



wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 05:02 pm BST

PDB ID : 3HYX
Title : 3-D X-Ray structure of the sulfide:quinone oxidoreductase from Aquifex aeolicus in complex with Aurachin C
Authors : Marcia, M.; Ermler, U.; Peng, G.H.; Michel, H.
Deposited on : 2009-06-23
Resolution : 2.90 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

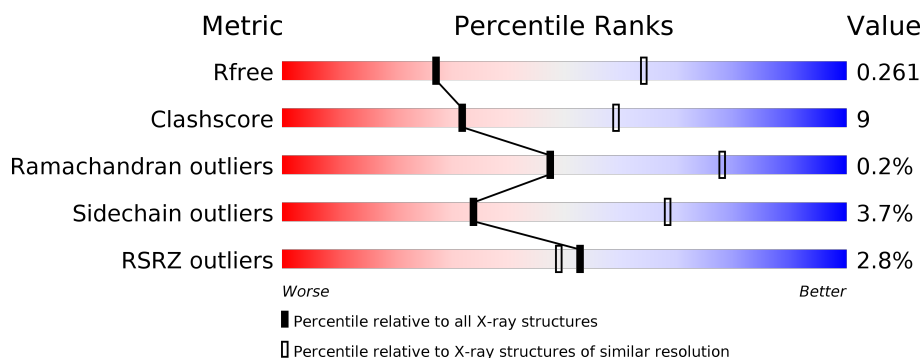
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 on 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	430	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>16%</div> </div> </div>
1	B	430	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>16%</div> </div> </div>
1	C	430	<div> <div>%</div> <div> <div></div> <div>79%</div> <div>20%</div> </div> </div>
1	D	430	<div> <div>8%</div> <div> <div></div> <div>82%</div> <div>17%</div> </div> </div>
1	E	430	<div> <div>3%</div> <div> <div></div> <div>82%</div> <div>17%</div> </div> </div>
1	F	430	<div> <div>2%</div> <div> <div></div> <div>82%</div> <div>18%</div> </div> </div>

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
2	SO4	D	432	-	-	X	-
2	SO4	E	434	-	-	X	-
2	SO4	F	434	-	-	-	X
4	AUK	A	501	-	-	-	X
4	AUK	B	501	-	-	-	X
4	AUK	C	501	-	-	X	-
4	AUK	D	501	-	-	X	-
4	AUK	E	501	-	-	-	X
4	AUK	F	501	-	-	-	X
5	LMT	A	600	-	-	-	X
5	LMT	B	600	-	-	-	X
5	LMT	C	600	-	-	-	X
5	LMT	E	600	-	-	X	X
5	LMT	F	600	-	-	-	X
7	PS9	A	800	-	-	X	X
7	PS9	B	800	-	-	X	X
7	PS9	C	800	-	-	X	X
7	PS9	D	800	-	-	X	X
7	PS9	E	800	-	-	X	X
7	PS9	F	800	-	-	-	X

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 21163 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 Sulfide-quinone reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	429	Total	C	N	O	S	0	4	0
			3345	2165	553	604	23			
1	B	429	Total	C	N	O	S	0	6	0
			3357	2173	553	608	23			
1	C	429	Total	C	N	O	S	0	5	0
			3351	2169	553	606	23			
1	D	429	Total	C	N	O	S	0	5	0
			3351	2169	553	606	23			
1	E	429	Total	C	N	O	S	0	5	0
			3351	2169	553	606	23			
1	F	429	Total	C	N	O	S	0	4	0
			3345	2165	553	604	23			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



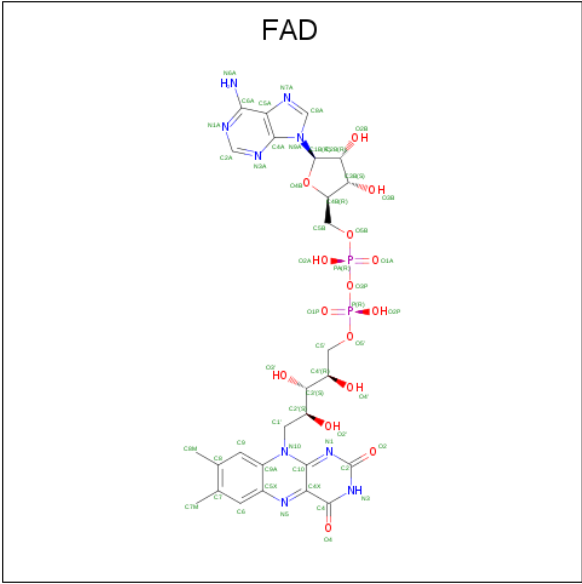
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0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

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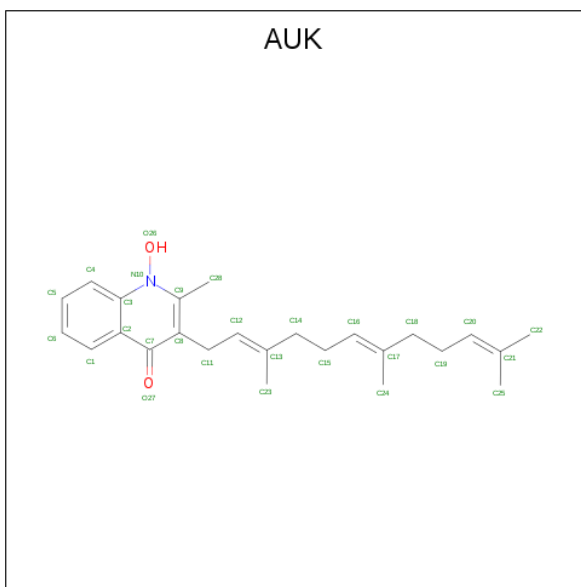
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



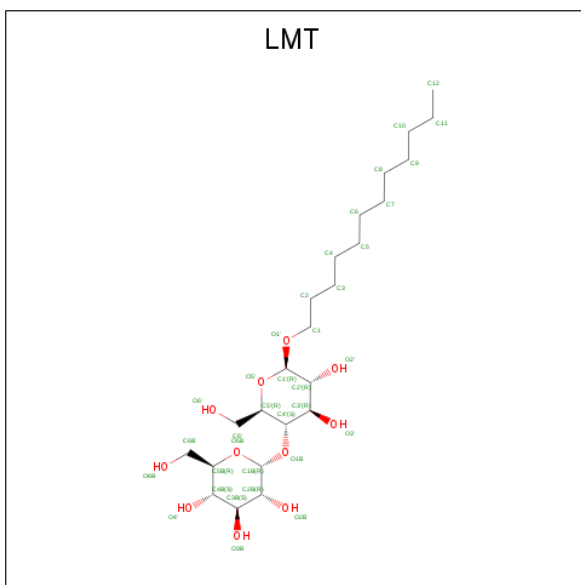
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	E	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	F	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is 1-hydroxy-2-methyl-3-[(2E,6E)-3,7,11-trimethyldodeca-2,6,10-trien-1-yl]quinol in-4(1H)-one (three-letter code: AUK) (formula: C₂₅H₃₃NO₂).



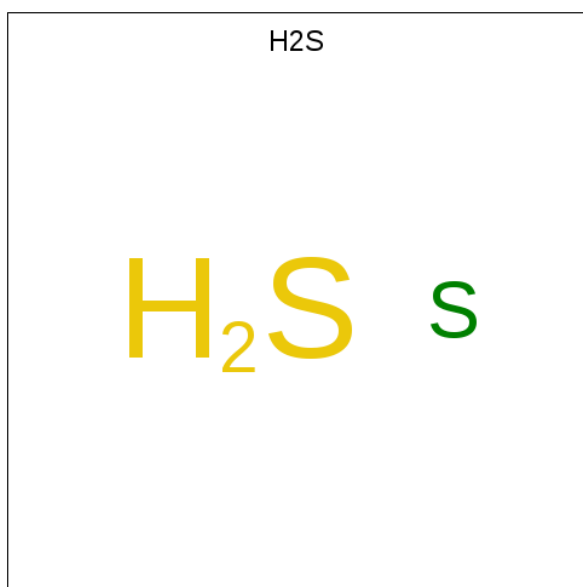
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			28	25	1	2		
4	B	1	Total	C	N	O	0	0
			28	25	1	2		
4	C	1	Total	C	N	O	0	0
			28	25	1	2		
4	D	1	Total	C	N	O	0	0
			28	25	1	2		
4	E	1	Total	C	N	O	0	0
			28	25	1	2		
4	F	1	Total	C	N	O	0	0
			28	25	1	2		

- Molecule 5 is DODECYL-BETA-D-MALTOSE (three-letter code: LMT) (formula: $C_{24}H_{46}O_{11}$).



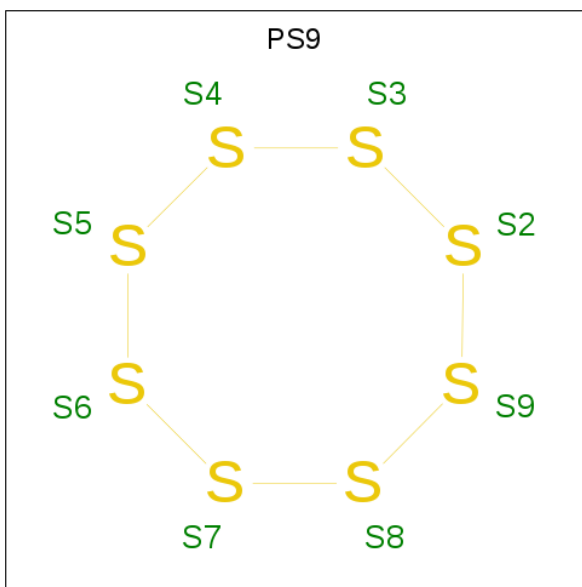
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 35	C 24	O 11	0	0
5	B	1	Total 35	C 24	O 11	0	0
5	C	1	Total 35	C 24	O 11	0	0
5	D	1	Total 35	C 24	O 11	0	0
5	E	1	Total 35	C 24	O 11	0	0
5	F	1	Total 35	C 24	O 11	0	0

- Molecule 6 is HYDROSULFURIC ACID (three-letter code: H2S) (formula: H_2S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total S 1 1	0	0
6	B	1	Total S 1 1	0	0
6	C	1	Total S 1 1	0	0
6	D	1	Total S 1 1	0	0
6	E	1	Total S 1 1	0	0
6	F	1	Total S 1 1	0	0

- Molecule 7 is octathiocane (three-letter code: PS9) (formula: S₈).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total S 7 7	0	0
7	B	1	Total S 8 8	0	0
7	C	1	Total S 8 8	0	0
7	D	1	Total S 8 8	0	0
7	E	1	Total S 8 8	0	0
7	F	1	Total S 8 8	0	0

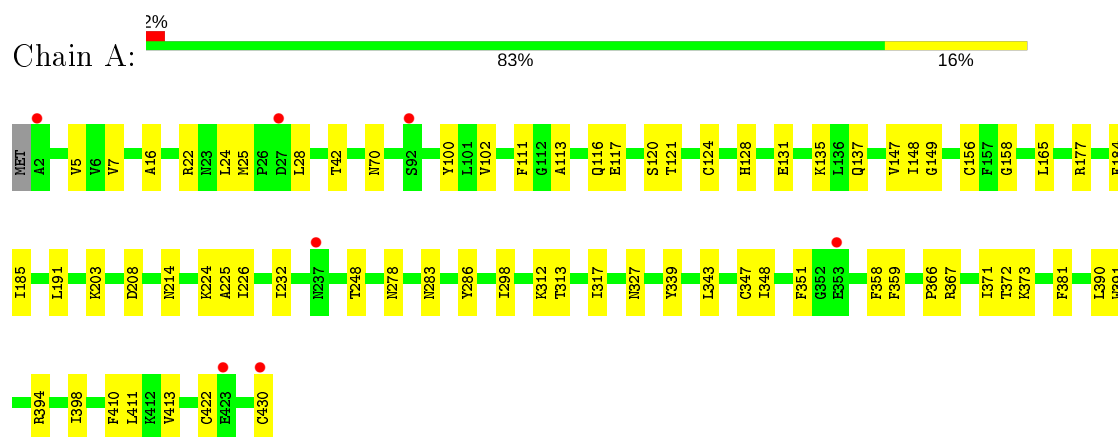
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	47	Total O 47 47	0	0
8	B	33	Total O 33 33	0	0
8	C	33	Total O 33 33	0	0
8	D	22	Total O 22 22	0	0
8	E	25	Total O 25 25	0	0
8	F	34	Total O 34 34	0	0

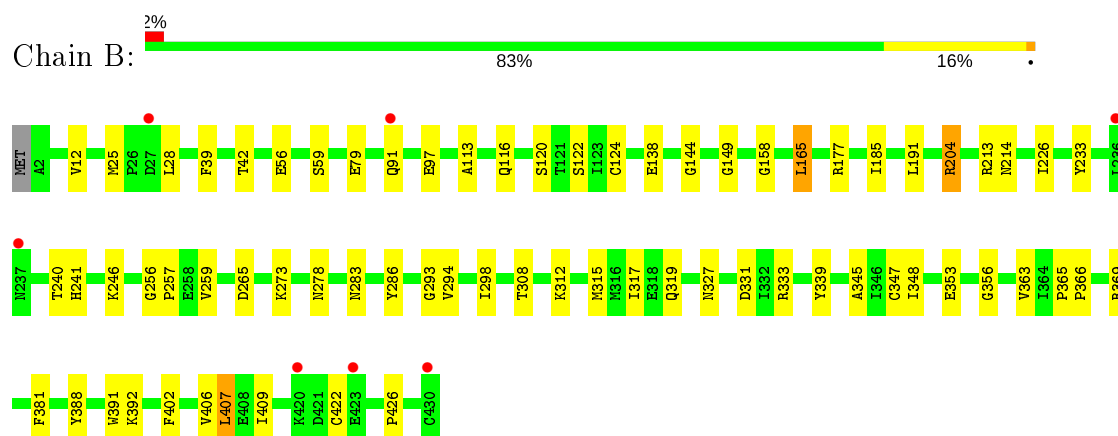
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

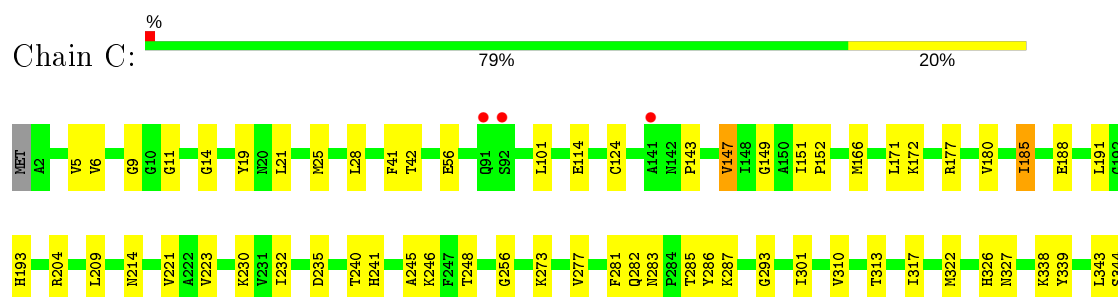
- Molecule 1: Sulfide-quinone reductase



- Molecule 1: Sulfide-quinone reductase

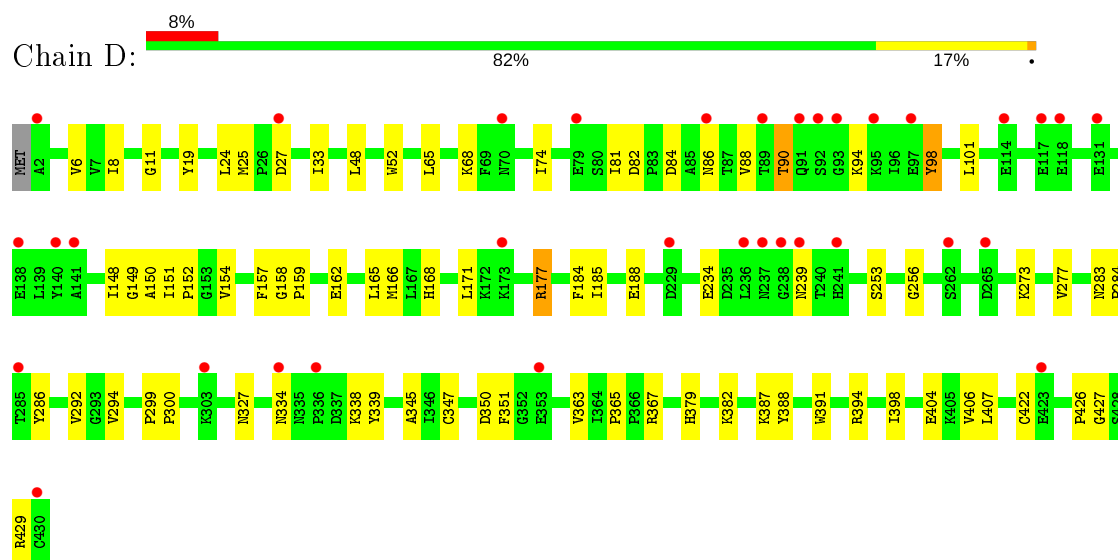


- Molecule 1: Sulfide-quinone reductase

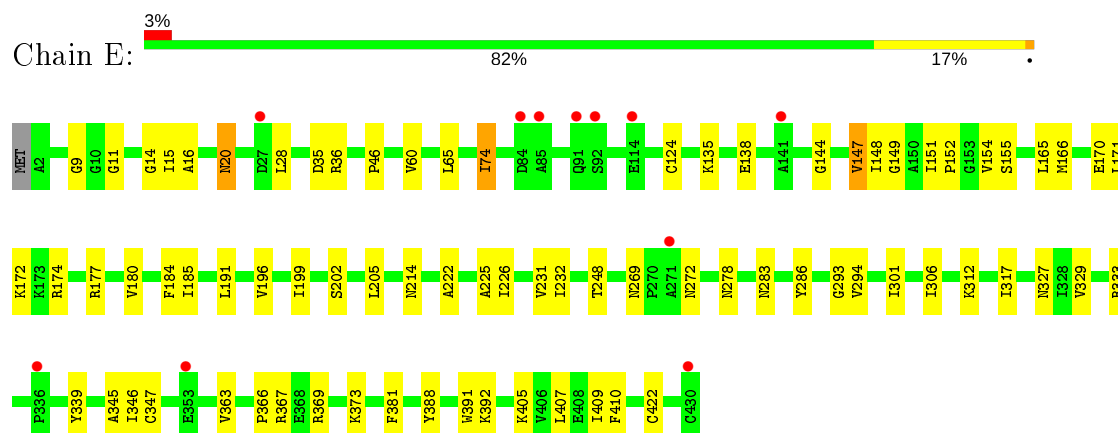




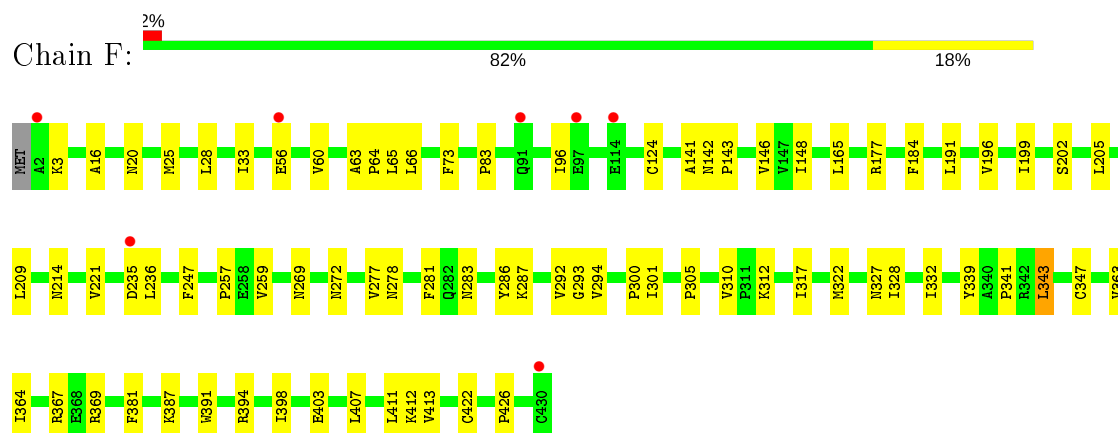
• Molecule 1: Sulfide-quinone reductase



• Molecule 1: Sulfide-quinone reductase



• Molecule 1: Sulfide-quinone reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	111.18Å 154.23Å 176.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.13 – 2.90 20.13 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (20.13-2.90) 98.9 (20.13-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.88Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.181 , 0.240 0.217 , 0.261	Depositor DCC
R_{free} test set	3388 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	49.4	Xtriage
Anisotropy	0.104	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	21163	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% 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: CSS, AUK, LMT, H2S, PS9, SO4, FAD

