



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 03:59 PM UTC

PDB ID : 3HDQ / pdb_00003hdq
Title : Crystal structure of UDP-galactopyranose mutase (oxidized form) in complex with substrate
Authors : Partha, S.K.; van Straaten, K.E.; Sanders, D.A.
Deposited on : 2009-05-07
Resolution : 2.36 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

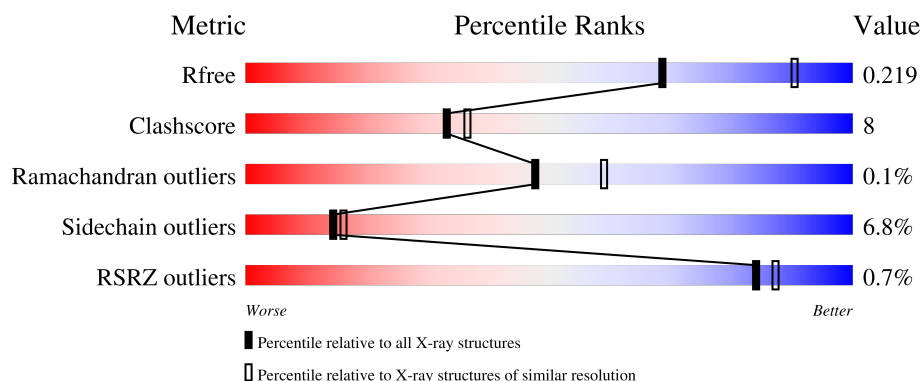
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.36 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	397	76% 13% • 8%
1	B	397	75% 15% • 8%
1	C	397	2% 71% 18% • 9%
1	D	397	72% 16% • 9%
1	E	397	76% 14% • 8%

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Mol	Chain	Length	Quality of chain			
1	F	397	76%	14%	9%	
1	G	397	76%	14%	9%	
1	H	397	76%	14%	8%	
1	I	397	74%	14%	9%	
1	J	397	70%	18%	9%	

2 Entry composition

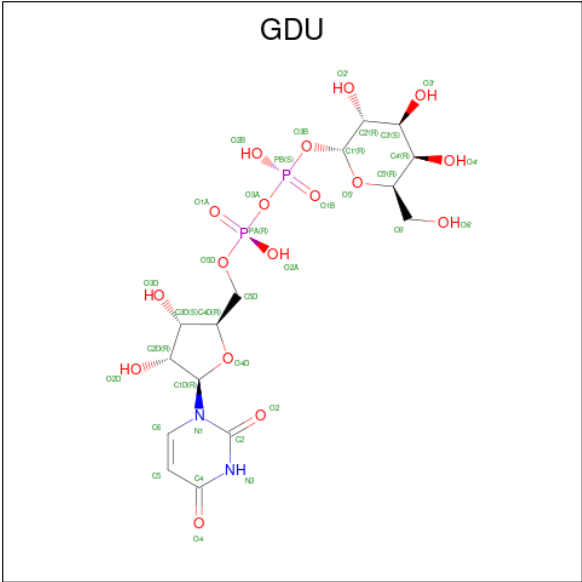
There are 4 unique types of molecules in this entry. The entry contains 31875 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 UDP-galactopyranose mutase.

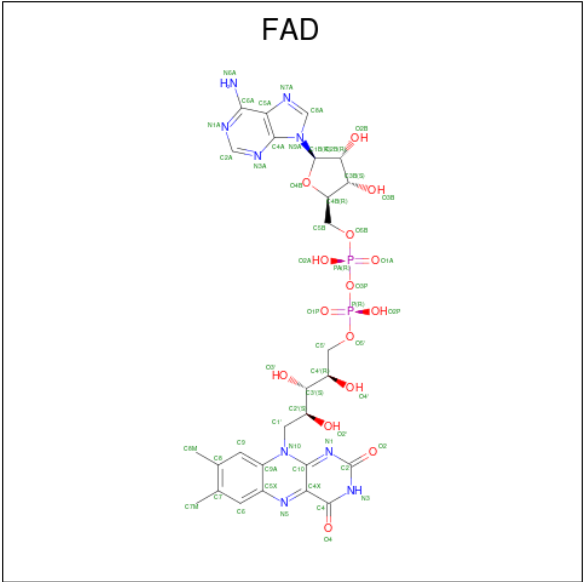
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	365	Total	C	N	O	S	0	1	0
			2992	1909	521	554	8			
1	B	364	Total	C	N	O	S	4	2	0
			2990	1909	522	551	8			
1	C	361	Total	C	N	O	S	23	1	0
			2964	1894	516	546	8			
1	D	360	Total	C	N	O	S	0	1	0
			2955	1888	514	545	8			
1	E	364	Total	C	N	O	S	8	0	0
			2975	1899	516	552	8			
1	F	363	Total	C	N	O	S	4	1	0
			2977	1901	519	549	8			
1	G	363	Total	C	N	O	S	4	1	0
			2974	1899	518	549	8			
1	H	364	Total	C	N	O	S	0	1	0
			2983	1904	520	551	8			
1	I	363	Total	C	N	O	S	4	1	0
			2975	1899	517	551	8			
1	J	361	Total	C	N	O	S	4	1	0
			2959	1890	515	546	8			

- Molecule 2 is GALACTOSE-URIDINE-5'-DIPHOSPHATE (CCD ID: GDU) (formula: $C_{15}H_{24}N_2O_{17}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	B	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	C	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	D	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	E	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	F	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	G	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	H	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	I	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	J	1	Total	C	N	O	P	0	0
			36	15	2	17	2		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: 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		
3	G	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	H	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	I	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	J	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	164	Total	O	0	0
			164	164		
4	B	104	Total	O	0	0
			104	104		

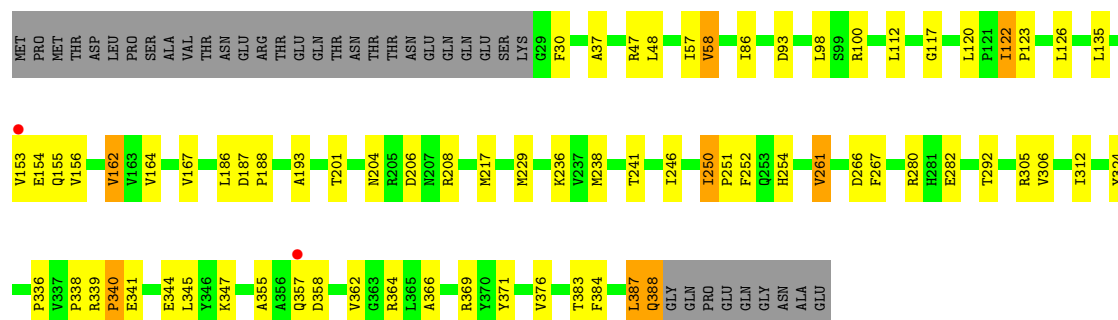
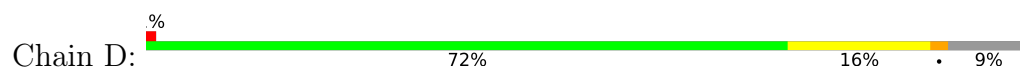
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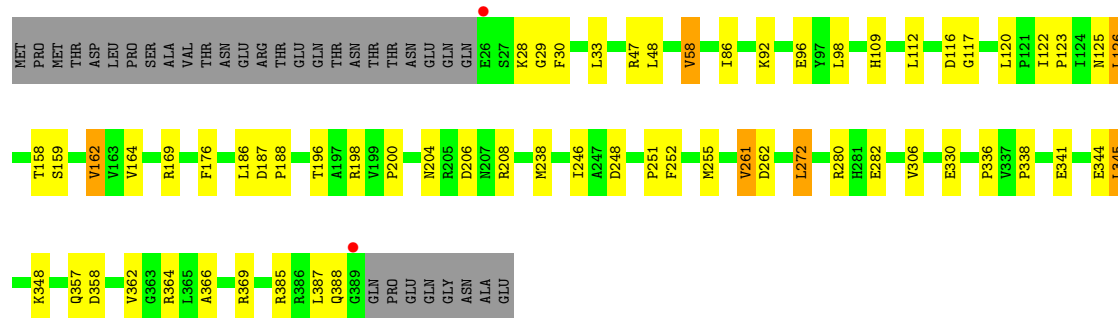
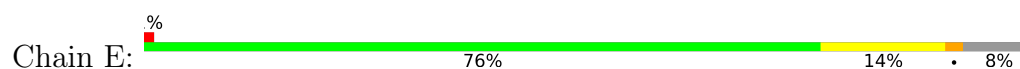
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	88	Total 88	O 88	0	0
4	D	86	Total 86	O 86	0	0
4	E	110	Total 110	O 110	0	0
4	F	143	Total 143	O 143	0	0
4	G	116	Total 116	O 116	0	0
4	H	143	Total 143	O 143	0	0
4	I	160	Total 160	O 160	0	0
4	J	127	Total 127	O 127	0	0



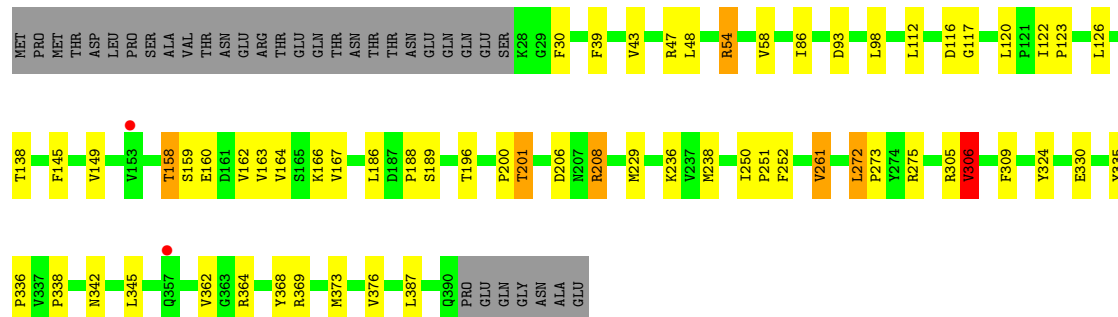
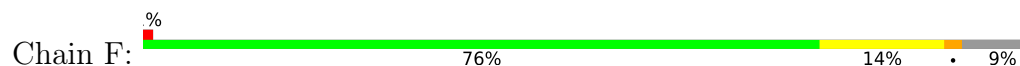
• Molecule 1: UDP-galactopyranose mutase



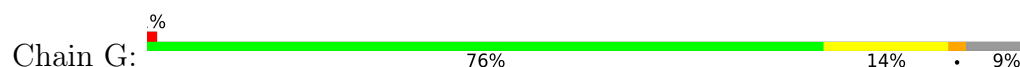
• Molecule 1: UDP-galactopyranose mutase

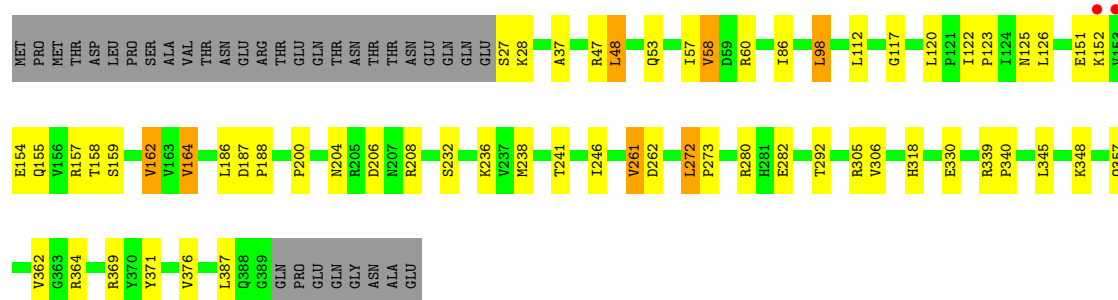


• Molecule 1: UDP-galactopyranose mutase

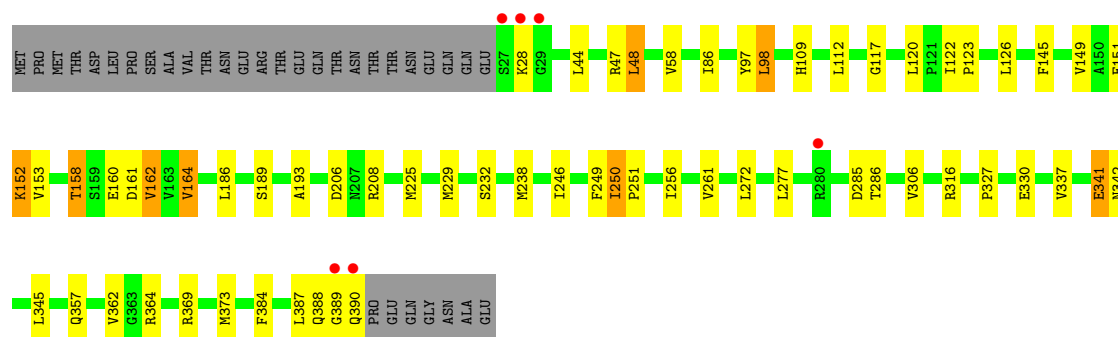
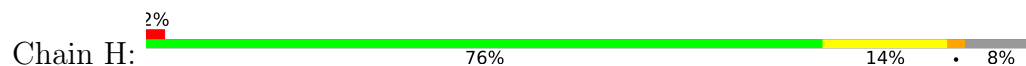


• Molecule 1: UDP-galactopyranose mutase

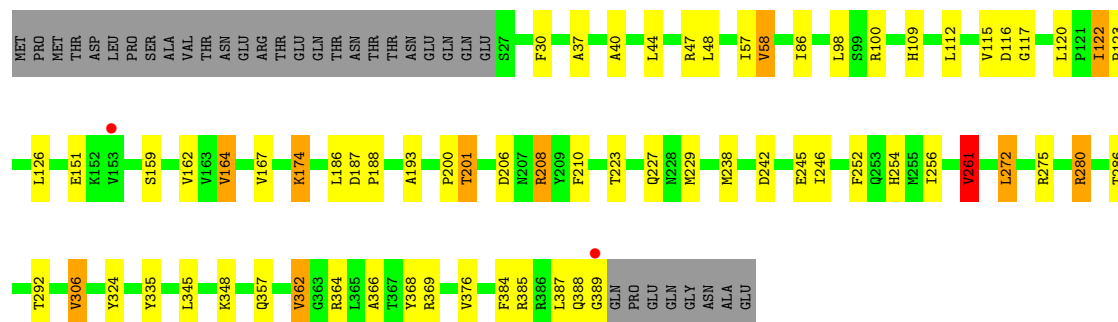
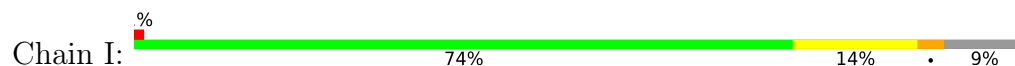




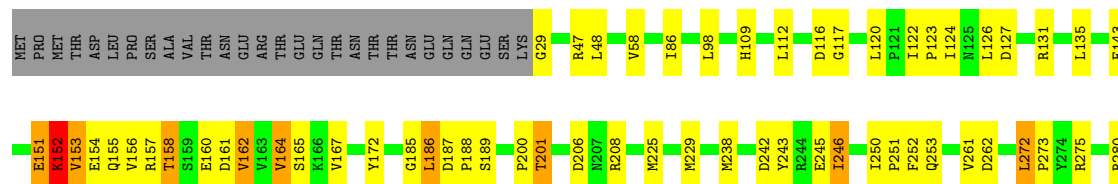
• Molecule 1: UDP-galactopyranose mutase



• Molecule 1: UDP-galactopyranose mutase



• Molecule 1: UDP-galactopyranose mutase



E281	E282	R305	V306	Y326	E330	Y335	P336	P337	P338	R339	P340	E341	N342	L345	Y346	K347	E350	Q357	V362	A366	T367	Y368	V376	F384	L387	Q388	G389	GLN	PRO	GLU	GLN	GLY	ASN	ALA	GLU
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	134.02Å 176.65Å 220.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.88 – 2.36 19.88 – 2.36	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.88-2.36) 99.7 (19.88-2.36)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.30Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.177 , 0.226 0.174 , 0.219	Depositor DCC
R_{free} test set	11275 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	35.7	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	31875	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.70% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GDU, 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	0.53	0/3079	0.82	5/4185 (0.1%)
1	B	0.49	0/3081	0.81	3/4188 (0.1%)
1	C	0.43	0/3051	0.81	0/4148
1	D	0.50	0/3042	0.81	3/4137 (0.1%)
1	E	0.42	0/3059	0.79	0/4159
1	F	0.47	0/3064	0.79	3/4165 (0.1%)
1	G	0.50	0/3061	0.78	2/4161 (0.0%)
1	H	0.48	0/3070	0.81	4/4173 (0.1%)
1	I	0.50	0/3059	0.82	2/4159 (0.0%)
1	J	0.49	1/3046 (0.0%)	0.82	6/4142 (0.1%)
All	All	0.48	1/30612 (0.0%)	0.81	28/41617 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	153	VAL	N-CA	-5.78	1.39	1.46

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	151	GLU	CA-C-N	-6.70	111.13	122.92
1	J	151	GLU	C-N-CA	-6.70	111.13	122.92
1	I	306	VAL	CB-CA-C	-6.45	101.01	110.62
1	J	153	VAL	N-CA-C	-6.28	99.00	108.17
1	F	306	VAL	CB-CA-C	-6.27	101.27	110.62

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2992	0	2867	51	0
1	B	2990	0	2868	45	0
1	C	2964	0	2845	59	0
1	D	2955	0	2832	48	0
1	E	2975	0	2846	40	0
1	F	2977	0	2856	43	0
1	G	2974	0	2853	37	0
1	H	2983	0	2861	50	0
1	I	2975	0	2847	53	0
1	J	2959	0	2835	72	0
2	A	36	0	22	0	0
2	B	36	0	22	3	0
2	C	36	0	22	1	0
2	D	36	0	22	2	0
2	E	36	0	22	1	0
2	F	36	0	22	2	0
2	G	36	0	22	3	0
2	H	36	0	22	1	0
2	I	36	0	22	3	0
2	J	36	0	22	2	0
3	A	53	0	30	1	0
3	B	53	0	31	2	0
3	C	53	0	30	1	0
3	D	53	0	31	0	0
3	E	53	0	31	0	0
3	F	53	0	29	2	0
3	G	53	0	31	4	0
3	H	53	0	31	1	0
3	I	53	0	31	1	0
3	J	53	0	30	1	0
4	A	164	0	0	2	0
4	B	104	0	0	3	0
4	C	88	0	0	2	0
4	D	86	0	0	1	0
4	E	110	0	0	3	0
4	F	143	0	0	0	0
4	G	116	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	143	0	0	0	0
4	I	160	0	0	2	0
4	J	127	0	0	0	0
All	All	31875	0	29035	464	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 8.

