



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 07:21 PM UTC

PDB ID : 3HDY / pdb_00003hdy
Title : Crystal Structure of UDP-galactopyranose mutase (reduced form) in complex with substrate
Authors : Partha, S.K.; van Straaten, K.E.; Sanders, D.A.R.
Deposited on : 2009-05-07
Resolution : 2.40 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

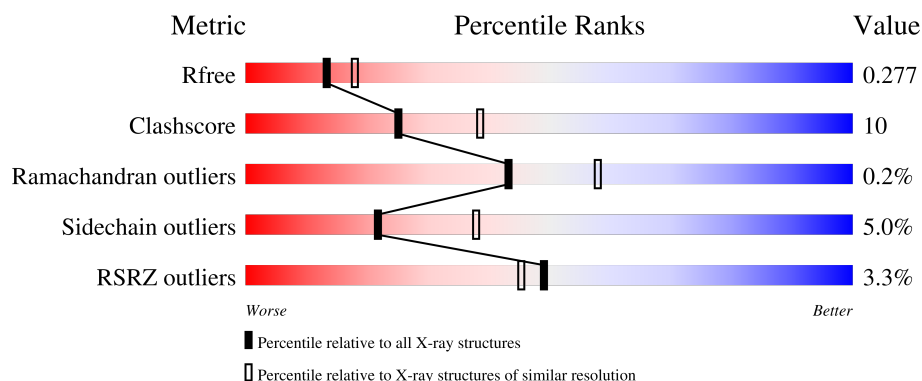
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	2% 70% 21% 8%
1	B	397	% 73% 16% 9%
1	C	397	14% 58% 26% 12%
1	D	397	4% 66% 23% 9%
1	E	397	2% 69% 20% 9%

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Mol	Chain	Length	Quality of chain
1	F	397	
1	G	397	
1	H	397	
1	I	397	
1	J	397	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	FDA	B	1385	X	-	-	-
4	FDA	D	1385	X	-	-	-
4	FDA	G	1385	X	-	-	-

2 Entry composition

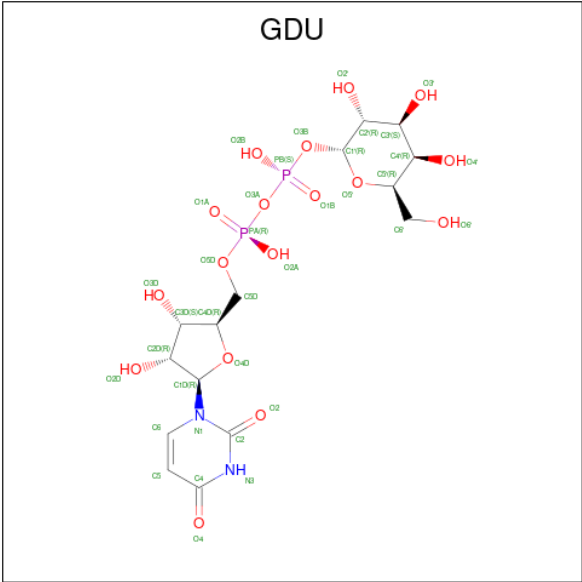
There are 5 unique types of molecules in this entry. The entry contains 30890 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

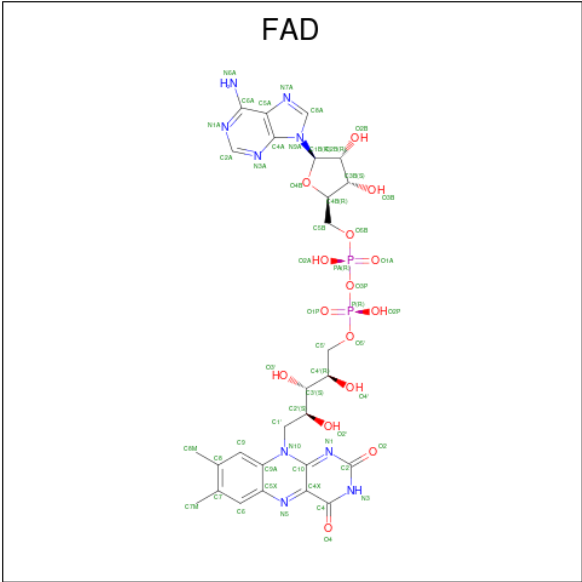
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	365	Total	C	N	O	S	0	0	0
			2984	1904	518	554	8			
1	B	361	Total	C	N	O	S	0	0	0
			2951	1885	512	546	8			
1	C	349	Total	C	N	O	S	12	0	0
			2850	1820	493	529	8			
1	D	361	Total	C	N	O	S	9	0	0
			2951	1885	512	546	8			
1	E	361	Total	C	N	O	S	12	0	0
			2951	1885	512	546	8			
1	F	362	Total	C	N	O	S	19	0	0
			2960	1891	514	547	8			
1	G	360	Total	C	N	O	S	0	0	0
			2947	1883	511	545	8			
1	H	361	Total	C	N	O	S	0	0	0
			2956	1889	513	546	8			
1	I	361	Total	C	N	O	S	1	0	0
			2951	1885	512	546	8			
1	J	359	Total	C	N	O	S	1	0	0
			2943	1881	510	544	8			

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



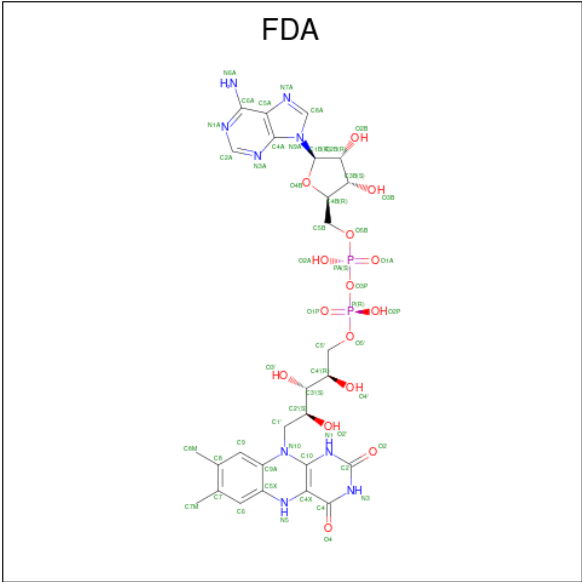
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	B	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	C	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	D	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	E	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	F	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	G	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	C	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	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 DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (CCD ID: FDA) (formula: C₂₇H₃₅N₉O₁₅P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
4	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
4	G	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	70	Total	O	0	0
			70	70		
5	B	51	Total	O	0	0
			51	51		
5	C	41	Total	O	0	0
			41	41		
5	D	48	Total	O	0	0
			48	48		
5	E	44	Total	O	0	0
			44	44		
5	F	60	Total	O	0	0
			60	60		
5	G	47	Total	O	0	0
			47	47		
5	H	75	Total	O	0	0
			75	75		
5	I	53	Total	O	0	0
			53	53		

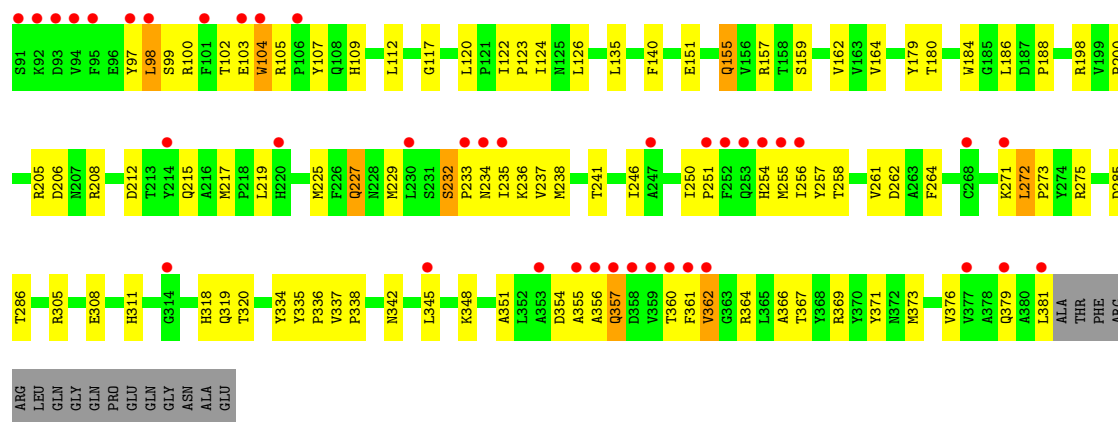
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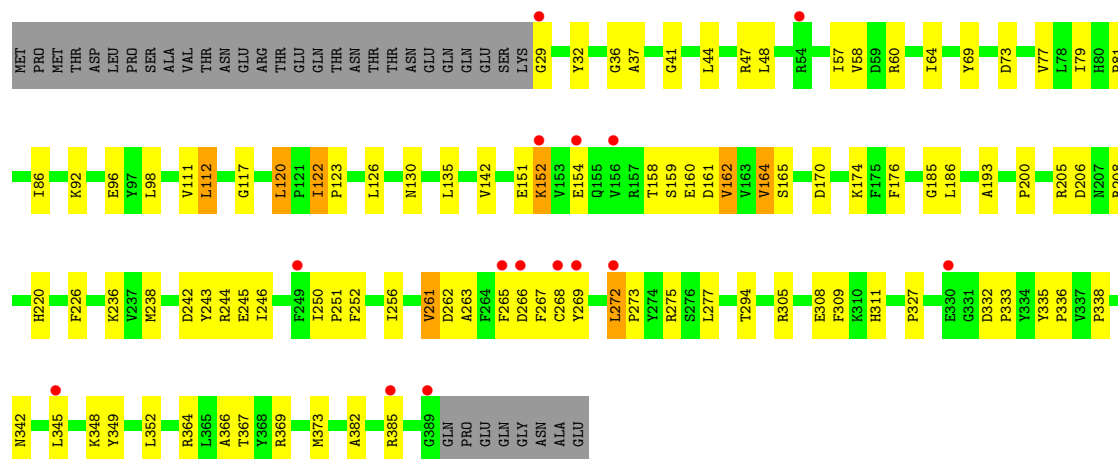
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	J	67	Total	O	0	0
			67	67		

- Molecule 1: UDP-galactopyranose mutase

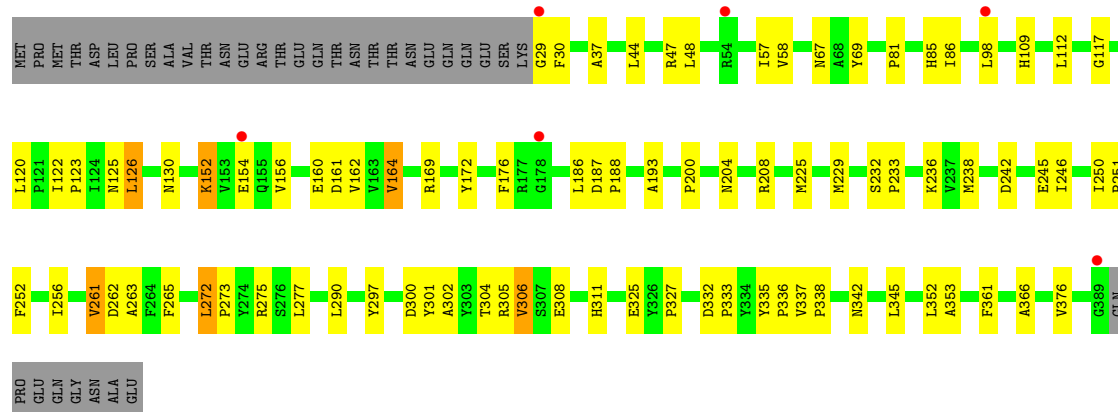




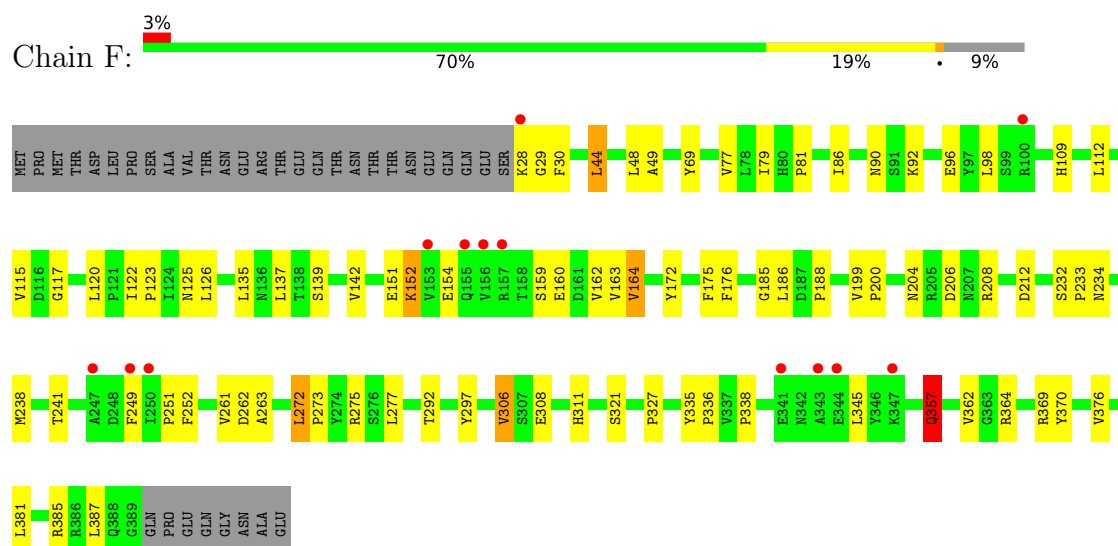
• Molecule 1: UDP-galactopyranose mutase



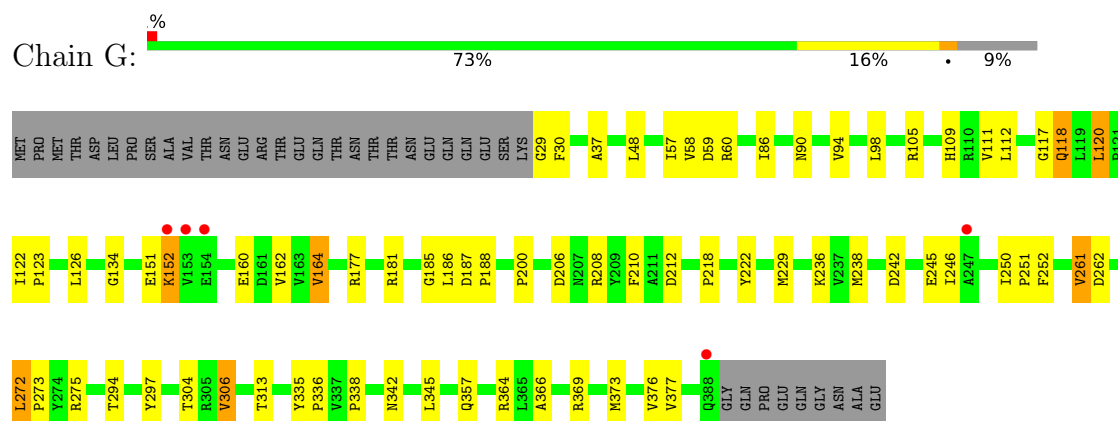
• Molecule 1: UDP-galactopyranose mutase



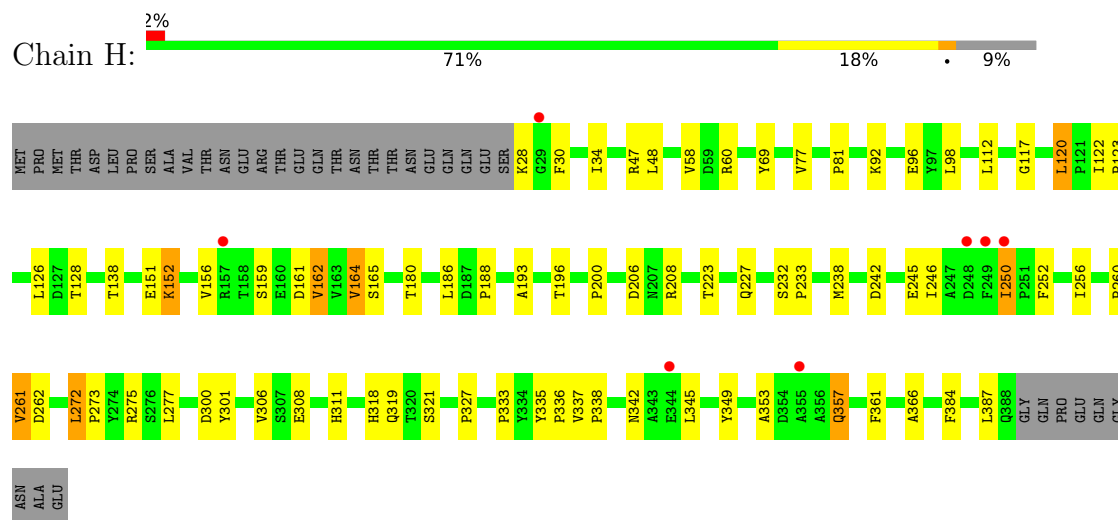
• Molecule 1: UDP-galactopyranose mutase