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	0.50	1/3439 (0.0%)	0.58	0/4668
1	B	0.48	0/3457	0.56	0/4692
1	C	0.48	0/3448	0.58	0/4680
1	D	0.50	4/3448 (0.1%)	0.58	1/4680 (0.0%)
1	E	0.45	0/3448	0.56	0/4680
1	F	0.45	0/3439	0.56	0/4668
All	All	0.48	5/20679 (0.0%)	0.57	1/28068 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	430	CYS	CB-SG	5.94	1.92	1.82
1	D	82	ASP	C-O	5.66	1.34	1.23
1	D	86	ASN	C-N	5.40	1.46	1.34
1	D	84	ASP	CG-OD2	5.23	1.37	1.25
1	D	98	TYR	CE2-CZ	5.11	1.45	1.38

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	98	TYR	CB-CG-CD2	-6.01	117.40	121.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3345	0	3346	40	0
1	B	3357	0	3358	41	0
1	C	3351	0	3352	55	0
1	D	3351	0	3352	50	0
1	E	3351	0	3352	52	0
1	F	3345	0	3346	57	0
2	A	15	0	0	1	0
2	B	25	0	0	2	0
2	C	20	0	0	2	0
2	D	25	0	0	4	0
2	E	25	0	0	4	0
2	F	10	0	0	1	0
3	A	53	0	30	1	0
3	B	53	0	30	3	0
3	C	53	0	29	1	0
3	D	53	0	29	1	0
3	E	53	0	29	2	0
3	F	53	0	29	2	0
4	A	28	0	33	16	0
4	B	28	0	33	15	0
4	C	28	0	33	25	0
4	D	28	0	33	26	0
4	E	28	0	33	20	0
4	F	28	0	33	6	0
5	A	35	0	46	15	0
5	B	35	0	46	10	0
5	C	35	0	46	11	0
5	D	35	0	46	4	0
5	E	35	0	46	26	0
5	F	35	0	46	5	0
6	A	1	0	0	1	0
6	B	1	0	0	1	0
6	C	1	0	0	1	0
6	D	1	0	0	0	0
6	E	1	0	0	1	0
6	F	1	0	0	1	0
7	A	7	0	0	4	0
7	B	8	0	0	3	0
7	C	8	0	0	2	0
7	D	8	0	0	4	0
7	E	8	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	F	8	0	0	1	0
8	A	47	0	0	1	0
8	B	33	0	0	1	0
8	C	33	0	0	1	0
8	D	22	0	0	0	0
8	E	25	0	0	1	0
8	F	34	0	0	3	0
All	All	21163	0	20756	372	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 372 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:C:501:AUK:H23A	4:D:501:AUK:C25	1.18	1.59
4:C:501:AUK:C23	4:D:501:AUK:H25	1.31	1.58
4:E:501:AUK:C21	5:E:600:LMT:H12	1.56	1.33
4:E:501:AUK:H25B	5:E:600:LMT:O1'	1.27	1.30
4:C:501:AUK:C23	4:D:501:AUK:C25	1.95	1.29

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	429/430 (100%)	414 (96%)	14 (3%)	1 (0%)	47	78
1	B	431/430 (100%)	417 (97%)	14 (3%)	0	100	100
1	C	430/430 (100%)	421 (98%)	9 (2%)	0	100	100
1	D	430/430 (100%)	416 (97%)	12 (3%)	2 (0%)	29	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	430/430 (100%)	413 (96%)	17 (4%)	0	100	100
1	F	429/430 (100%)	413 (96%)	15 (4%)	1 (0%)	47	78
All	All	2579/2580 (100%)	2494 (97%)	81 (3%)	4 (0%)	47	78

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	334	ASN
1	F	287	LYS
1	A	158	GLY
1	D	284	PRO

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	358/356 (101%)	347 (97%)	11 (3%)	40	74
1	B	360/356 (101%)	342 (95%)	18 (5%)	24	57
1	C	359/356 (101%)	338 (94%)	21 (6%)	20	50
1	D	359/356 (101%)	348 (97%)	11 (3%)	40	74
1	E	359/356 (101%)	347 (97%)	12 (3%)	38	72
1	F	358/356 (101%)	350 (98%)	8 (2%)	52	81
All	All	2153/2136 (101%)	2072 (96%)	81 (4%)	34	67

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	172	LYS
1	C	338	LYS
1	F	142	ASN
1	C	177	ARG
1	C	246	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	241	HIS
1	C	395	ASN
1	F	237	ASN
1	C	283	ASN
1	C	327	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

12 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z > 2$
1	CSS	B	156[B]	7	4,6,7	1.11	0	1,6,8	1.36	0
1	CSS	E	156[B]	7	4,6,7	0.99	0	1,6,8	1.39	0
1	CSS	E	156[A]	-	4,5,7	1.04	0	1,5,8	0.05	0
1	CSS	A	156[B]	7	4,6,7	1.16	0	1,6,8	0.46	0
1	CSS	A	156[A]	-	4,5,7	1.15	0	1,5,8	1.09	0
1	CSS	C	156[A]	-	4,5,7	1.14	0	1,5,8	0.24	0
1	CSS	D	156[B]	7	4,6,7	1.09	0	1,6,8	0.36	0
1	CSS	C	156[B]	7	4,6,7	1.12	0	1,6,8	1.45	0
1	CSS	D	156[A]	-	4,5,7	1.28	0	1,5,8	1.80	0
1	CSS	F	156[A]	-	4,5,7	1.22	0	1,5,8	0.74	0
1	CSS	F	156[B]	7	4,6,7	1.21	0	1,6,8	0.90	0
1	CSS	B	156[A]	-	4,5,7	1.22	0	1,5,8	0.97	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
1	CSS	B	156[B]	7	-	1/1/5/7	-
1	CSS	E	156[B]	7	-	1/1/5/7	-
1	CSS	E	156[A]	-	-	1/1/4/7	-
1	CSS	A	156[B]	7	-	0/1/5/7	-
1	CSS	A	156[A]	-	-	1/1/4/7	-
1	CSS	C	156[A]	-	-	1/1/4/7	-
1	CSS	D	156[B]	7	-	0/1/5/7	-
1	CSS	C	156[B]	7	-	1/1/5/7	-
1	CSS	D	156[A]	-	-	1/1/4/7	-
1	CSS	F	156[A]	-	-	1/1/4/7	-
1	CSS	F	156[B]	7	-	1/1/5/7	-
1	CSS	B	156[A]	-	-	1/1/4/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	E	156[B]	CSS	N-CA-CB-SG
1	E	156[A]	CSS	N-CA-CB-SG
1	A	156[A]	CSS	N-CA-CB-SG
1	C	156[B]	CSS	N-CA-CB-SG
1	D	156[A]	CSS	N-CA-CB-SG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	156[A]	CSS	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 54 ligands modelled in this entry, 6 are modelled with single atom - leaving 48 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	FAD	D	441	6	51,58,58	1.13	3 (5%)	60,89,89	1.65	9 (15%)
7	PS9	B	800	1	8,8,8	0.83	0	8,8,8	1.09	0
4	AUK	B	501	-	27,29,29	2.65	4 (14%)	31,39,39	1.39	6 (19%)
2	SO4	C	432	-	4,4,4	0.11	0	6,6,6	0.27	0
3	FAD	A	441	6	51,58,58	1.16	2 (3%)	60,89,89	1.67	11 (18%)
4	AUK	D	501	-	27,29,29	2.67	4 (14%)	31,39,39	1.56	7 (22%)
4	AUK	C	501	-	27,29,29	2.63	4 (14%)	31,39,39	1.45	6 (19%)
4	AUK	A	501	-	27,29,29	2.61	4 (14%)	31,39,39	1.50	4 (12%)
2	SO4	C	434	-	4,4,4	0.15	0	6,6,6	0.23	0
2	SO4	E	434	-	4,4,4	0.15	0	6,6,6	0.15	0
2	SO4	B	431	-	4,4,4	0.14	0	6,6,6	0.31	0
2	SO4	D	432	-	4,4,4	0.17	0	6,6,6	0.30	0
2	SO4	F	434	-	4,4,4	0.12	0	6,6,6	0.33	0
5	LMT	A	600	-	36,36,36	0.55	1 (2%)	47,47,47	1.01	3 (6%)
5	LMT	E	600	-	36,36,36	0.50	0	47,47,47	1.07	5 (10%)
2	SO4	E	435	-	4,4,4	0.19	0	6,6,6	0.40	0
2	SO4	B	435	-	4,4,4	0.16	0	6,6,6	0.24	0
2	SO4	E	431	-	4,4,4	0.16	0	6,6,6	0.11	0
2	SO4	B	432	-	4,4,4	0.11	0	6,6,6	0.26	0
5	LMT	B	600	-	36,36,36	0.61	1 (2%)	47,47,47	1.05	3 (6%)
7	PS9	C	800	1	8,8,8	0.88	0	8,8,8	1.11	0
2	SO4	D	433	-	4,4,4	0.15	0	6,6,6	0.10	0
2	SO4	B	433	-	4,4,4	0.17	0	6,6,6	0.39	0
3	FAD	C	441	6	51,58,58	1.09	2 (3%)	60,89,89	1.77	13 (21%)
7	PS9	E	800	1	8,8,8	0.86	0	8,8,8	0.99	0
2	SO4	D	434	-	4,4,4	0.13	0	6,6,6	0.13	0
5	LMT	C	600	-	36,36,36	0.51	0	47,47,47	1.05	4 (8%)
3	FAD	B	441	6	51,58,58	1.11	3 (5%)	60,89,89	1.60	11 (18%)
2	SO4	B	434	-	4,4,4	0.12	0	6,6,6	0.20	0
3	FAD	E	441	6	51,58,58	1.05	1 (1%)	60,89,89	1.80	11 (18%)
2	SO4	A	431	-	4,4,4	0.14	0	6,6,6	0.20	0
2	SO4	E	433	-	4,4,4	0.13	0	6,6,6	0.17	0
2	SO4	D	435	-	4,4,4	0.16	0	6,6,6	0.15	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	AUK	F	501	-	27,29,29	2.69	4 (14%)	31,39,39	1.70	7 (22%)
2	SO4	D	431	-	4,4,4	0.13	0	6,6,6	0.14	0
5	LMT	F	600	-	36,36,36	0.64	1 (2%)	47,47,47	1.15	3 (6%)
2	SO4	A	434	-	4,4,4	0.17	0	6,6,6	0.18	0
2	SO4	C	433	-	4,4,4	0.13	0	6,6,6	0.37	0
2	SO4	A	433	-	4,4,4	0.14	0	6,6,6	0.14	0
7	PS9	D	800	1	8,8,8	0.81	0	8,8,8	1.15	0
2	SO4	F	433	-	4,4,4	0.13	0	6,6,6	0.26	0
2	SO4	E	432	-	4,4,4	0.14	0	6,6,6	0.19	0
7	PS9	F	800	1	8,8,8	0.86	0	8,8,8	0.96	0
5	LMT	D	600	-	36,36,36	0.86	2 (5%)	47,47,47	1.00	1 (2%)
2	SO4	C	431	-	4,4,4	0.18	0	6,6,6	0.28	0
4	AUK	E	501	-	27,29,29	2.59	4 (14%)	31,39,39	1.57	6 (19%)
7	PS9	A	800	1	4,6,8	1.54	0	3,5,8	1.26	0
3	FAD	F	441	6	51,58,58	1.11	3 (5%)	60,89,89	1.73	10 (16%)

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
3	FAD	D	441	6	-	10/30/50/50	0/6/6/6
7	PS9	B	800	1	-	-	0/1/1/1
4	AUK	B	501	-	-	6/17/17/17	0/2/2/2
3	FAD	A	441	6	-	10/30/50/50	0/6/6/6
4	AUK	D	501	-	-	5/17/17/17	0/2/2/2
4	AUK	C	501	-	-	7/17/17/17	0/2/2/2
4	AUK	A	501	-	-	7/17/17/17	0/2/2/2
3	FAD	B	441	6	-	10/30/50/50	0/6/6/6
3	FAD	C	441	6	-	6/30/50/50	0/6/6/6
5	LMT	A	600	-	-	9/21/61/61	0/2/2/2
5	LMT	E	600	-	-	14/21/61/61	0/2/2/2
5	LMT	D	600	-	-	13/21/61/61	0/2/2/2
5	LMT	B	600	-	-	14/21/61/61	0/2/2/2
7	PS9	E	800	1	-	-	0/1/1/1
3	FAD	E	441	6	-	5/30/50/50	0/6/6/6
5	LMT	C	600	-	-	15/21/61/61	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	AUK	F	501	-	-	8/17/17/17	0/2/2/2
5	LMT	F	600	-	-	12/21/61/61	0/2/2/2
7	PS9	C	800	1	-	-	0/1/1/1
7	PS9	A	800	1	-	0/4/4/8	-
7	PS9	D	800	1	-	-	0/1/1/1
7	PS9	F	800	1	-	-	0/1/1/1
4	AUK	E	501	-	-	7/17/17/17	0/2/2/2
3	FAD	F	441	6	-	10/30/50/50	0/6/6/6

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	501	AUK	C2-C3	10.87	1.49	1.41
4	D	501	AUK	C2-C3	10.84	1.49	1.41
4	B	501	AUK	C2-C3	10.80	1.49	1.41
4	A	501	AUK	C2-C3	10.33	1.49	1.41
4	E	501	AUK	C2-C3	10.30	1.49	1.41

The worst 5 of 120 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	441	FAD	C4-N3-C2	6.62	120.73	115.14
3	D	441	FAD	C4-N3-C2	6.32	120.48	115.14
3	F	441	FAD	C4-N3-C2	6.07	120.27	115.14
3	C	441	FAD	C4-N3-C2	6.01	120.22	115.14
3	C	441	FAD	C1'-N10-C9A	5.84	122.89	118.29

There are no chirality outliers.

5 of 168 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	441	FAD	C5B-O5B-PA-O1A
3	D	441	FAD	PA-O3P-P-O5'
4	B	501	AUK	C12-C11-C8-C9
4	B	501	AUK	C13-C14-C15-C16
4	B	501	AUK	C16-C17-C18-C19

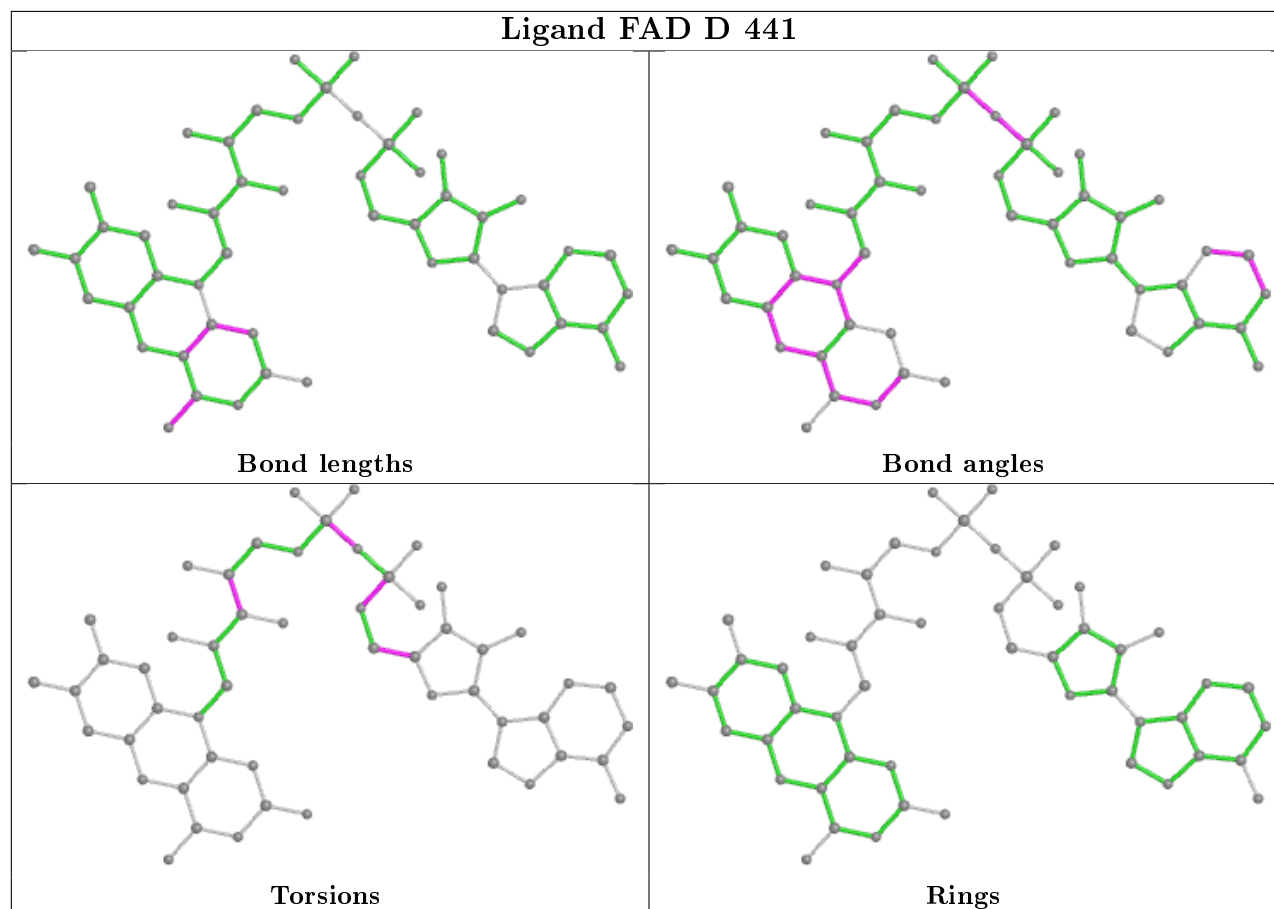
There are no ring outliers.

