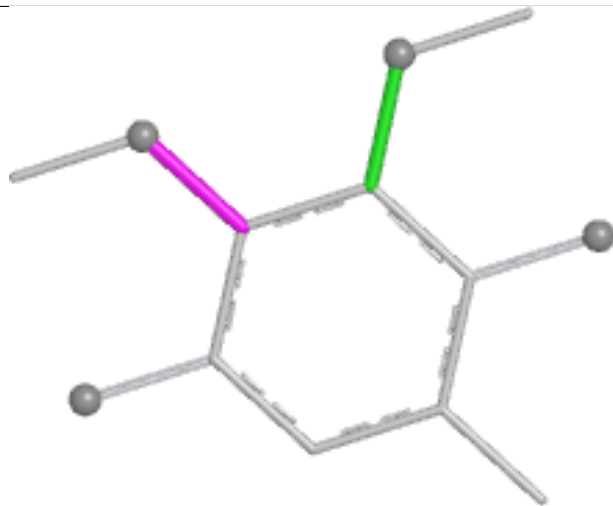
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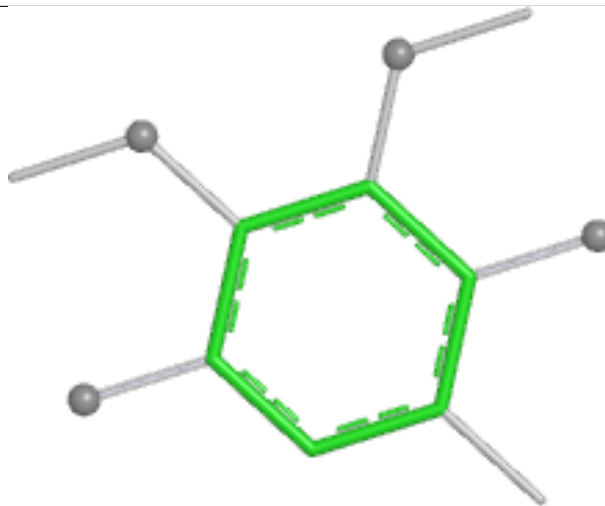
Bond lengths



Bond angles

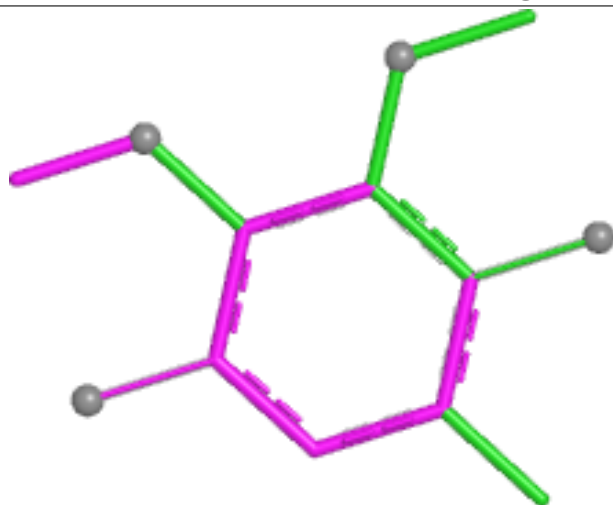


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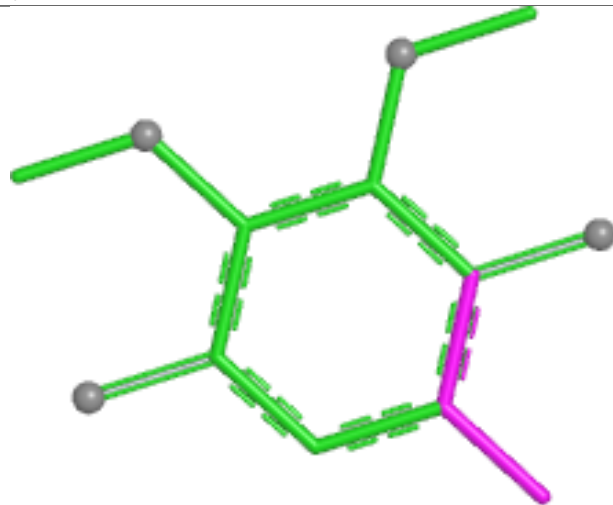


Rings

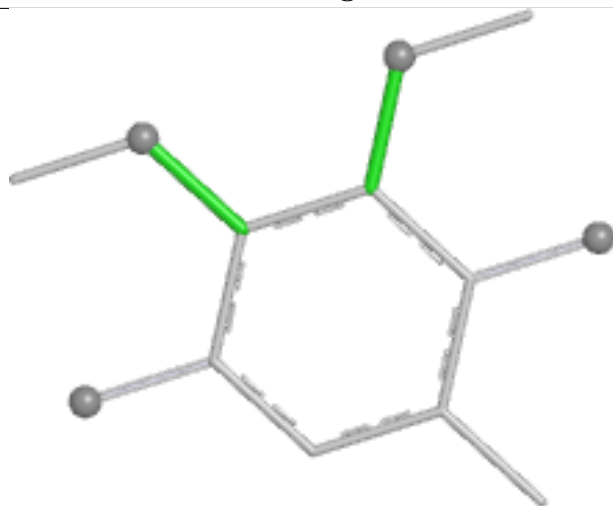
Ligand UQ1 F 605



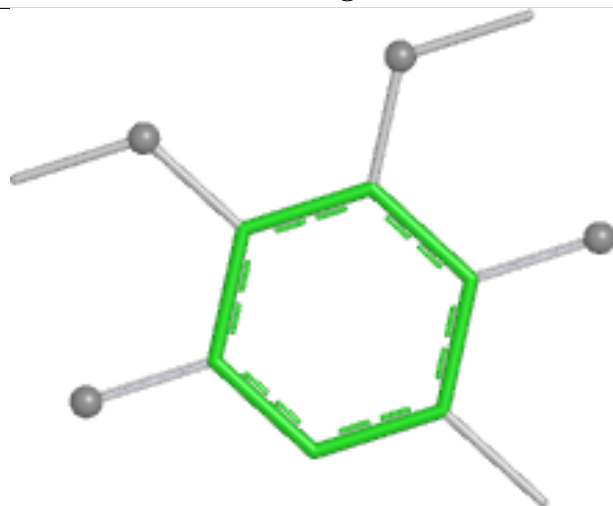
Bond lengths



Bond angles

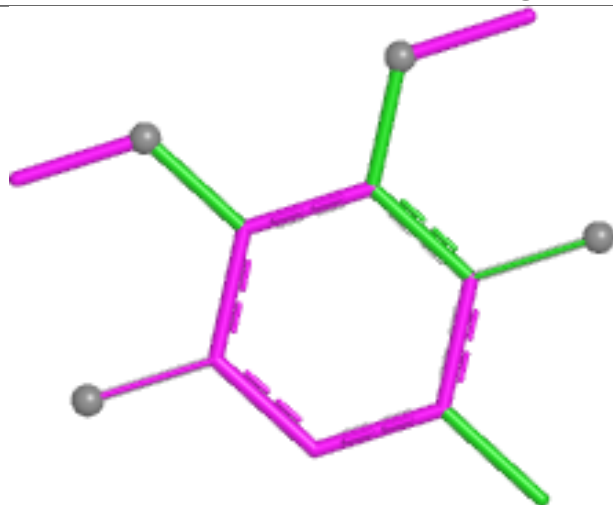


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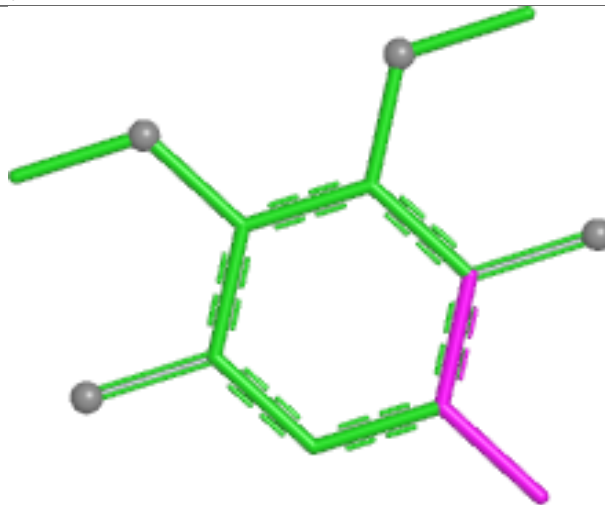


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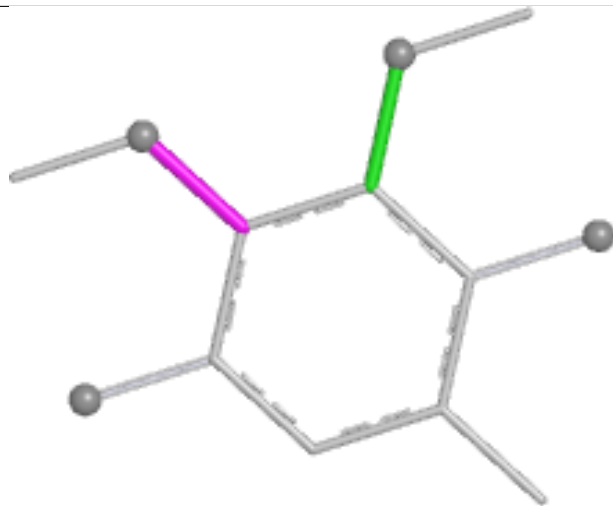
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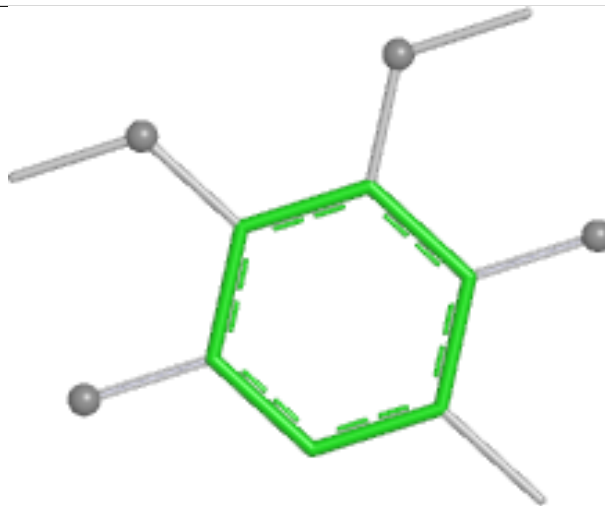
Bond lengths



Bond angles

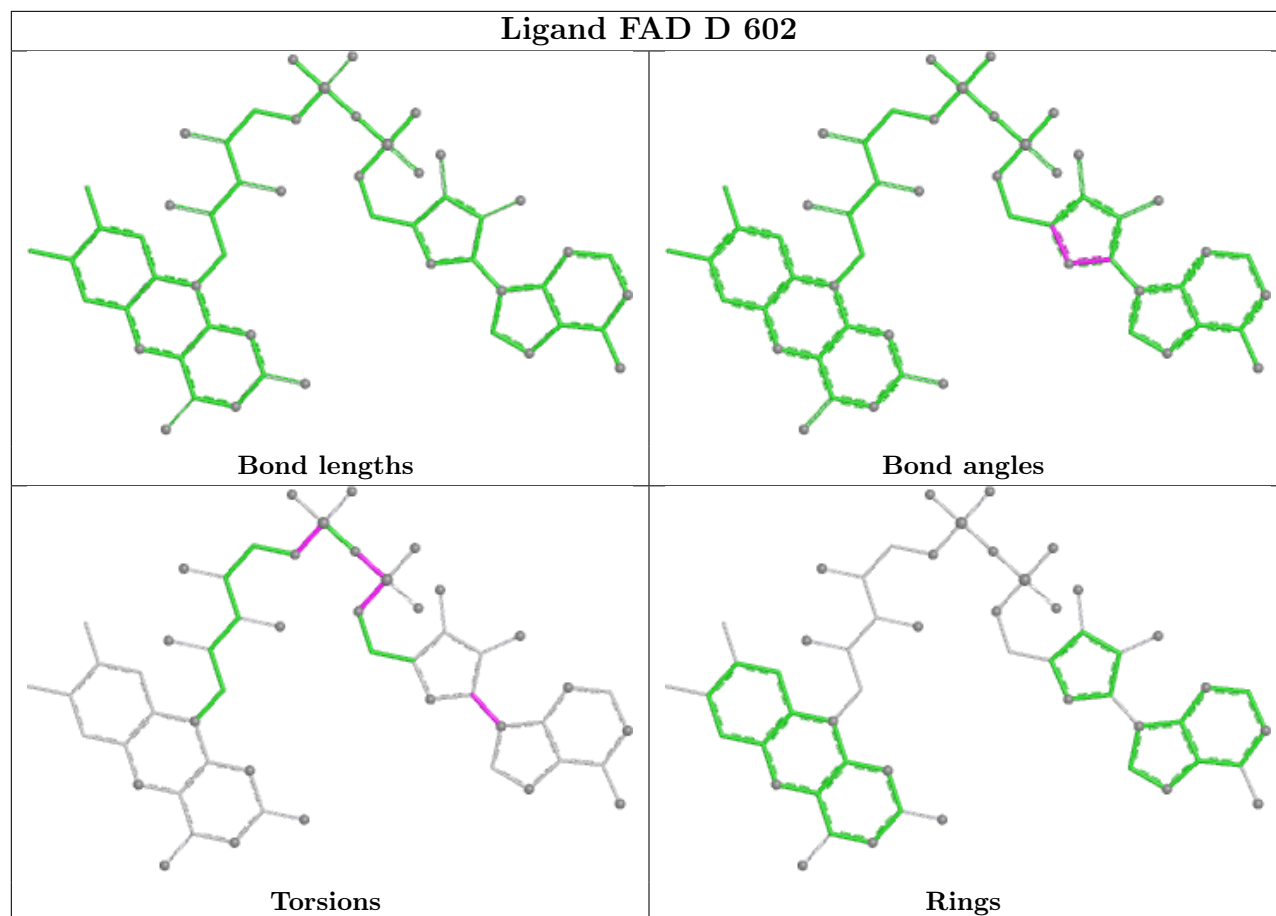


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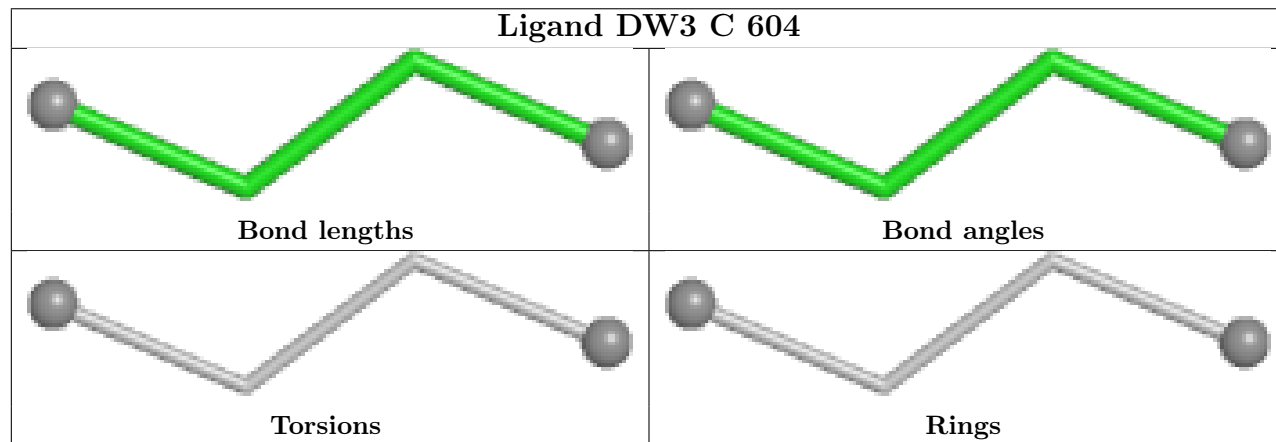


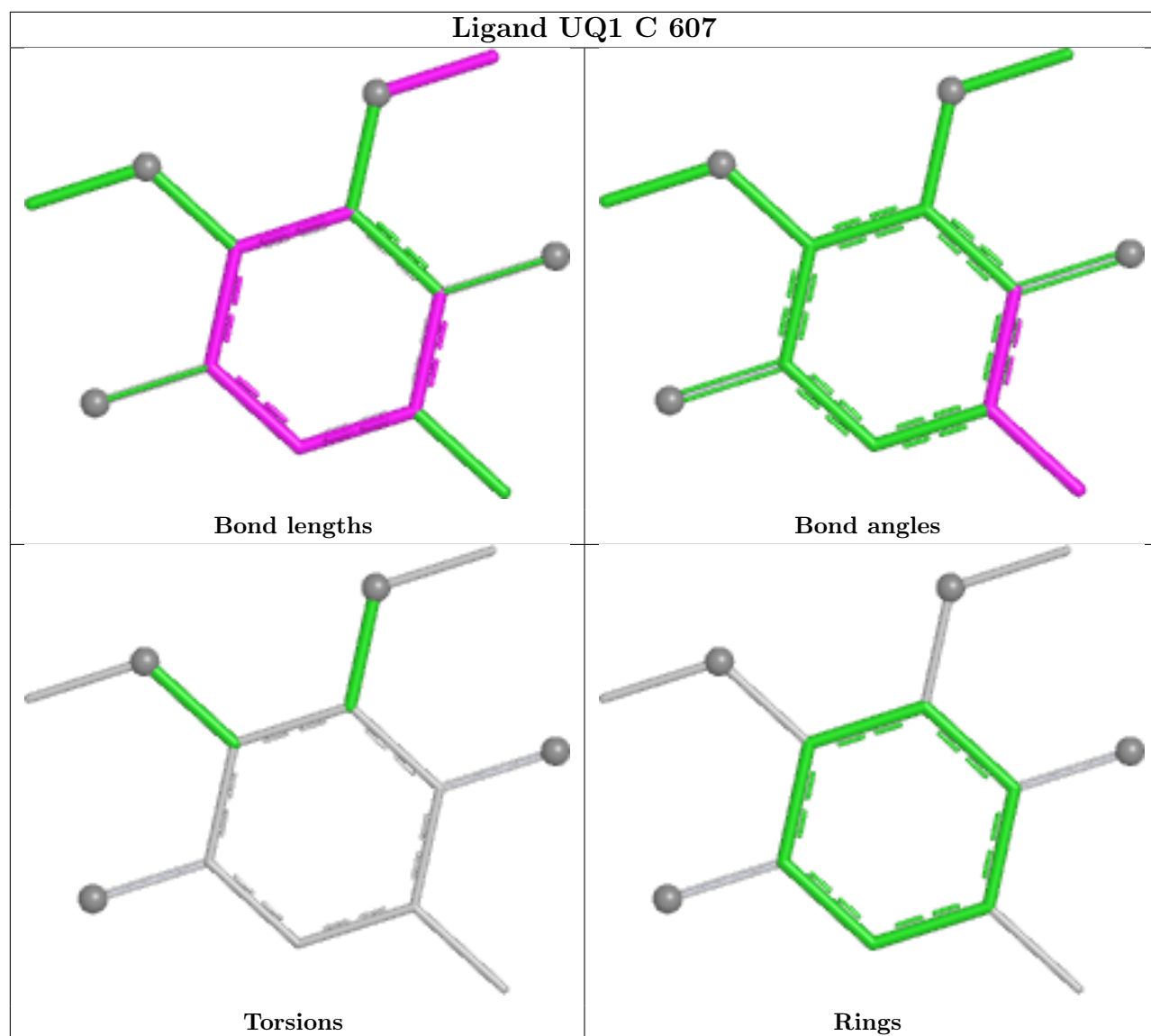
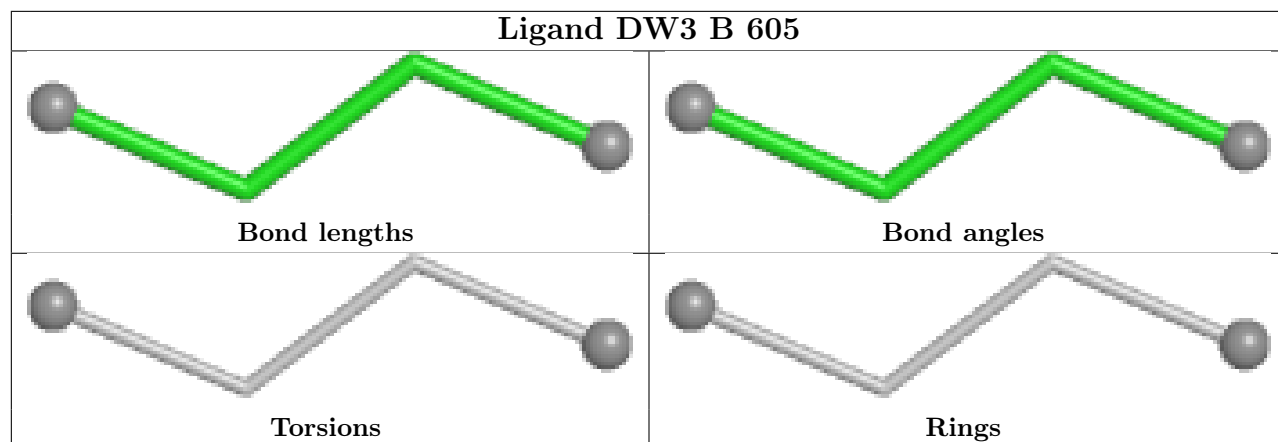
Rings

Ligand FAD D 602

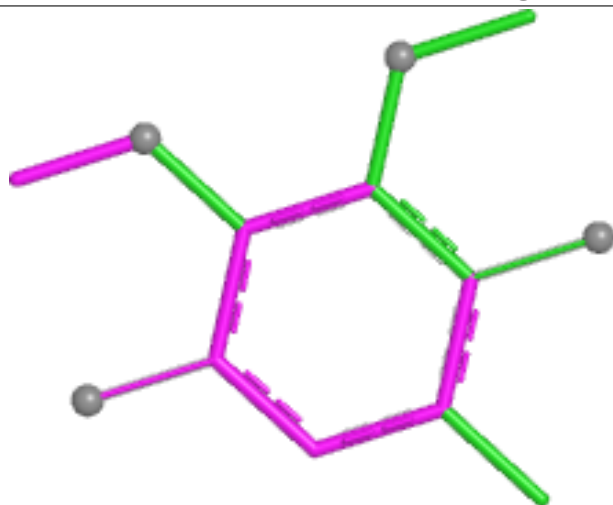


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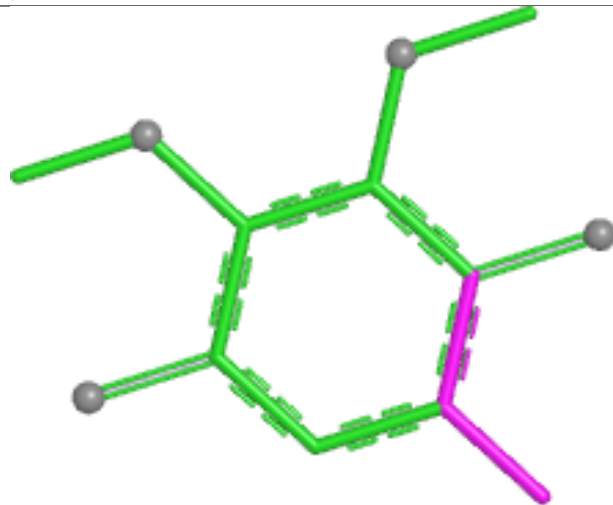




