



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 24, 2023 – 04:03 PM EDT

PDB ID : 3EYA
Title : Structural basis for membrane binding and catalytic activation of the peripheral membrane enzyme pyruvate oxidase from Escherichia coli
Authors : Neumann, P.; Weidner, A.; Pech, A.; Stubbs, M.T.; Tittmann, K.
Deposited on : 2008-10-20
Resolution : 2.50 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

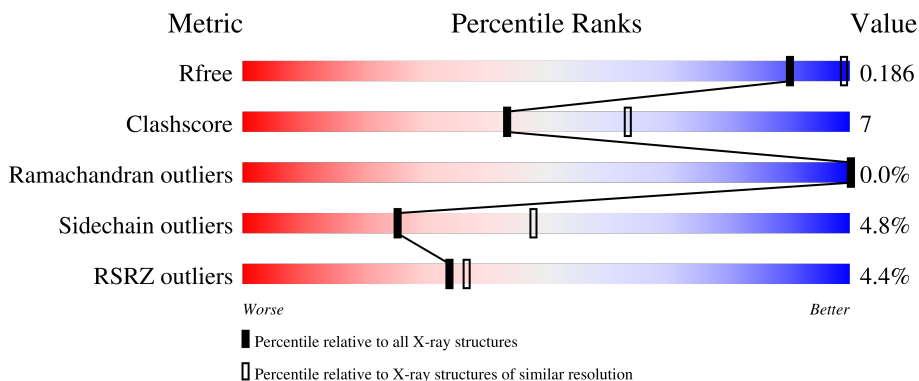
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	549	 3% 81% 12% . . 5%
1	B	549	 4% 82% 11% . 5%
1	C	549	 4% 82% 11% . 5%
1	D	549	 3% 81% 12% . 5%
1	E	549	 5% 82% 10% . 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	549	
1	G	549	
1	H	549	
1	I	549	
1	J	549	
1	K	549	
1	L	549	

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
5	PO4	A	616	-	-	X	-
5	PO4	A	618	-	-	X	-
5	PO4	A	619	-	-	X	-
5	PO4	D	616	-	-	-	X

2 Entry composition [i](#)

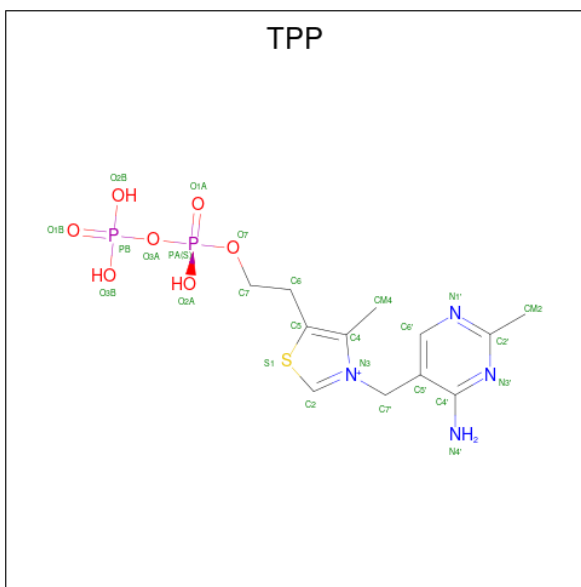
There are 6 unique types of molecules in this entry. The entry contains 50360 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Pyruvate dehydrogenase [cytochrome].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	527	Total 4066	C 2579	N 708	O 752	S 27	0	12	0
1	B	524	Total 3999	C 2529	N 694	O 749	S 27	0	5	0
1	C	522	Total 4001	C 2530	N 697	O 748	S 26	0	6	0
1	D	520	Total 3977	C 2516	N 693	O 741	S 27	0	6	0
1	E	522	Total 3975	C 2513	N 693	O 743	S 26	0	3	0
1	F	521	Total 3969	C 2510	N 693	O 739	S 27	0	3	0
1	G	519	Total 3939	C 2490	N 684	O 738	S 27	0	2	0
1	H	522	Total 3973	C 2515	N 688	O 743	S 27	0	4	0
1	I	523	Total 3978	C 2516	N 694	O 741	S 27	0	2	0
1	J	522	Total 3993	C 2527	N 696	O 743	S 27	0	6	0
1	K	523	Total 4005	C 2533	N 702	O 743	S 27	0	5	0
1	L	523	Total 4016	C 2541	N 704	O 744	S 27	0	8	0

- Molecule 2 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: C₁₂H₁₉N₄O₇P₂S).



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

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

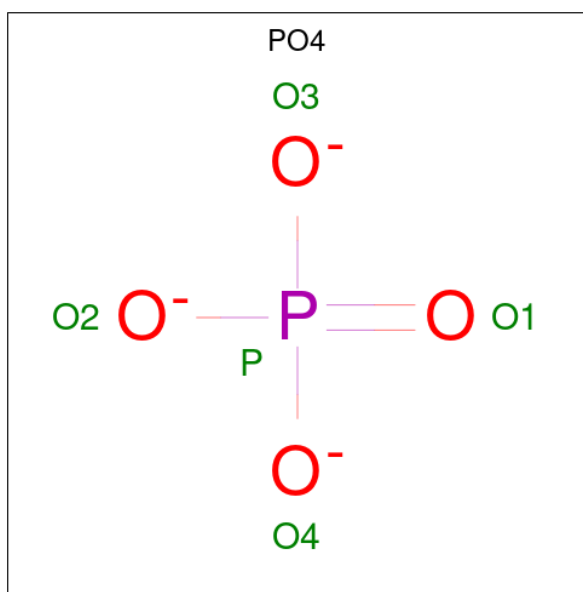


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	Total 53	C 27	N 9	O 15	P 2	0	0
3	B	1	Total 53	C 27	N 9	O 15	P 2	0	0
3	C	1	Total 53	C 27	N 9	O 15	P 2	0	0
3	D	1	Total 53	C 27	N 9	O 15	P 2	0	0
3	E	1	Total 53	C 27	N 9	O 15	P 2	0	0
3	F	1	Total 53	C 27	N 9	O 15	P 2	0	0
3	G	1	Total 53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

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Mg 1 1	0	0
4	B	1	Total Mg 1 1	0	0
4	C	1	Total Mg 1 1	0	0
4	D	1	Total Mg 1 1	0	0
4	E	1	Total Mg 1 1	0	0
4	F	1	Total Mg 1 1	0	0
4	G	1	Total Mg 1 1	0	0
4	H	1	Total Mg 1 1	0	0
4	I	1	Total Mg 1 1	0	0
4	J	1	Total Mg 1 1	0	0
4	K	1	Total Mg 1 1	0	0
4	L	1	Total Mg 1 1	0	0

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	G	1	Total	O	P	0	0
			5	4	1		
5	G	1	Total	O	P	0	0
			5	4	1		
5	G	1	Total	O	P	0	0
			5	4	1		
5	H	1	Total	O	P	0	0
			5	4	1		
5	H	1	Total	O	P	0	0
			5	4	1		
5	I	1	Total	O	P	0	0
			5	4	1		
5	I	1	Total	O	P	0	0
			5	4	1		
5	J	1	Total	O	P	0	0
			5	4	1		
5	K	1	Total	O	P	0	0
			5	4	1		
5	L	1	Total	O	P	0	0
			5	4	1		
5	L	1	Total	O	P	0	0
			5	4	1		
5	L	1	Total	O	P	0	0
			5	4	1		
5	L	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	280	Total	O	0	0
			280	280		
6	B	60	Total	O	0	0
			60	60		
6	C	73	Total	O	0	0
			73	73		
6	D	88	Total	O	0	0
			88	88		
6	E	43	Total	O	0	0
			43	43		

Continued on next page...

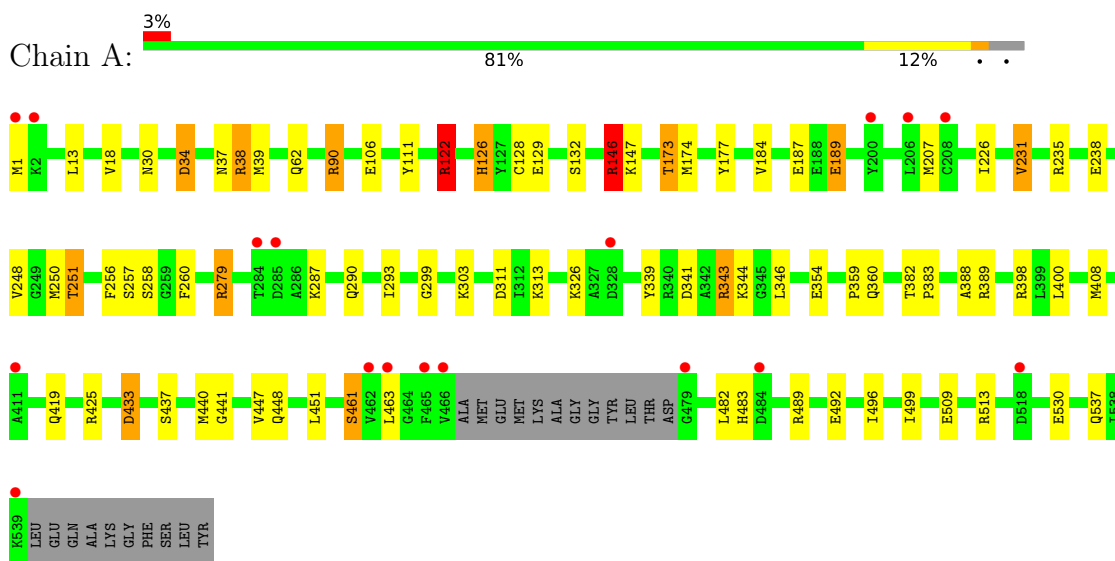
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	41	Total 41	O 41	0	0
6	G	40	Total 40	O 40	0	0
6	H	64	Total 64	O 64	0	0
6	I	62	Total 62	O 62	0	0
6	J	50	Total 50	O 50	0	0
6	K	77	Total 77	O 77	0	0
6	L	451	Total 451	O 451	0	0

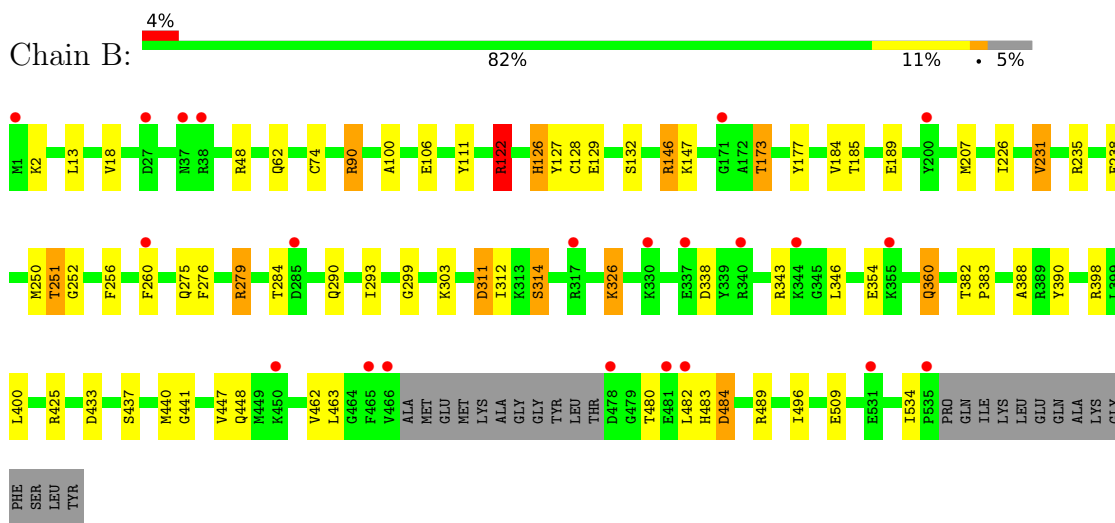
3 Residue-property plots [i](#)

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

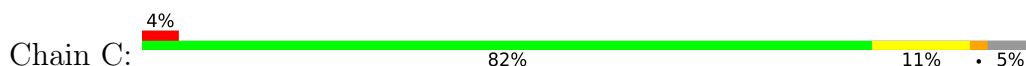
- Molecule 1: Pyruvate dehydrogenase [cytochrome]

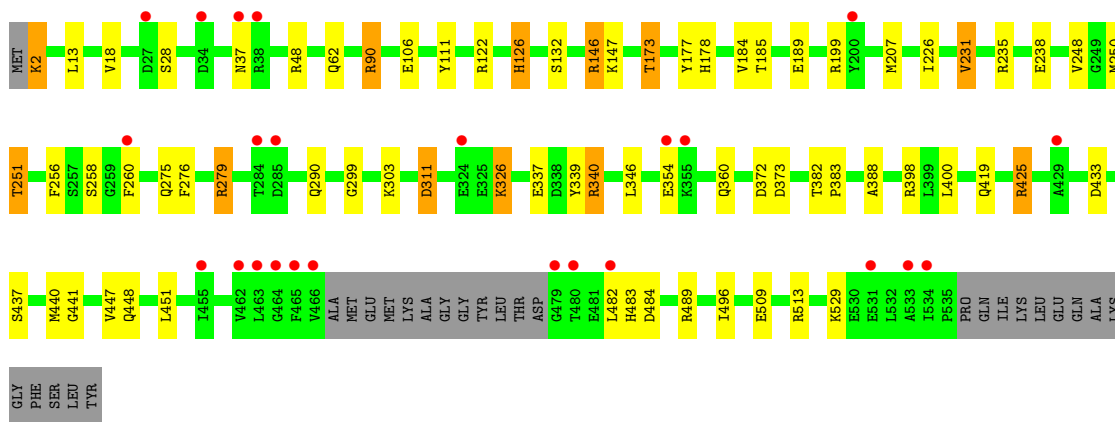


- Molecule 1: Pyruvate dehydrogenase [cytochrome]

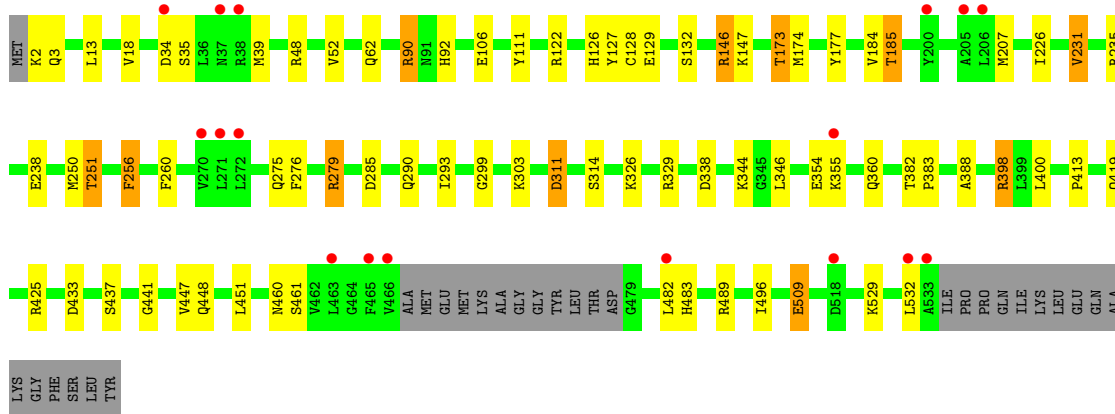
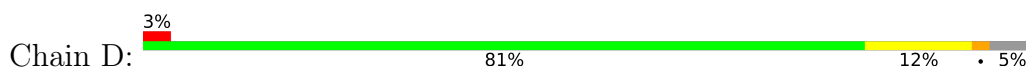


- Molecule 1: Pyruvate dehydrogenase [cytochrome]

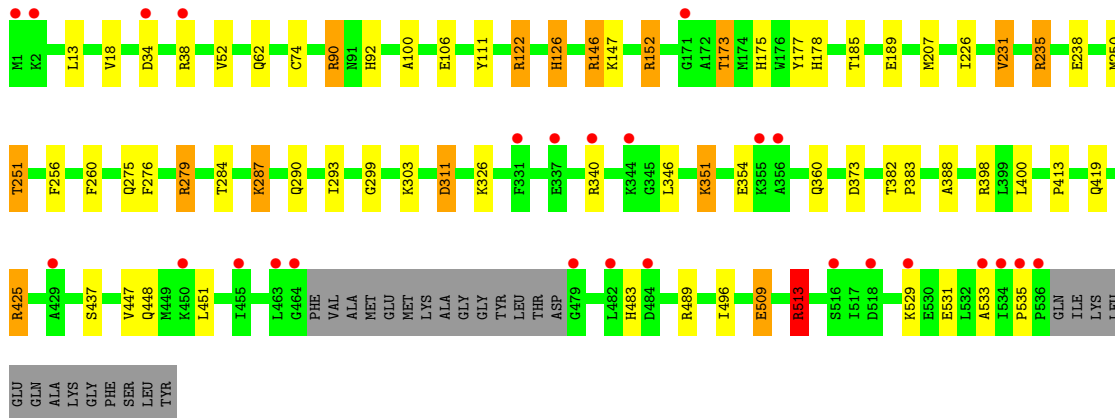
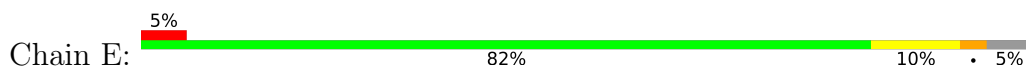




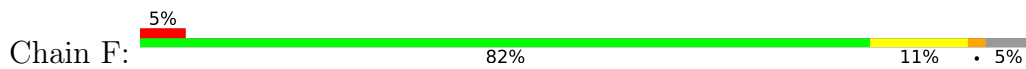
● Molecule 1: Pyruvate dehydrogenase [cytochrome]

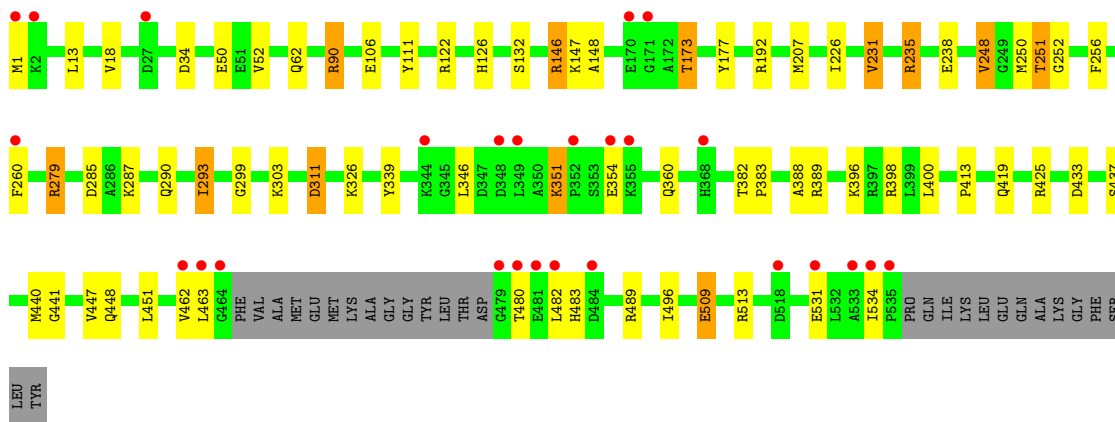


● Molecule 1: Pyruvate dehydrogenase [cytochrome]

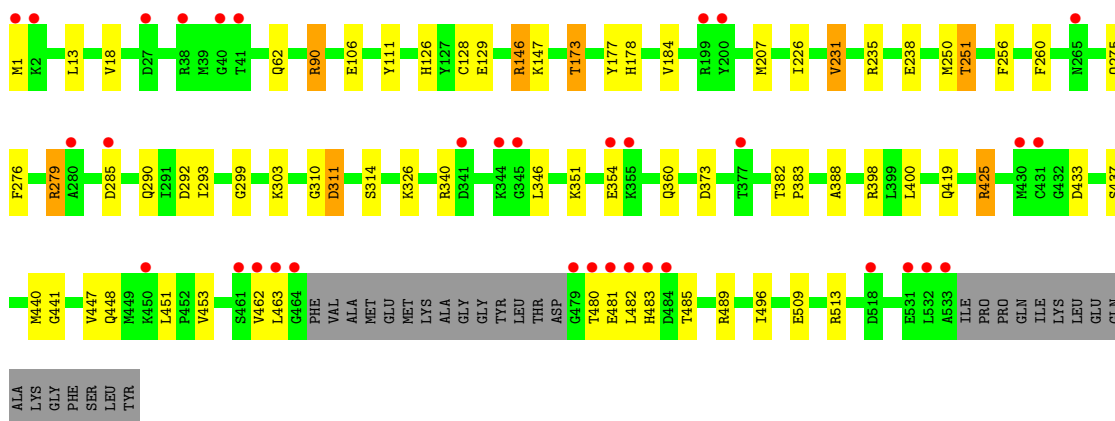
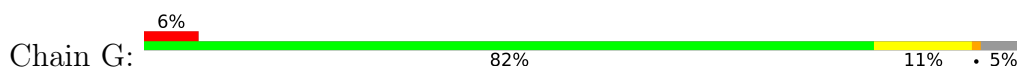