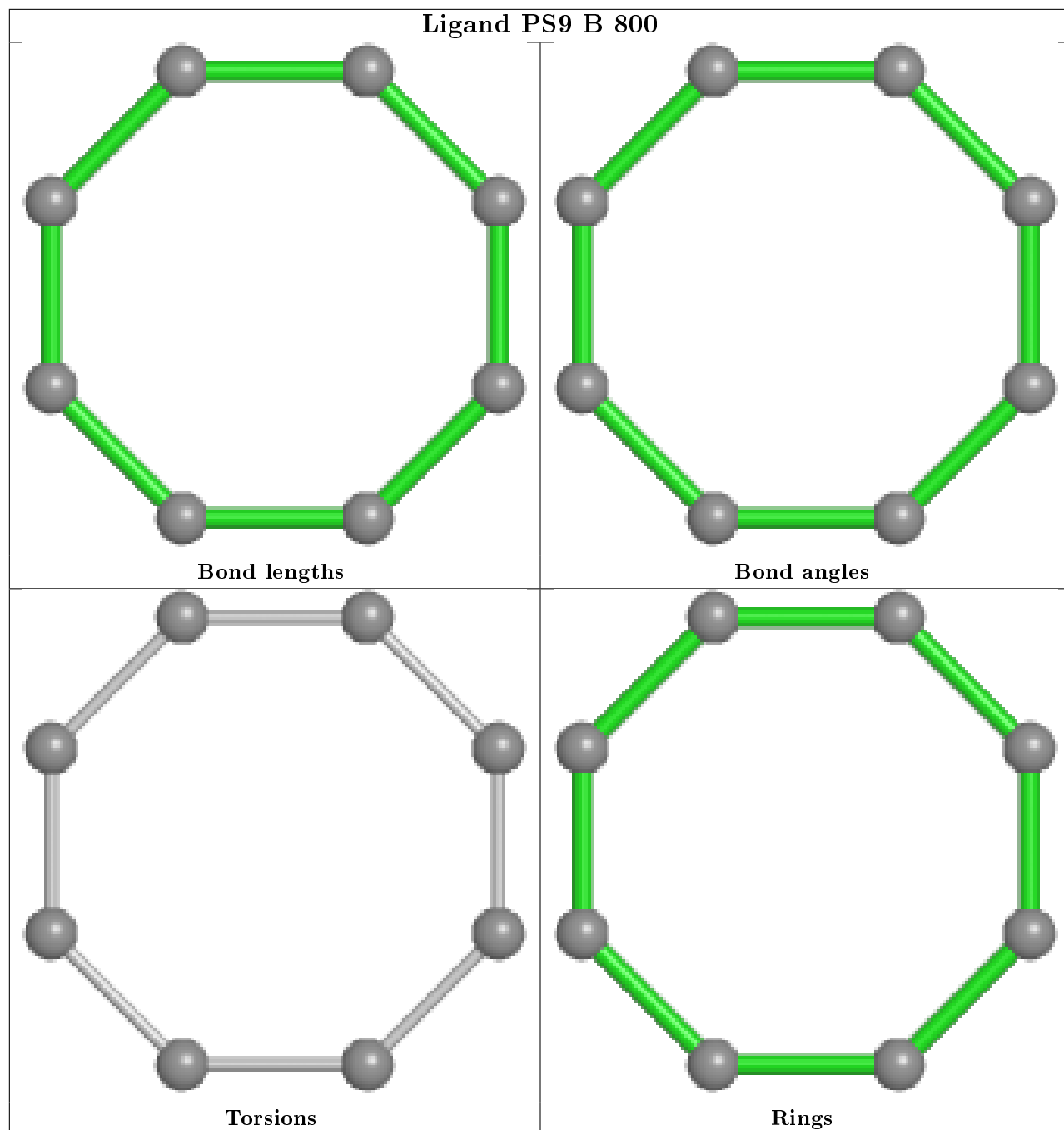
34 monomers are involved in 144 short contacts:

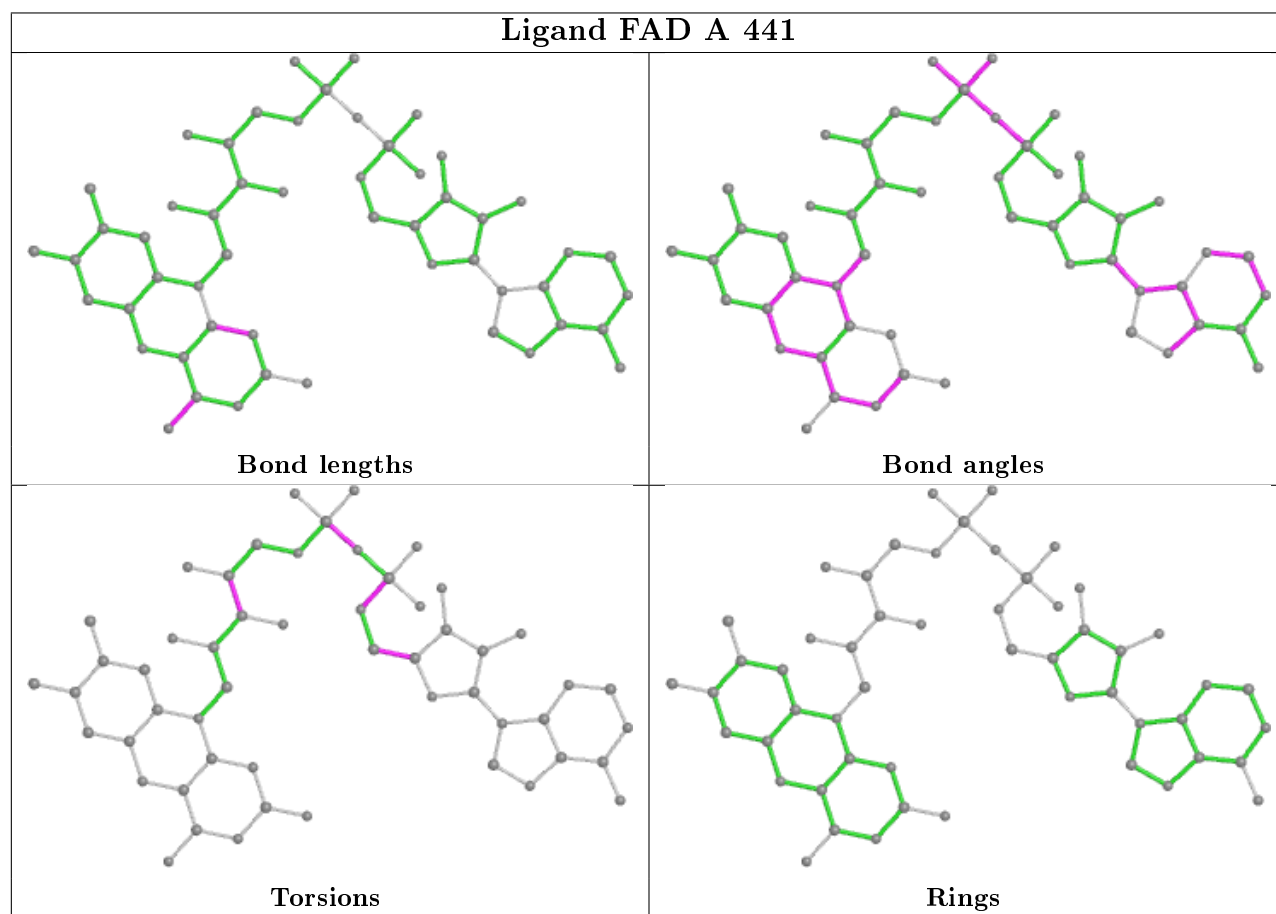
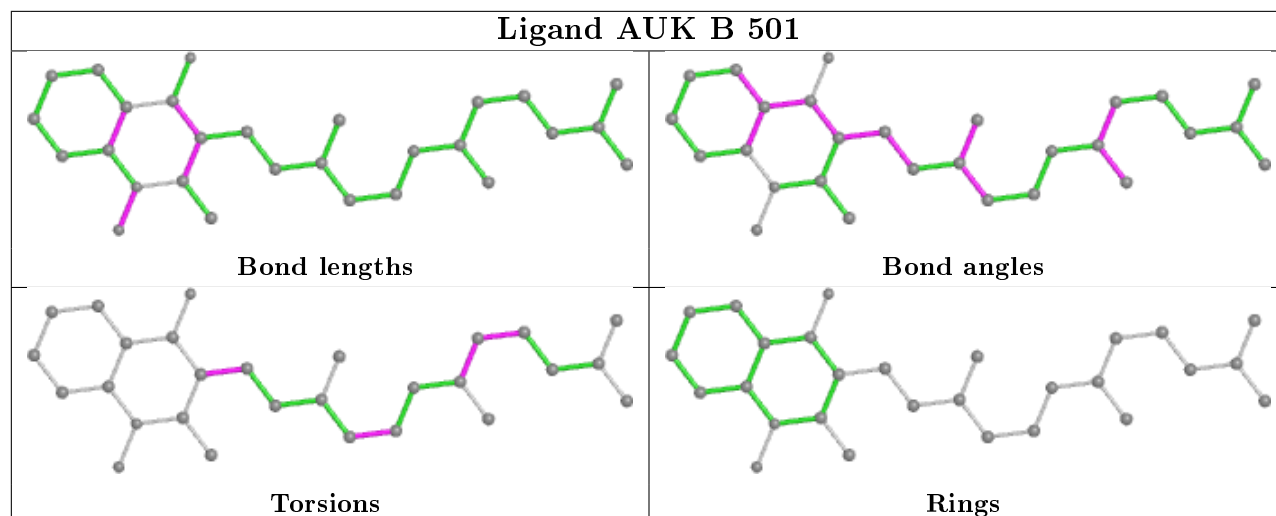
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	441	FAD	1	0
7	B	800	PS9	3	0
4	B	501	AUK	15	0
3	A	441	FAD	1	0
4	D	501	AUK	26	0
4	C	501	AUK	25	0
4	A	501	AUK	16	0
2	C	434	SO4	1	0
2	E	434	SO4	4	0
2	D	432	SO4	2	0
2	F	434	SO4	1	0
5	A	600	LMT	15	0
5	E	600	LMT	26	0
2	B	435	SO4	1	0
2	B	432	SO4	1	0
5	B	600	LMT	10	0
7	C	800	PS9	2	0
3	C	441	FAD	1	0
7	E	800	PS9	3	0
2	D	434	SO4	1	0
5	C	600	LMT	11	0
3	B	441	FAD	3	0
3	E	441	FAD	2	0
4	F	501	AUK	6	0
2	D	431	SO4	1	0
5	F	600	LMT	5	0
2	A	434	SO4	1	0
7	D	800	PS9	4	0
7	F	800	PS9	1	0
5	D	600	LMT	4	0
2	C	431	SO4	1	0
4	E	501	AUK	20	0
7	A	800	PS9	4	0
3	F	441	FAD	2	0

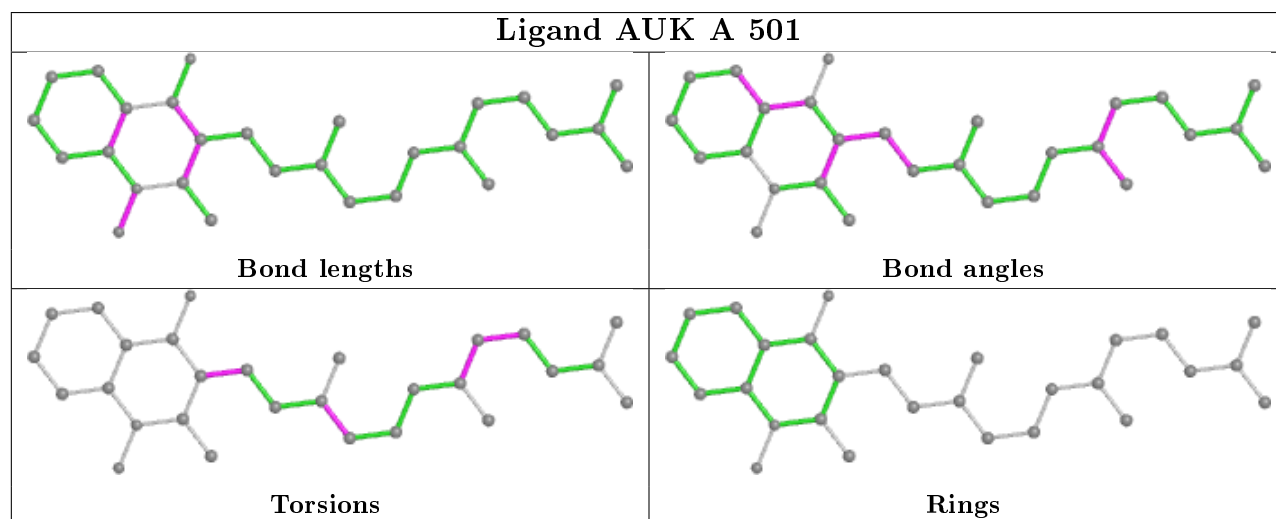
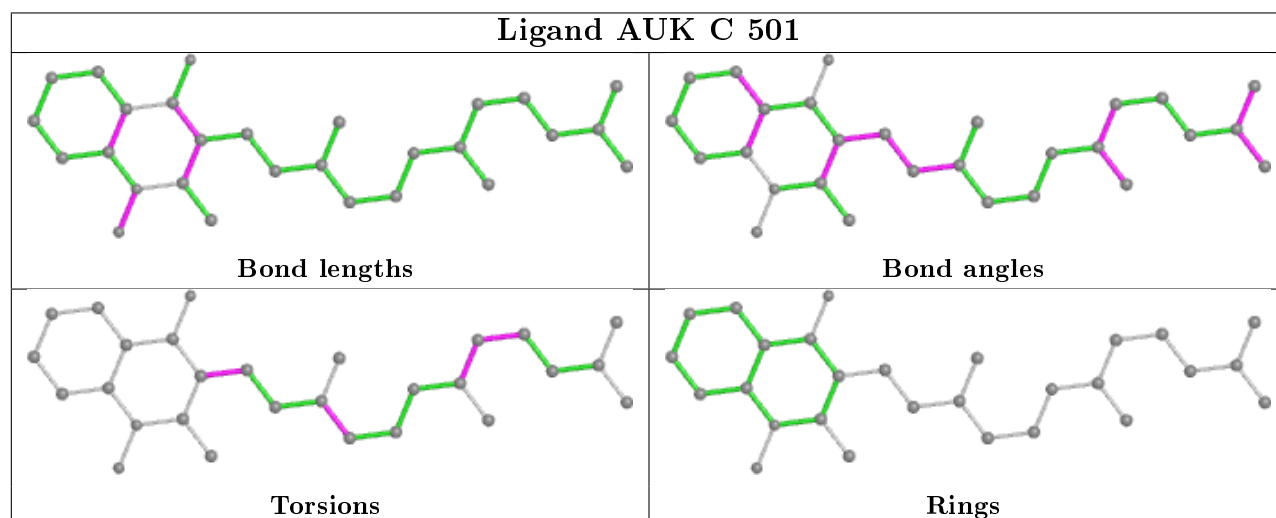
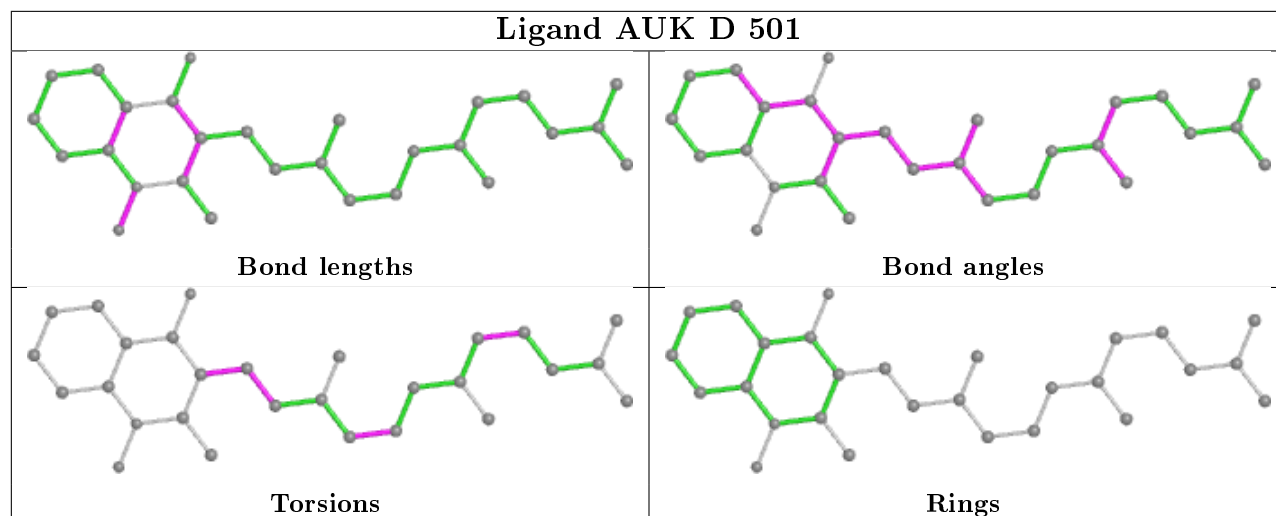
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

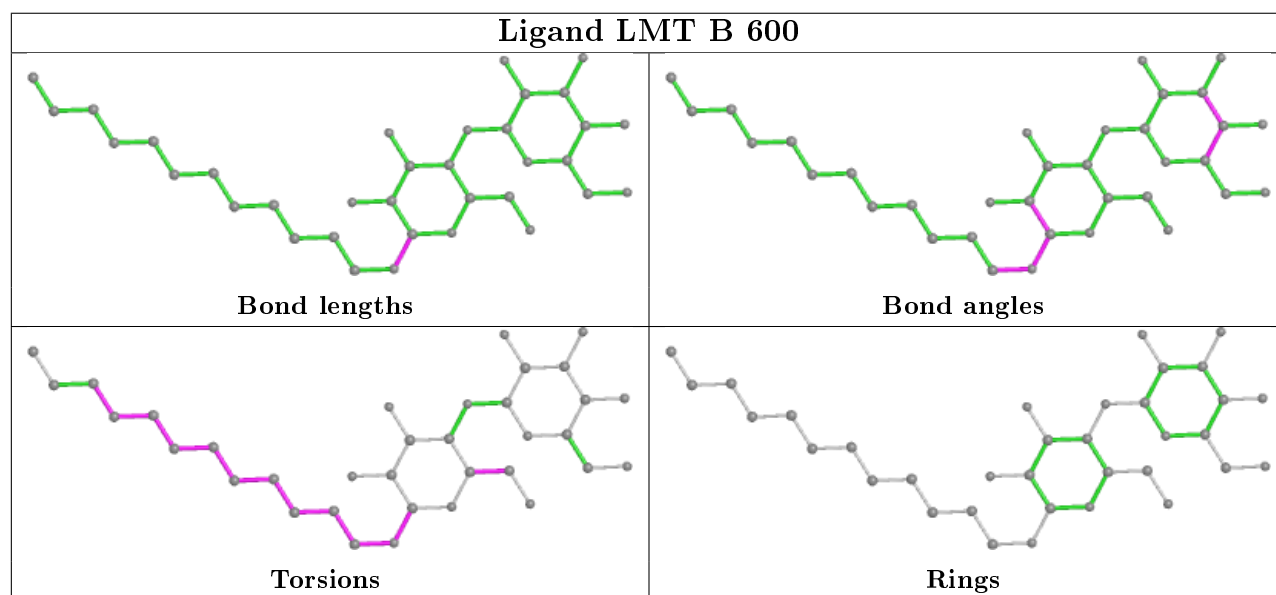
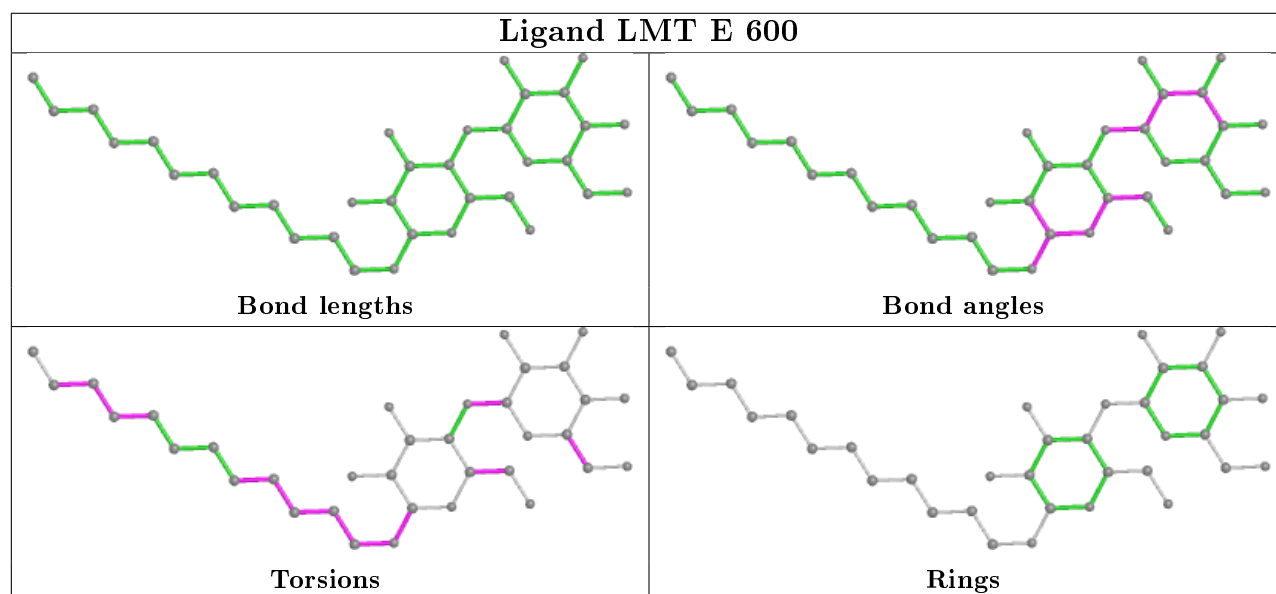
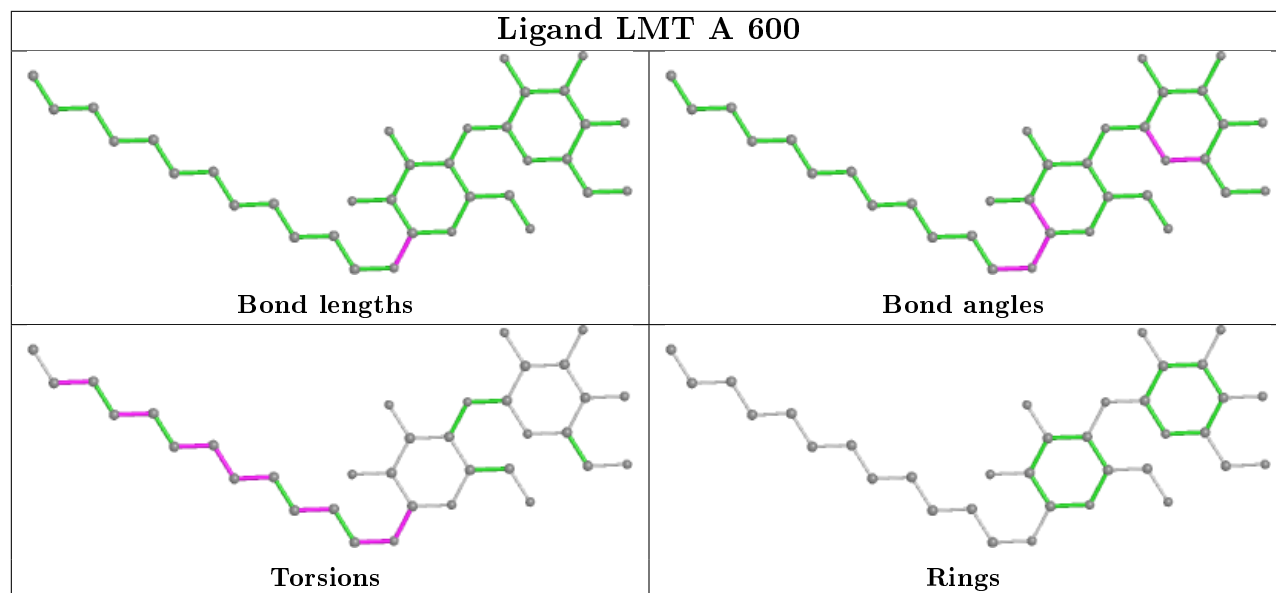
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

