



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 10:18 AM UTC

PDB ID : 3UKP / pdb_00003ukp
Title : Crystal structure of R327A UDP-galactopyranose mutase from *Aspergillus fumigatus* in complex with UDPgalp
Authors : Van Straaten, K.E.; Sanders, D.A.R.
Deposited on : 2011-11-09
Resolution : 3.10 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

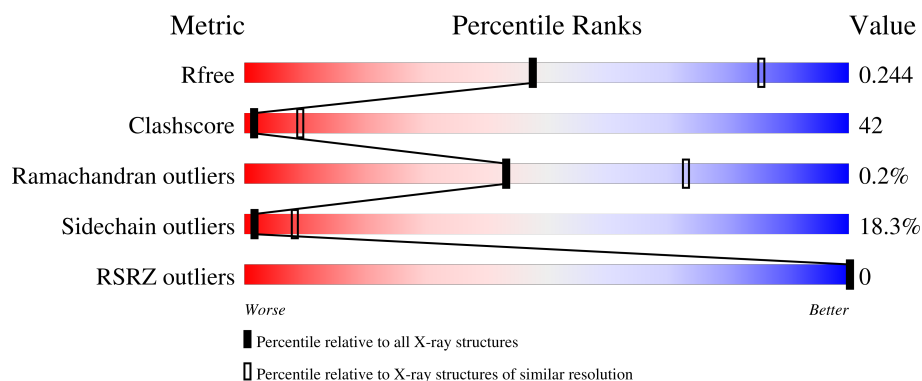
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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.



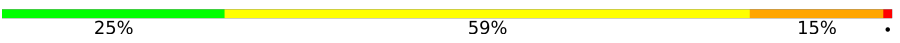
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	509	
1	B	509	
1	C	509	
1	D	509	
1	E	509	

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Mol	Chain	Length	Quality of chain
1	F	509	
1	G	509	
1	H	509	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FAD	A	601	X	-	-	-
2	FAD	D	601	-	-	X	-
2	FAD	F	601	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 32560 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	509	Total	C	N	O	S	0	0	0
			3990	2531	683	755	21			
1	B	509	Total	C	N	O	S	0	0	0
			3990	2531	683	755	21			
1	C	509	Total	C	N	O	S	0	0	0
			3990	2531	683	755	21			
1	D	509	Total	C	N	O	S	0	0	0
			3990	2531	683	755	21			
1	E	509	Total	C	N	O	S	0	0	0
			3990	2531	683	755	21			
1	F	509	Total	C	N	O	S	0	0	0
			3990	2531	683	755	21			
1	G	509	Total	C	N	O	S	0	0	0
			3990	2531	683	755	21			
1	H	509	Total	C	N	O	S	0	0	0
			3990	2531	683	755	21			

There are 8 discrepancies between the modelled and reference sequences:

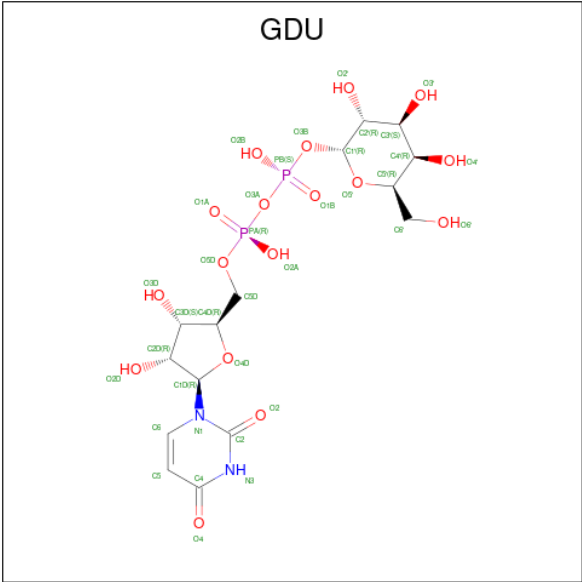
Chain	Residue	Modelled	Actual	Comment	Reference
A	327	ALA	ARG	engineered mutation	UNP Q4W1X2
B	327	ALA	ARG	engineered mutation	UNP Q4W1X2
C	327	ALA	ARG	engineered mutation	UNP Q4W1X2
D	327	ALA	ARG	engineered mutation	UNP Q4W1X2
E	327	ALA	ARG	engineered mutation	UNP Q4W1X2
F	327	ALA	ARG	engineered mutation	UNP Q4W1X2
G	327	ALA	ARG	engineered mutation	UNP Q4W1X2
H	327	ALA	ARG	engineered mutation	UNP Q4W1X2

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



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

- Molecule 3 is GALACTOSE-URIDINE-5'-DIPHOSPHATE (CCD ID: GDU) (formula: C₁₅H₂₄N₂O₁₇P₂).

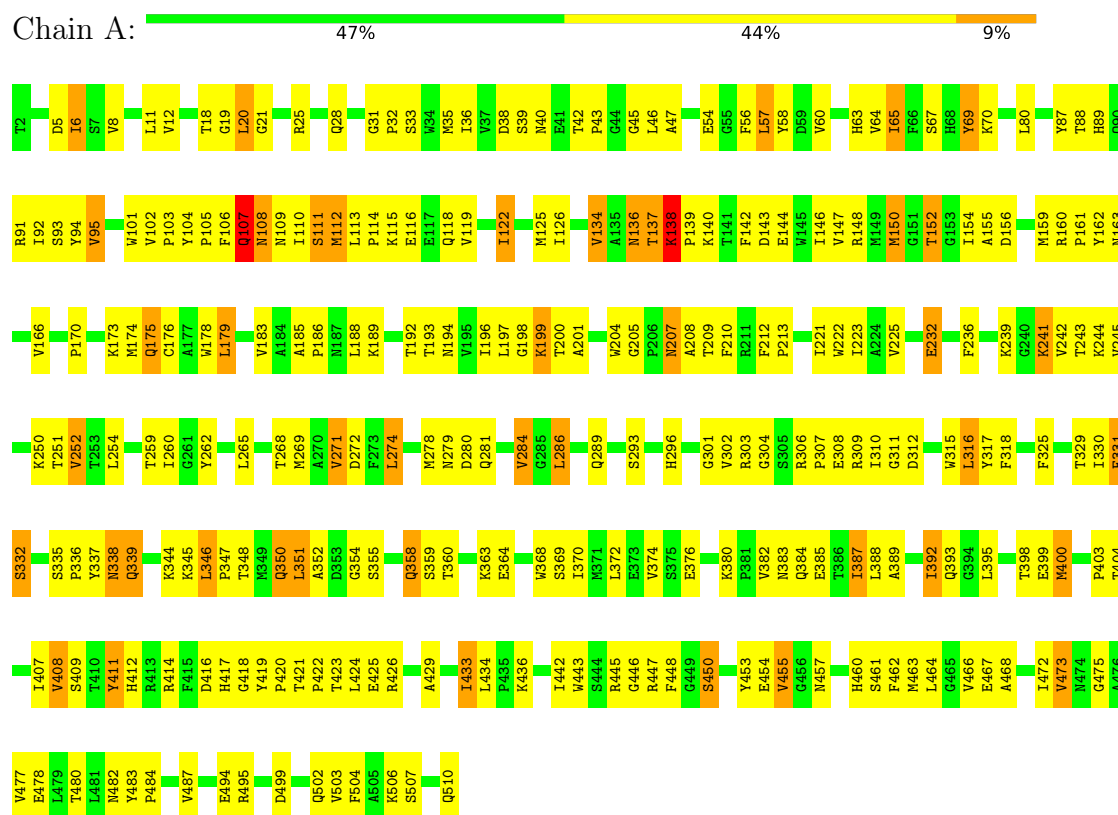


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
3	B	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
3	C	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
3	D	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
3	E	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
3	F	1	Total	C	N	O	P	0	0
			36	15	2	17	2		