● Molecule 1: Pyruvate dehydrogenase [cytochrome]

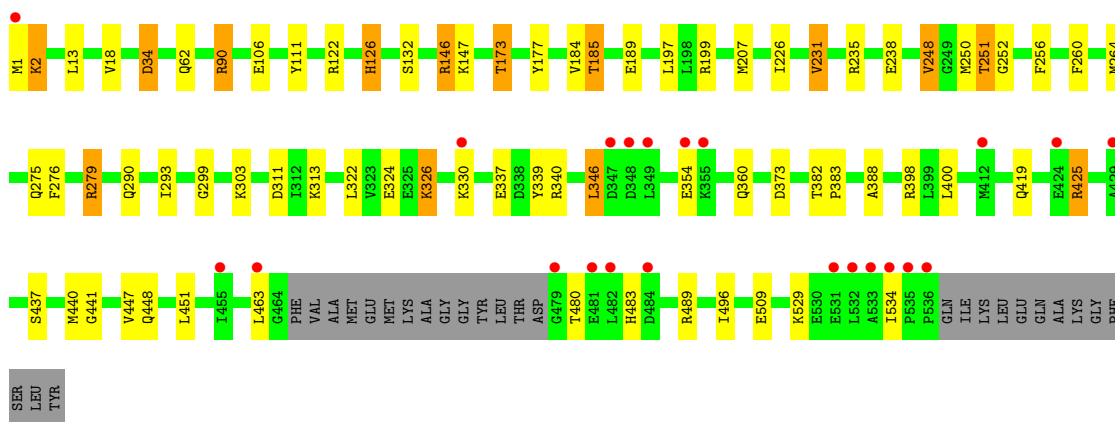
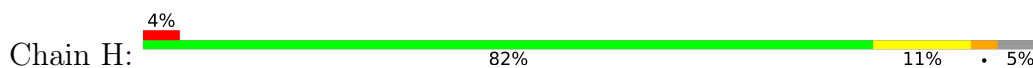




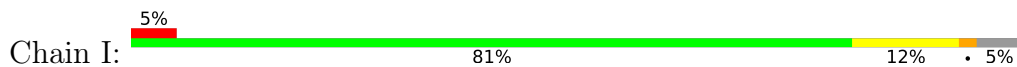
• Molecule 1: Pyruvate dehydrogenase [cytochrome]

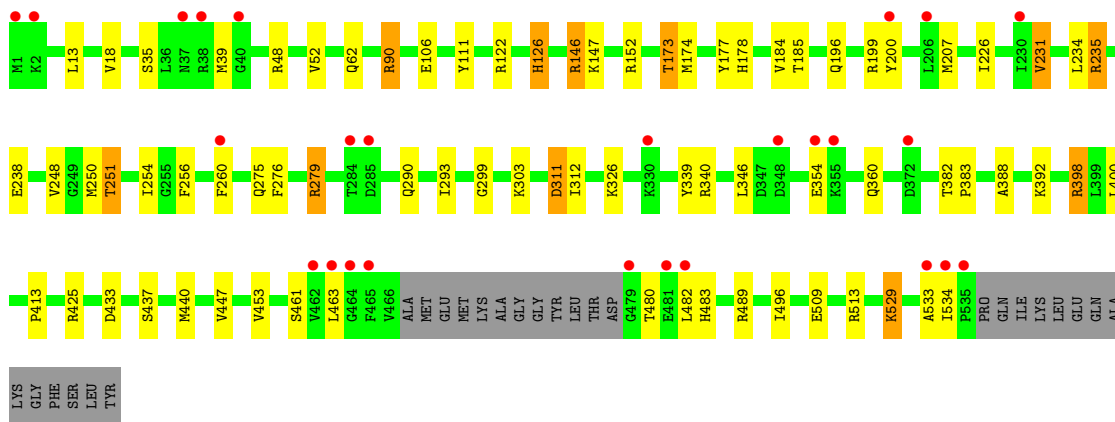


• Molecule 1: Pyruvate dehydrogenase [cytochrome]

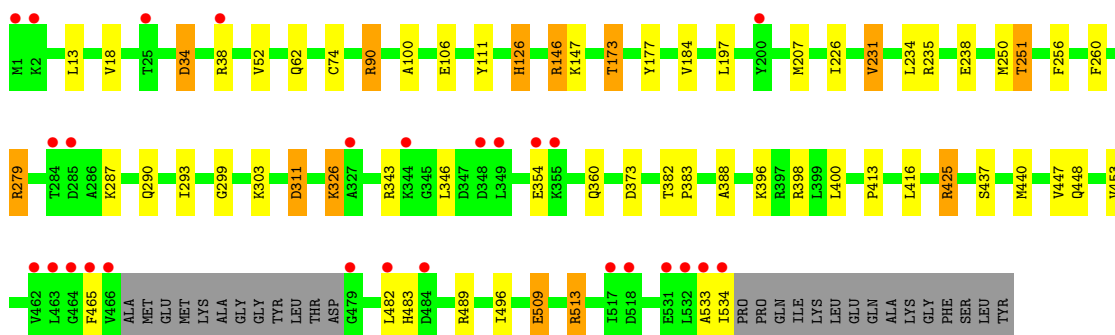
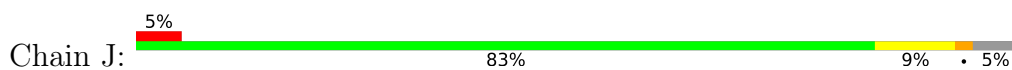


• Molecule 1: Pyruvate dehydrogenase [cytochrome]

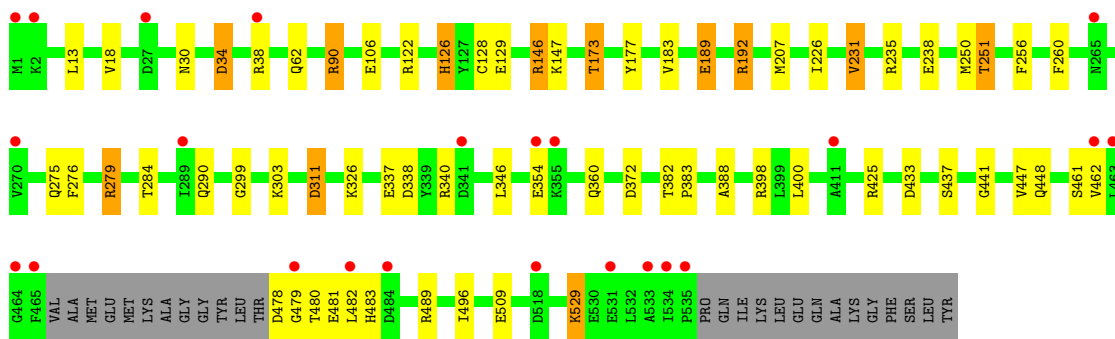
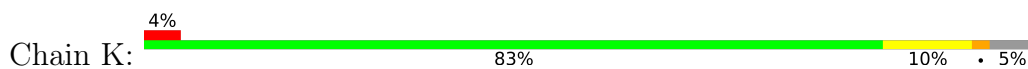




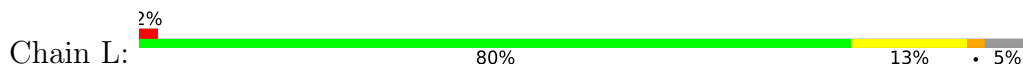
• Molecule 1: Pyruvate dehydrogenase [cytochrome]

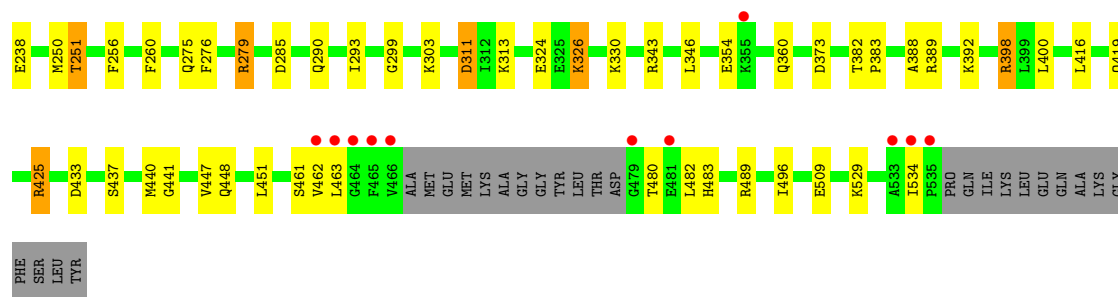


• Molecule 1: Pyruvate dehydrogenase [cytochrome]



• Molecule 1: Pyruvate dehydrogenase [cytochrome]





4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	203.24Å 207.05Å 214.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.50 29.99 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (30.00-2.50) 99.6 (29.99-2.50)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.51Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.183 , 0.198 0.186 , 0.186	Depositor DCC
R_{free} test set	15607 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	45.7	Xtrriage
Anisotropy	0.004	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 38.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.007 for k,h,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	50360	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.92% 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: TPP, MG, FAD, PO4

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	0.68	1/4186 (0.0%)	0.76	12/5670 (0.2%)
1	B	0.61	0/4096	0.73	10/5550 (0.2%)
1	C	0.66	3/4088 (0.1%)	0.77	12/5540 (0.2%)
1	D	0.65	0/4076	0.74	8/5522 (0.1%)
1	E	0.63	4/4063 (0.1%)	0.70	8/5508 (0.1%)
1	F	0.57	1/4060 (0.0%)	0.69	9/5502 (0.2%)
1	G	0.55	1/4024 (0.0%)	0.67	6/5453 (0.1%)
1	H	0.62	1/4066 (0.0%)	0.72	9/5513 (0.2%)
1	I	0.66	8/4065 (0.2%)	0.81	16/5507 (0.3%)
1	J	0.64	6/4092 (0.1%)	0.82	11/5543 (0.2%)
1	K	0.64	0/4102	0.75	9/5556 (0.2%)
1	L	0.68	2/4123 (0.0%)	0.75	10/5584 (0.2%)
All	All	0.63	27/49041 (0.1%)	0.74	120/66448 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	E	0	2

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	351	LYS	CG-CD	12.22	1.94	1.52
1	E	351	LYS	CE-NZ	12.20	1.79	1.49
1	E	513[A]	ARG	CD-NE	11.85	1.66	1.46
1	E	513[B]	ARG	CD-NE	11.85	1.66	1.46
1	I	513[A]	ARG	NE-CZ	9.84	1.45	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	513[A]	ARG	NE-CZ-NH1	18.57	129.59	120.30
1	J	513[B]	ARG	NE-CZ-NH1	18.57	129.59	120.30
1	C	340	ARG	NE-CZ-NH1	-14.26	113.17	120.30
1	I	513[A]	ARG	NE-CZ-NH1	14.22	127.41	120.30
1	I	513[B]	ARG	NE-CZ-NH1	14.22	127.41	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	513[A]	ARG	Sidechain
1	E	513[B]	ARG	Sidechain

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	4066	0	4095	79	2
1	B	3999	0	3991	51	0
1	C	4001	0	3990	63	0
1	D	3977	0	3975	71	0
1	E	3975	0	3967	57	0
1	F	3969	0	3969	53	0
1	G	3939	0	3938	56	0
1	H	3973	0	3982	65	0
1	I	3978	0	3978	47	0
1	J	3993	0	3999	43	0
1	K	4005	0	4014	69	0
1	L	4016	0	4027	61	2
2	A	26	0	16	3	0
2	B	26	0	16	1	0
2	C	26	0	16	2	0
2	D	26	0	16	1	0
2	E	26	0	16	2	0
2	F	26	0	16	2	0
2	G	26	0	16	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	26	0	16	2	0
2	I	26	0	16	3	0
2	J	26	0	16	2	0
2	K	26	0	16	6	0
2	L	26	0	16	4	0
3	A	53	0	31	1	0
3	B	53	0	31	3	0
3	C	53	0	31	1	0
3	D	53	0	31	3	0
3	E	53	0	31	5	0
3	F	53	0	31	4	0
3	G	53	0	31	4	0
3	H	53	0	31	2	0
3	I	53	0	31	6	0
3	J	53	0	31	4	0
3	K	53	0	31	2	0
3	L	53	0	31	2	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
4	I	1	0	0	0	0
4	J	1	0	0	0	0
4	K	1	0	0	0	0
4	L	1	0	0	0	0
5	A	30	0	0	8	0
5	B	15	0	0	1	0
5	C	10	0	0	0	0
5	D	35	0	0	3	0
5	E	10	0	0	1	0
5	F	10	0	0	1	0
5	G	15	0	0	0	0
5	H	10	0	0	1	0
5	I	10	0	0	1	0
5	J	5	0	0	0	0
5	K	5	0	0	1	0
5	L	25	0	0	2	0
6	A	280	0	0	15	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	60	0	0	0	0
6	C	73	0	0	4	0
6	D	88	0	0	6	0
6	E	43	0	0	8	0
6	F	41	0	0	2	0
6	G	40	0	0	1	0
6	H	64	0	0	4	0
6	I	62	0	0	1	0
6	J	50	0	0	3	0
6	K	77	0	0	4	0
6	L	451	0	0	28	0
All	All	50360	0	48489	649	2

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 7.

The worst 5 of 649 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:K:337:GLU:CG	1:K:340:ARG:HH22	1.26	1.49
1:C:337:GLU:CG	1:C:340:ARG:HH21	1.25	1.46
1:F:351:LYS:CD	1:F:351:LYS:CG	1.94	1.42
1:E:351:LYS:NZ	1:E:351:LYS:CE	1.79	1.41
1:C:337:GLU:CG	1:C:340:ARG:NH2	1.80	1.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:GLU:OE1	1:L:200:TYR:OH[4_545]	1.76	0.44
1:A:344:LYS:NZ	1:L:330:LYS:CE[4_545]	1.92	0.28

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	535/549 (97%)	513 (96%)	22 (4%)	0	100	100
1	B	525/549 (96%)	505 (96%)	20 (4%)	0	100	100
1	C	524/549 (95%)	509 (97%)	14 (3%)	1 (0%)	47	68
1	D	522/549 (95%)	503 (96%)	19 (4%)	0	100	100
1	E	521/549 (95%)	504 (97%)	17 (3%)	0	100	100
1	F	520/549 (95%)	502 (96%)	18 (4%)	0	100	100
1	G	517/549 (94%)	502 (97%)	15 (3%)	0	100	100
1	H	522/549 (95%)	507 (97%)	15 (3%)	0	100	100
1	I	521/549 (95%)	506 (97%)	15 (3%)	0	100	100
1	J	524/549 (95%)	507 (97%)	17 (3%)	0	100	100
1	K	524/549 (95%)	504 (96%)	19 (4%)	1 (0%)	47	68
1	L	527/549 (96%)	509 (97%)	18 (3%)	0	100	100
All	All	6282/6588 (95%)	6071 (97%)	209 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	484	ASP
1	K	479	GLY

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	434/439 (99%)	411 (95%)	23 (5%)	22	43
1	B	424/439 (97%)	401 (95%)	23 (5%)	22	42
1	C	423/439 (96%)	402 (95%)	21 (5%)	24	46
1	D	421/439 (96%)	401 (95%)	20 (5%)	25	48

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	420/439 (96%)	399 (95%)	21 (5%)	24	46
1	F	420/439 (96%)	400 (95%)	20 (5%)	25	48
1	G	417/439 (95%)	401 (96%)	16 (4%)	33	58
1	H	422/439 (96%)	397 (94%)	25 (6%)	19	37
1	I	420/439 (96%)	399 (95%)	21 (5%)	24	46
1	J	423/439 (96%)	402 (95%)	21 (5%)	24	46
1	K	424/439 (97%)	404 (95%)	20 (5%)	26	49
1	L	426/439 (97%)	407 (96%)	19 (4%)	27	51
All	All	5074/5268 (96%)	4824 (95%)	250 (5%)	25	47

5 of 250 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	248	VAL
1	K	338	ASP
1	G	513	ARG
1	K	284	THR
1	L	231	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 93 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	151	ASN
1	I	448	GLN
1	H	290	GLN
1	I	151	ASN
1	J	364	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 72 ligands modelled in this entry, 12 are monoatomic - leaving 60 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
5	PO4	A	614	-	4,4,4	0.69	0	6,6,6	1.39	1 (16%)
5	PO4	C	615	-	4,4,4	0.60	0	6,6,6	0.70	0
5	PO4	B	615	-	4,4,4	0.95	0	6,6,6	0.66	0
5	PO4	H	614	-	4,4,4	0.50	0	6,6,6	0.70	0
5	PO4	J	614	-	4,4,4	0.77	0	6,6,6	0.90	0
5	PO4	A	616	-	4,4,4	1.03	0	6,6,6	0.79	0
5	PO4	L	614	-	4,4,4	0.71	0	6,6,6	0.54	0
2	TPP	I	611	4	22,27,27	1.08	2 (9%)	29,40,40	1.96	9 (31%)
5	PO4	I	614	-	4,4,4	0.85	0	6,6,6	0.84	0
2	TPP	K	611	4	22,27,27	1.40	2 (9%)	29,40,40	2.56	10 (34%)
5	PO4	B	616	-	4,4,4	0.66	0	6,6,6	0.65	0
5	PO4	K	614	-	4,4,4	0.69	0	6,6,6	1.44	2 (33%)
5	PO4	G	615	-	4,4,4	0.91	0	6,6,6	1.05	0
2	TPP	E	611	4	22,27,27	0.91	1 (4%)	29,40,40	2.40	10 (34%)
2	TPP	F	611	4	22,27,27	0.98	0	29,40,40	2.61	10 (34%)
5	PO4	A	617	-	4,4,4	0.86	0	6,6,6	1.30	1 (16%)
5	PO4	G	616	-	4,4,4	0.65	0	6,6,6	0.68	0
5	PO4	E	614	-	4,4,4	0.81	0	6,6,6	0.42	0
5	PO4	D	615	-	4,4,4	0.61	0	6,6,6	1.53	1 (16%)
3	FAD	F	612	-	53,58,58	1.14	4 (7%)	68,89,89	1.51	15 (22%)
2	TPP	L	611	4	22,27,27	1.88	1 (4%)	29,40,40	2.49	11 (37%)
2	TPP	G	611	4	22,27,27	1.07	1 (4%)	29,40,40	2.55	13 (44%)
2	TPP	B	611	4	22,27,27	1.17	2 (9%)	29,40,40	2.39	14 (48%)
5	PO4	A	618	-	4,4,4	0.78	0	6,6,6	0.81	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	FAD	D	612	-	53,58,58	1.26	7 (13%)	68,89,89	1.54	15 (22%)
5	PO4	D	620	-	4,4,4	0.53	0	6,6,6	0.63	0
2	TPP	H	611	4	22,27,27	0.87	1 (4%)	29,40,40	2.27	11 (37%)
3	FAD	A	612	-	53,58,58	1.12	4 (7%)	68,89,89	1.55	11 (16%)
5	PO4	A	615	-	4,4,4	0.79	0	6,6,6	0.73	0
5	PO4	F	615	-	4,4,4	0.64	0	6,6,6	0.84	0
5	PO4	D	618	-	4,4,4	0.67	0	6,6,6	0.94	0
5	PO4	D	619	-	4,4,4	0.67	0	6,6,6	0.53	0
5	PO4	H	615	-	4,4,4	0.71	0	6,6,6	0.67	0
5	PO4	A	619	-	4,4,4	0.81	0	6,6,6	0.48	0
3	FAD	L	612	-	53,58,58	1.11	6 (11%)	68,89,89	1.66	13 (19%)
3	FAD	H	612	-	53,58,58	1.26	5 (9%)	68,89,89	1.48	12 (17%)
5	PO4	G	614	-	4,4,4	0.88	0	6,6,6	0.72	0
3	FAD	I	612	-	53,58,58	1.11	4 (7%)	68,89,89	1.41	10 (14%)
3	FAD	J	612	-	53,58,58	1.17	4 (7%)	68,89,89	1.44	10 (14%)
2	TPP	J	611	4	22,27,27	1.12	2 (9%)	29,40,40	2.56	13 (44%)
3	FAD	C	612	-	53,58,58	1.23	6 (11%)	68,89,89	1.58	14 (20%)
3	FAD	B	612	-	53,58,58	1.21	5 (9%)	68,89,89	1.50	15 (22%)
5	PO4	L	617	-	4,4,4	0.70	0	6,6,6	0.89	0
5	PO4	D	617	-	4,4,4	1.05	0	6,6,6	0.89	0
3	FAD	K	612	-	53,58,58	0.89	2 (3%)	68,89,89	1.62	17 (25%)
5	PO4	D	614	-	4,4,4	0.85	0	6,6,6	0.80	0
5	PO4	D	616	-	4,4,4	0.45	0	6,6,6	1.21	1 (16%)
5	PO4	E	615	-	4,4,4	0.72	0	6,6,6	0.78	0
5	PO4	I	615	-	4,4,4	0.75	0	6,6,6	0.85	0
5	PO4	B	614	-	4,4,4	0.38	0	6,6,6	1.57	1 (16%)
5	PO4	L	616	-	4,4,4	0.91	0	6,6,6	0.75	0
5	PO4	F	614	-	4,4,4	0.67	0	6,6,6	0.88	0
2	TPP	C	611	4	22,27,27	0.95	1 (4%)	29,40,40	2.29	11 (37%)
5	PO4	L	615	-	4,4,4	0.59	0	6,6,6	1.00	0
5	PO4	L	618	-	4,4,4	0.87	0	6,6,6	0.44	0
3	FAD	E	612	-	53,58,58	1.03	4 (7%)	68,89,89	1.45	11 (16%)
5	PO4	C	614	-	4,4,4	0.78	0	6,6,6	1.78	2 (33%)
2	TPP	D	611	4	22,27,27	1.69	3 (13%)	29,40,40	2.15	10 (34%)
2	TPP	A	611	4	22,27,27	1.32	3 (13%)	29,40,40	3.36	10 (34%)
3	FAD	G	612	-	53,58,58	1.08	4 (7%)	68,89,89	1.57	14 (20%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TPP	I	611	4	-	5/16/17/17	0/2/2/2
2	TPP	K	611	4	-	2/16/17/17	0/2/2/2
2	TPP	E	611	4	-	6/16/17/17	0/2/2/2
2	TPP	F	611	4	-	6/16/17/17	0/2/2/2
3	FAD	F	612	-	-	8/30/50/50	0/6/6/6
2	TPP	L	611	4	-	5/16/17/17	0/2/2/2
2	TPP	G	611	4	-	3/16/17/17	0/2/2/2
2	TPP	B	611	4	-	5/16/17/17	0/2/2/2
3	FAD	D	612	-	-	7/30/50/50	0/6/6/6
2	TPP	H	611	4	-	5/16/17/17	0/2/2/2
3	FAD	A	612	-	-	4/30/50/50	0/6/6/6
3	FAD	L	612	-	-	8/30/50/50	0/6/6/6
3	FAD	H	612	-	-	8/30/50/50	0/6/6/6
3	FAD	I	612	-	-	8/30/50/50	0/6/6/6
3	FAD	J	612	-	-	8/30/50/50	0/6/6/6
2	TPP	J	611	4	-	5/16/17/17	0/2/2/2
3	FAD	C	612	-	-	10/30/50/50	0/6/6/6
3	FAD	B	612	-	-	9/30/50/50	0/6/6/6
3	FAD	K	612	-	-	8/30/50/50	0/6/6/6
2	TPP	C	611	4	-	4/16/17/17	0/2/2/2
3	FAD	E	612	-	-	7/30/50/50	0/6/6/6
2	TPP	D	611	4	-	6/16/17/17	0/2/2/2
2	TPP	A	611	4	-	4/16/17/17	0/2/2/2
3	FAD	G	612	-	-	10/30/50/50	0/6/6/6