- Molecule 1: UDP-galactopyranose mutase

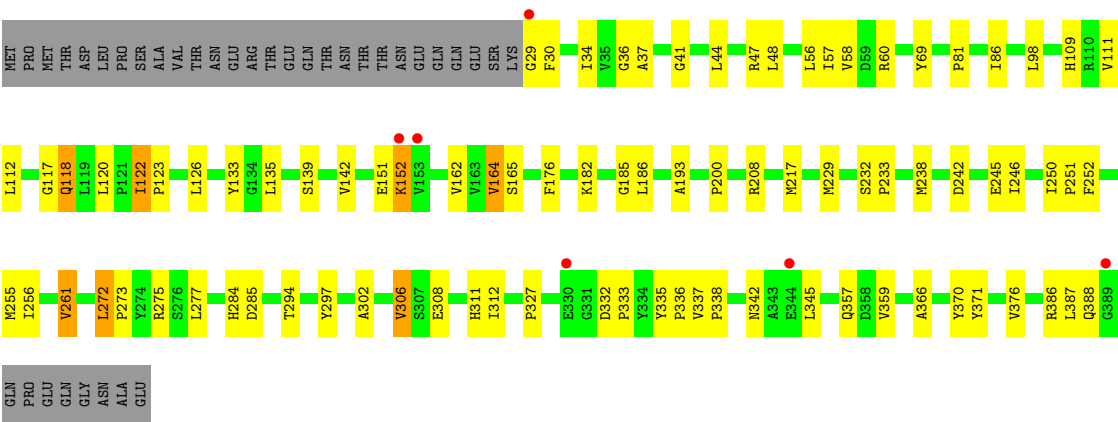


- Molecule 1: UDP-galactopyranose mutase

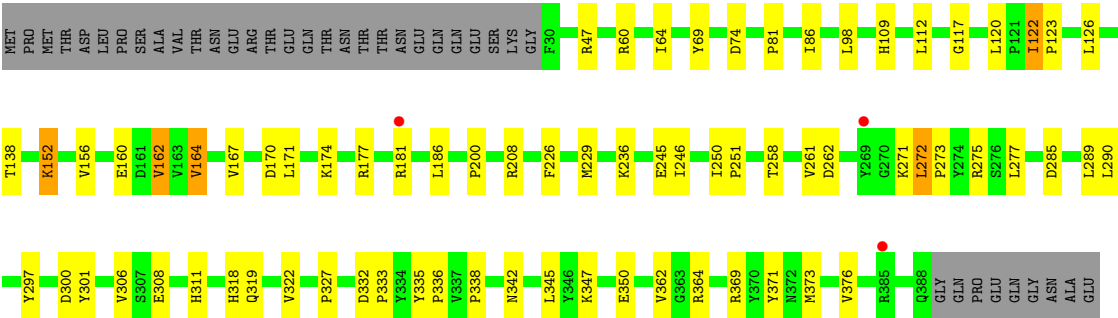


- Molecule 1: UDP-galactopyranose mutase





● Molecule 1: UDP-galactopyranose mutase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	132.82Å 174.63Å 218.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.94 – 2.40 39.94 – 2.40	Depositor EDS
% Data completeness (in resolution range)	95.8 (39.94-2.40) 95.7 (39.94-2.40)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	0.19	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.74 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.235 , 0.280 0.236 , 0.277	Depositor DCC
R_{free} test set	9506 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	43.8	Xtriage
Anisotropy	0.198	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	30890	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.22% 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: FDA, 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	0.33	0/3068	0.71	0/4171
1	B	0.37	0/3035	0.73	2/4128 (0.0%)
1	C	0.55	2/2931 (0.1%)	0.84	8/3989 (0.2%)
1	D	0.35	1/3035 (0.0%)	0.72	0/4128
1	E	0.35	1/3035 (0.0%)	0.71	0/4128
1	F	0.33	0/3044	0.73	0/4139
1	G	0.35	0/3031	0.72	0/4123
1	H	0.33	0/3040	0.73	2/4134 (0.0%)
1	I	0.31	0/3035	0.73	0/4128
1	J	0.35	2/3027 (0.1%)	0.73	2/4118 (0.0%)
All	All	0.37	6/30281 (0.0%)	0.74	14/41186 (0.0%)

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

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

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	301	TYR	C-N	-7.89	1.21	1.33
1	J	300	ASP	C-N	-6.94	1.24	1.33
1	C	57	ILE	CA-CB	-6.67	1.46	1.54
1	D	263	ALA	C-N	-6.64	1.24	1.33
1	E	302	ALA	CA-CB	-5.30	1.44	1.53

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	104	TRP	N-CA-C	9.56	122.66	110.33
1	C	105	ARG	CA-C-N	8.66	129.20	119.93
1	C	105	ARG	C-N-CA	8.66	129.20	119.93
1	C	55	VAL	N-CA-C	7.27	119.30	108.46
1	C	357	GLN	N-CA-C	6.88	121.95	112.04

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	50	SER	Peptide

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	2984	0	2854	57	0
1	B	2951	0	2822	54	0
1	C	2850	0	2728	104	0
1	D	2951	0	2822	69	0
1	E	2951	0	2822	48	0
1	F	2960	0	2835	58	0
1	G	2947	0	2819	48	0
1	H	2956	0	2832	51	0
1	I	2951	0	2822	51	0
1	J	2943	0	2816	46	0
2	A	36	0	22	4	0
2	B	36	0	22	4	0
2	C	36	0	22	6	0
2	D	36	0	22	6	0
2	E	36	0	22	2	0
2	F	36	0	22	3	0
2	G	36	0	22	2	0
2	H	36	0	22	1	0
2	I	36	0	22	1	0
2	J	36	0	22	0	0
3	A	53	0	31	3	0
3	C	53	0	31	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	53	0	31	2	0
3	F	53	0	31	4	0
3	H	53	0	31	2	0
3	I	53	0	31	3	0
3	J	53	0	31	3	0
4	B	53	0	28	2	0
4	D	53	0	29	5	0
4	G	53	0	28	6	0
5	A	70	0	0	1	0
5	B	51	0	0	0	0
5	C	41	0	0	3	0
5	D	48	0	0	2	0
5	E	44	0	0	0	0
5	F	60	0	0	0	0
5	G	47	0	0	1	0
5	H	75	0	0	0	0
5	I	53	0	0	1	0
5	J	67	0	0	0	0
All	All	30890	0	28694	572	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 10.

The worst 5 of 572 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:F:152:LYS:HE2	1:F:152:LYS:HA	1.48	0.96
1:J:152:LYS:HE2	1:J:152:LYS:HA	1.50	0.91
1:I:152:LYS:HE2	1:I:152:LYS:HA	1.52	0.91
1:D:152:LYS:HE2	1:D:152:LYS:HA	1.51	0.89
1:B:152:LYS:HA	1:B:152:LYS:HE2	1.55	0.88

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	363/397 (91%)	347 (96%)	16 (4%)	0	100	100
1	B	359/397 (90%)	347 (97%)	12 (3%)	0	100	100
1	C	347/397 (87%)	314 (90%)	30 (9%)	3 (1%)	14	22
1	D	359/397 (90%)	342 (95%)	17 (5%)	0	100	100
1	E	359/397 (90%)	347 (97%)	12 (3%)	0	100	100
1	F	360/397 (91%)	343 (95%)	15 (4%)	2 (1%)	21	32
1	G	358/397 (90%)	342 (96%)	16 (4%)	0	100	100
1	H	359/397 (90%)	347 (97%)	12 (3%)	0	100	100
1	I	359/397 (90%)	343 (96%)	15 (4%)	1 (0%)	36	50
1	J	357/397 (90%)	341 (96%)	16 (4%)	0	100	100
All	All	3580/3970 (90%)	3413 (95%)	161 (4%)	6 (0%)	43	58

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	51	SER
1	C	233	PRO
1	F	357	GLN
1	F	370	TYR
1	I	370	TYR

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	317/346 (92%)	302 (95%)	15 (5%)	23	41
1	B	313/346 (90%)	299 (96%)	14 (4%)	24	42
1	C	304/346 (88%)	283 (93%)	21 (7%)	14	24
1	D	313/346 (90%)	299 (96%)	14 (4%)	24	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	313/346 (90%)	299 (96%)	14 (4%)	24	42
1	F	314/346 (91%)	295 (94%)	19 (6%)	17	30
1	G	313/346 (90%)	298 (95%)	15 (5%)	23	40
1	H	314/346 (91%)	299 (95%)	15 (5%)	23	40
1	I	313/346 (90%)	297 (95%)	16 (5%)	21	37
1	J	313/346 (90%)	301 (96%)	12 (4%)	29	49
All	All	3127/3460 (90%)	2972 (95%)	155 (5%)	22	38

5 of 155 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	120	LEU
1	J	98	LEU
1	H	164	VAL
1	I	118	GLN
1	J	164	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	227	GLN
1	J	53	GLN
1	H	357	GLN
1	I	311	HIS
1	J	284	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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	E	450	-	58,58,58	1.23	5 (8%)	85,89,89	1.61	13 (15%)
2	GDU	J	500	-	37,38,38	2.67	4 (10%)	55,58,58	3.56	16 (29%)
3	FAD	H	450	-	58,58,58	1.23	5 (8%)	85,89,89	1.60	12 (14%)
2	GDU	B	500	-	37,38,38	2.64	4 (10%)	55,58,58	3.61	20 (36%)
3	FAD	F	450	-	58,58,58	1.23	5 (8%)	85,89,89	1.60	12 (14%)
2	GDU	H	500	-	37,38,38	2.67	4 (10%)	55,58,58	3.54	18 (32%)
2	GDU	C	500	-	37,38,38	2.66	4 (10%)	55,58,58	3.65	19 (34%)
3	FAD	C	450	-	58,58,58	1.23	5 (8%)	85,89,89	1.61	13 (15%)
4	FDA	B	1385	-	57,58,58	2.79	28 (49%)	78,89,89	2.60	30 (38%)
2	GDU	F	500	-	37,38,38	2.66	4 (10%)	55,58,58	3.58	17 (30%)
2	GDU	G	500	-	37,38,38	2.68	4 (10%)	55,58,58	3.58	18 (32%)
3	FAD	J	450	-	58,58,58	1.23	5 (8%)	85,89,89	1.60	12 (14%)
4	FDA	G	1385	-	57,58,58	2.80	27 (47%)	78,89,89	2.60	31 (39%)
2	GDU	E	500	-	37,38,38	2.66	4 (10%)	55,58,58	3.60	19 (34%)
3	FAD	A	450	-	58,58,58	1.23	5 (8%)	85,89,89	1.61	12 (14%)
2	GDU	D	500	-	37,38,38	2.66	4 (10%)	55,58,58	3.63	17 (30%)
2	GDU	I	500	-	37,38,38	2.67	4 (10%)	55,58,58	3.57	17 (30%)
4	FDA	D	1385	-	57,58,58	2.50	17 (29%)	78,89,89	2.47	28 (35%)
2	GDU	A	500	-	37,38,38	2.70	4 (10%)	55,58,58	3.60	21 (38%)
3	FAD	I	450	-	58,58,58	1.23	5 (8%)	85,89,89	1.61	12 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FAD	E	450	-	-	0/34/50/50	0/6/6/6
2	GDU	J	500	-	-	7/23/59/59	0/3/3/3
3	FAD	H	450	-	-	0/34/50/50	0/6/6/6
2	GDU	B	500	-	-	8/23/59/59	0/3/3/3
3	FAD	F	450	-	-	0/34/50/50	0/6/6/6
2	GDU	H	500	-	-	7/23/59/59	0/3/3/3
2	GDU	C	500	-	-	12/23/59/59	0/3/3/3
3	FAD	C	450	-	-	0/34/50/50	0/6/6/6
4	FDA	B	1385	-	2/2/9/9	2/34/50/50	0/6/6/6
2	GDU	F	500	-	-	8/23/59/59	0/3/3/3
2	GDU	G	500	-	-	9/23/59/59	0/3/3/3
3	FAD	J	450	-	-	0/34/50/50	0/6/6/6
4	FDA	G	1385	-	2/2/9/9	5/34/50/50	0/6/6/6
2	GDU	E	500	-	-	6/23/59/59	0/3/3/3
3	FAD	A	450	-	-	0/34/50/50	0/6/6/6
2	GDU	D	500	-	-	10/23/59/59	0/3/3/3
2	GDU	I	500	-	-	8/23/59/59	0/3/3/3
4	FDA	D	1385	-	4/4/9/9	5/34/50/50	0/6/6/6
2	GDU	A	500	-	-	4/23/59/59	0/3/3/3
3	FAD	I	450	-	-	0/34/50/50	0/6/6/6

The worst 5 of 147 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	500	GDU	O2-C2	11.58	1.43	1.23
2	F	500	GDU	O2-C2	11.57	1.43	1.23
2	H	500	GDU	O2-C2	11.56	1.43	1.23
2	A	500	GDU	O2-C2	11.53	1.43	1.23
2	B	500	GDU	O2-C2	11.53	1.43	1.23

The worst 5 of 357 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	GDU	N3-C2-N1	16.64	136.55	114.89
2	J	500	GDU	N3-C2-N1	16.35	136.18	114.89
2	I	500	GDU	N3-C2-N1	16.27	136.07	114.89
2	B	500	GDU	N3-C2-N1	16.26	136.05	114.89
2	C	500	GDU	N3-C2-N1	16.25	136.03	114.89

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	B	1385	FDA	C1B
4	B	1385	FDA	C2B
4	D	1385	FDA	C3B
4	D	1385	FDA	C2B
4	D	1385	FDA	C4B

5 of 91 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	GDU	O5'-C1'-O3B-PB
2	B	500	GDU	C1'-O3B-PB-O3A
2	B	500	GDU	C1'-O3B-PB-O2B
2	B	500	GDU	O5'-C1'-O3B-PB
2	C	500	GDU	O4D-C4D-C5D-O5D

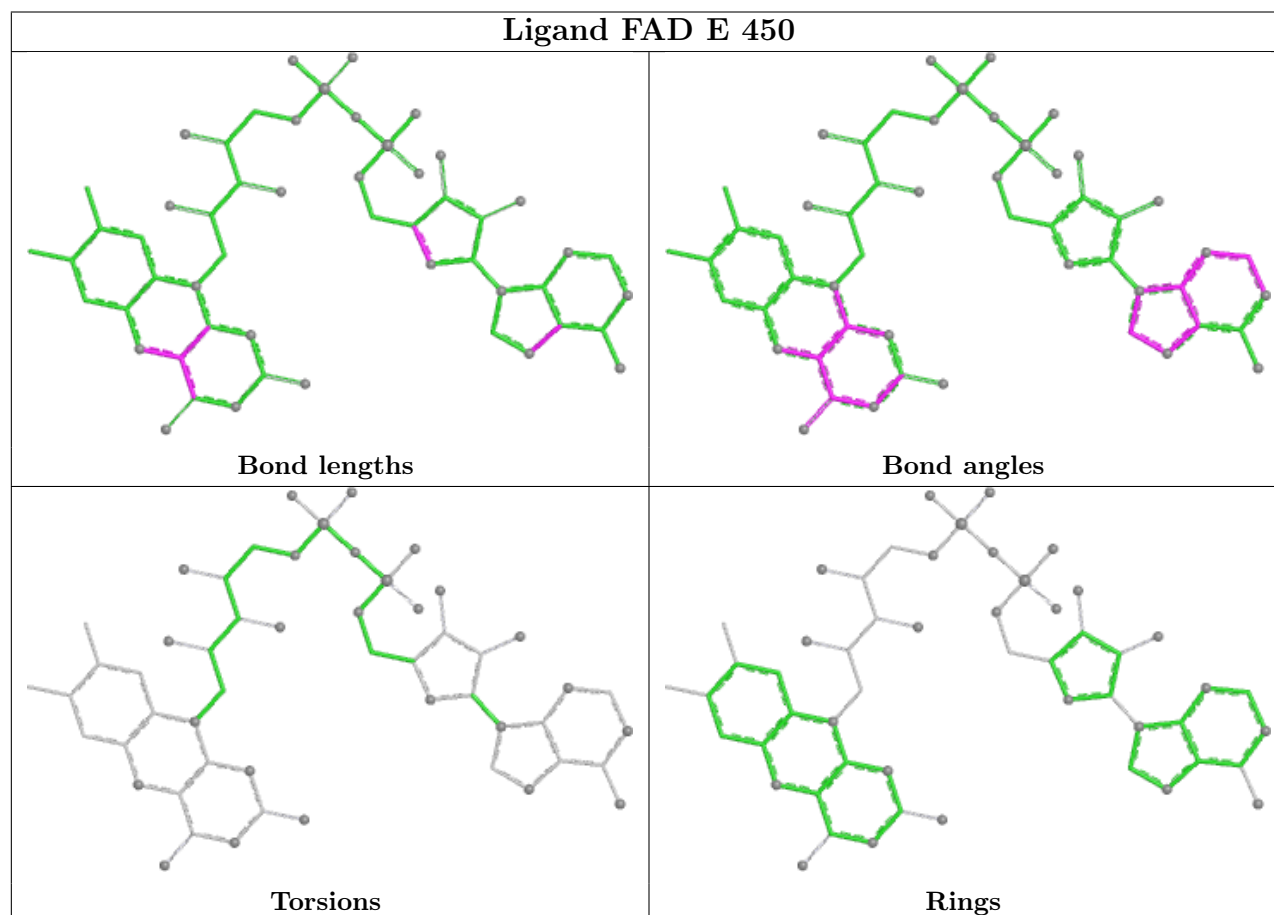
There are no ring outliers.