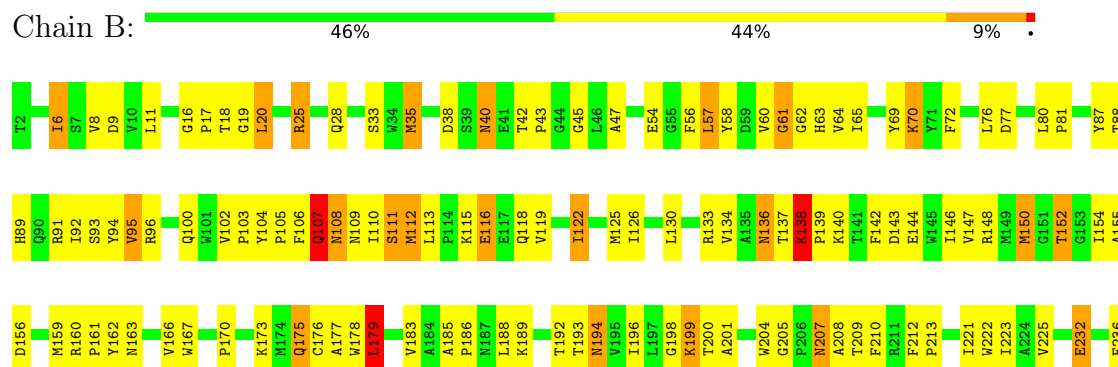
3 Residue-property plots

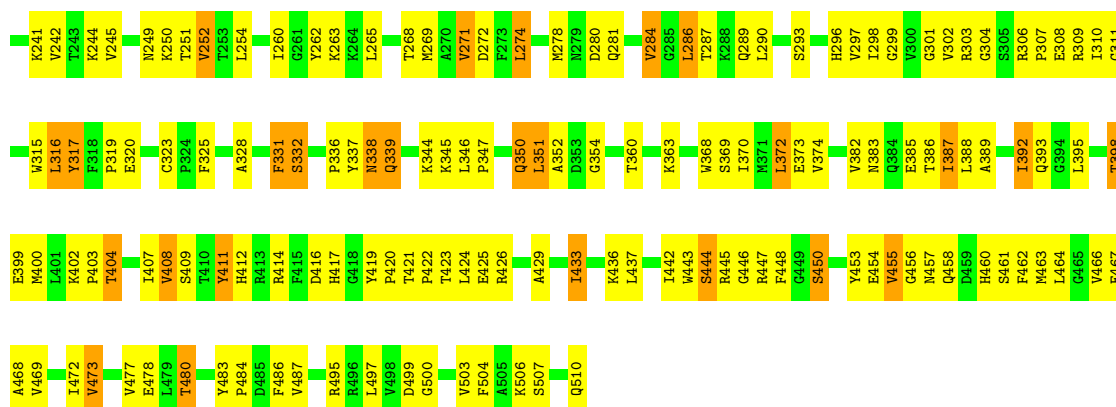
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: UDP-galactopyranose mutase