The worst 5 of 74 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	611	TPP	C6-C5	-8.00	1.47	1.50
2	D	611	TPP	C4-N3	-5.94	1.34	1.39
2	K	611	TPP	C6-C5	-4.08	1.49	1.50
2	A	611	TPP	C6-C5	-4.06	1.49	1.50
3	D	612	FAD	C4X-N5	3.99	1.38	1.30

The worst 5 of 298 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	611	TPP	C6-C5-C4	13.35	138.15	127.43
2	F	611	TPP	C6-C5-C4	8.41	134.19	127.43
2	G	611	TPP	C6-C5-C4	7.74	133.64	127.43
2	L	611	TPP	CM4-C4-N3	7.18	131.69	122.53
2	A	611	TPP	CM4-C4-N3	6.96	131.41	122.53

There are no chirality outliers.

5 of 151 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	611	TPP	C5-C6-C7-O7
2	A	611	TPP	PA-O3A-PB-O3B
2	B	611	TPP	C4-C5-C6-C7
2	B	611	TPP	C5-C6-C7-O7
2	B	611	TPP	C7-O7-PA-O1A

There are no ring outliers.

39 monomers are involved in 79 short contacts:

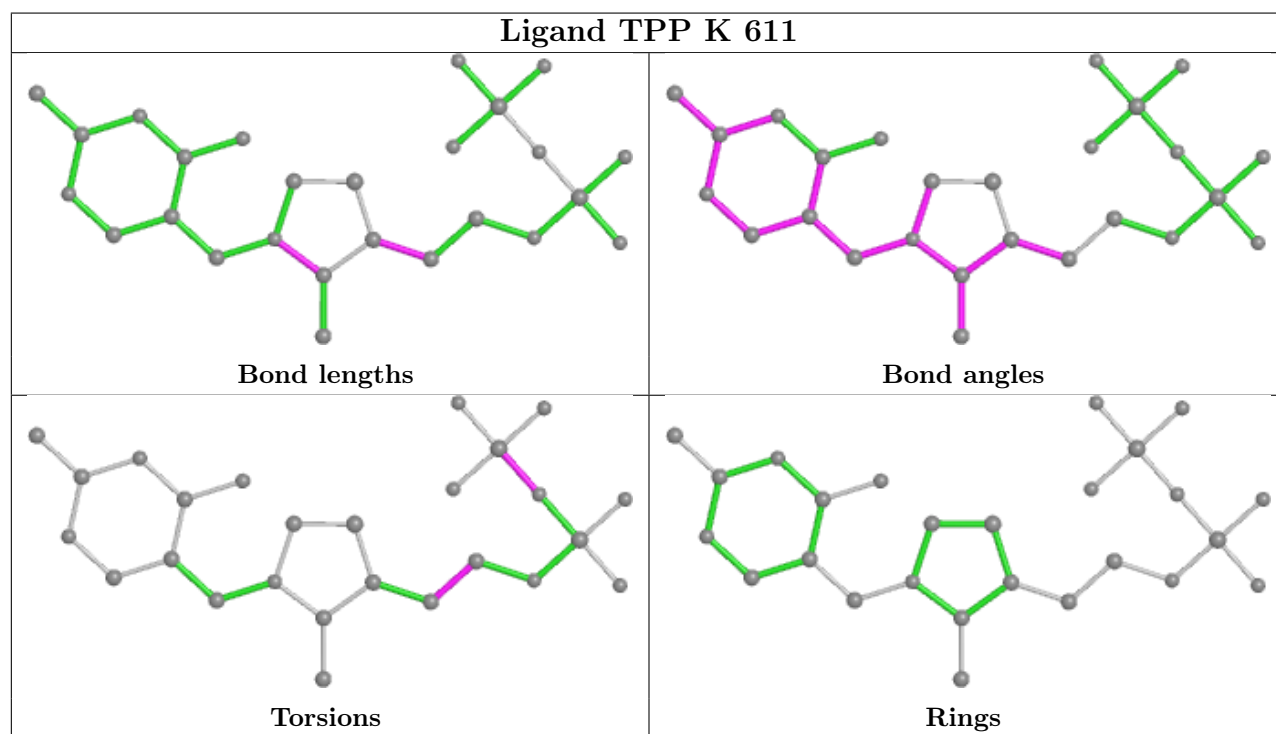
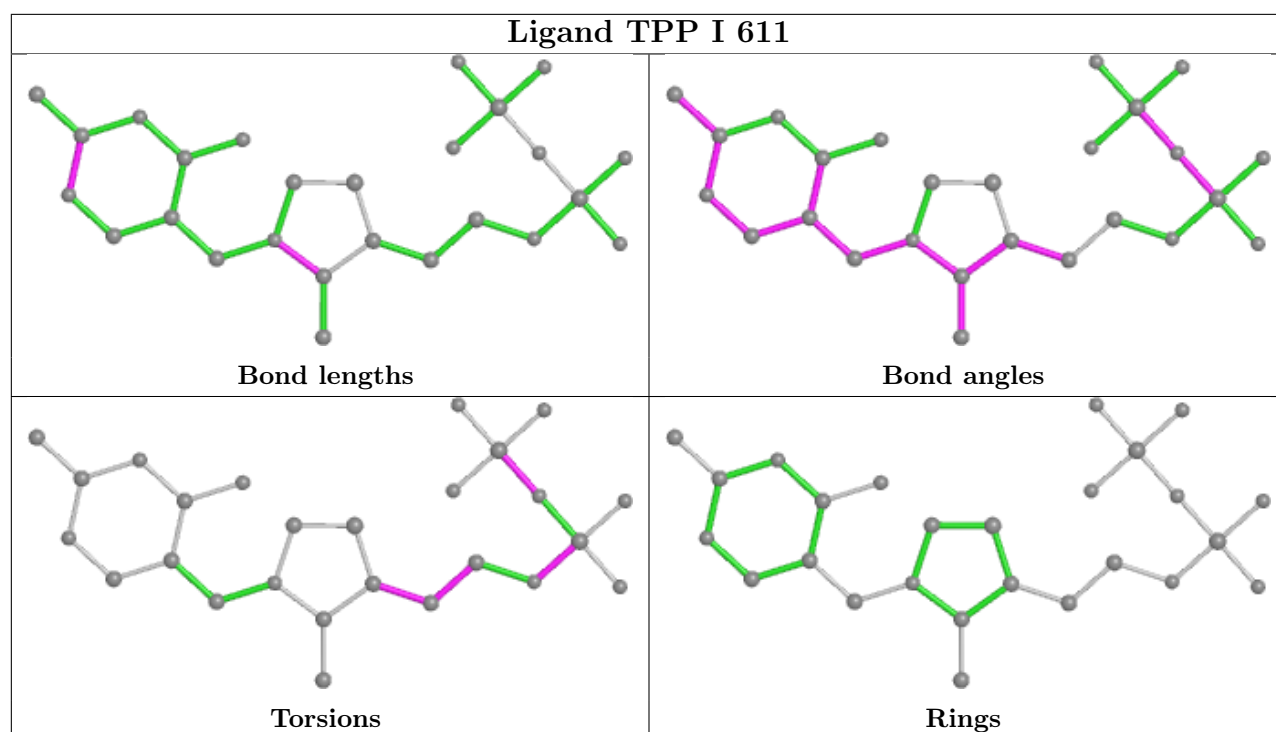
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	616	PO4	2	0
2	I	611	TPP	3	0
5	I	614	PO4	1	0
2	K	611	TPP	6	0
5	K	614	PO4	1	0
2	E	611	TPP	2	0
2	F	611	TPP	2	0
5	A	617	PO4	1	0
5	E	614	PO4	1	0
5	D	615	PO4	1	0
3	F	612	FAD	4	0
2	L	611	TPP	4	0
2	G	611	TPP	2	0
2	B	611	TPP	1	0
5	A	618	PO4	2	0
3	D	612	FAD	3	0
2	H	611	TPP	2	0
3	A	612	FAD	1	0
5	D	618	PO4	1	0
5	H	615	PO4	1	0
5	A	619	PO4	3	0

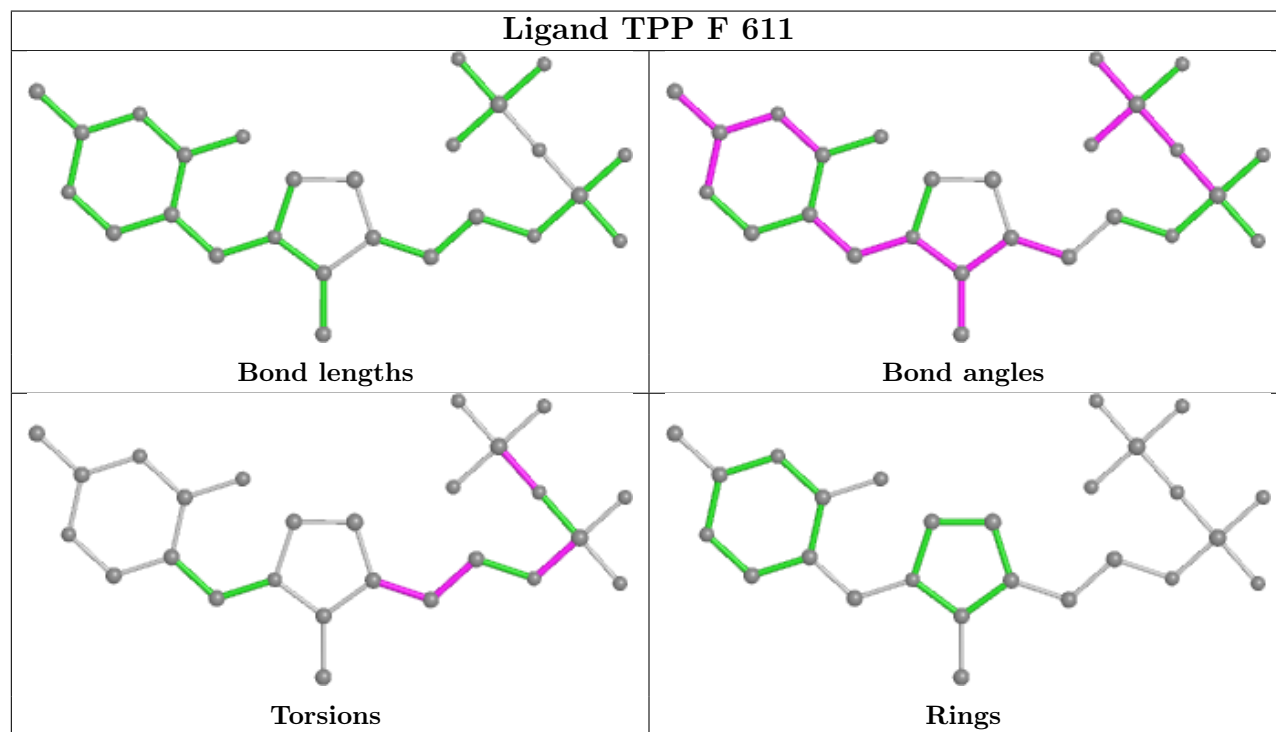
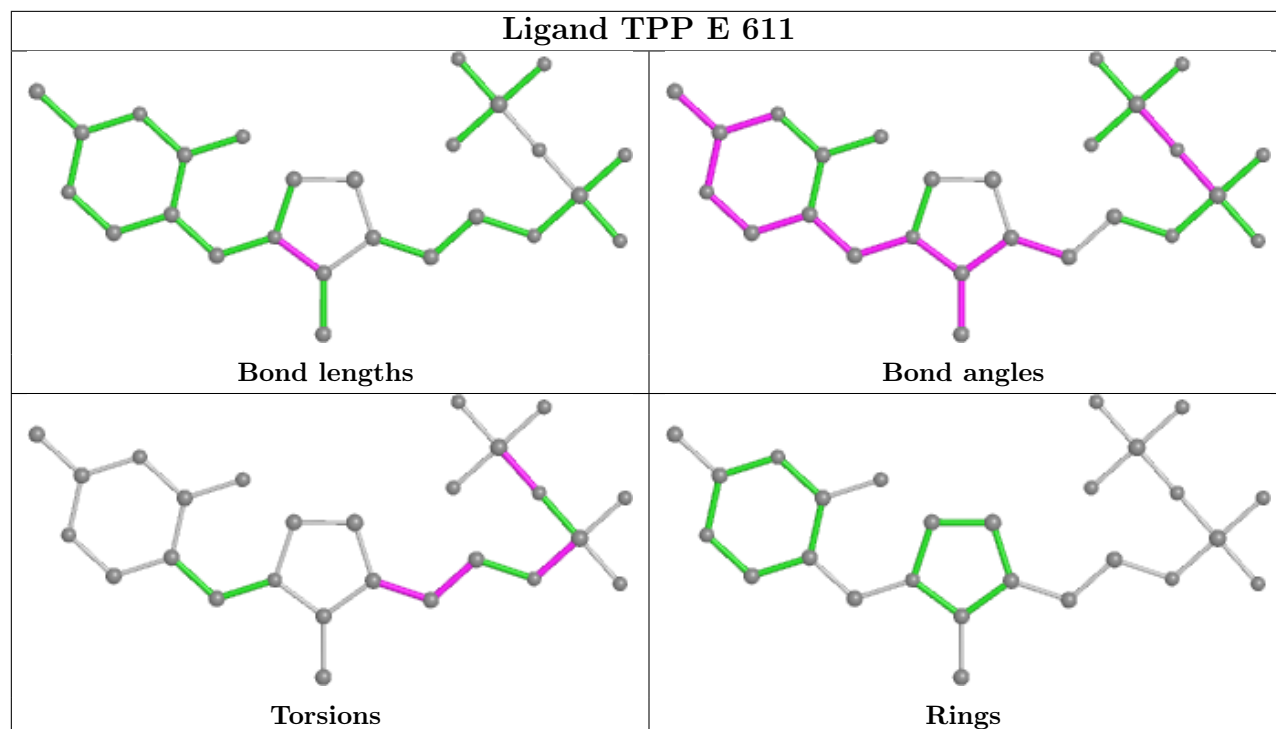
Continued on next page...

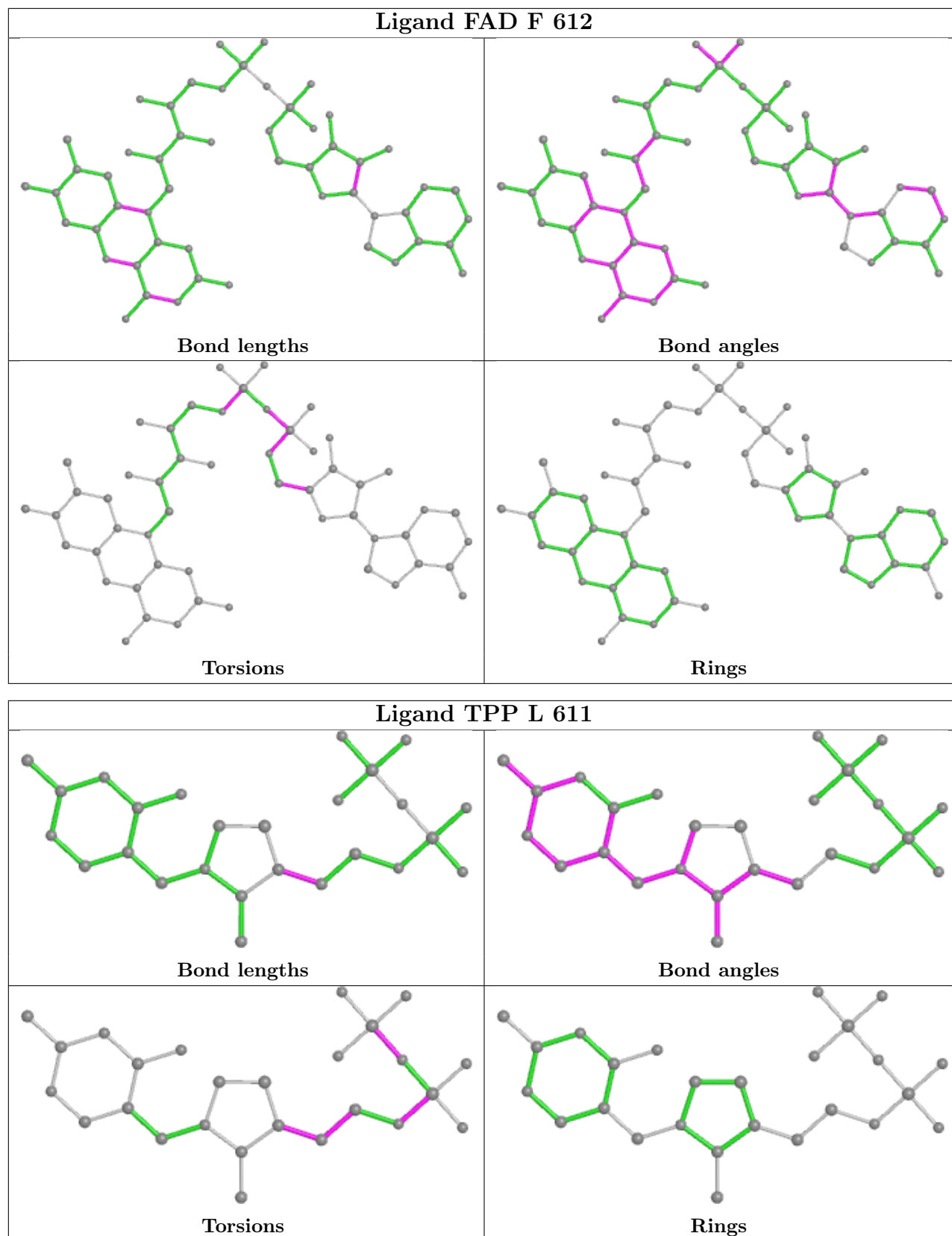
Continued from previous page...