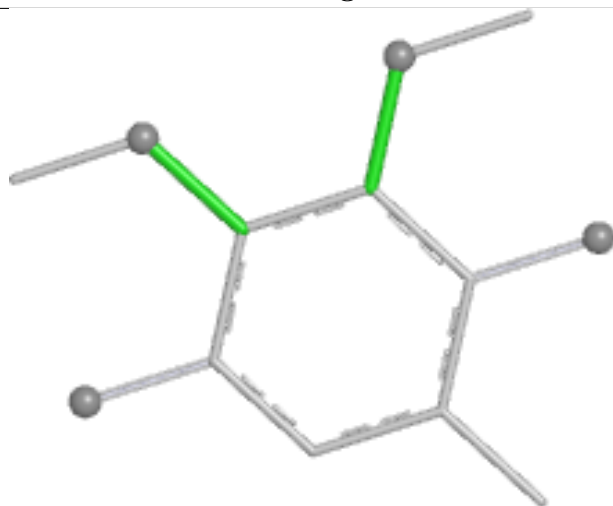
Ligand UQ1 D 607



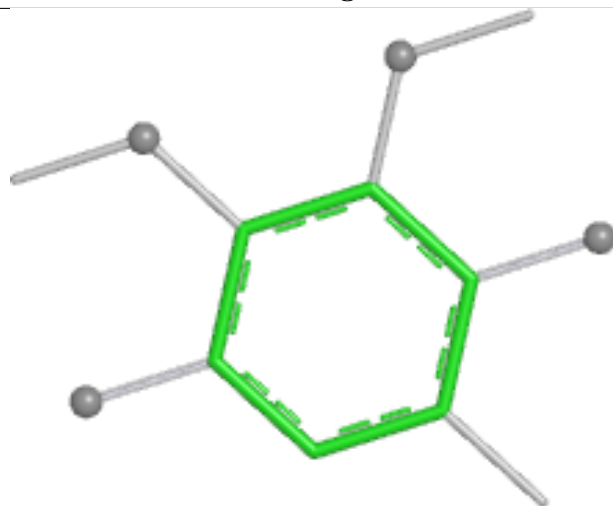
Bond lengths



Bond angles

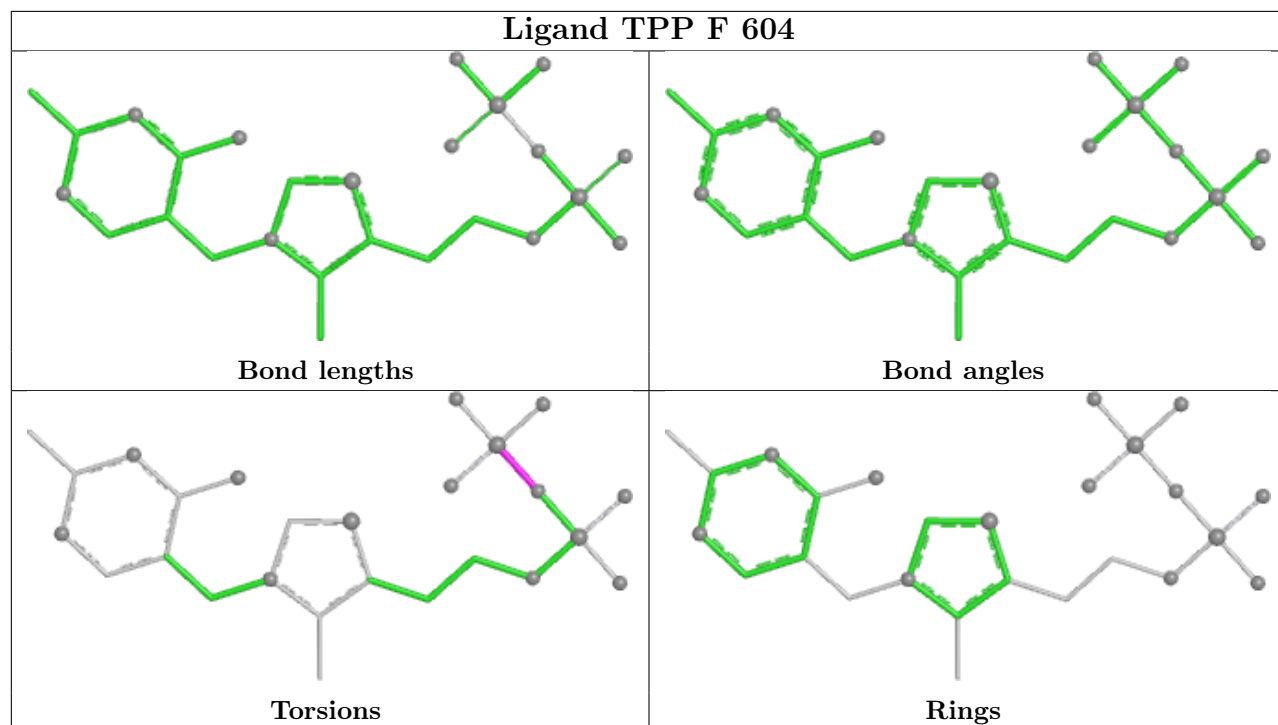


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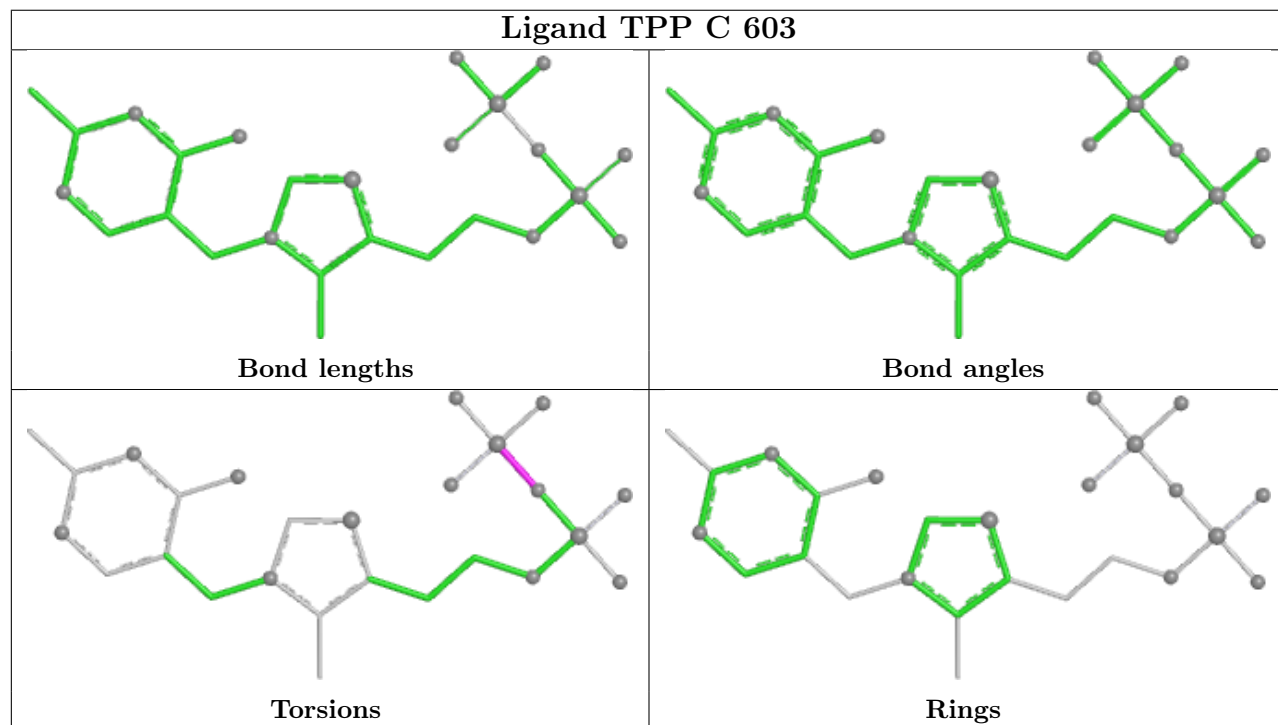


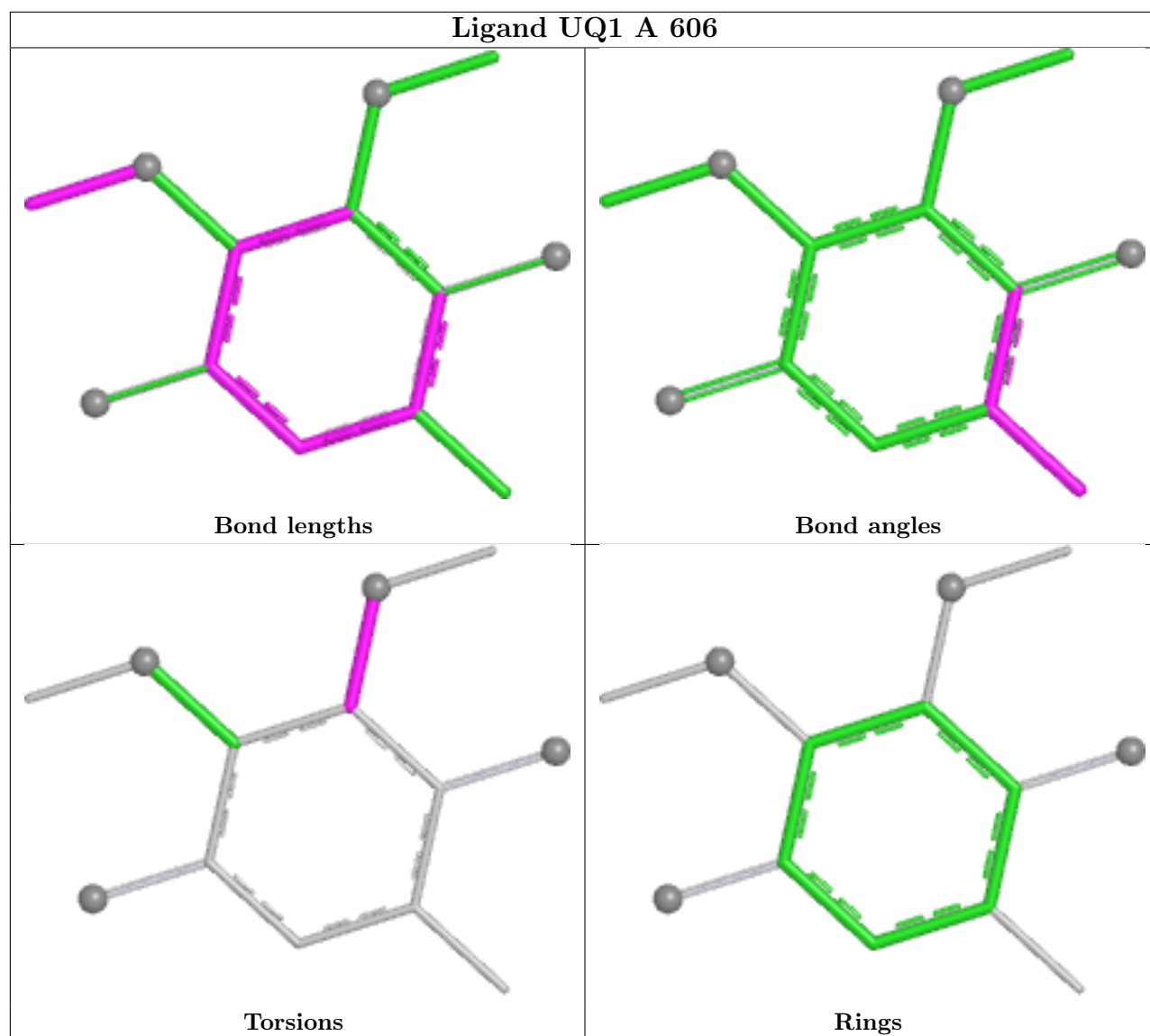
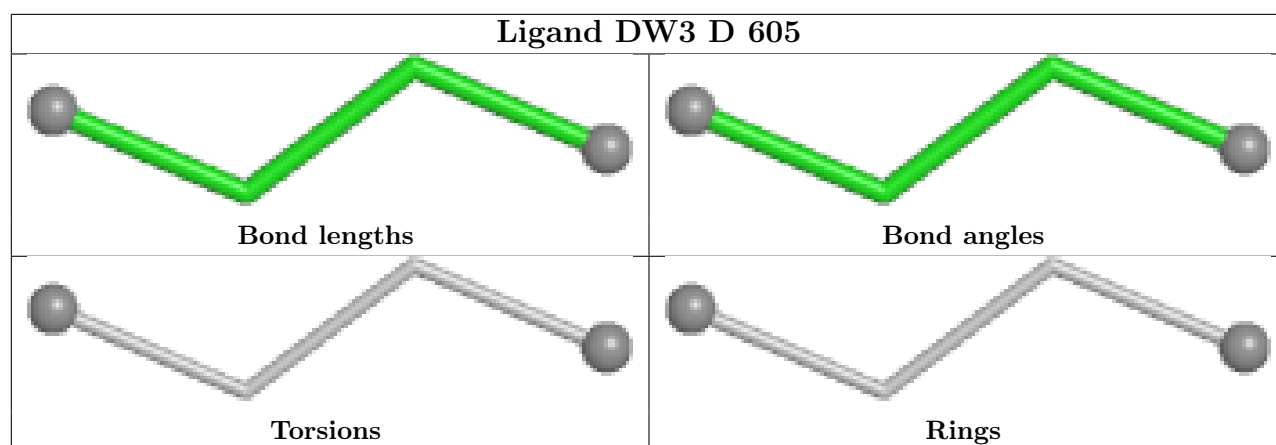
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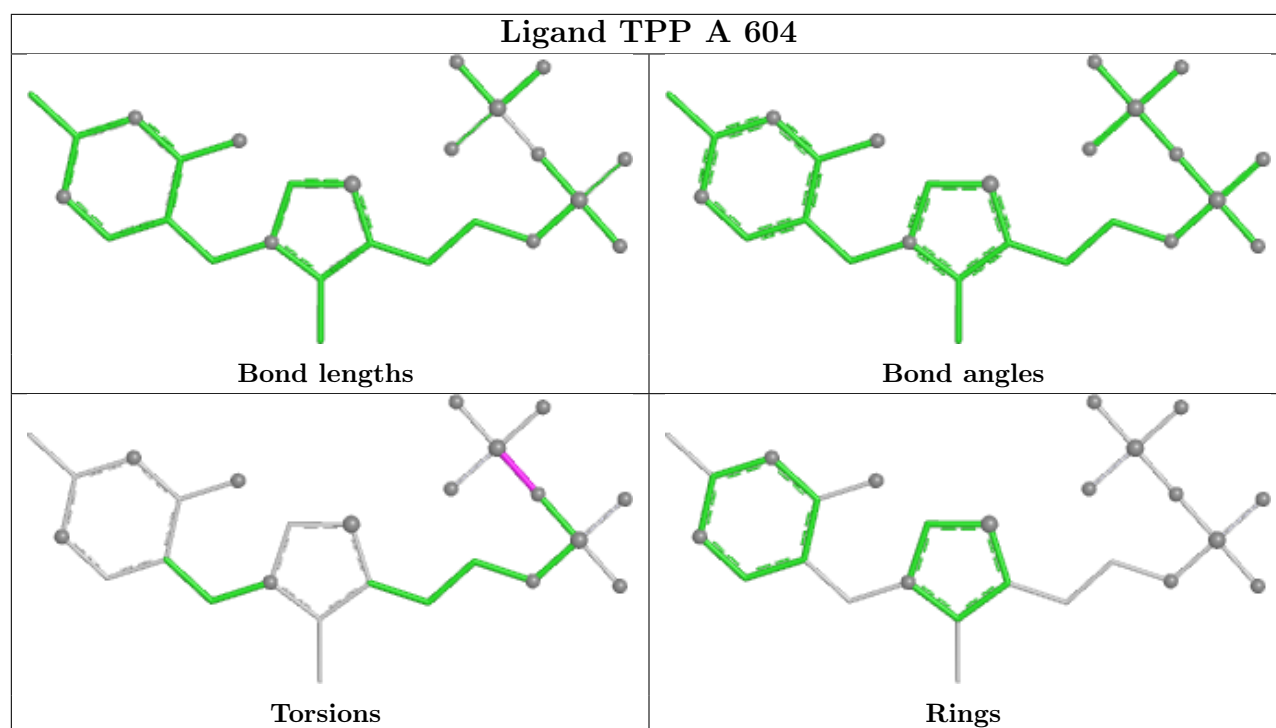
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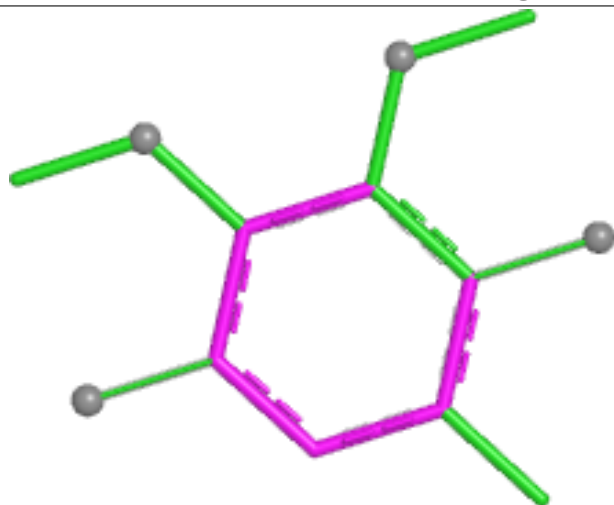
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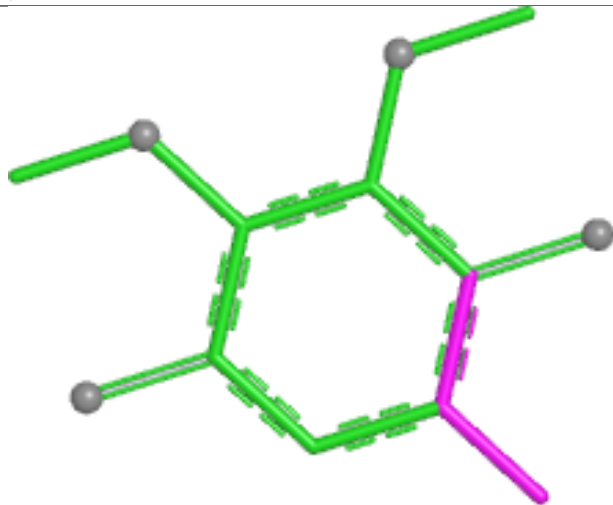




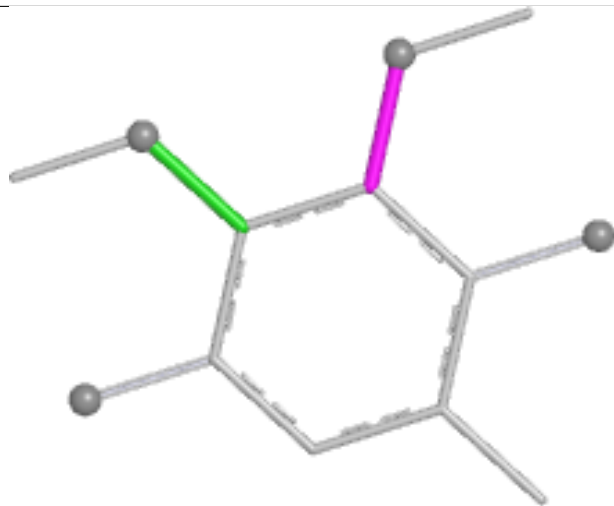
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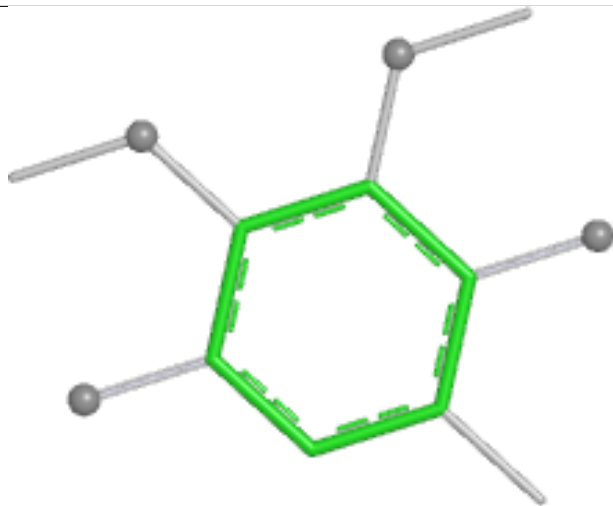
Bond lengths



Bond angles

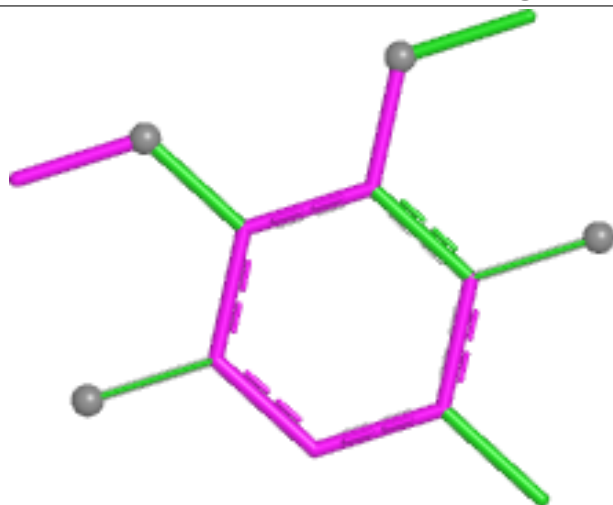


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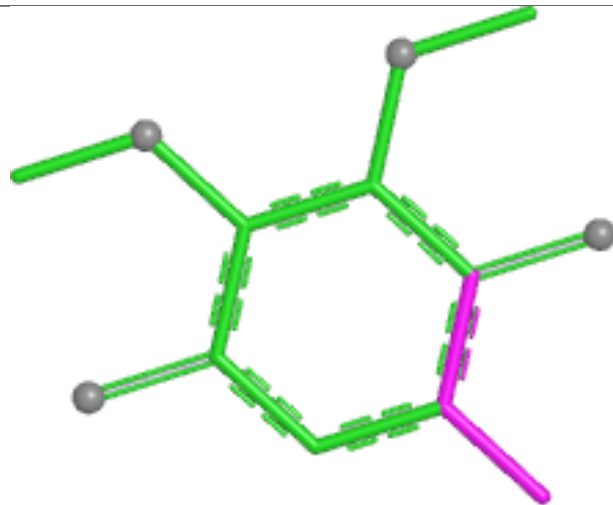


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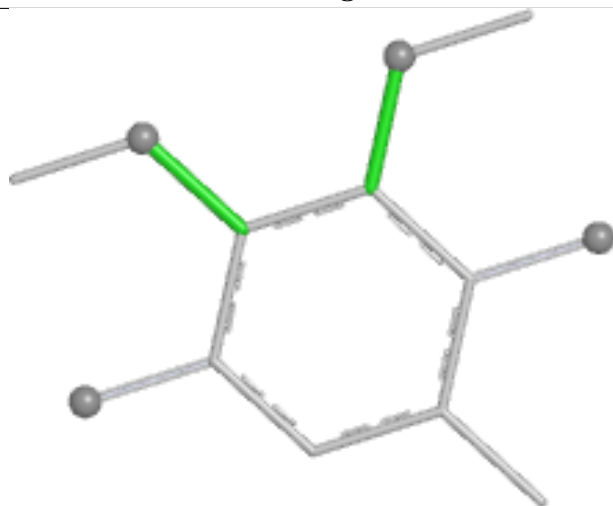
Ligand UQ1 E 604