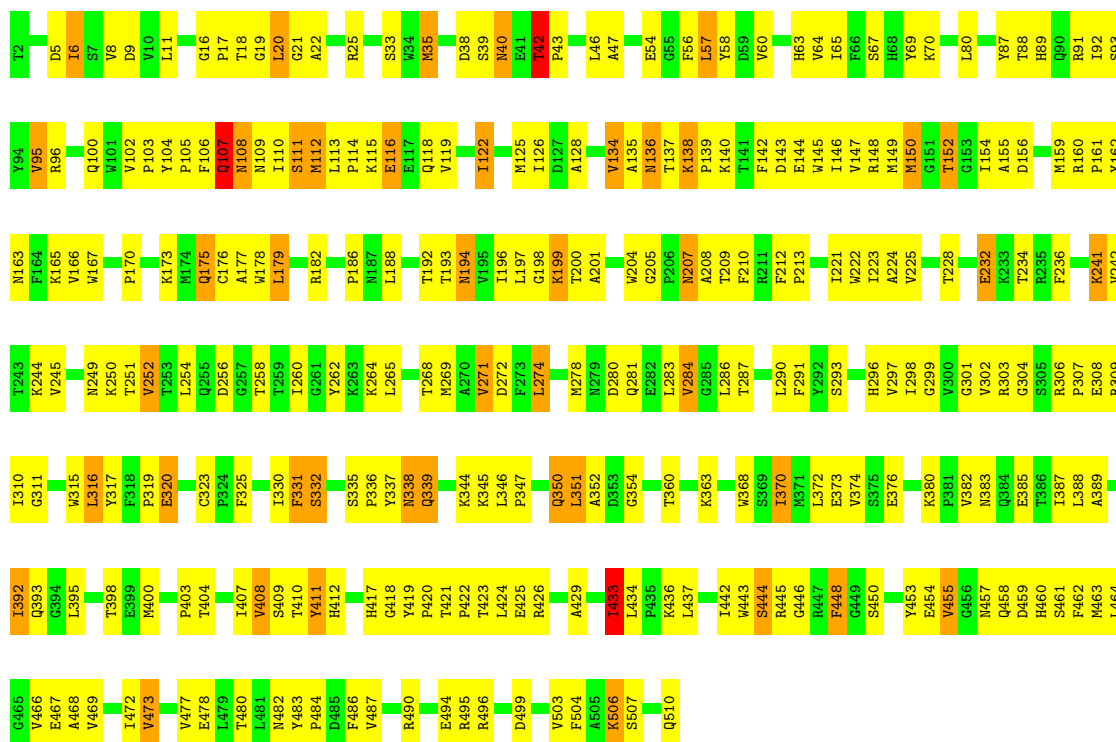


• Molecule 1: UDP-galactopyranose mutase

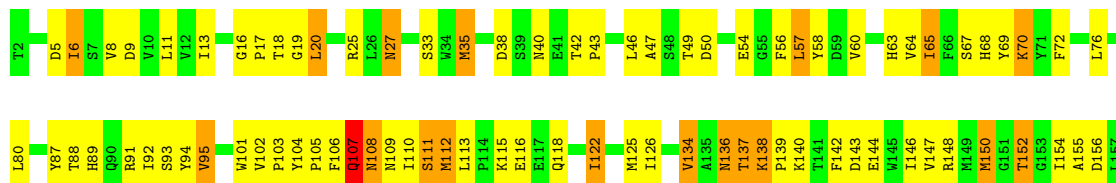


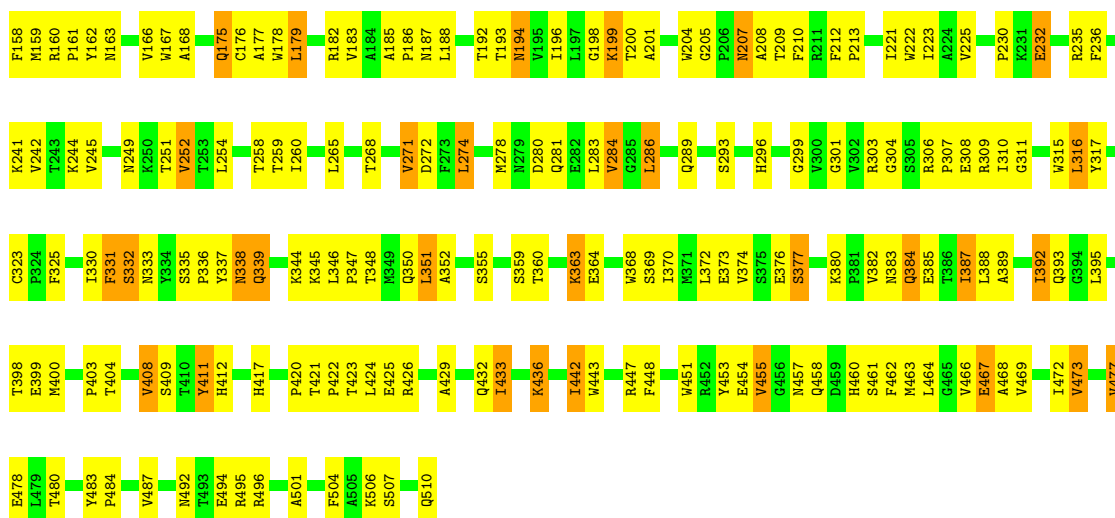


• Molecule 1: UDP-galactopyranose mutase



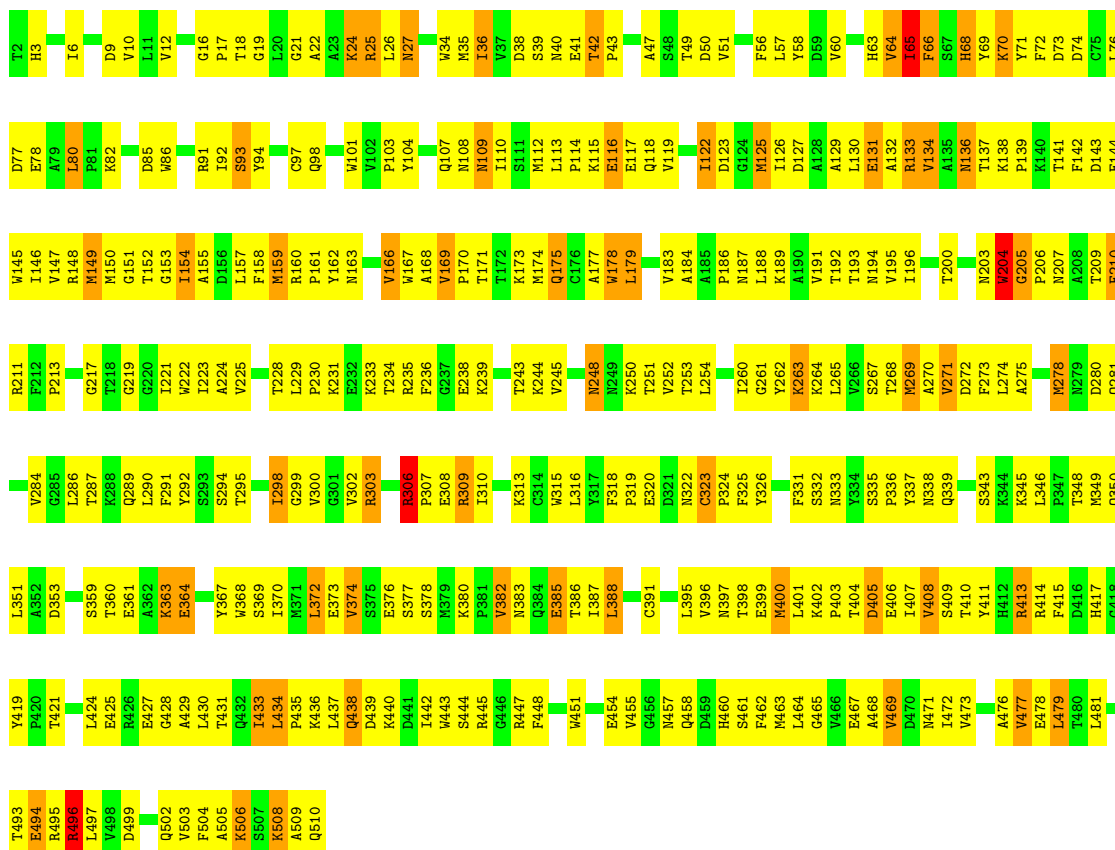
• Molecule 1: UDP-galactopyranose mutase





• Molecule 1: UDP-galactopyranose mutase

Chain E: 34% 54% 11%

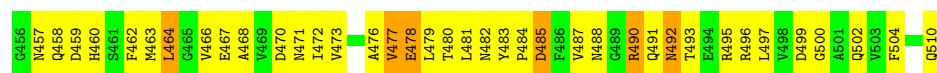


• Molecule 1: UDP-galactopyranose mutase

Chain F: 33% 55% 11%

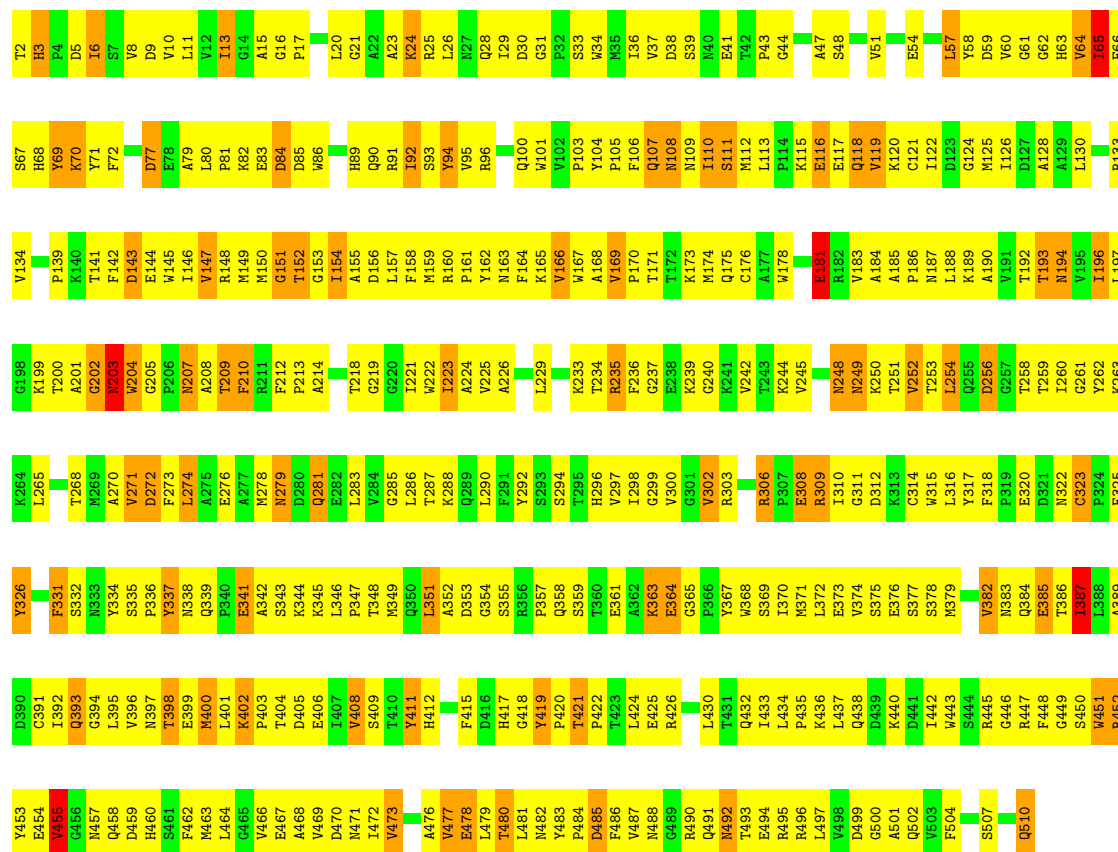


Q393	S332	W269	T200	M136	H68	T2				
							A201	H89	H3	
							G202	P139	P4	Y69
							N203	K140	K70	D6
							W204	L141	Y71	I6
							G205	F142	F72	S7
							P206	D143	V8	
							V207	E144	D9	
							A208	W145	V10	
							T209	L146	A79	L11
Q400	Q339	M278	F210	M149	D77	D9				
							N279	L147	V11	
							T280	P211	L80	L12
							G281	F212	P81	I13
							W282	A213	M150	G14
							L283	D214	D84	A15
							W284	P215	G16	G16
							G285	E152	W86	P17
							T286	T218	G17	P18
							N287	L154	H89	G19
Q402	Q340	M278	F211	M150	D77	D9				
							N279	L147	V11	
							T280	P211	L80	L12
							G281	F212	P81	I13
							W282	A213	D84	A15
							L283	D214	G16	G16
							W284	P215	W86	P17
							G285	E152	G17	P18
							T286	T218	H89	G19
							N287	L154	Q90	L20
Q403	Q342	M278	F212	M150	D77	D9				
							N279	L147	V11	
							T280	P211	L80	L12
							G281	F212	P81	I13
							W282	A213	D84	A15
							L283	D214	G16	G16
							W284	P215	W86	P17
							G285	E152	G17	P18
							T286	T218	H89	G19
							N287	L154	Q90	L20
Q404	Q343	M278	F213	M150	D77	D9				
							N279	L147	V11	
							T280	P211	L80	L12
							G281	F212	P81	I13
							W282	A213	D84	A15
							L283	D214	G16	G16
							W284	P215	W86	P17
							G285	E152	G17	P18
							T286	T218	H89	G19
							N287	L154	Q90	L20
Q405	Q344	M278	F214	M150	D77	D9				
							N279	L147	V11	
							T280	P211	L80	L12
							G281	F212	P81	I13
							W282	A213	D84	A15
							L283	D214	G16	G16
							W284	P215	W86	P17
							G285	E152	G17	P18
							T286	T218	H89	G19
							N287	L154	Q90	L20
Q406	Q345	M278	F215	M150	D77	D9				
							N279	L147	V11	
							T280	P211	L80	L12
							G281	F212	P81	I13
							W282	A213	D84	A15
							L283	D214	G16	G16
							W284	P215	W86	P17
							G285	E152	G17	P18
							T286	T218	H89	G19
							N287	L154	Q90	L20
Q407	Q346	M278	F216	M150	D77	D9				
							N279	L147	V11	
							T280	P211	L80	L12
							G281	F212	P81	I13
							W282	A213	D84	A15
							L283	D214	G16	G16
							W284	P215	W86	P17
							G285	E152	G17	P18
							T286	T218	H89	G19
							N287	L154	Q90	L20
Q408	Q347	M278	F217	M150	D77	D9				
							N279	L147	V11	
							T280	P211	L80	L12
							G281	F212	P81	I13
							W282	A213	D84	A15
							L283	D214	G16	G16
							W284	P215	W86	P17
							G285	E152	G17	P18
							T286	T218	H89	G19
							N287	L154	Q90	L20
Q409	Q348	M278	F218	M150	D77	D9				
							N279	L147	V11	
							T280	P211	L80	L12
							G281	F212	P81	I13
							W282	A213	D84	A15
							L283	D214	G16	G16
							W284	P215	W86	P17
							G285	E152	G17	P18
							T286	T218	H89	G19
							N287	L154	Q90	L20
Q410	Q349	M278	F219	M150	D77	D9				
							N279	L147	V11	
							T280	P211	L80	L12
							G281	F212	P	