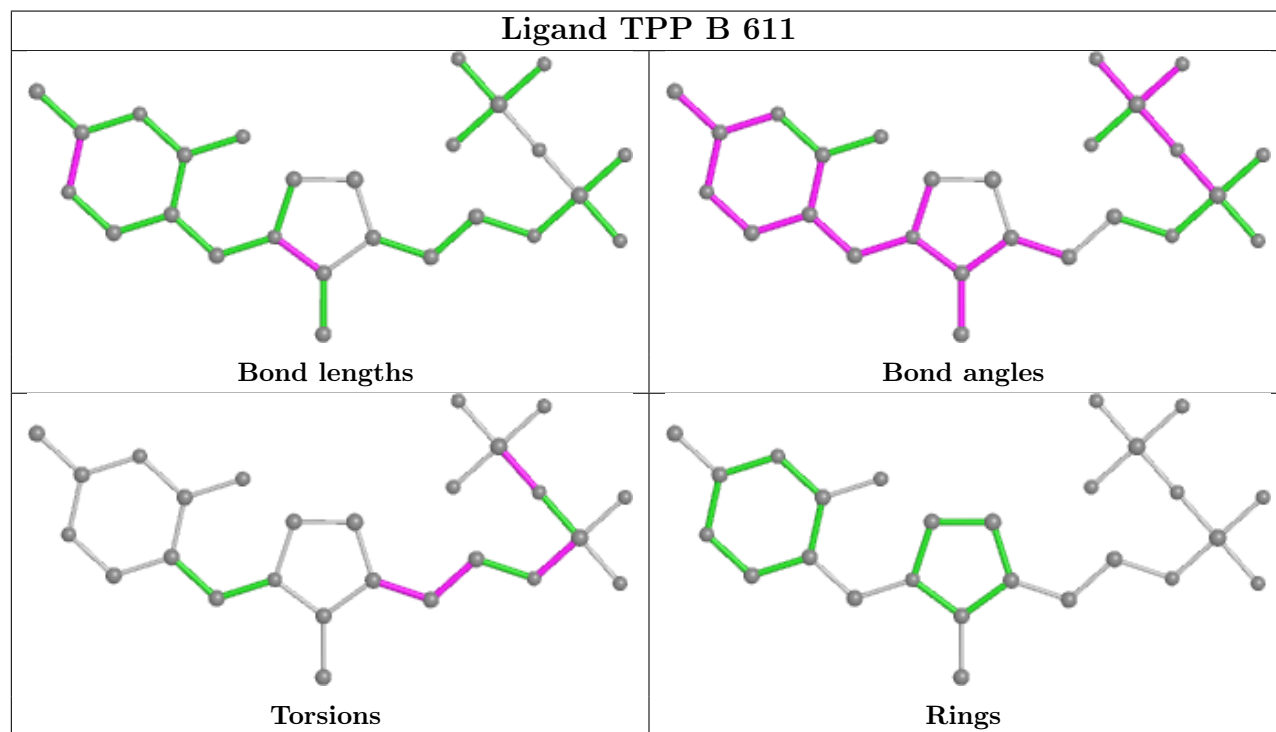
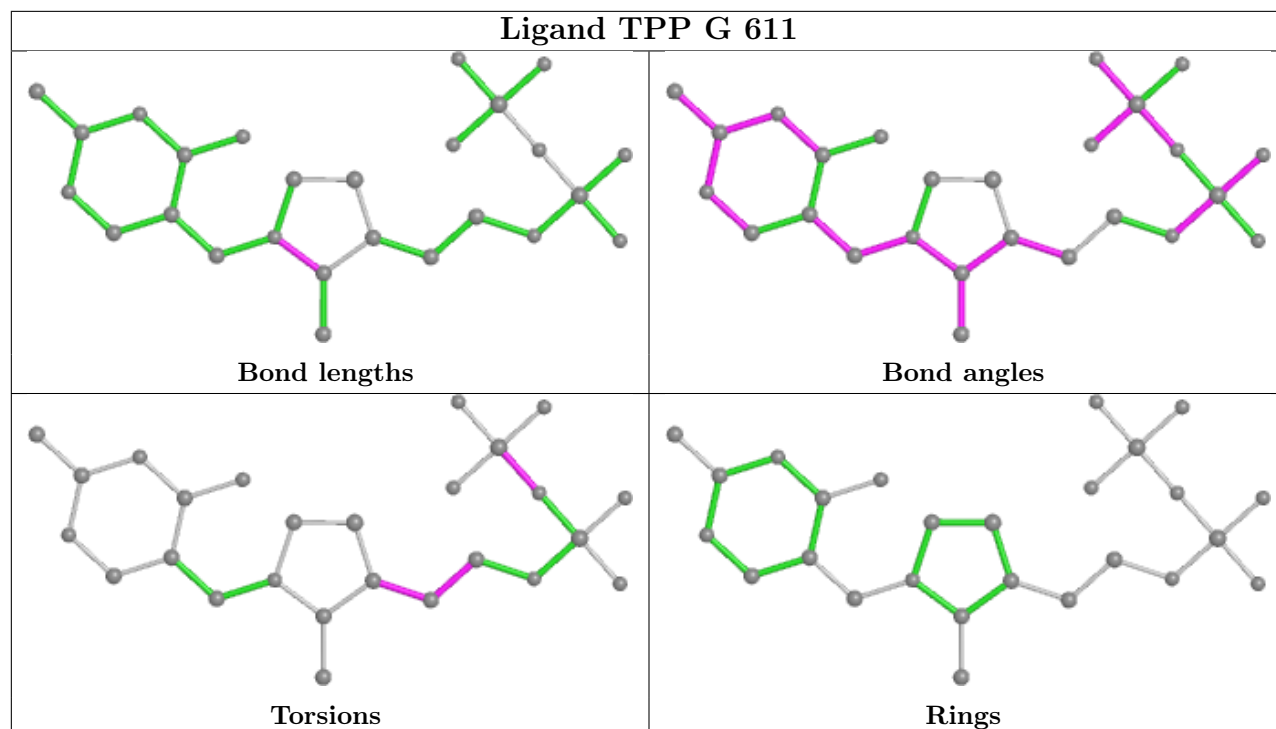
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	612	FAD	2	0
3	H	612	FAD	2	0
3	I	612	FAD	6	0
3	J	612	FAD	4	0
2	J	611	TPP	2	0
3	C	612	FAD	1	0
3	B	612	FAD	3	0
5	L	617	PO4	1	0
3	K	612	FAD	2	0
5	D	614	PO4	1	0
5	B	614	PO4	1	0
5	L	616	PO4	1	0
5	F	614	PO4	1	0
2	C	611	TPP	2	0
3	E	612	FAD	5	0
2	D	611	TPP	1	0
2	A	611	TPP	3	0
3	G	612	FAD	4	0

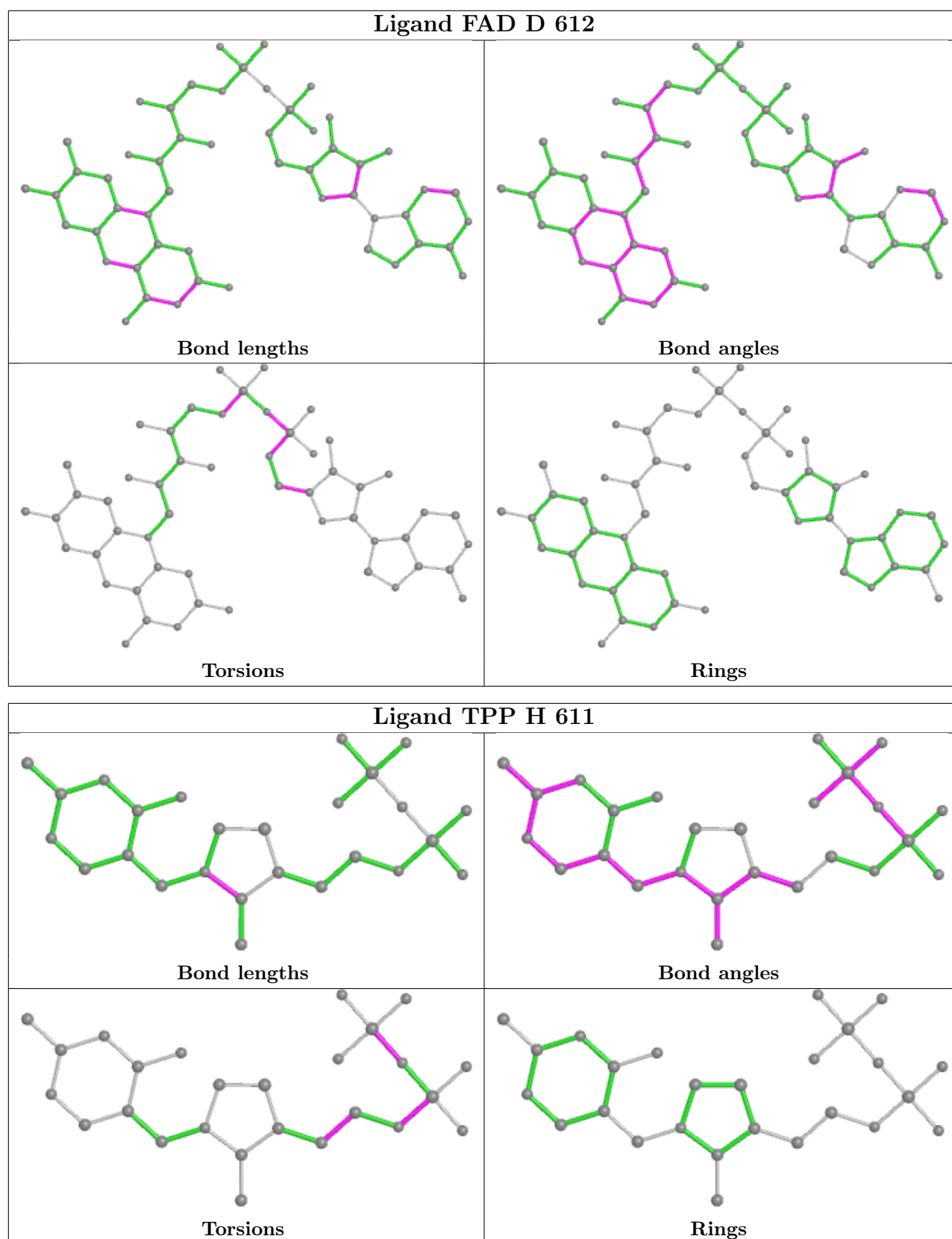
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