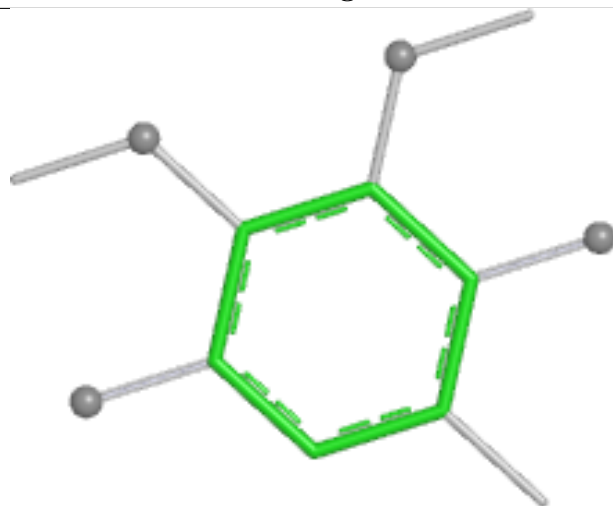
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Bond angles

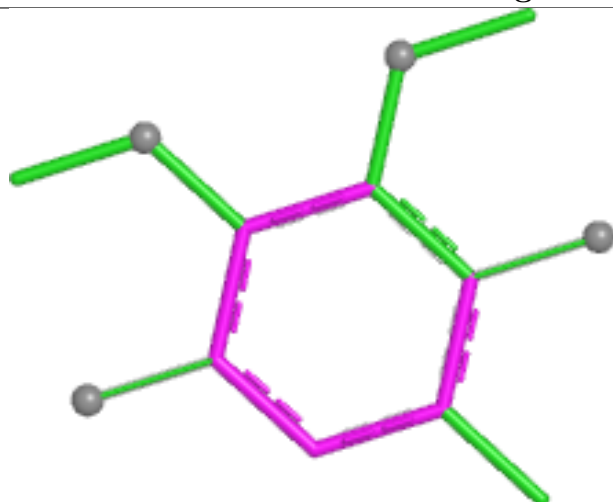


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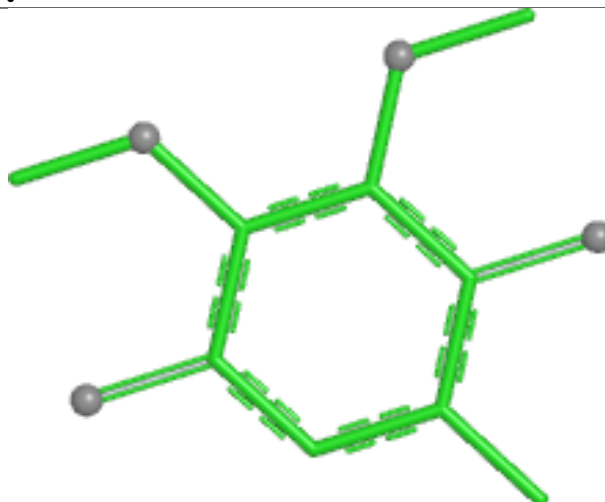


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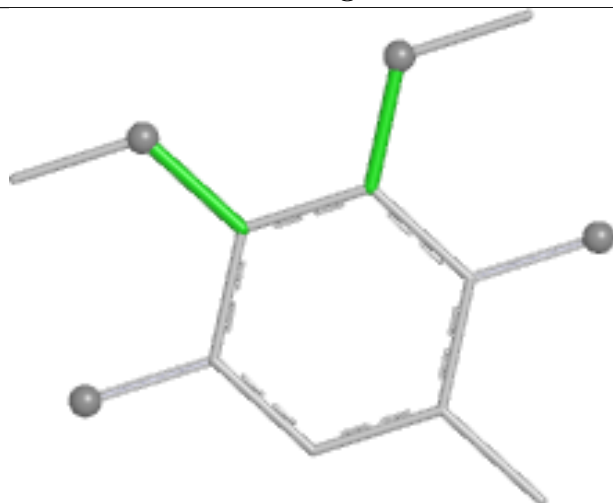
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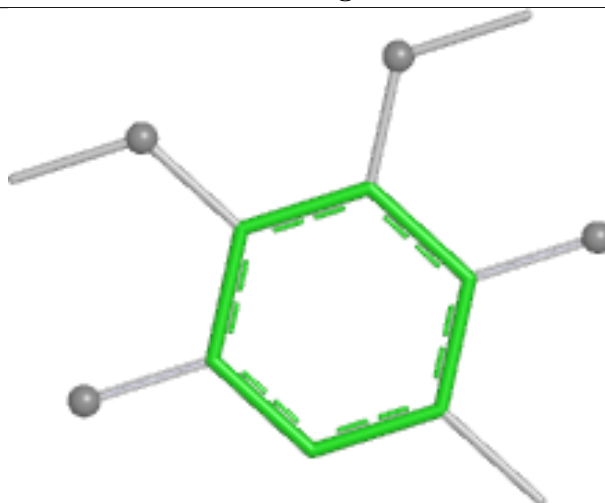
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Bond angles

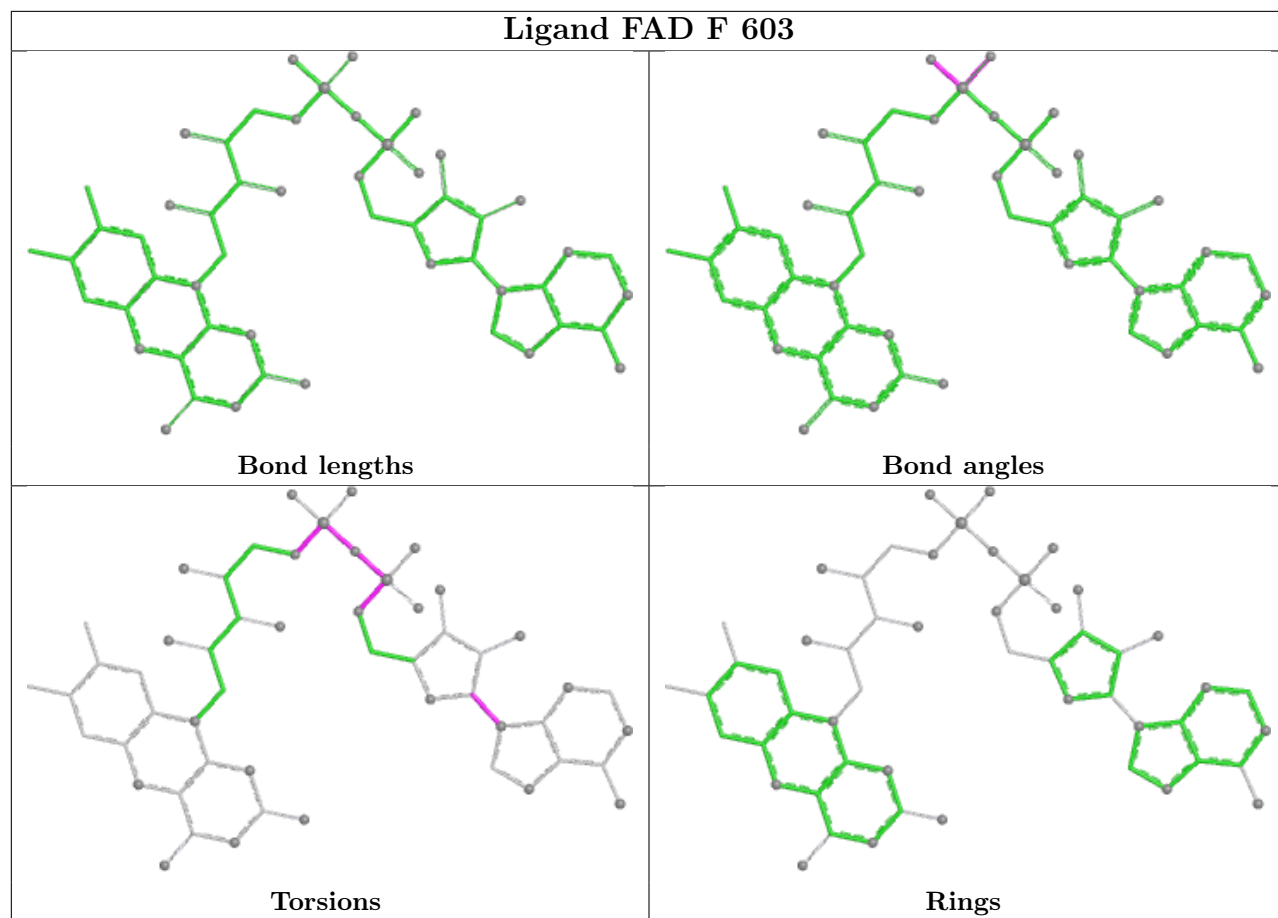


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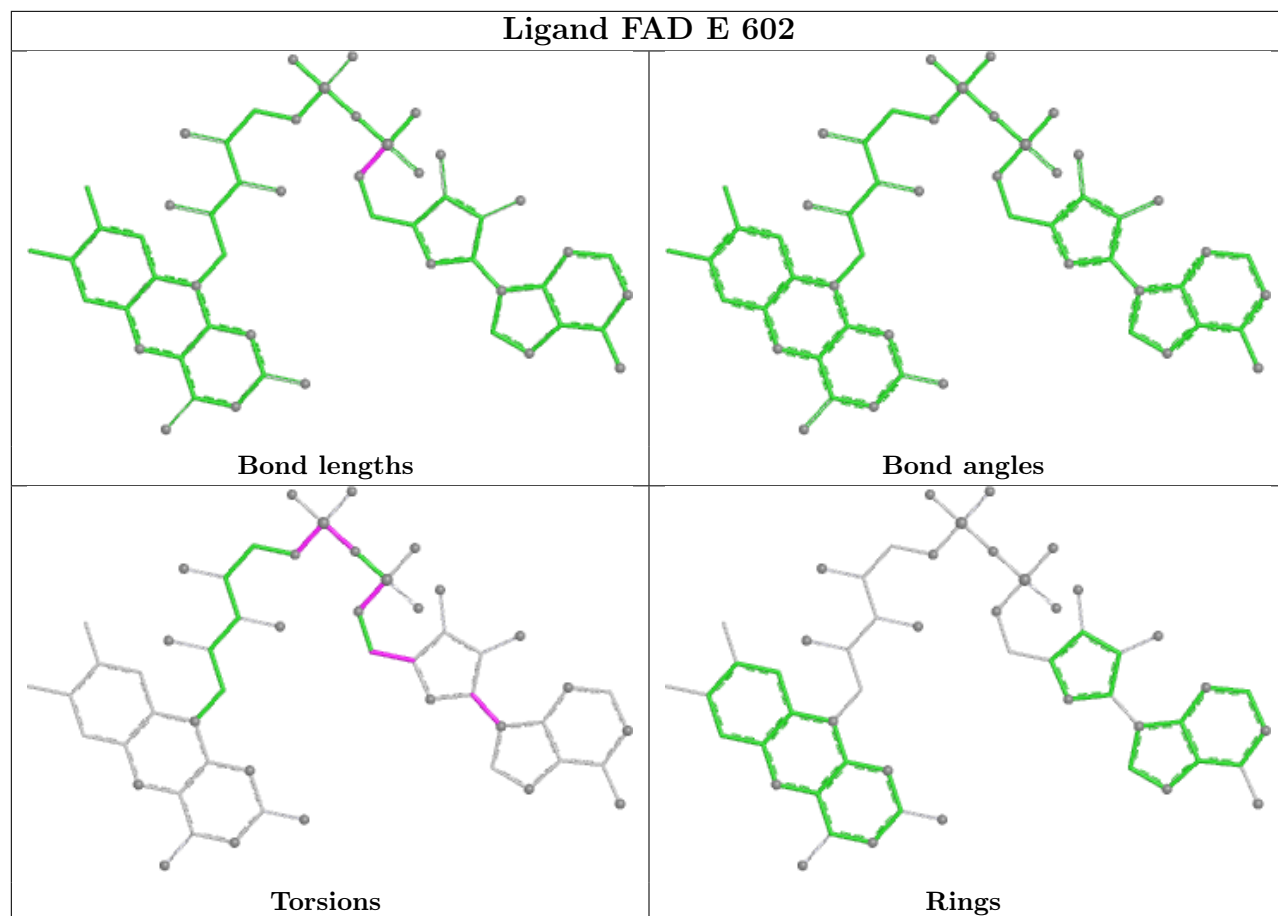


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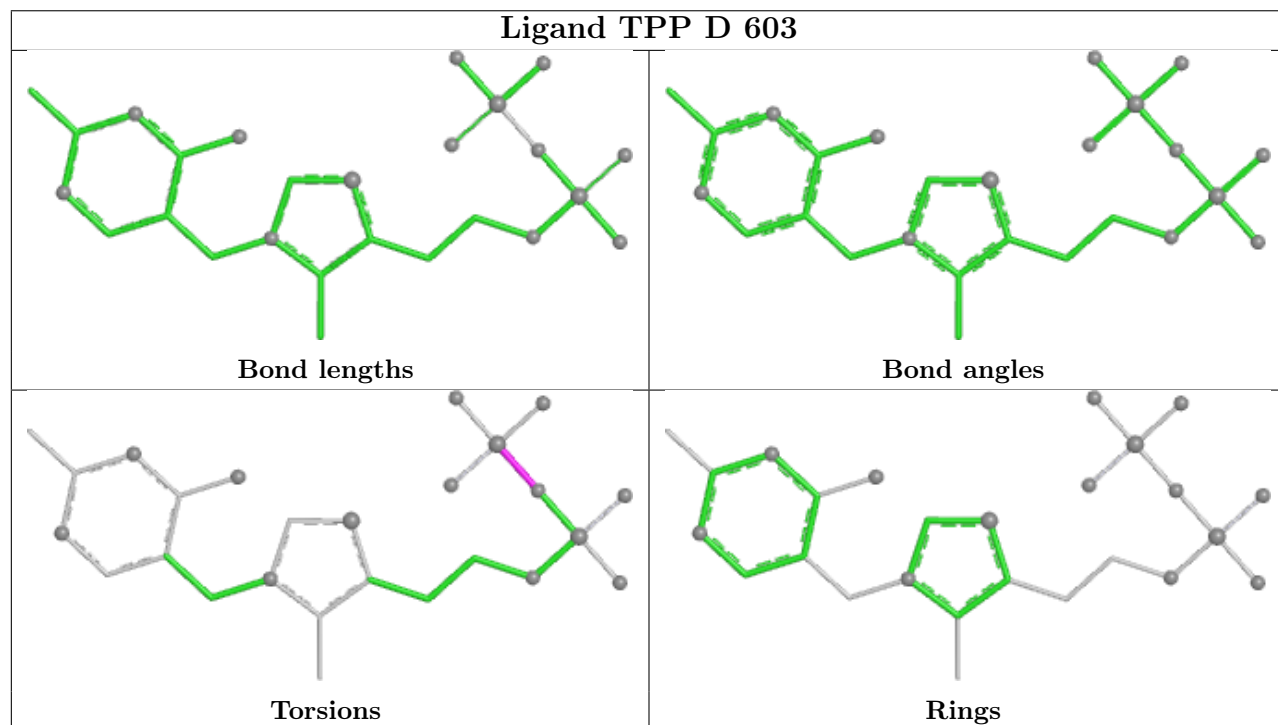
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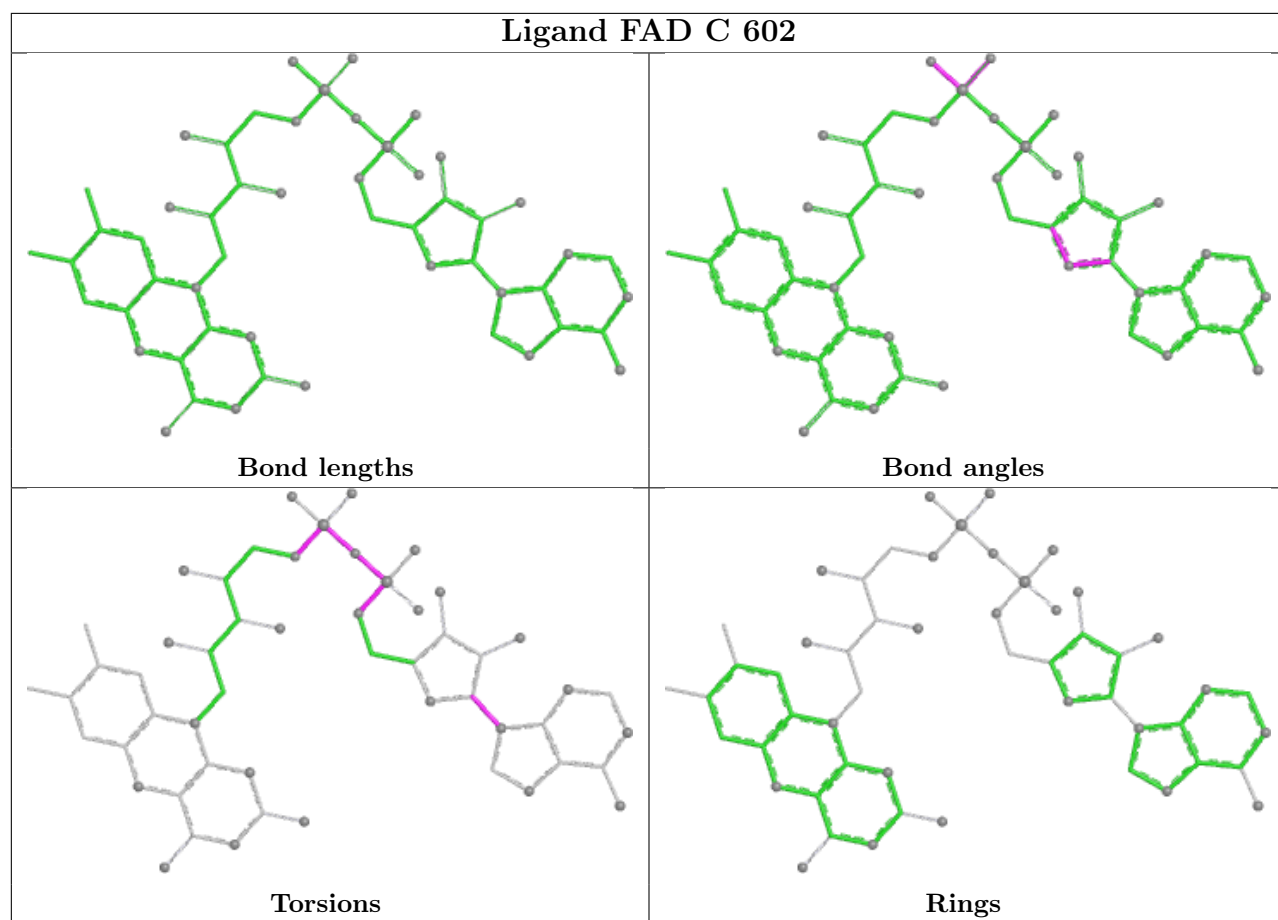
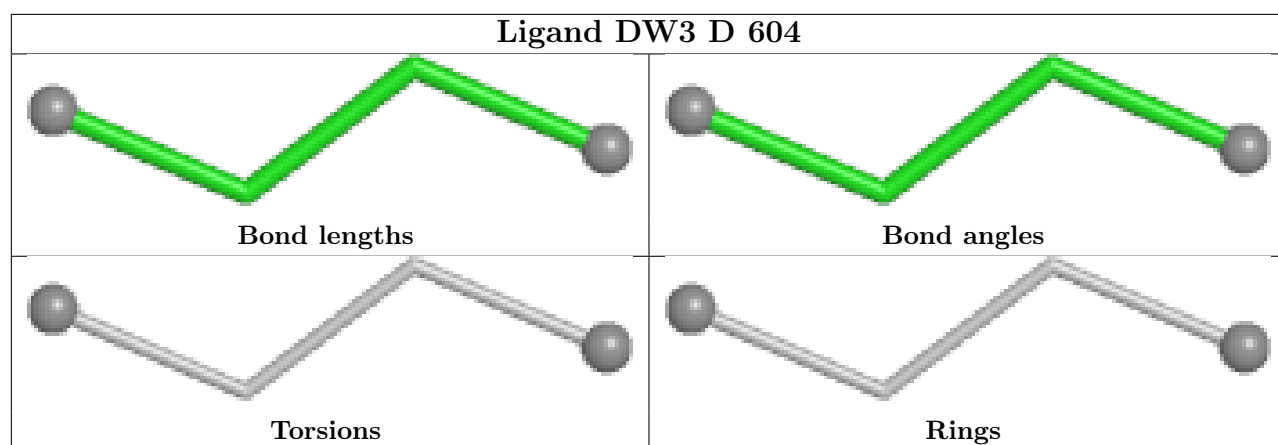