• Molecule 1: UDP-galactopyranose mutase

Chain H: 25% 59% 15%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	129.60Å 175.71Å 135.35Å 90.00° 90.01° 90.00°	Depositor
Resolution (Å)	34.77 – 3.10 34.77 – 3.10	Depositor EDS
% Data completeness (in resolution range)	96.3 (34.77-3.10) 96.2 (34.77-3.10)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	0.24	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.74 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.7.1_743	Depositor
R, R_{free}	0.202 , 0.260 0.201 , 0.244	Depositor DCC
R_{free} test set	5333 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	53.6	Xtriage
Anisotropy	0.517	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 66.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.000 for l,k,-h 0.327 for h,-k,-l 0.000 for l,-k,h	Xtriage
Reported twinning fraction	0.479 for h,-k,-l	Depositor
Outliers	2 of 105627 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	32560	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.04 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.6278e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FAD, GDU

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	0.38	0/4089	0.93	17/5558 (0.3%)
1	B	0.39	0/4089	0.92	10/5558 (0.2%)
1	C	0.38	0/4089	0.92	11/5558 (0.2%)
1	D	0.38	0/4089	0.91	7/5558 (0.1%)
1	E	0.40	0/4089	1.03	26/5558 (0.5%)
1	F	0.40	0/4089	1.00	21/5558 (0.4%)
1	G	0.41	0/4089	1.03	20/5558 (0.4%)
1	H	0.39	0/4089	0.99	19/5558 (0.3%)
All	All	0.39	0/32712	0.97	131/44464 (0.3%)

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	G	0	1

There are no bond length outliers.

The worst 5 of 131 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	205	GLY	O-C-N	-12.82	108.95	121.77
1	F	80	LEU	CA-C-N	10.67	130.34	119.56
1	F	80	LEU	C-N-CA	10.67	130.34	119.56
1	G	306	ARG	CA-C-N	10.41	130.20	120.21
1	G	306	ARG	C-N-CA	10.41	130.20	120.21

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	65	ILE	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3990	0	3906	258	0
1	B	3990	0	3906	278	0
1	C	3990	0	3906	281	0
1	D	3990	0	3906	243	0
1	E	3990	0	3906	394	0
1	F	3990	0	3906	375	0
1	G	3990	0	3906	468	0
1	H	3990	0	3906	449	0
2	A	53	0	29	9	0
2	B	53	0	30	13	0
2	C	53	0	30	12	0
2	D	53	0	30	22	0
2	E	53	0	30	18	0
2	F	53	0	29	13	0
2	G	53	0	29	13	0
2	H	53	0	30	10	0
3	A	36	0	22	11	0
3	B	36	0	22	17	0
3	C	36	0	22	9	0
3	D	36	0	22	4	0
3	E	36	0	22	14	0
3	F	36	0	22	10	0
All	All	32560	0	31617	2702	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 42.

The worst 5 of 2702 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:E:70:LYS:HG3	1:E:496:ARG:HH22	0.96	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:70:LYS:HG3	1:F:496:ARG:HH22	1.12	1.10
1:F:461:SER:HA	1:F:464:LEU:HD12	1.37	1.06
1:D:303:ARG:NH2	1:D:346:LEU:O	1.90	1.05
1:E:461:SER:HA	1:E:464:LEU:HD12	1.38	1.05

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	507/509 (100%)	476 (94%)	30 (6%)	1 (0%)	43	73
1	B	507/509 (100%)	476 (94%)	29 (6%)	2 (0%)	30	61
1	C	507/509 (100%)	476 (94%)	30 (6%)	1 (0%)	43	73
1	D	507/509 (100%)	481 (95%)	25 (5%)	1 (0%)	43	73
1	E	507/509 (100%)	456 (90%)	51 (10%)	0	100	100
1	F	507/509 (100%)	457 (90%)	49 (10%)	1 (0%)	43	73
1	G	507/509 (100%)	462 (91%)	45 (9%)	0	100	100
1	H	507/509 (100%)	460 (91%)	46 (9%)	1 (0%)	43	73
All	All	4056/4072 (100%)	3744 (92%)	305 (8%)	7 (0%)	43	73

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	203	ASN
1	B	61	GLY
1	A	107	GLN
1	B	107	GLN
1	C	107	GLN

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	430/430 (100%)	358 (83%)	72 (17%)	2	10
1	B	430/430 (100%)	360 (84%)	70 (16%)	2	11
1	C	430/430 (100%)	359 (84%)	71 (16%)	2	11
1	D	430/430 (100%)	357 (83%)	73 (17%)	2	10
1	E	430/430 (100%)	348 (81%)	82 (19%)	1	7
1	F	430/430 (100%)	343 (80%)	87 (20%)	1	5
1	G	430/430 (100%)	342 (80%)	88 (20%)	1	5
1	H	430/430 (100%)	344 (80%)	86 (20%)	1	6
All	All	3440/3440 (100%)	2811 (82%)	629 (18%)	2	8

5 of 629 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	57	LEU
1	H	193	THR
1	G	143	ASP
1	G	42	THR
1	G	361	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	90	GLN
1	H	203	ASN
1	D	40	ASN
1	C	458	GLN
1	H	339	GLN

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 ⓘ

14 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	$\# Z > 2$
2	FAD	H	601	-	58,58,58	3.15	18 (31%)	85,89,89	2.04	24 (28%)
3	GDU	A	602	-	37,38,38	1.95	9 (24%)	55,58,58	1.82	11 (20%)
2	FAD	A	601	-	58,58,58	3.03	15 (25%)	85,89,89	2.30	26 (30%)
2	FAD	G	601	-	58,58,58	2.46	24 (41%)	85,89,89	2.37	31 (36%)
3	GDU	C	602	-	37,38,38	1.99	10 (27%)	55,58,58	1.75	13 (23%)
3	GDU	E	602	-	37,38,38	1.96	10 (27%)	55,58,58	1.75	9 (16%)
3	GDU	D	602	-	37,38,38	2.02	10 (27%)	55,58,58	1.84	13 (23%)
2	FAD	E	601	-	58,58,58	3.13	16 (27%)	85,89,89	2.06	24 (28%)
2	FAD	D	601	-	58,58,58	3.11	15 (25%)	85,89,89	2.09	26 (30%)
3	GDU	B	602	-	37,38,38	1.96	10 (27%)	55,58,58	1.95	13 (23%)
3	GDU	F	602	-	37,38,38	1.95	9 (24%)	55,58,58	1.83	13 (23%)
2	FAD	B	601	-	58,58,58	3.06	17 (29%)	85,89,89	2.10	23 (27%)
2	FAD	F	601	-	58,58,58	3.09	15 (25%)	85,89,89	2.11	24 (28%)
2	FAD	C	601	-	58,58,58	3.10	15 (25%)	85,89,89	2.13	22 (25%)