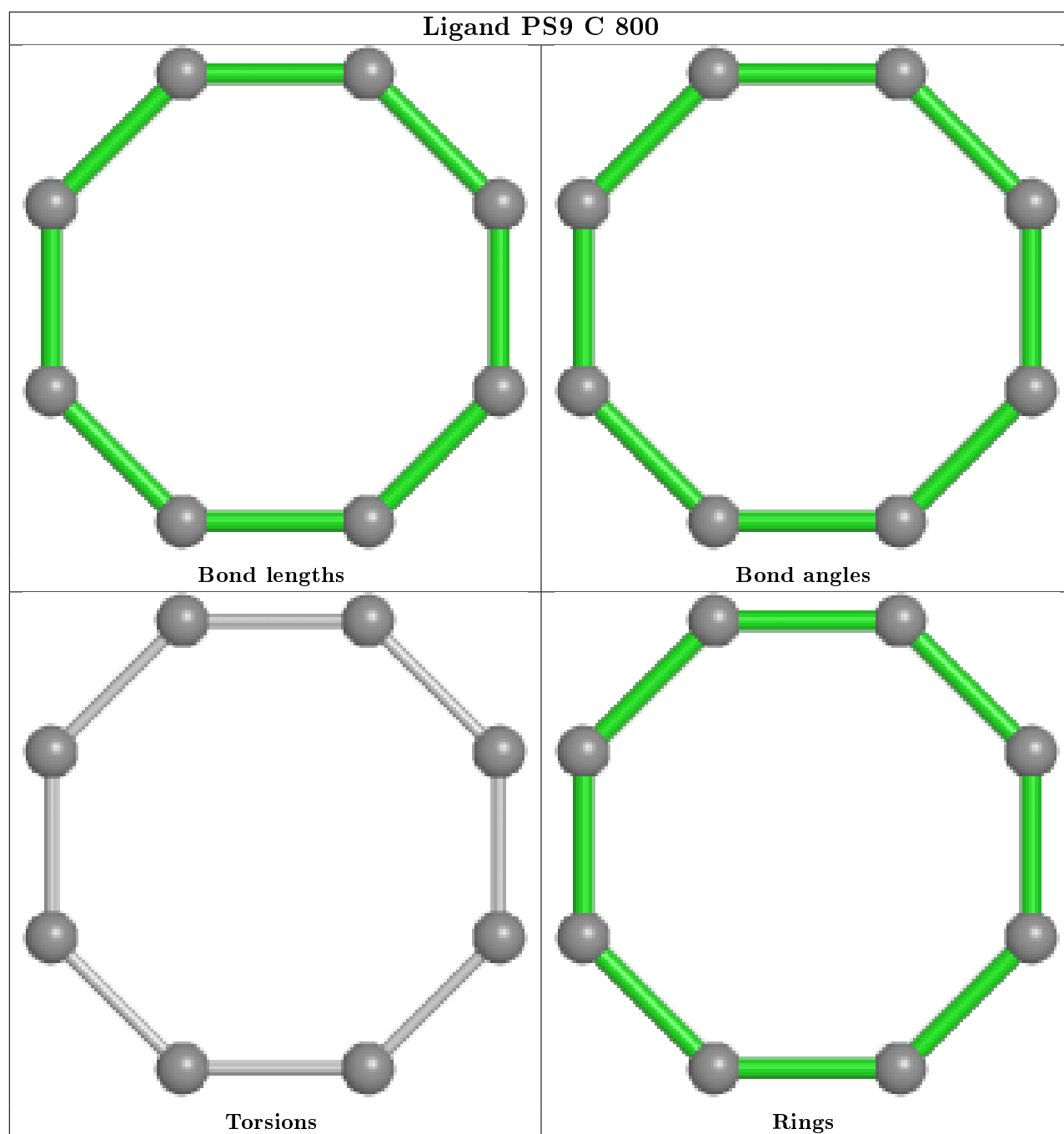


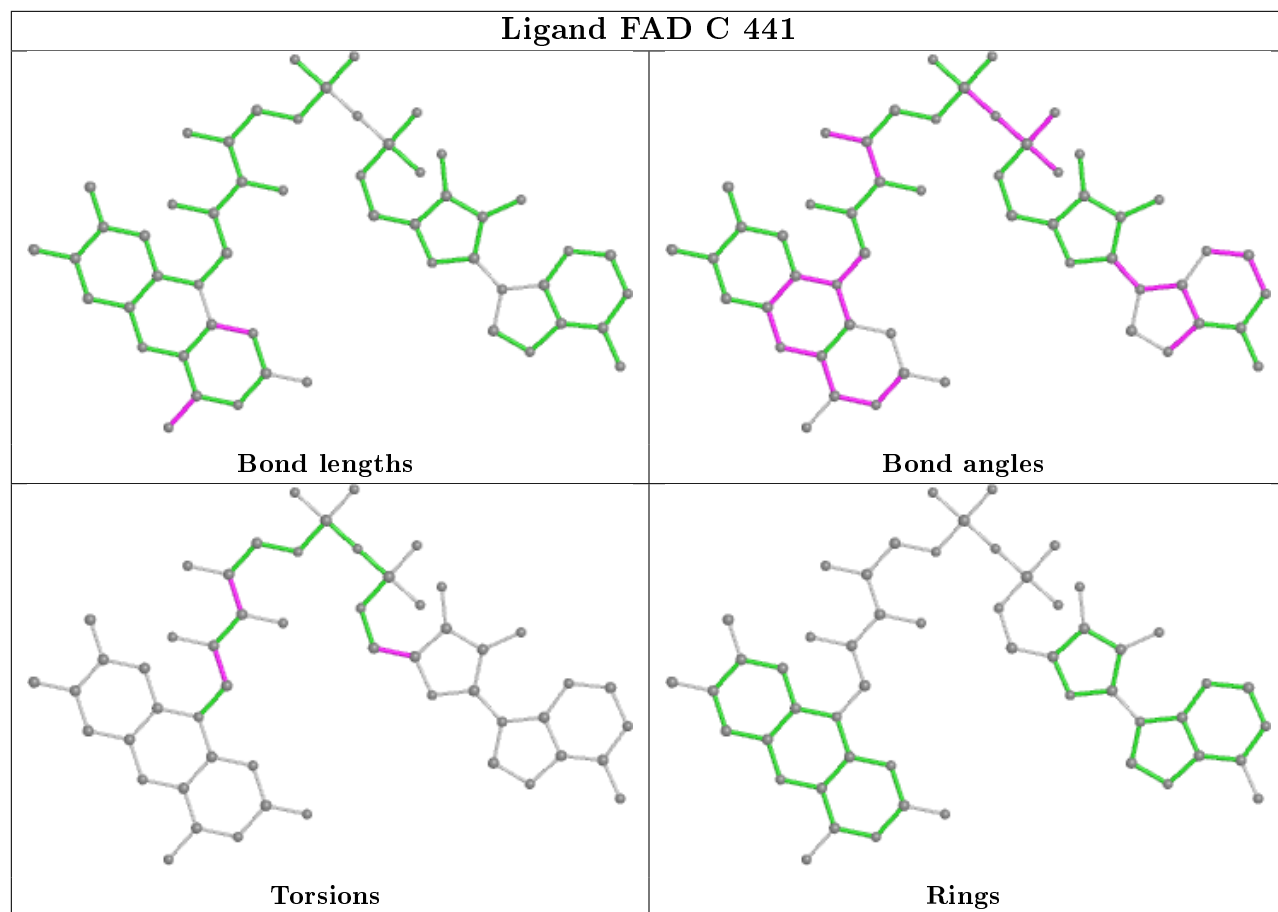


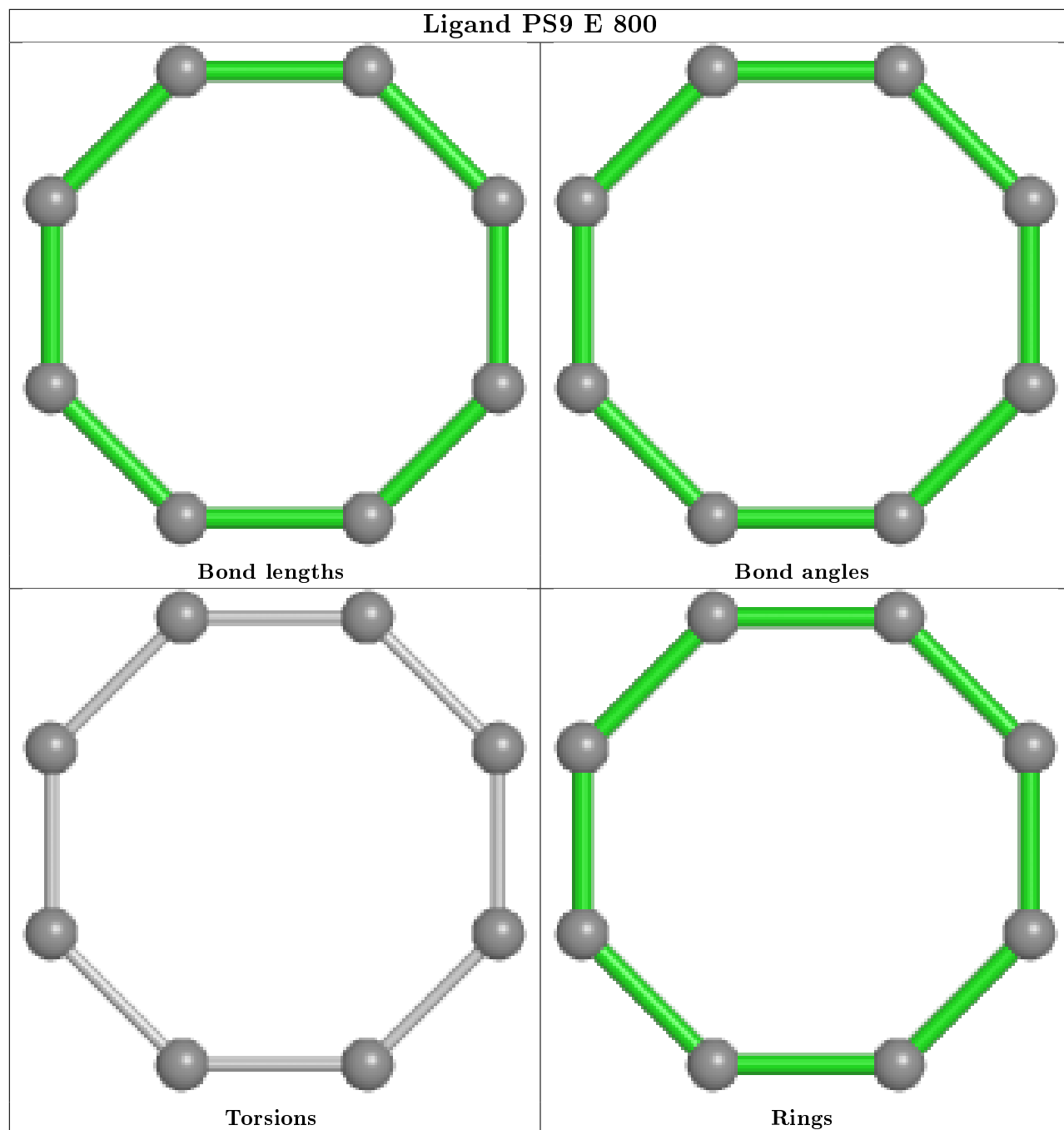


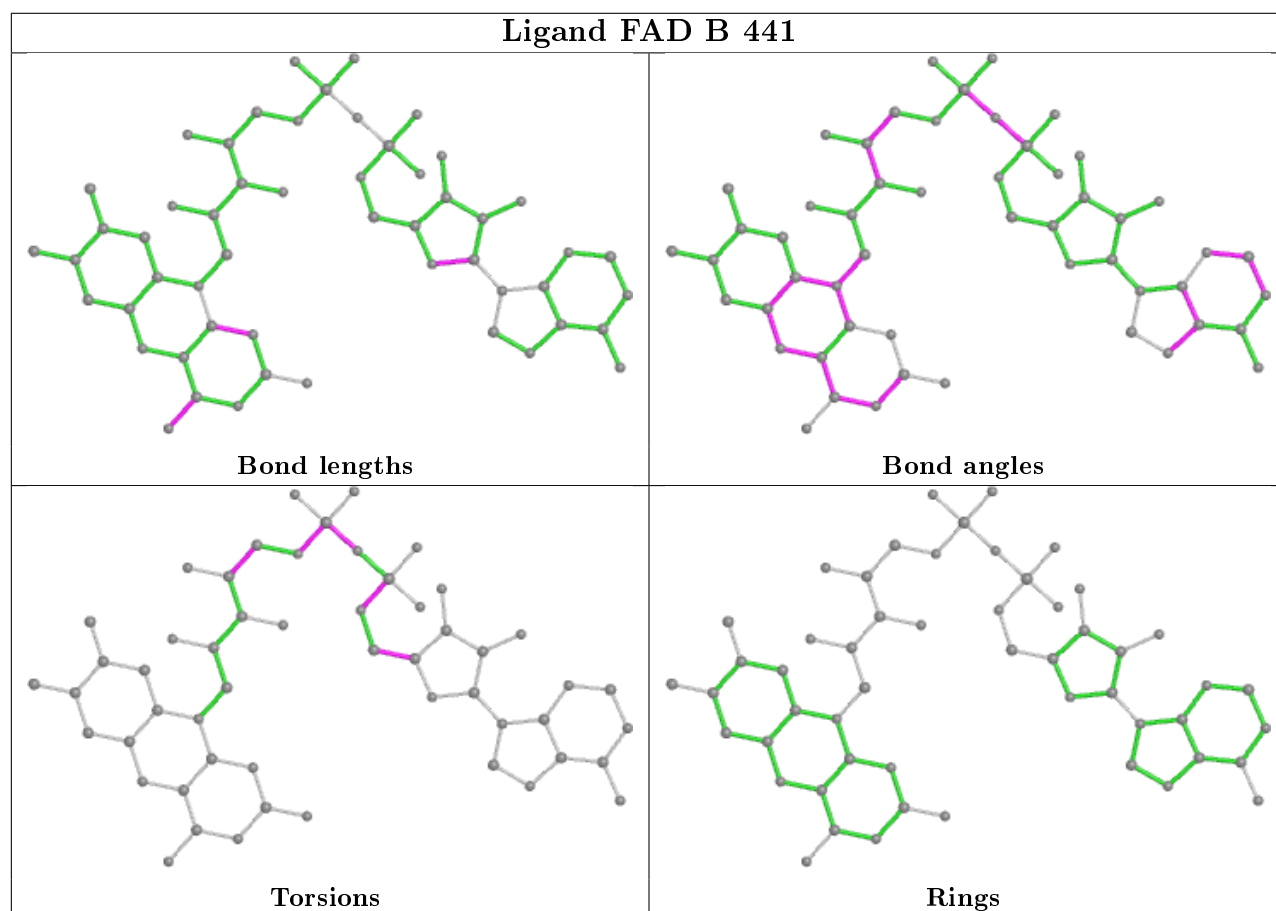
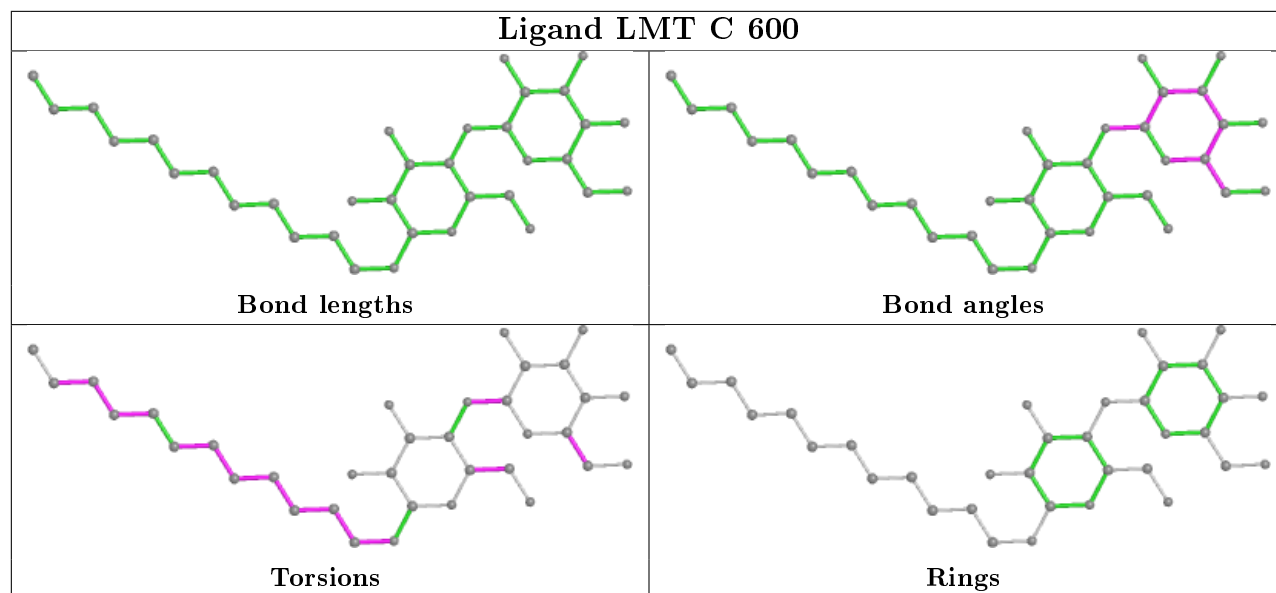