Ligand FAD E 602

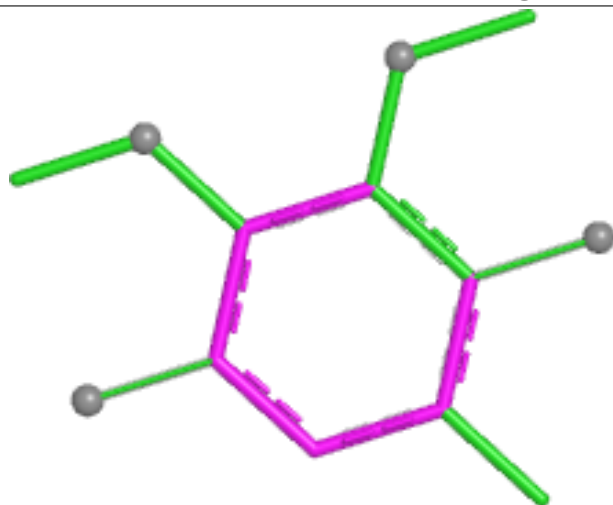


Ligand TPP D 603

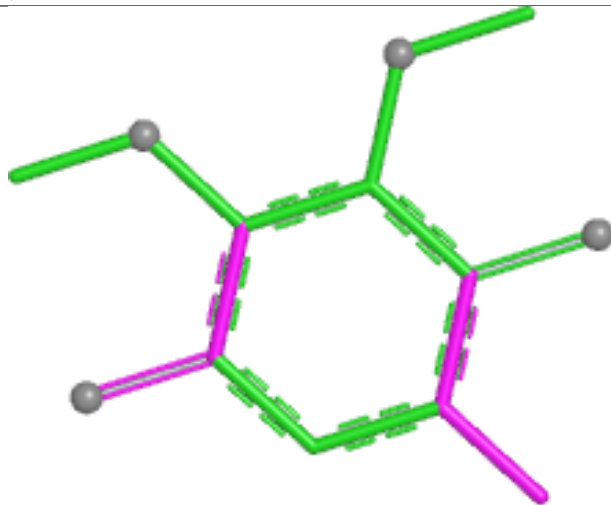




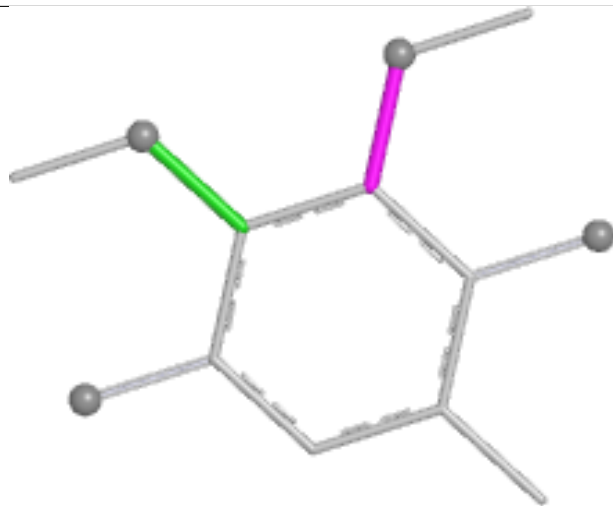
Ligand UQ1 B 606



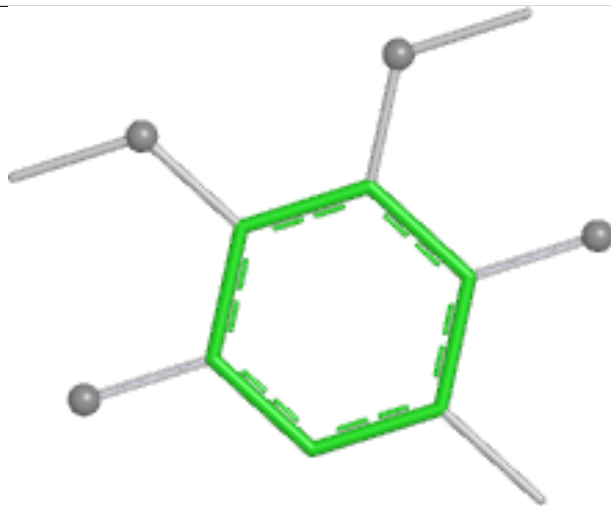
Bond lengths



Bond angles

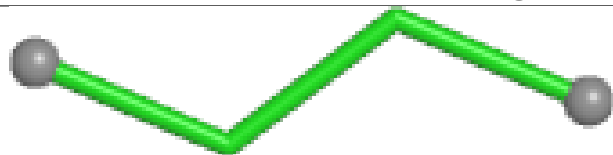


Torsions

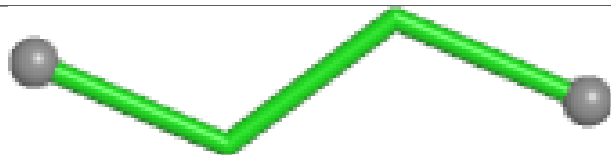


Rings

Ligand DW3 A 605



Bond lengths



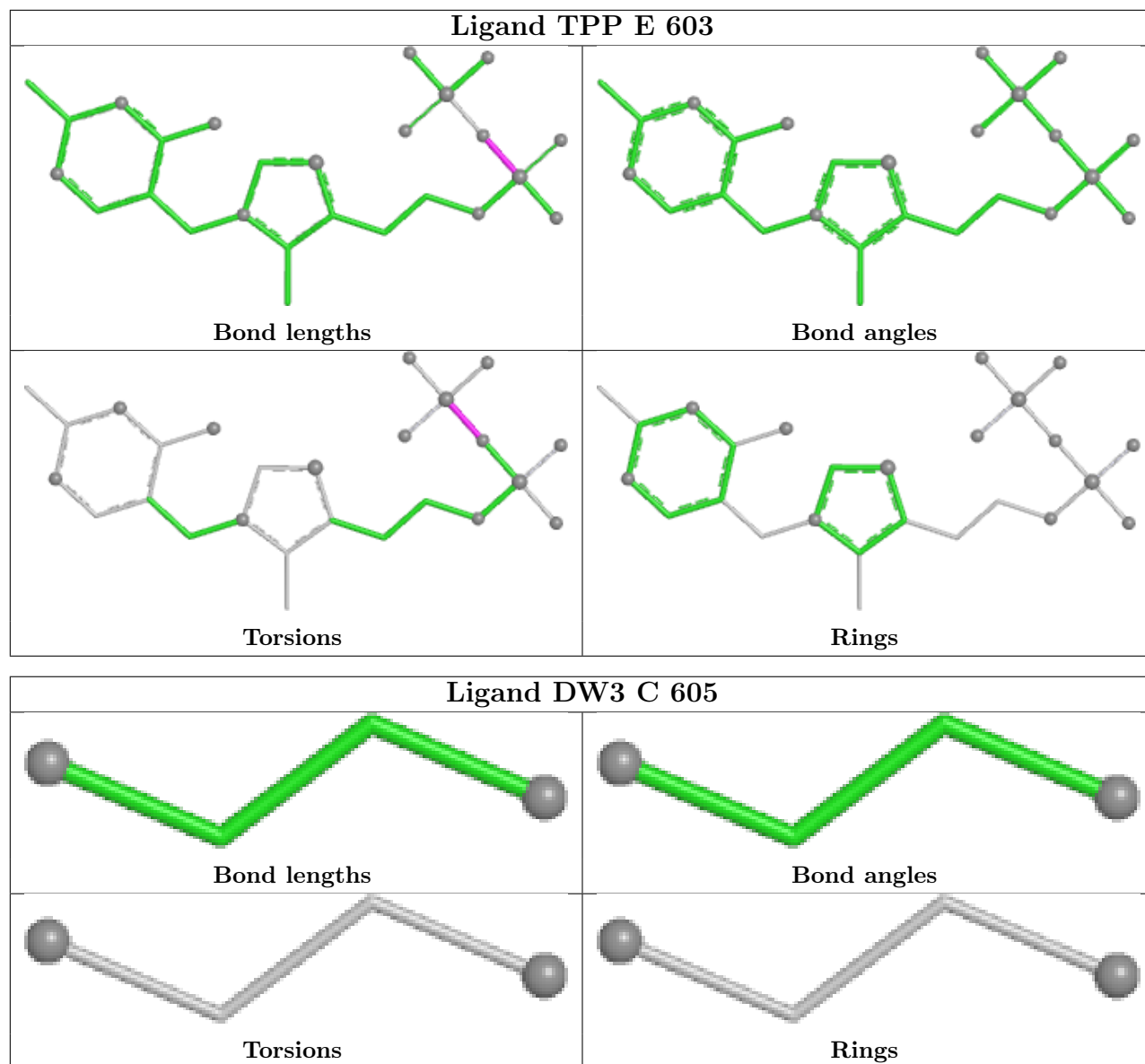
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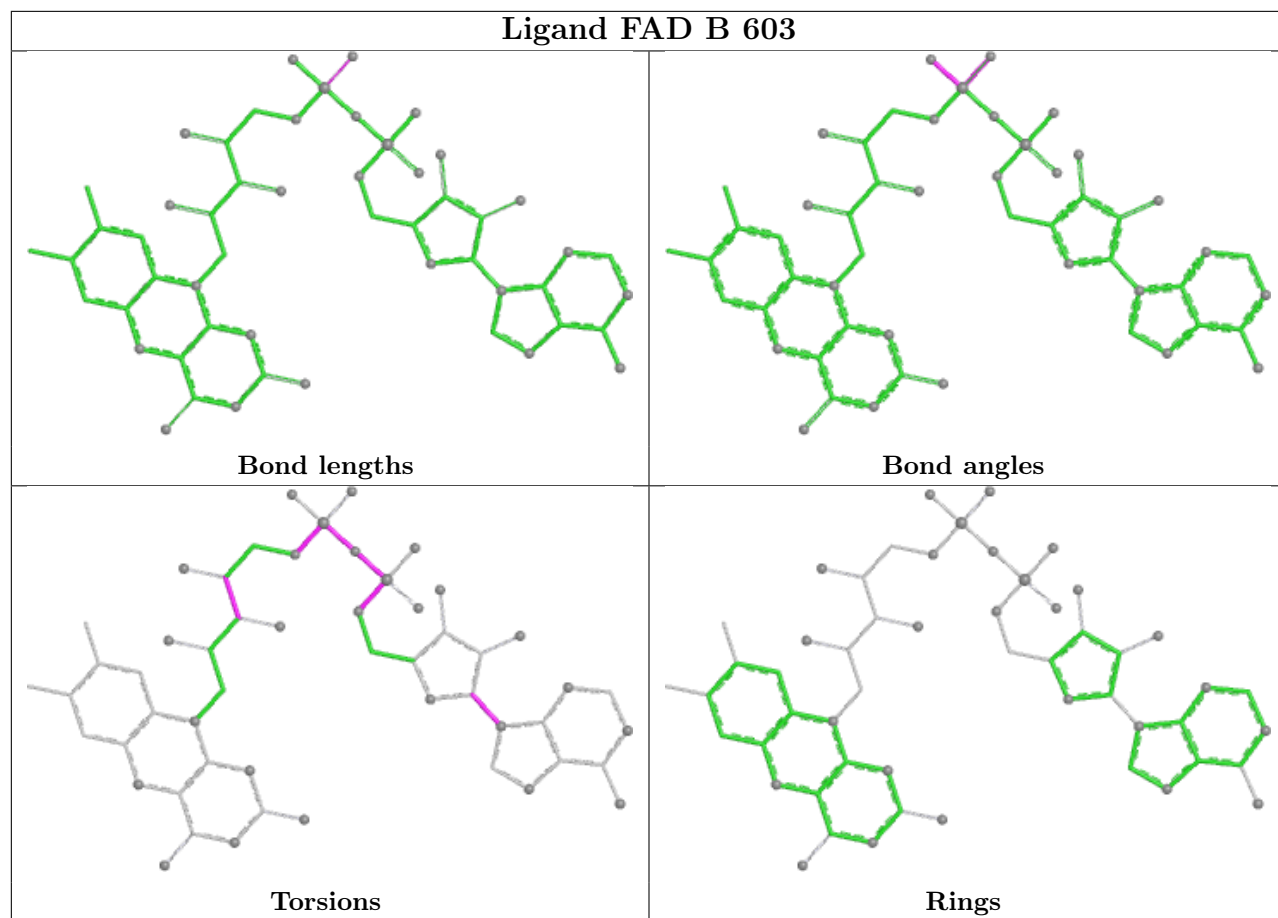


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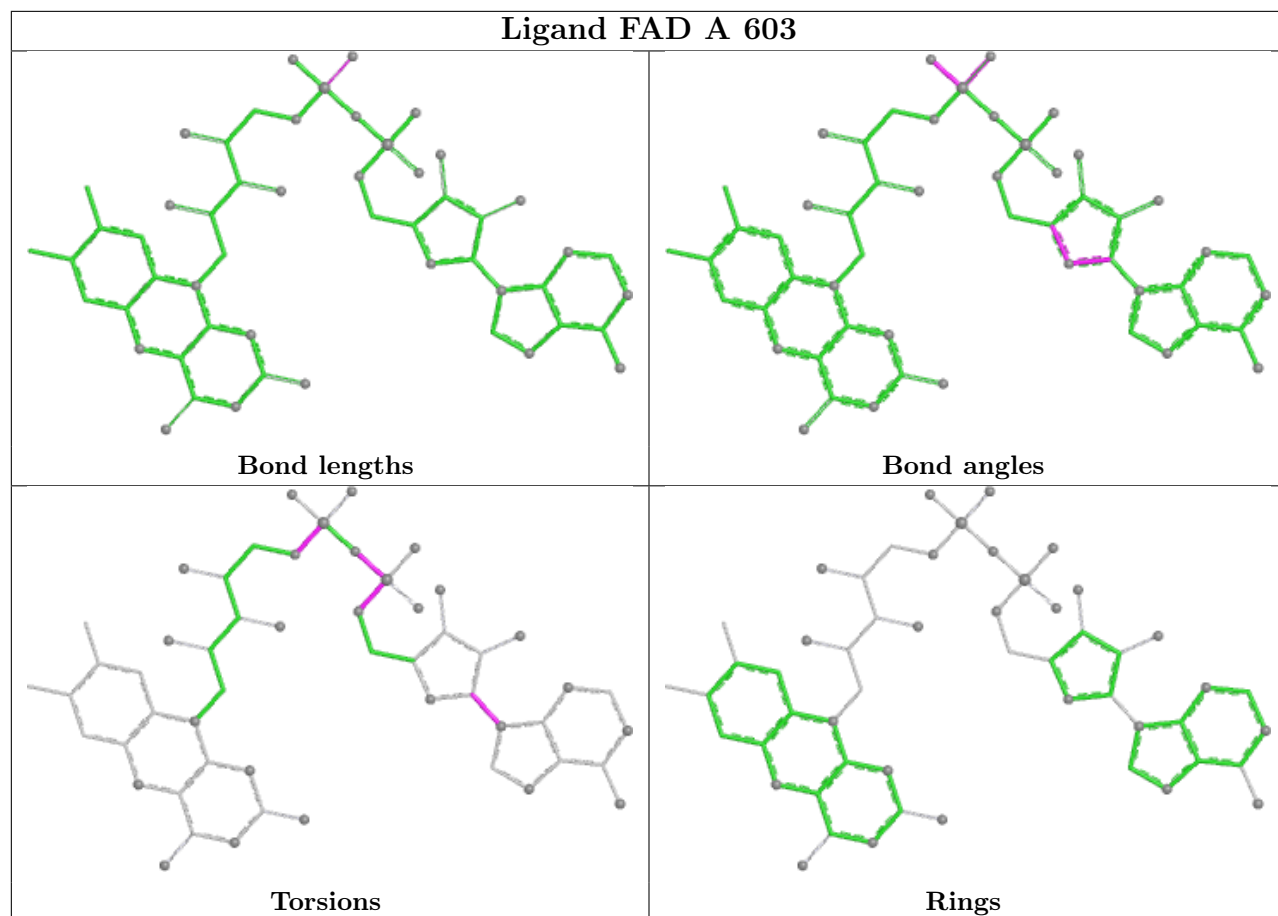


Rings

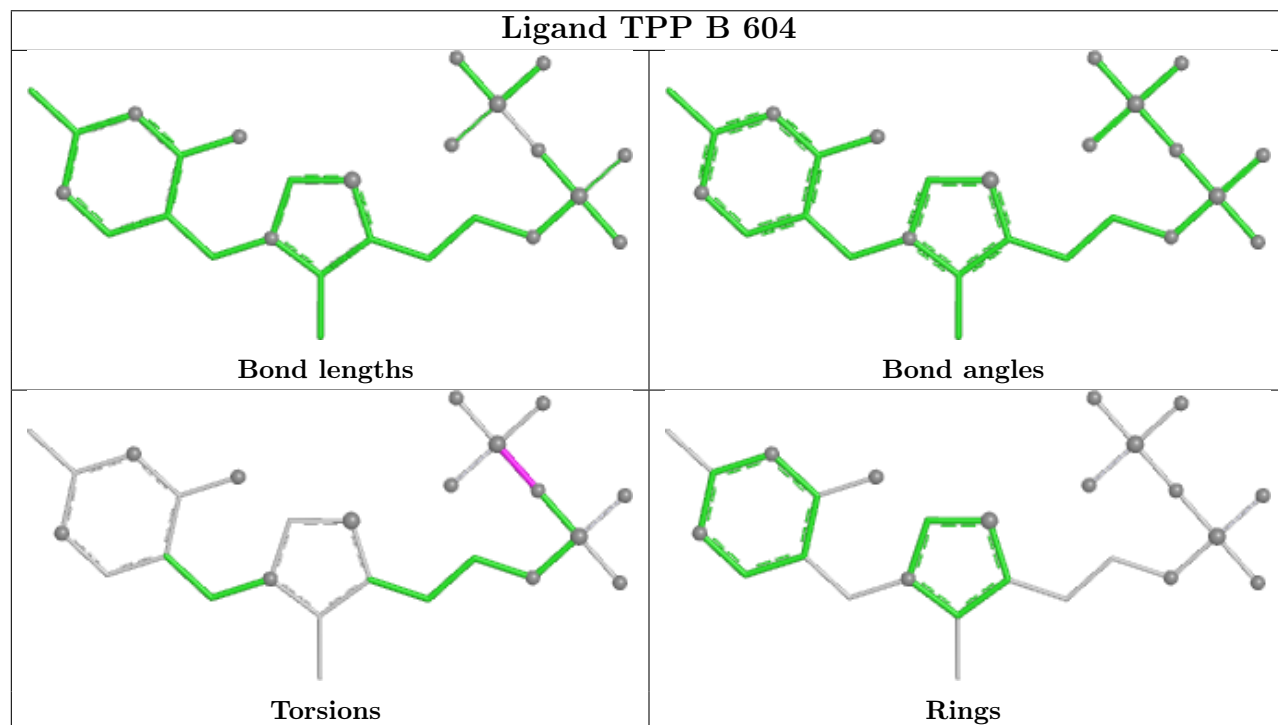




Ligand FAD A 603



Ligand TPP B 604



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	594/594 (100%)	-0.43	6 (1%) 79 79	16, 21, 35, 57	0
1	B	594/594 (100%)	-0.25	11 (1%) 66 66	18, 24, 39, 66	0
1	C	594/594 (100%)	-0.12	9 (1%) 72 71	23, 30, 44, 73	0
1	D	594/594 (100%)	-0.12	5 (0%) 82 82	22, 30, 46, 69	0
1	E	594/594 (100%)	-0.02	14 (2%) 59 59	23, 32, 48, 69	0
1	F	594/594 (100%)	0.04	10 (1%) 69 68	22, 32, 47, 77	0
All	All	3564/3564 (100%)	-0.15	55 (1%) 72 71	16, 29, 45, 77	0

The worst 5 of 55 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	593	GLU	5.0
1	B	111	LYS	3.9
1	B	316	LEU	3.9
1	F	593	GLU	3.7
1	D	593	GLU	3.7

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 ⓘ

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
6	UQ1	C	608	13/18	0.29	0.37	84,93,107,111	0
6	UQ1	A	607	13/18	0.35	0.35	67,75,86,87	0
6	UQ1	E	604	13/18	0.35	0.31	70,81,93,94	0
6	UQ1	B	607	13/18	0.40	0.29	73,79,86,92	0
6	UQ1	F	605	13/18	0.45	0.29	77,85,99,100	0
6	UQ1	D	607	13/18	0.54	0.29	90,93,101,103	0
5	DW3	D	604	4/4	0.78	0.19	54,60,66,73	0
5	DW3	C	604	4/4	0.82	0.17	47,52,58,62	0
6	UQ1	C	607	13/18	0.84	0.14	49,53,57,59	0
5	DW3	C	605	4/4	0.86	0.16	48,54,58,63	0
6	UQ1	E	605	13/18	0.87	0.13	62,71,75,76	0
5	DW3	D	605	4/4	0.88	0.13	51,56,64,67	0
6	UQ1	A	606	13/18	0.88	0.12	39,45,48,49	0
5	DW3	B	605	4/4	0.91	0.13	35,39,42,46	0
6	UQ1	B	606	13/18	0.91	0.11	30,35,40,48	0
5	DW3	A	605	4/4	0.91	0.17	28,36,43,45	0
6	UQ1	F	606	13/18	0.91	0.12	43,47,57,58	0
6	UQ1	D	606	13/18	0.92	0.11	39,44,50,53	0
3	FAD	E	602	53/53	0.95	0.07	26,29,33,34	0
3	FAD	C	602	53/53	0.96	0.07	22,27,31,32	0
3	FAD	D	602	53/53	0.96	0.07	23,27,31,33	0
3	FAD	B	603	53/53	0.96	0.07	17,22,27,36	0
3	FAD	F	603	53/53	0.96	0.07	23,28,36,37	0
4	TPP	D	603	26/26	0.96	0.07	26,29,32,35	0
4	TPP	F	604	26/26	0.96	0.07	27,31,35,37	0
3	FAD	A	603	53/53	0.97	0.06	18,19,23,24	0
4	TPP	E	603	26/26	0.97	0.07	26,30,33,35	0
4	TPP	C	603	26/26	0.97	0.07	23,28,32,34	0
4	TPP	A	604	26/26	0.98	0.05	18,20,23,25	0
4	TPP	B	604	26/26	0.98	0.06	19,23,25,26	0
2	MG	C	601	1/1	0.99	0.04	26,26,26,26	0
2	MG	C	606	1/1	0.99	0.04	27,27,27,27	0
2	MG	D	601	1/1	0.99	0.02	26,26,26,26	0
2	MG	E	601	1/1	0.99	0.02	27,27,27,27	0
2	MG	F	601	1/1	0.99	0.04	29,29,29,29	0
2	MG	F	602	1/1	0.99	0.04	26,26,26,26	0
2	MG	A	601	1/1	0.99	0.02	20,20,20,20	0

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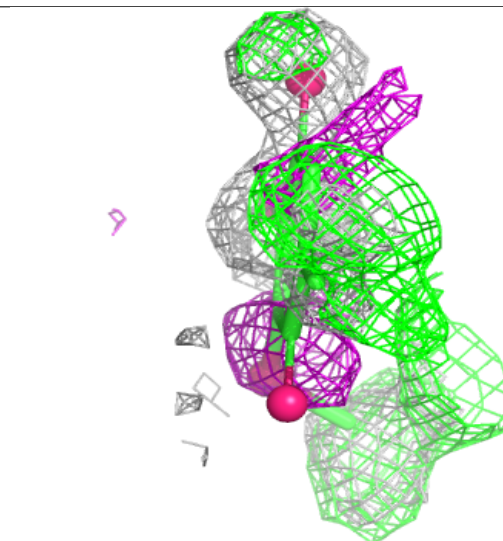
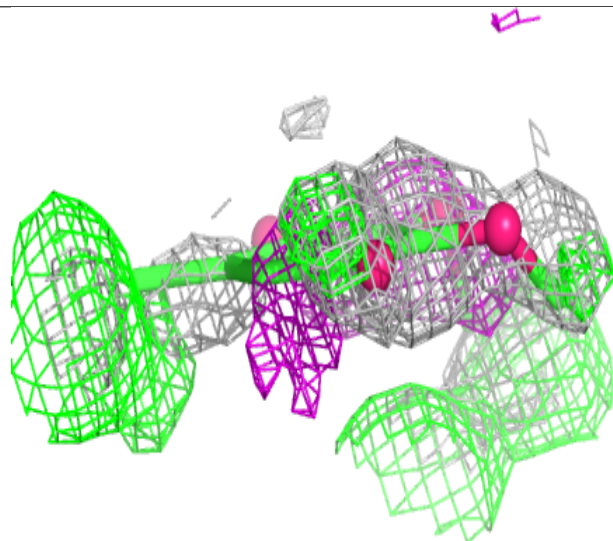
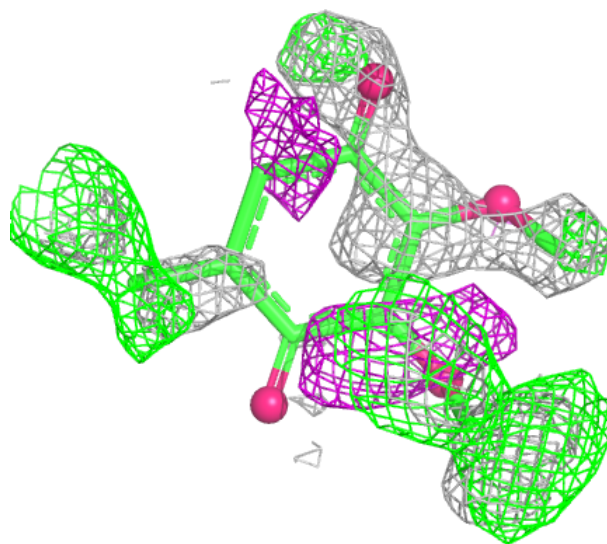
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MG	A	602	1/1	0.99	0.09	17,17,17,17	1
2	MG	B	601	1/1	0.99	0.01	21,21,21,21	0
2	MG	B	602	1/1	1.00	0.04	19,19,19,19	1

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.