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
2	FAD	H	601	-	-	9/34/50/50	0/6/6/6
3	GDU	A	602	-	-	7/23/59/59	0/3/3/3
2	FAD	A	601	-	1/1/9/9	17/34/50/50	0/6/6/6
2	FAD	G	601	-	-	7/34/50/50	0/6/6/6
3	GDU	C	602	-	-	8/23/59/59	0/3/3/3
3	GDU	E	602	-	-	8/23/59/59	0/3/3/3
3	GDU	D	602	-	-	13/23/59/59	0/3/3/3
2	FAD	E	601	-	-	12/34/50/50	0/6/6/6
2	FAD	D	601	-	-	8/34/50/50	0/6/6/6
3	GDU	B	602	-	-	5/23/59/59	0/3/3/3
3	GDU	F	602	-	-	9/23/59/59	0/3/3/3
2	FAD	B	601	-	-	23/34/50/50	0/6/6/6
2	FAD	F	601	-	1/1/9/9	12/34/50/50	0/6/6/6
2	FAD	C	601	-	-	7/34/50/50	0/6/6/6

The worst 5 of 193 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	FAD	PA-O3P	-12.19	1.46	1.59
2	F	601	FAD	PA-O3P	-11.89	1.46	1.59
2	C	601	FAD	PA-O3P	-11.85	1.46	1.59
2	E	601	FAD	PA-O3P	-11.81	1.46	1.59
2	A	601	FAD	PA-O3P	-11.65	1.46	1.59

The worst 5 of 272 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	FAD	O4B-C1B-N9A	7.09	121.70	108.09
3	A	602	GDU	N3-C2-N1	6.67	123.58	114.89
3	C	602	GDU	N3-C2-N1	6.63	123.52	114.89
2	D	601	FAD	O4B-C1B-N9A	6.52	120.61	108.09
2	G	601	FAD	O2P-P-O3P	6.46	124.75	107.27

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	601	FAD	C2'
2	F	601	FAD	C2'

5 of 145 torsion outliers are listed below:

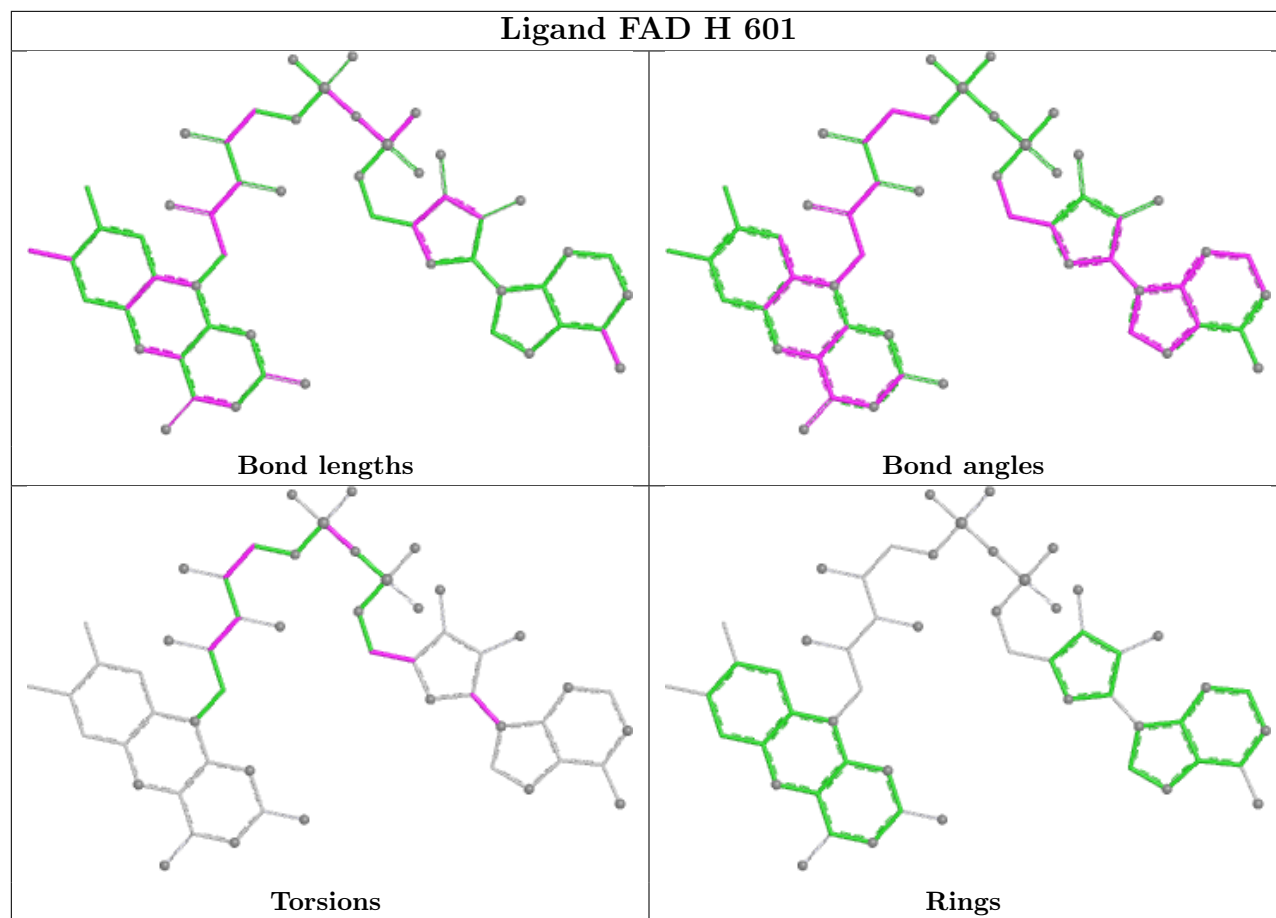
Mol	Chain	Res	Type	Atoms
2	A	601	FAD	C5B-O5B-PA-O3P
2	A	601	FAD	C2'-C1'-N10-C9A
2	A	601	FAD	C2'-C1'-N10-C10
2	A	601	FAD	N10-C1'-C2'-O2'
2	A	601	FAD	C1'-C2'-C3'-O3'

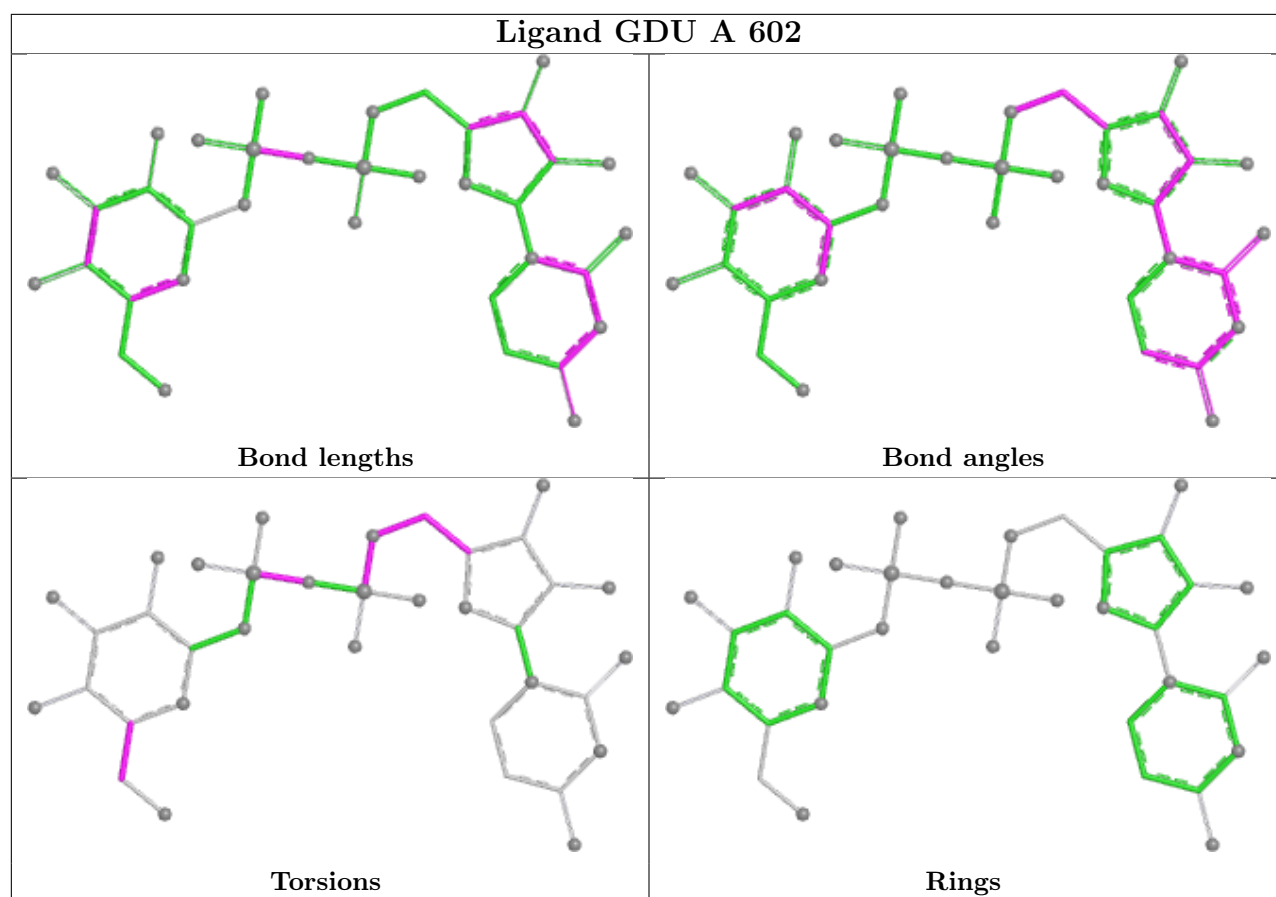
There are no ring outliers.