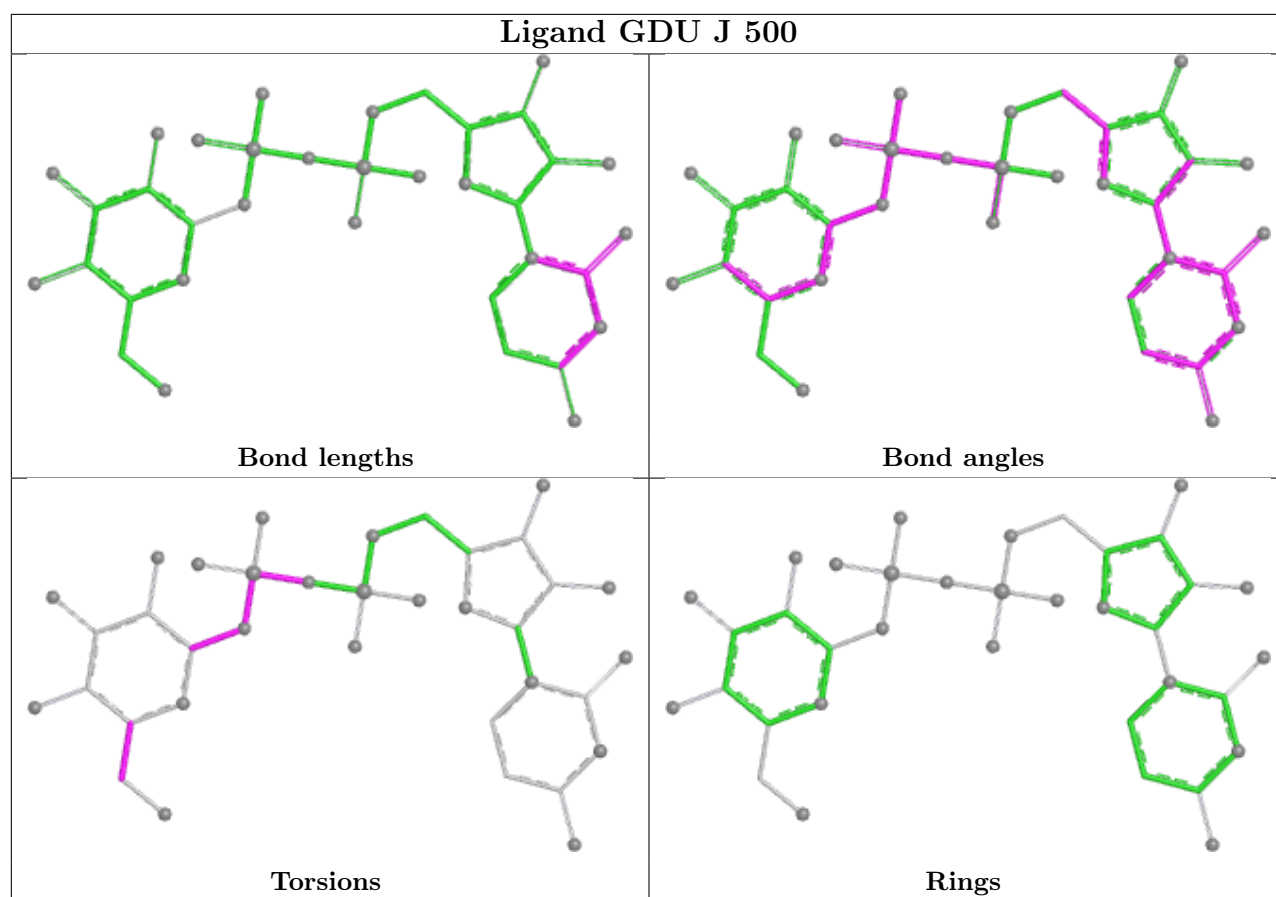
19 monomers are involved in 53 short contacts:

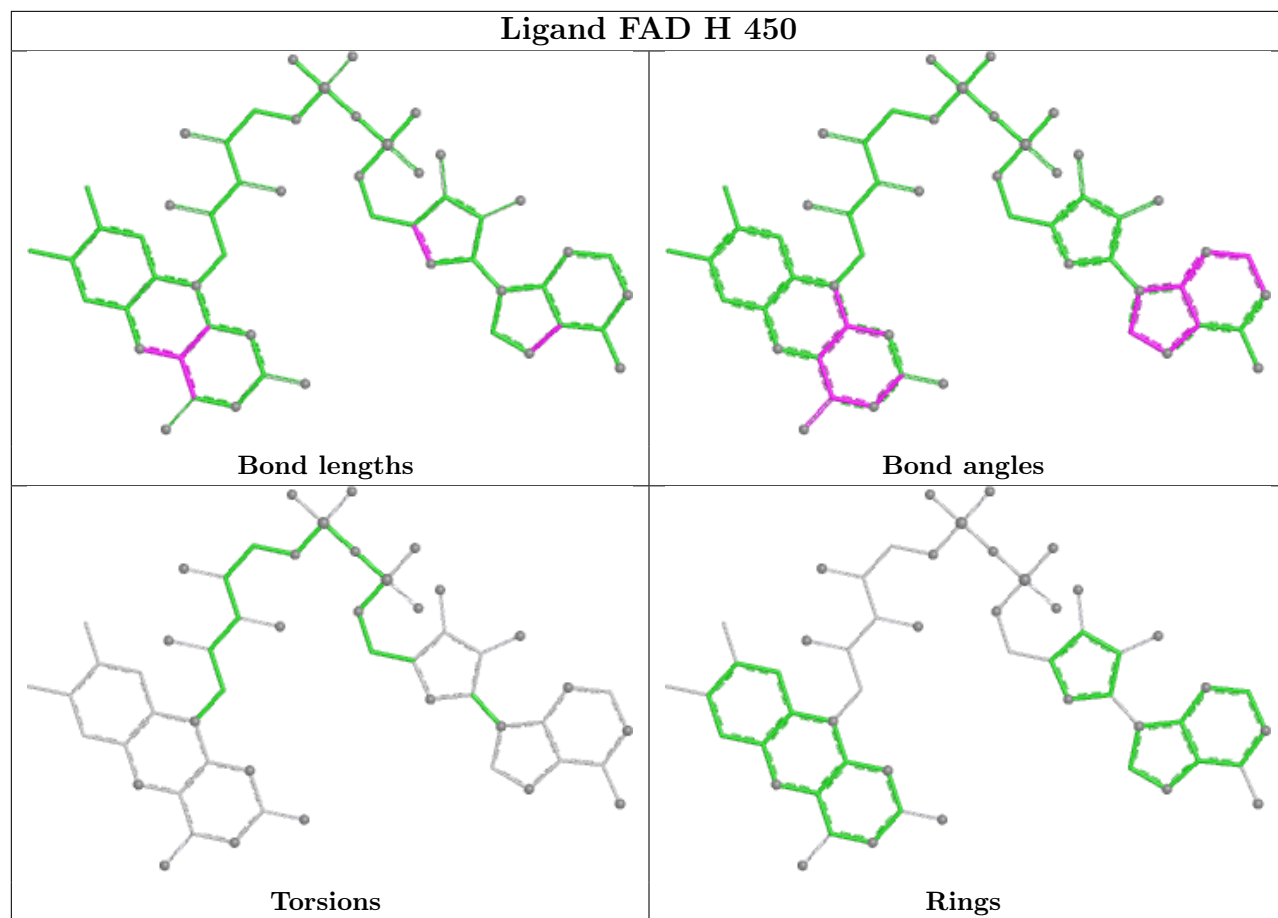
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	450	FAD	2	0
3	H	450	FAD	2	0
2	B	500	GDU	4	0
3	F	450	FAD	4	0
2	H	500	GDU	1	0
2	C	500	GDU	6	0
3	C	450	FAD	6	0
4	B	1385	FDA	2	0
2	F	500	GDU	3	0
2	G	500	GDU	2	0
3	J	450	FAD	3	0
4	G	1385	FDA	6	0
2	E	500	GDU	2	0
3	A	450	FAD	3	0
2	D	500	GDU	6	0
2	I	500	GDU	1	0
4	D	1385	FDA	5	0
2	A	500	GDU	4	0
3	I	450	FAD	3	0

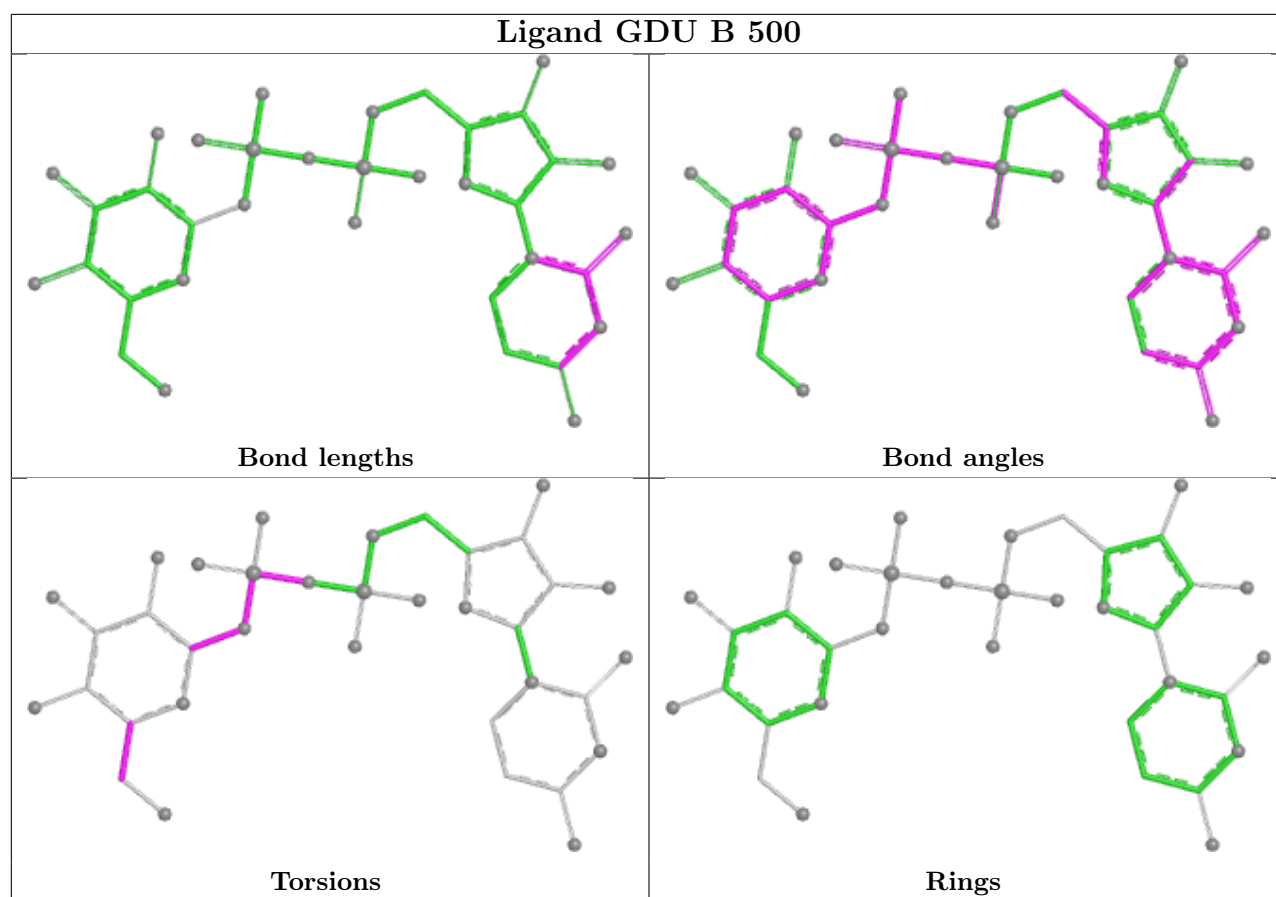
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

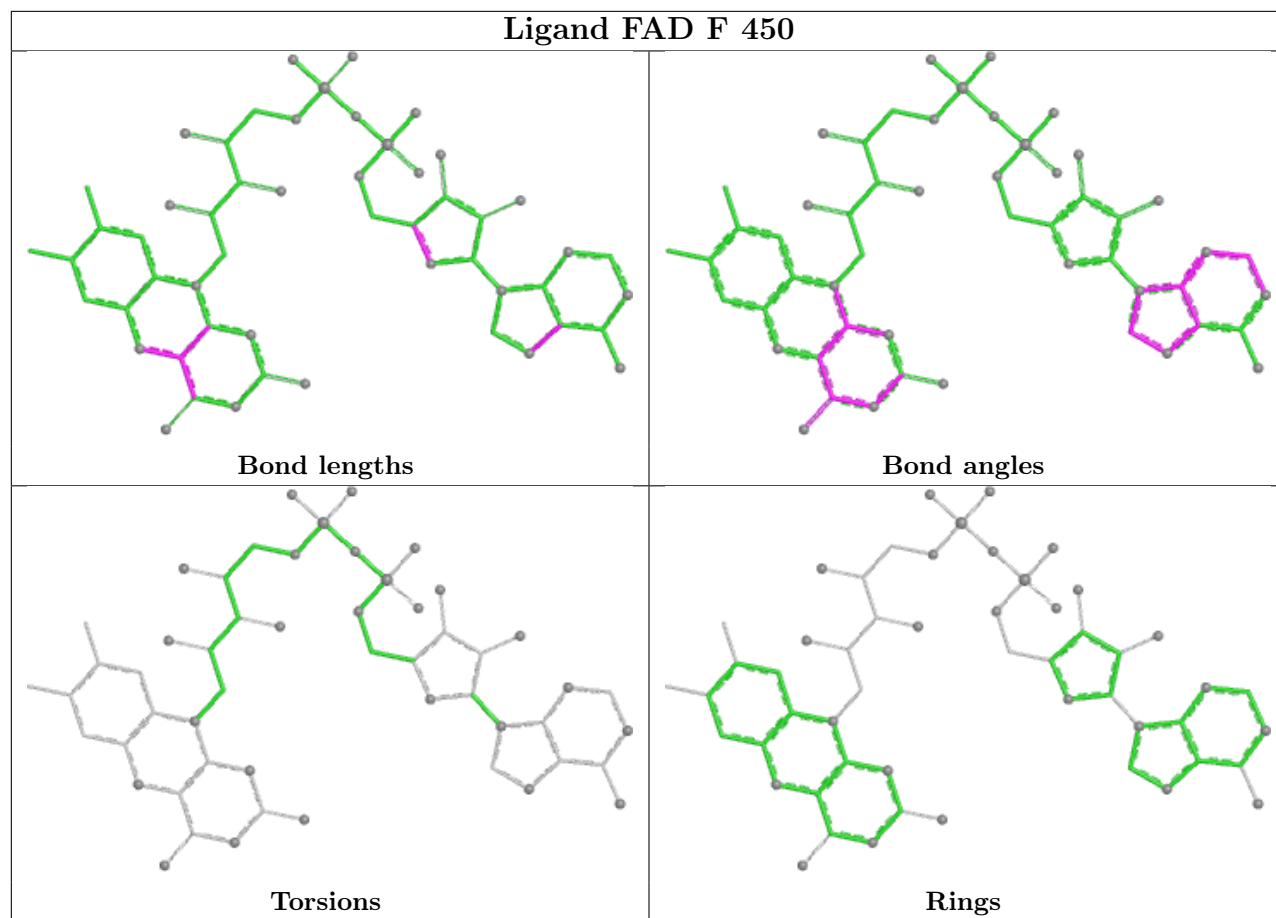
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question 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.