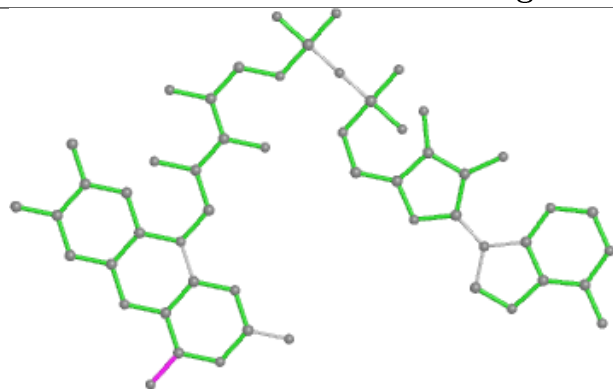




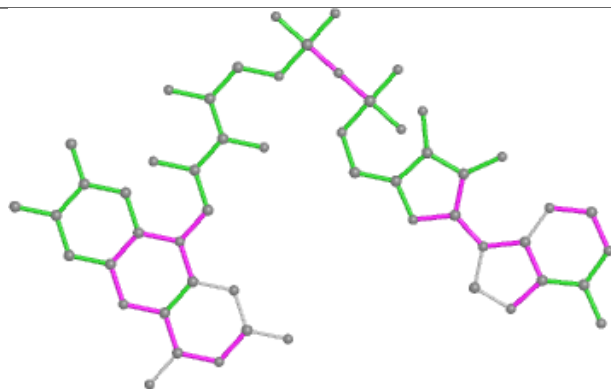




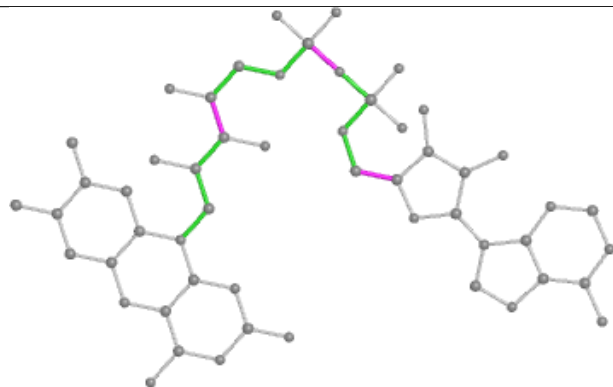
Ligand FAD E 441



Bond lengths



Bond angles

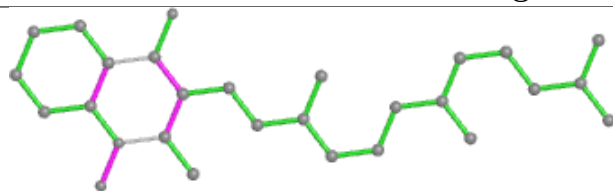


Torsions

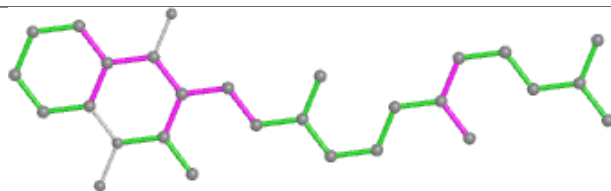


Rings

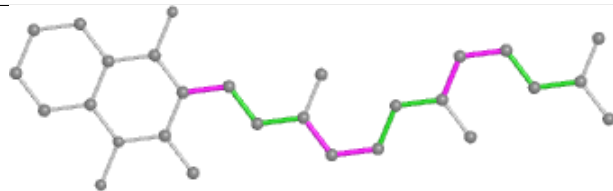
Ligand AUK F 501



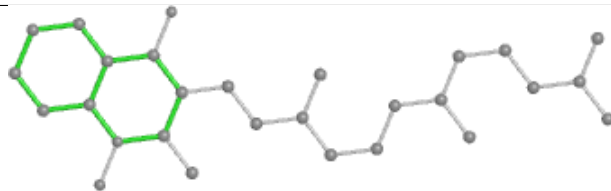
Bond lengths



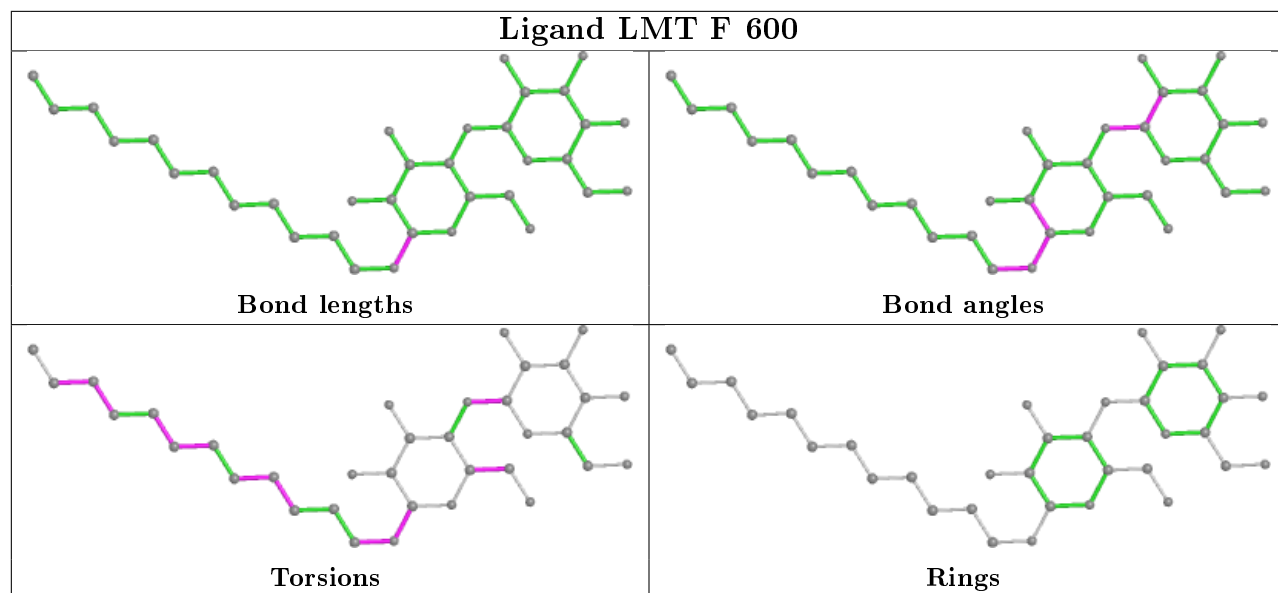
Bond angles

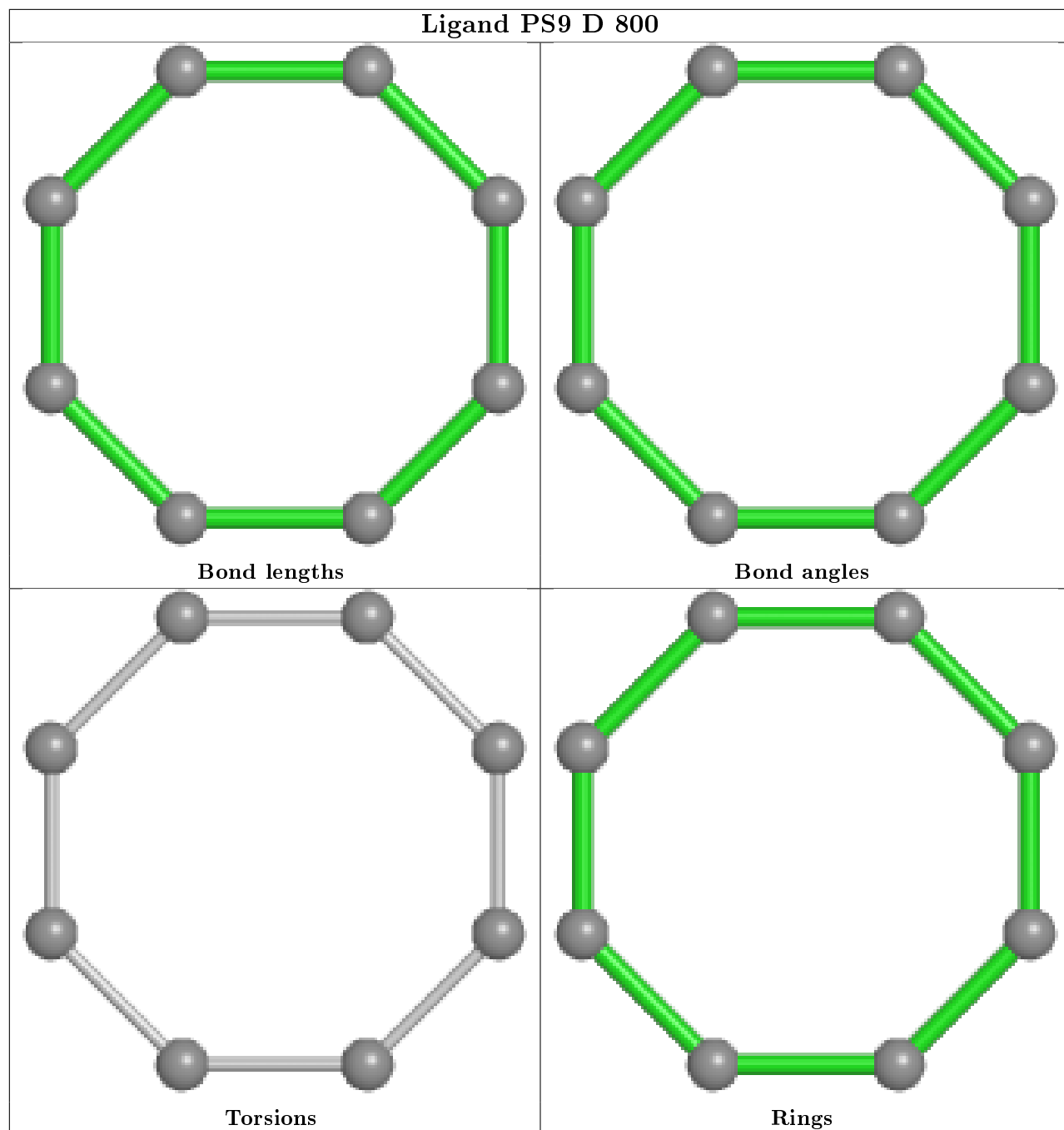


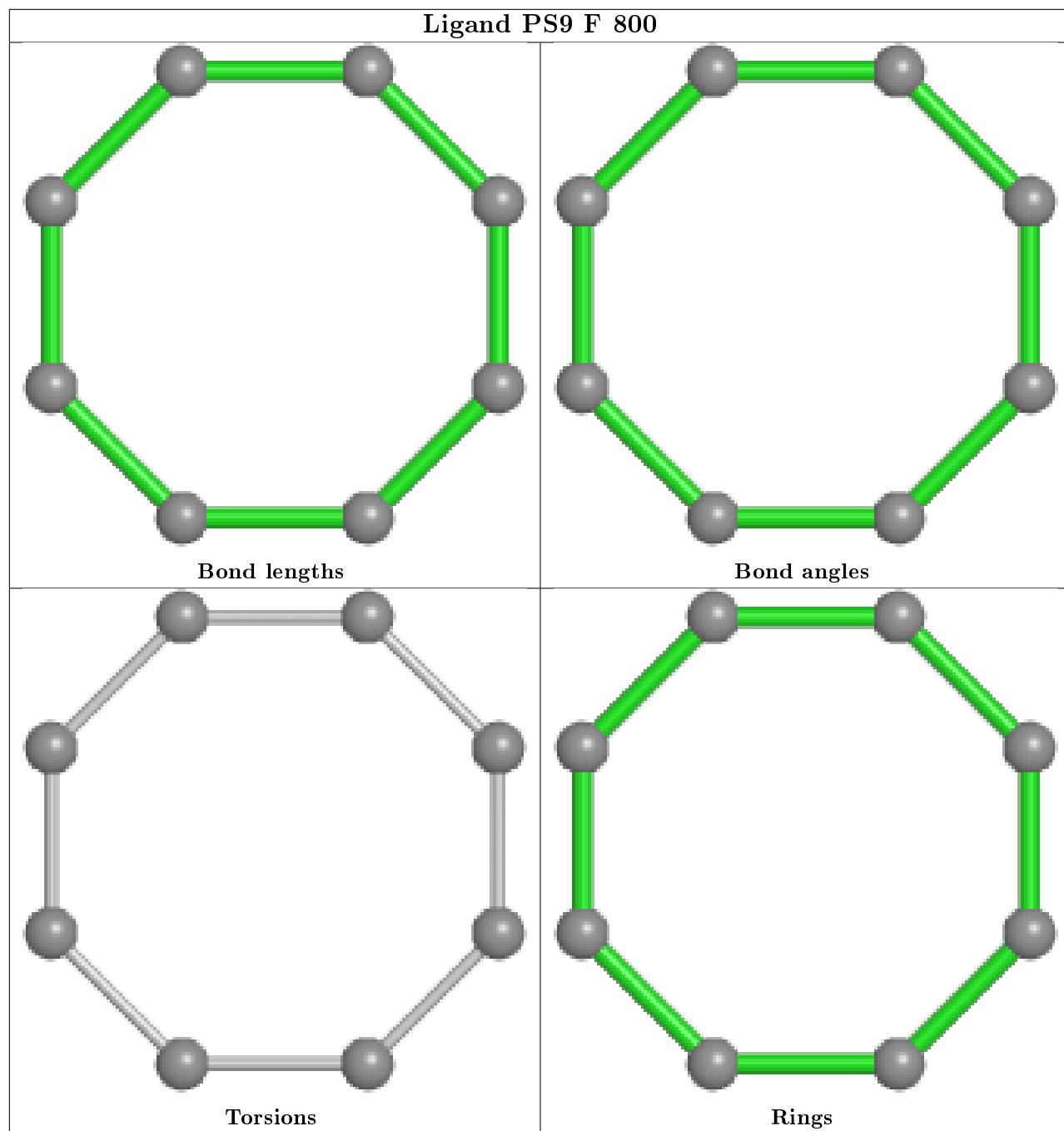
Torsions

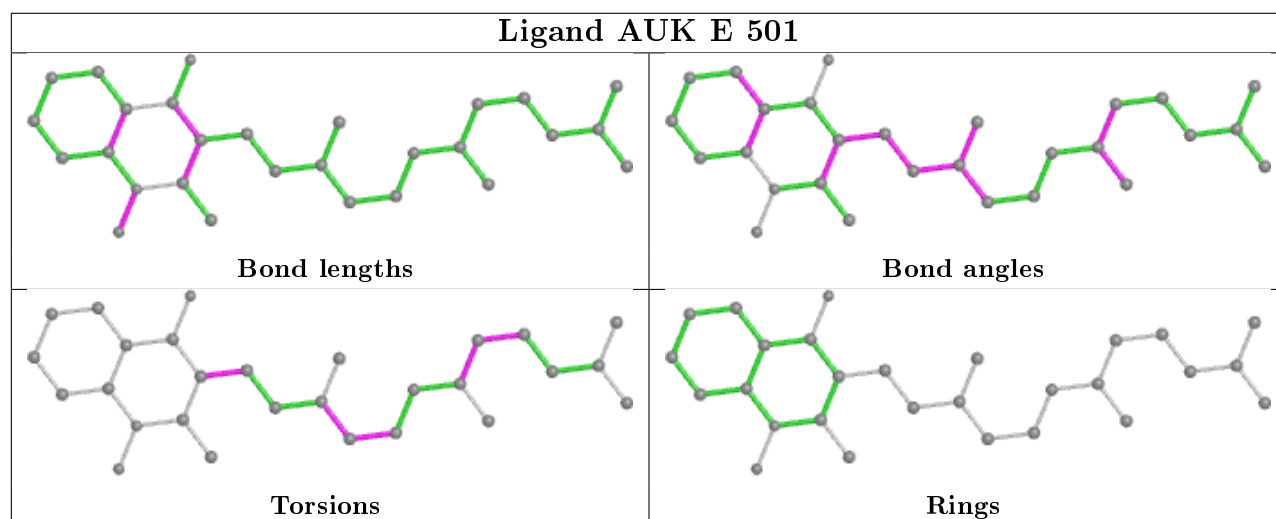
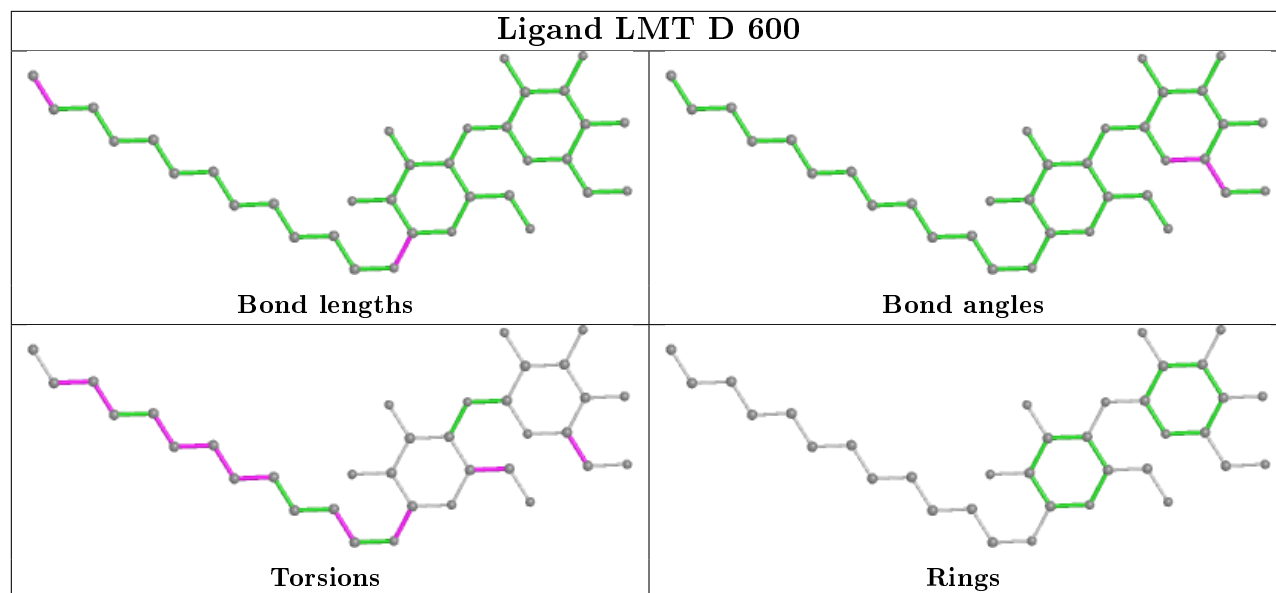