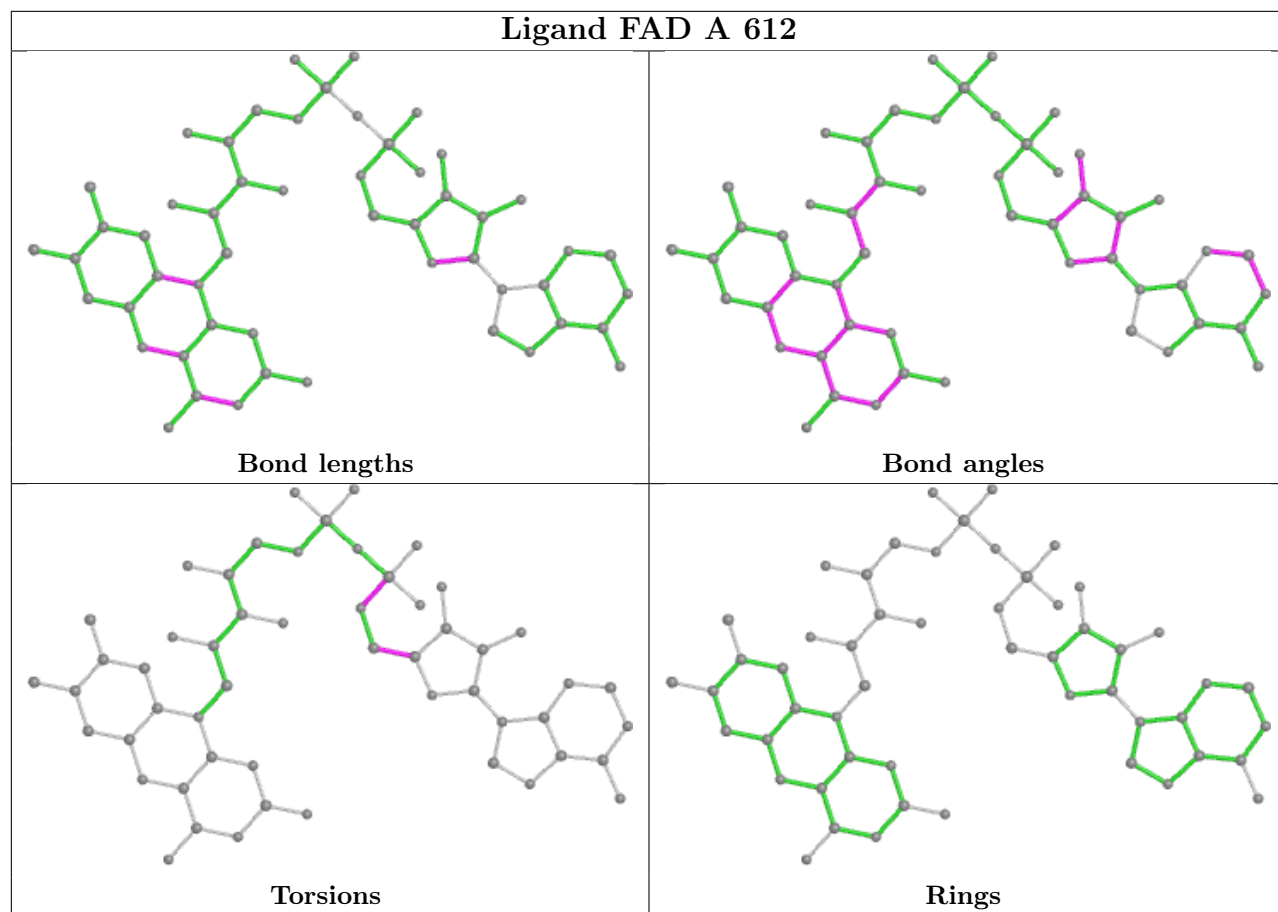


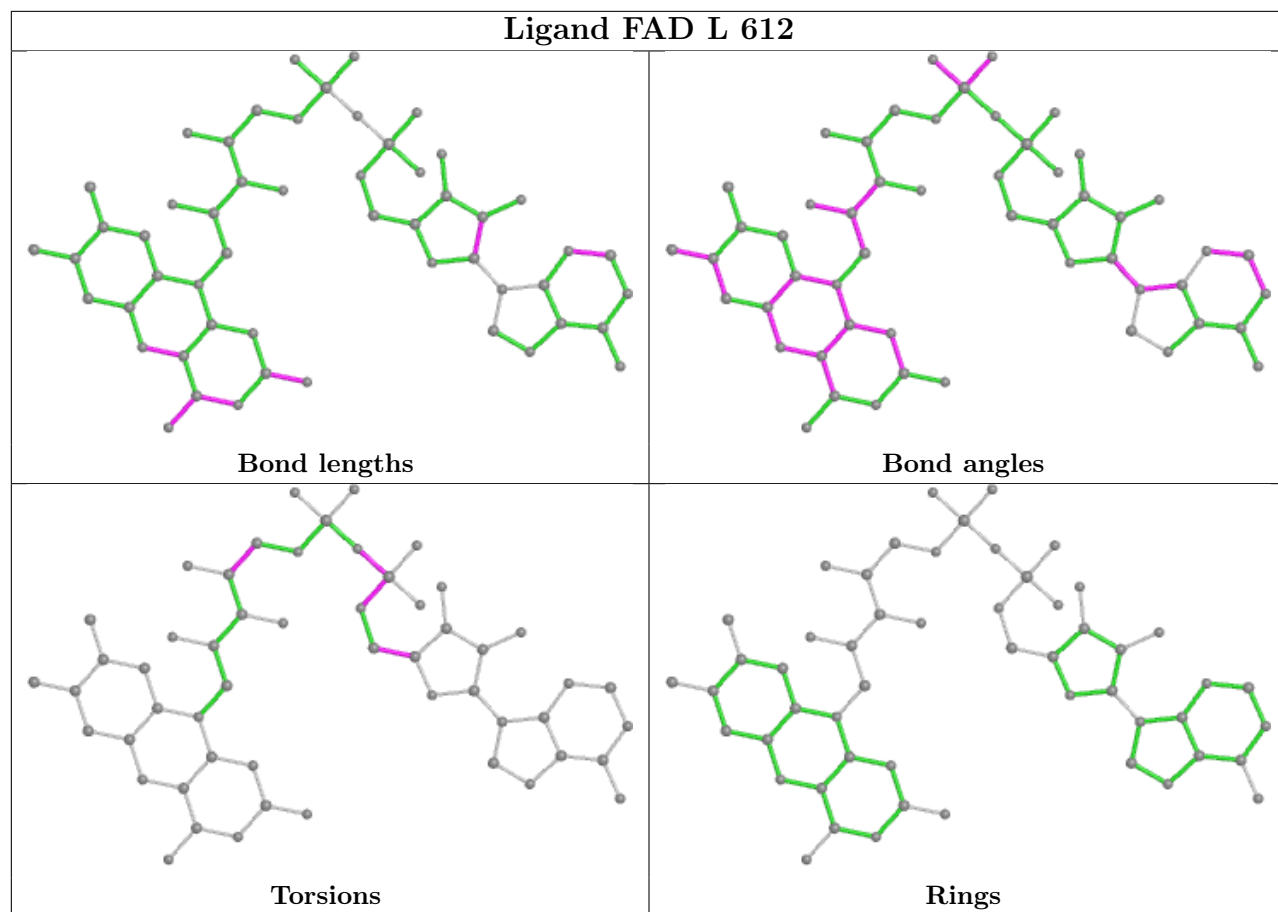


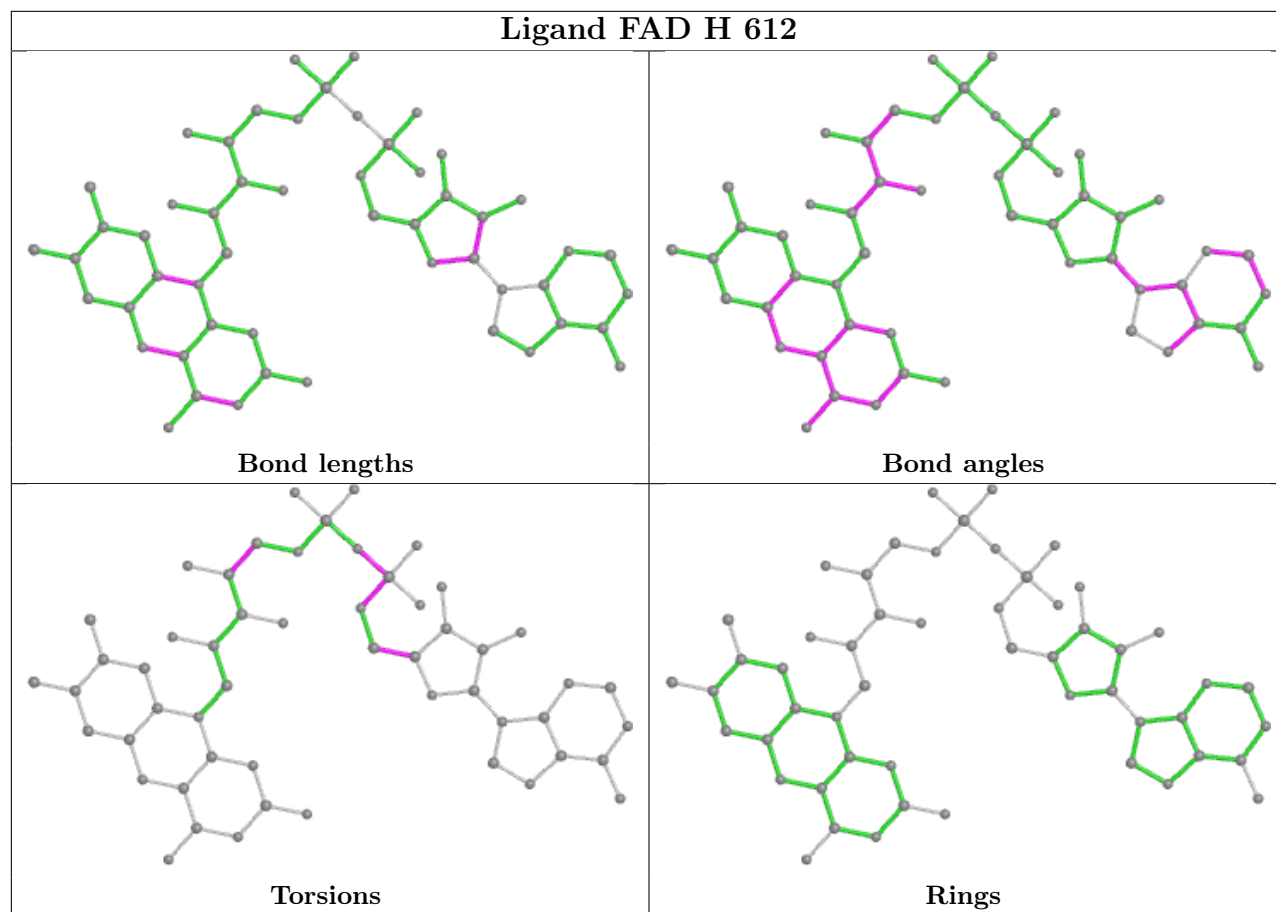


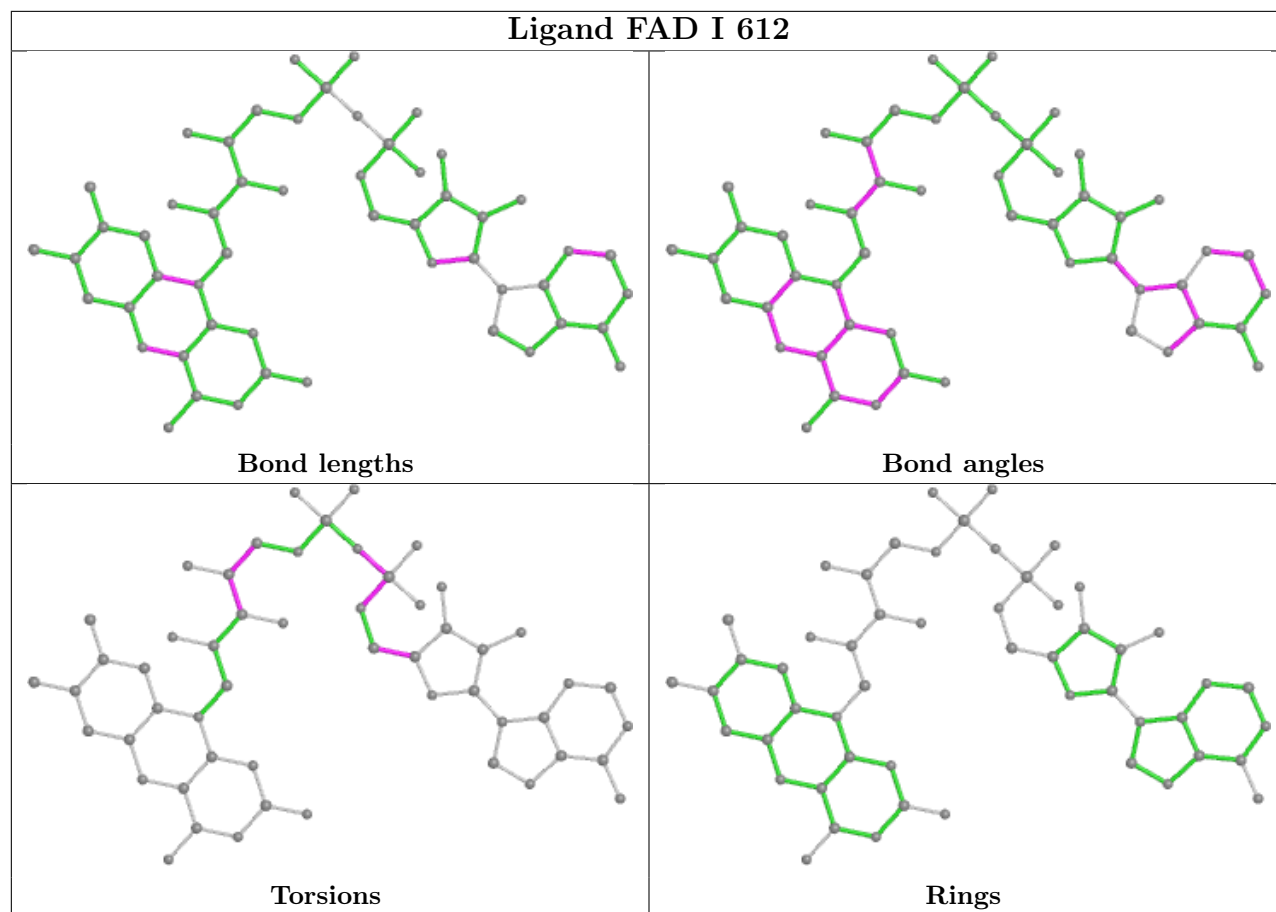


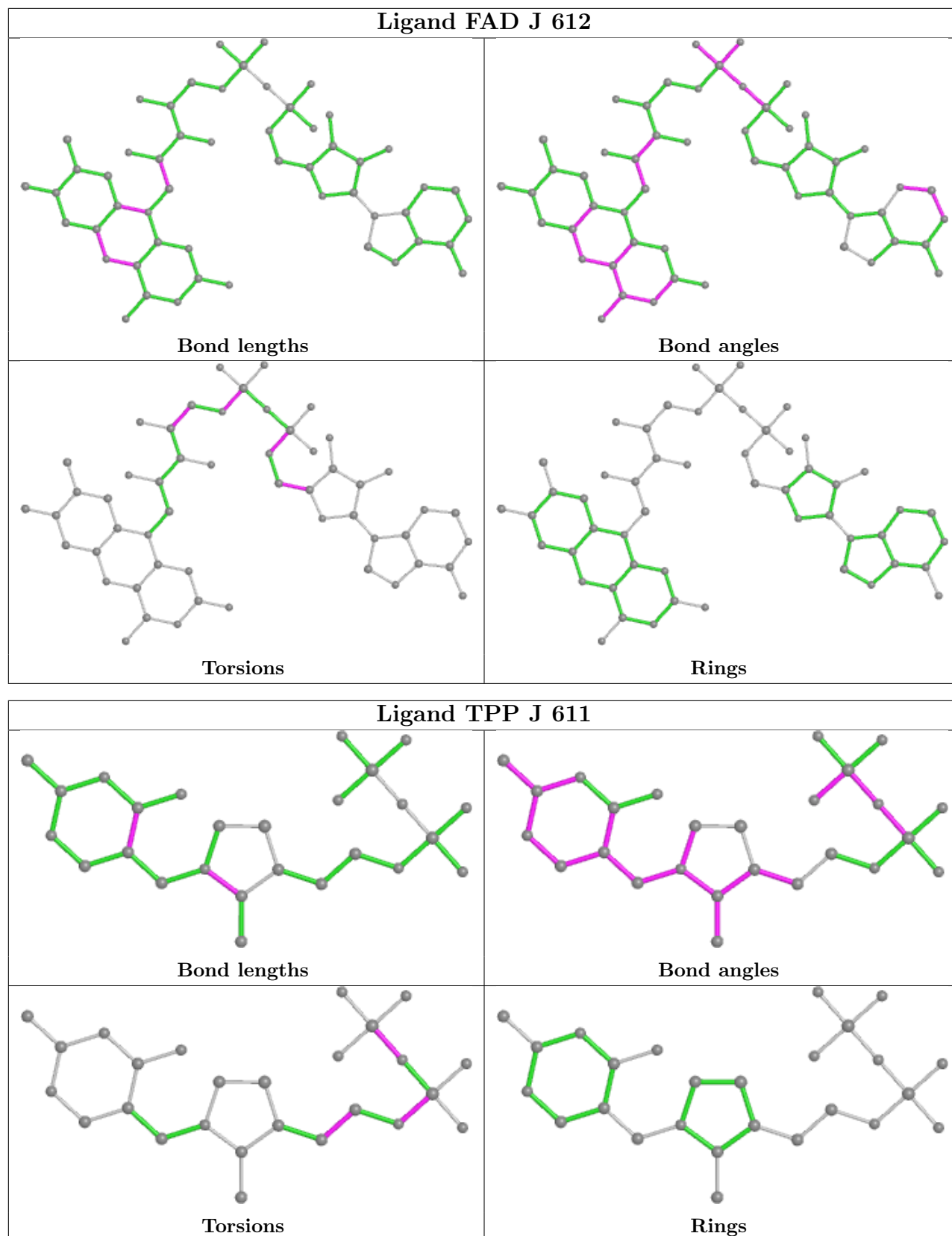


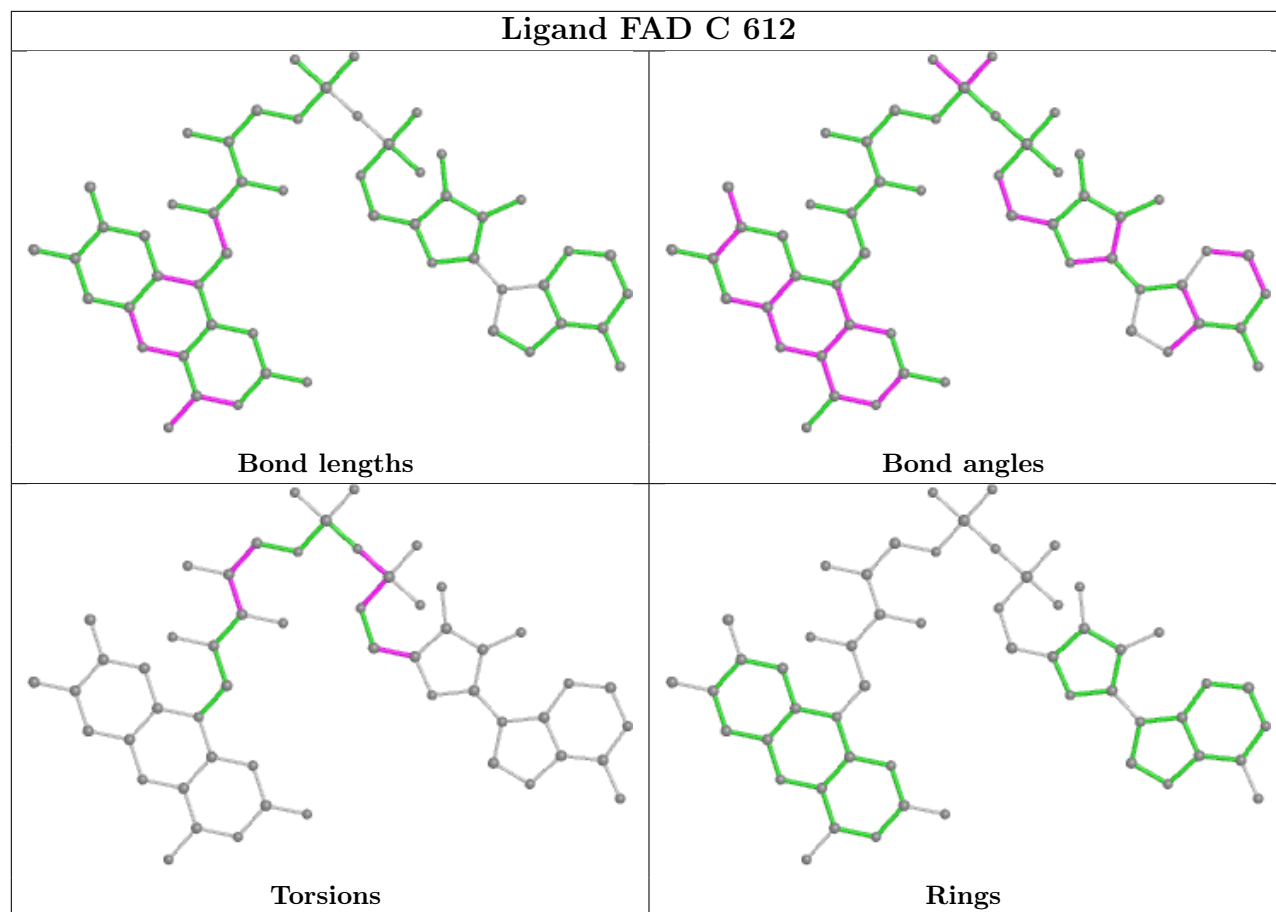


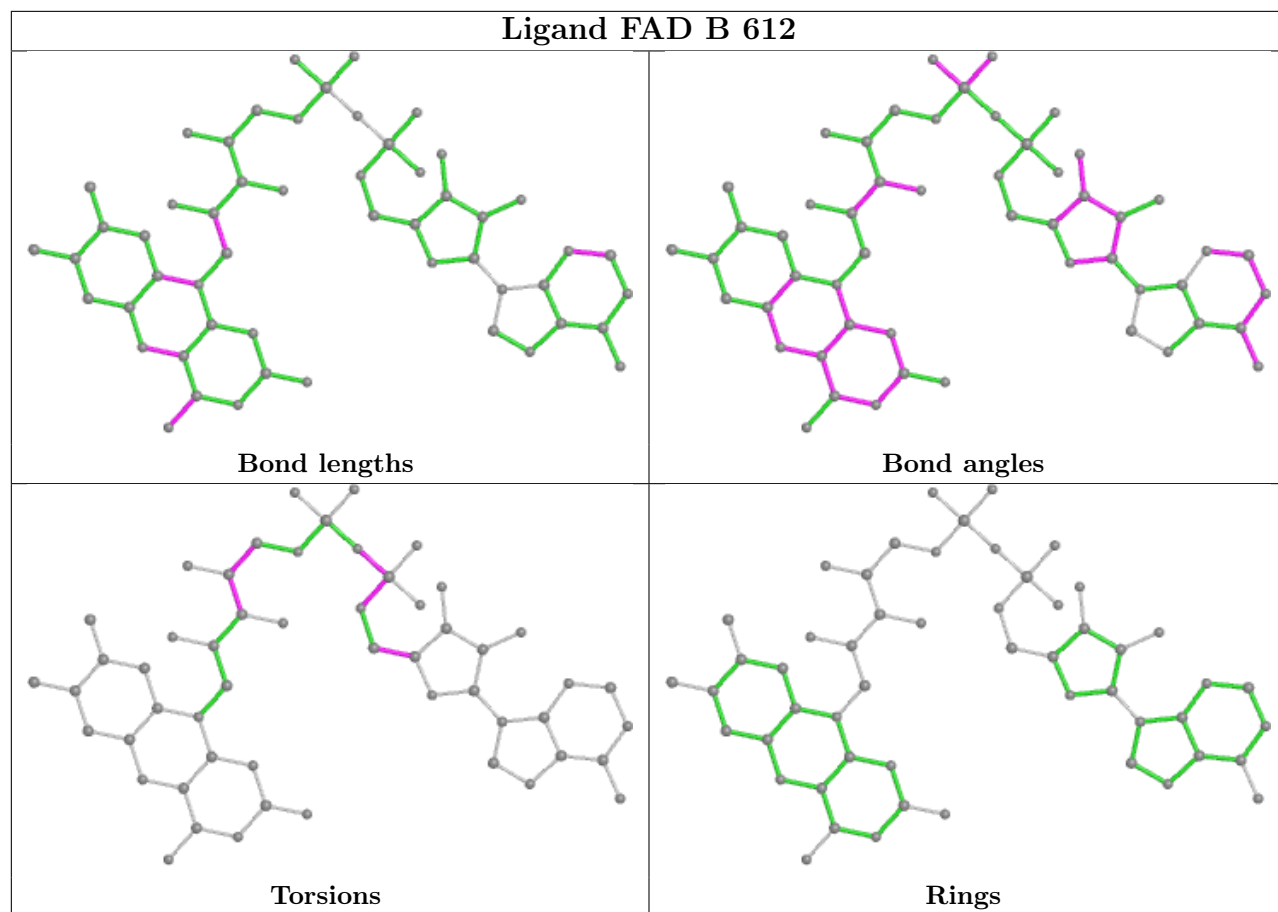


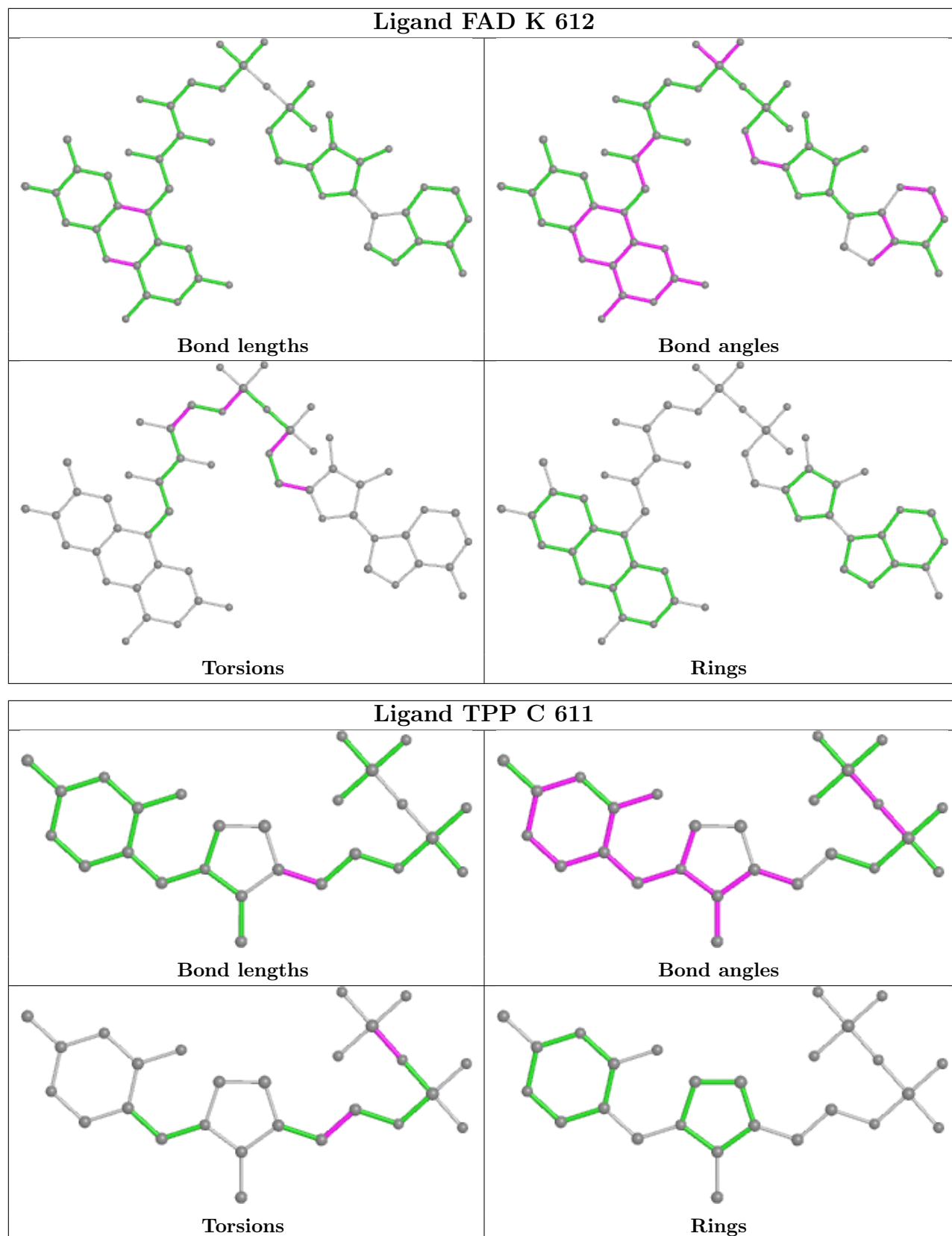


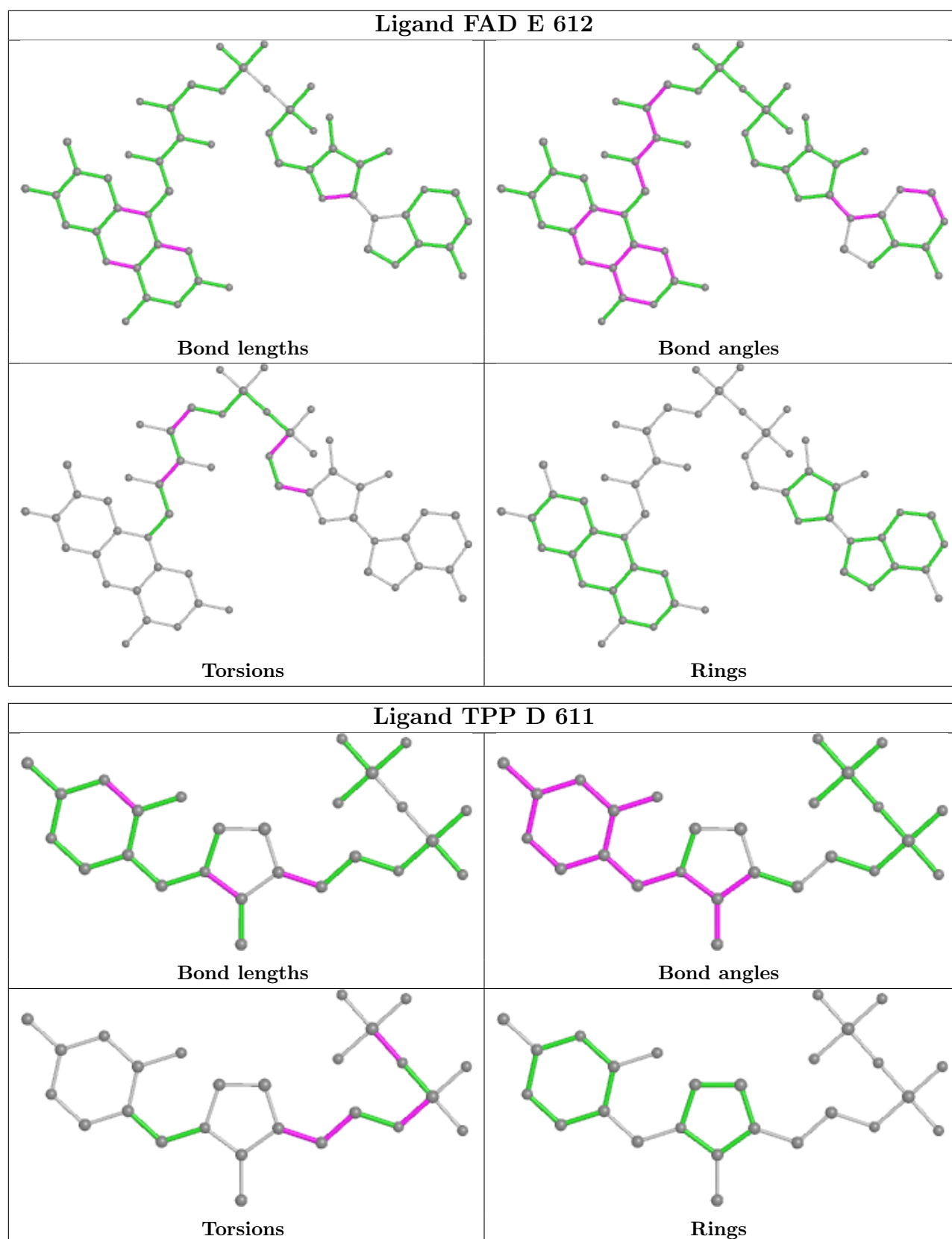


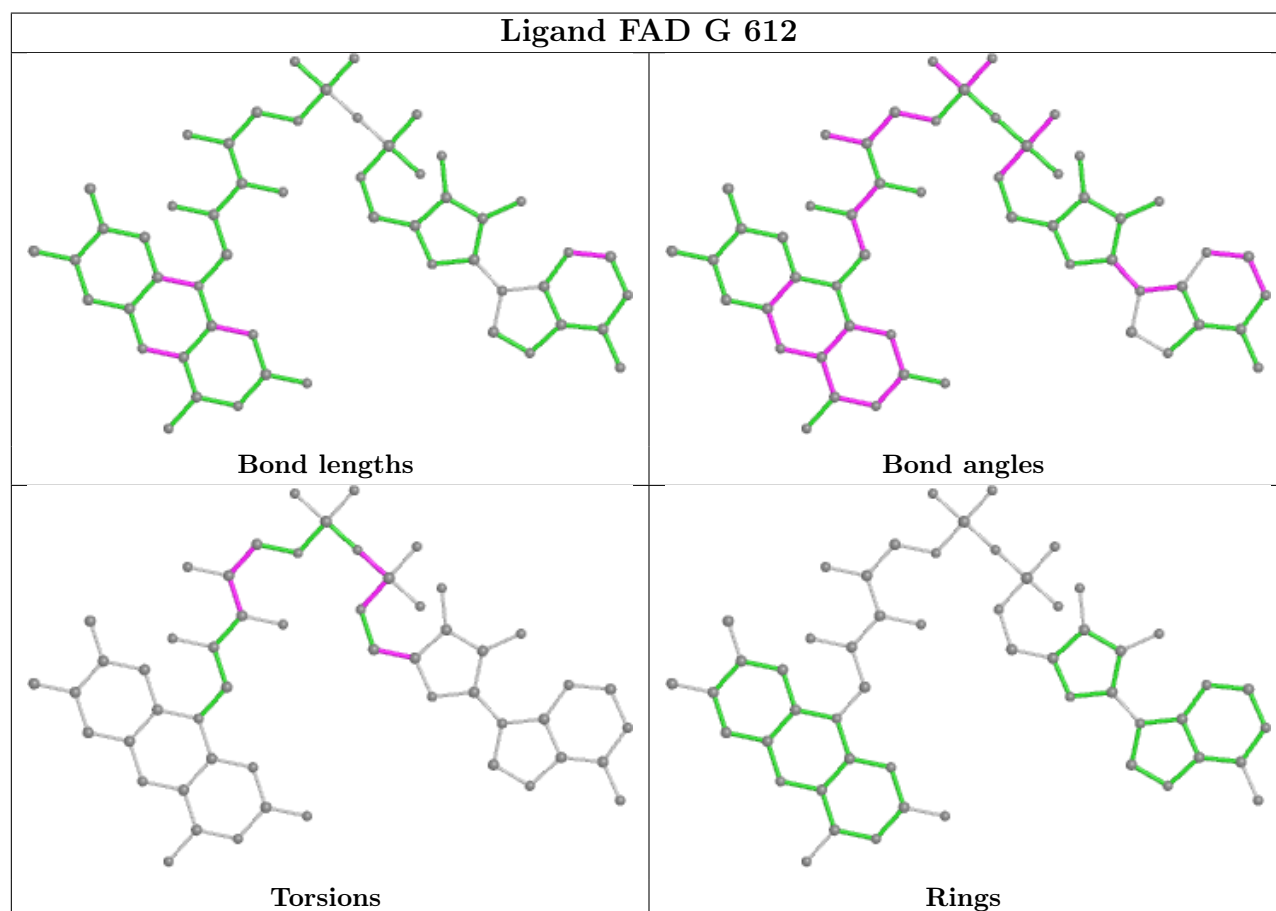
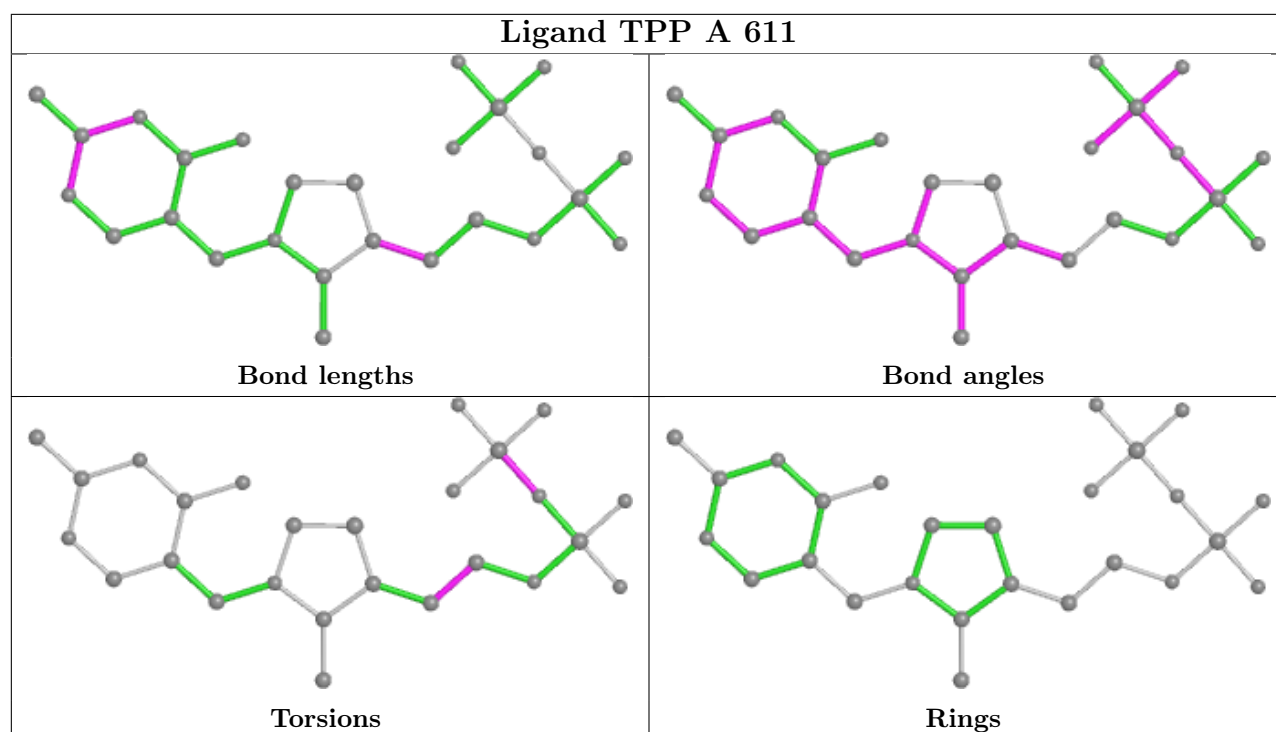












5.7 Other polymers [i](#)

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	527/549 (95%)	-0.13	17 (3%) 47 51	37, 50, 73, 115	10 (1%)
1	B	524/549 (95%)	-0.05	22 (4%) 36 39	39, 60, 92, 128	11 (2%)
1	C	522/549 (95%)	-0.09	24 (4%) 32 34	39, 57, 84, 124	10 (1%)
1	D	520/549 (94%)	-0.09	17 (3%) 46 50	39, 54, 78, 94	10 (1%)
1	E	522/549 (95%)	0.07	26 (4%) 28 30	45, 70, 110, 169	8 (1%)
1	F	521/549 (94%)	0.02	26 (4%) 28 30	48, 71, 103, 143	9 (1%)
1	G	519/549 (94%)	0.09	34 (6%) 18 19	46, 71, 104, 137	8 (1%)
1	H	522/549 (95%)	-0.07	22 (4%) 36 39	45, 62, 96, 147	8 (1%)
1	I	523/549 (95%)	0.01	26 (4%) 28 30	44, 64, 98, 137	10 (1%)
1	J	522/549 (95%)	0.06	27 (5%) 27 29	42, 66, 98, 132	10 (1%)
1	K	523/549 (95%)	-0.06	23 (4%) 34 37	39, 55, 81, 118	10 (1%)
1	L	523/549 (95%)	-0.24	13 (2%) 57 61	38, 51, 75, 119	10 (1%)
All	All	6268/6588 (95%)	-0.04	277 (4%) 34 37	37, 60, 96, 169	114 (1%)

The worst 5 of 277 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	534	ILE	6.8
1	J	465	PHE	6.8
1	J	466	VAL	6.7
1	F	1	MET	6.2
1	H	535	PRO	6.1

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 monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	PO4	D	616	5/5	0.61	0.45	67,67,69,69	5
5	PO4	C	615	5/5	0.69	0.33	72,73,73,74	5
4	MG	F	613	1/1	0.70	0.08	76,76,76,76	0
4	MG	G	613	1/1	0.70	0.10	67,67,67,67	0
4	MG	E	613	1/1	0.72	0.07	70,70,70,70	0
4	MG	K	613	1/1	0.76	0.19	50,50,50,50	0
4	MG	L	613	1/1	0.76	0.12	47,47,47,47	0
5	PO4	A	615	5/5	0.77	0.30	62,62,64,66	5
5	PO4	H	614	5/5	0.79	0.28	98,99,99,100	0
4	MG	B	613	1/1	0.80	0.12	55,55,55,55	0
5	PO4	A	619	5/5	0.81	0.32	72,73,74,74	5
5	PO4	E	615	5/5	0.81	0.25	73,73,74,74	5
4	MG	J	613	1/1	0.81	0.13	72,72,72,72	0
4	MG	D	613	1/1	0.82	0.16	57,57,57,57	0
5	PO4	B	616	5/5	0.82	0.41	71,71,72,73	5
4	MG	C	613	1/1	0.82	0.12	63,63,63,63	0
5	PO4	B	615	5/5	0.84	0.22	71,71,72,72	5
5	PO4	A	617	5/5	0.84	0.21	66,67,68,68	5
4	MG	A	613	1/1	0.85	0.11	52,52,52,52	0
5	PO4	L	617	5/5	0.85	0.24	58,58,60,61	5