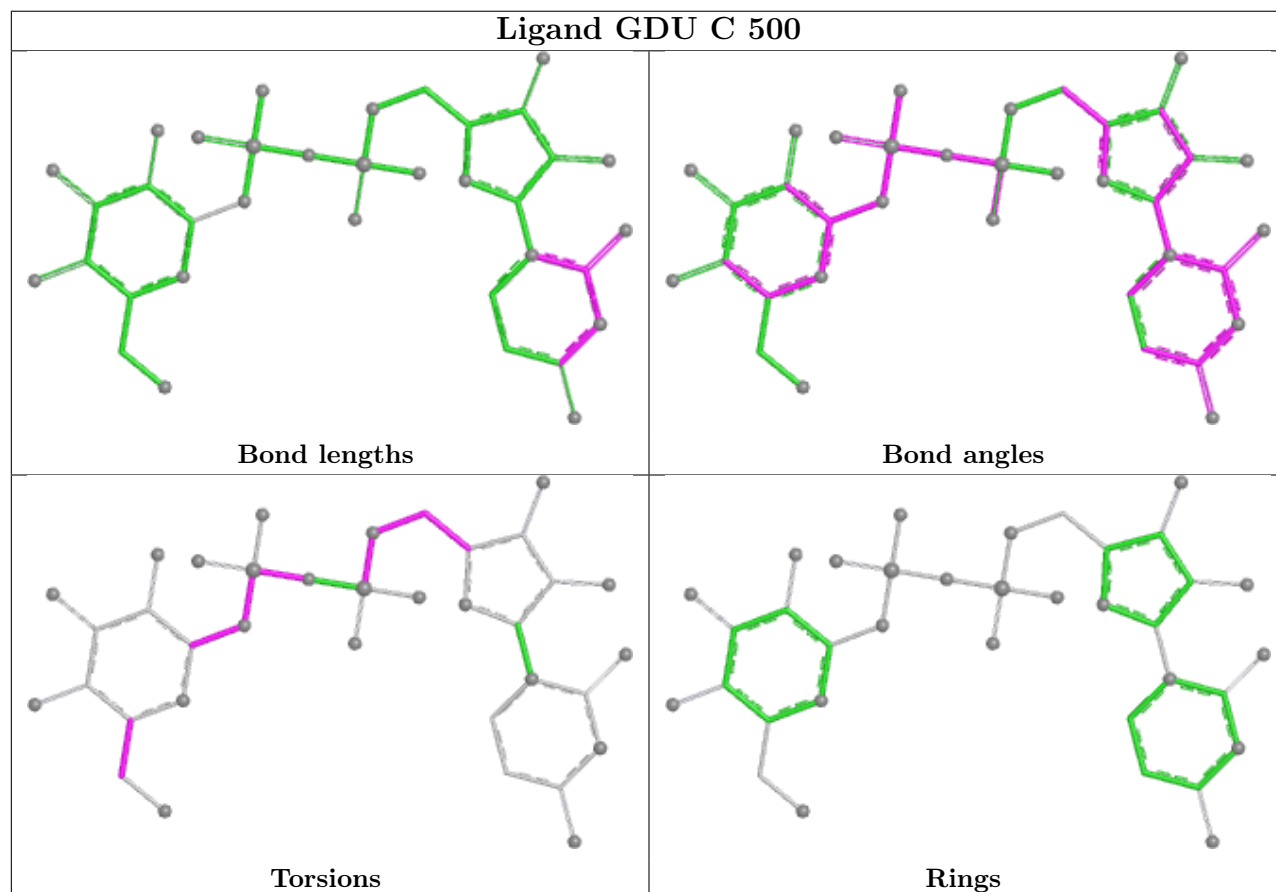
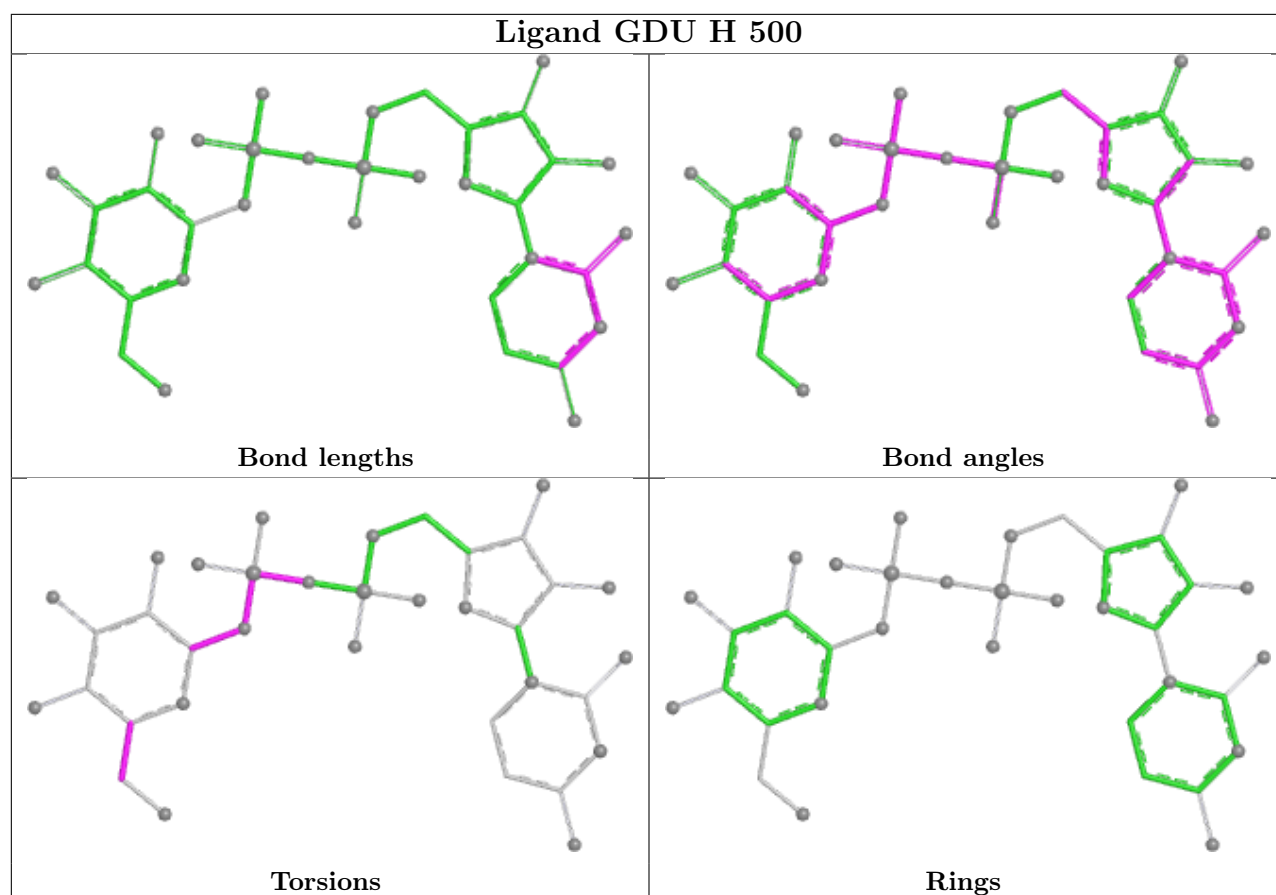


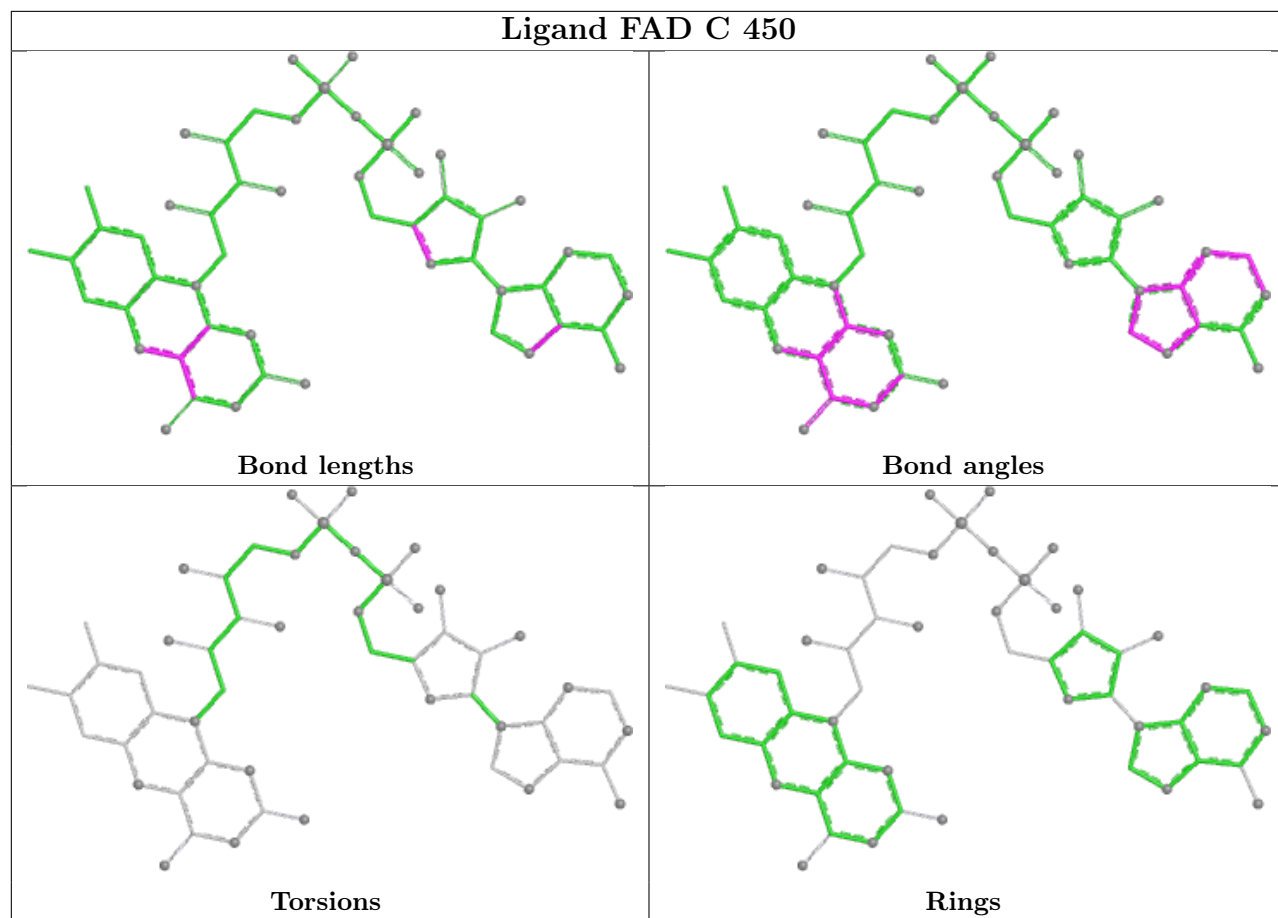


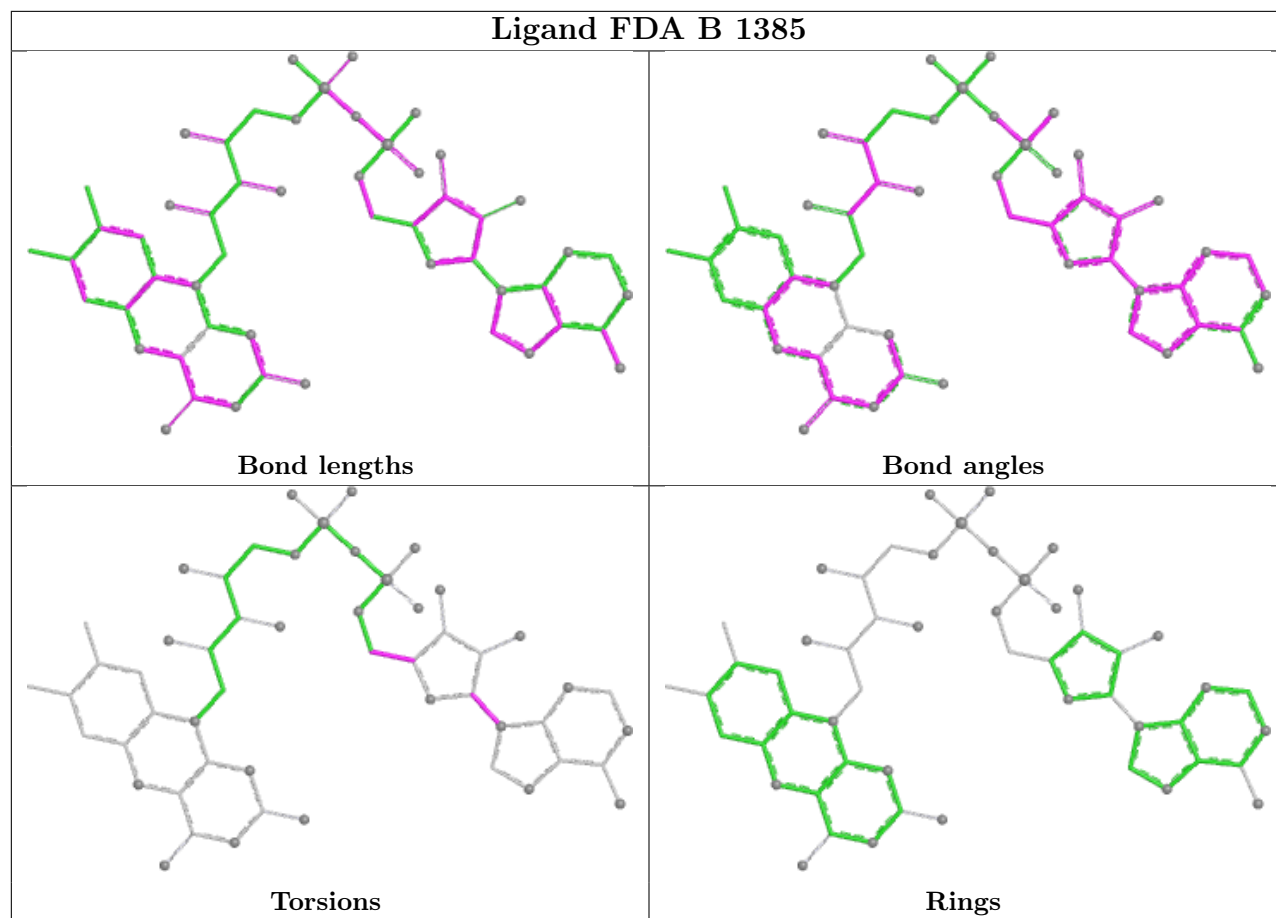


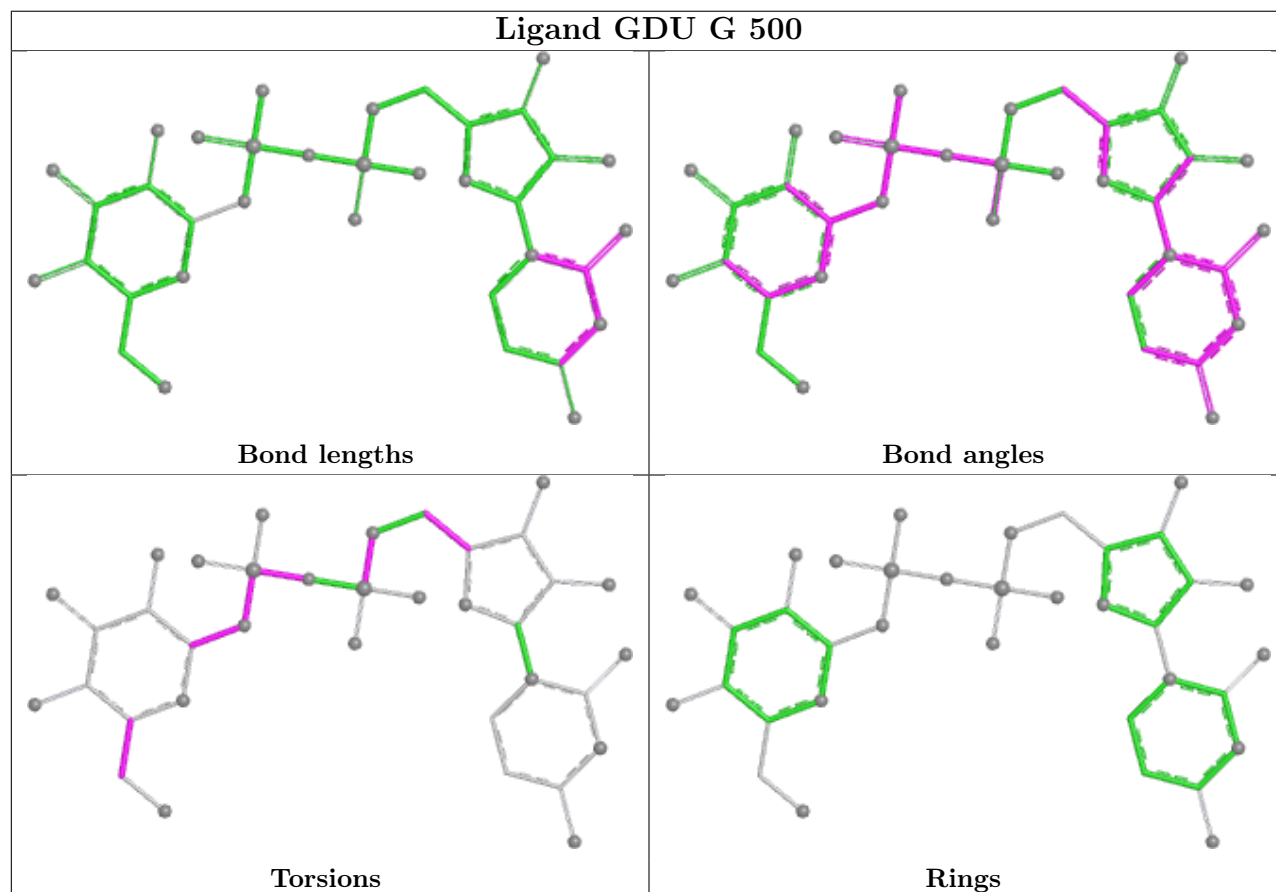
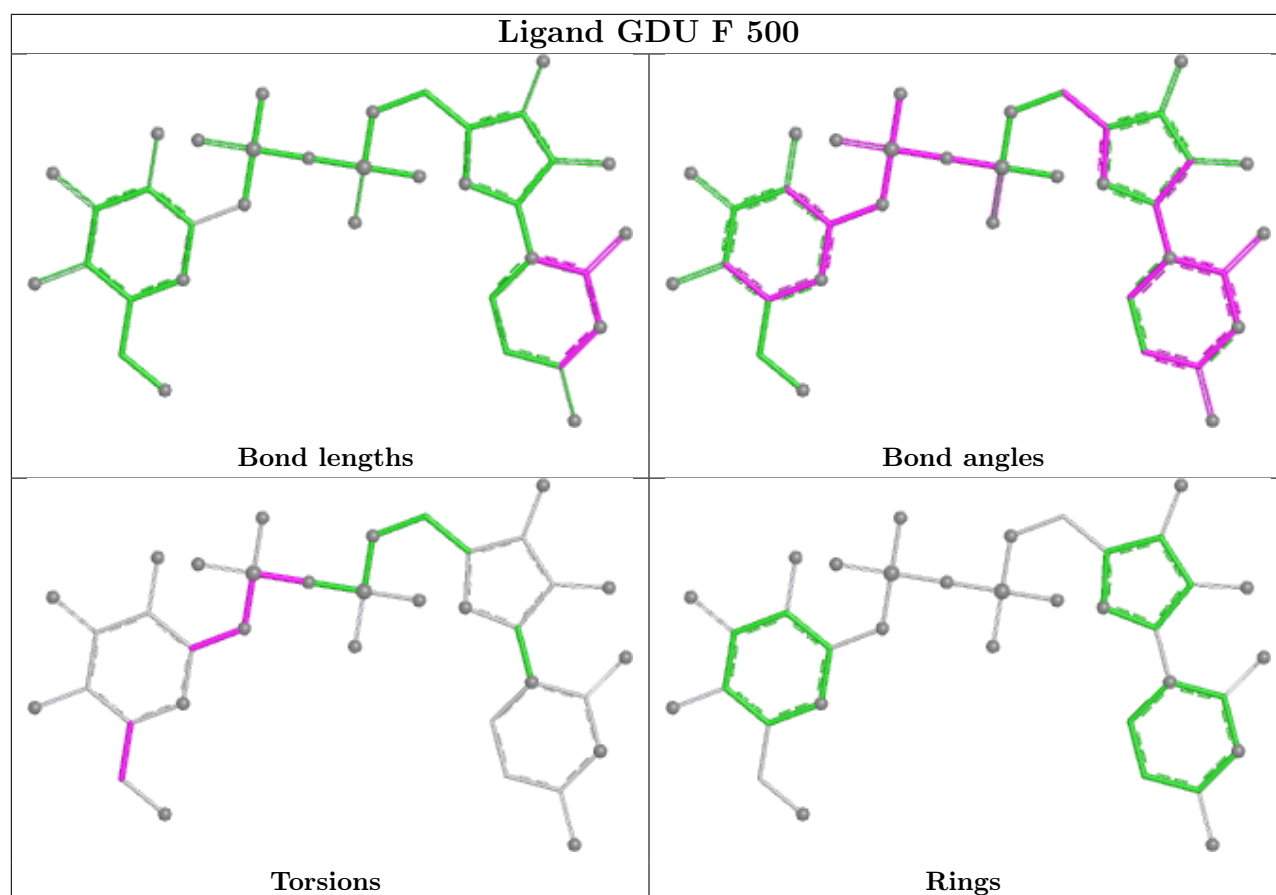