The worst 5 of 464 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:A:152:LYS:CD	1:A:153:VAL:H	1.54	1.18
1:J:357:GLN:HE21	1:J:357:GLN:HA	1.15	1.10
1:A:152:LYS:HD3	1:A:153:VAL:N	1.72	1.04
1:E:58:VAL:HG22	1:E:238:MET:HB3	1.42	1.01
1:H:152:LYS:HE2	1:H:152:LYS:HA	1.38	1.01

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	364/397 (92%)	355 (98%)	9 (2%)	0	100	100
1	B	364/397 (92%)	352 (97%)	12 (3%)	0	100	100
1	C	360/397 (91%)	347 (96%)	13 (4%)	0	100	100
1	D	359/397 (90%)	345 (96%)	13 (4%)	1 (0%)	36	43
1	E	362/397 (91%)	353 (98%)	9 (2%)	0	100	100
1	F	362/397 (91%)	356 (98%)	6 (2%)	0	100	100
1	G	362/397 (91%)	355 (98%)	6 (2%)	1 (0%)	36	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	363/397 (91%)	353 (97%)	10 (3%)	0	100	100
1	I	362/397 (91%)	353 (98%)	9 (2%)	0	100	100
1	J	360/397 (91%)	353 (98%)	7 (2%)	0	100	100
All	All	3618/3970 (91%)	3522 (97%)	94 (3%)	2 (0%)	48	59

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	340	PRO
1	G	154	GLU

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	318/346 (92%)	293 (92%)	25 (8%)	11	12
1	B	318/346 (92%)	298 (94%)	20 (6%)	16	19
1	C	315/346 (91%)	292 (93%)	23 (7%)	13	14
1	D	314/346 (91%)	293 (93%)	21 (7%)	15	17
1	E	316/346 (91%)	296 (94%)	20 (6%)	16	19
1	F	316/346 (91%)	295 (93%)	21 (7%)	15	17
1	G	316/346 (91%)	294 (93%)	22 (7%)	14	15
1	H	317/346 (92%)	296 (93%)	21 (7%)	15	17
1	I	316/346 (91%)	294 (93%)	22 (7%)	14	15
1	J	314/346 (91%)	294 (94%)	20 (6%)	16	18
All	All	3160/3460 (91%)	2945 (93%)	215 (7%)	14	16

5 of 215 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	120	LEU

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Mol	Chain	Res	Type
1	G	272	LEU
1	J	126	LEU
1	F	164	VAL
1	G	27	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	215	GLN
1	I	319	GLN
1	J	311	HIS
1	E	53	GLN
1	D	388	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

20 ligands 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
3	FAD	F	450	-	58,58,58	1.79	18 (31%)	85,89,89	1.61	15 (17%)
3	FAD	G	450	-	58,58,58	1.66	15 (25%)	85,89,89	1.63	14 (16%)
3	FAD	I	450	-	58,58,58	1.77	17 (29%)	85,89,89	1.60	18 (21%)
2	GDU	F	500	-	37,38,38	2.69	4 (10%)	55,58,58	3.73	22 (40%)
2	GDU	B	500	-	37,38,38	2.68	4 (10%)	55,58,58	3.61	19 (34%)
2	GDU	D	500	-	37,38,38	2.75	5 (13%)	55,58,58	3.63	20 (36%)
3	FAD	H	450	-	58,58,58	1.80	17 (29%)	85,89,89	1.57	16 (18%)
3	FAD	A	450	-	58,58,58	1.84	19 (32%)	85,89,89	1.78	20 (23%)
2	GDU	C	500	-	37,38,38	2.72	4 (10%)	55,58,58	3.60	20 (36%)
2	GDU	I	500	-	37,38,38	2.66	4 (10%)	55,58,58	3.75	20 (36%)
2	GDU	J	500	-	37,38,38	2.65	4 (10%)	55,58,58	3.70	20 (36%)
2	GDU	E	500	-	37,38,38	2.70	4 (10%)	55,58,58	3.51	19 (34%)
3	FAD	E	450	-	58,58,58	1.76	18 (31%)	85,89,89	1.71	18 (21%)
3	FAD	D	450	-	58,58,58	1.76	20 (34%)	85,89,89	1.80	19 (22%)
2	GDU	G	500	-	37,38,38	2.65	4 (10%)	55,58,58	3.61	20 (36%)
3	FAD	B	450	-	58,58,58	1.72	18 (31%)	85,89,89	1.61	16 (18%)
2	GDU	H	500	-	37,38,38	2.75	5 (13%)	55,58,58	3.49	16 (29%)
2	GDU	A	500	-	37,38,38	2.66	5 (13%)	55,58,58	3.55	16 (29%)
3	FAD	J	450	-	58,58,58	1.76	16 (27%)	85,89,89	1.65	14 (16%)
3	FAD	C	450	-	58,58,58	1.83	19 (32%)	85,89,89	1.86	20 (23%)

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	F	450	-	-	1/34/50/50	0/6/6/6
3	FAD	G	450	-	-	1/34/50/50	0/6/6/6
3	FAD	I	450	-	-	4/34/50/50	0/6/6/6
2	GDU	F	500	-	-	5/23/59/59	0/3/3/3
2	GDU	B	500	-	-	2/23/59/59	0/3/3/3
2	GDU	D	500	-	-	6/23/59/59	0/3/3/3
3	FAD	H	450	-	-	5/34/50/50	0/6/6/6
3	FAD	A	450	-	-	5/34/50/50	0/6/6/6
2	GDU	C	500	-	-	5/23/59/59	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GDU	I	500	-	-	5/23/59/59	0/3/3/3
2	GDU	J	500	-	-	5/23/59/59	0/3/3/3
2	GDU	E	500	-	-	5/23/59/59	0/3/3/3
3	FAD	E	450	-	-	6/34/50/50	0/6/6/6
3	FAD	D	450	-	-	2/34/50/50	0/6/6/6
2	GDU	G	500	-	-	5/23/59/59	0/3/3/3
3	FAD	B	450	-	-	1/34/50/50	0/6/6/6
2	GDU	H	500	-	-	5/23/59/59	0/3/3/3
2	GDU	A	500	-	-	4/23/59/59	0/3/3/3
3	FAD	J	450	-	-	2/34/50/50	0/6/6/6
3	FAD	C	450	-	-	0/34/50/50	0/6/6/6

The worst 5 of 220 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	500	GDU	O2-C2	11.62	1.43	1.23
2	G	500	GDU	O2-C2	11.60	1.43	1.23
2	E	500	GDU	O2-C2	11.58	1.43	1.23
2	C	500	GDU	O2-C2	11.48	1.43	1.23
2	F	500	GDU	O2-C2	11.35	1.43	1.23

The worst 5 of 362 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	500	GDU	N3-C2-N1	16.97	136.98	114.89
2	A	500	GDU	N3-C2-N1	16.94	136.93	114.89
2	J	500	GDU	N3-C2-N1	16.92	136.91	114.89
2	F	500	GDU	N3-C2-N1	16.73	136.66	114.89
2	B	500	GDU	N3-C2-N1	16.71	136.64	114.89

There are no chirality outliers.

5 of 74 torsion outliers are listed below:

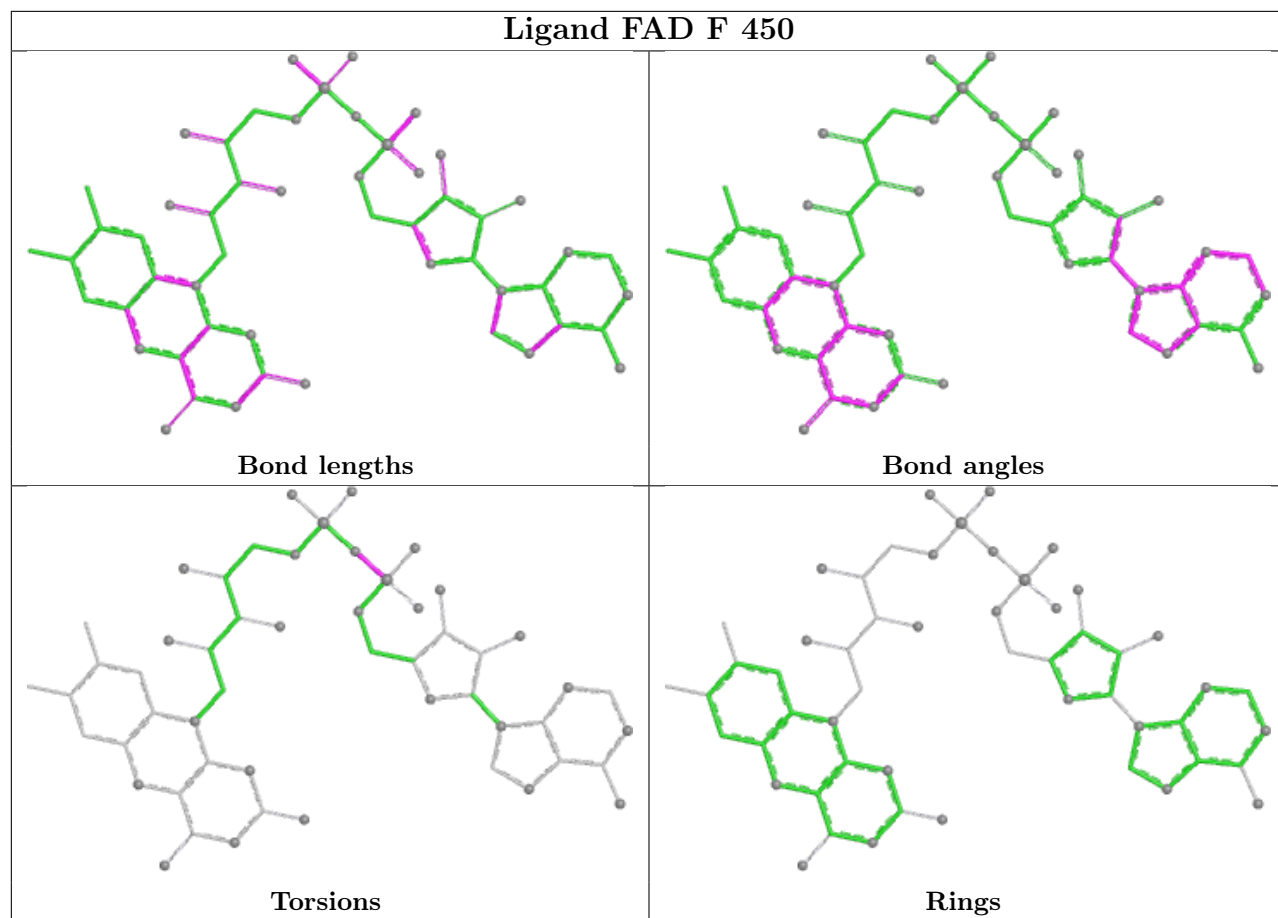
Mol	Chain	Res	Type	Atoms
2	A	500	GDU	O5'-C1'-O3B-PB
2	B	500	GDU	O5'-C1'-O3B-PB
2	C	500	GDU	C1'-O3B-PB-O3A
2	C	500	GDU	C1'-O3B-PB-O2B
2	C	500	GDU	C2'-C1'-O3B-PB

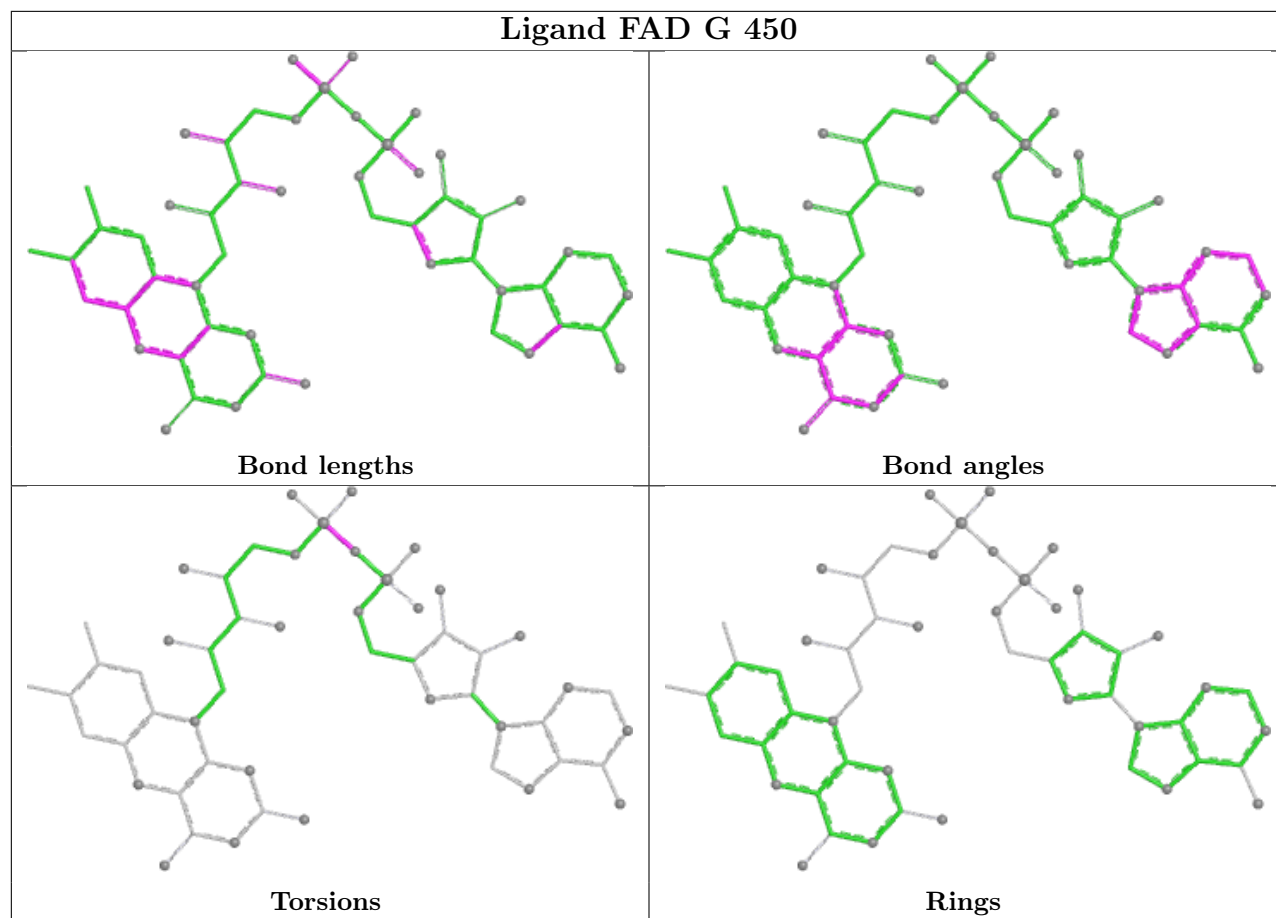
There are no ring outliers.