5	PO4	D	620	5/5	0.86	0.27	51,53,54,55	5
5	PO4	A	616	5/5	0.86	0.31	56,57,58,58	5
5	PO4	I	614	5/5	0.87	0.15	68,68,68,69	5
5	PO4	L	615	5/5	0.88	0.32	91,92,93,93	0
5	PO4	D	619	5/5	0.89	0.18	68,69,69,70	5
5	PO4	L	614	5/5	0.89	0.20	97,97,98,98	0
5	PO4	G	616	5/5	0.89	0.20	71,71,71,72	5
5	PO4	D	618	5/5	0.89	0.21	67,68,69,69	5
5	PO4	D	614	5/5	0.90	0.21	68,68,69,69	5
5	PO4	D	617	5/5	0.91	0.26	61,61,62,62	5
5	PO4	F	615	5/5	0.91	0.21	61,61,62,64	5
5	PO4	L	618	5/5	0.91	0.20	63,63,64,65	5

Continued on next page...

Continued from previous page...

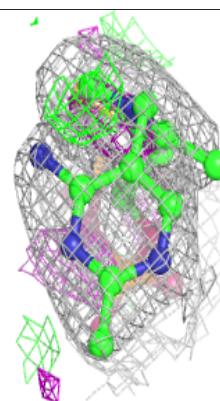
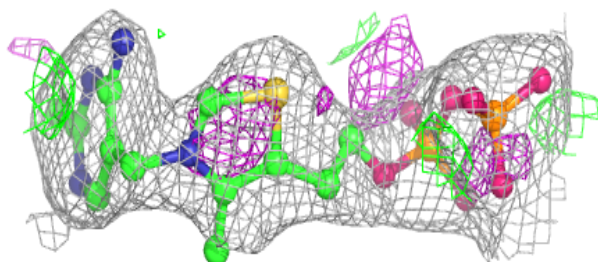
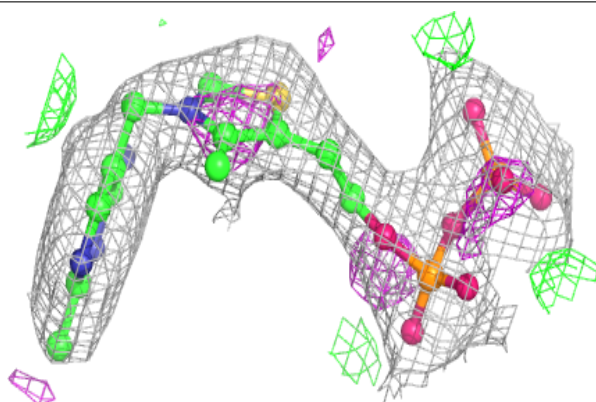
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	MG	I	613	1/1	0.92	0.08	62,62,62,62	0
5	PO4	A	618	5/5	0.93	0.13	56,56,57,57	5
4	MG	H	613	1/1	0.93	0.07	59,59,59,59	0
5	PO4	J	614	5/5	0.94	0.15	89,89,90,91	0
5	PO4	C	614	5/5	0.94	0.12	73,74,75,77	0
5	PO4	G	614	5/5	0.94	0.20	65,65,66,66	5
5	PO4	G	615	5/5	0.94	0.16	84,85,86,86	0
5	PO4	I	615	5/5	0.94	0.15	91,91,92,93	0
5	PO4	K	614	5/5	0.95	0.19	69,72,72,73	0
2	TPP	E	611	26/26	0.95	0.13	59,65,67,69	0
5	PO4	E	614	5/5	0.95	0.13	96,96,97,98	0
2	TPP	G	611	26/26	0.95	0.14	56,59,62,63	0
5	PO4	F	614	5/5	0.95	0.13	91,91,92,93	0
3	FAD	G	612	53/53	0.96	0.11	52,57,64,64	0
2	TPP	J	611	26/26	0.96	0.11	48,61,63,65	0
5	PO4	D	615	5/5	0.96	0.15	73,73,74,75	0
5	PO4	B	614	5/5	0.96	0.16	69,70,72,73	0
3	FAD	F	612	53/53	0.97	0.09	50,55,59,63	0
2	TPP	F	611	26/26	0.97	0.11	50,61,63,65	0
3	FAD	I	612	53/53	0.97	0.10	45,49,53,57	0
3	FAD	J	612	53/53	0.97	0.10	47,52,57,60	0
3	FAD	K	612	53/53	0.97	0.10	40,45,52,55	0
5	PO4	H	615	5/5	0.97	0.11	82,83,84,85	0
5	PO4	A	614	5/5	0.97	0.11	70,70,72,73	0
2	TPP	C	611	26/26	0.97	0.11	43,49,53,54	0
2	TPP	I	611	26/26	0.97	0.11	44,56,58,60	0
2	TPP	B	611	26/26	0.97	0.10	42,50,54,58	0
2	TPP	L	611	26/26	0.97	0.10	43,46,49,50	0
3	FAD	C	612	53/53	0.97	0.10	38,46,50,53	0
3	FAD	D	612	53/53	0.97	0.11	39,43,48,49	0
3	FAD	E	612	53/53	0.97	0.10	53,57,63,65	0
3	FAD	L	612	53/53	0.98	0.10	40,45,47,50	0
2	TPP	K	611	26/26	0.98	0.10	39,45,48,50	0
2	TPP	H	611	26/26	0.98	0.09	55,58,60,63	0
3	FAD	A	612	53/53	0.98	0.10	36,41,44,45	0
3	FAD	H	612	53/53	0.98	0.09	45,49,53,54	0
3	FAD	B	612	53/53	0.98	0.09	43,47,52,52	0
2	TPP	D	611	26/26	0.98	0.11	42,48,51,51	0
2	TPP	A	611	26/26	0.98	0.10	39,46,49,50	0
5	PO4	L	616	5/5	0.99	0.10	67,67,68,69	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.