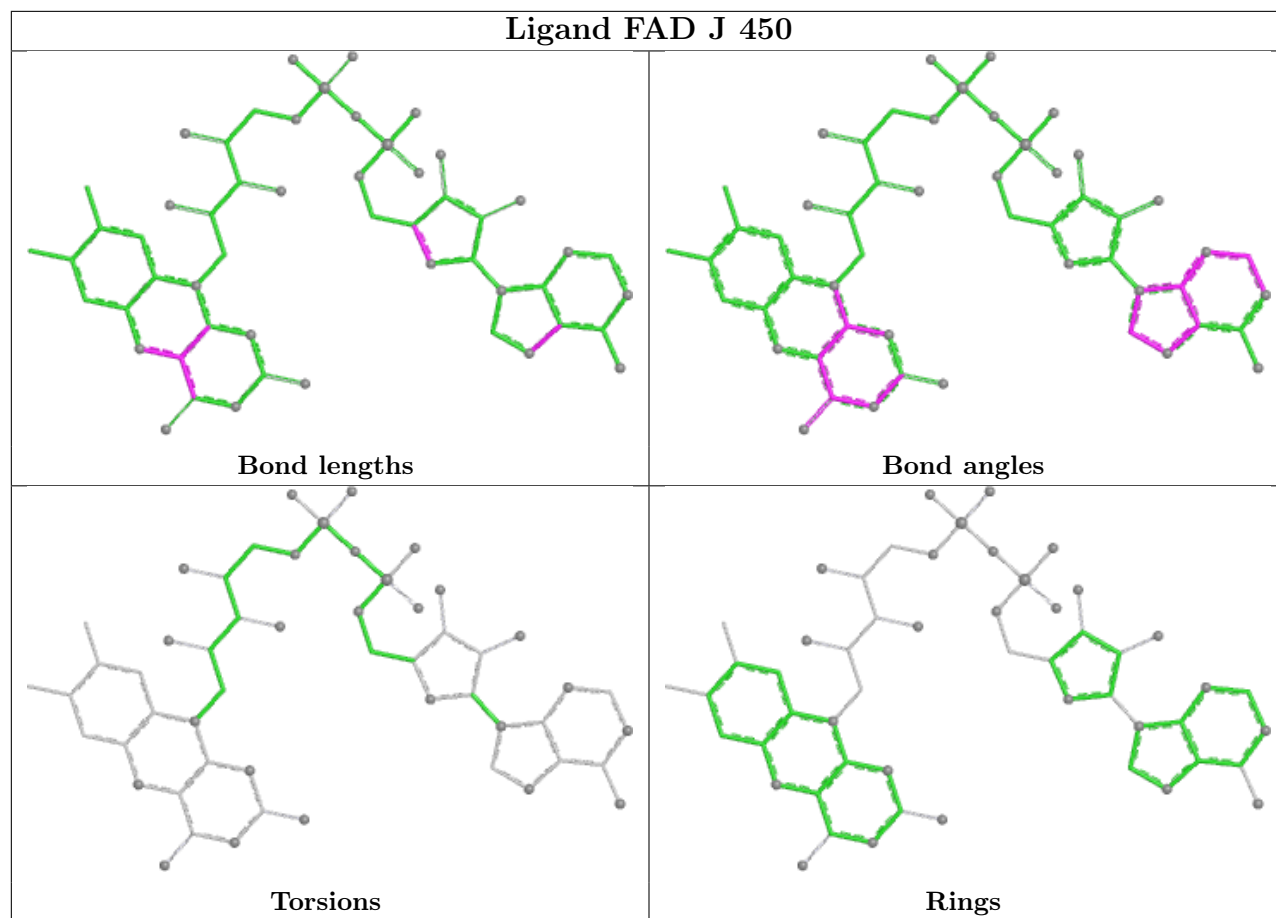


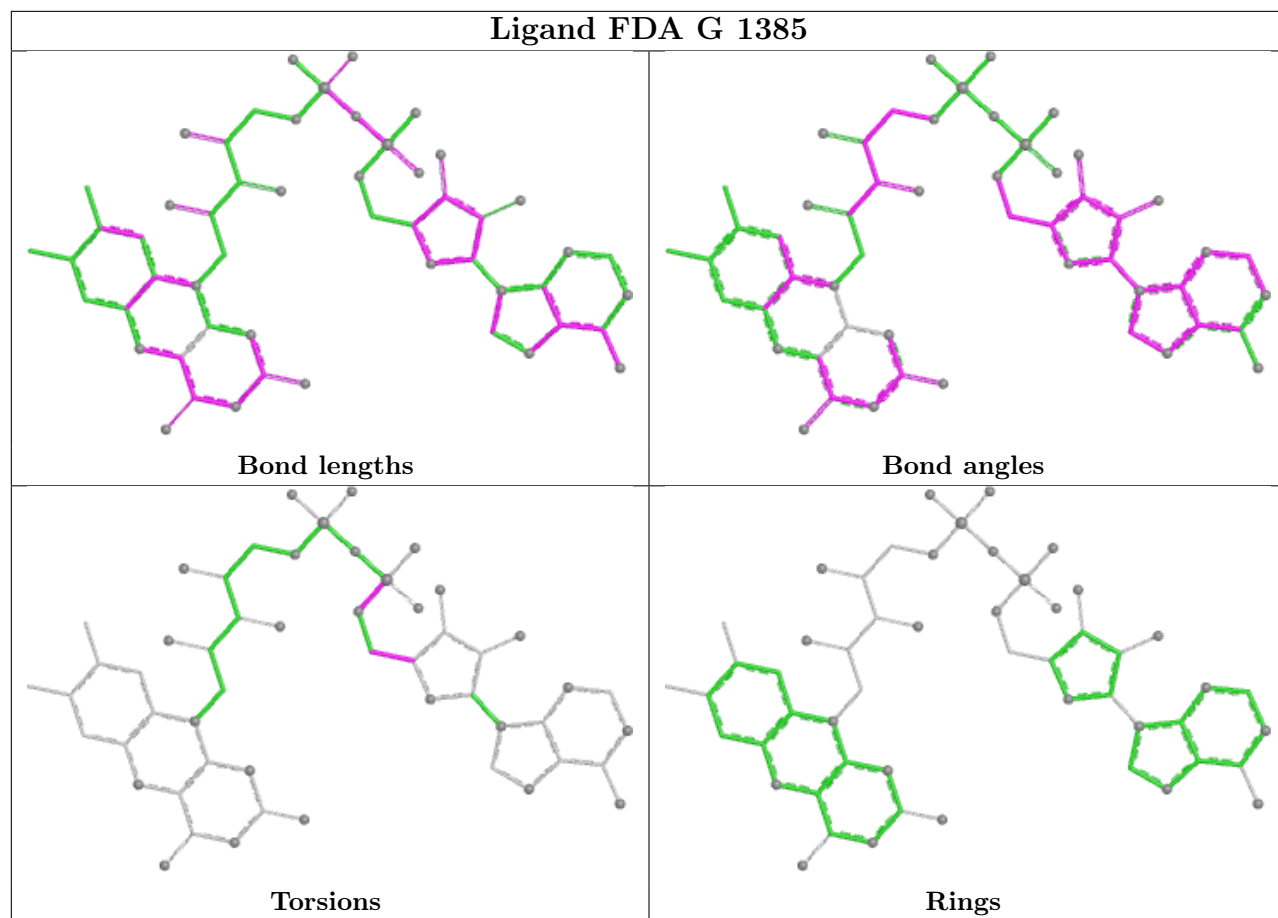


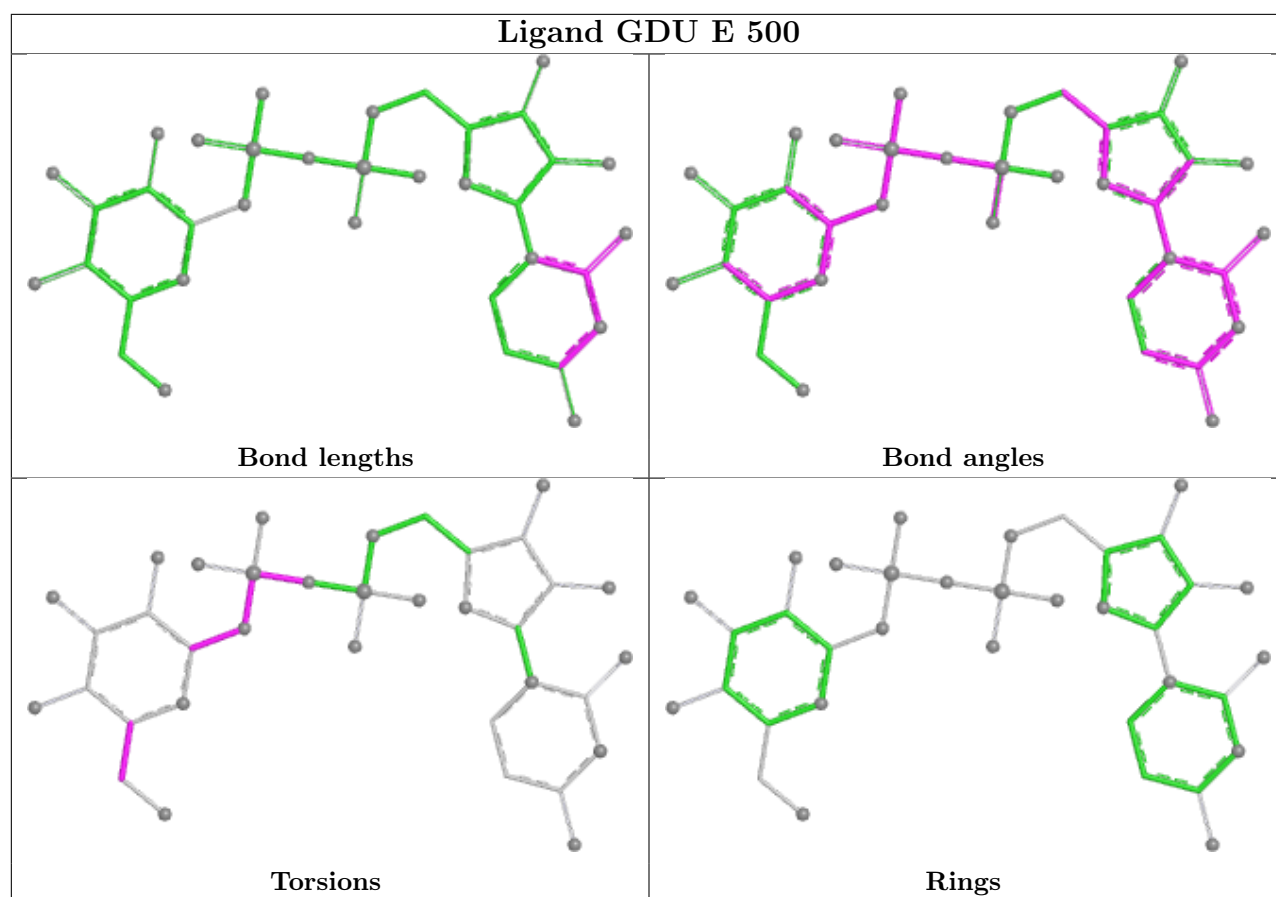


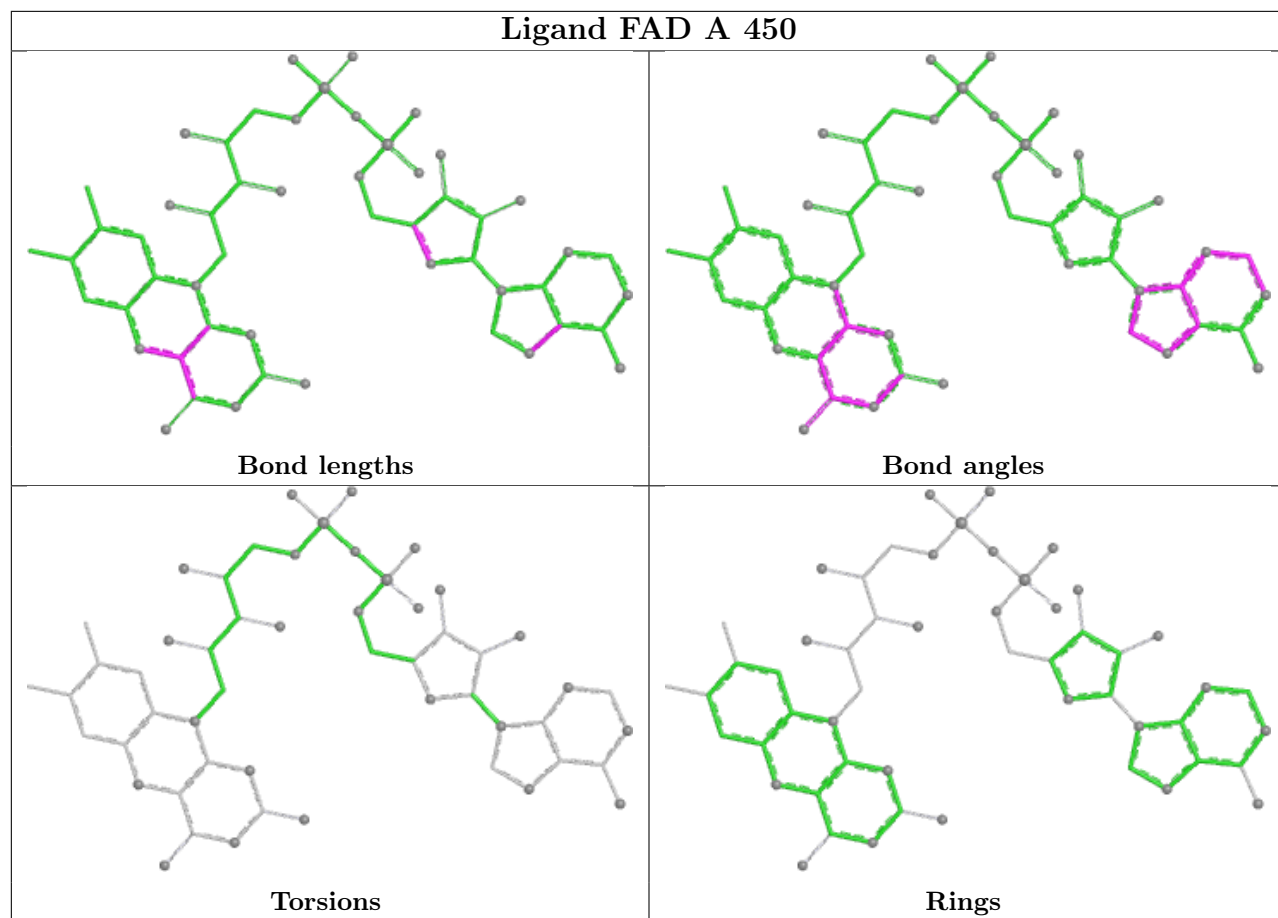


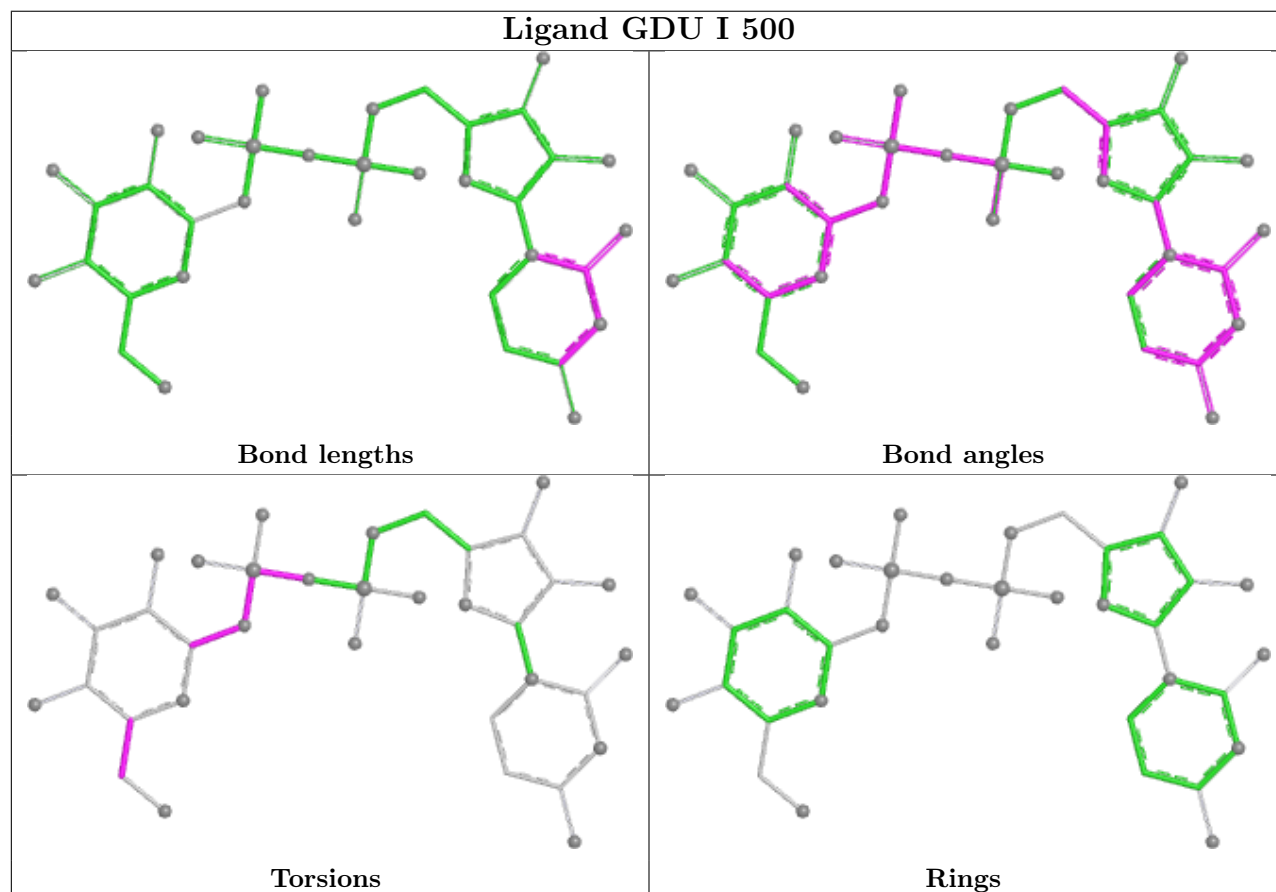
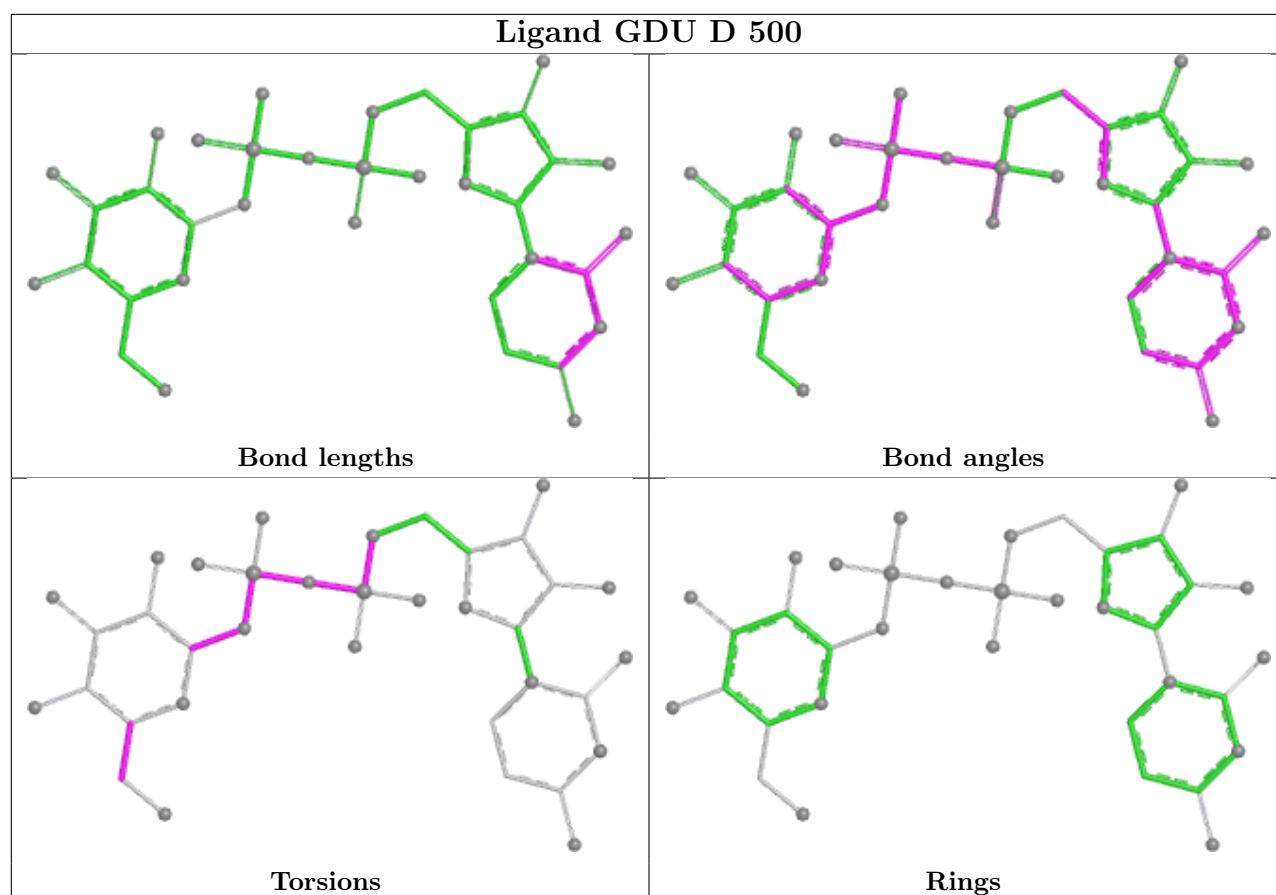


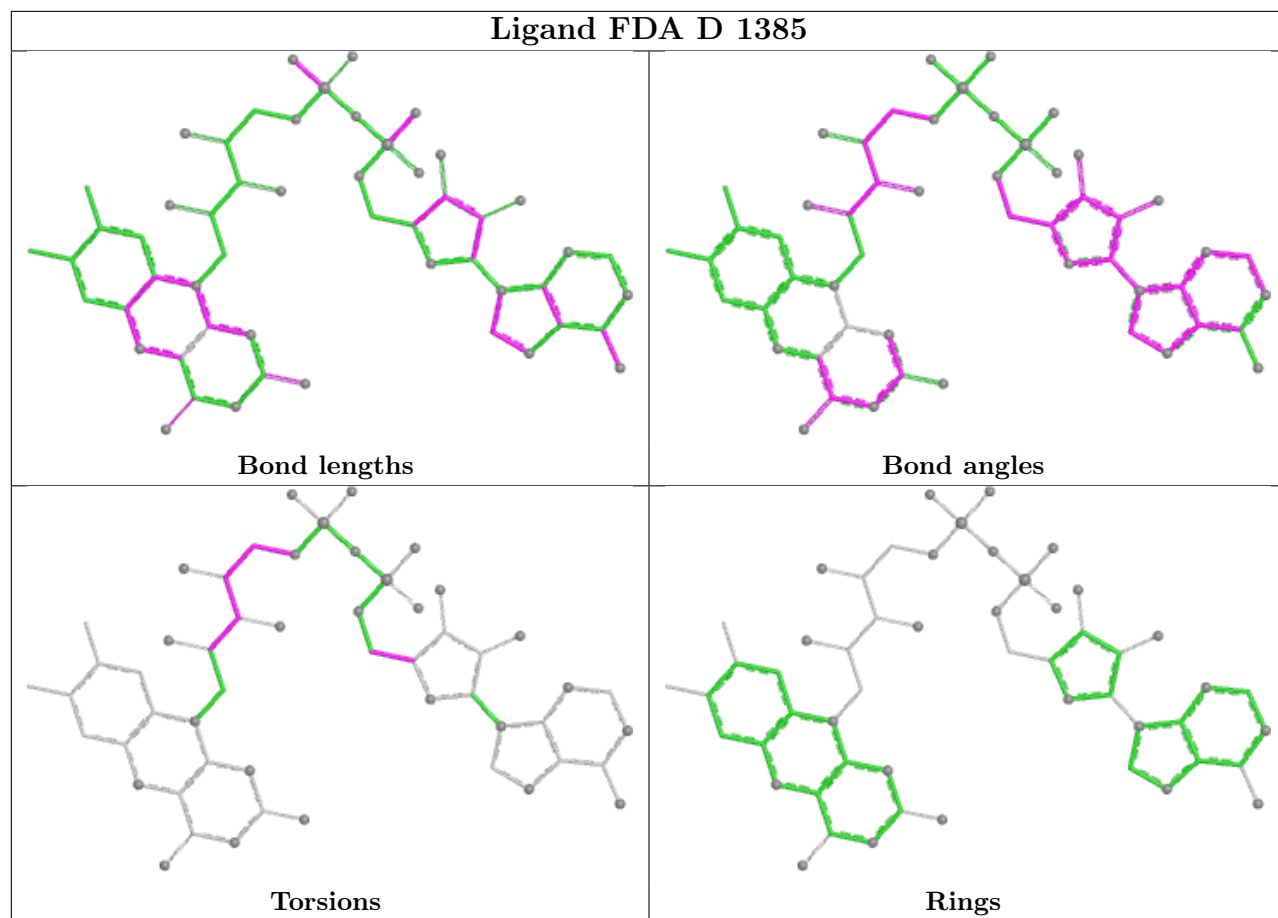


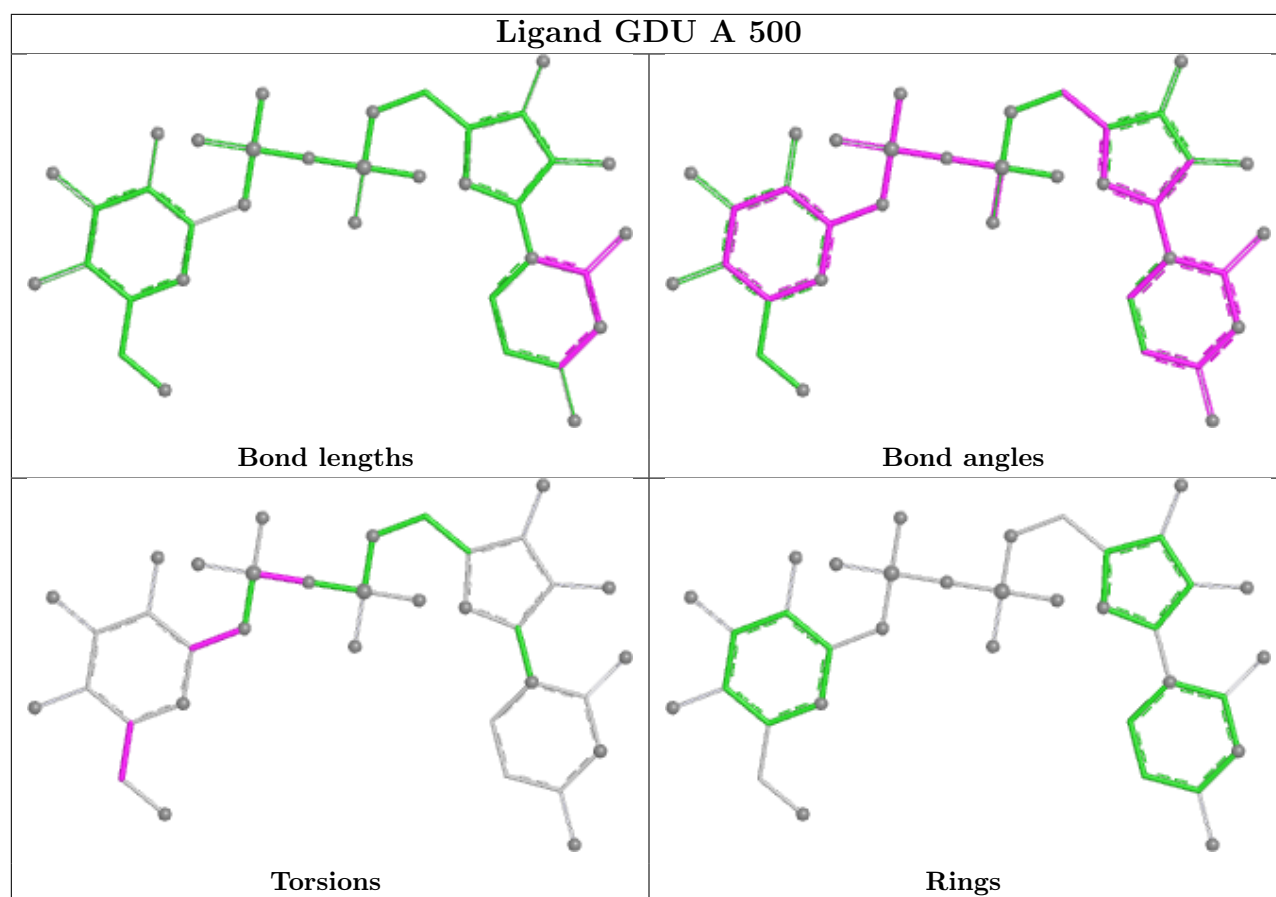


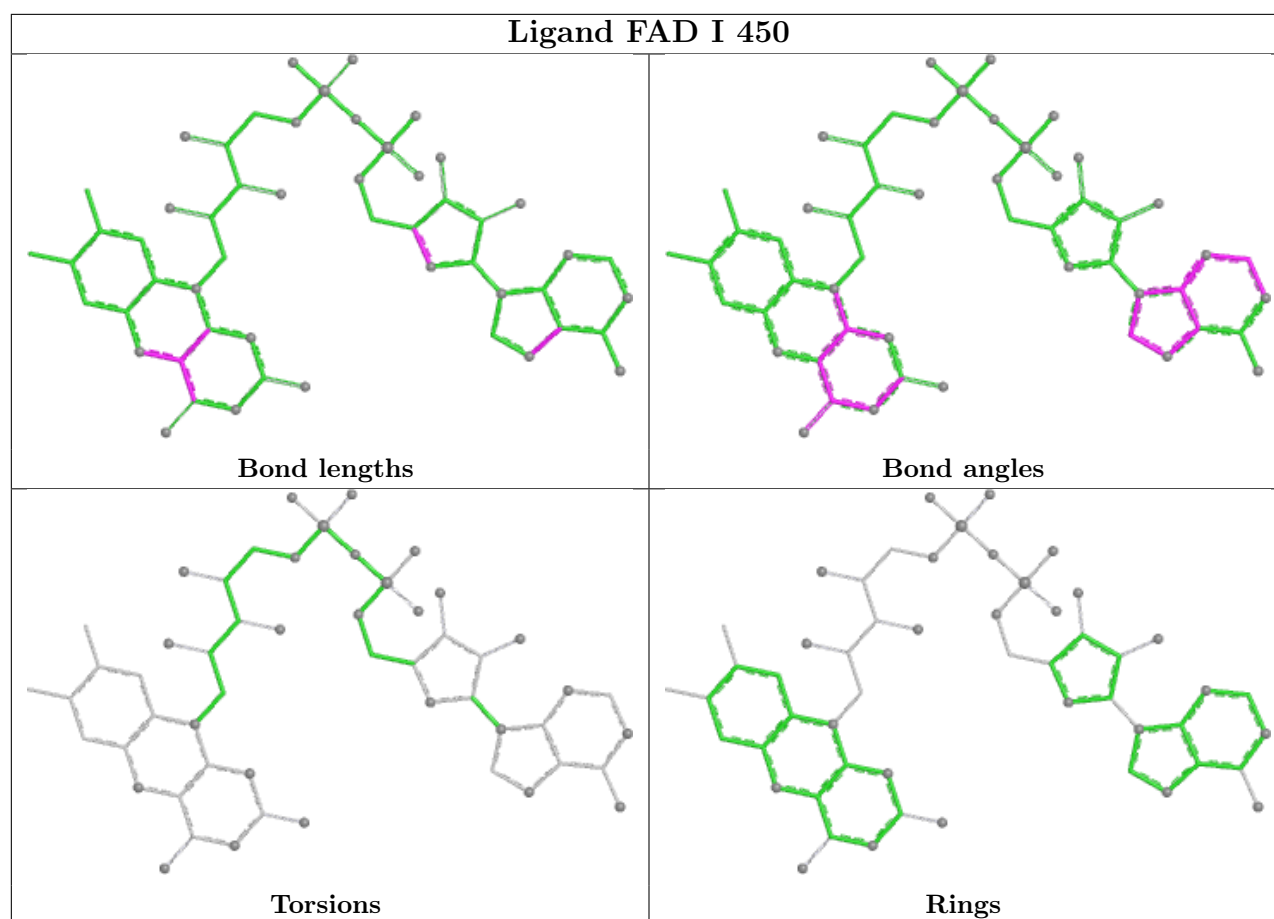












5.7 Other polymers [i](#)

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	365/397 (91%)	0.12	6 (1%) 70 66	35, 45, 65, 109	1 (0%)
1	B	361/397 (90%)	0.12	4 (1%) 78 74	36, 48, 66, 98	0
1	C	348/397 (87%)	0.91	55 (15%) 5 4	20, 55, 89, 122	1 (0%)
1	D	360/397 (90%)	0.36	15 (4%) 40 36	37, 53, 77, 102	1 (0%)
1	E	360/397 (90%)	0.36	6 (1%) 69 65	40, 55, 76, 101	1 (0%)
1	F	360/397 (90%)	0.20	13 (3%) 46 42	37, 48, 73, 97	1 (0%)
1	G	360/397 (90%)	0.27	5 (1%) 73 69	35, 50, 69, 102	0
1	H	361/397 (90%)	0.25	7 (1%) 66 62	37, 50, 70, 89	1 (0%)
1	I	361/397 (90%)	0.15	6 (1%) 69 65	38, 47, 65, 92	1 (0%)
1	J	359/397 (90%)	0.23	3 (0%) 82 80	36, 50, 74, 95	1 (0%)
All	All	3595/3970 (90%)	0.29	120 (3%) 49 45	20, 50, 75, 122	8 (0%)