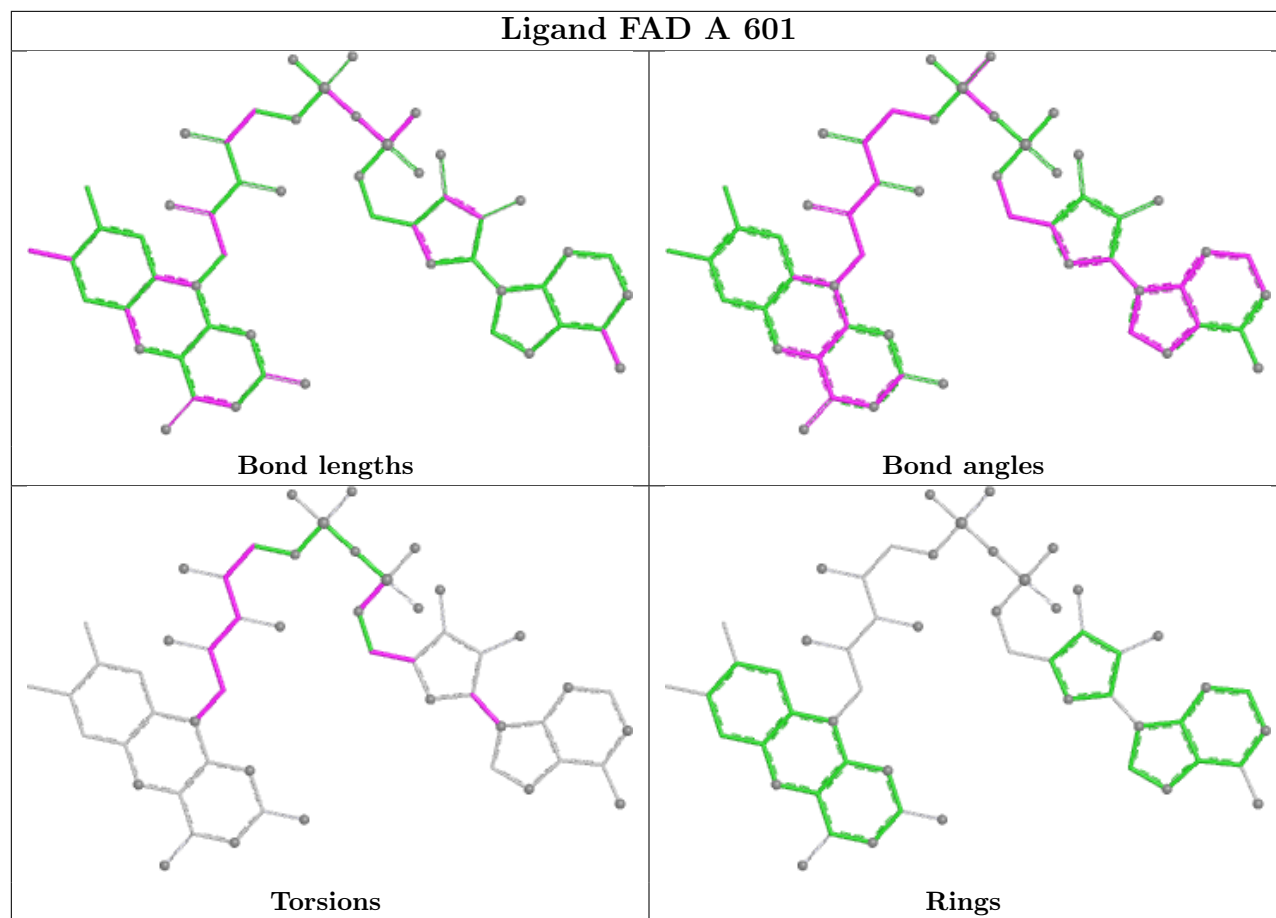
14 monomers are involved in 172 short contacts:

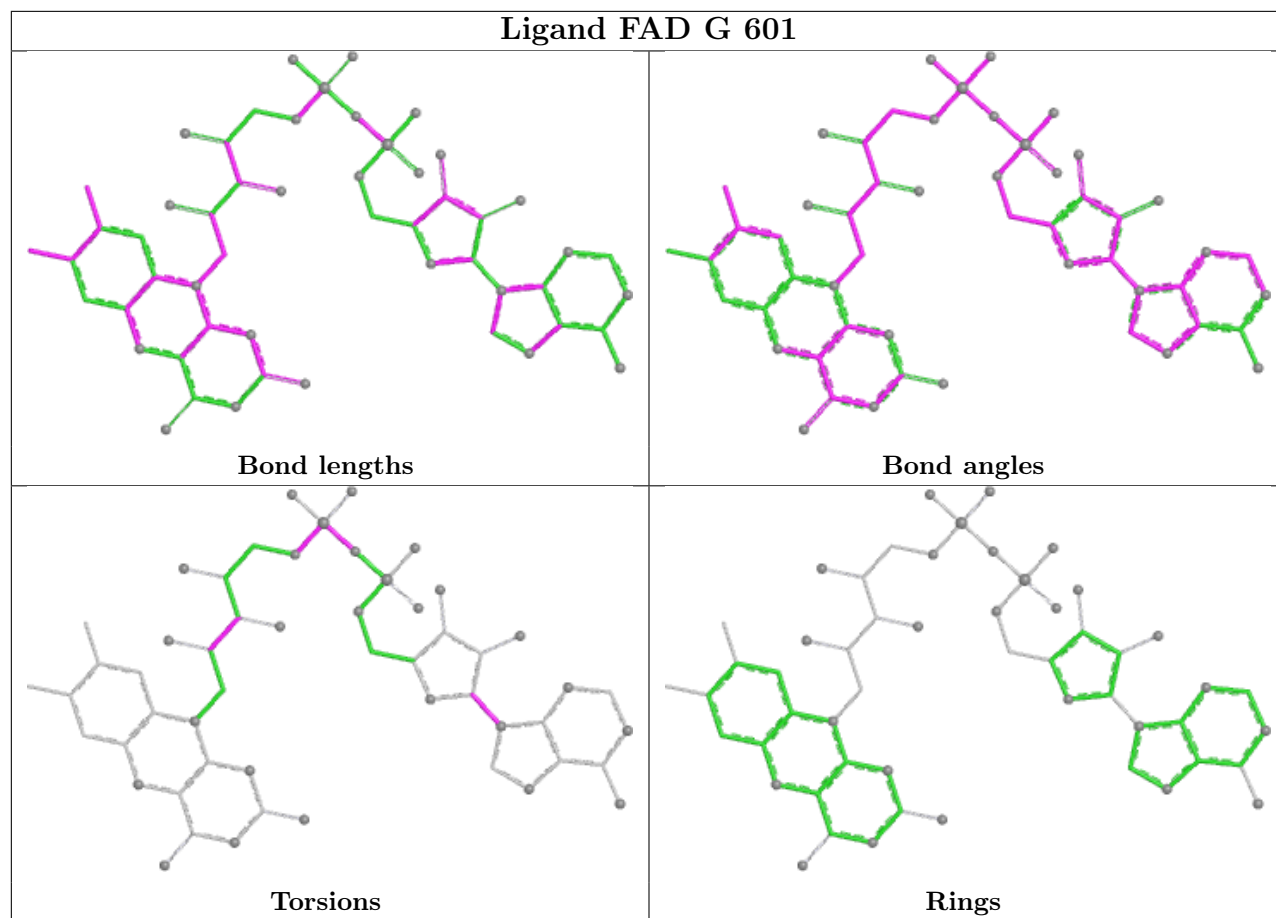
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	601	FAD	10	0
3	A	602	GDU	11	0
2	A	601	FAD	9	0
2	G	601	FAD	13	0
3	C	602	GDU	9	0
3	E	602	GDU	14	0
3	D	602	GDU	4	0
2	E	601	FAD	18	0
2	D	601	FAD	22	0
3	B	602	GDU	17	0
3	F	602	GDU	10	0
2	B	601	FAD	13	0
2	F	601	FAD	13	0
2	C	601	FAD	12	0