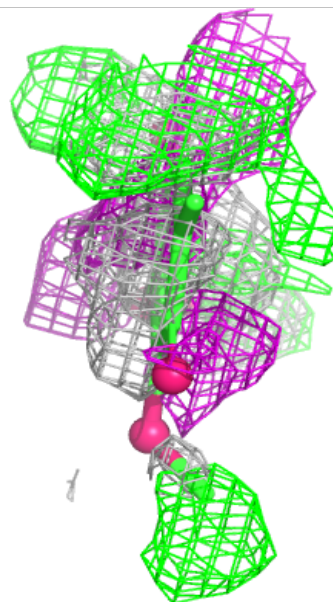
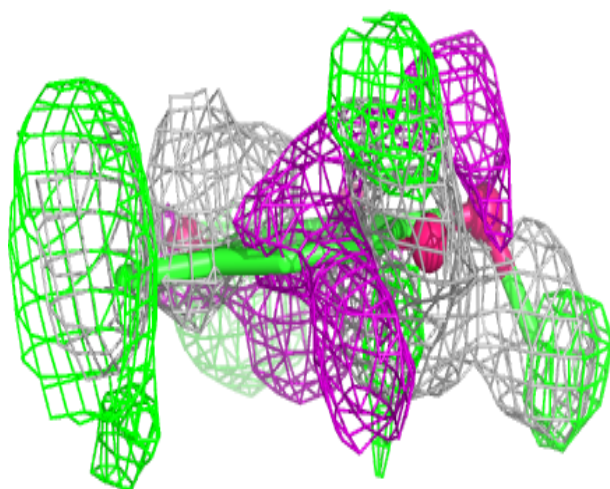
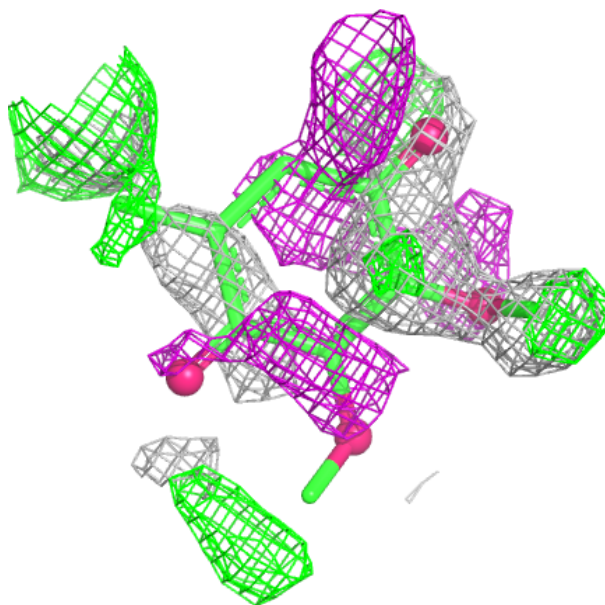
Electron density around UQ1 C 608:

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



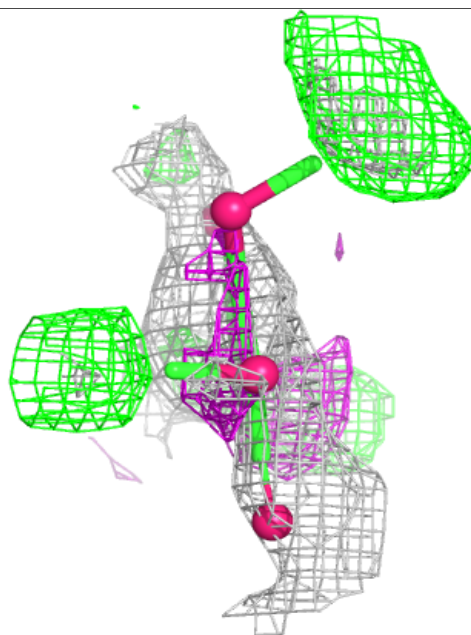
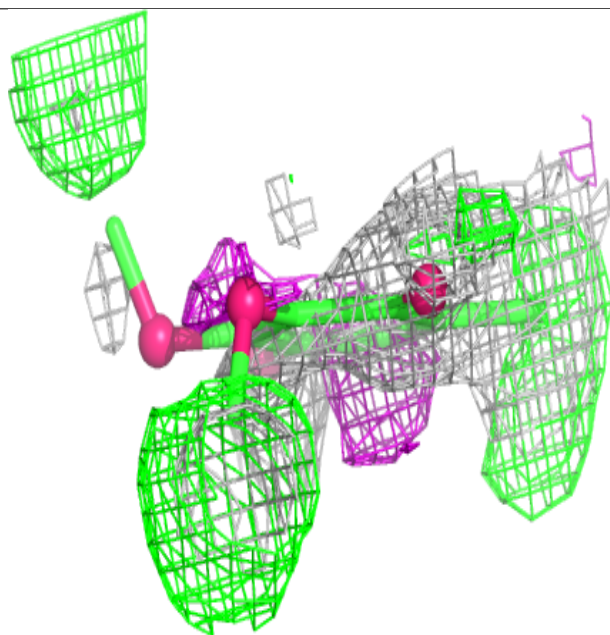
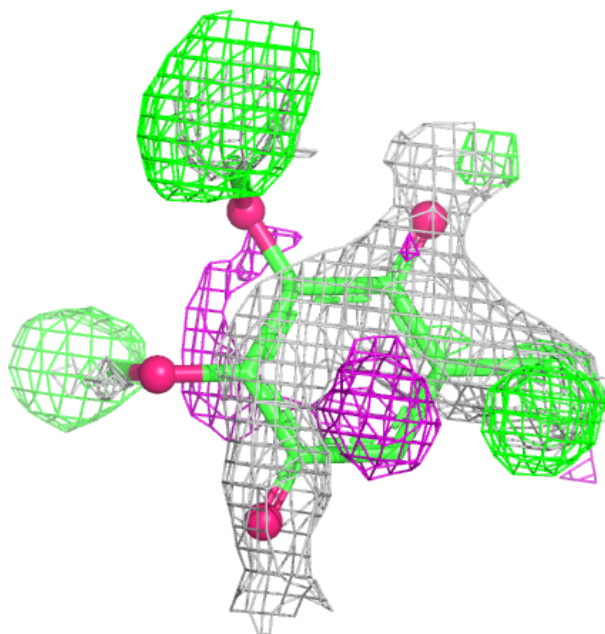
Electron density around UQ1 A 607:

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



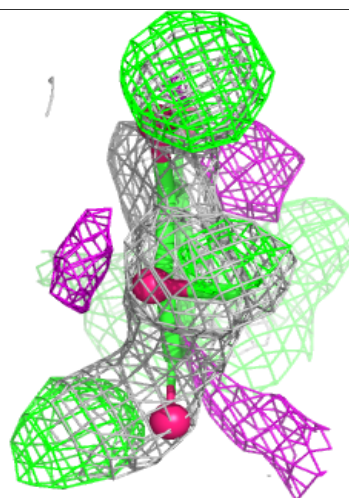
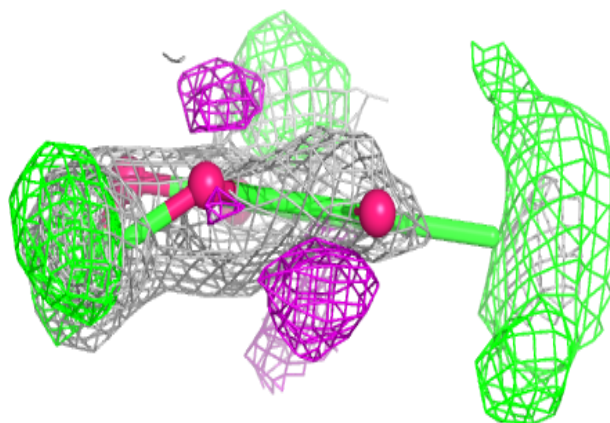
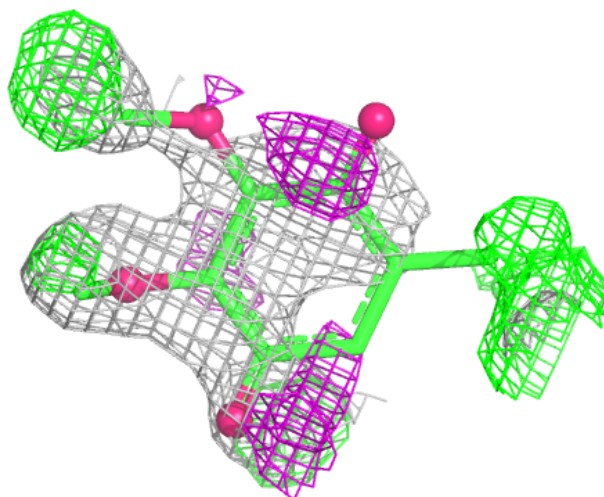
Electron density around UQ1 E 604:

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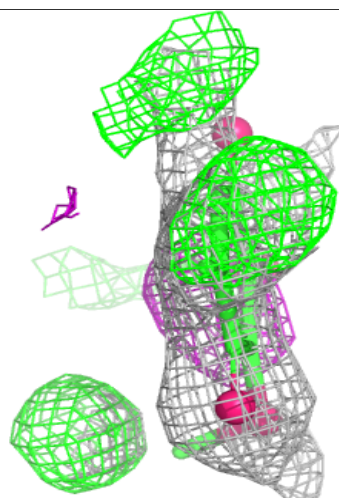
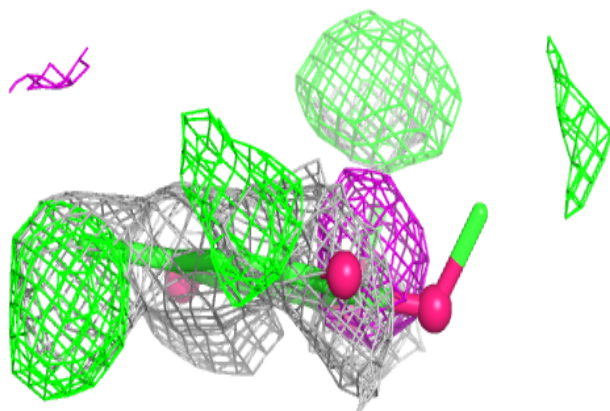
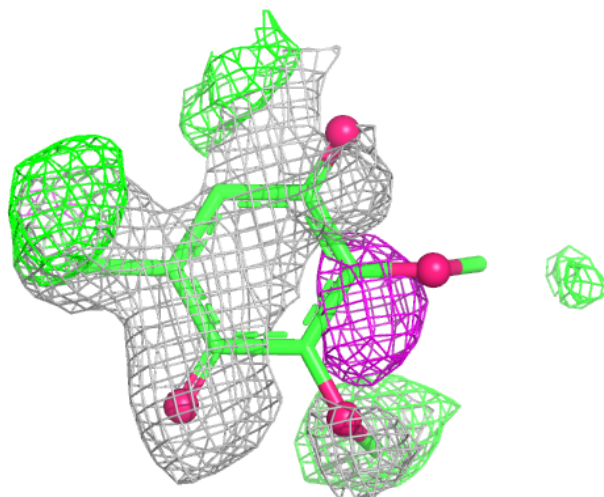
Electron density around UQ1 B 607:

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and green (positive)



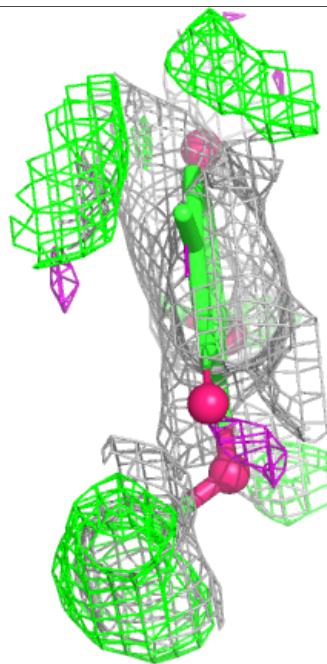
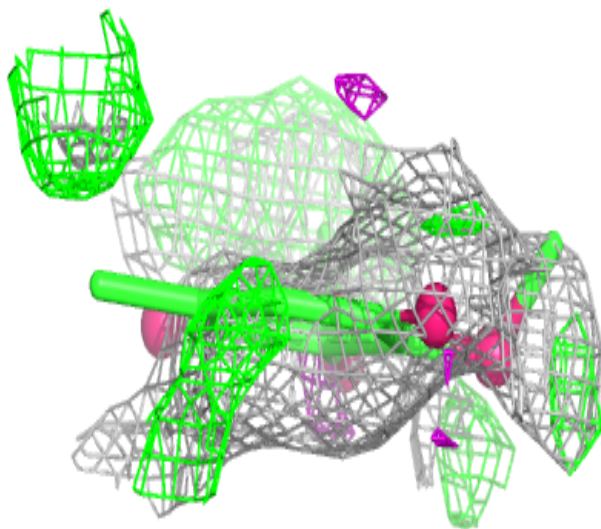
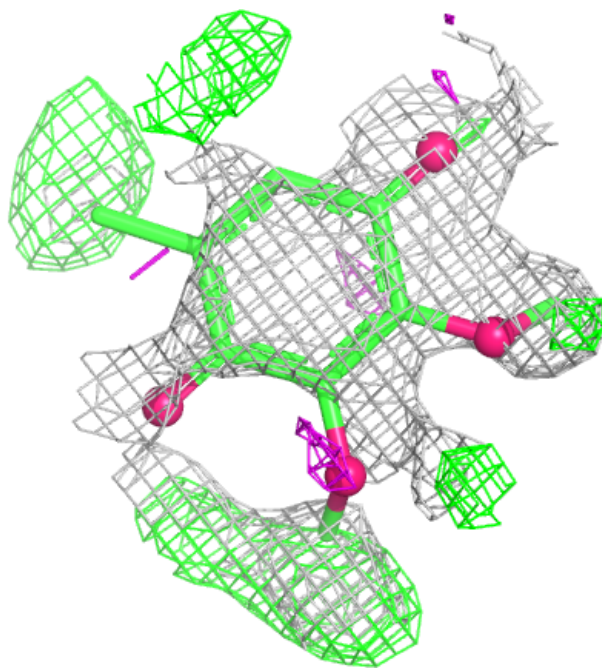
Electron density around UQ1 F 605:

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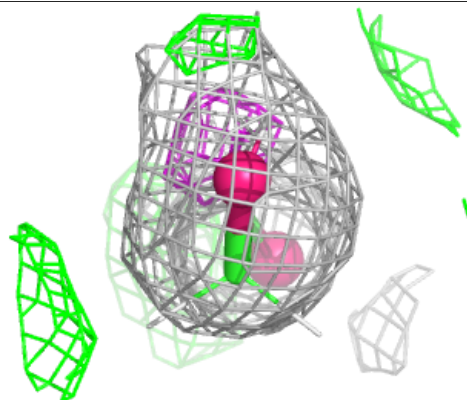
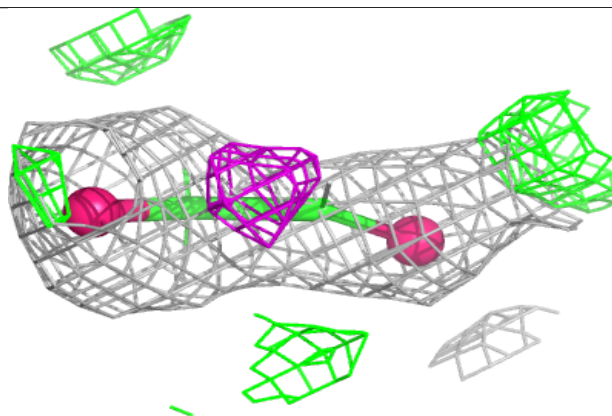
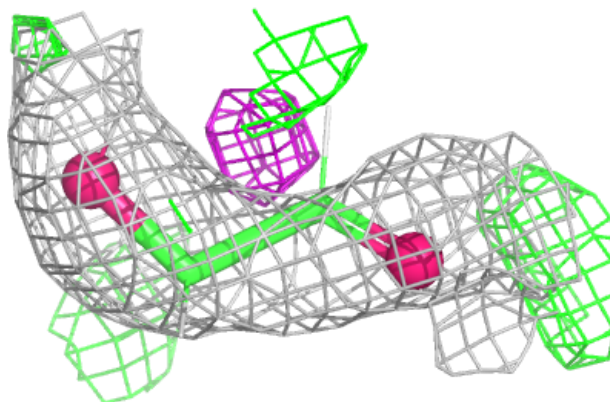
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and green (positive)



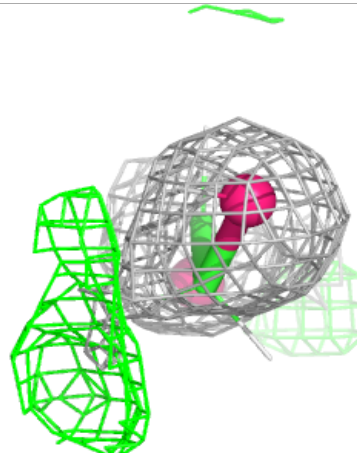
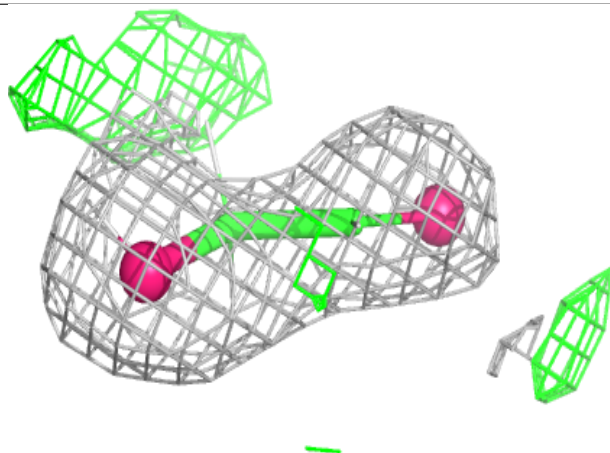
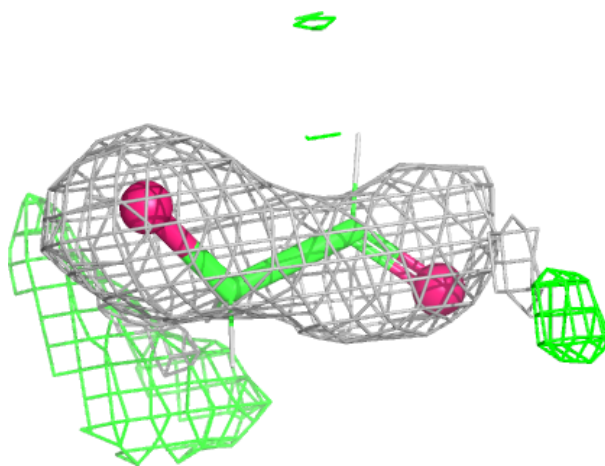
Electron density around DW3 D 604:

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and green (positive)



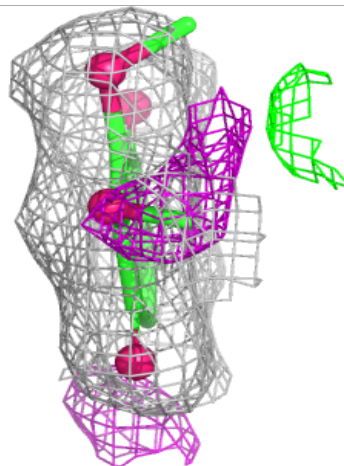
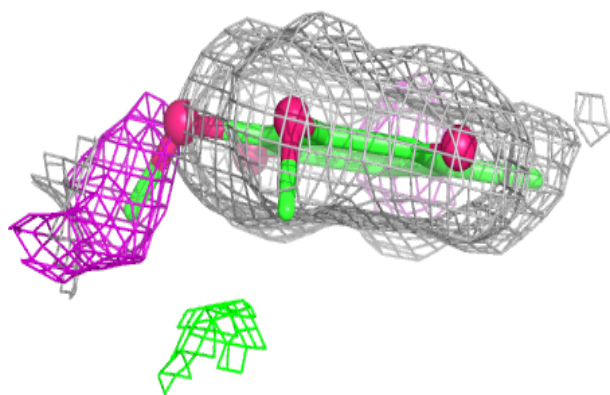
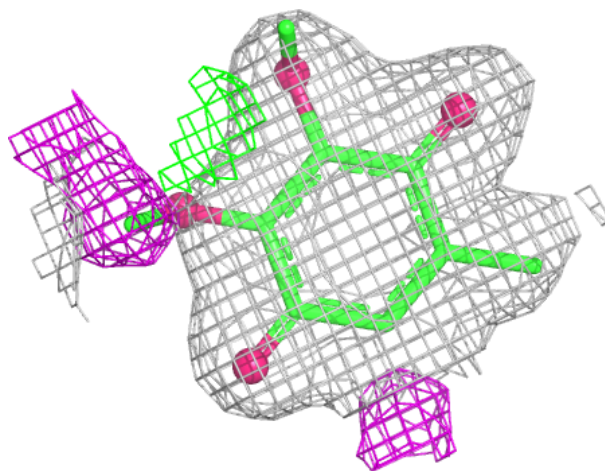
Electron density around DW3 C 604:

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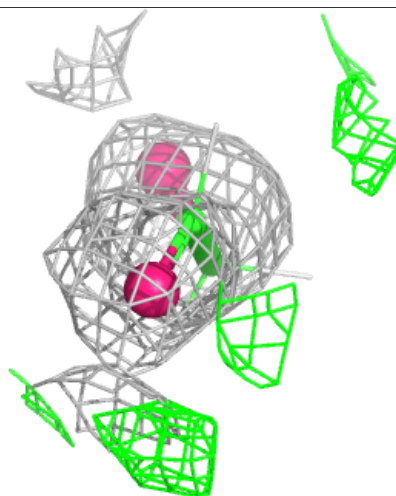
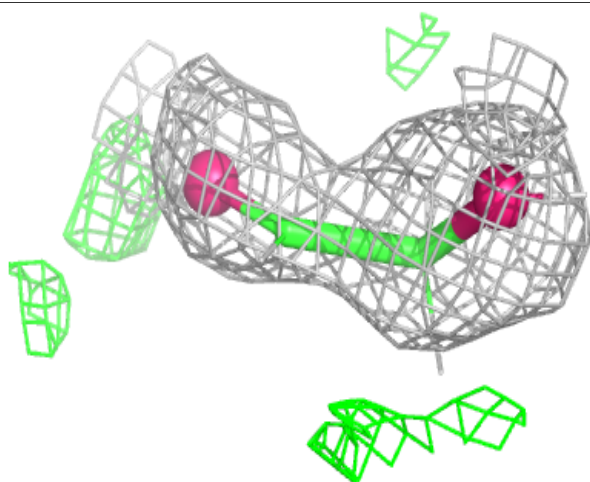
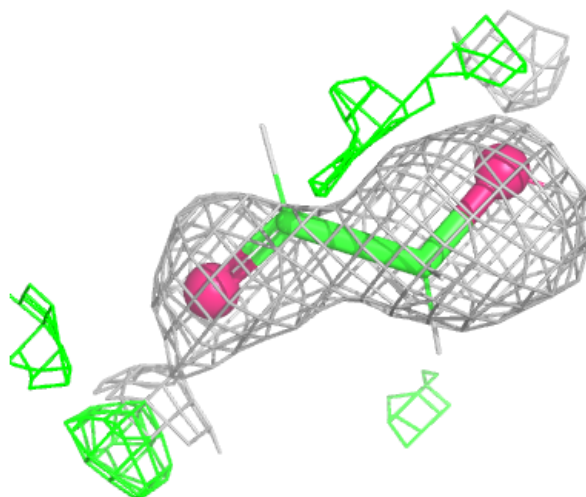
Electron density around UQ1 C 607:

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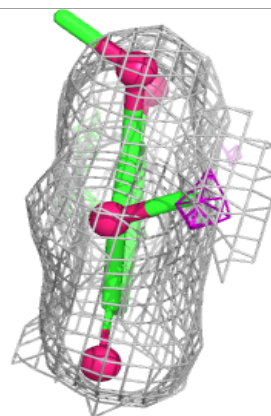
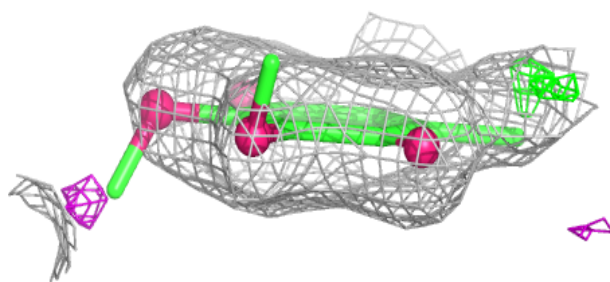
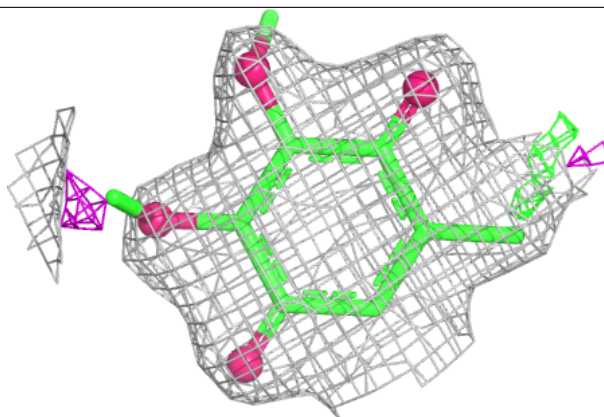
Electron density around DW3 C 605:

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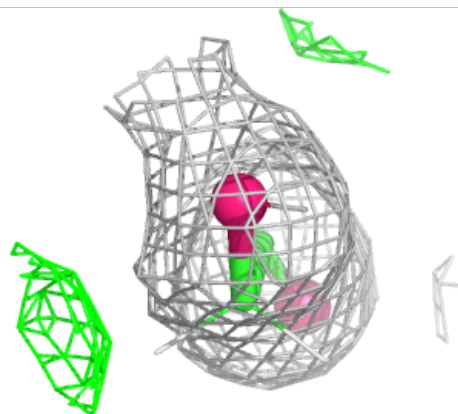
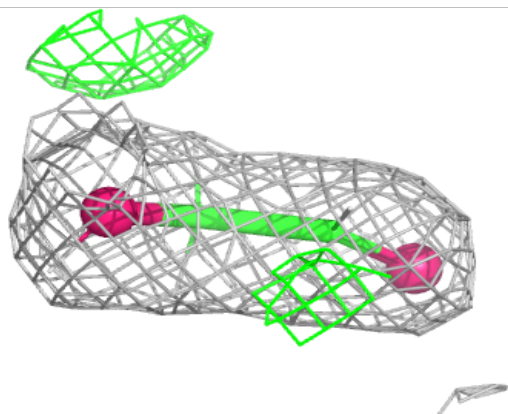
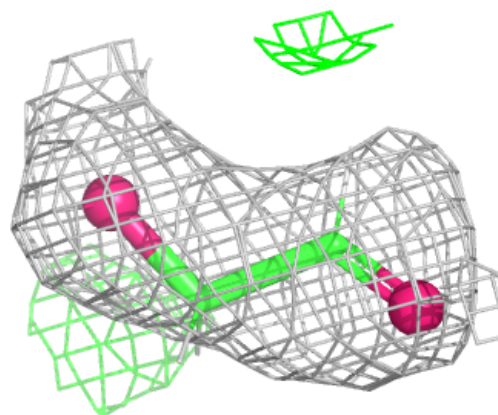


Electron density around UQ1 E 605:

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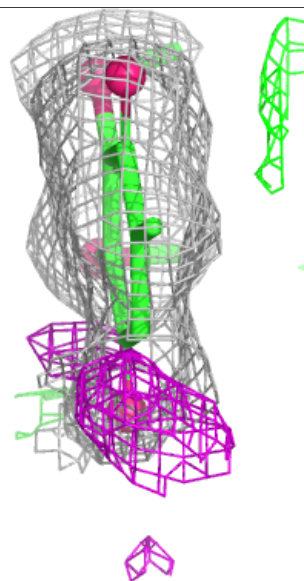
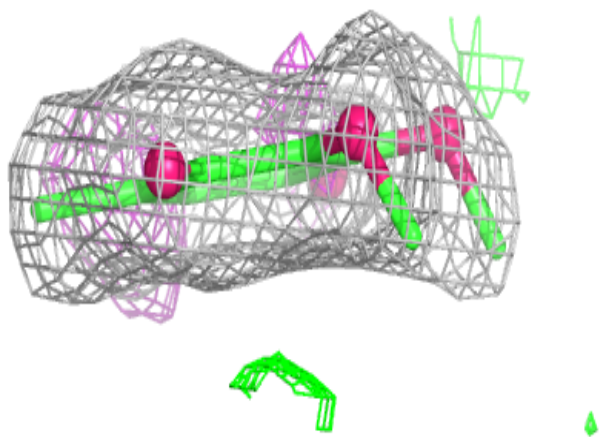
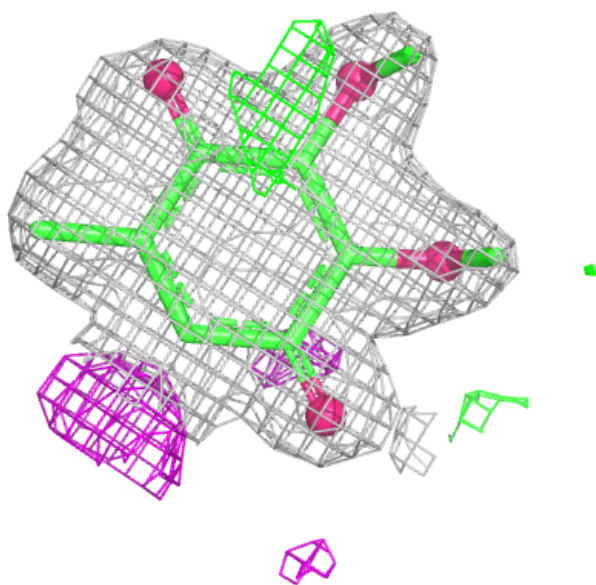
**Electron density around DW3 D 605:**

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and green (positive)



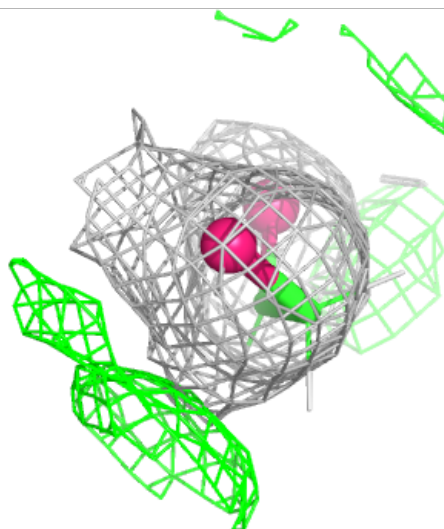
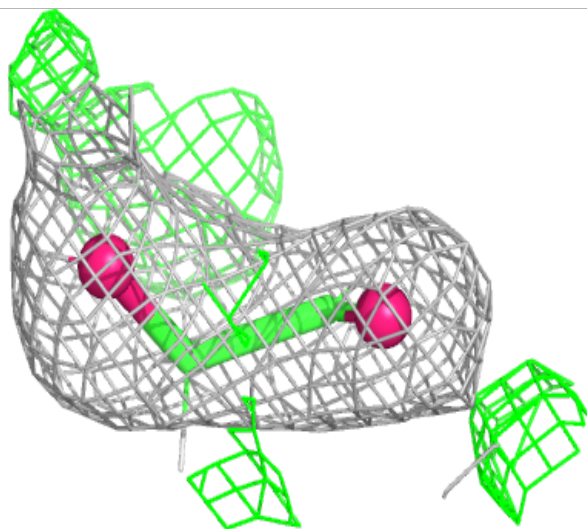
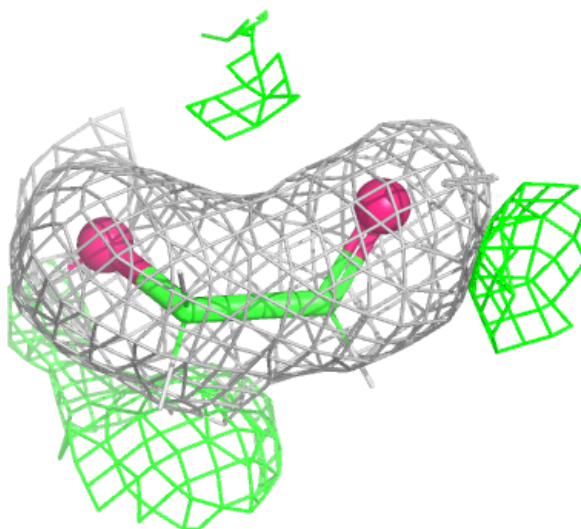
Electron density around UQ1 A 606:

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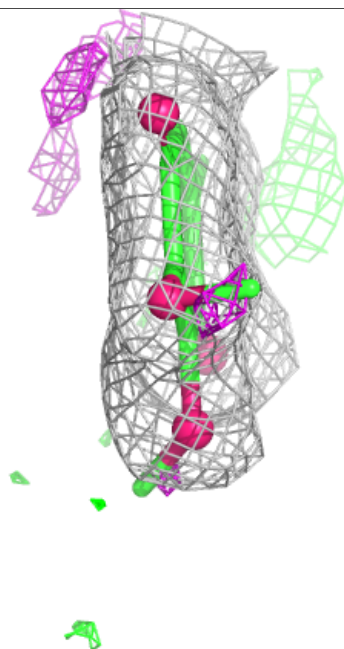
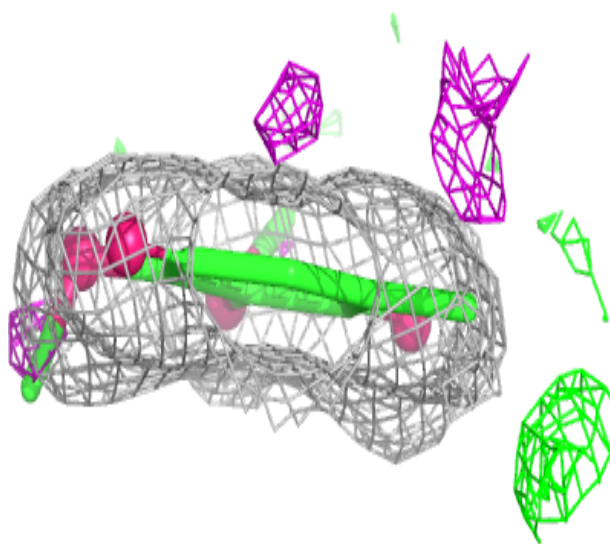
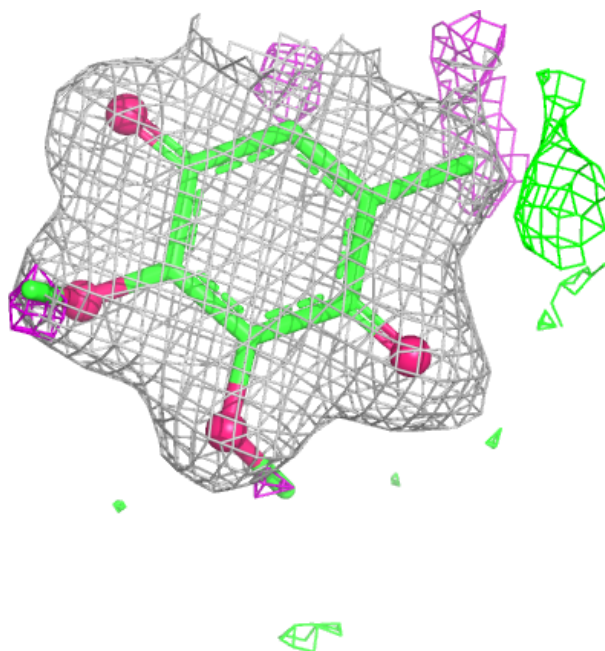
Electron density around DW3 B 605:

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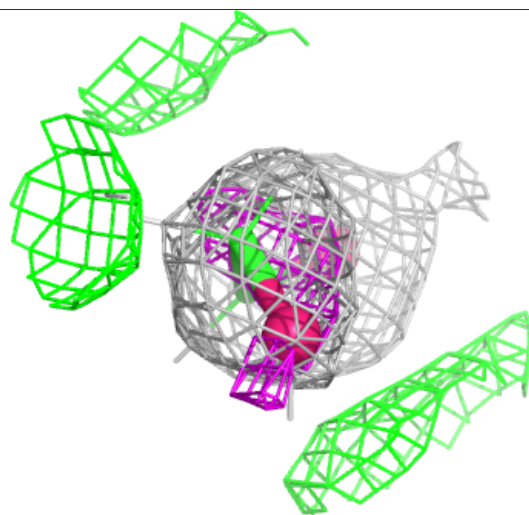
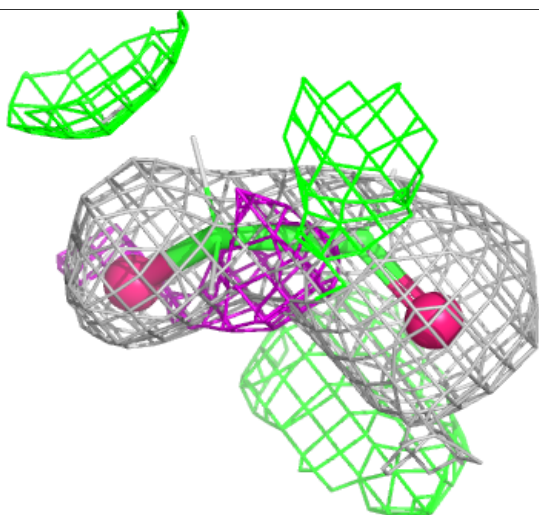
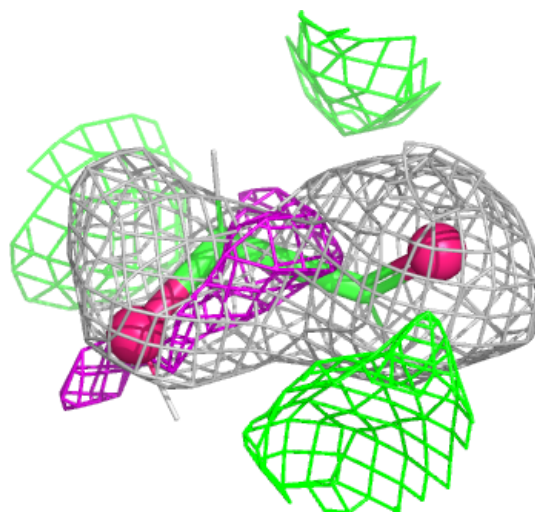
Electron density around UQ1 B 606:

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



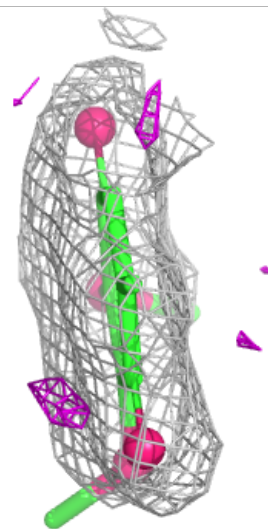
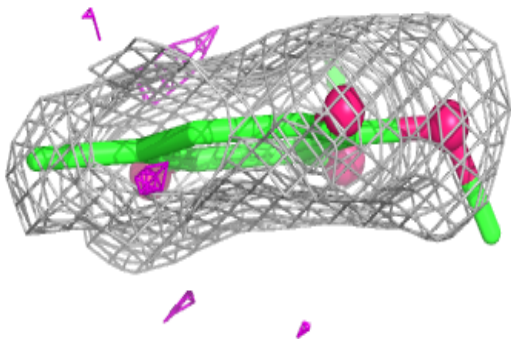
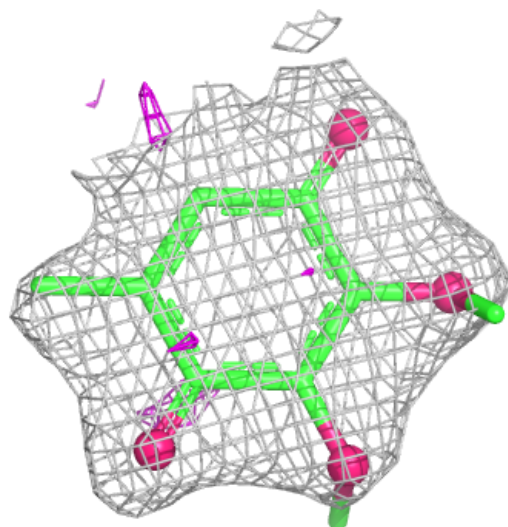
Electron density around DW3 A 605:

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



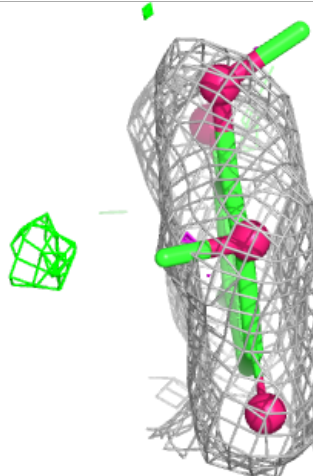
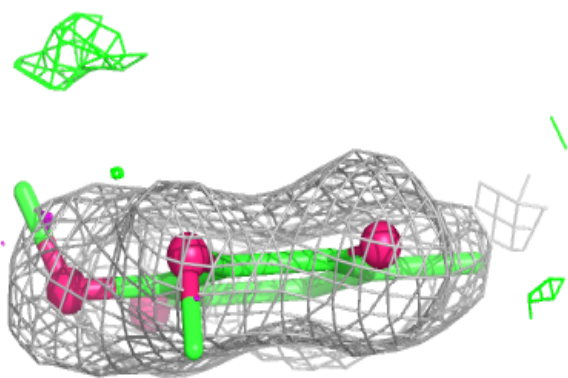
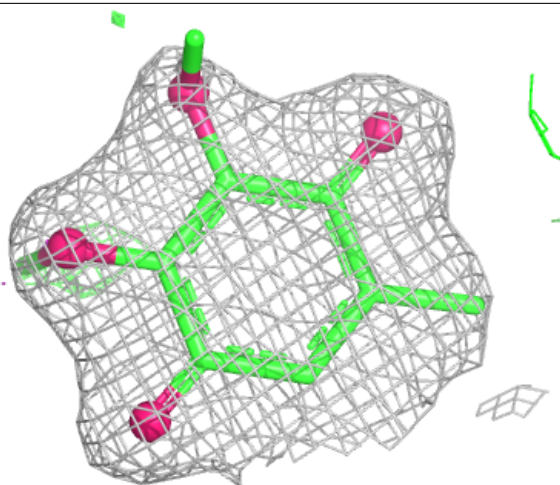
Electron density around UQ1 F 606:

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



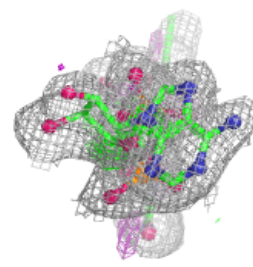
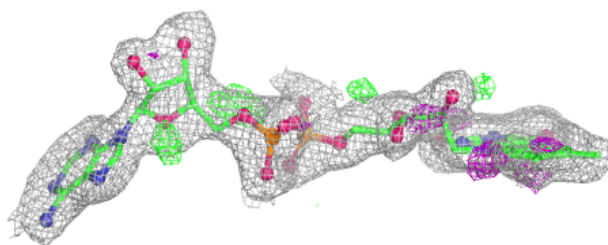
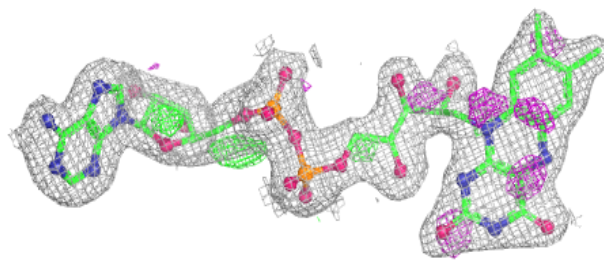
Electron density around UQ1 D 606:

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

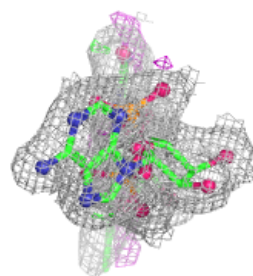
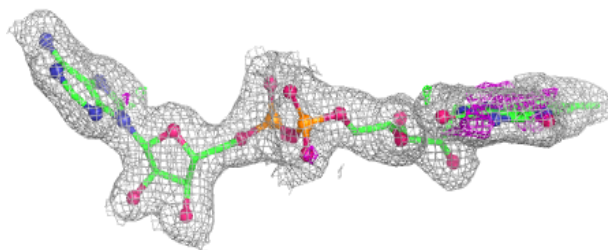
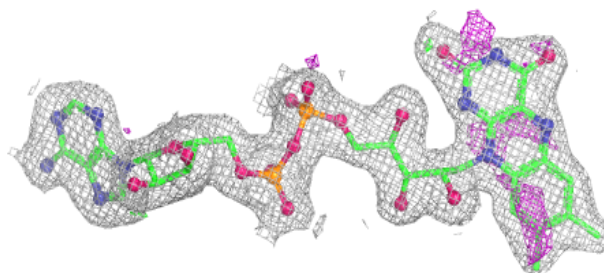


Electron density around FAD E 602:

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

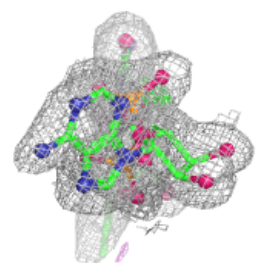
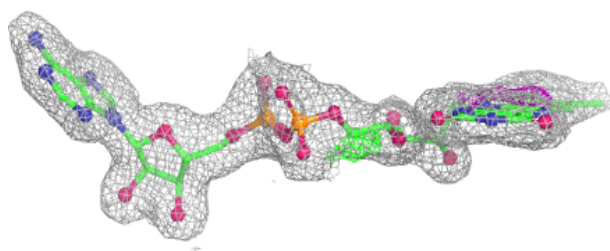
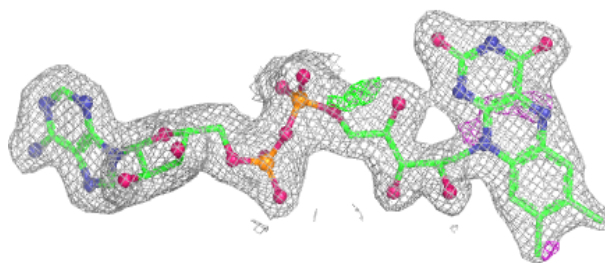
**Electron density around FAD C 602:**