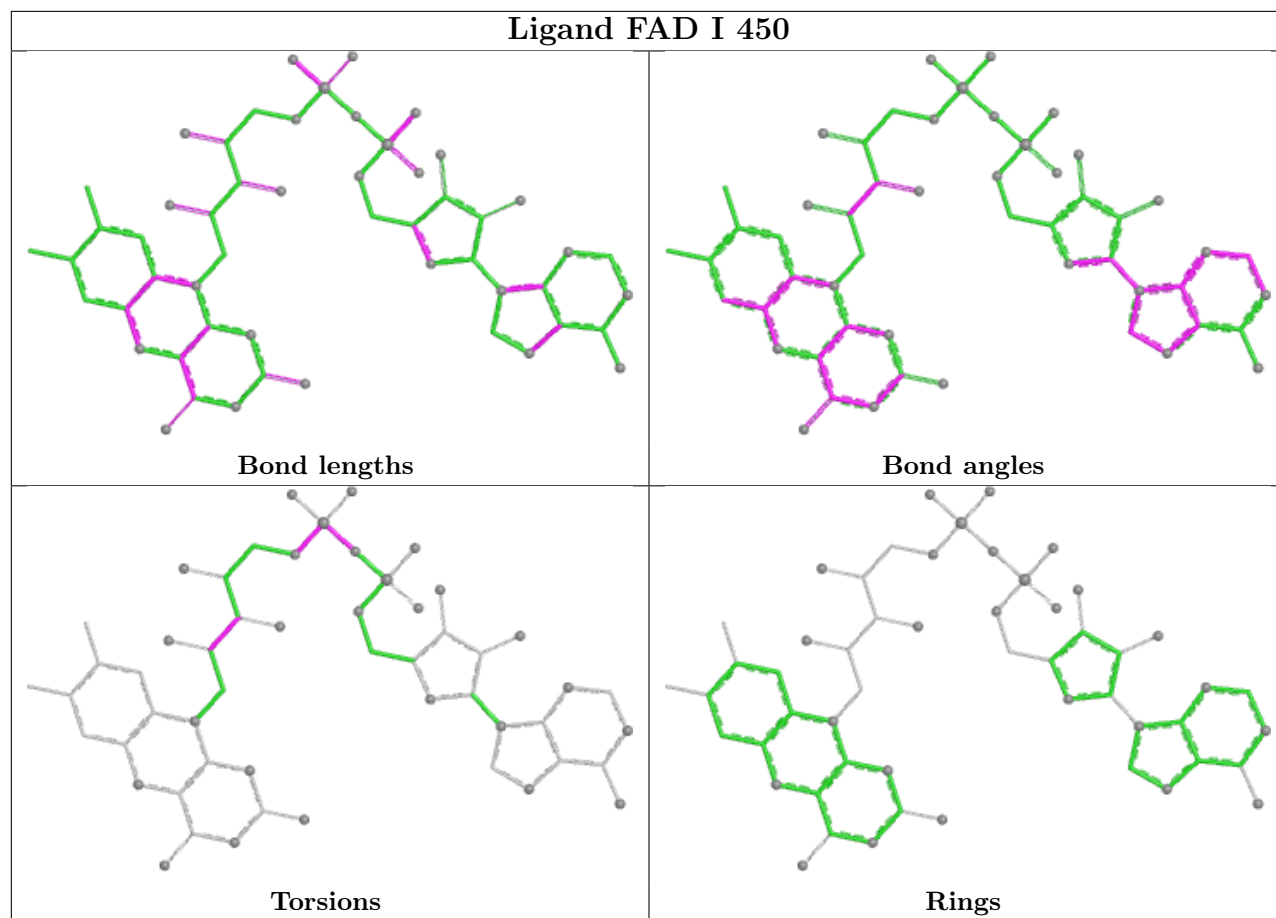
17 monomers are involved in 29 short contacts:

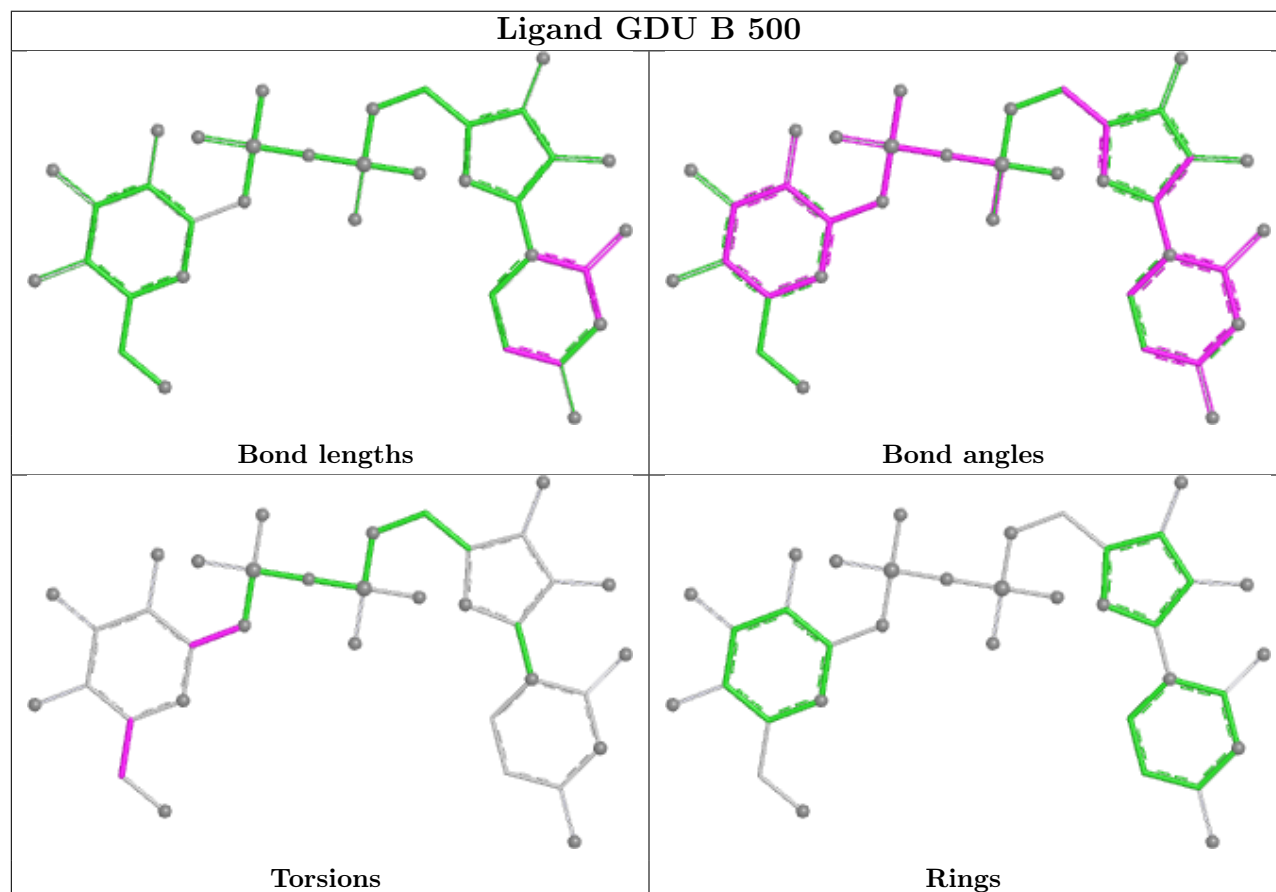
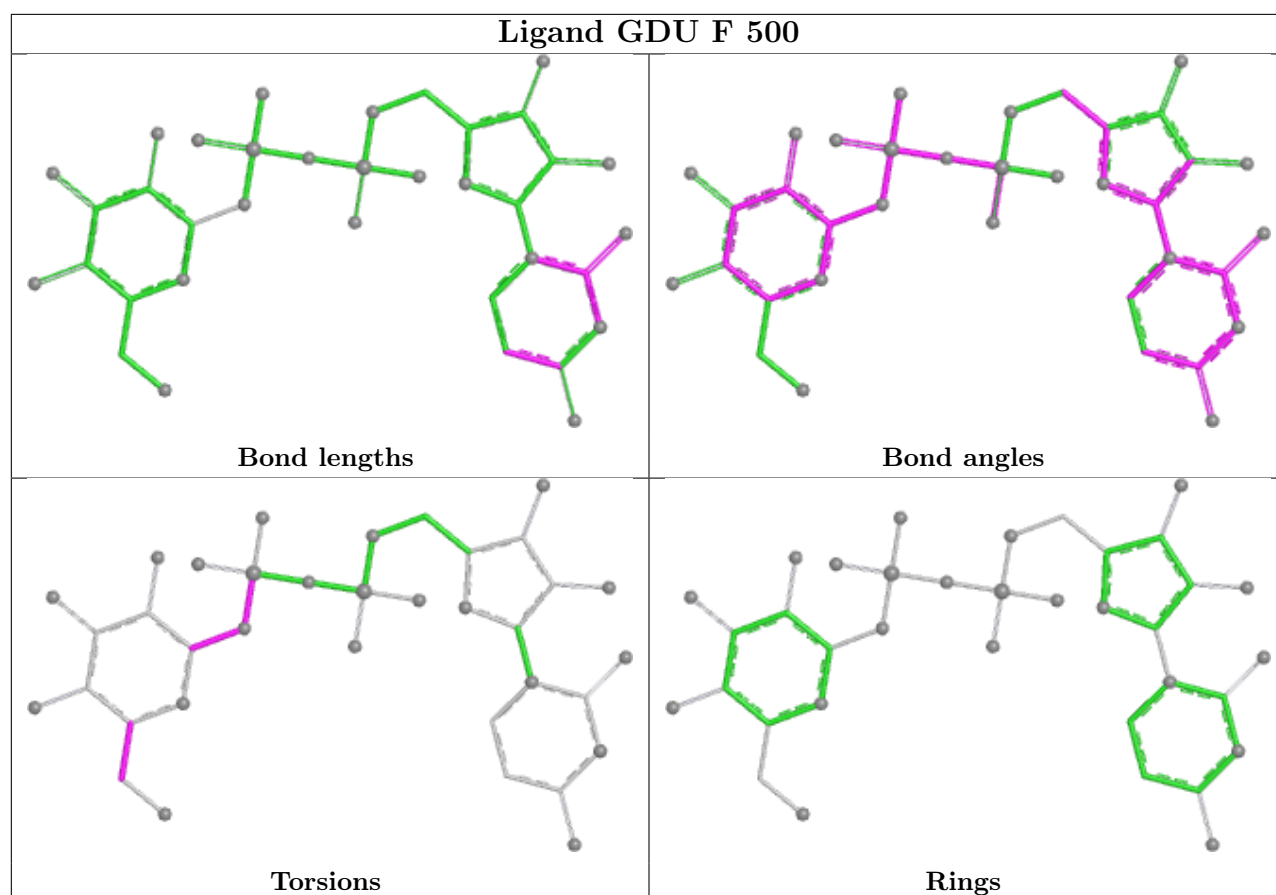
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	450	FAD	2	0
3	G	450	FAD	4	0
3	I	450	FAD	1	0
2	F	500	GDU	2	0
2	B	500	GDU	3	0
2	D	500	GDU	2	0
3	H	450	FAD	1	0
3	A	450	FAD	1	0
2	C	500	GDU	1	0
2	I	500	GDU	3	0
2	J	500	GDU	2	0
2	E	500	GDU	1	0
2	G	500	GDU	3	0
3	B	450	FAD	2	0
2	H	500	GDU	1	0
3	J	450	FAD	1	0
3	C	450	FAD	1	0

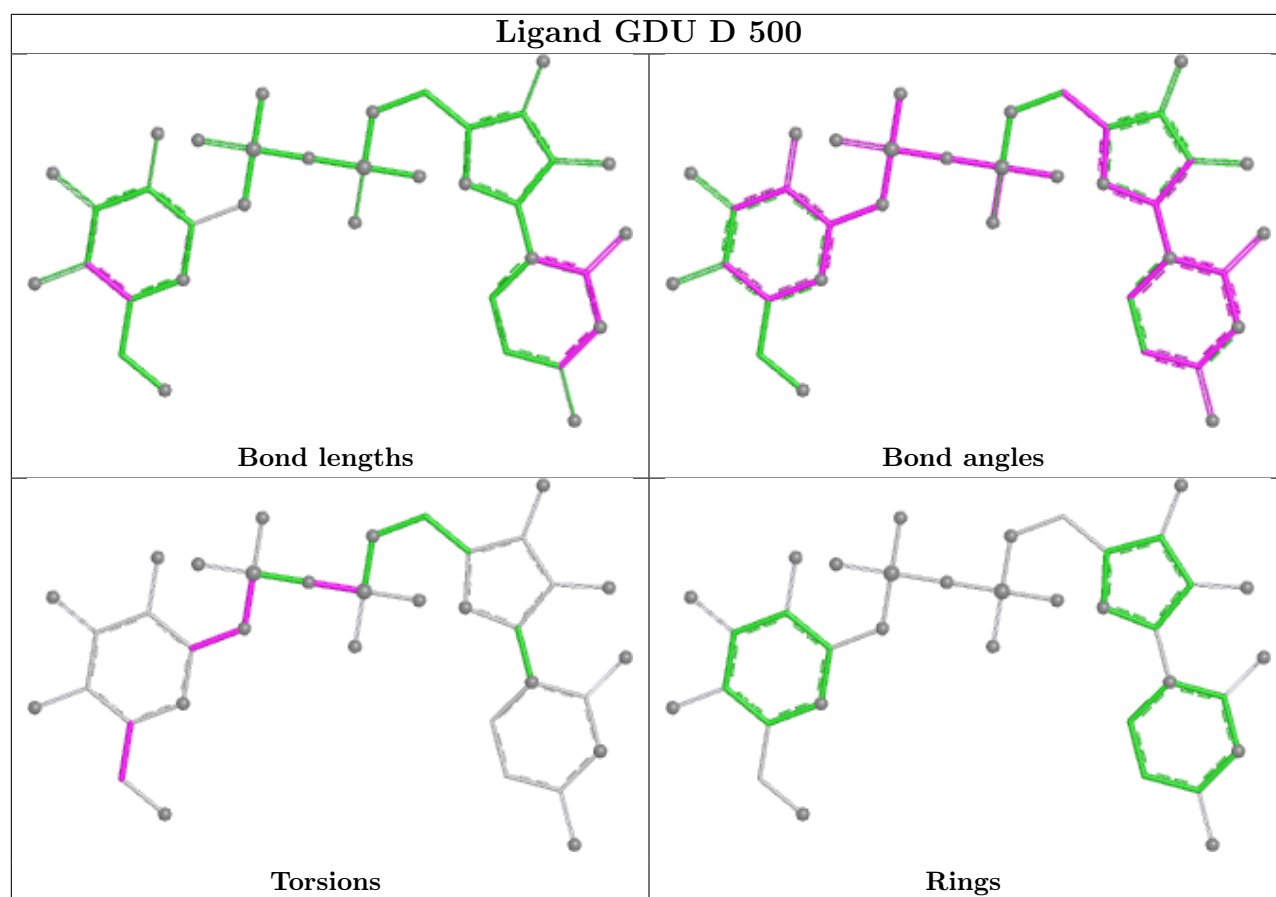
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