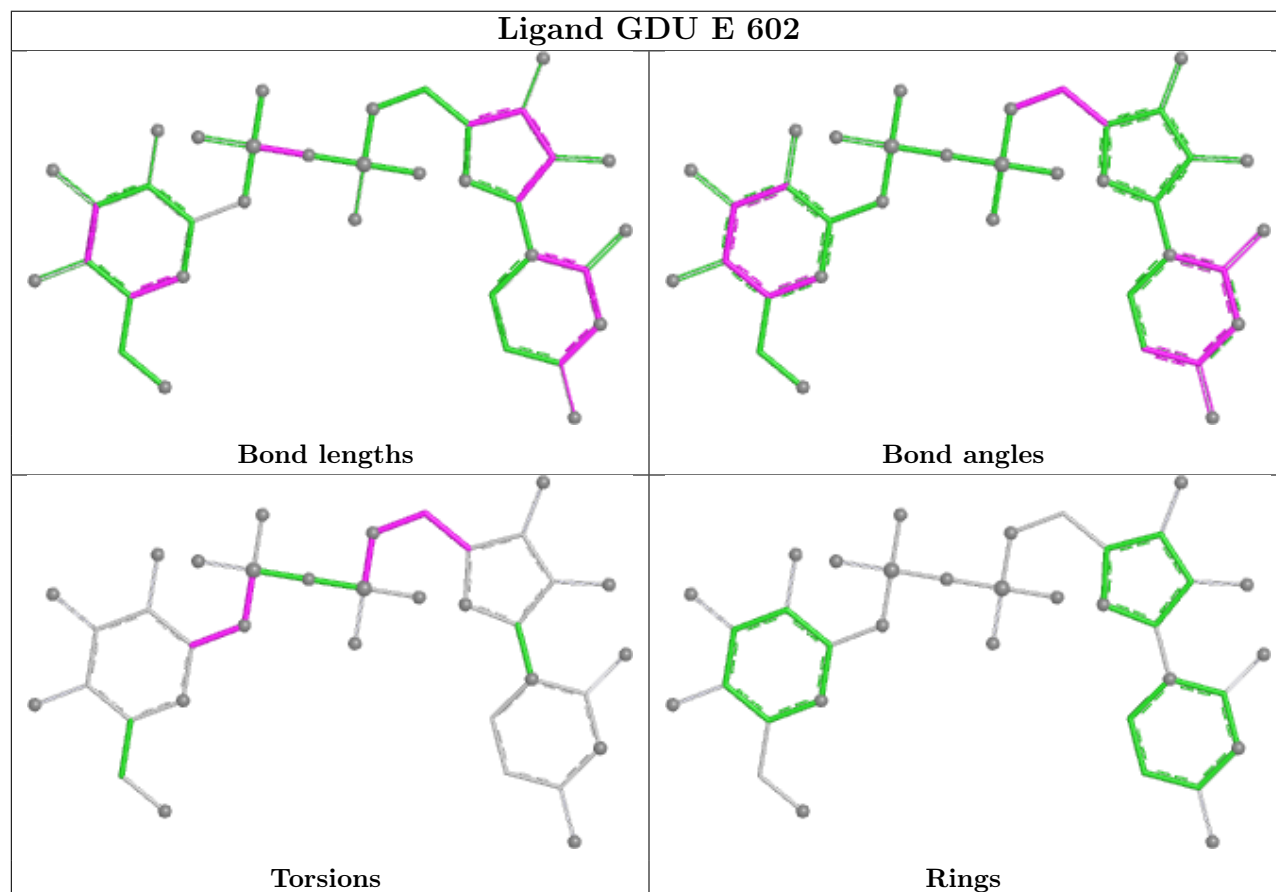
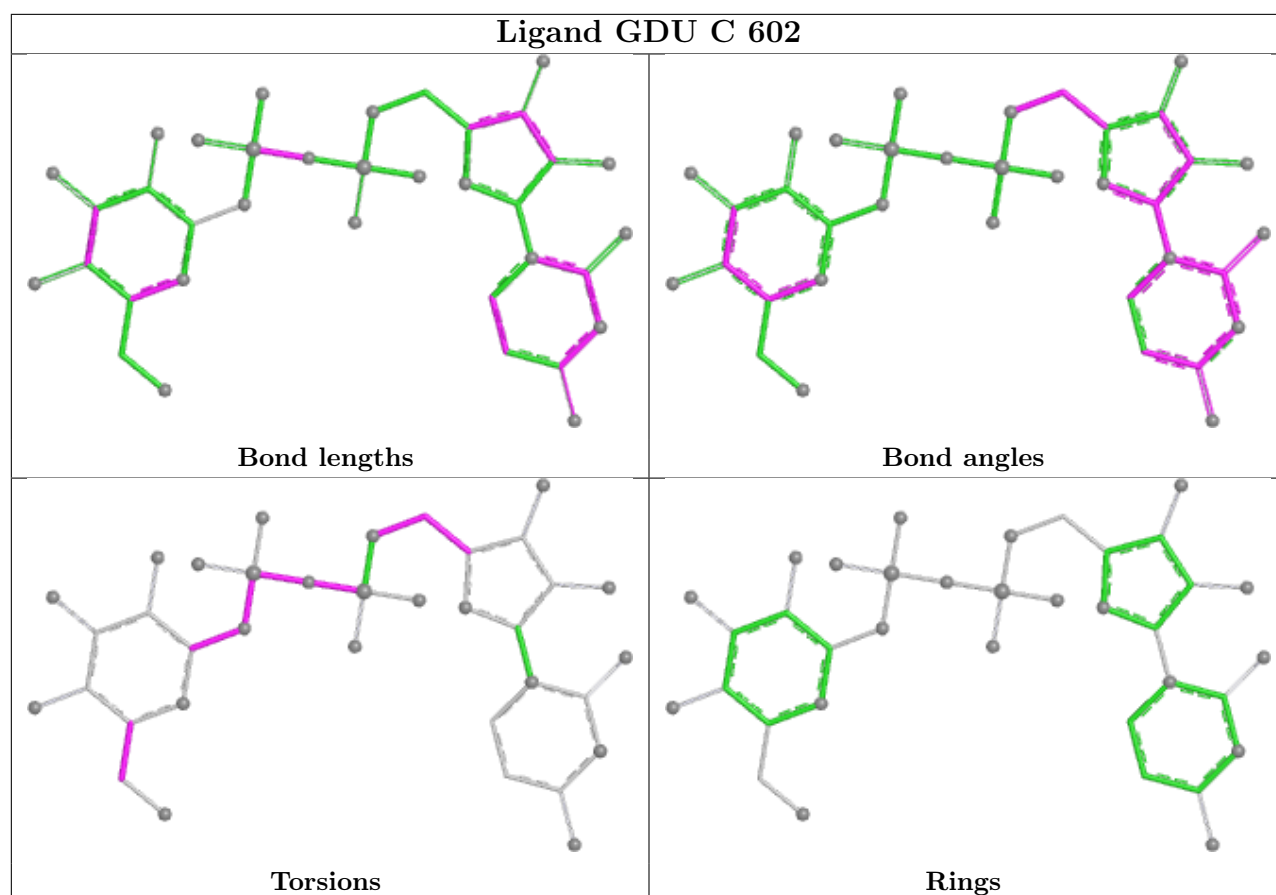
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