The worst 5 of 120 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	55	VAL	7.0
1	C	360	THR	6.2
1	C	359	VAL	5.8
1	C	234	ASN	5.7
1	C	361	PHE	5.6

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 ⓘ

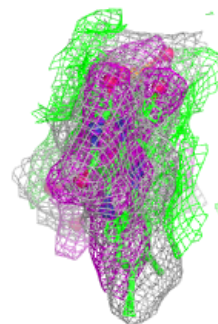
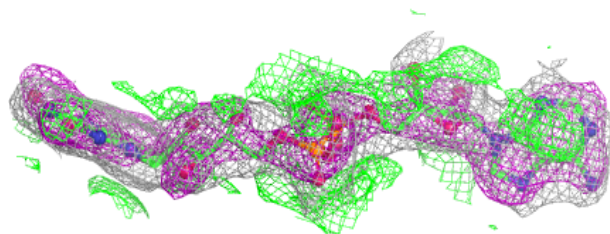
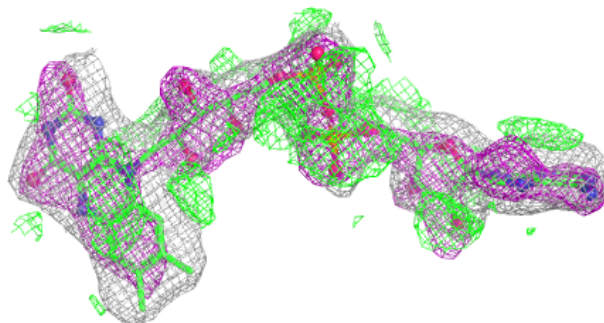
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	FAD	C	450	53/53	0.84	0.12	20,20,20,20	0
3	FAD	E	450	53/53	0.88	0.11	20,20,20,20	0
3	FAD	H	450	53/53	0.88	0.11	20,20,20,20	0
3	FAD	I	450	53/53	0.88	0.11	20,20,20,20	0
3	FAD	J	450	53/53	0.88	0.11	20,20,20,20	0
3	FAD	F	450	53/53	0.89	0.10	20,20,20,20	0
2	GDU	C	500	36/36	0.90	0.12	36,48,61,68	0
4	FDA	D	1385	53/53	0.91	0.11	42,53,66,71	0
2	GDU	I	500	36/36	0.92	0.11	40,49,64,65	0
2	GDU	H	500	36/36	0.92	0.11	39,49,64,70	0
2	GDU	E	500	36/36	0.93	0.11	45,56,64,67	0
2	GDU	J	500	36/36	0.93	0.10	40,49,61,62	0
3	FAD	A	450	53/53	0.93	0.09	20,20,20,20	0
2	GDU	F	500	36/36	0.93	0.10	39,48,58,61	0
2	GDU	A	500	36/36	0.93	0.10	35,47,58,66	0
2	GDU	D	500	36/36	0.94	0.09	42,50,56,60	0
4	FDA	B	1385	53/53	0.94	0.08	42,49,55,57	0
2	GDU	B	500	36/36	0.94	0.08	43,50,59,64	0
4	FDA	G	1385	53/53	0.94	0.08	41,53,59,60	0
2	GDU	G	500	36/36	0.95	0.09	41,49,61,69	0

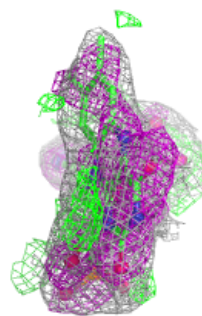
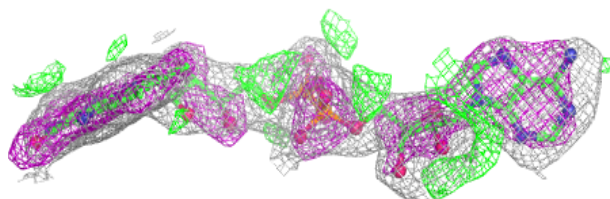
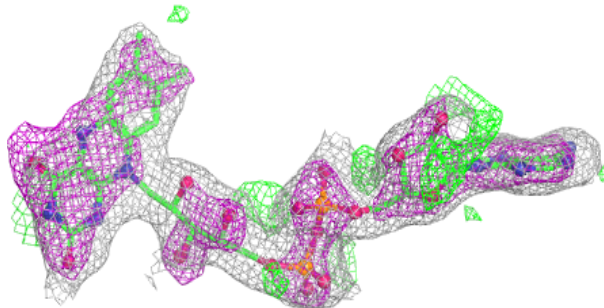
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 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)

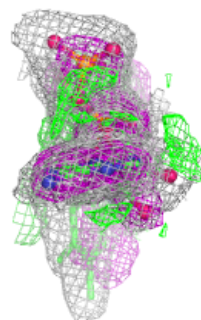
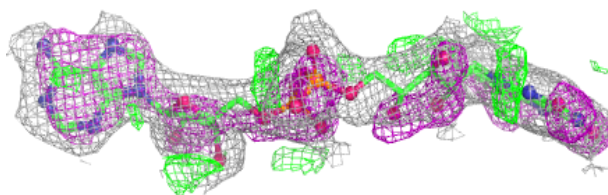
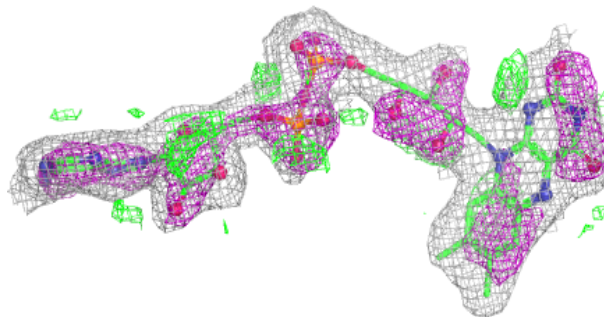
**Electron density around FAD E 450:**

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

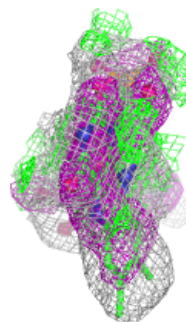
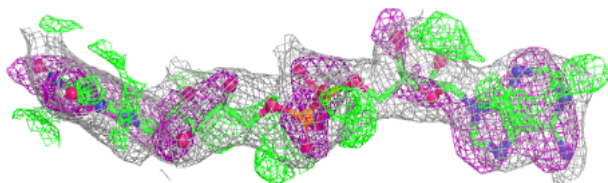
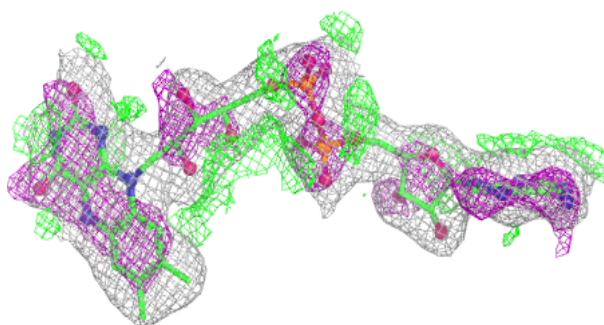


Electron density around FAD H 450:

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and green (positive)

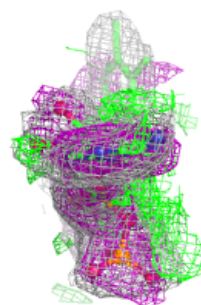
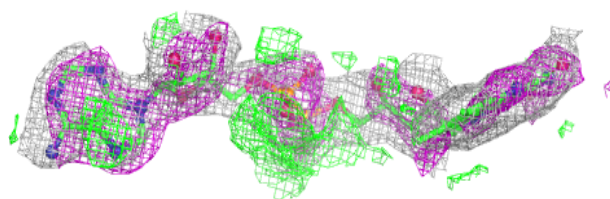
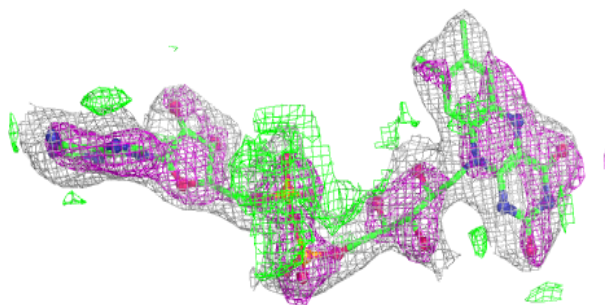
**Electron density around FAD I 450:**

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

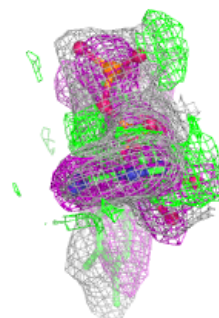
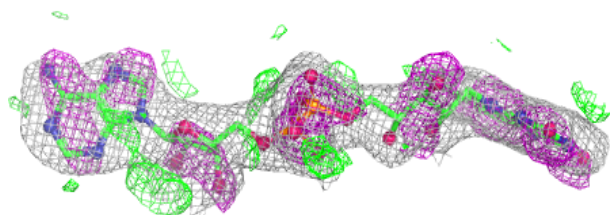
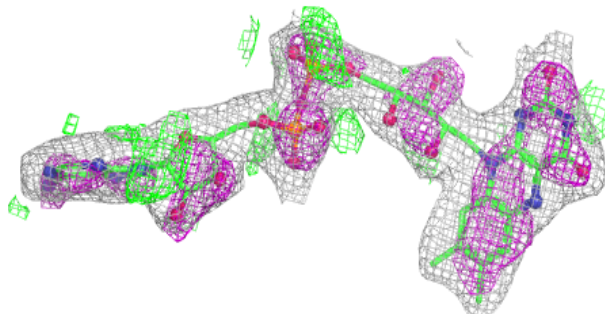


Electron density around FAD J 450:

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and green (positive)

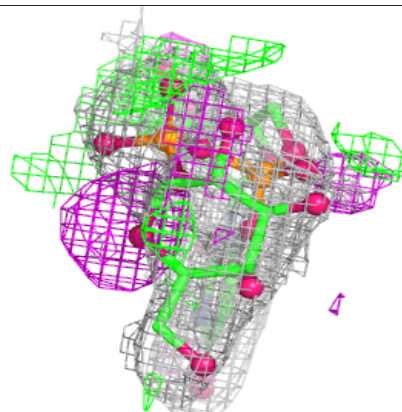
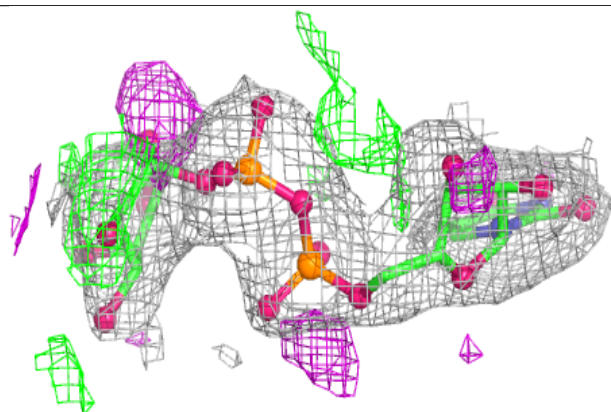
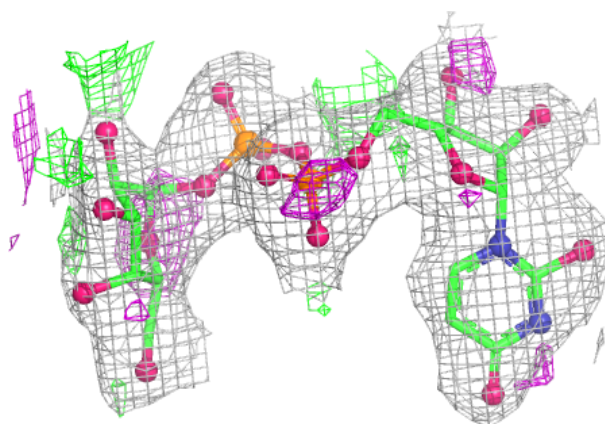
**Electron density around FAD F 450:**

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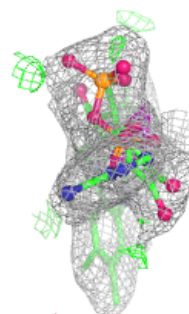
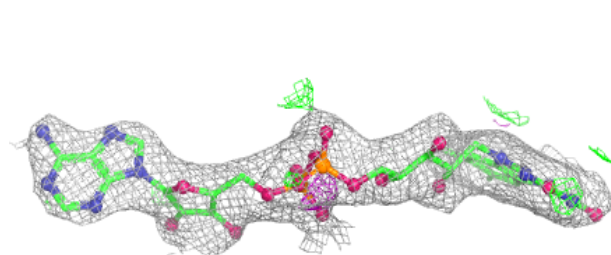
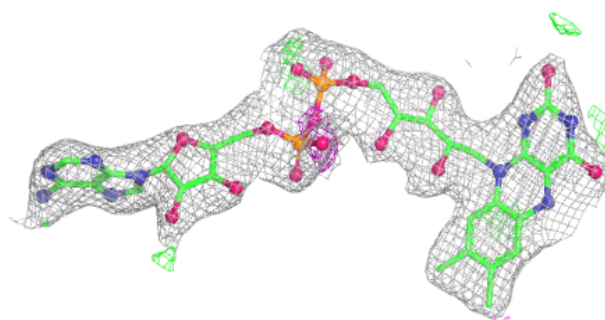


Electron density around GDU C 500:

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

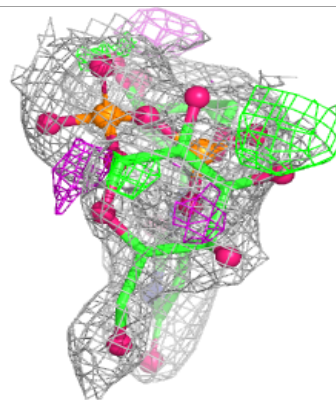
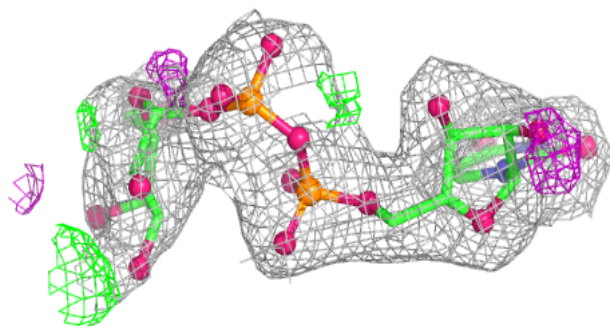
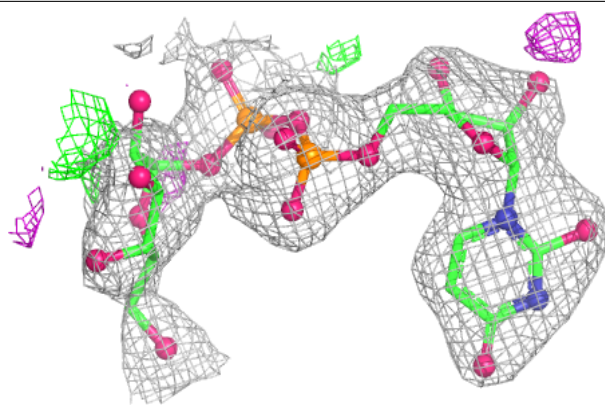
**Electron density around FDA D 1385:**

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

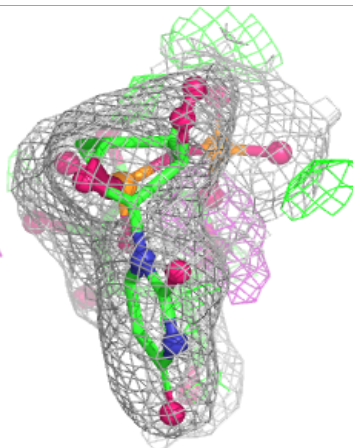
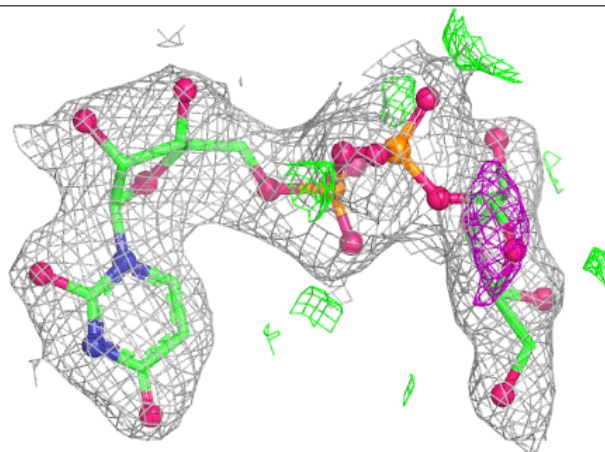


Electron density around GDU I 500:

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

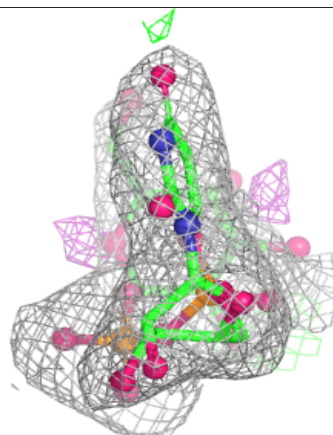
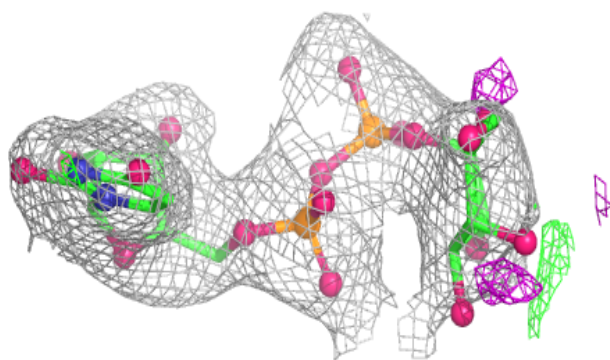
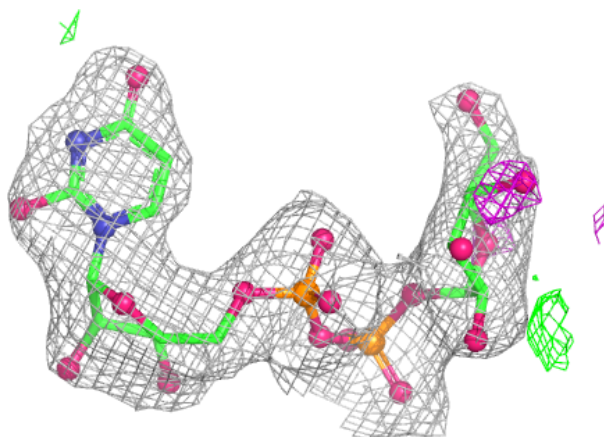
**Electron density around GDU H 500:**

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



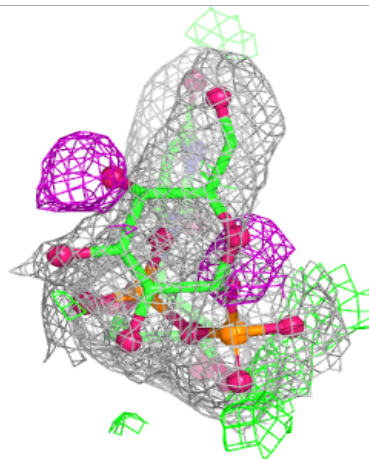
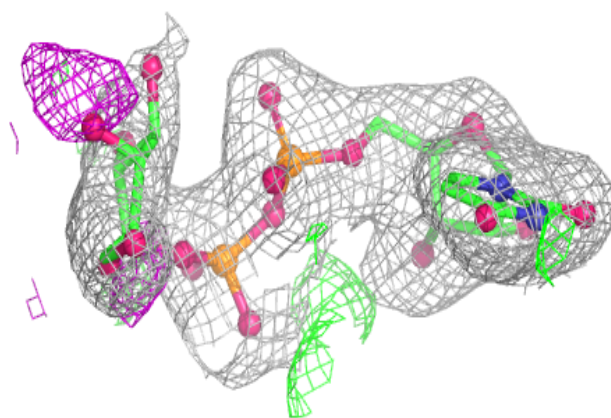
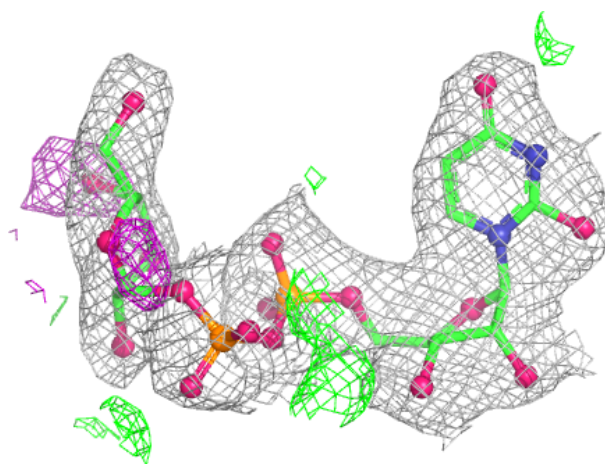
Electron density around GDU E 500:

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



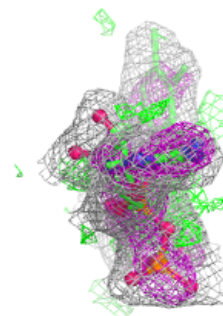
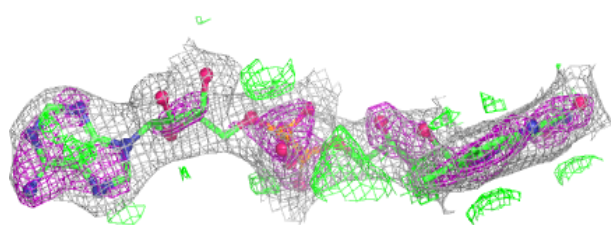
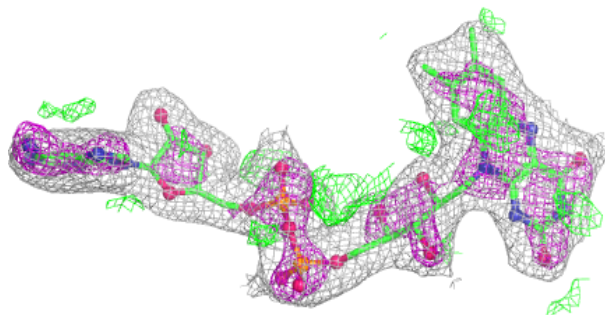
Electron density around GDU J 500:

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

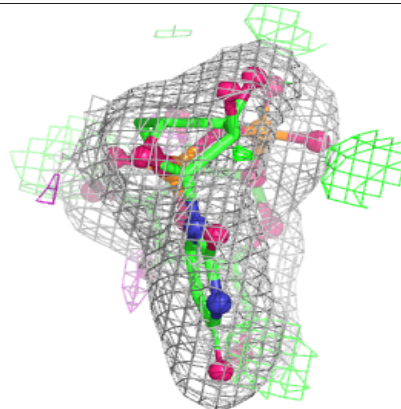
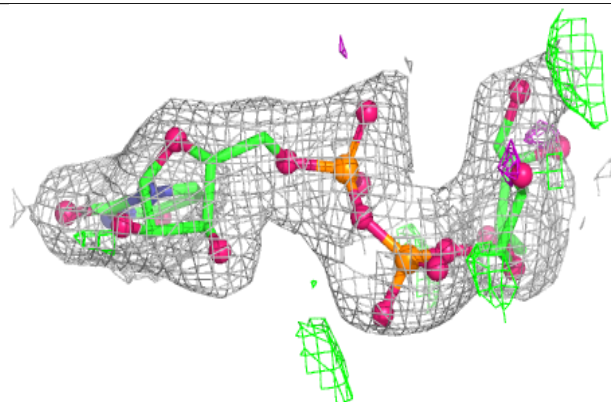
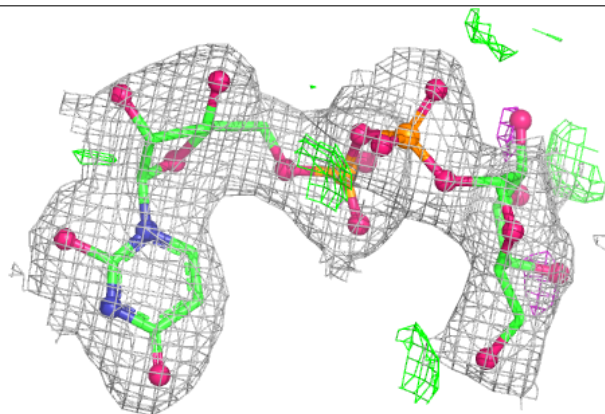


Electron density around FAD A 450:

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

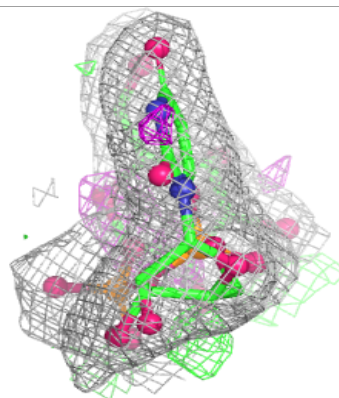
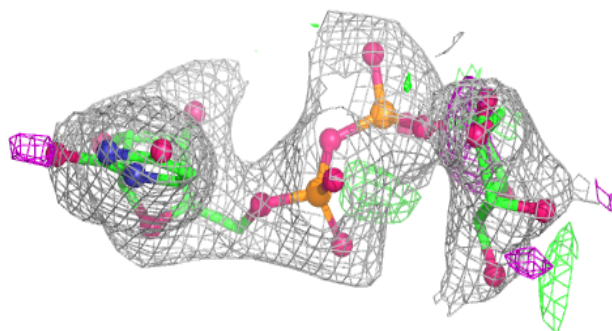
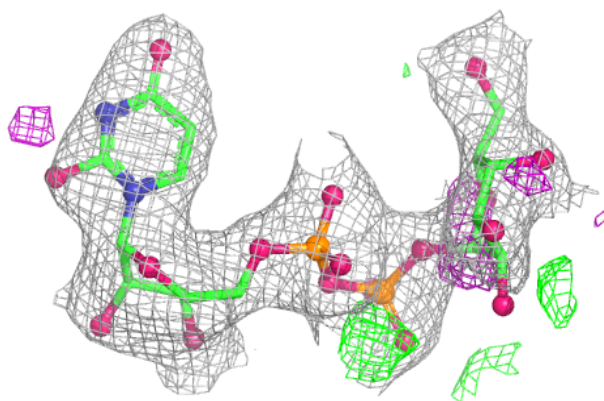
**Electron density around GDU F 500:**

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

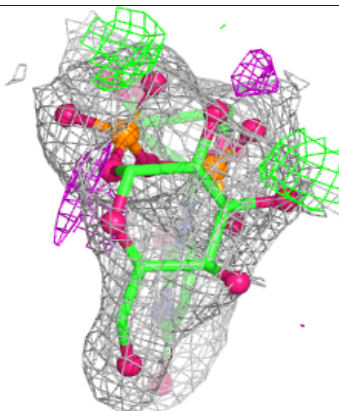
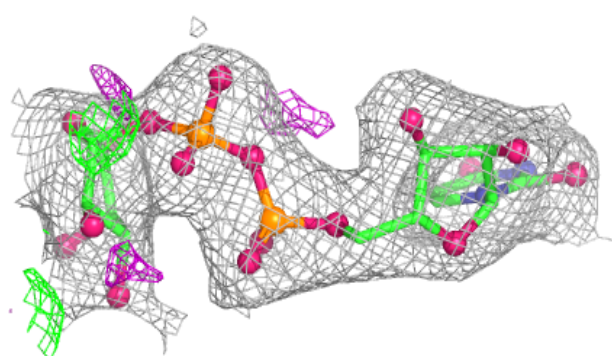
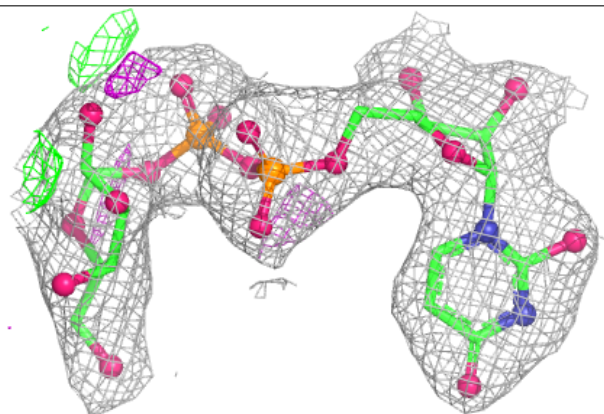


Electron density around GDU A 500:

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

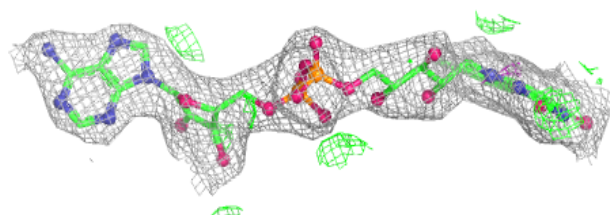
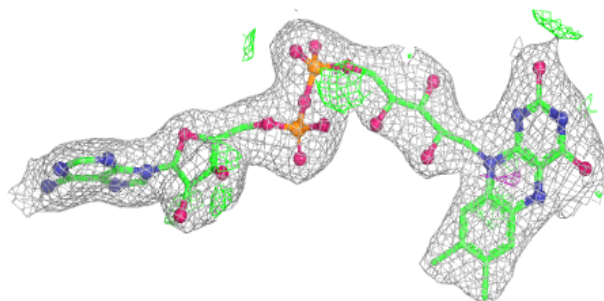
**Electron density around GDU D 500:**

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

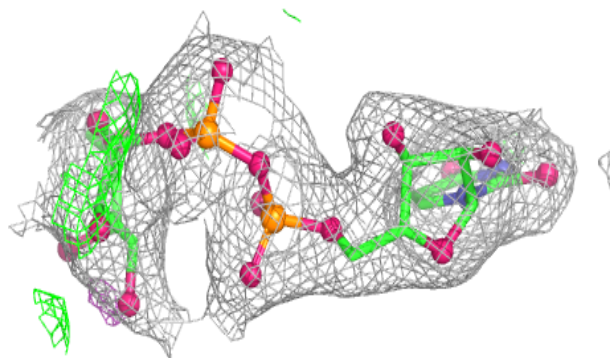
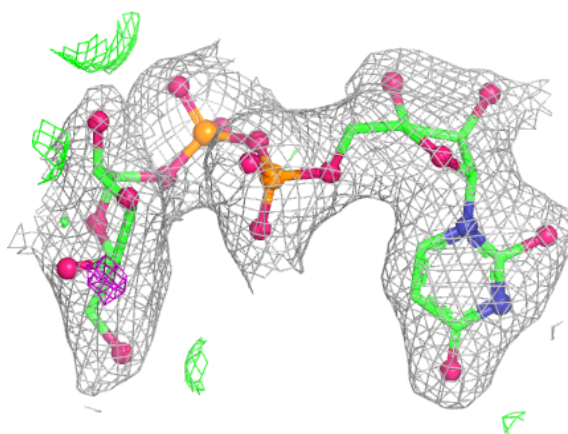


Electron density around FDA B 1385:

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

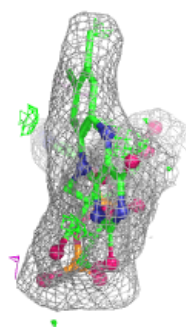
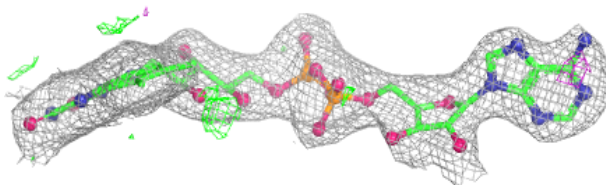
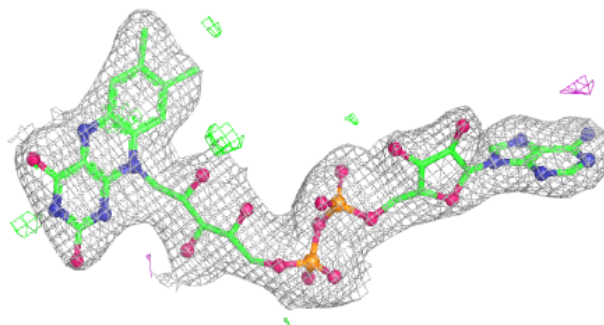
**Electron density around GDU B 500:**

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

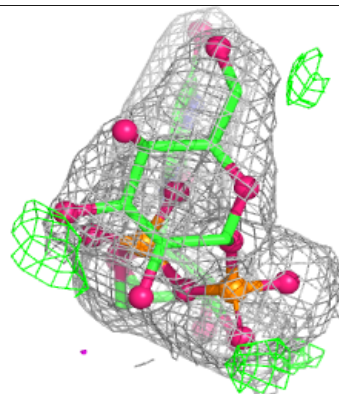
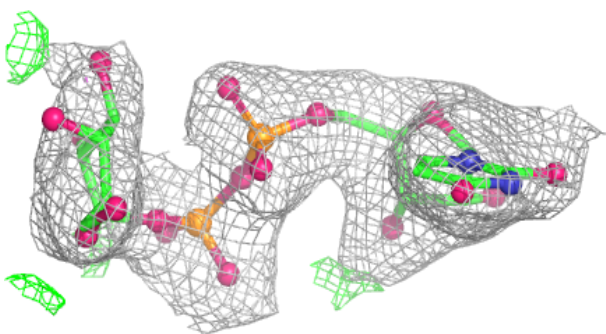
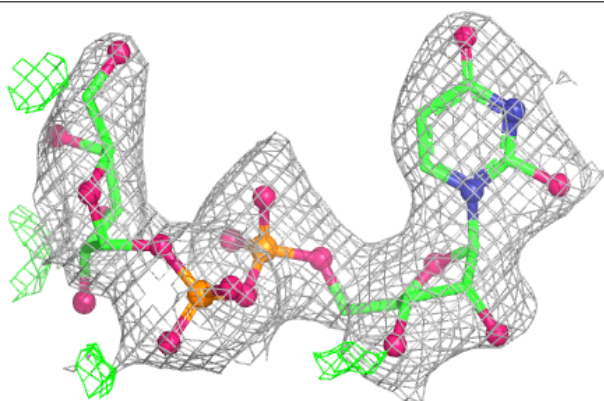


Electron density around FDA G 1385:

$2mF_o-DF_c$ (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.