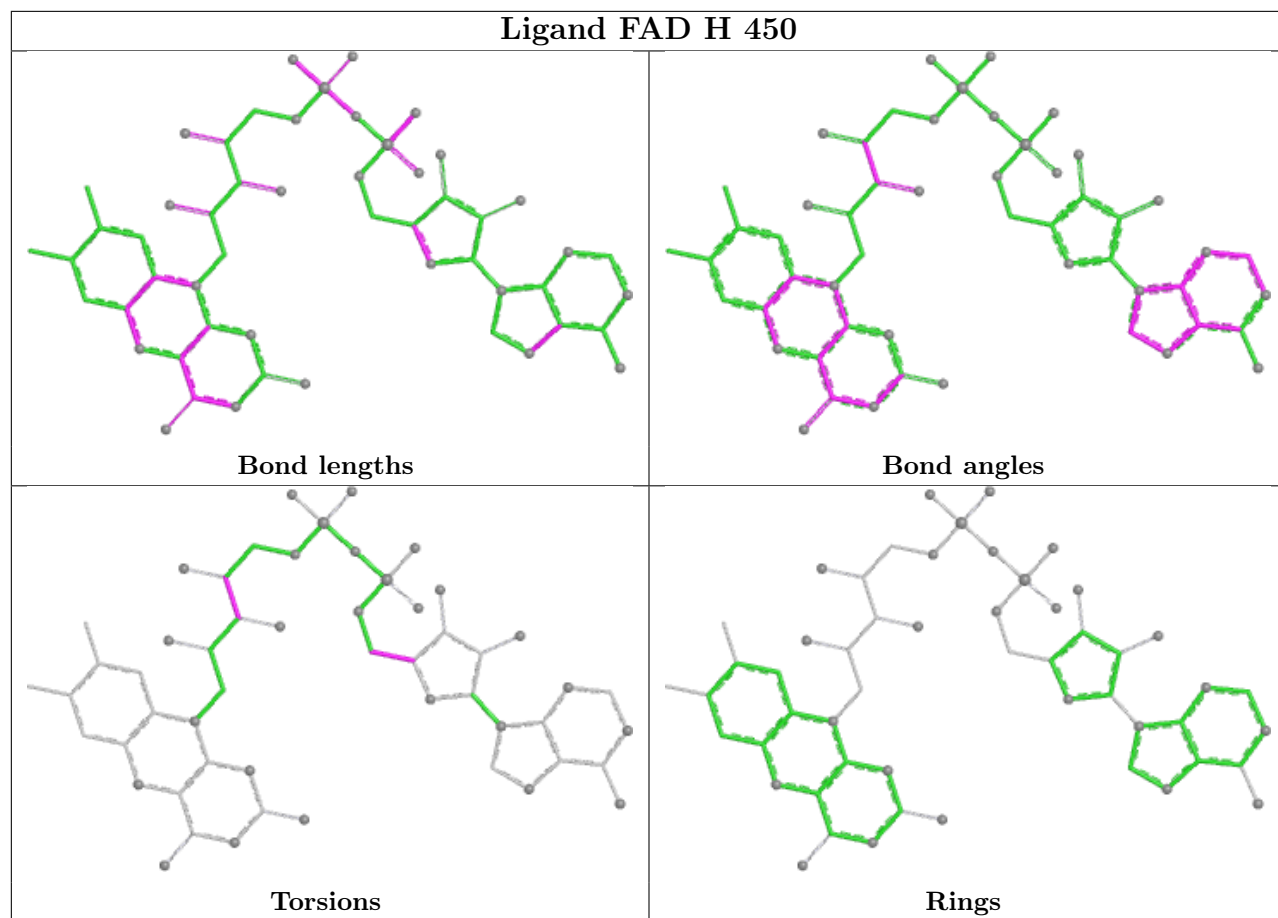


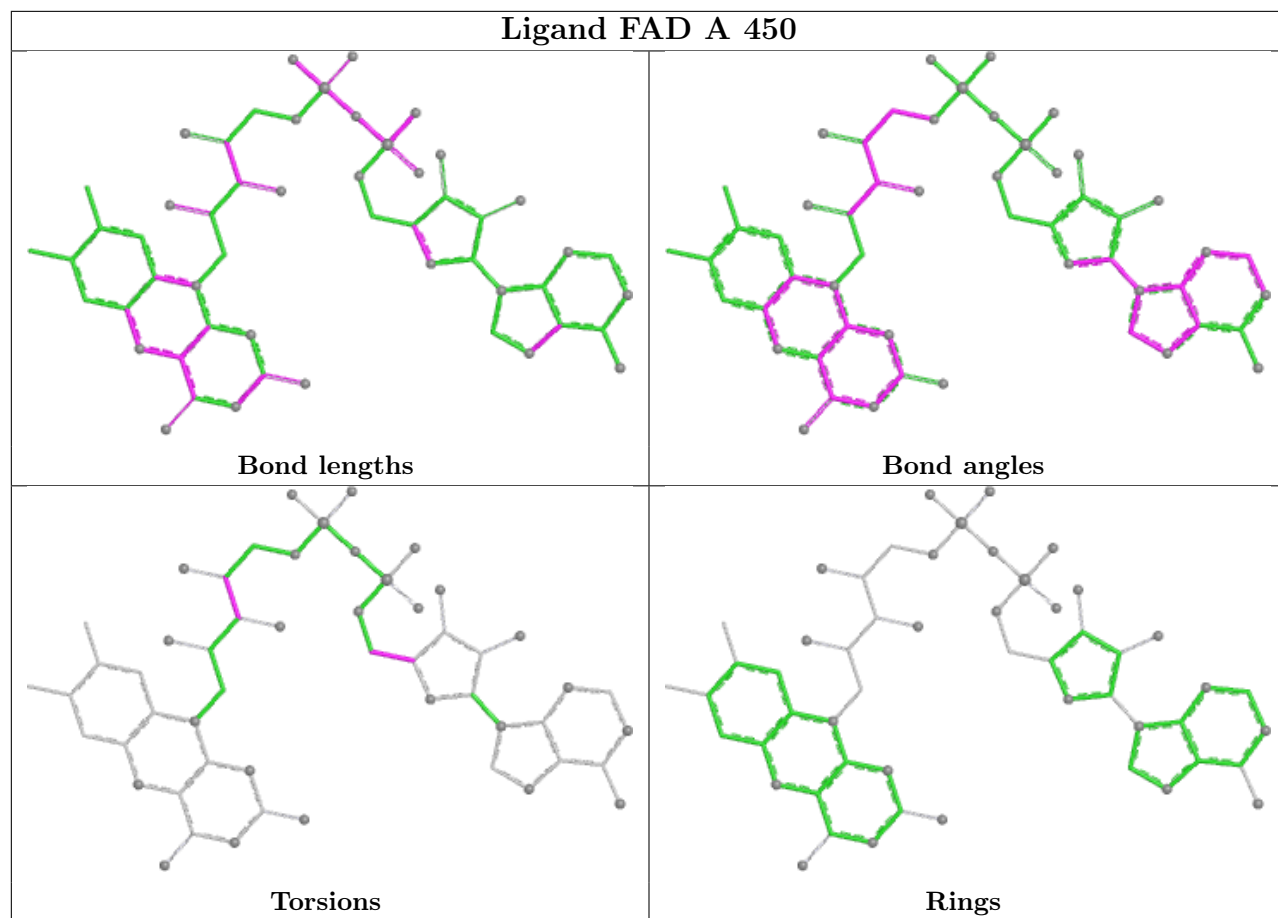


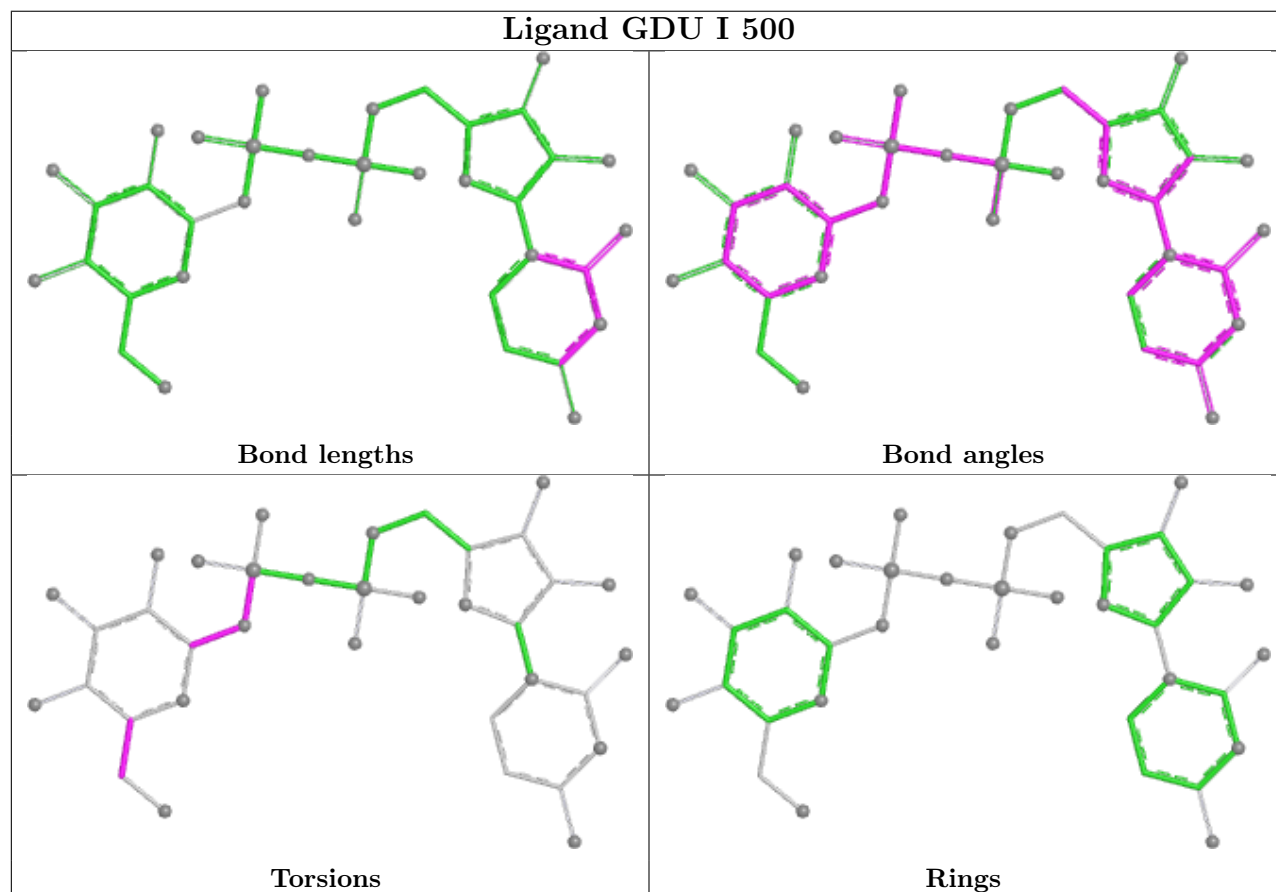
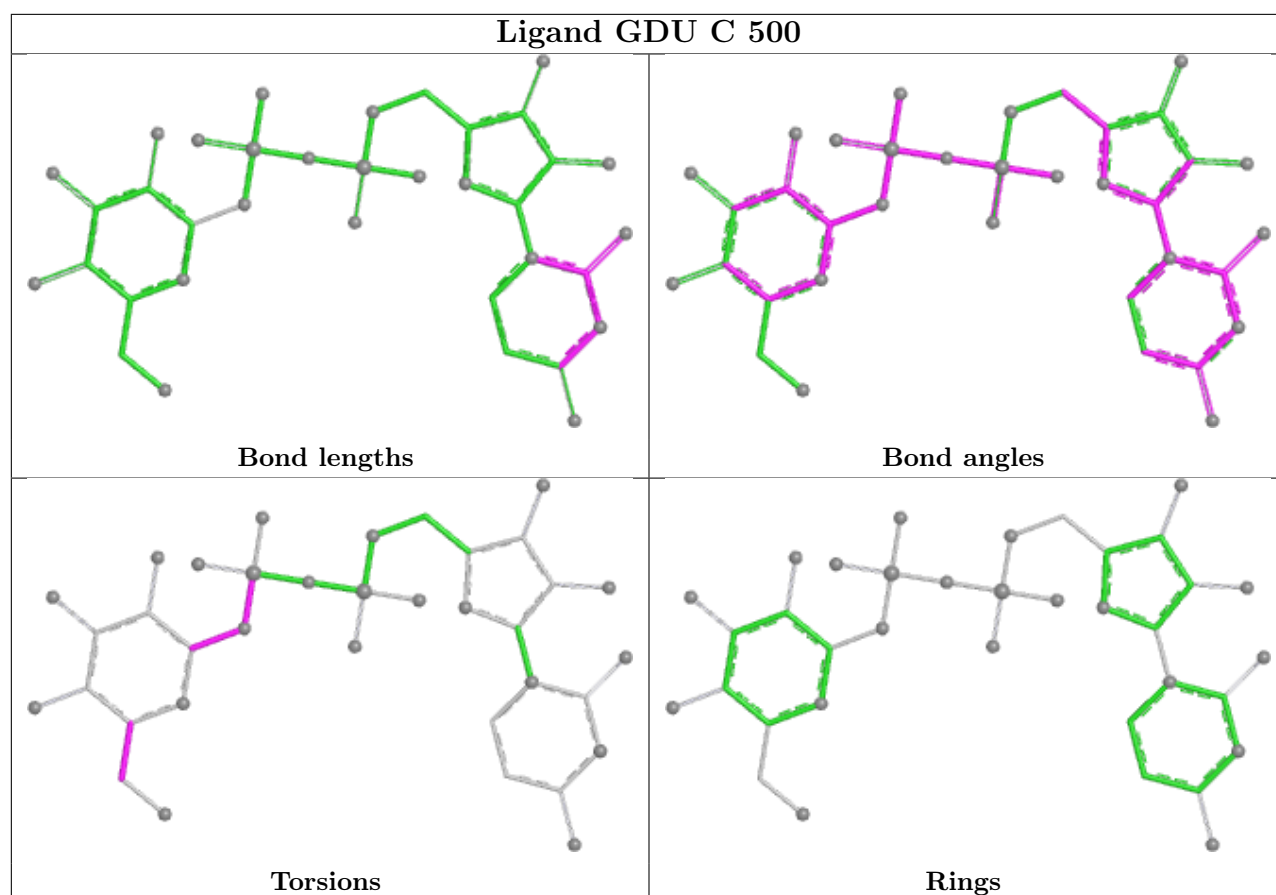


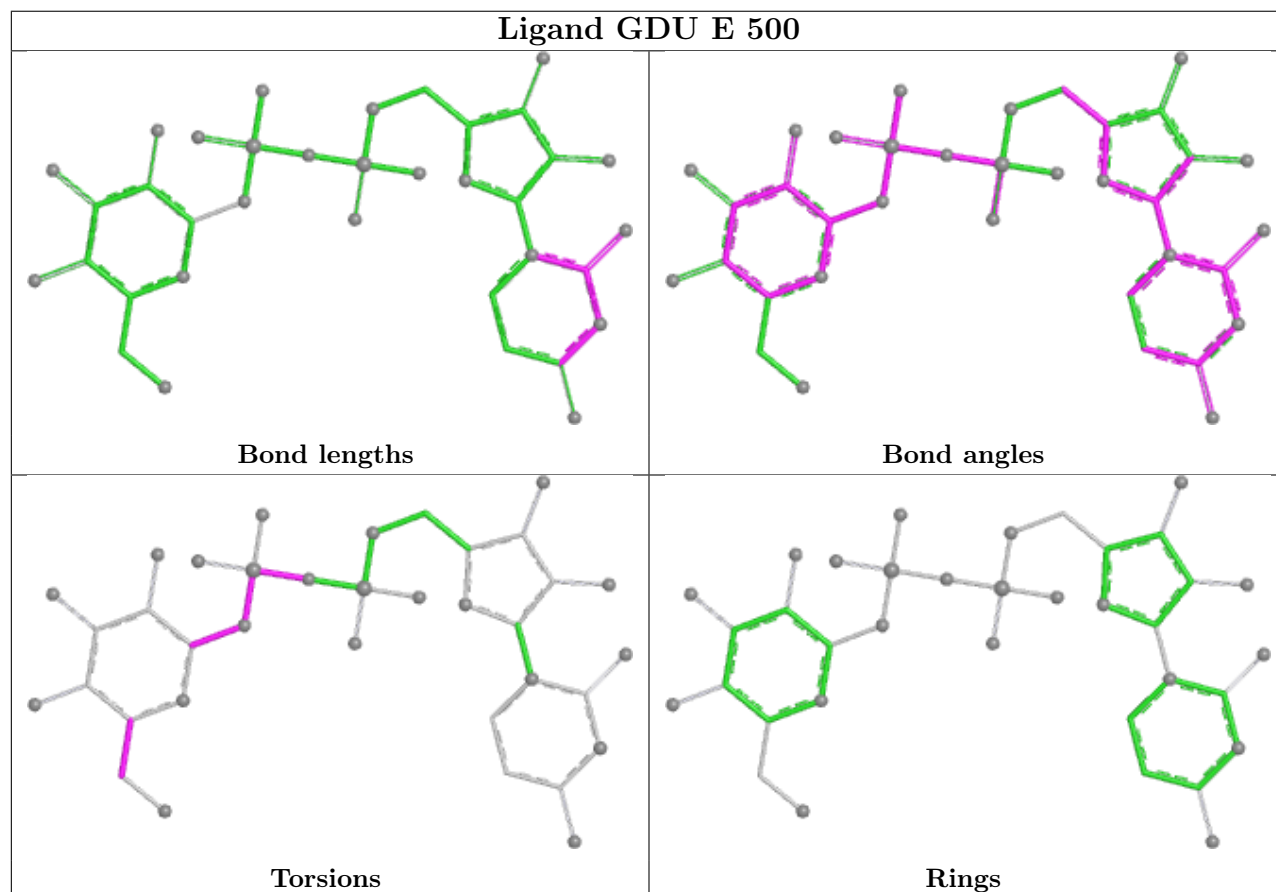
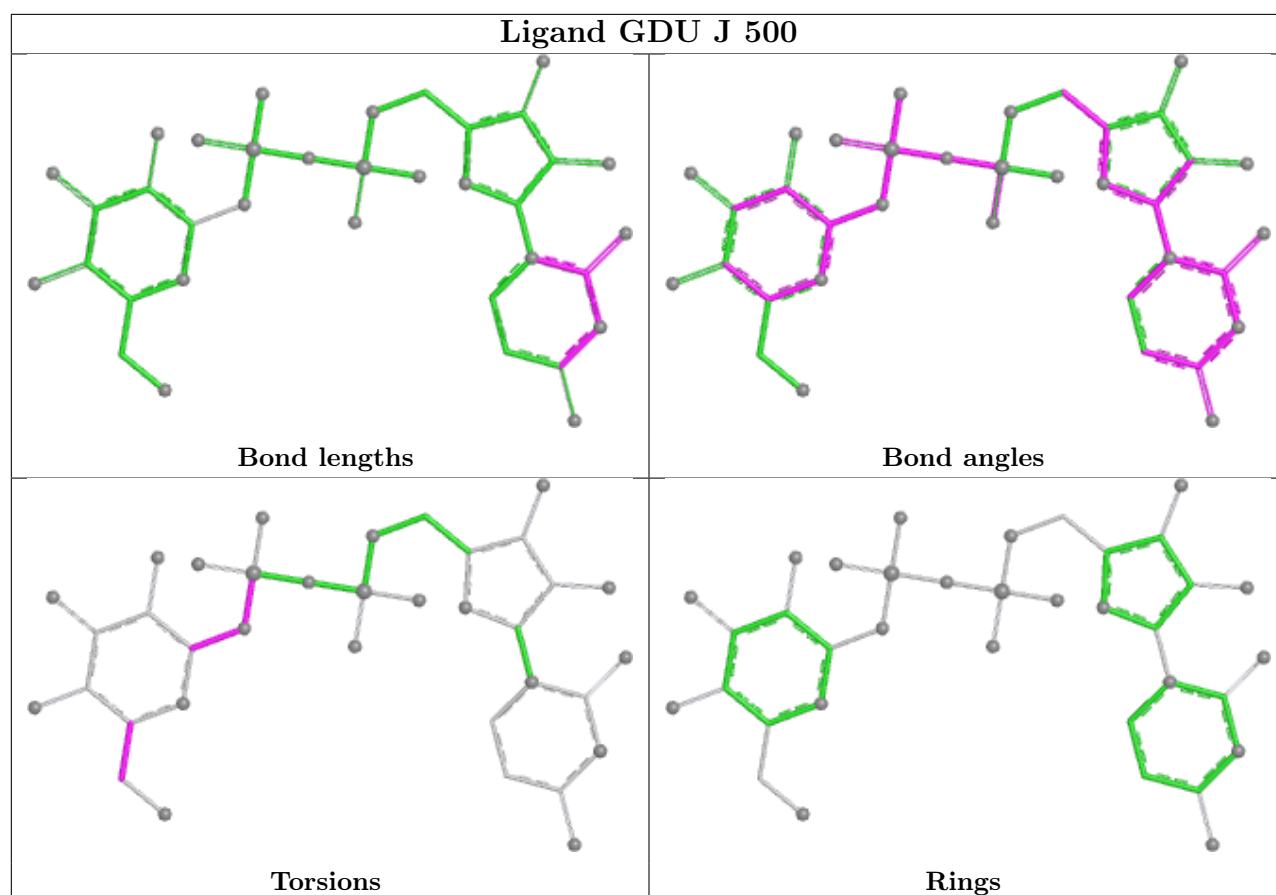