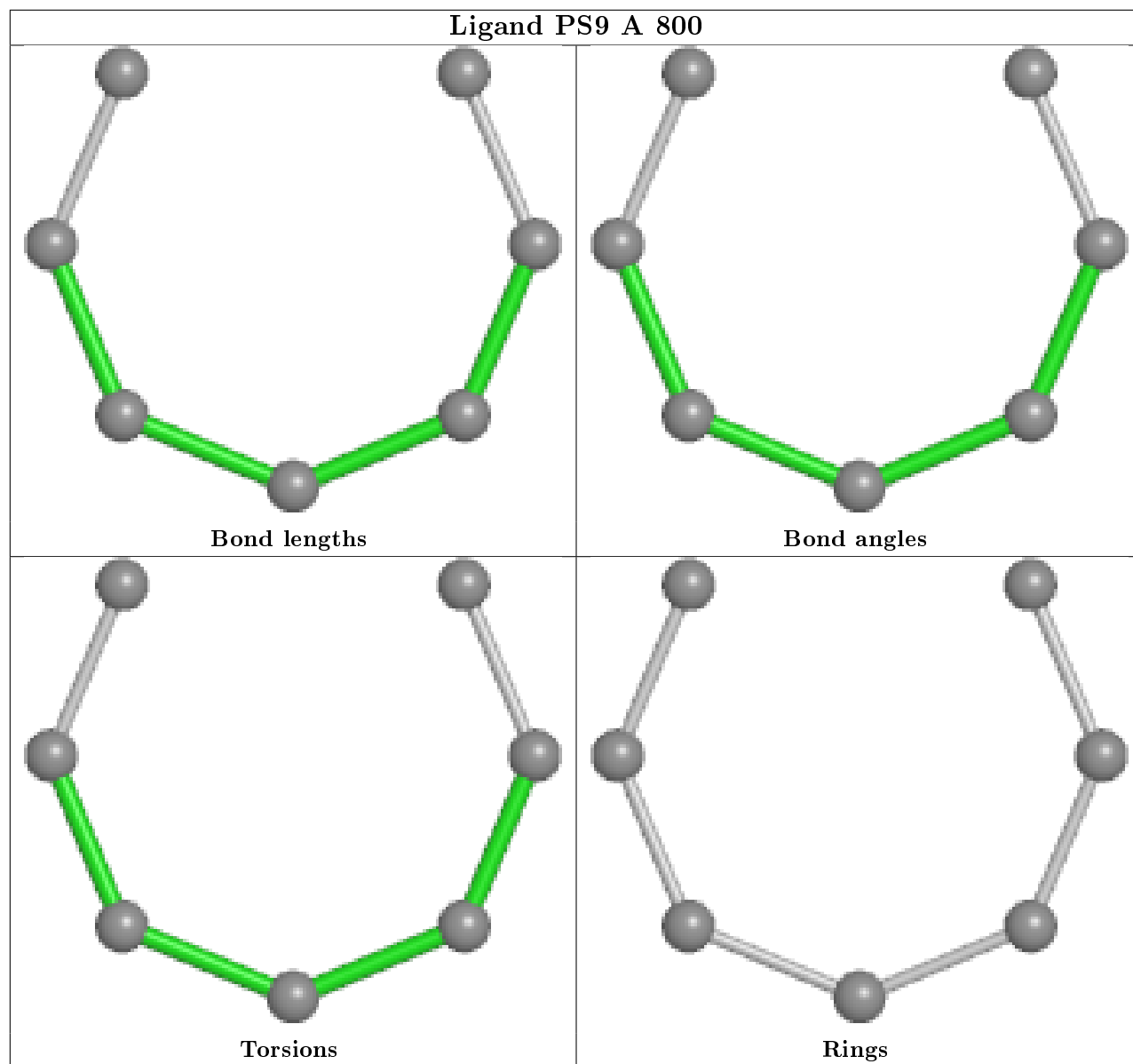
Rings

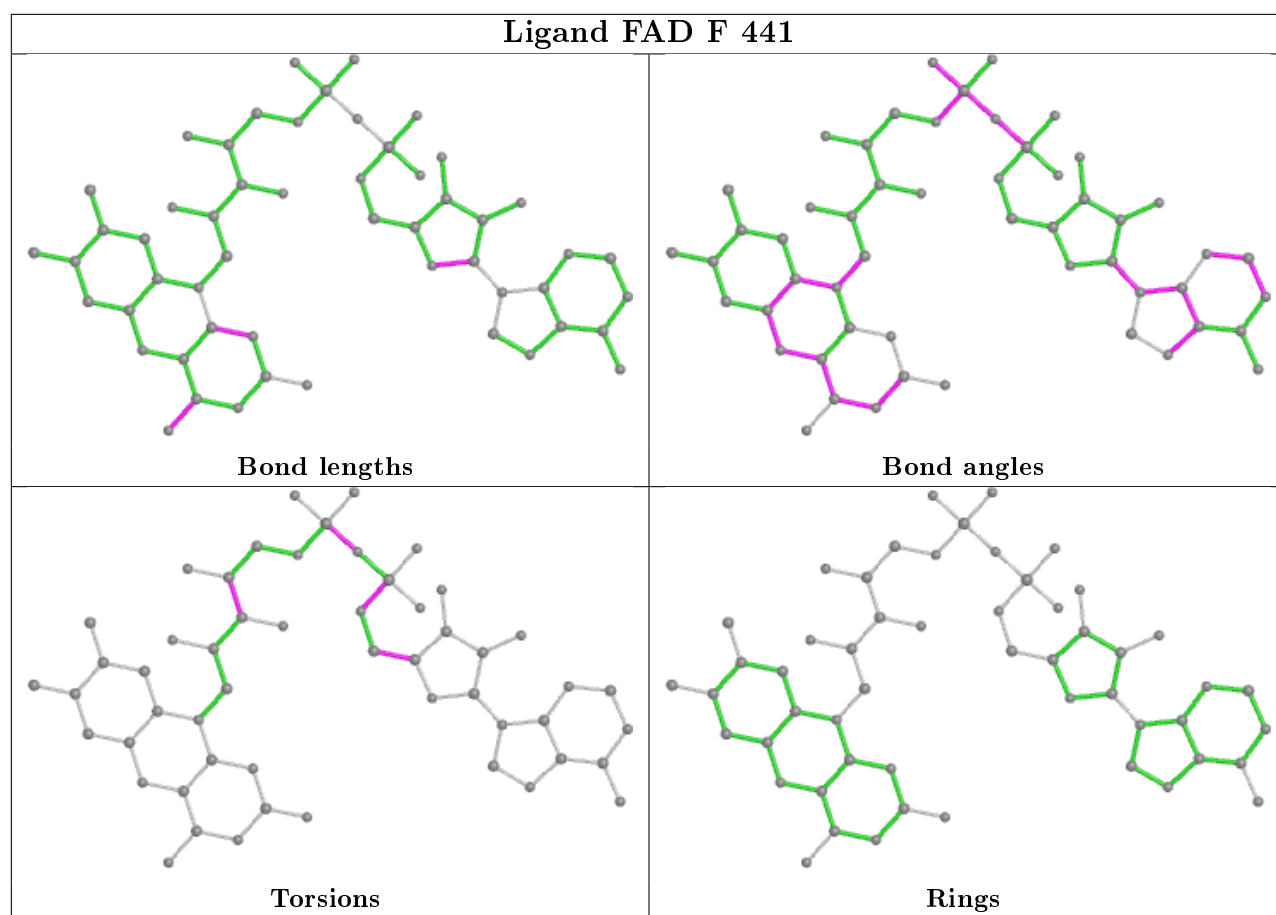












5.7 Other polymers [i](#)

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	428/430 (99%)	-0.05	7 (1%) 72 71	32, 41, 50, 54	0
1	B	428/430 (99%)	-0.05	7 (1%) 72 71	32, 41, 50, 54	0
1	C	428/430 (99%)	0.01	6 (1%) 75 75	32, 43, 53, 61	0
1	D	428/430 (99%)	0.32	34 (7%) 12 10	33, 43, 51, 56	0
1	E	428/430 (99%)	0.07	11 (2%) 56 52	32, 44, 51, 54	0
1	F	428/430 (99%)	-0.01	7 (1%) 72 71	35, 44, 51, 58	0
All	All	2568/2580 (99%)	0.05	72 (2%) 53 49	32, 42, 51, 61	0

The worst 5 of 72 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	430	CYS	5.9
1	D	430	CYS	5.0
1	E	430	CYS	4.9
1	F	430	CYS	4.6
1	A	430	CYS	4.5

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	CSS	B	156[B]	7/8	0.92	0.21	41,41,42,45	2
1	CSS	B	156[A]	6/8	0.92	0.21	41,41,42,42	1
1	CSS	E	156[A]	6/8	0.96	0.18	47,47,47,48	1
1	CSS	C	156[A]	6/8	0.96	0.20	45,45,45,46	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	CSS	D	156[B]	7/8	0.96	0.14	40,40,41,43	2
1	CSS	C	156[B]	7/8	0.96	0.20	45,45,46,48	2
1	CSS	D	156[A]	6/8	0.96	0.14	40,40,41,41	1
1	CSS	E	156[B]	7/8	0.96	0.18	47,47,48,50	2
1	CSS	F	156[B]	7/8	0.97	0.17	45,45,46,46	2
1	CSS	F	156[A]	6/8	0.97	0.17	45,45,45,46	1
1	CSS	A	156[A]	6/8	0.98	0.17	40,40,40,43	1
1	CSS	A	156[B]	7/8	0.98	0.17	40,40,41,43	2

6.3 Carbohydrates ⓘ

There are no carbohydrates 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(\AA^2)	Q<0.9
5	LMT	A	600	35/35	0.57	0.49	35,47,56,57	35
5	LMT	F	600	35/35	0.59	0.51	29,47,52,54	35
7	PS9	B	800	8/8	0.60	0.74	50,51,51,52	8
5	LMT	B	600	35/35	0.63	0.46	21,33,41,42	35
5	LMT	C	600	35/35	0.65	0.44	38,51,54,54	35
2	SO4	E	431	5/5	0.66	0.40	52,53,53,53	5
7	PS9	E	800	8/8	0.68	0.77	54,55,55,56	8
4	AUK	E	501	28/28	0.68	0.56	33,41,41,41	28
7	PS9	D	800	8/8	0.69	0.62	46,47,48,48	8
5	LMT	D	600	35/35	0.69	0.39	22,27,32,32	35
5	LMT	E	600	35/35	0.69	0.41	28,42,45,45	35
4	AUK	A	501	28/28	0.70	0.56	43,46,46,46	28
4	AUK	B	501	28/28	0.72	0.49	42,48,49,49	28
7	PS9	C	800	8/8	0.73	0.54	51,52,53,53	8
7	PS9	F	800	8/8	0.73	0.70	48,49,49,49	8
2	SO4	F	434	5/5	0.74	0.51	37,37,38,39	5
4	AUK	F	501	28/28	0.74	0.46	34,38,39,39	28
7	PS9	A	800	7/8	0.75	0.64	45,46,47,47	7
2	SO4	D	435	5/5	0.78	0.32	43,43,44,44	5

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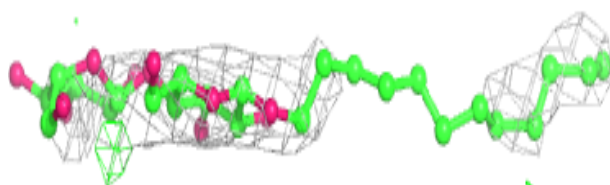
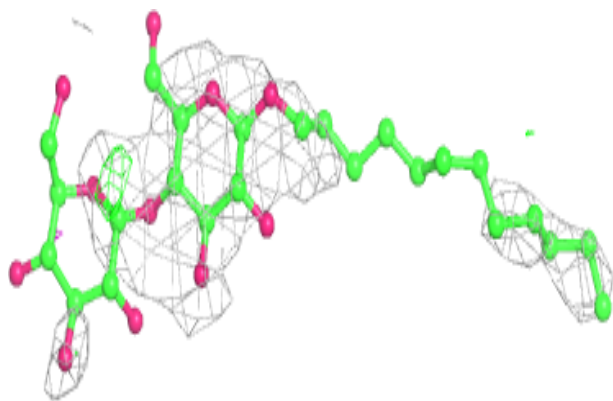
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	AUK	C	501	28/28	0.80	0.48	32,38,38,38	28
2	SO4	A	431	5/5	0.80	0.31	52,53,53,54	5
4	AUK	D	501	28/28	0.80	0.50	47,50,50,50	28
2	SO4	B	435	5/5	0.81	0.33	37,38,38,39	5
2	SO4	C	434	5/5	0.81	0.34	41,41,42,42	5
2	SO4	C	431	5/5	0.82	0.26	39,39,40,40	5
2	SO4	C	433	5/5	0.82	0.34	44,44,45,45	5
2	SO4	E	433	5/5	0.84	0.31	48,48,48,49	5
6	H2S	E	700	1/1	0.85	0.26	44,44,44,44	1
2	SO4	D	431	5/5	0.85	0.20	37,38,38,38	5
2	SO4	E	435	5/5	0.87	0.31	58,58,59,59	5
2	SO4	D	433	5/5	0.87	0.32	76,76,77,77	5
6	H2S	F	700	1/1	0.88	0.28	43,43,43,43	1
2	SO4	B	433	5/5	0.88	0.29	40,40,40,41	5
6	H2S	B	700	1/1	0.89	0.23	42,42,42,42	1
6	H2S	C	700	1/1	0.89	0.35	43,43,43,43	1
2	SO4	B	434	5/5	0.90	0.25	39,40,40,40	5
2	SO4	E	434	5/5	0.91	0.27	39,40,40,40	5
6	H2S	A	700	1/1	0.91	0.37	36,36,36,36	1
2	SO4	F	433	5/5	0.91	0.21	38,38,38,38	5
2	SO4	C	432	5/5	0.91	0.22	56,56,56,57	5
2	SO4	B	432	5/5	0.92	0.24	44,44,45,45	5
2	SO4	D	434	5/5	0.92	0.38	45,45,46,46	5
2	SO4	A	434	5/5	0.93	0.21	33,33,34,34	5
2	SO4	E	432	5/5	0.93	0.26	52,52,53,53	5
6	H2S	D	700	1/1	0.94	0.19	52,52,52,52	1
2	SO4	D	432	5/5	0.94	0.16	46,47,47,47	5
3	FAD	D	441	53/53	0.95	0.15	39,50,52,52	0
2	SO4	B	431	5/5	0.95	0.20	46,46,47,47	5
3	FAD	E	441	53/53	0.95	0.15	32,38,46,46	0
2	SO4	A	433	5/5	0.95	0.13	46,47,47,48	5
3	FAD	A	441	53/53	0.96	0.13	23,30,34,34	0
3	FAD	B	441	53/53	0.96	0.14	30,38,41,41	0
3	FAD	F	441	53/53	0.96	0.14	33,41,46,47	0
3	FAD	C	441	53/53	0.97	0.13	28,34,41,42	0

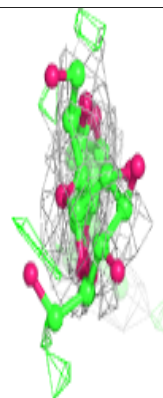
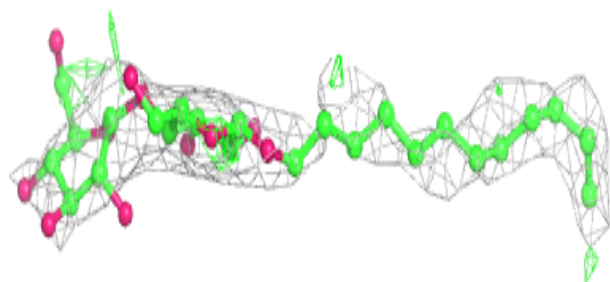
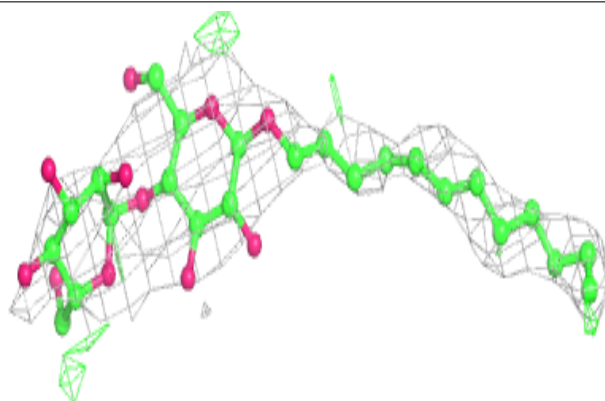
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around LMT A 600:

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

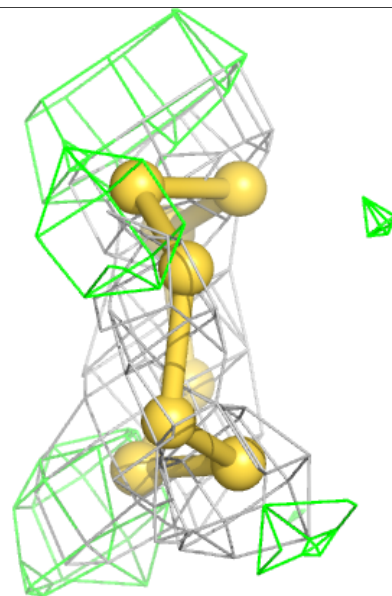
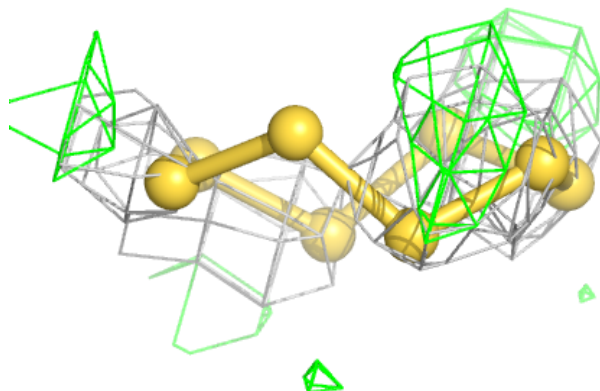
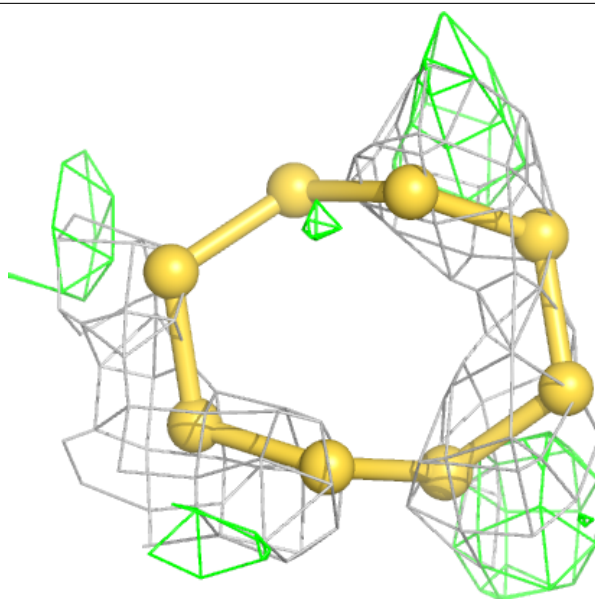
**Electron density around LMT F 600:**