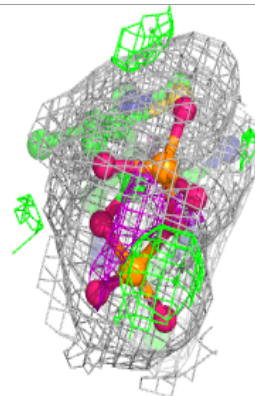
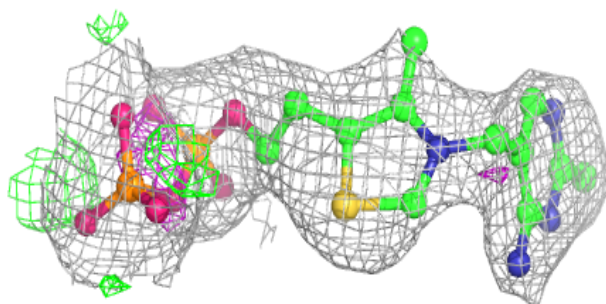
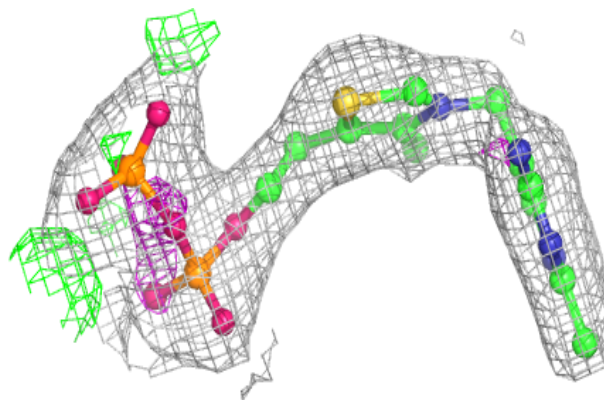
Electron density around TPP E 611:

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



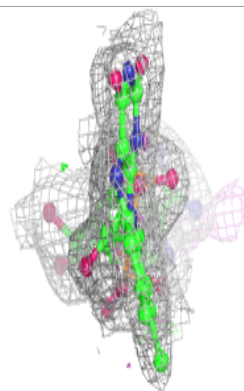
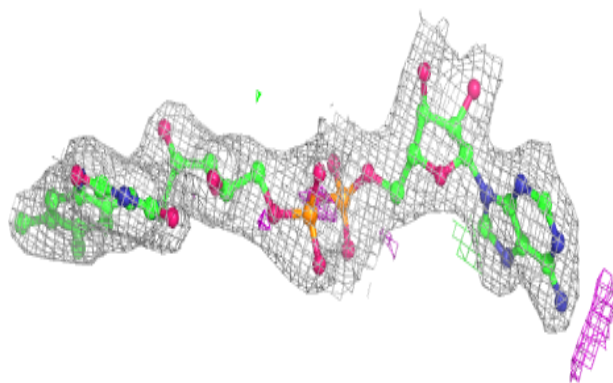
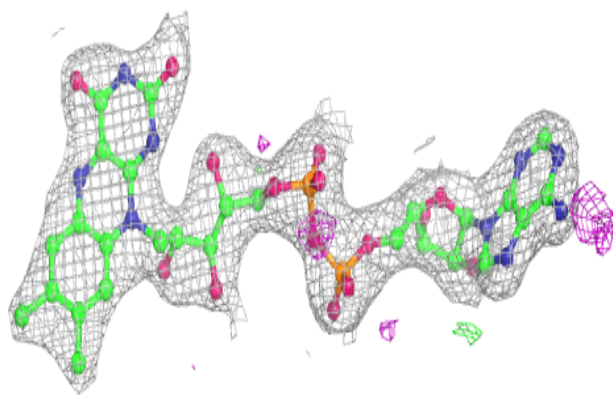
Electron density around TPP G 611:

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

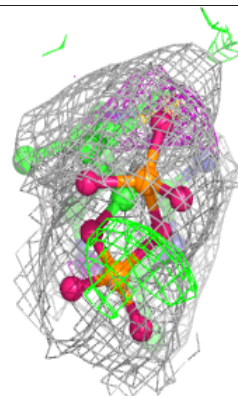
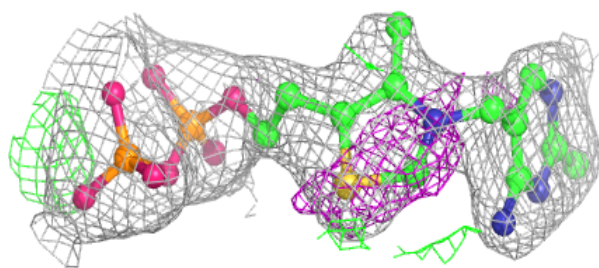
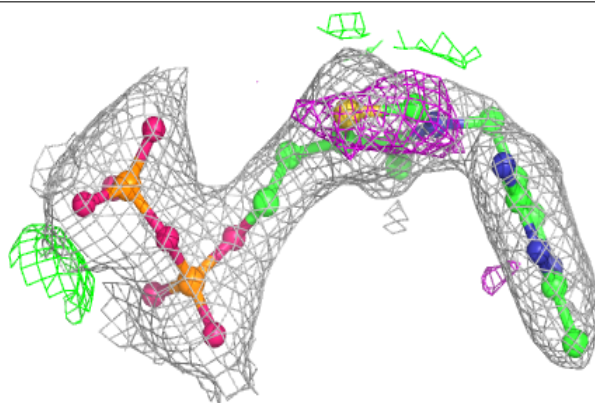


Electron density around FAD G 612:

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

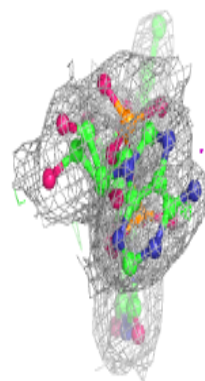
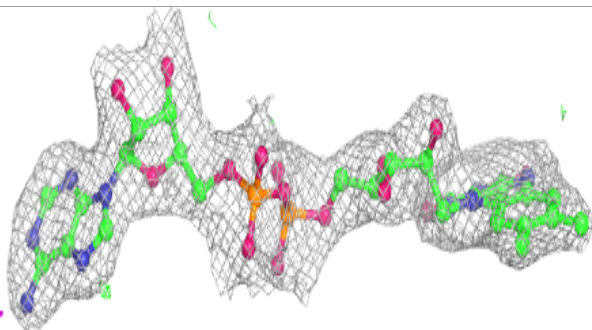
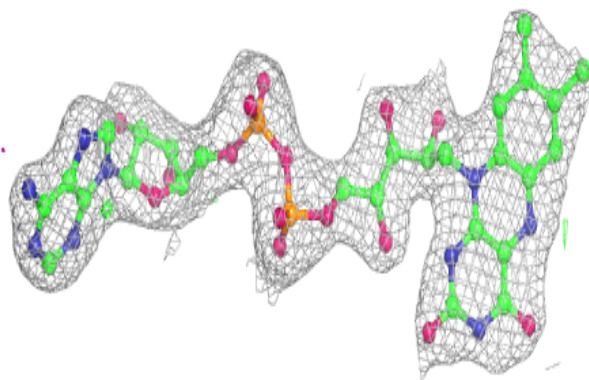
**Electron density around TPP J 611:**

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

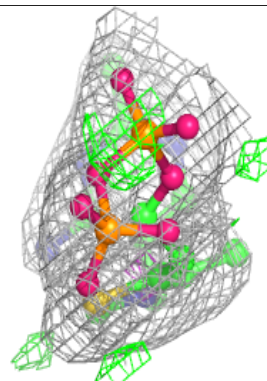
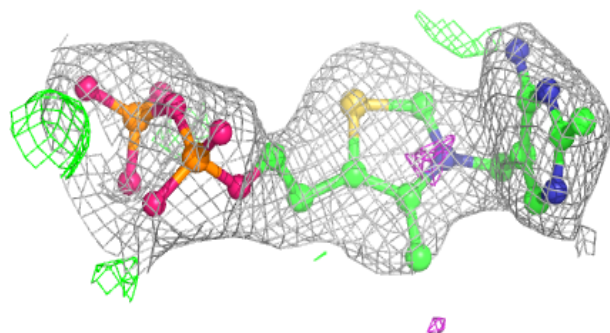
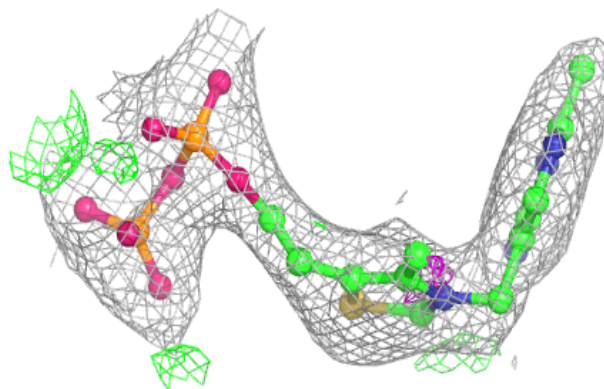


Electron density around FAD F 612:

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

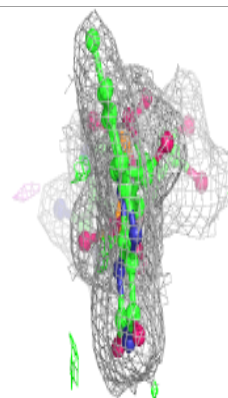
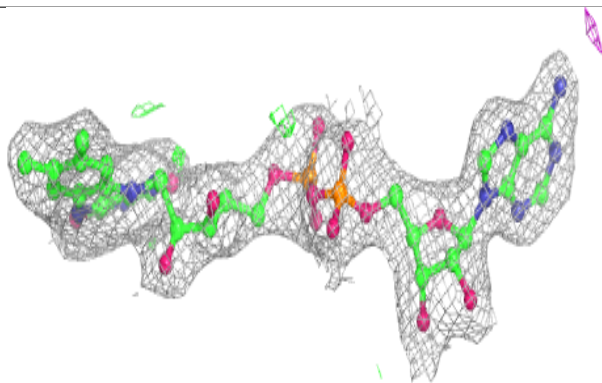
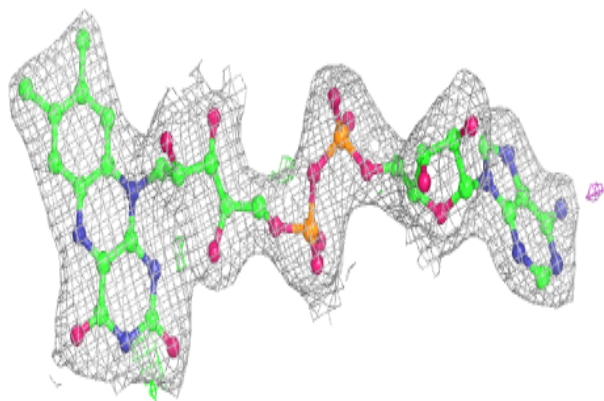
**Electron density around TPP F 611:**

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

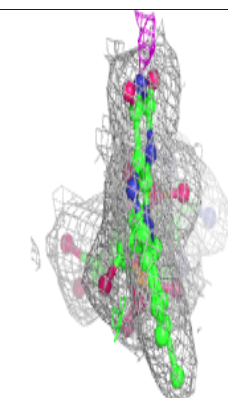
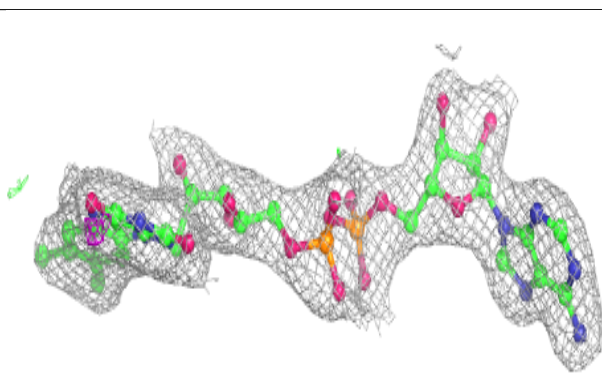
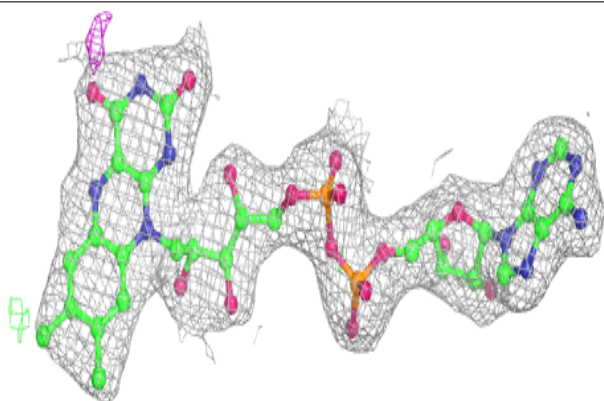


Electron density around FAD I 612:

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

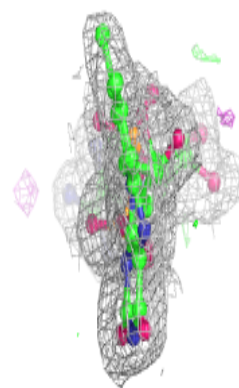
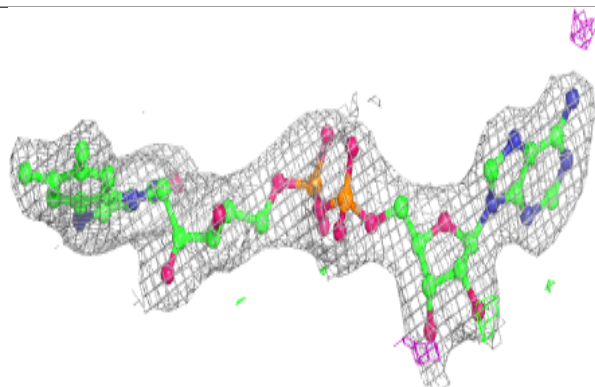
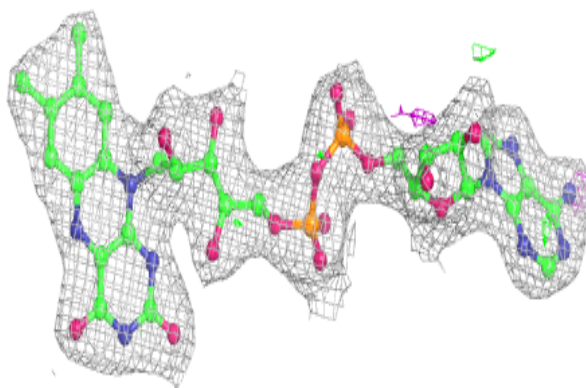
**Electron density around FAD J 612:**

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

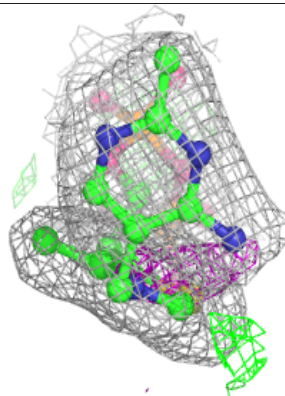
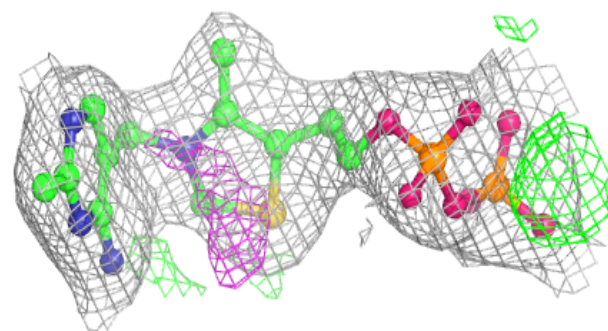
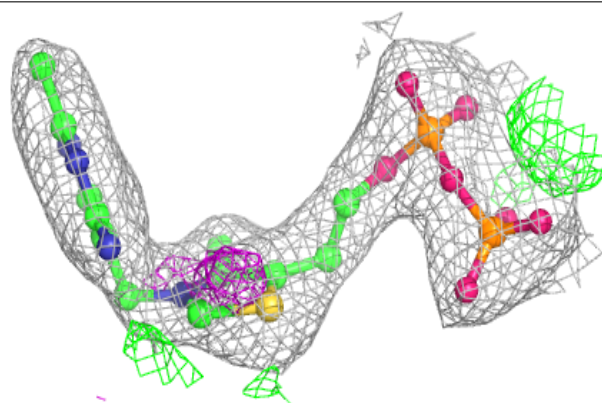


Electron density around FAD K 612:

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

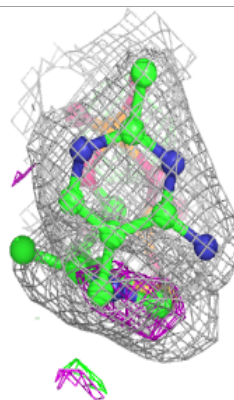
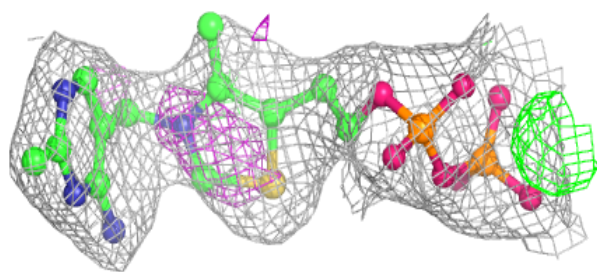
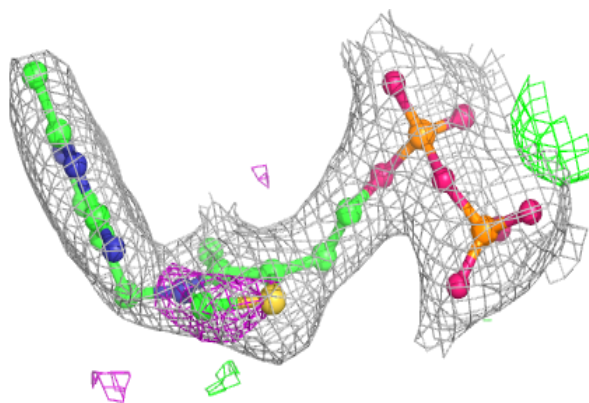
**Electron density around TPP C 611:**

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

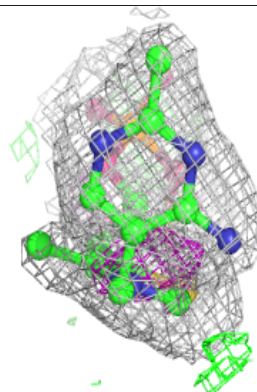
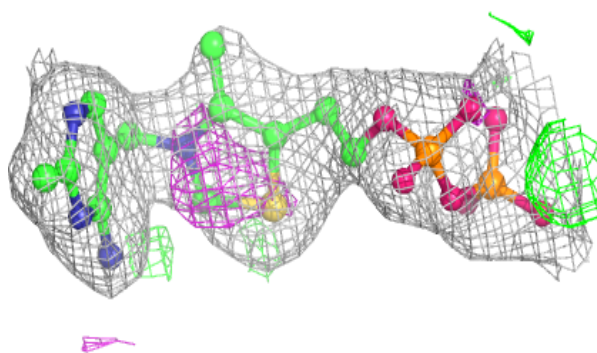
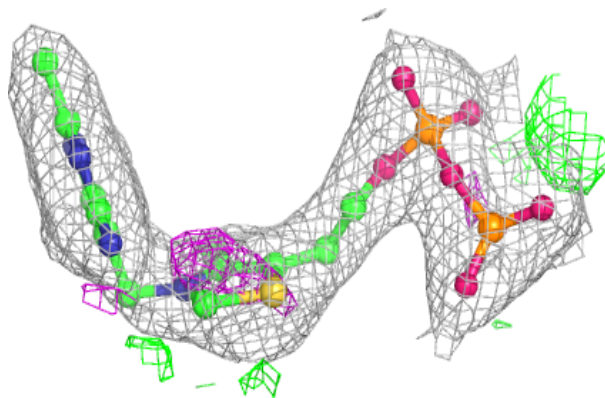


Electron density around TPP I 611:

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

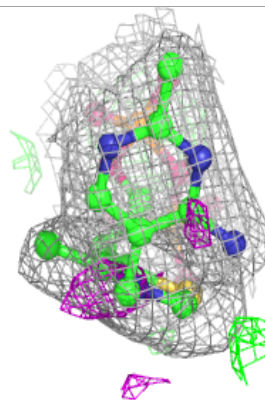
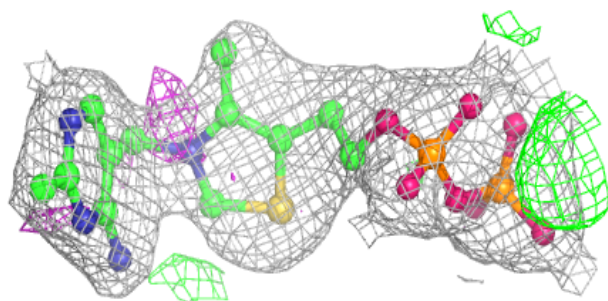
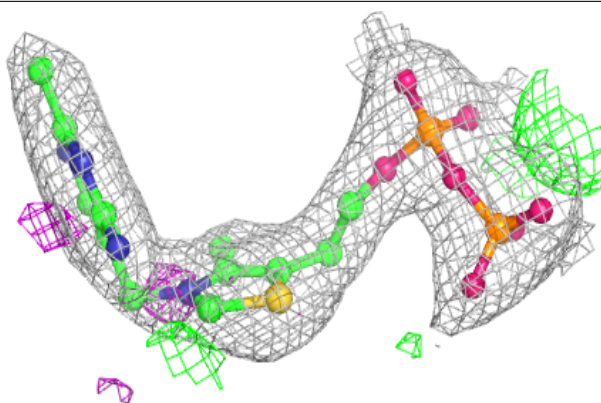
**Electron density around TPP B 611:**