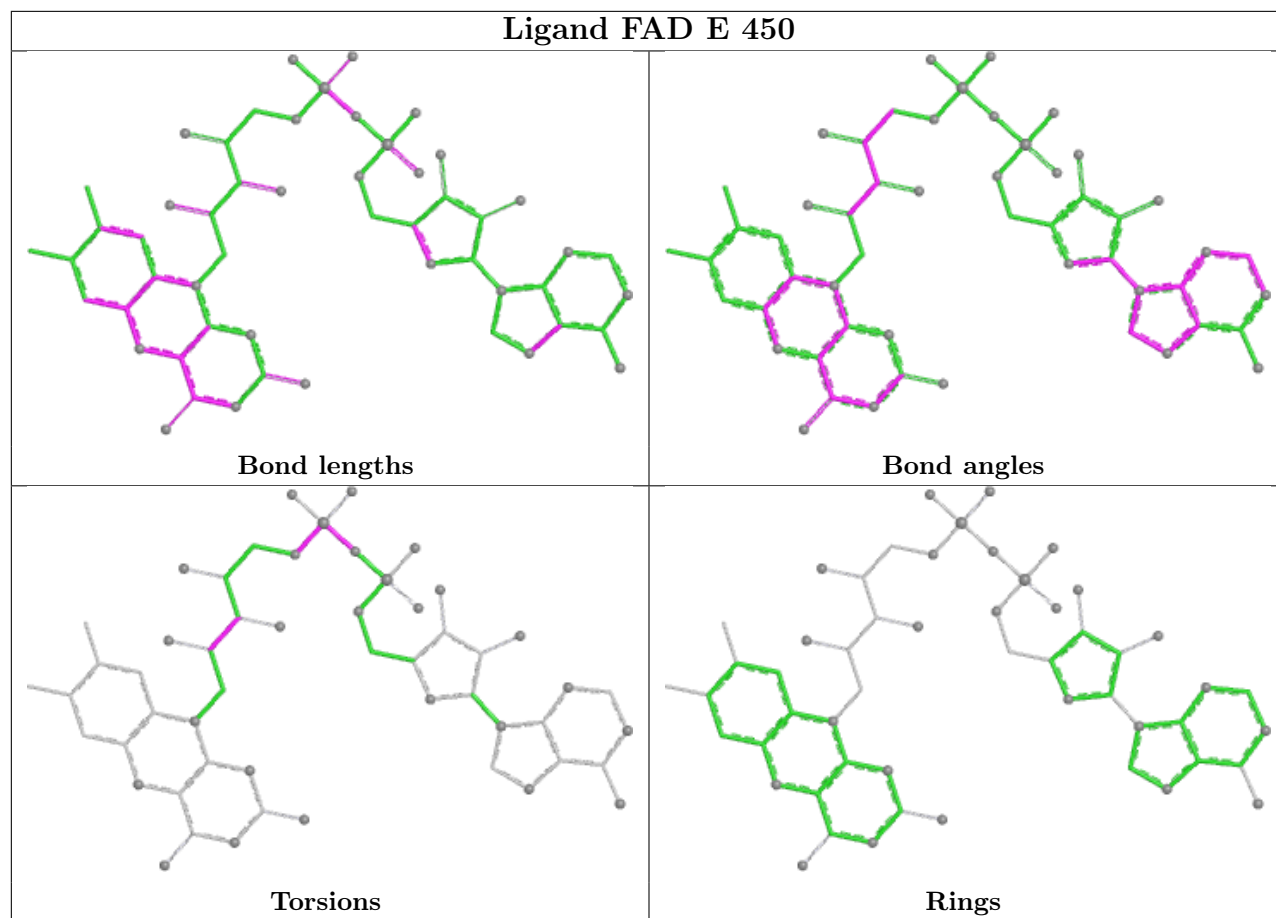


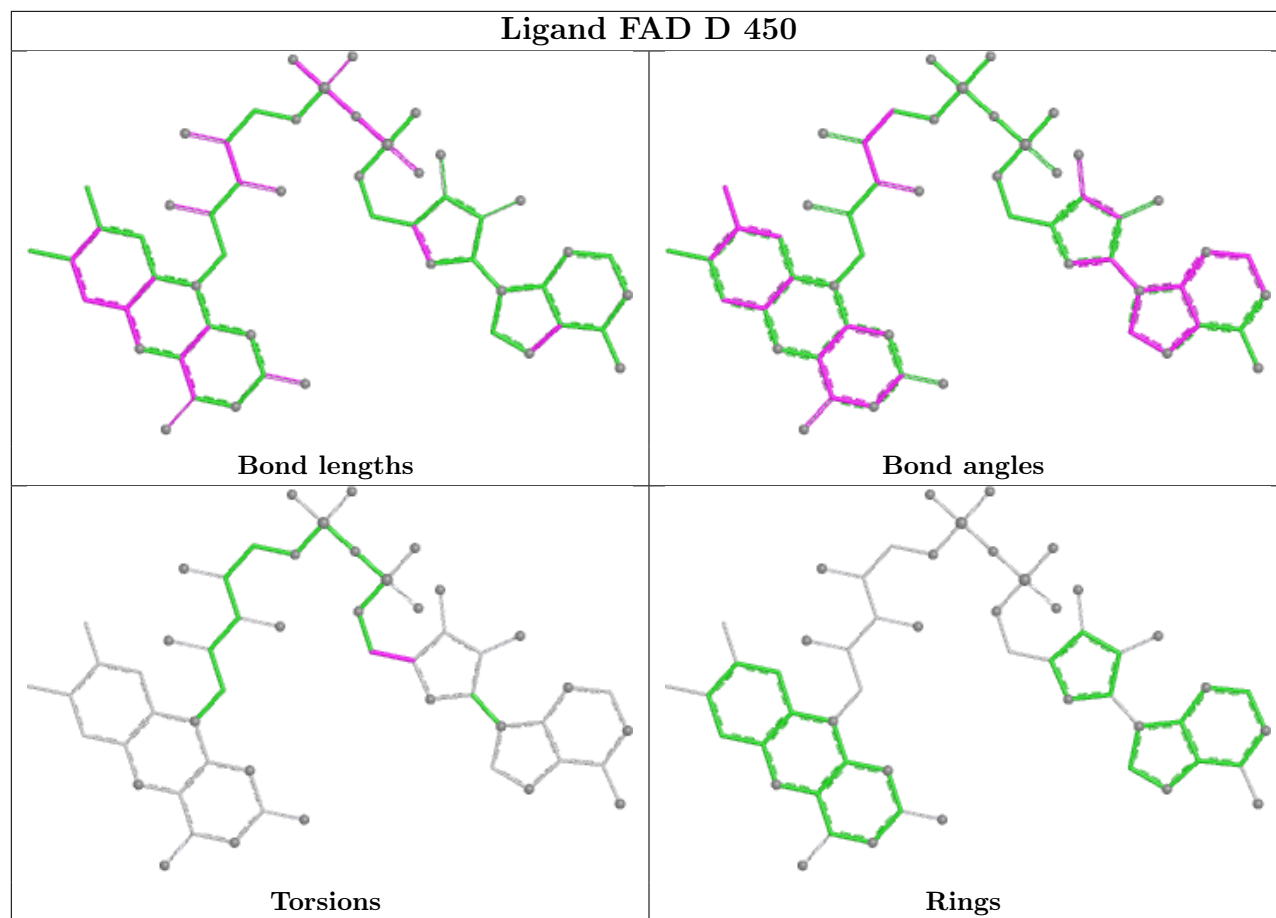


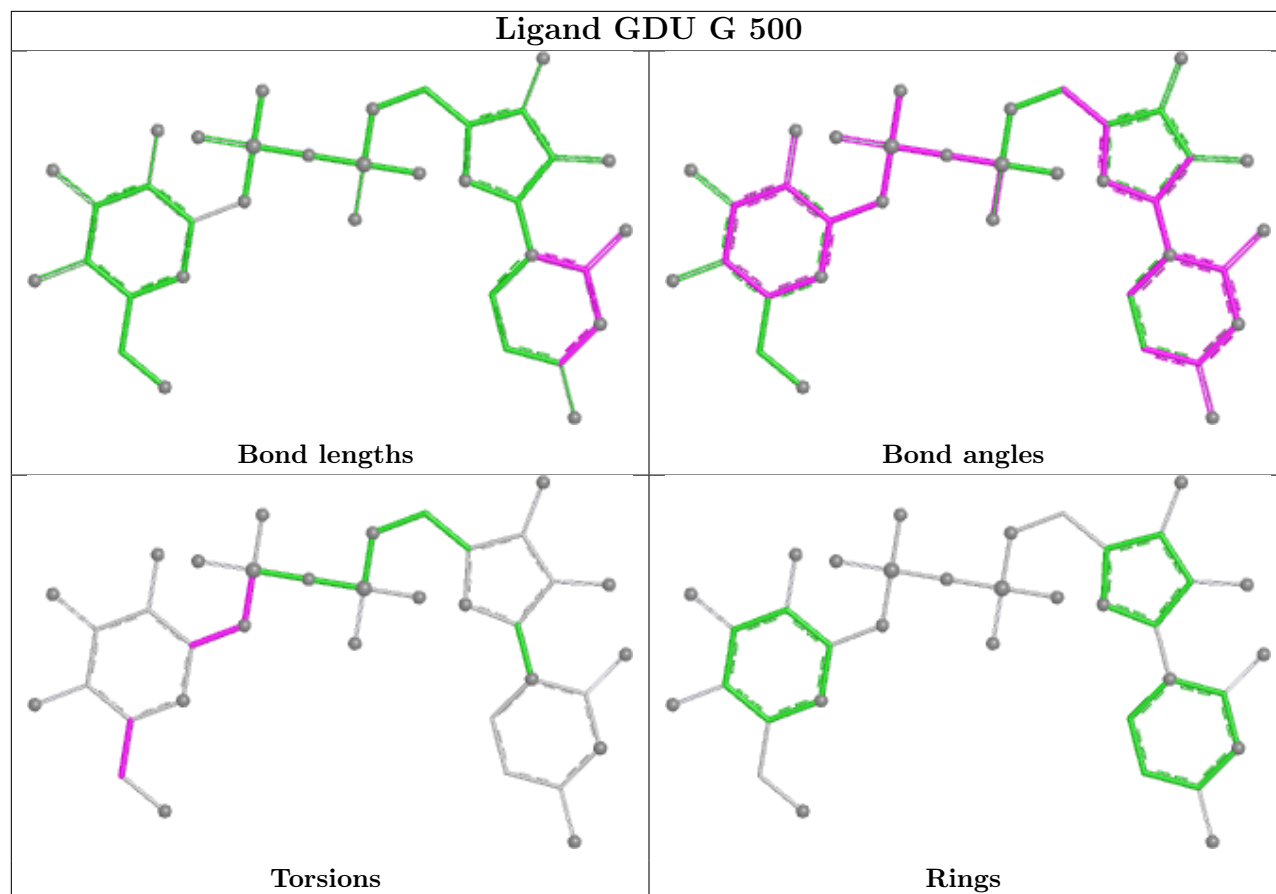


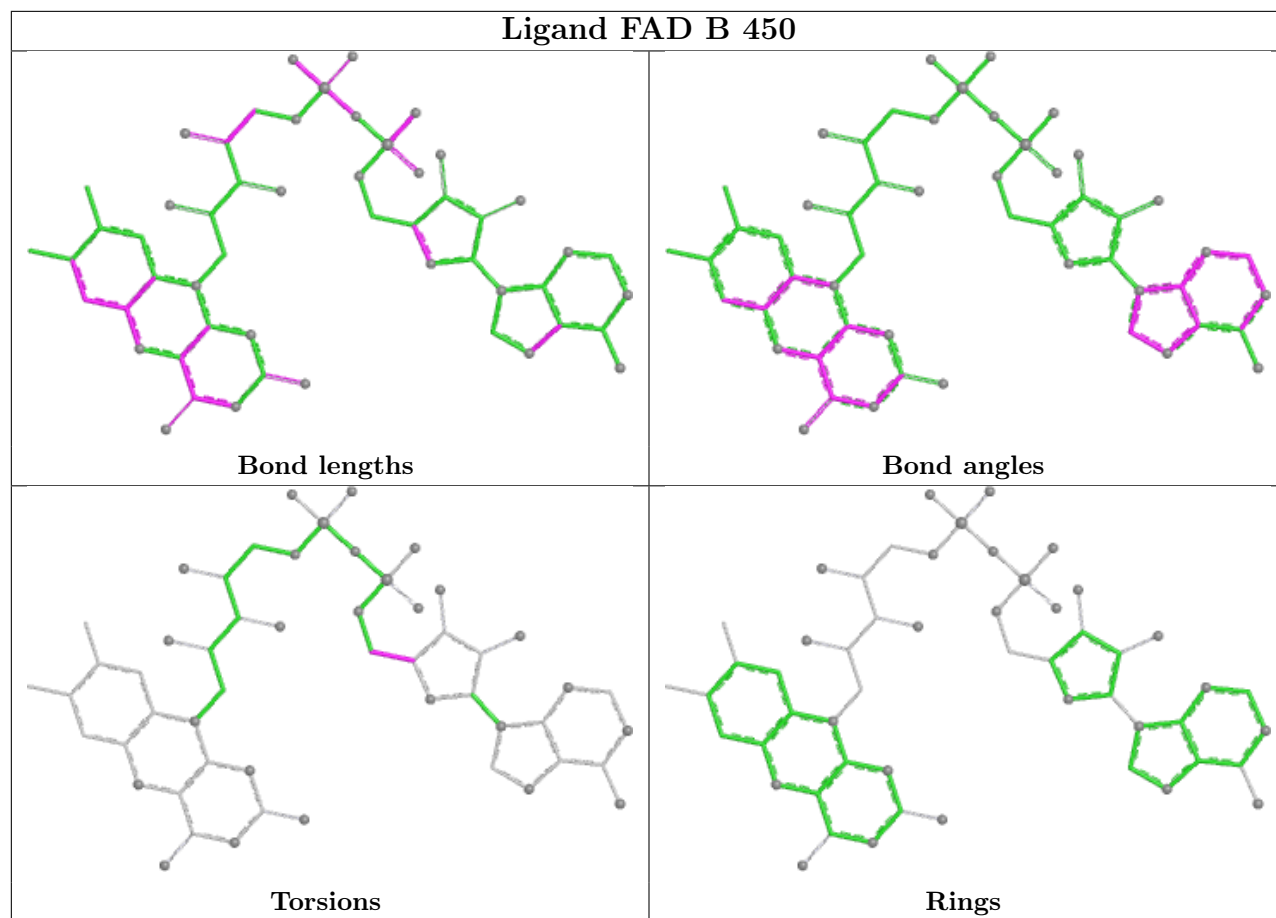


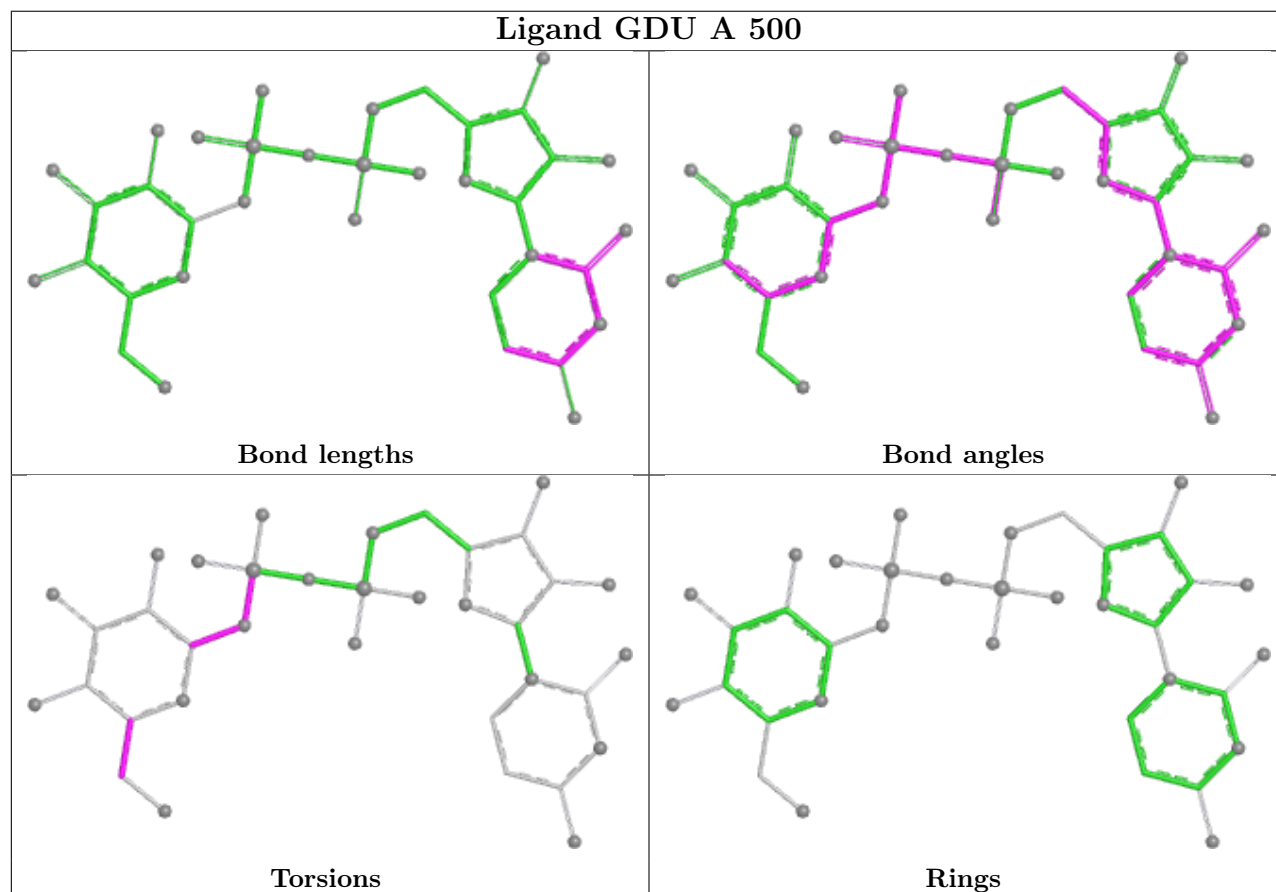
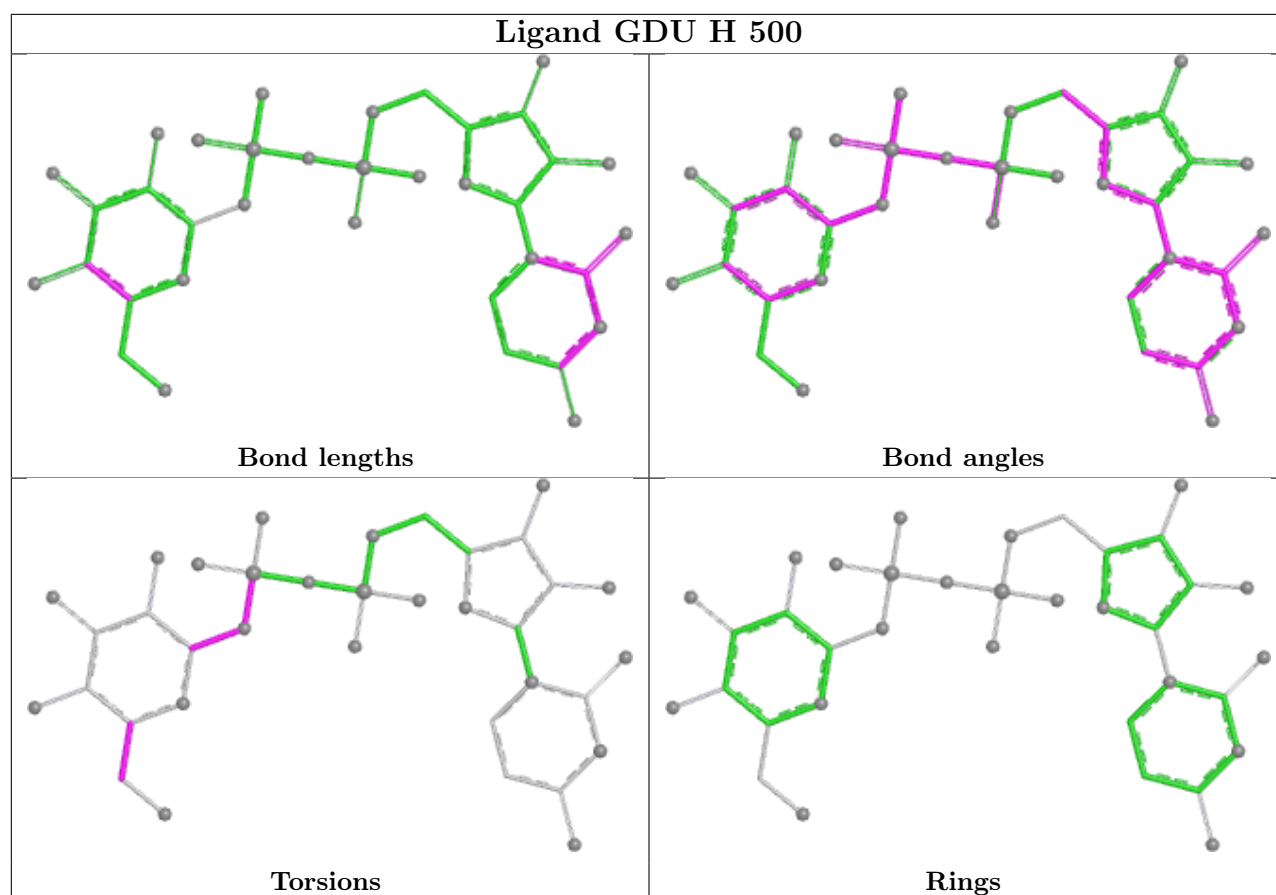




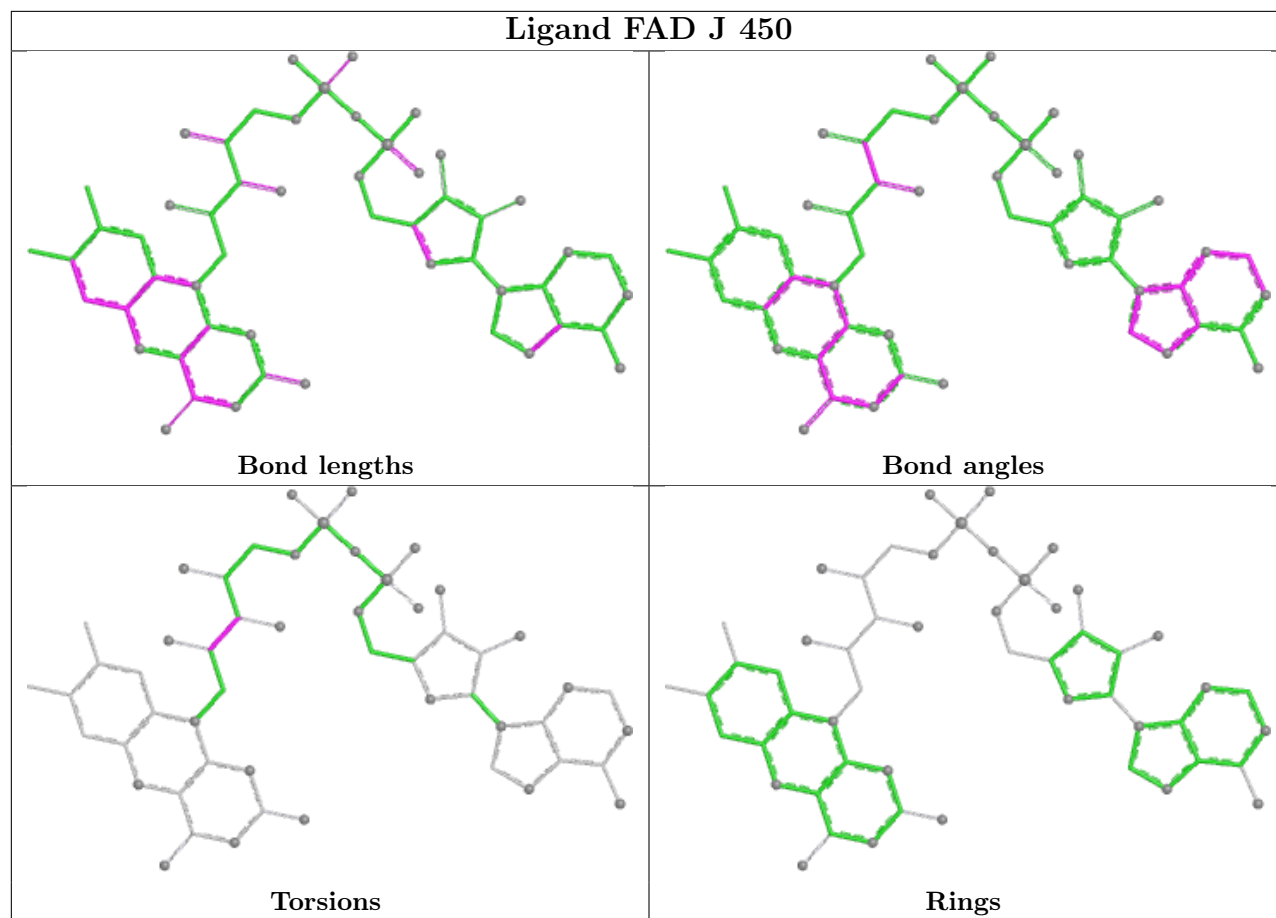


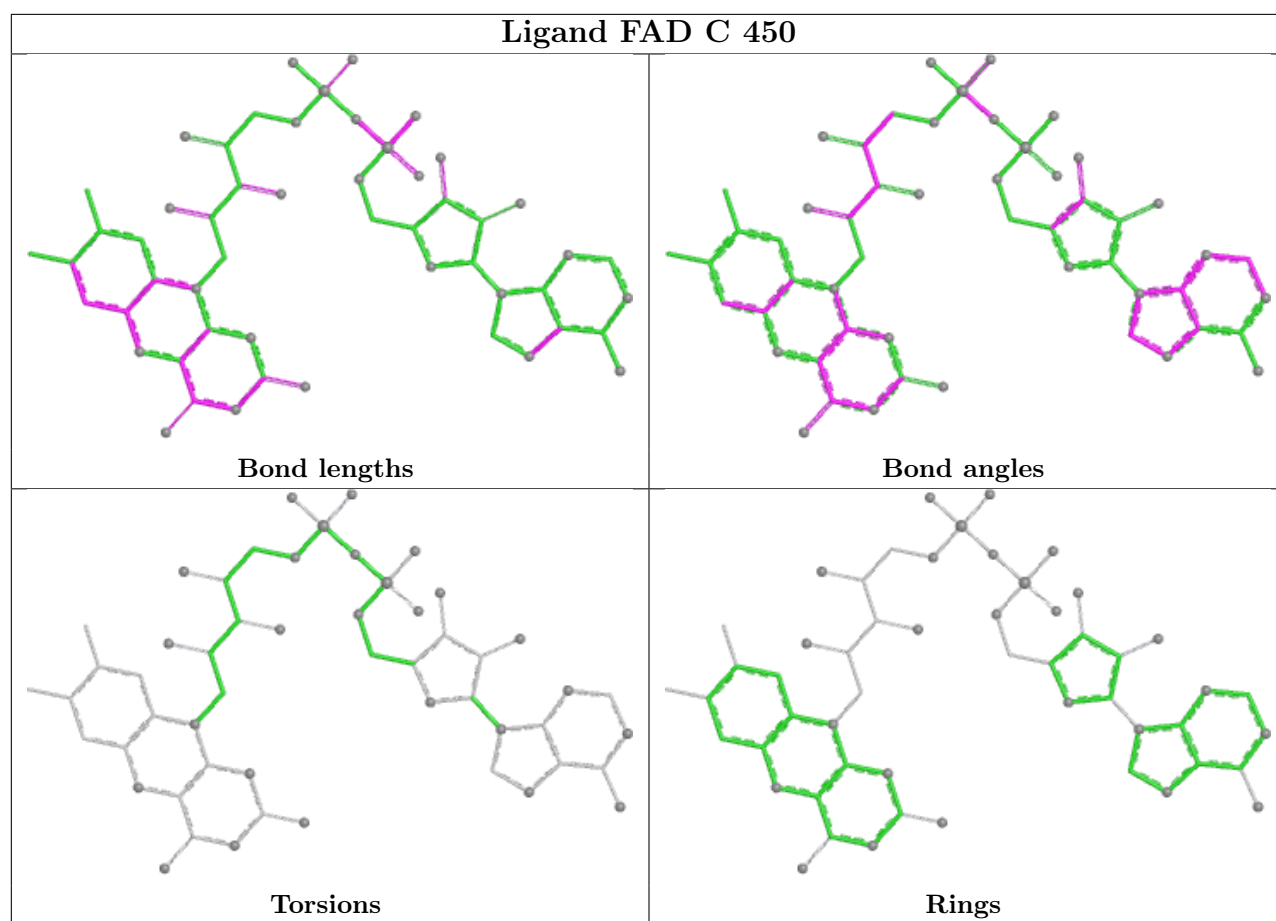






Ligand FAD J 450





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	365/397 (91%)	-0.60	3 (0%) 82 86	18, 30, 46, 75	1 (0%)
1	B	364/397 (91%)	-0.47	1 (0%) 90 92	19, 34, 54, 80	3 (0%)
1	C	361/397 (90%)	-0.06	6 (1%) 69 74	21, 39, 63, 82	7 (1%)
1	D	360/397 (90%)	-0.24	2 (0%) 85 89	20, 41, 65, 81	1 (0%)
1	E	364/397 (91%)	-0.49	2 (0%) 87 90	24, 37, 57, 98	2 (0%)
1	F	363/397 (91%)	-0.55	2 (0%) 85 89	19, 32, 50, 75	2 (0%)
1	G	363/397 (91%)	-0.46	2 (0%) 85 89	19, 35, 54, 78	2 (0%)
1	H	364/397 (91%)	-0.53	6 (1%) 70 76	20, 32, 52, 76	1 (0%)
1	I	363/397 (91%)	-0.60	2 (0%) 85 89	15, 32, 47, 70	2 (0%)
1	J	361/397 (90%)	-0.43	0 100 100	17, 35, 59, 81	2 (0%)
All	All	3628/3970 (91%)	-0.44	26 (0%) 84 87	15, 34, 58, 98	23 (0%)

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	357	GLN	6.3
1	H	27	SER	5.6
1	D	153	VAL	5.6
1	H	28	LYS	5.3