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



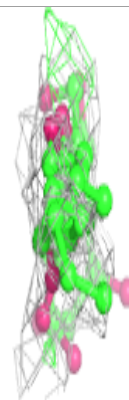
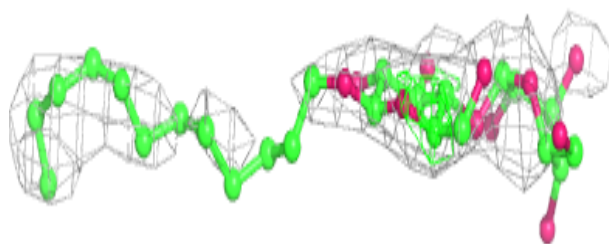
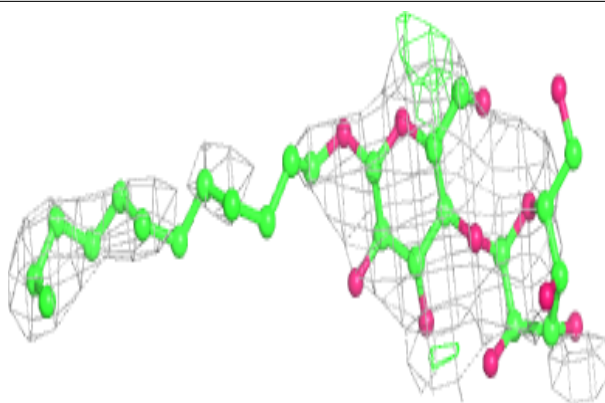
Electron density around PS9 B 800:

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and green (positive)

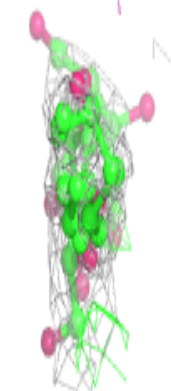
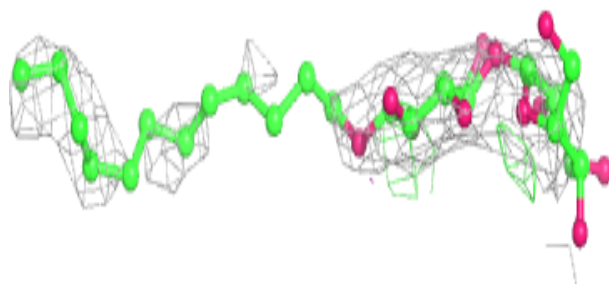
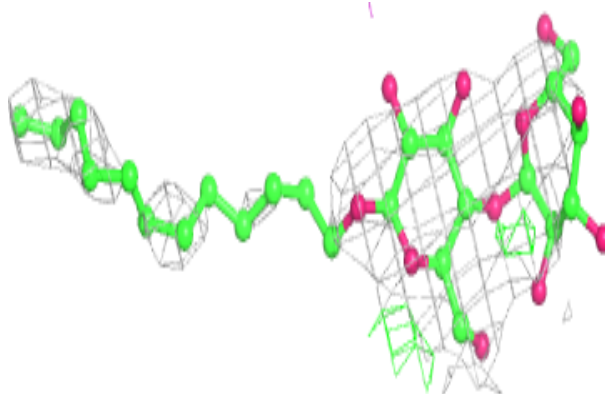


Electron density around LMT B 600:

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

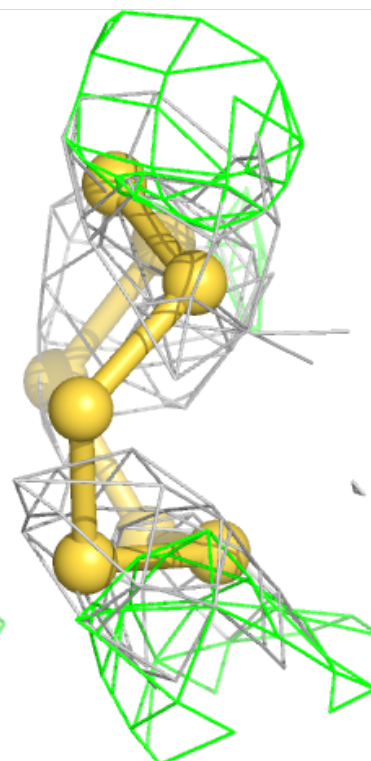
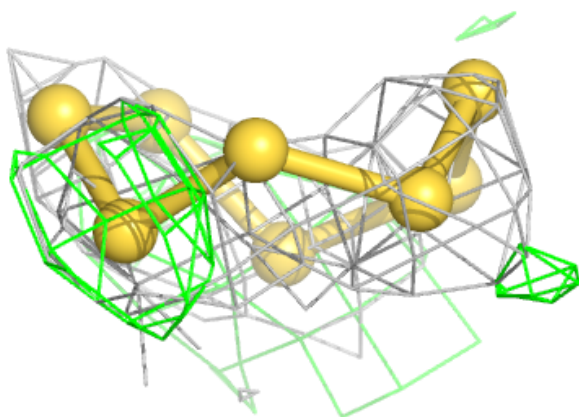
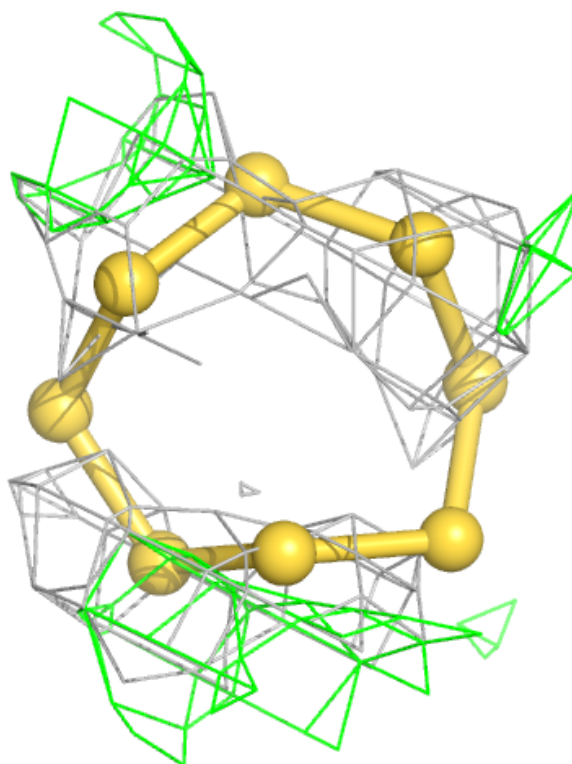
**Electron density around LMT C 600:**

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



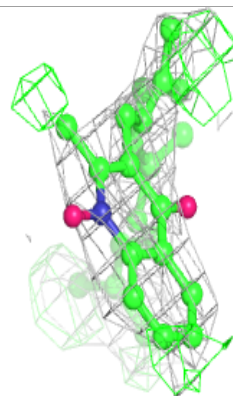
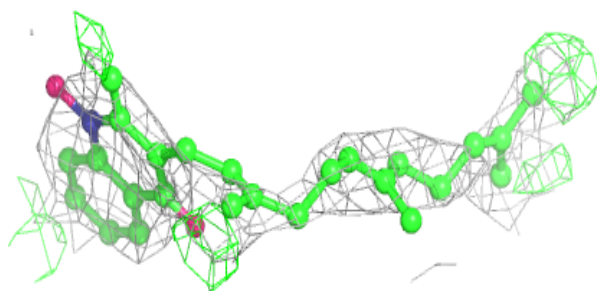
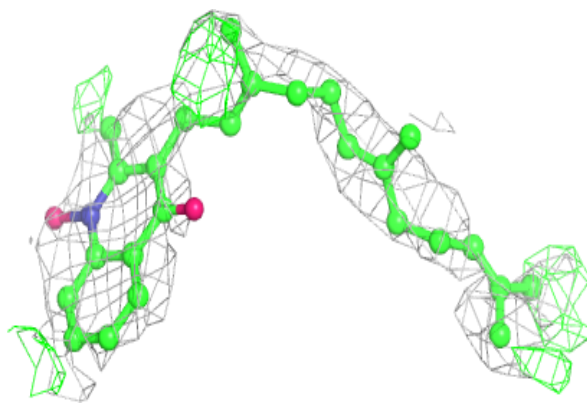
Electron density around PS9 E 800:

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



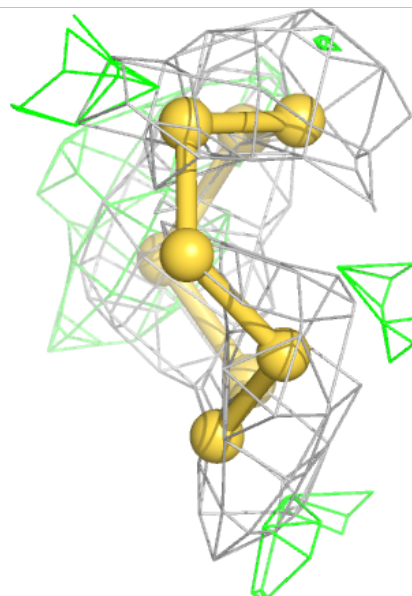
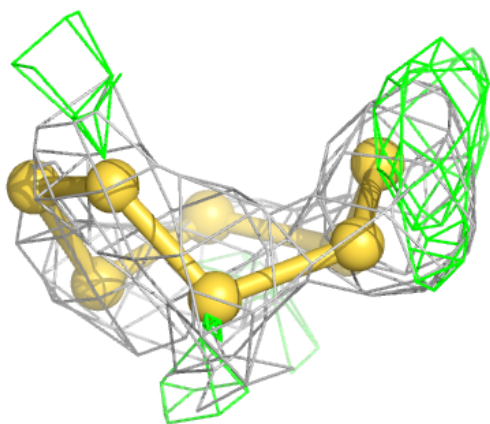
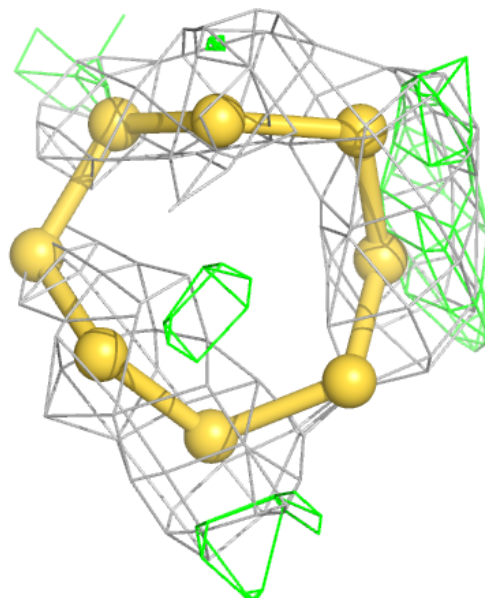
Electron density around AUK E 501:

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



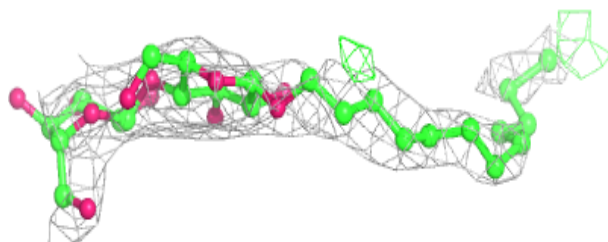
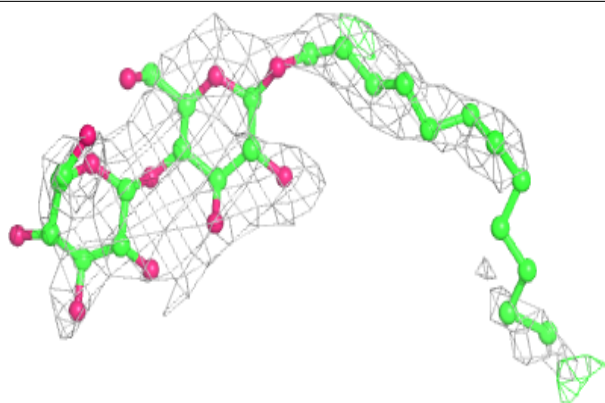
Electron density around PS9 D 800:

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and green (positive)

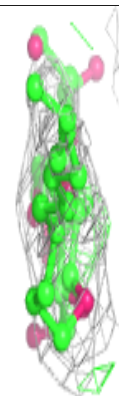
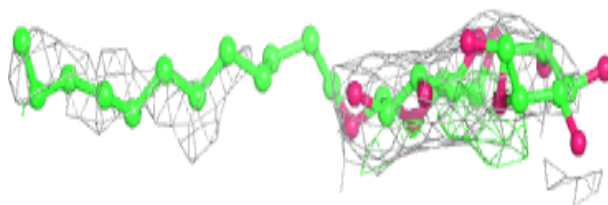
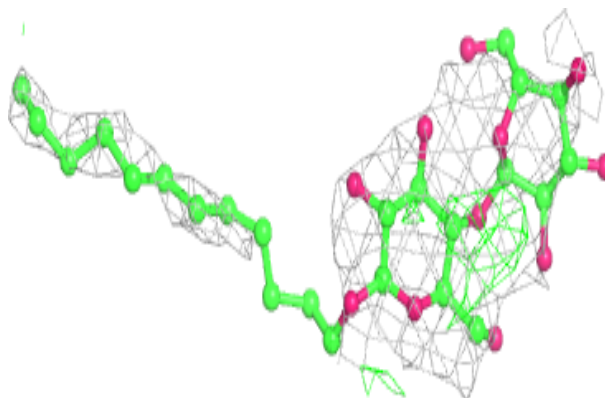


Electron density around LMT D 600:

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

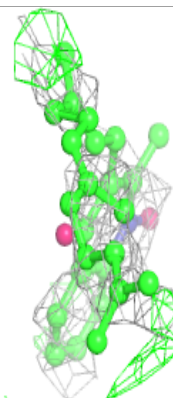
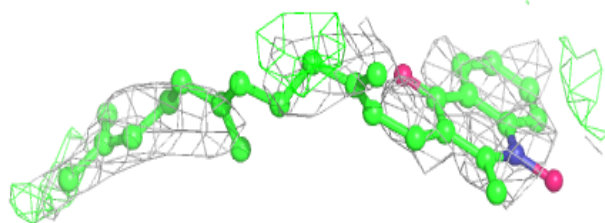
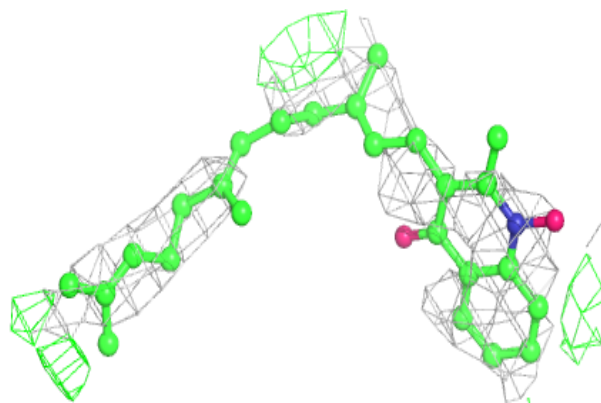
**Electron density around LMT E 600:**

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

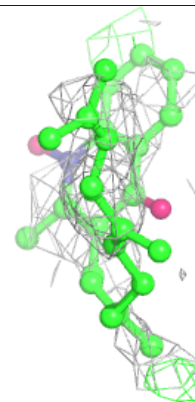
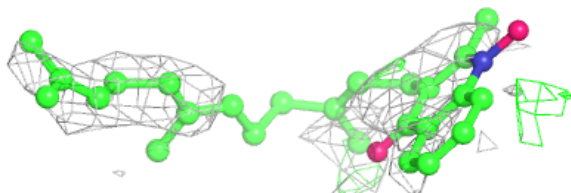
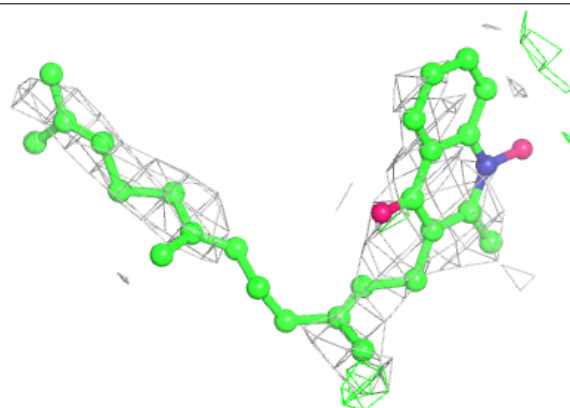


Electron density around AUK A 501:

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and green (positive)

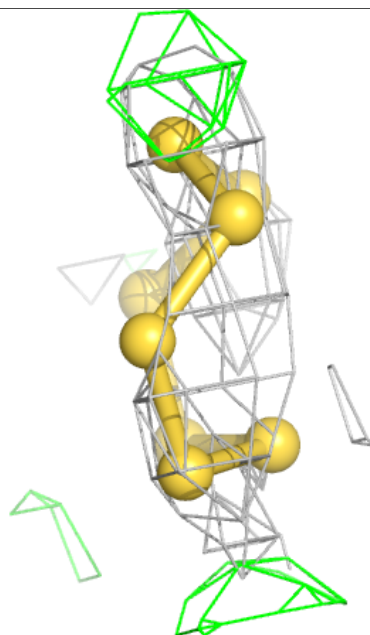
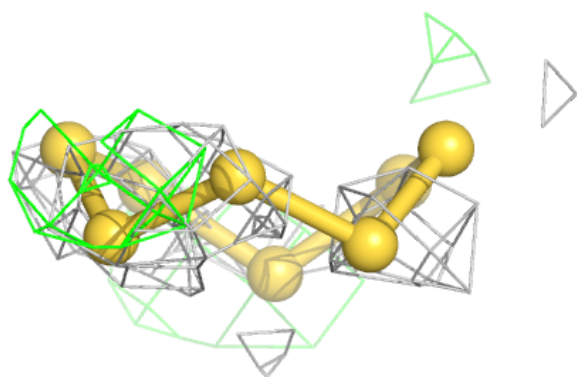
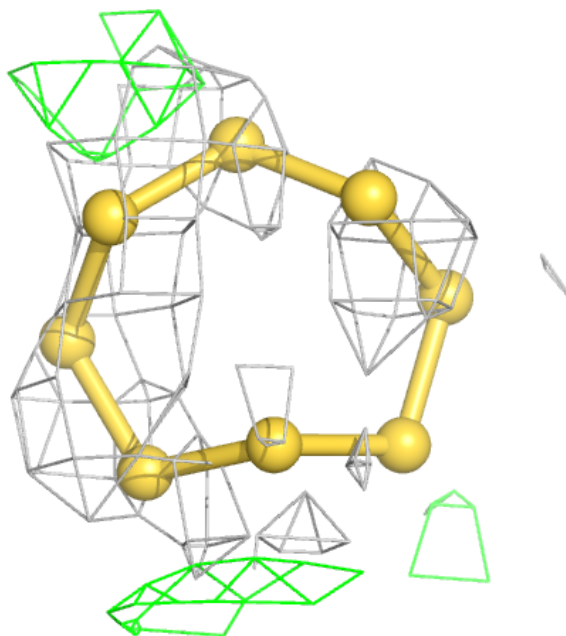
**Electron density around AUK B 501:**