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

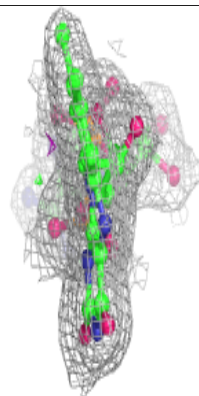
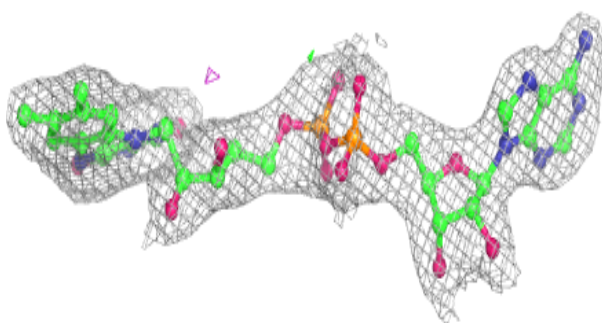
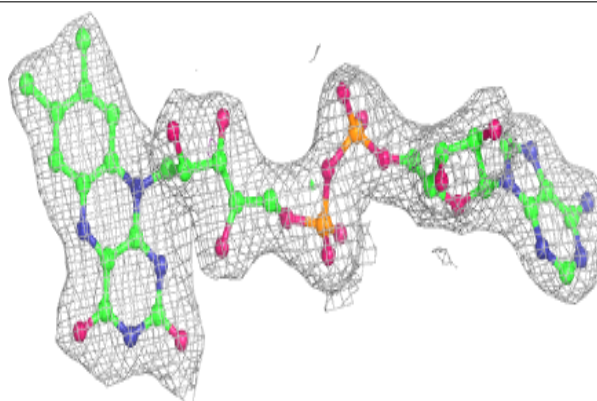


Electron density around TPP L 611:

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

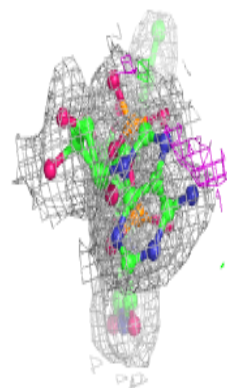
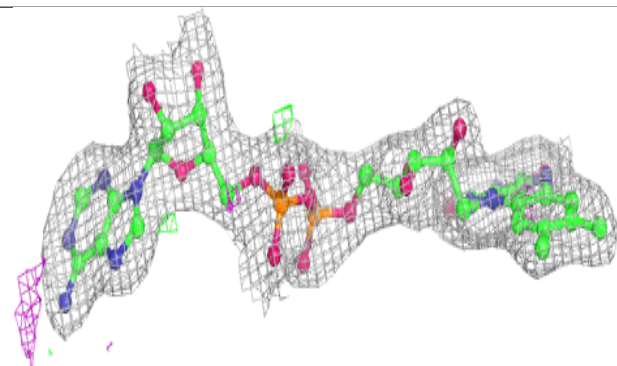
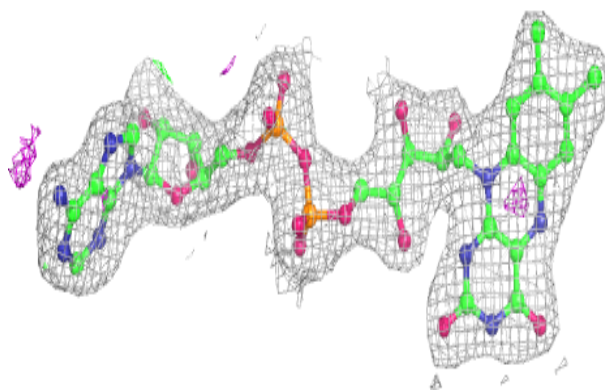
**Electron density around FAD C 612:**

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

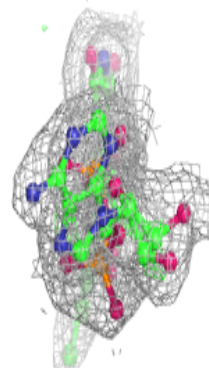
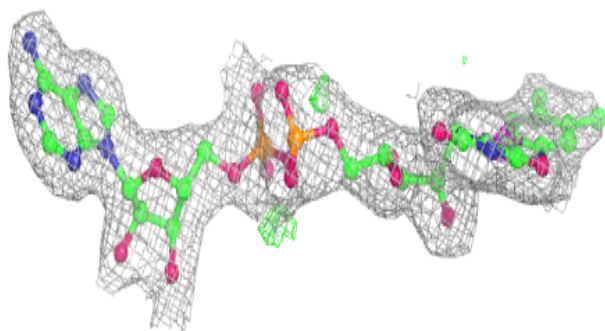
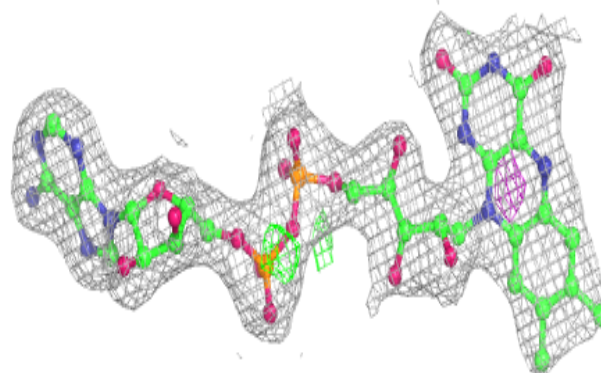


Electron density around FAD D 612:

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

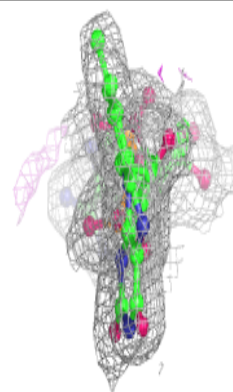
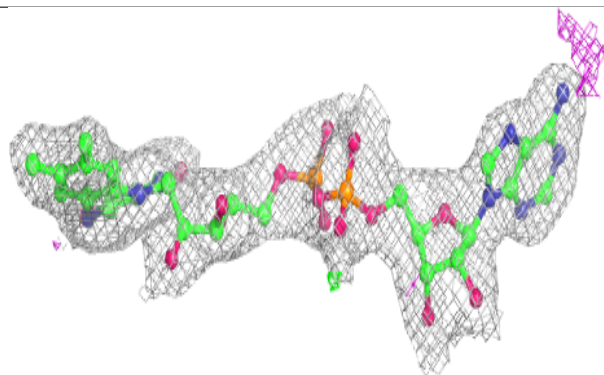
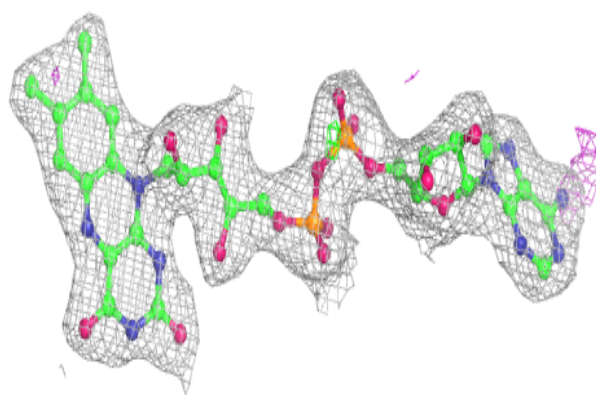
**Electron density around FAD E 612:**

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

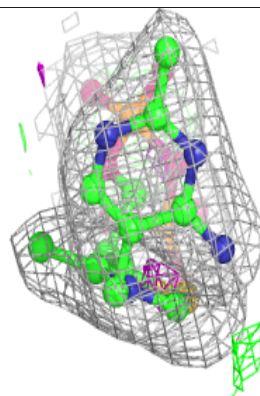
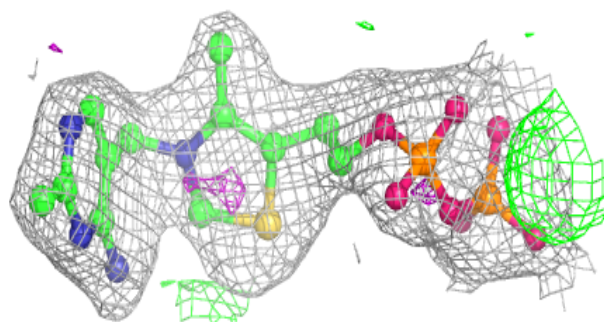
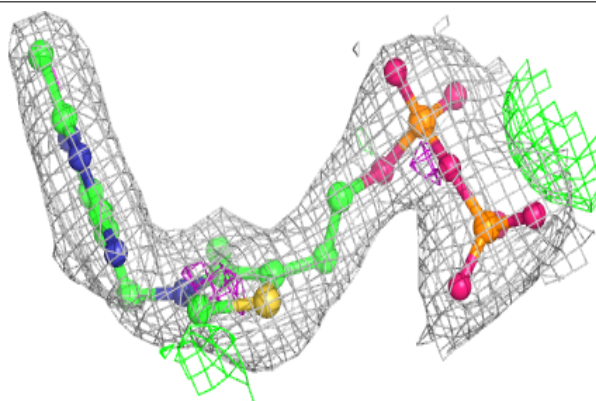


Electron density around FAD L 612:

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

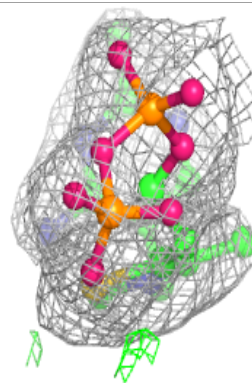
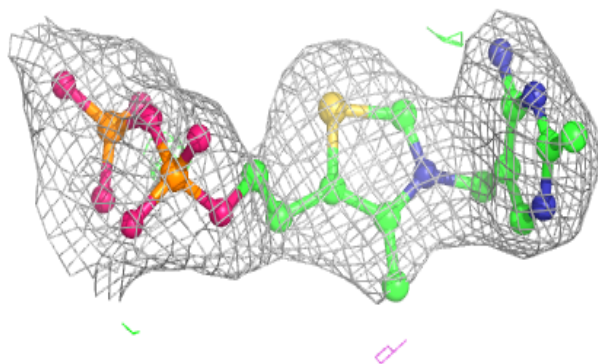
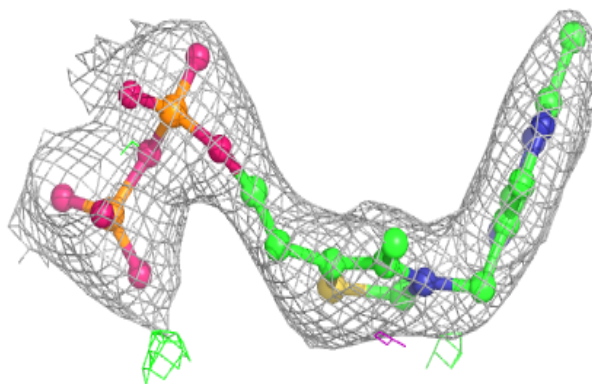
**Electron density around TPP K 611:**

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

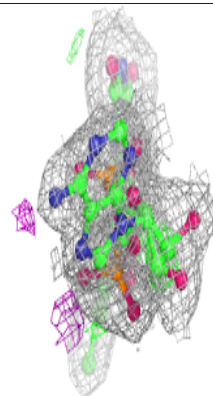
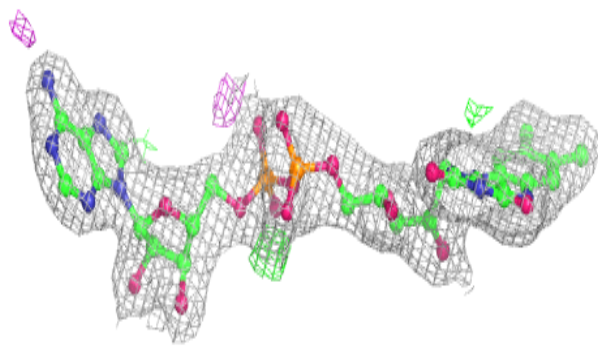
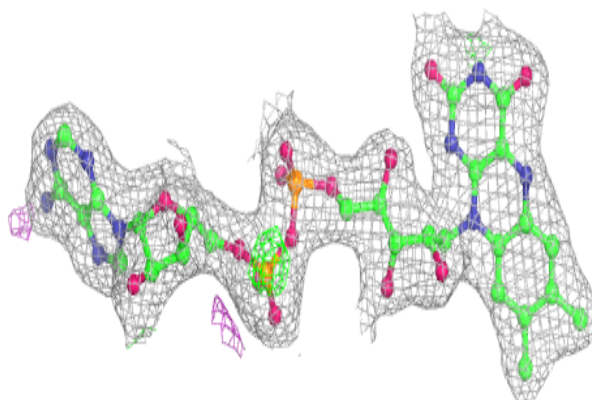


Electron density around TPP H 611:

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

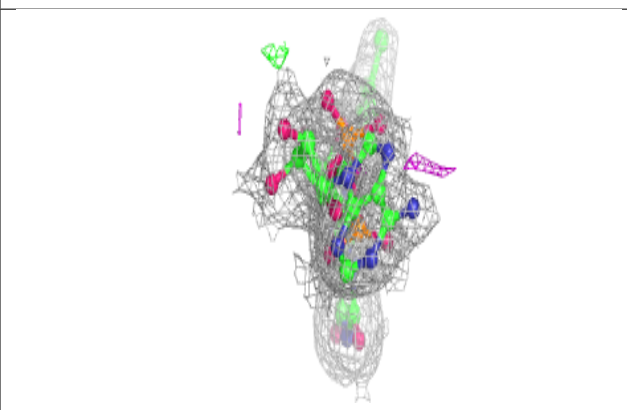
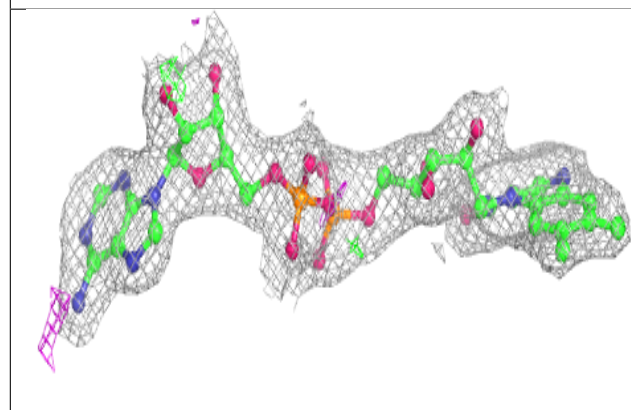
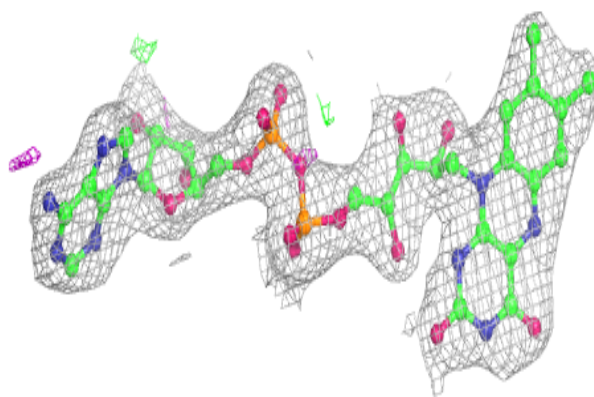
**Electron density around FAD A 612:**

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

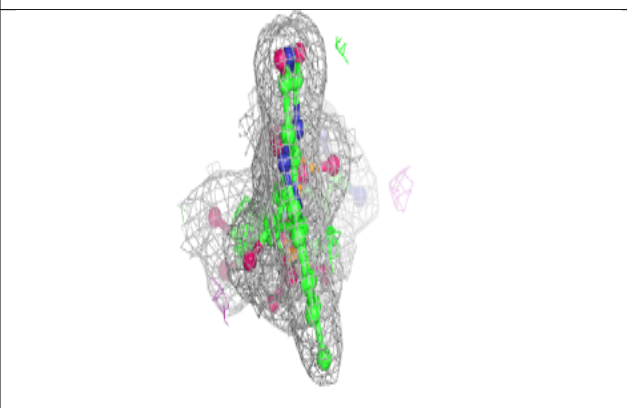
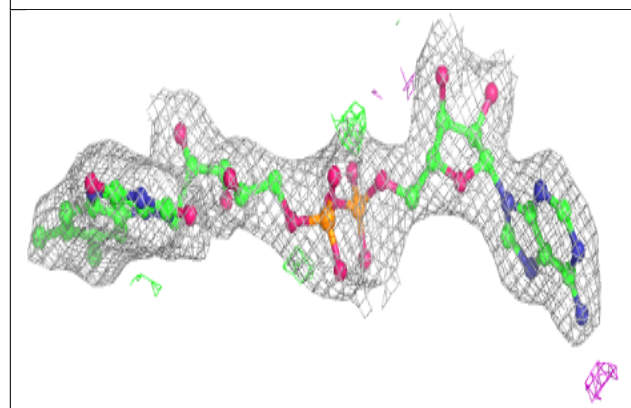
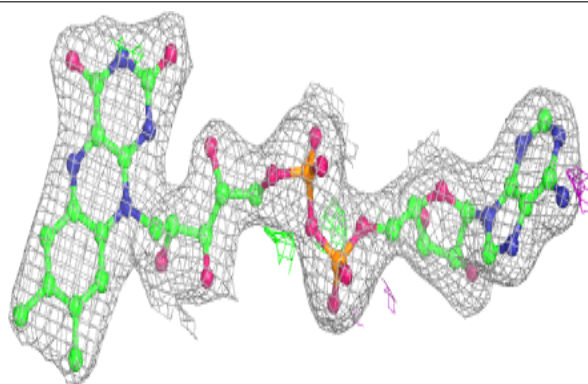


Electron density around FAD H 612:

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

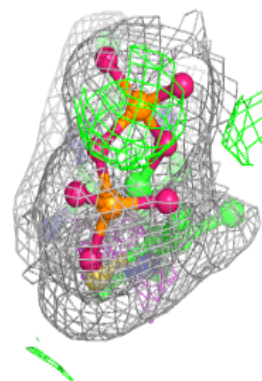
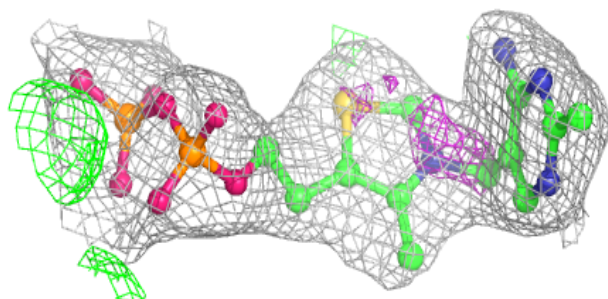
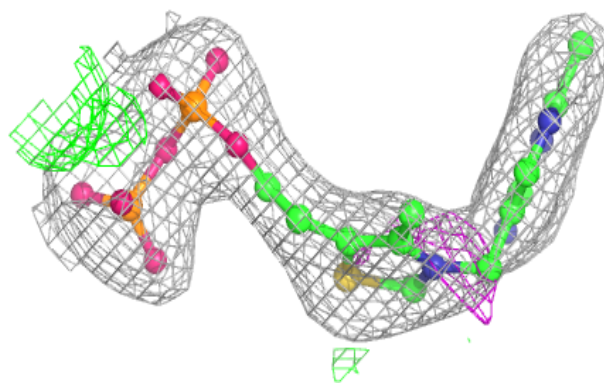
**Electron density around FAD B 612:**

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

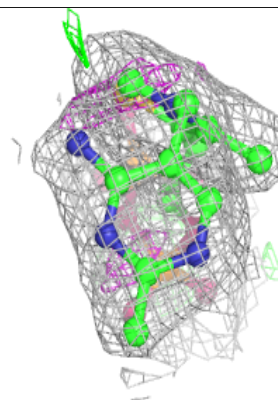
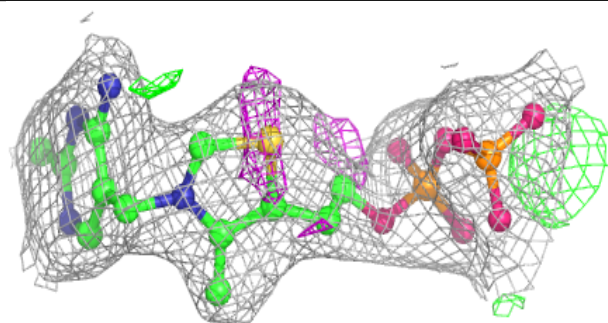
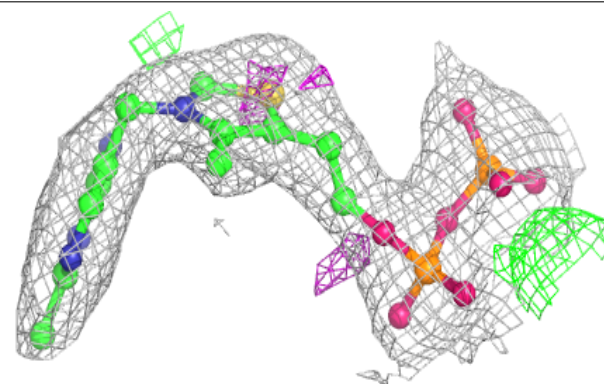


Electron density around TPP D 611:

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

**Electron density around TPP A 611:**

$2mF_o-DF_c$ (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.