1	F	153	VAL	4.6

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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

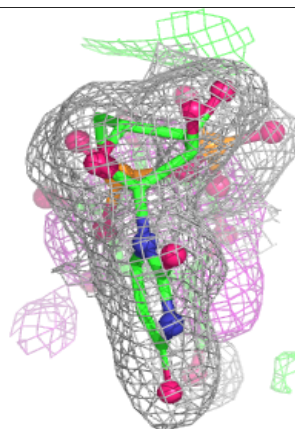
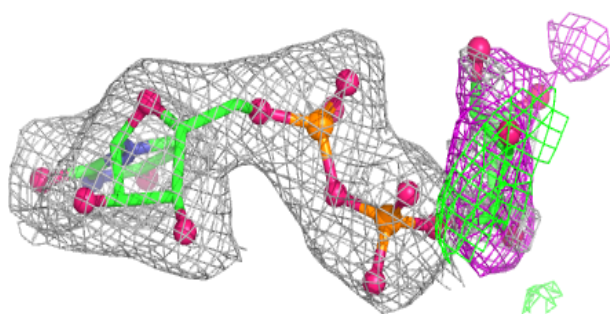
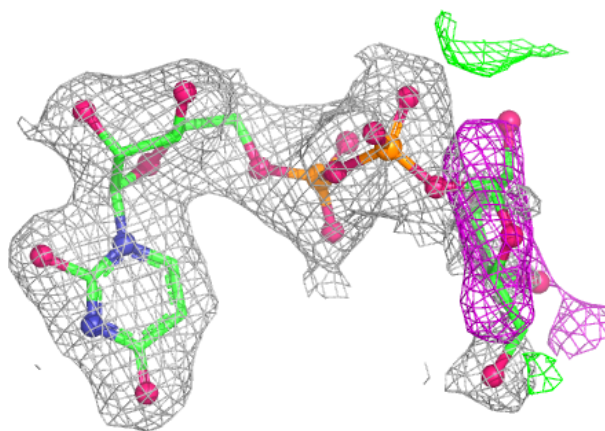
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GDU	D	500	36/36	0.92	0.11	35,44,65,69	0
2	GDU	B	500	36/36	0.93	0.10	31,39,57,61	0
3	FAD	C	450	53/53	0.93	0.09	23,29,36,51	0
2	GDU	I	500	36/36	0.94	0.10	29,34,54,58	0
2	GDU	C	500	36/36	0.94	0.09	29,39,63,64	0
3	FAD	D	450	53/53	0.94	0.09	23,29,36,51	0
2	GDU	E	500	36/36	0.95	0.09	28,36,55,58	0
2	GDU	J	500	36/36	0.95	0.09	25,32,54,57	0
3	FAD	B	450	53/53	0.95	0.07	23,29,36,51	0
2	GDU	F	500	36/36	0.95	0.08	26,35,50,53	0
2	GDU	H	500	36/36	0.95	0.09	25,31,48,52	0
3	FAD	E	450	53/53	0.95	0.08	23,29,36,51	0
3	FAD	G	450	53/53	0.95	0.08	23,29,36,51	0
3	FAD	J	450	53/53	0.95	0.08	23,29,36,51	0
3	FAD	A	450	53/53	0.96	0.06	23,29,36,51	0
3	FAD	H	450	53/53	0.96	0.07	23,29,36,51	0
3	FAD	F	450	53/53	0.96	0.07	23,29,36,51	0
3	FAD	I	450	53/53	0.97	0.06	23,29,36,51	0
2	GDU	G	500	36/36	0.97	0.07	31,36,40,43	11
2	GDU	A	500	36/36	0.98	0.06	25,29,32,34	12

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.