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



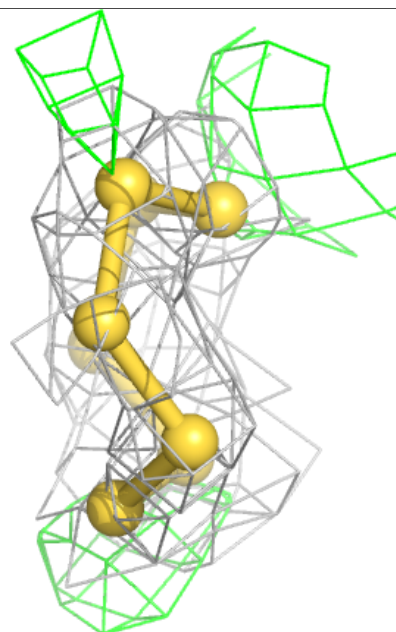
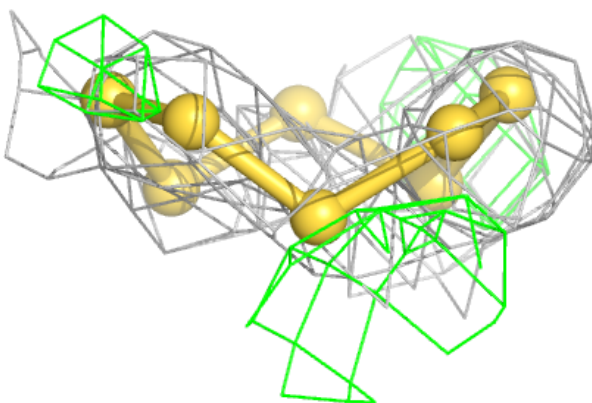
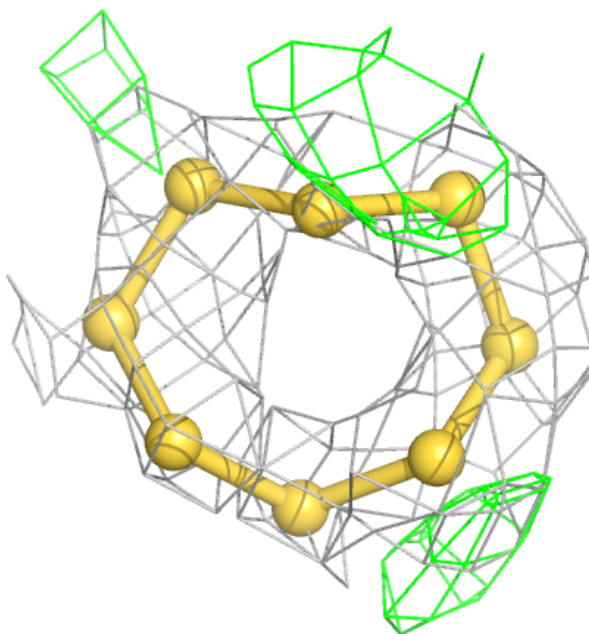
Electron density around PS9 C 800:

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and green (positive)



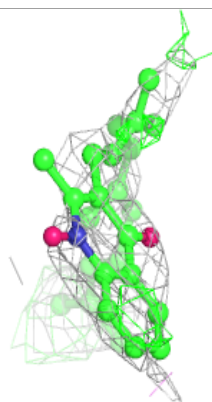
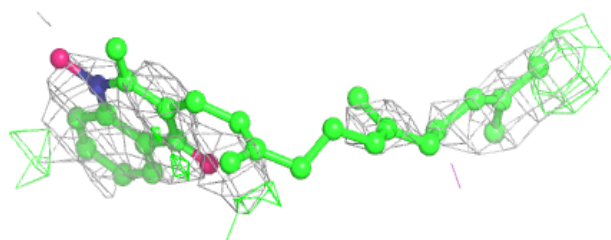
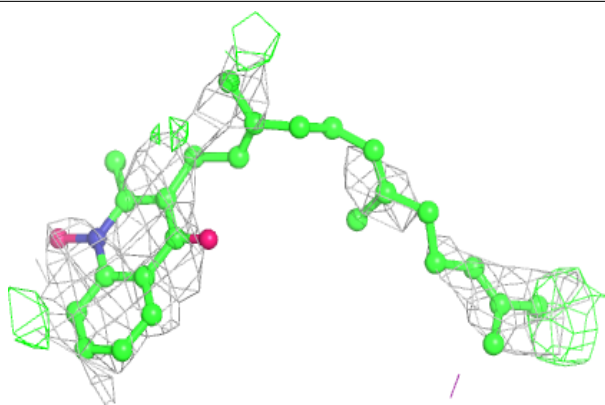
Electron density around PS9 F 800:

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and green (positive)



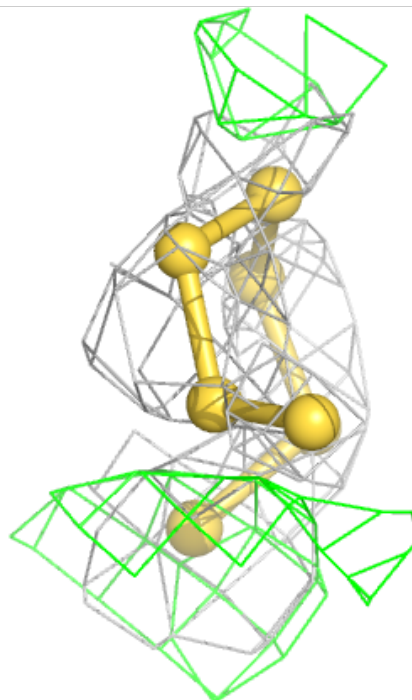
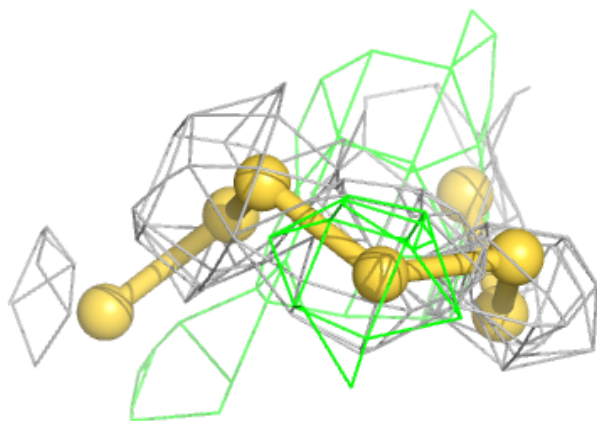
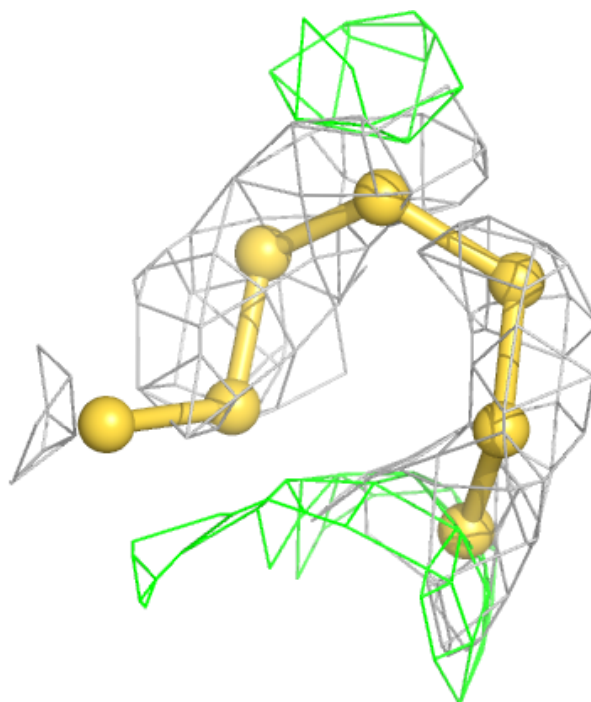
Electron density around AUK F 501:

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



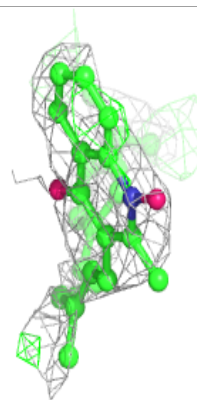
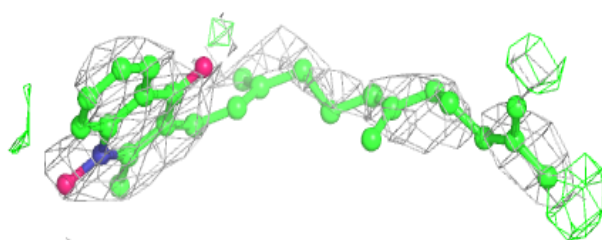
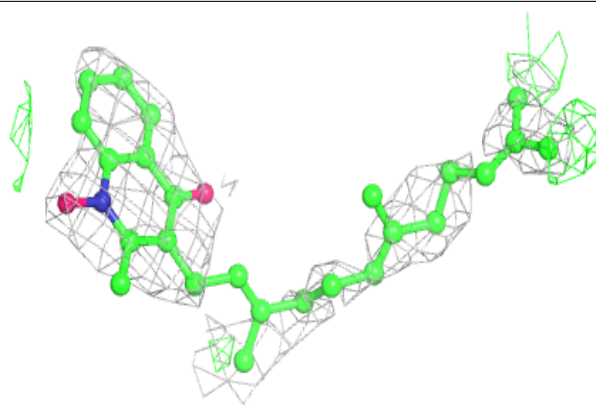
Electron density around PS9 A 800:

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

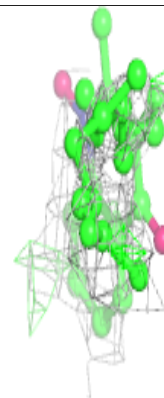
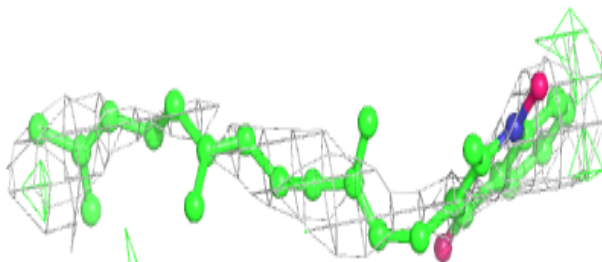
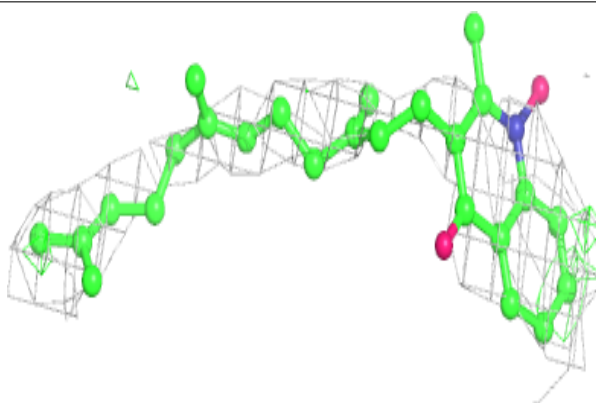


Electron density around AUK C 501:

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

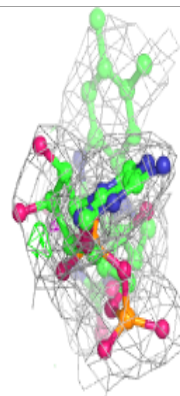
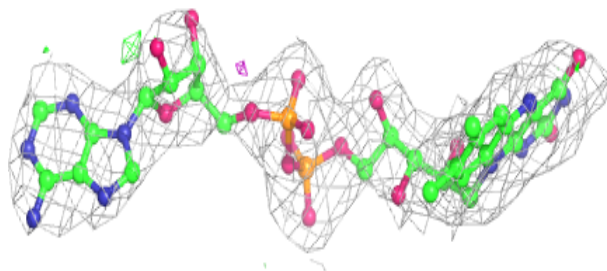
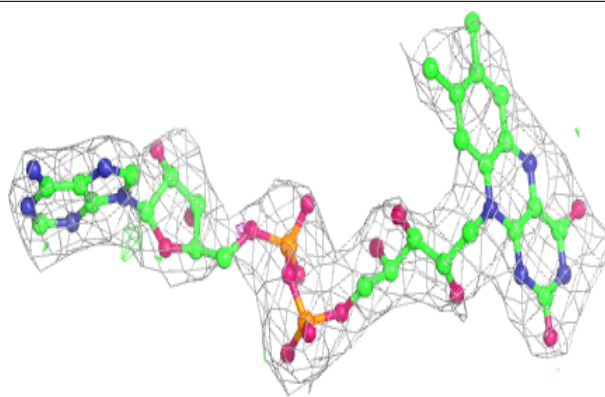
**Electron density around AUK D 501:**

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

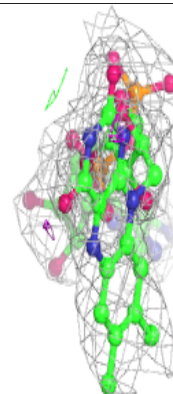
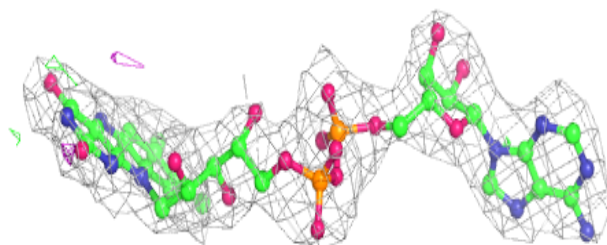
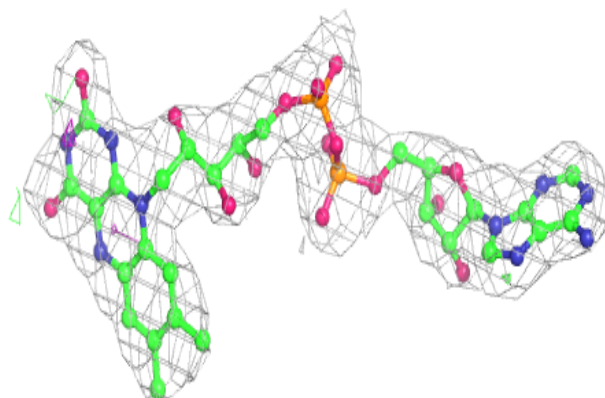


Electron density around FAD D 441:

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

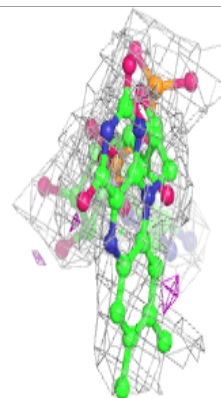
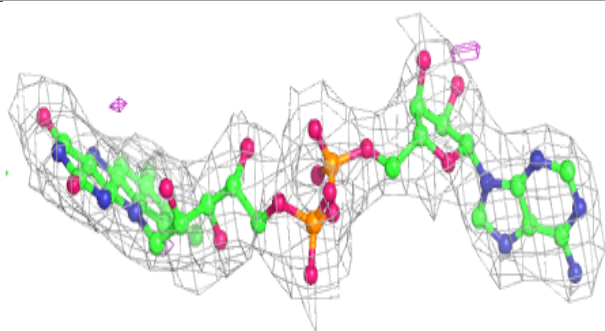
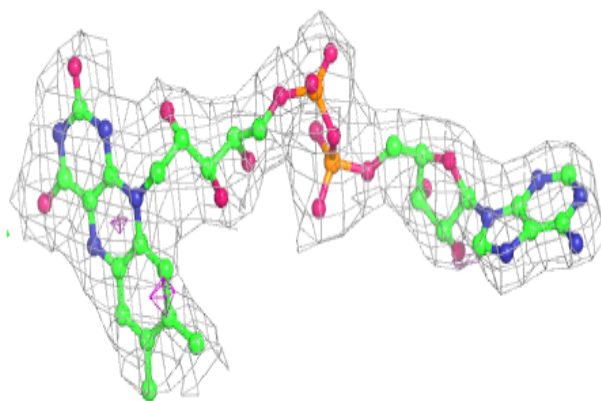
**Electron density around FAD E 441:**

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

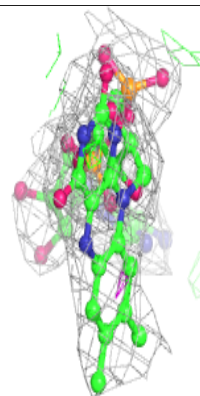
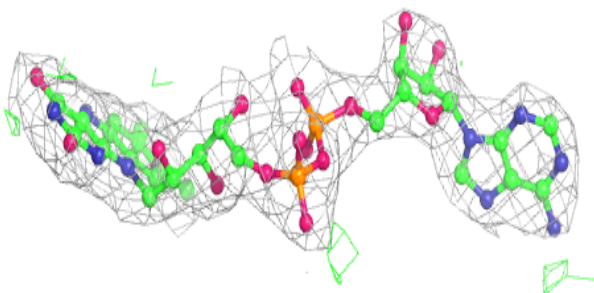
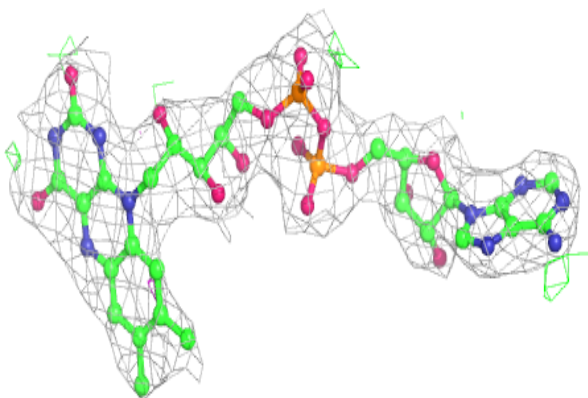


Electron density around FAD A 441:

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

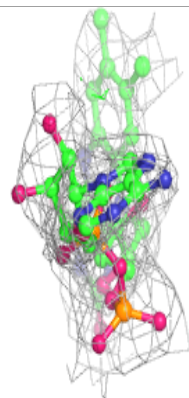
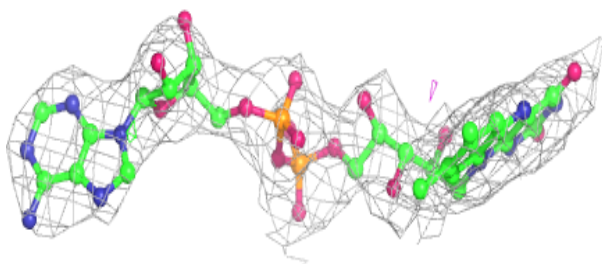
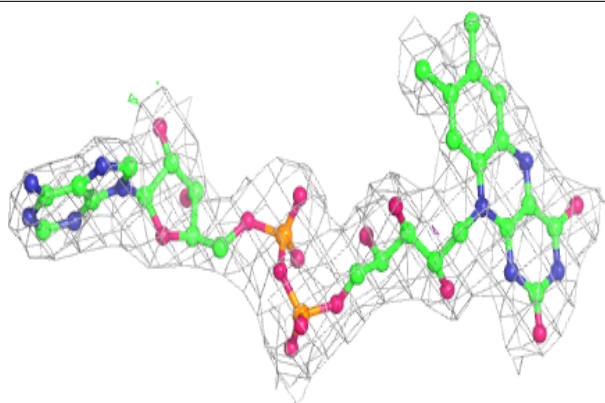
**Electron density around FAD B 441:**

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

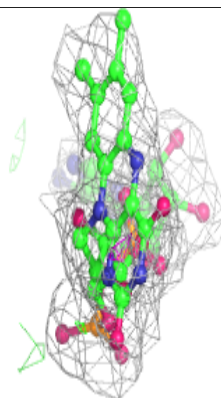
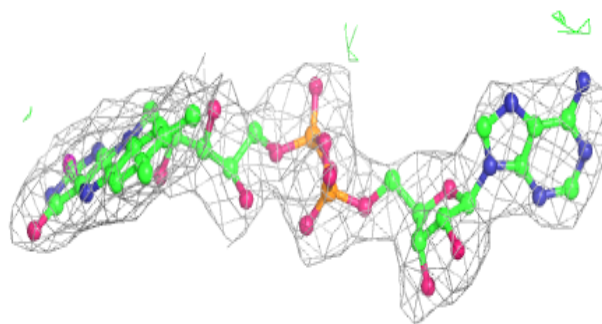
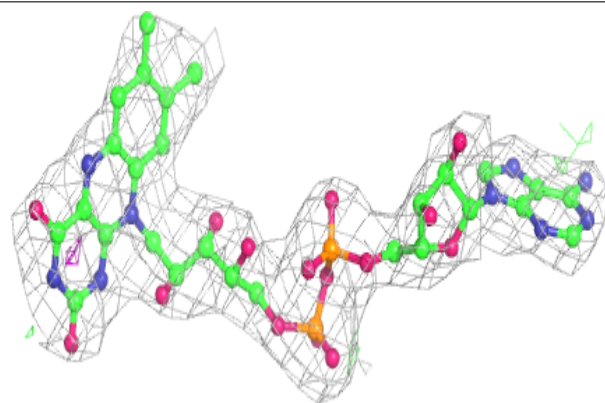


Electron density around FAD F 441:

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

**Electron density around FAD C 441:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.