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

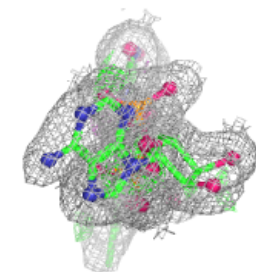
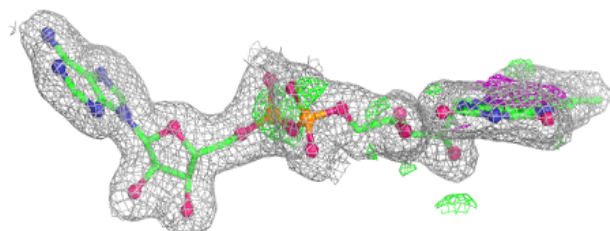
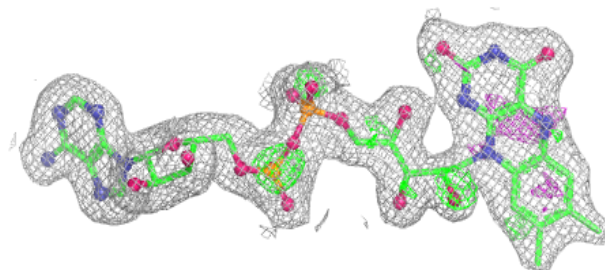


Electron density around FAD D 602:

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

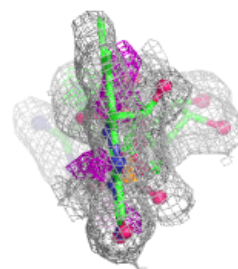
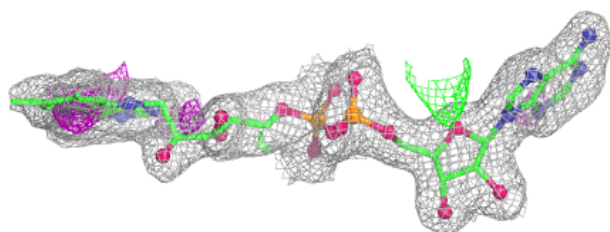
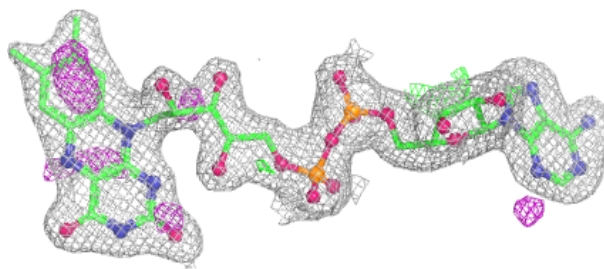
**Electron density around FAD B 603:**

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

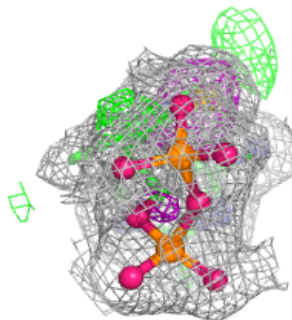
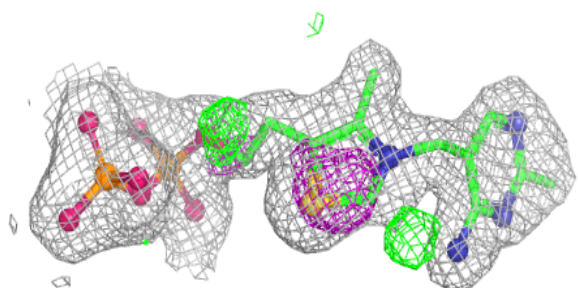
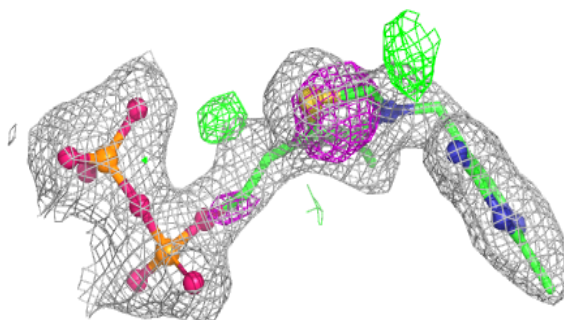


Electron density around FAD F 603:

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

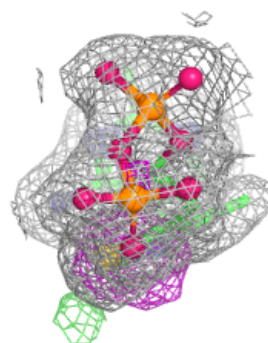
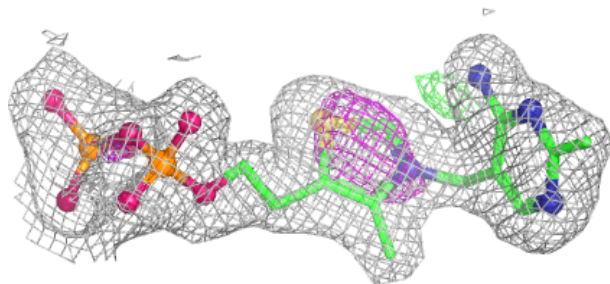
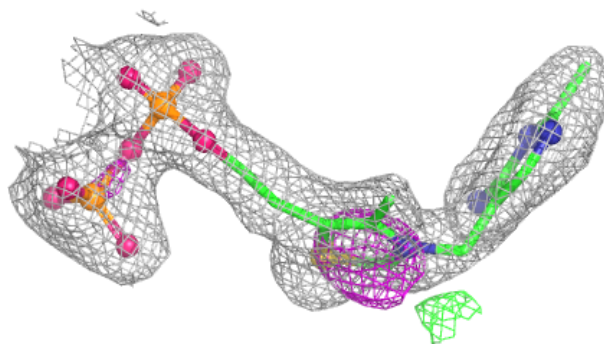
**Electron density around TPP D 603:**

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

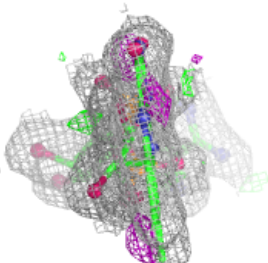
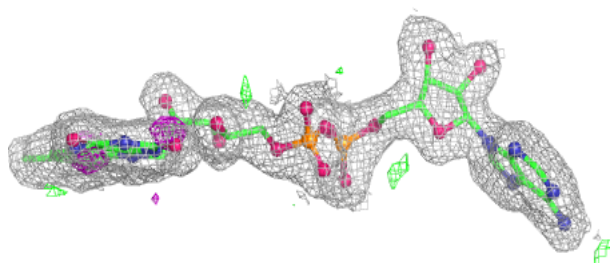
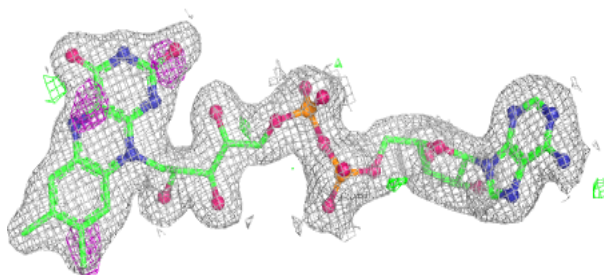


Electron density around TPP F 604:

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

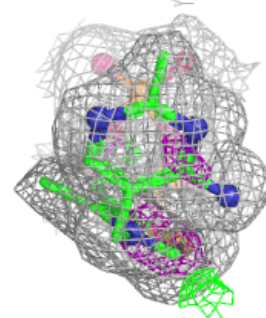
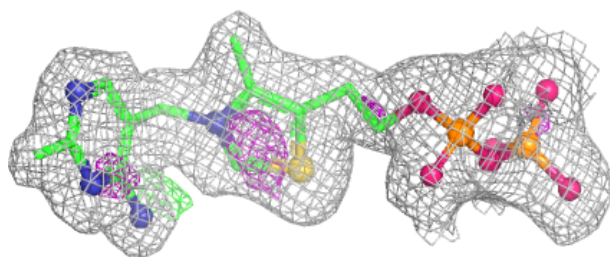
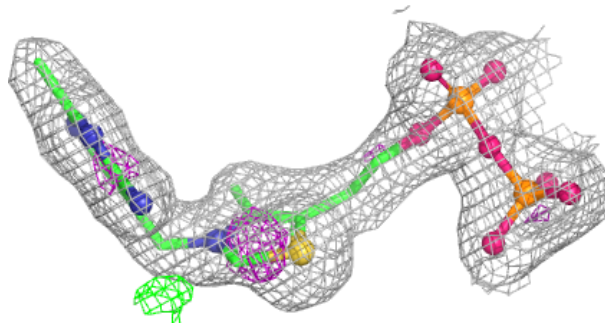
**Electron density around FAD A 603:**

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

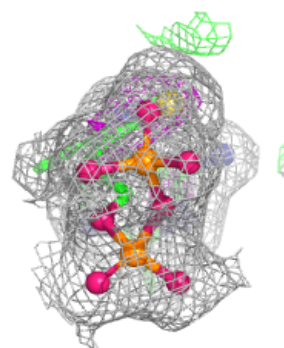
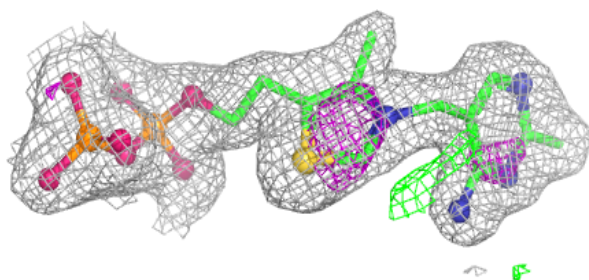
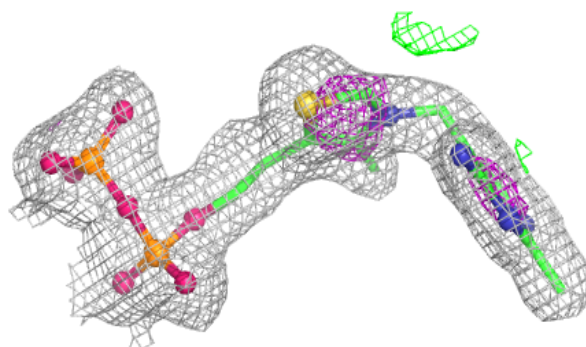


Electron density around TPP E 603:

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

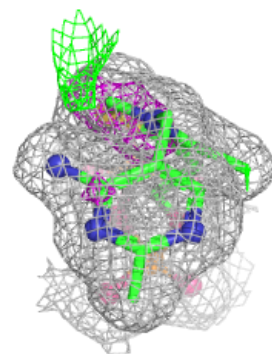
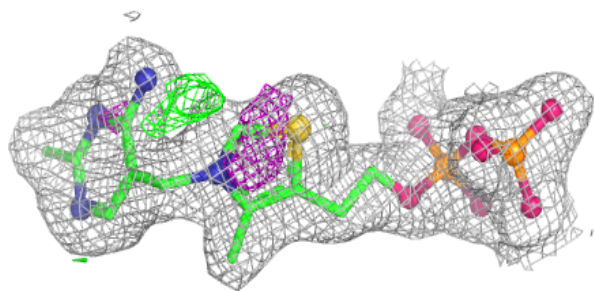
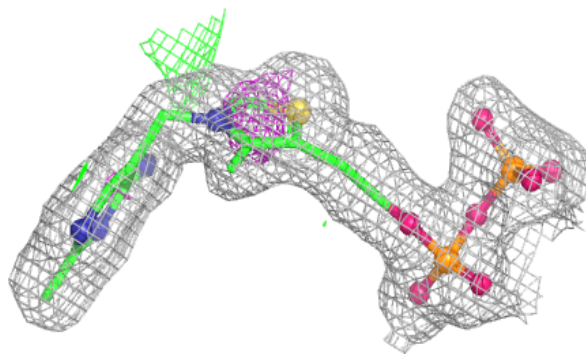
**Electron density around TPP C 603:**

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

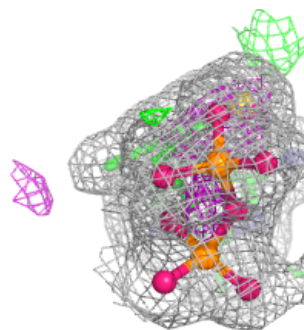
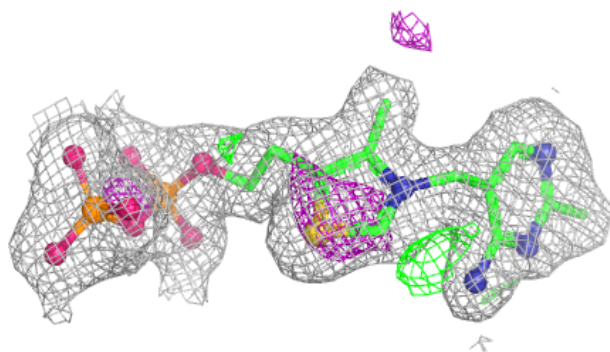
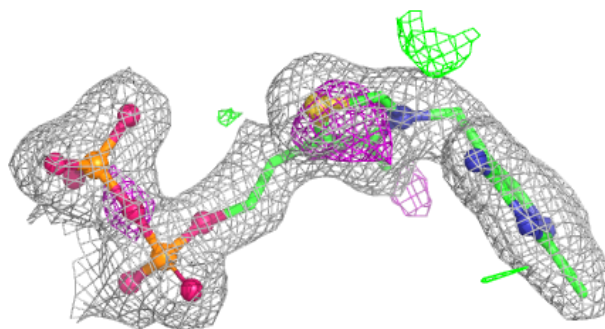


Electron density around TPP A 604:

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

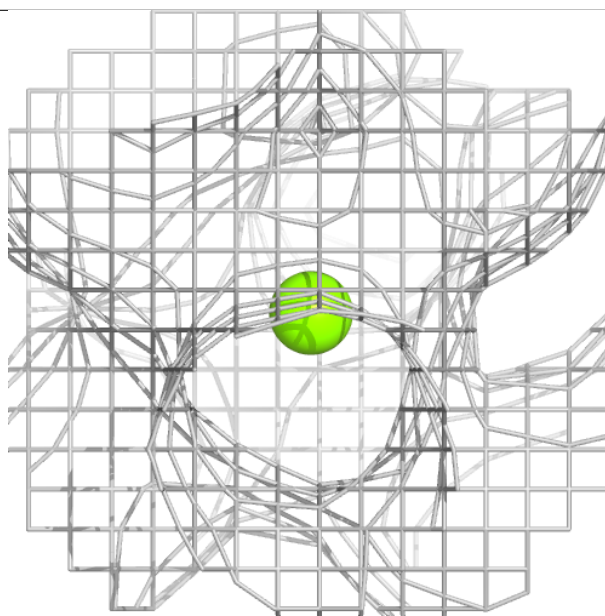
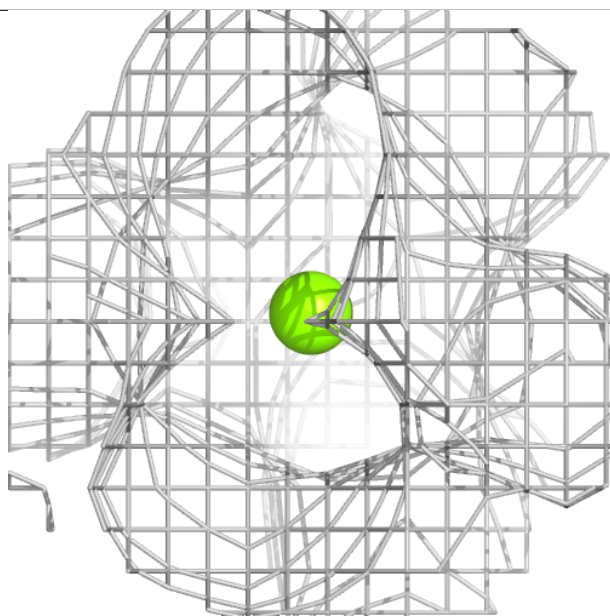
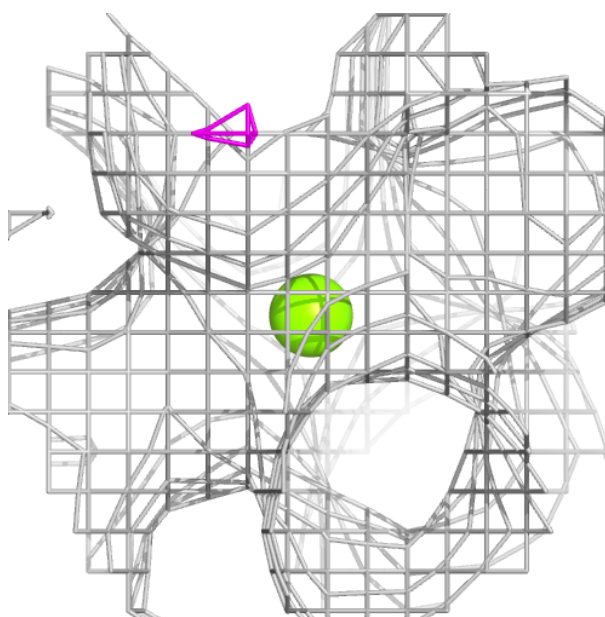
**Electron density around TPP B 604:**

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



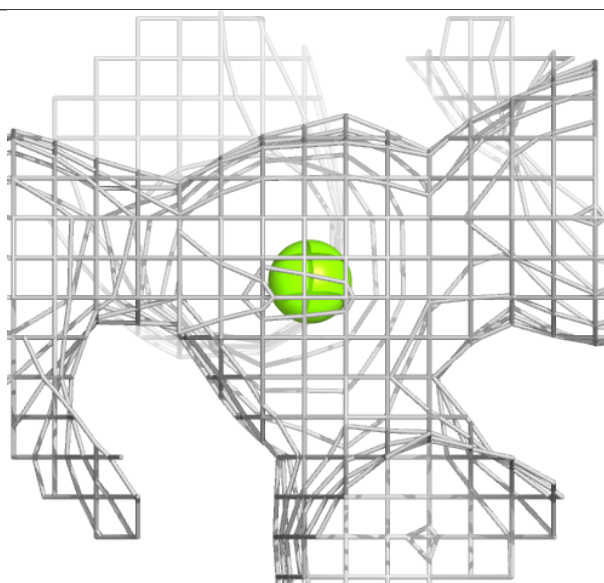
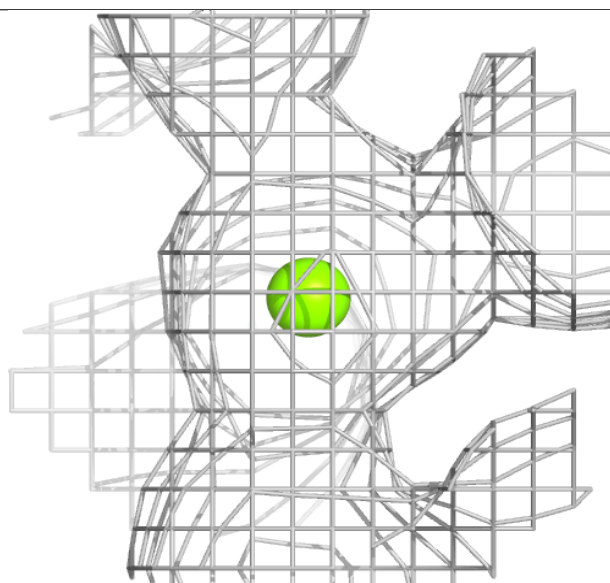
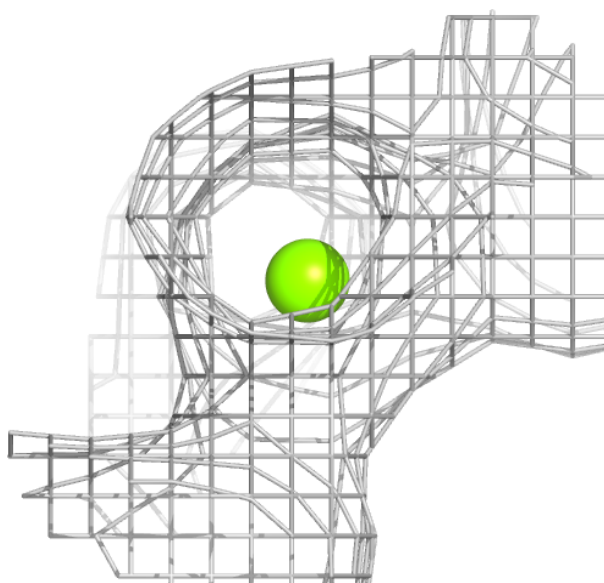
Electron density around MG C 601:

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



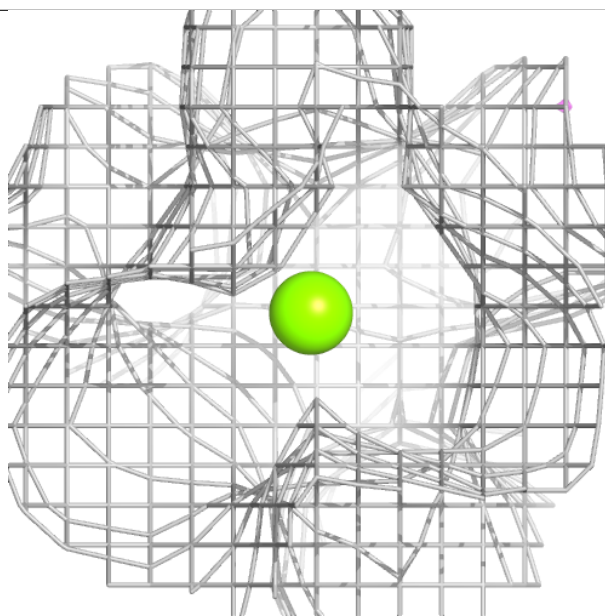
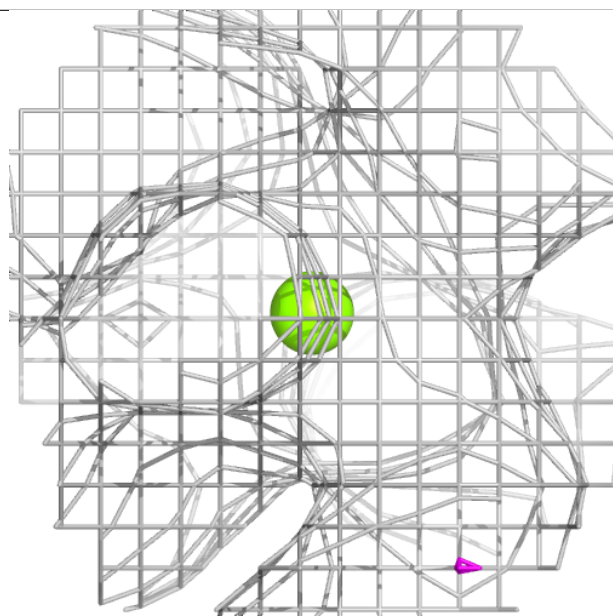
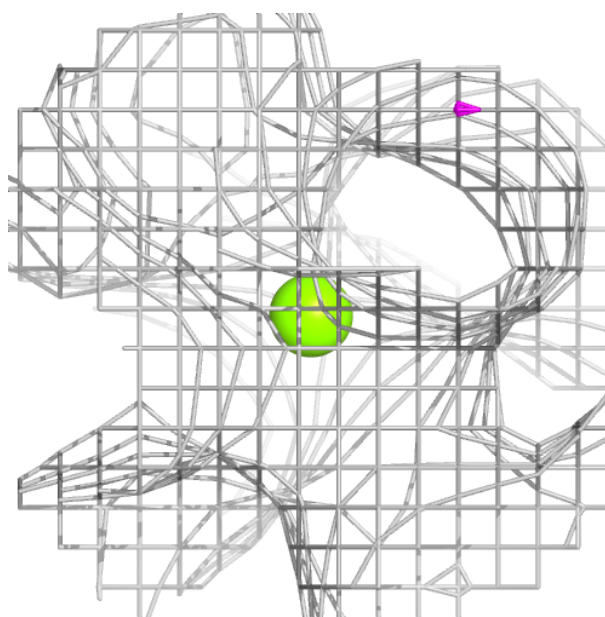
Electron density around MG C 606:

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



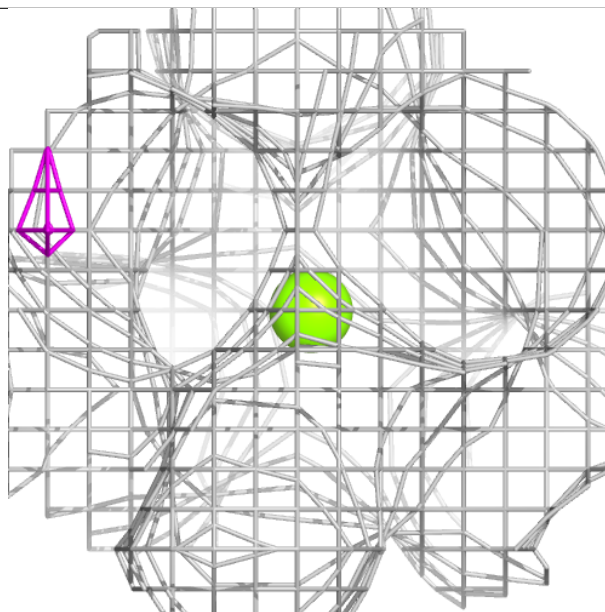
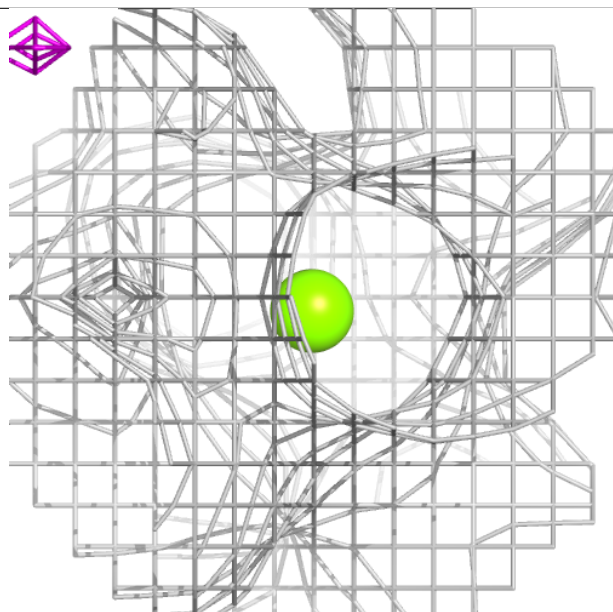
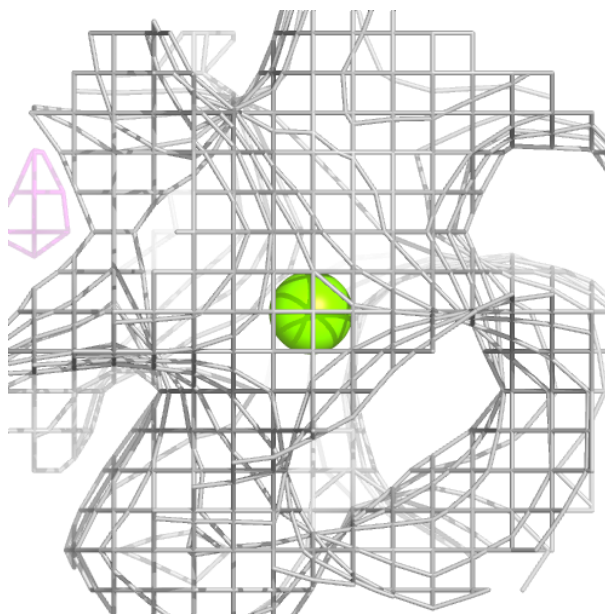
Electron density around MG D 601:

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



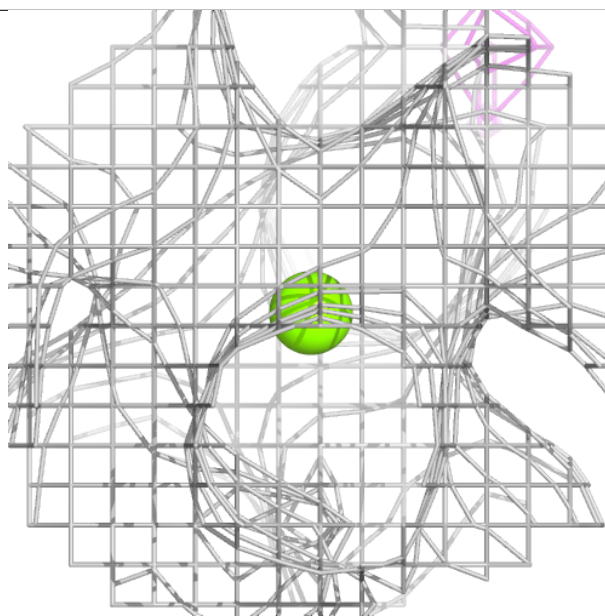
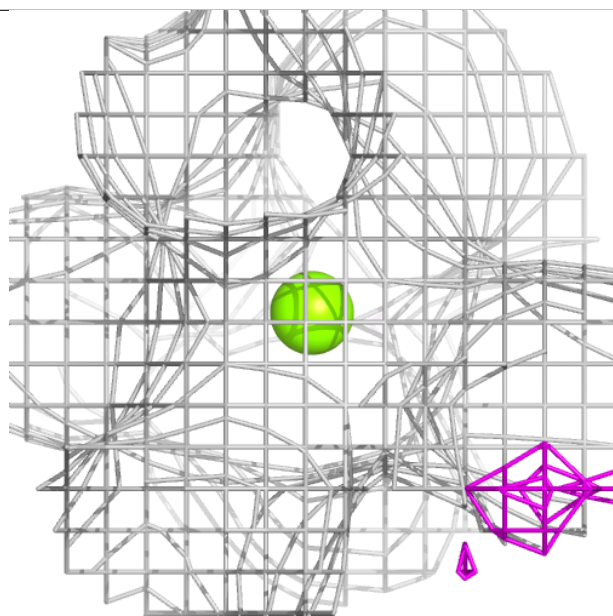
Electron density around MG E 601:

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



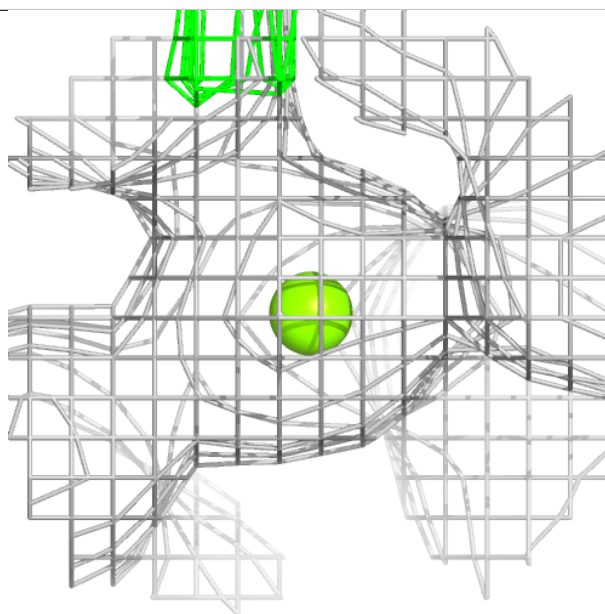
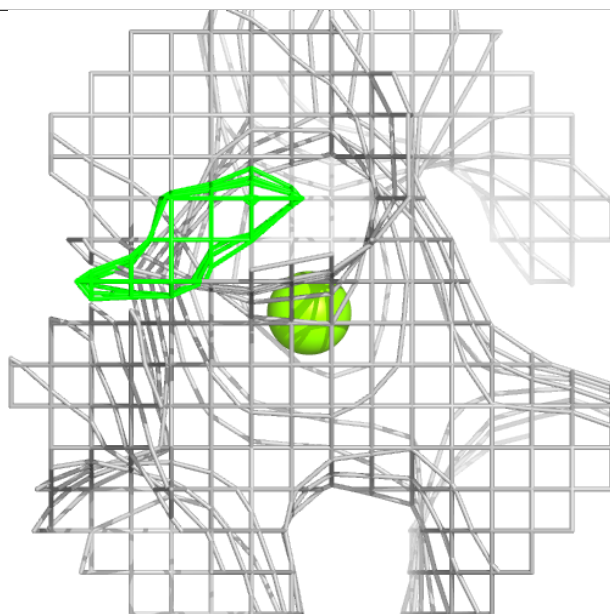
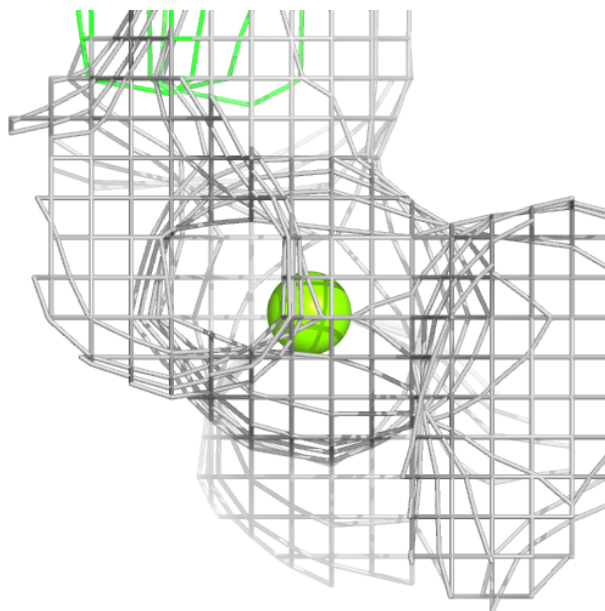
Electron density around MG F 601:

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



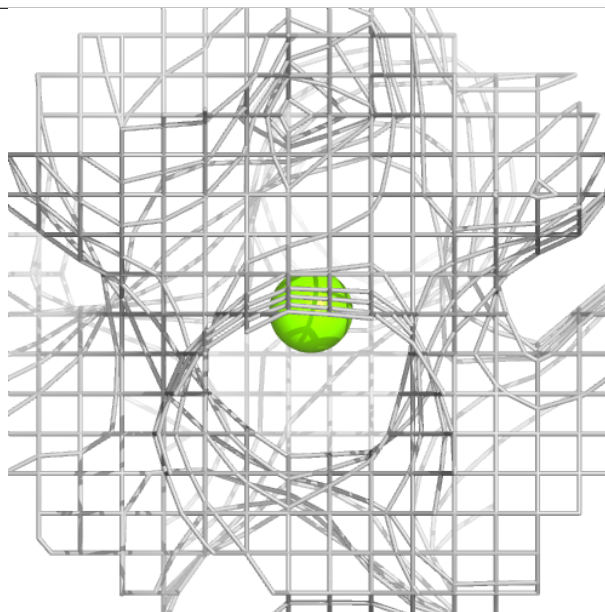
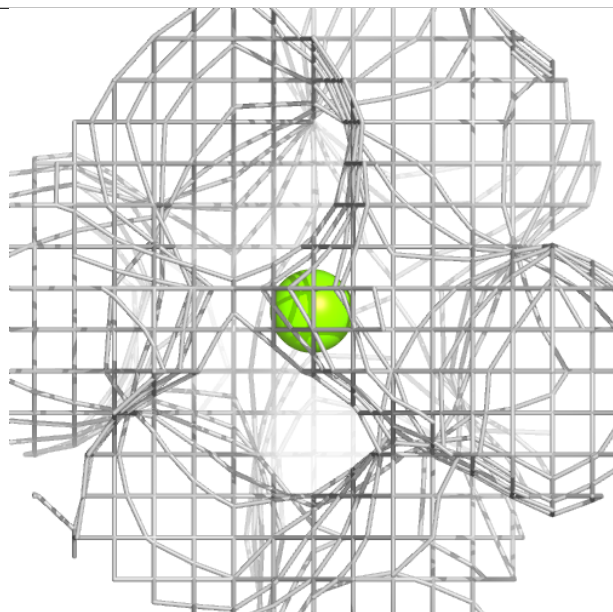
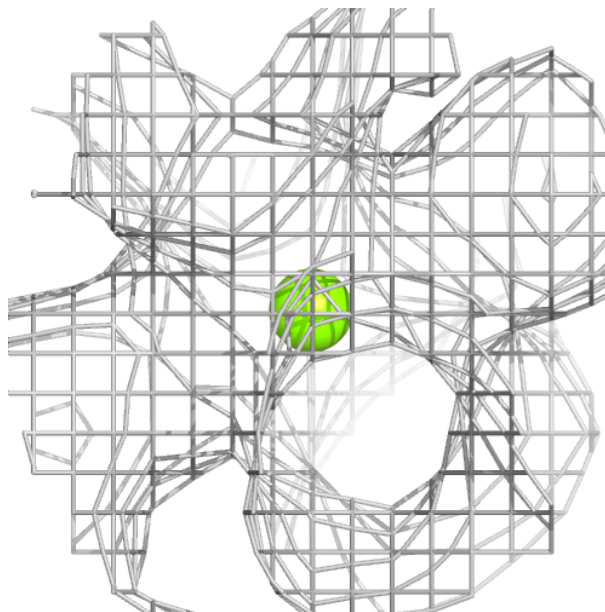
Electron density around MG F 602:

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



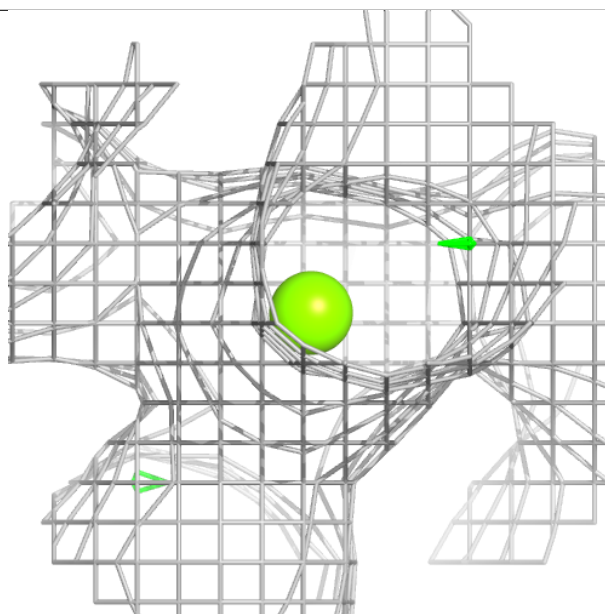
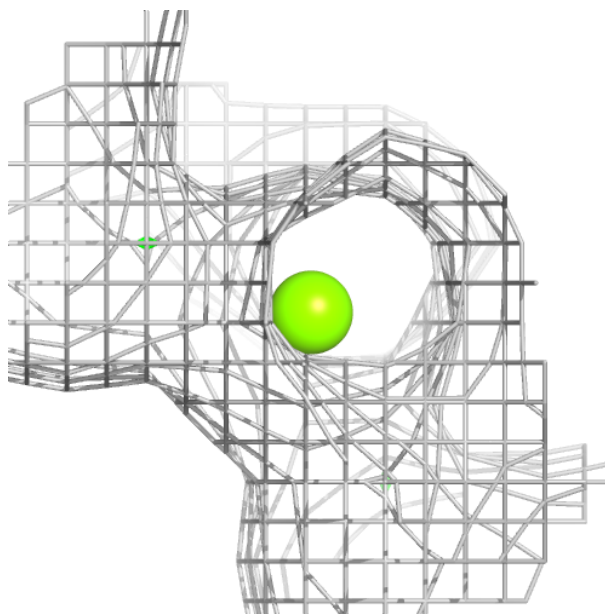
Electron density around MG A 601:

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



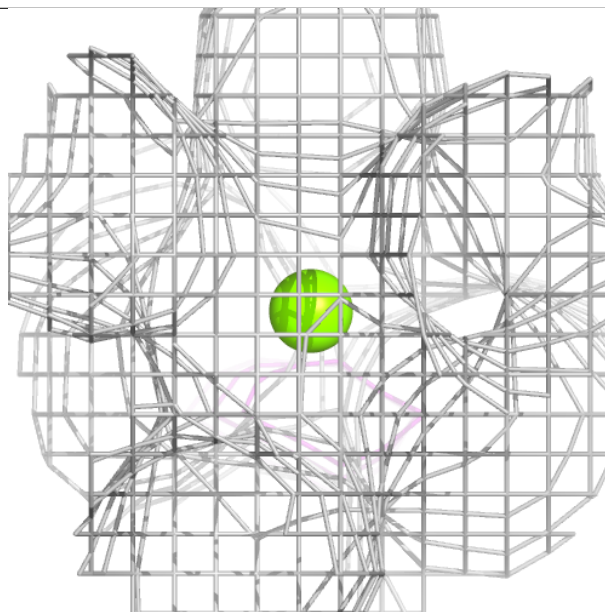
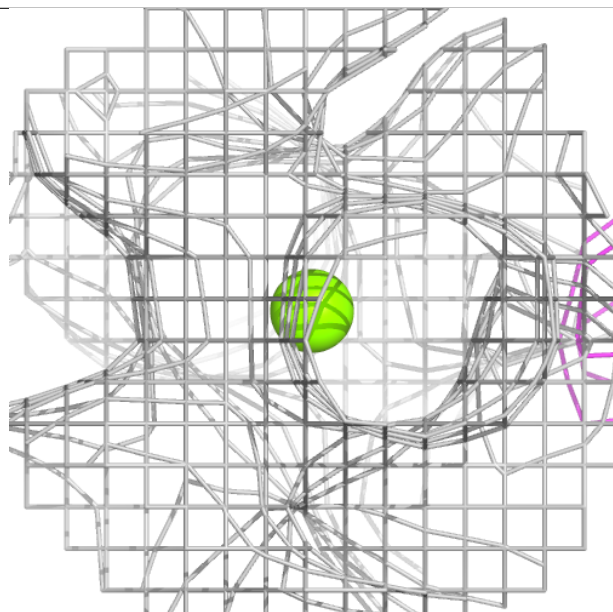
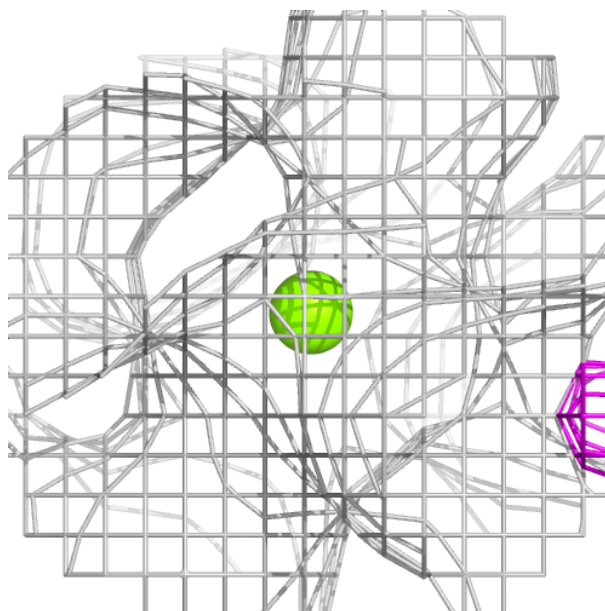
Electron density around MG A 602:

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



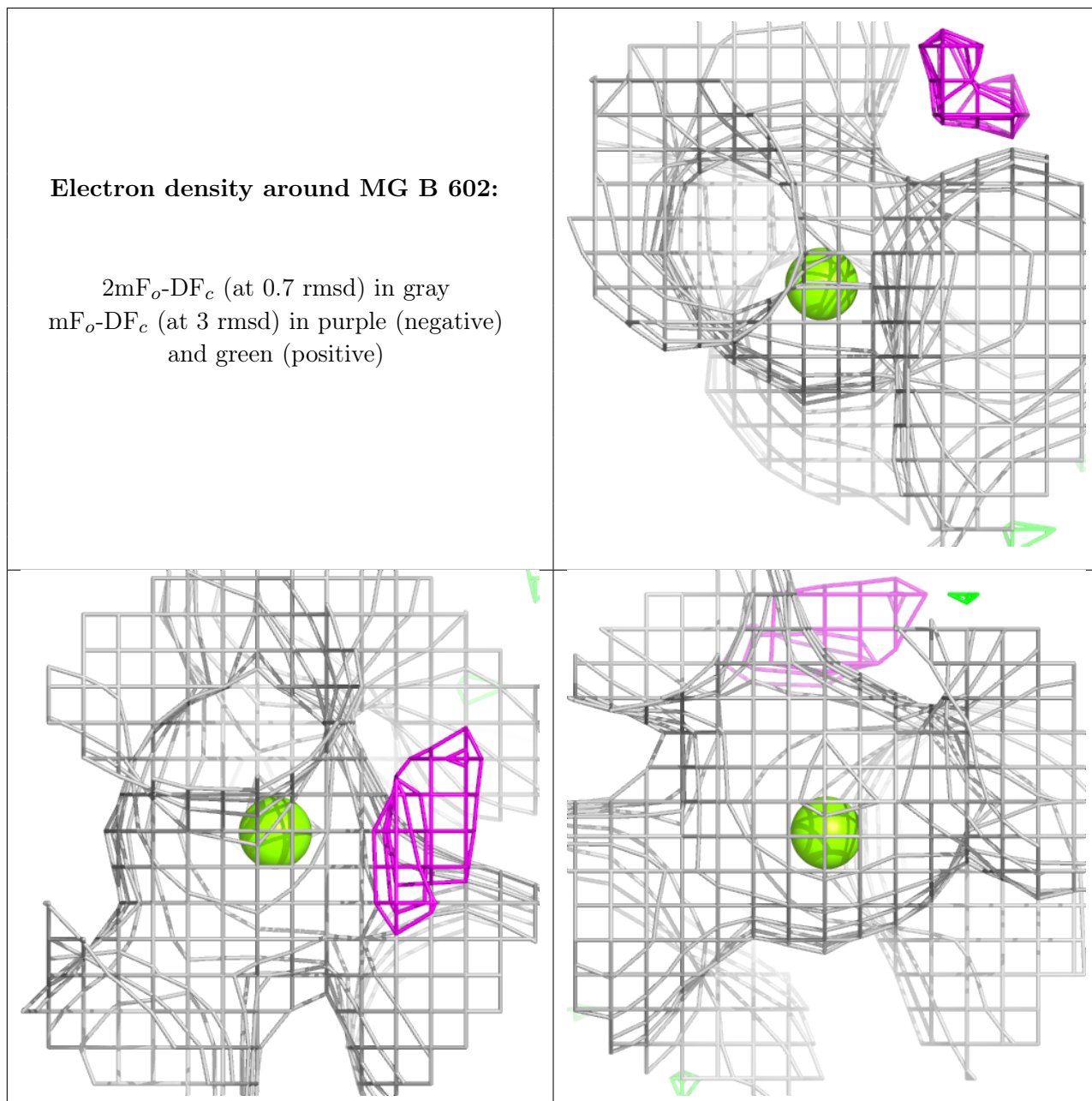
Electron density around MG B 601:

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



Electron density around MG B 602:

$2mF_o-DF_c$ (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.