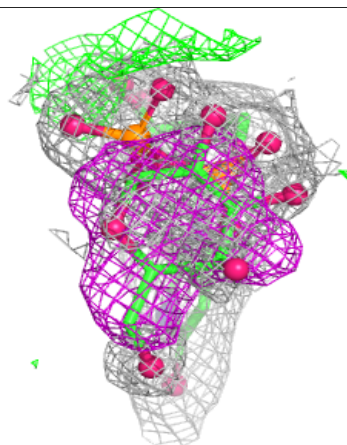
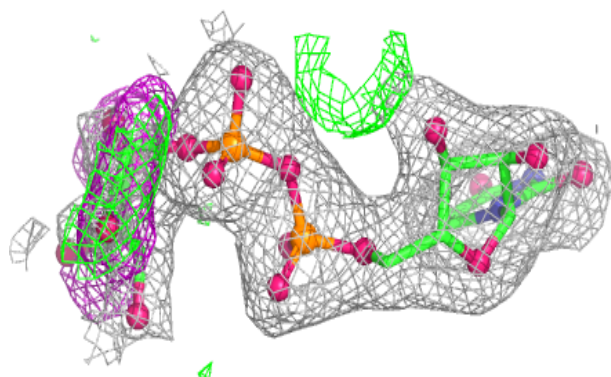
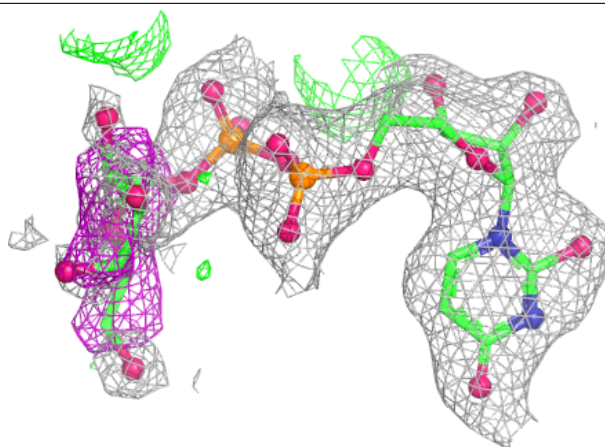
Electron density around GDU D 500:

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

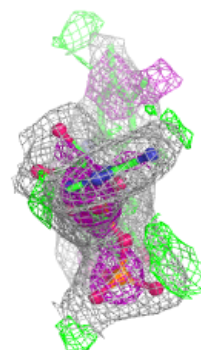
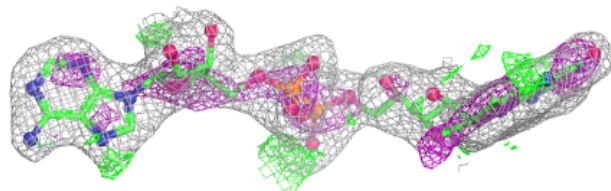
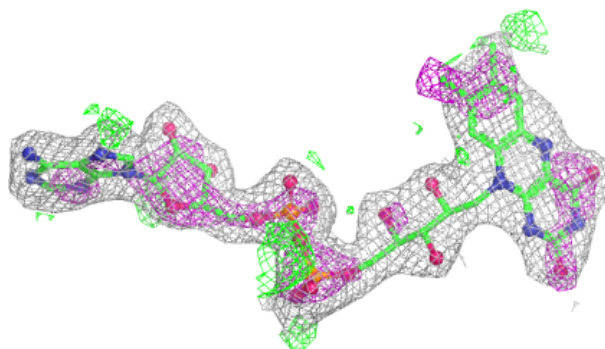


Electron density around GDU B 500:

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

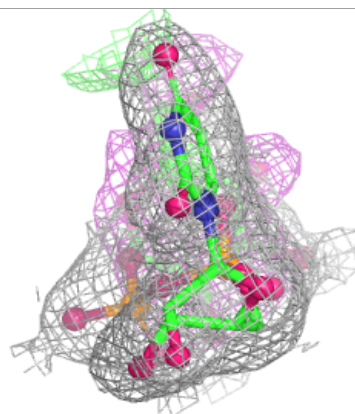
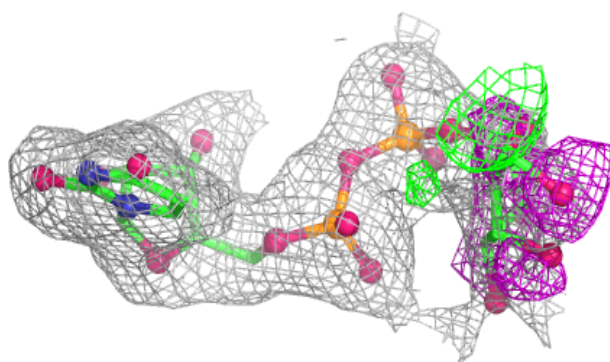
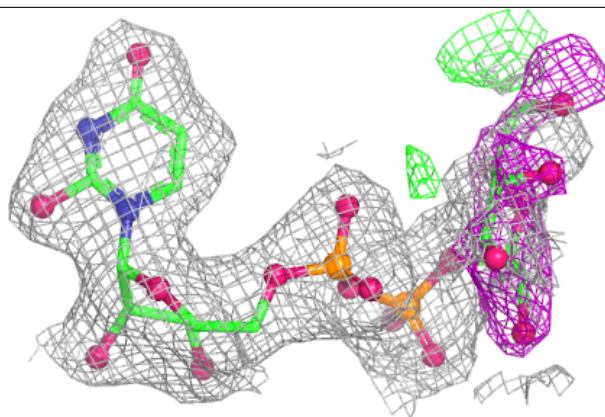
**Electron density around FAD C 450:**

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



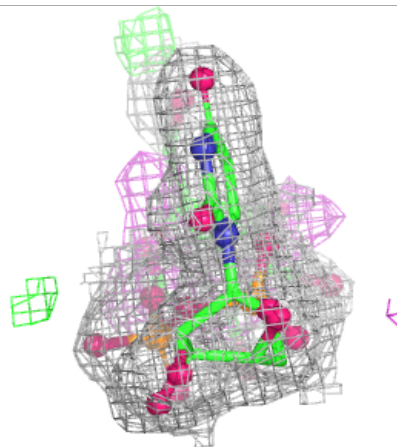
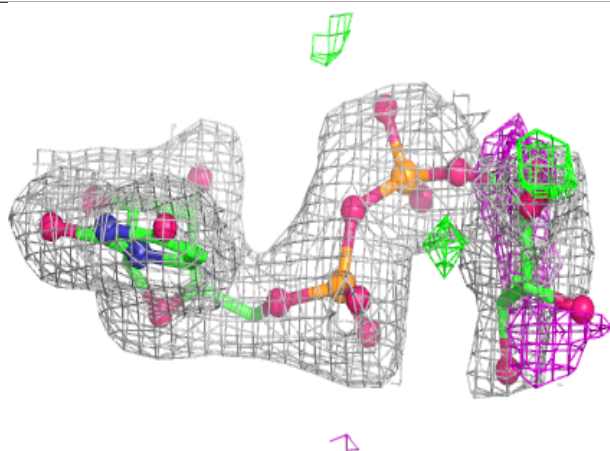
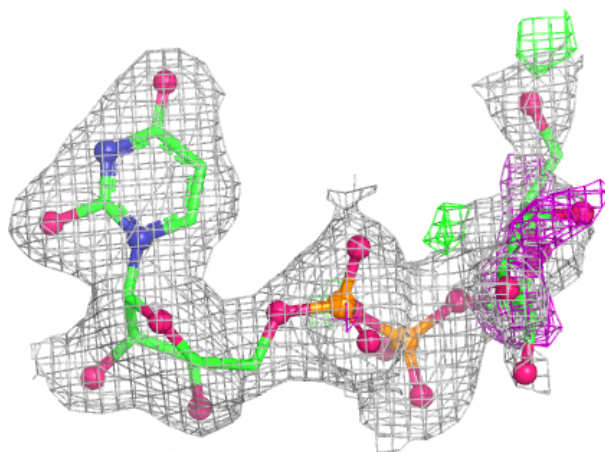
Electron density around GDU I 500:

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



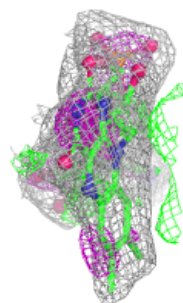
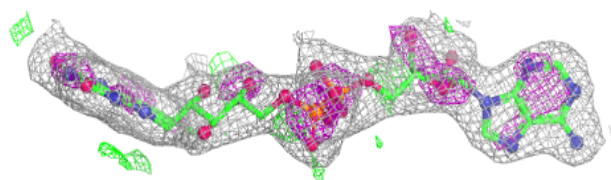
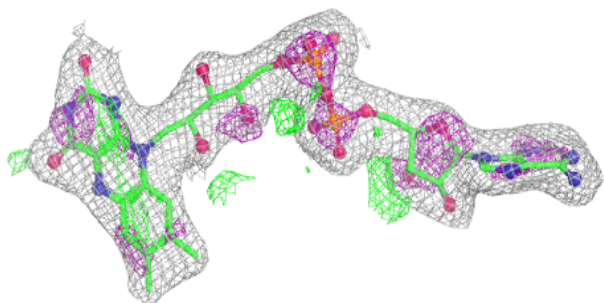
Electron density around GDU C 500:

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



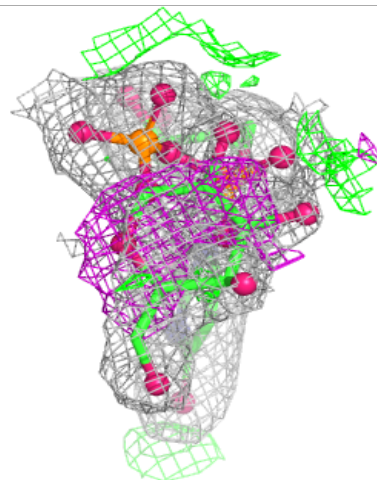
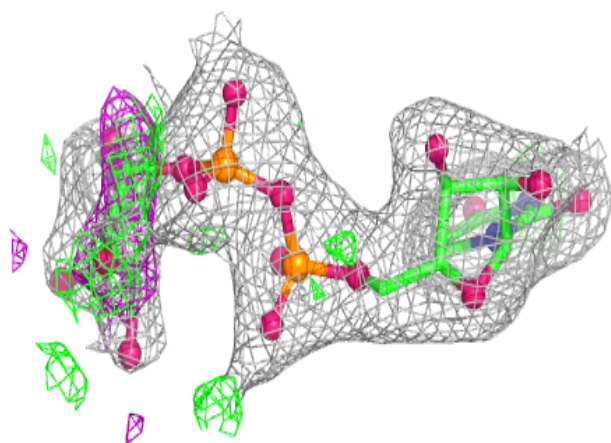
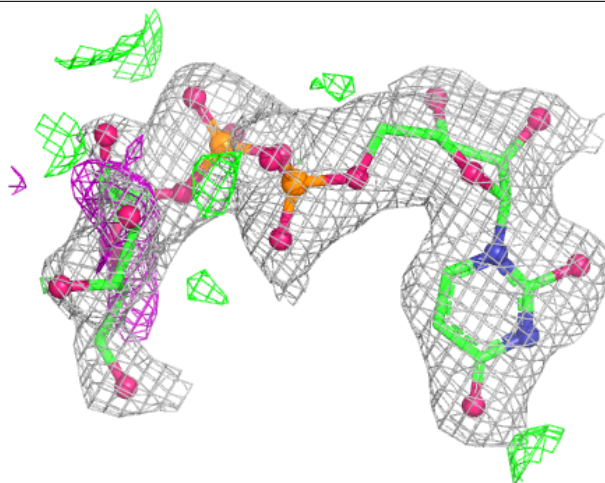
Electron density around FAD D 450:

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



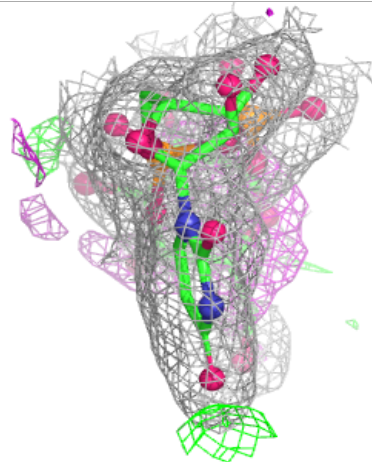
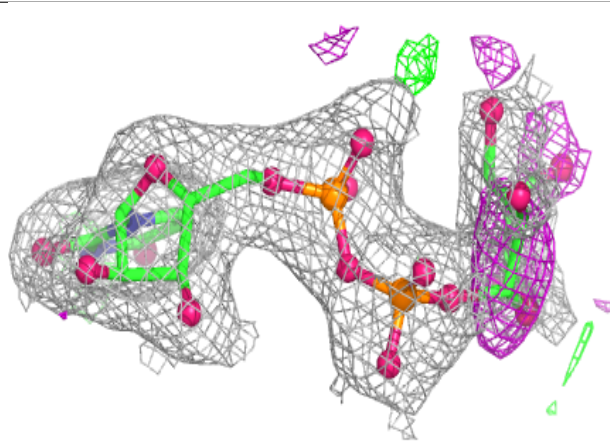
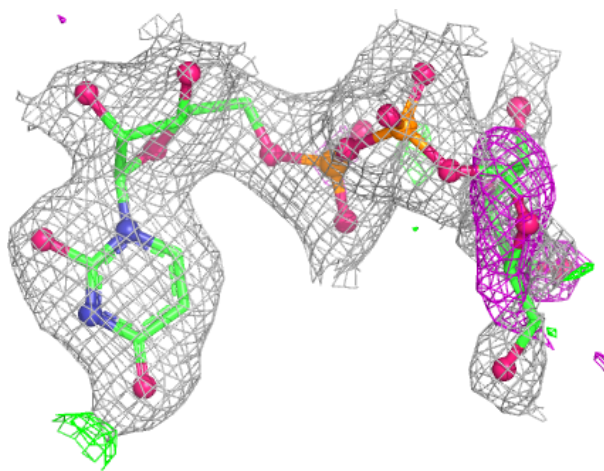
Electron density around GDU E 500:

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



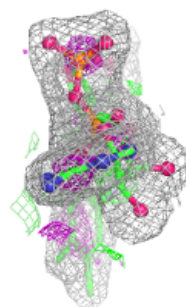
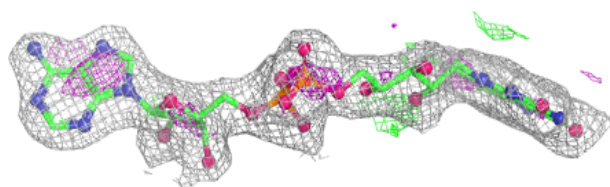
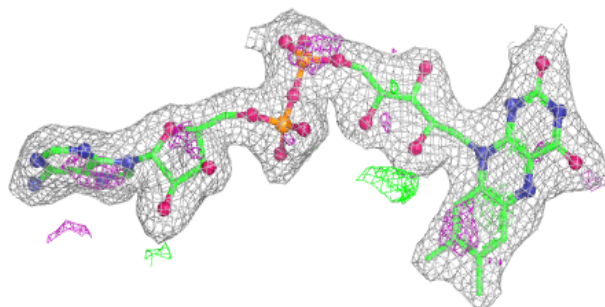
Electron density around GDU J 500:

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



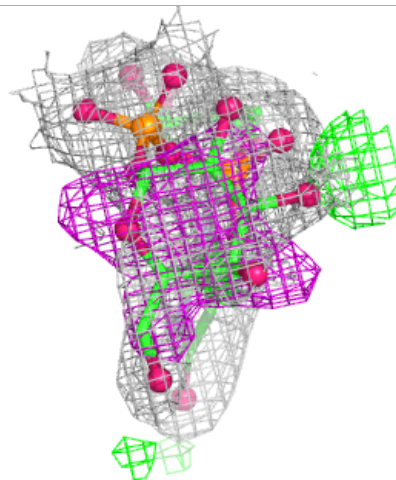
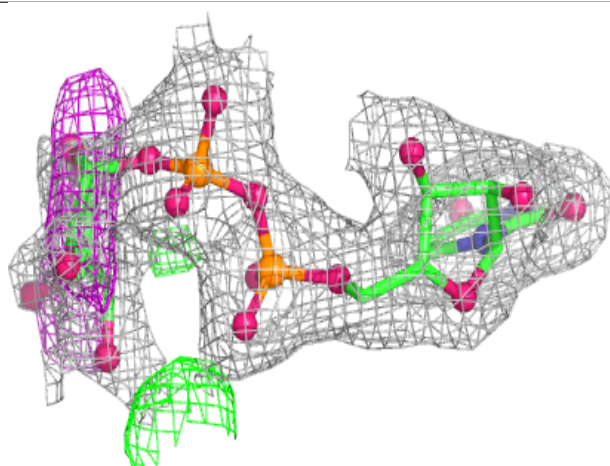
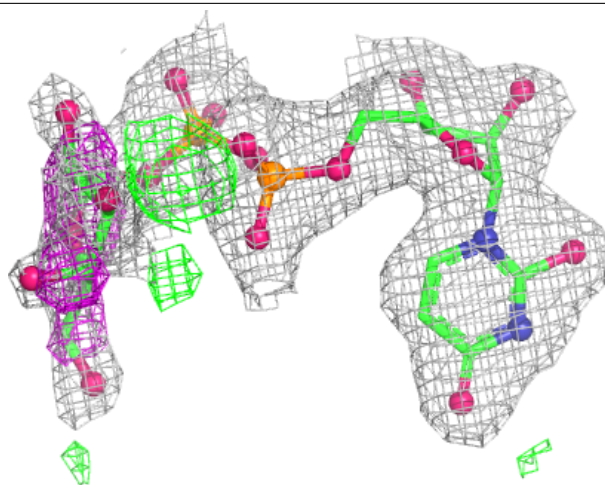
Electron density around FAD B 450:

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



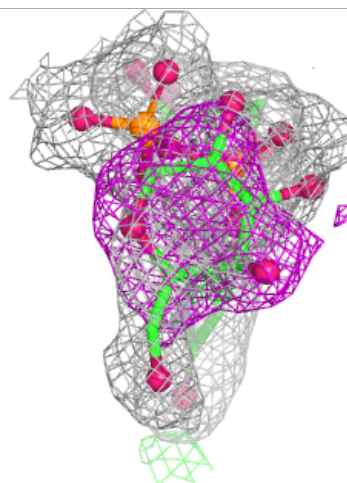
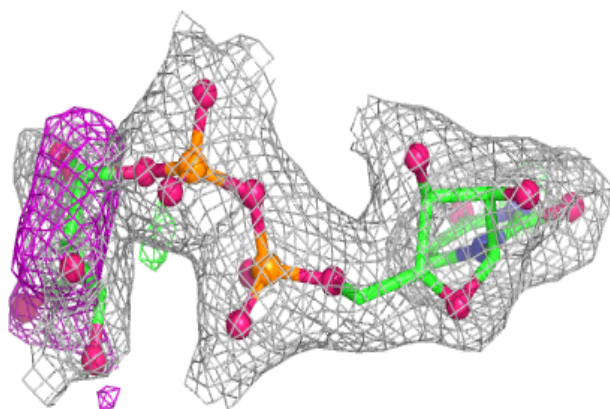
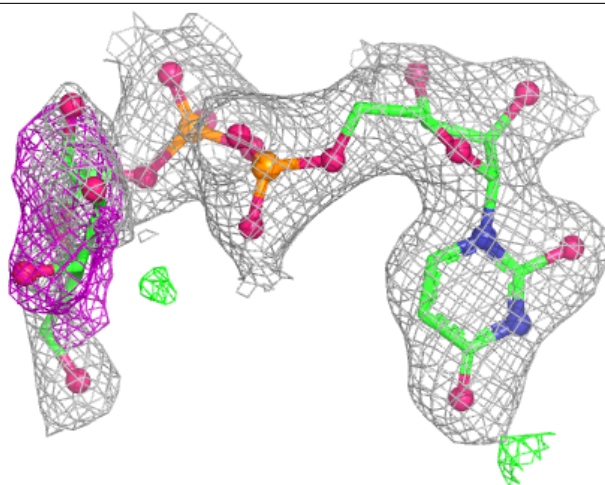
Electron density around GDU F 500:

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



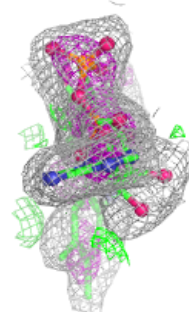
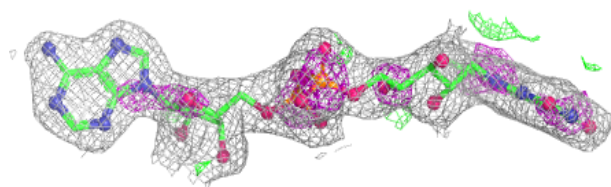
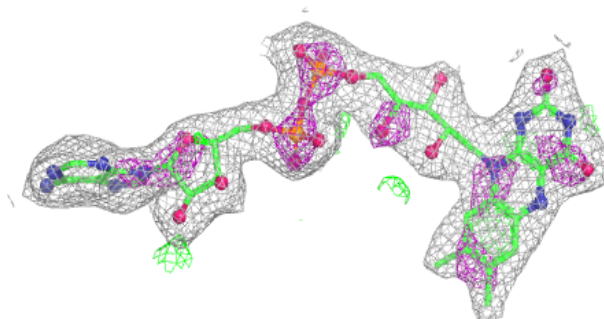
Electron density around GDU H 500:

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

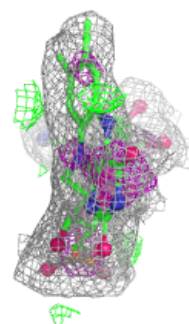
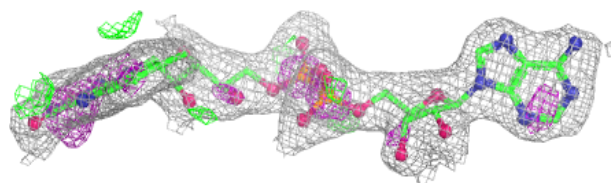
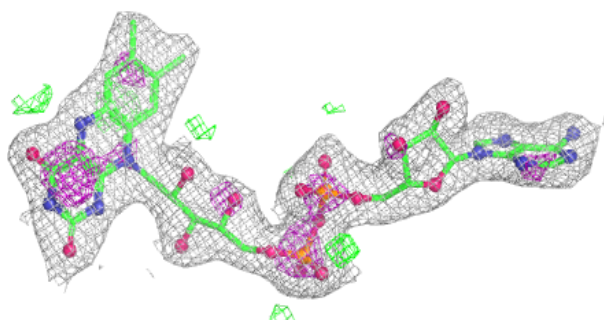


Electron density around FAD E 450:

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

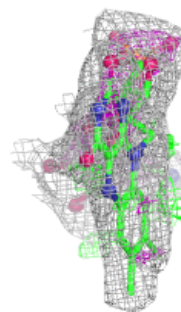
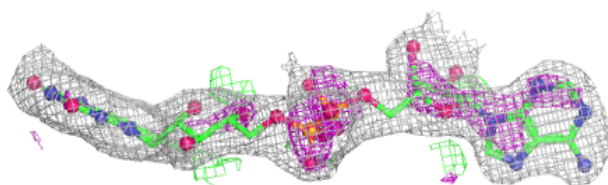
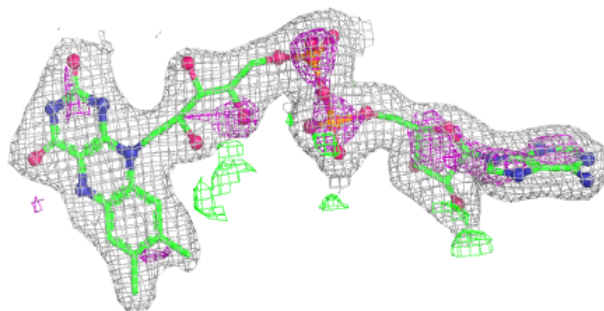
**Electron density around FAD G 450:**

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

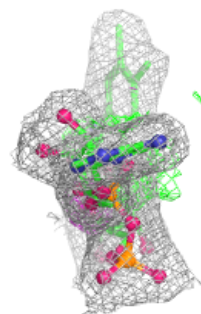
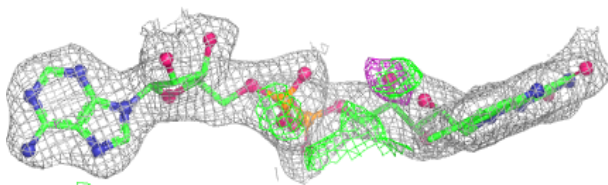
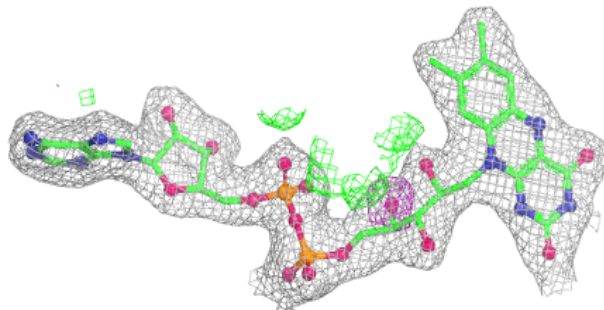


Electron density around FAD J 450:

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

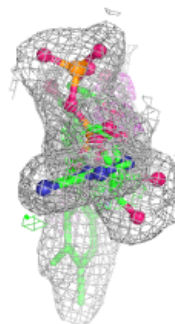
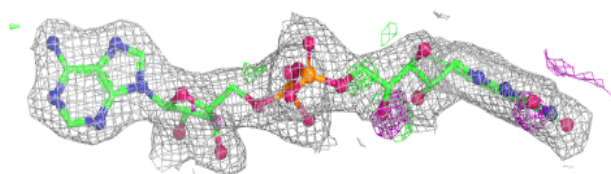
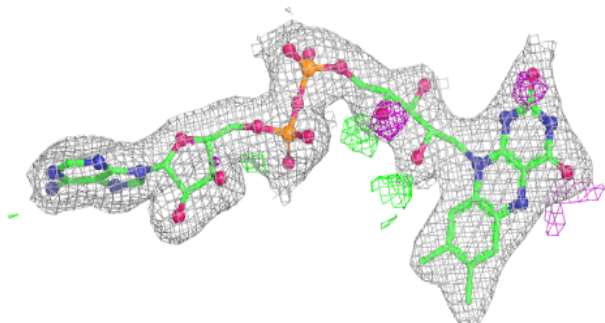
**Electron density around FAD A 450:**

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

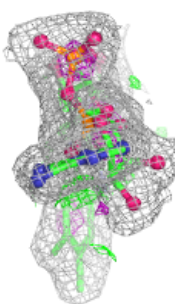
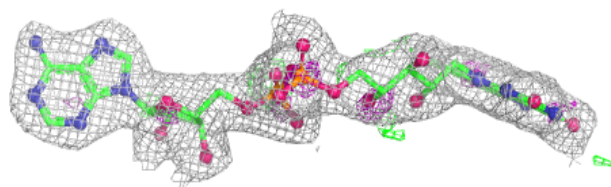
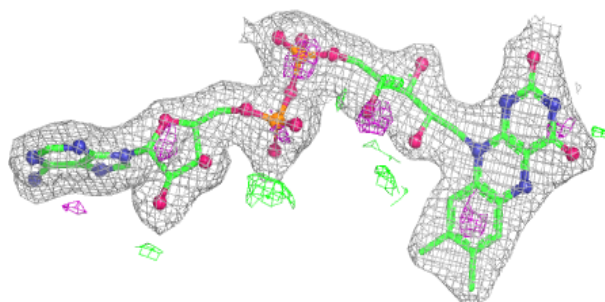


Electron density around FAD H 450:

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

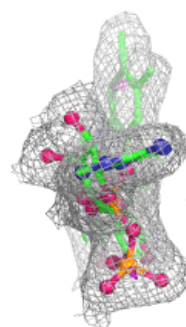
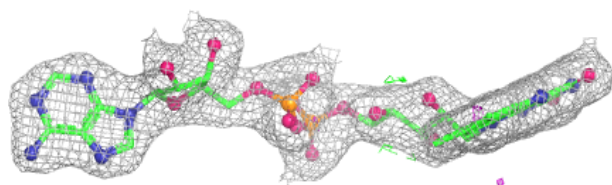
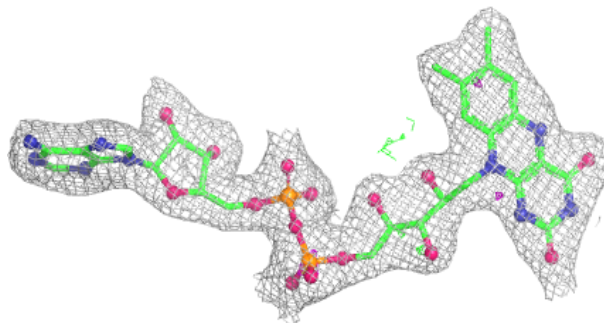
**Electron density around FAD F 450:**

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



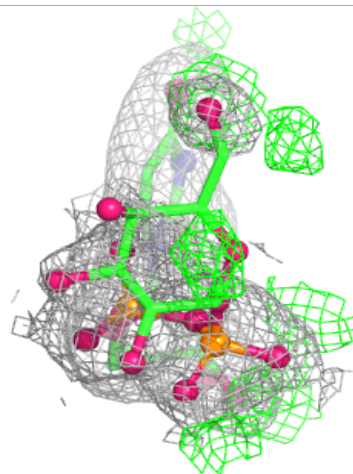
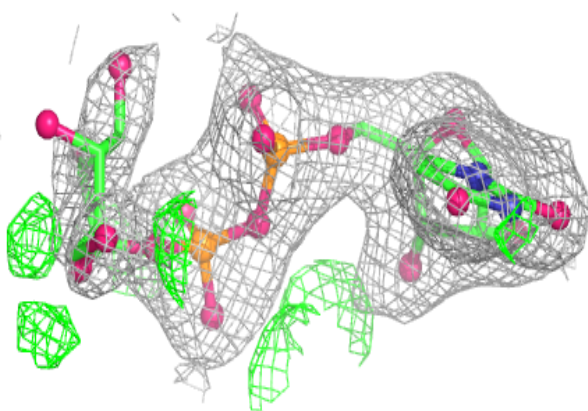
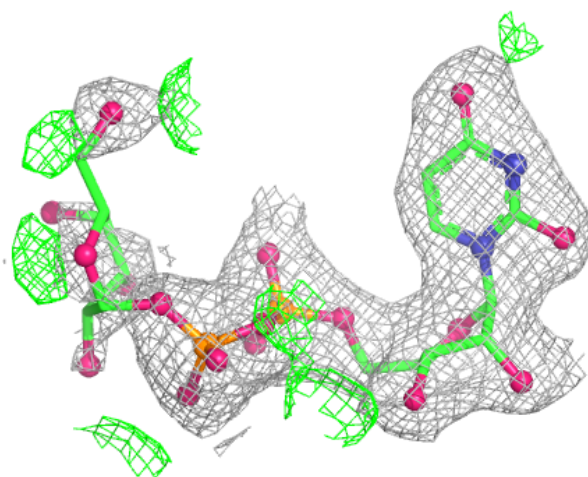
Electron density around FAD I 450:

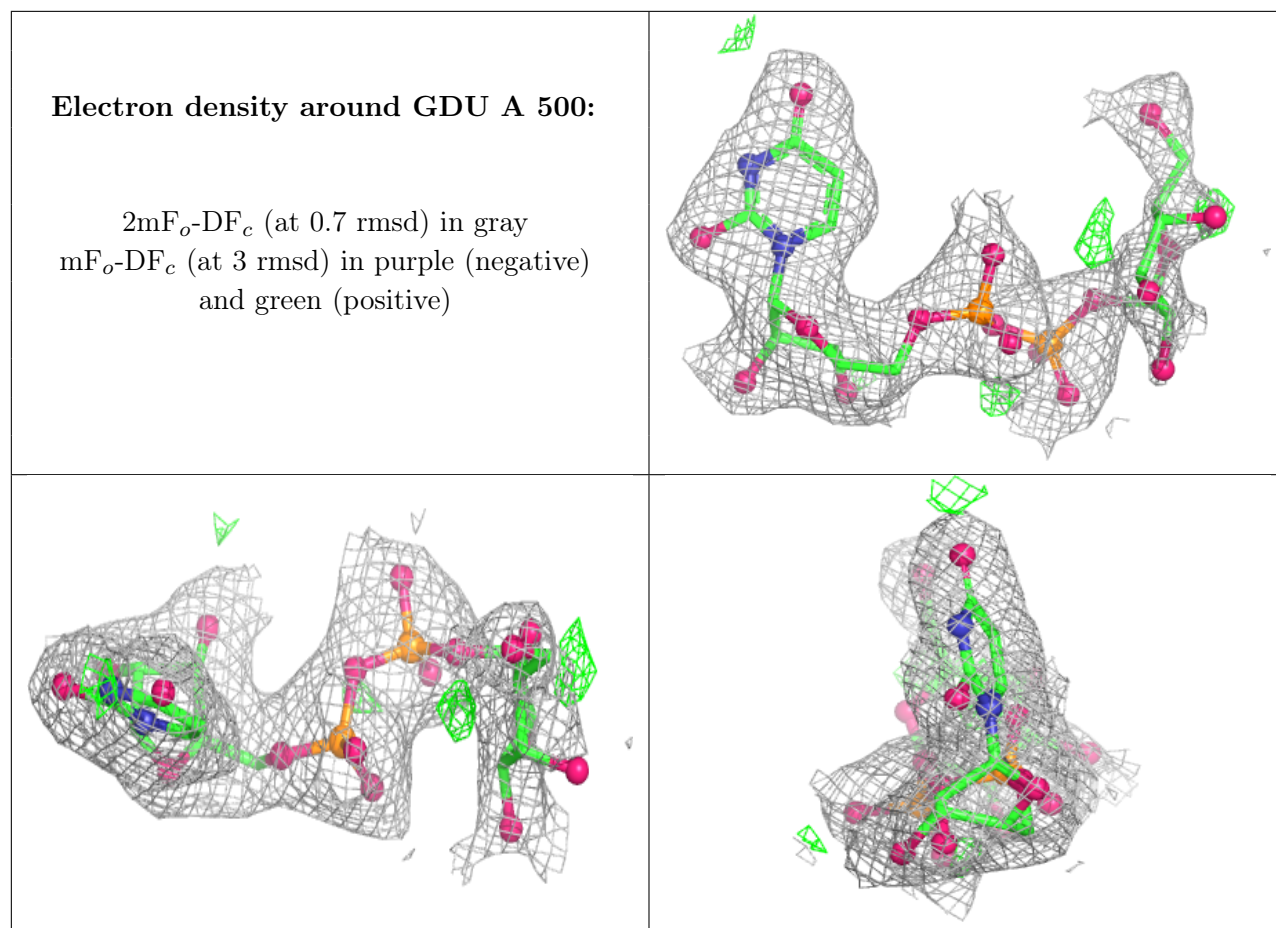
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around GDU G 500:

$2mF_o-DF_c$ (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.