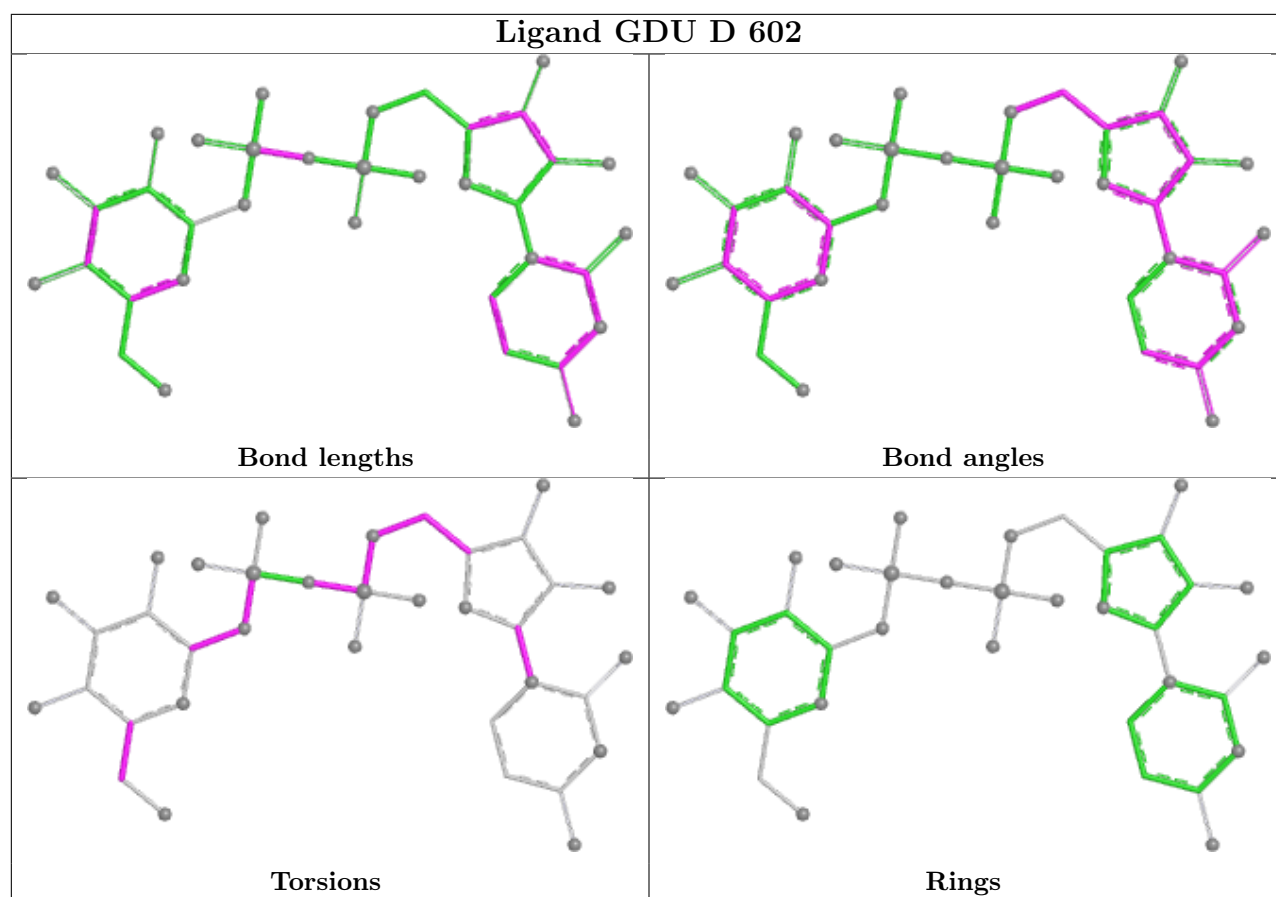


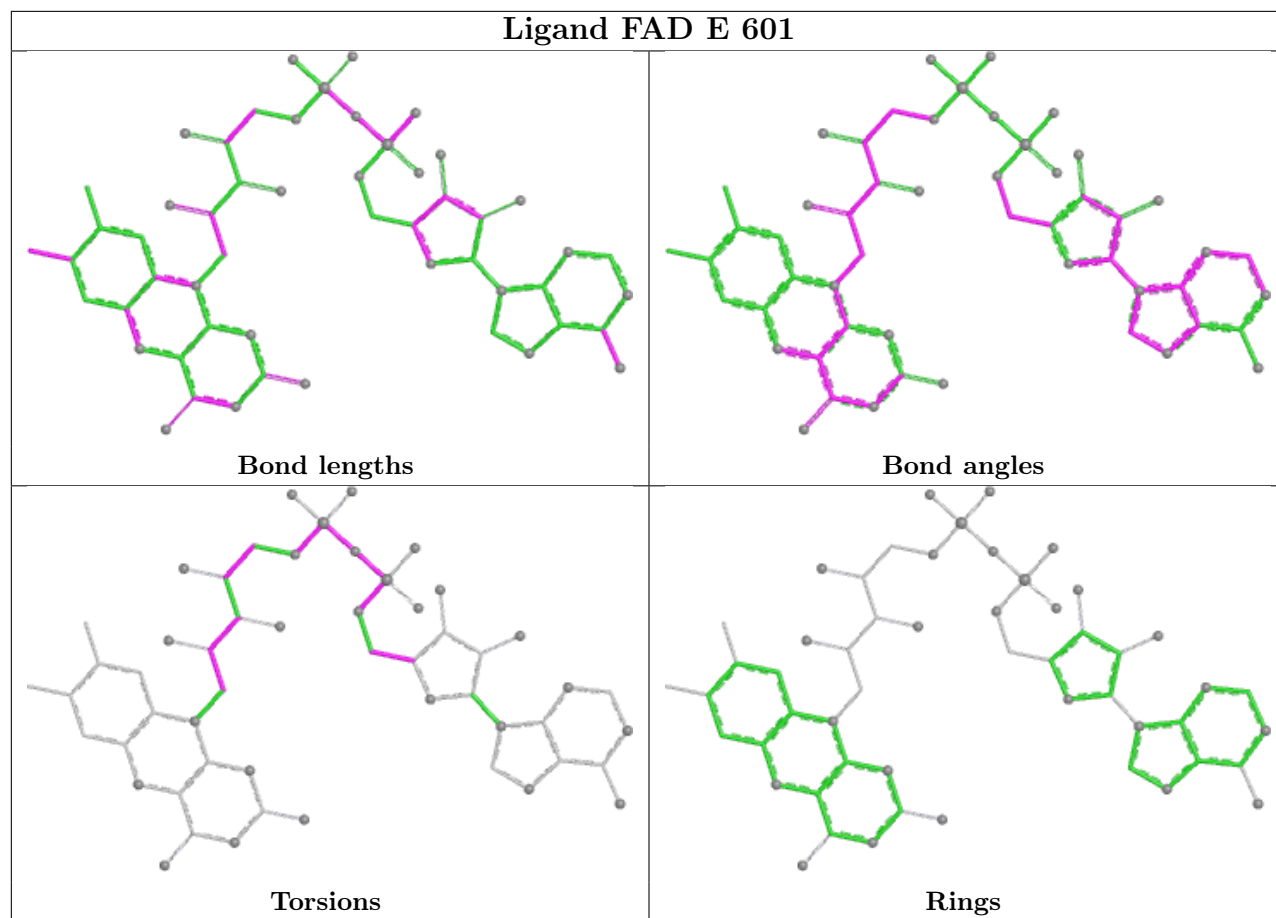


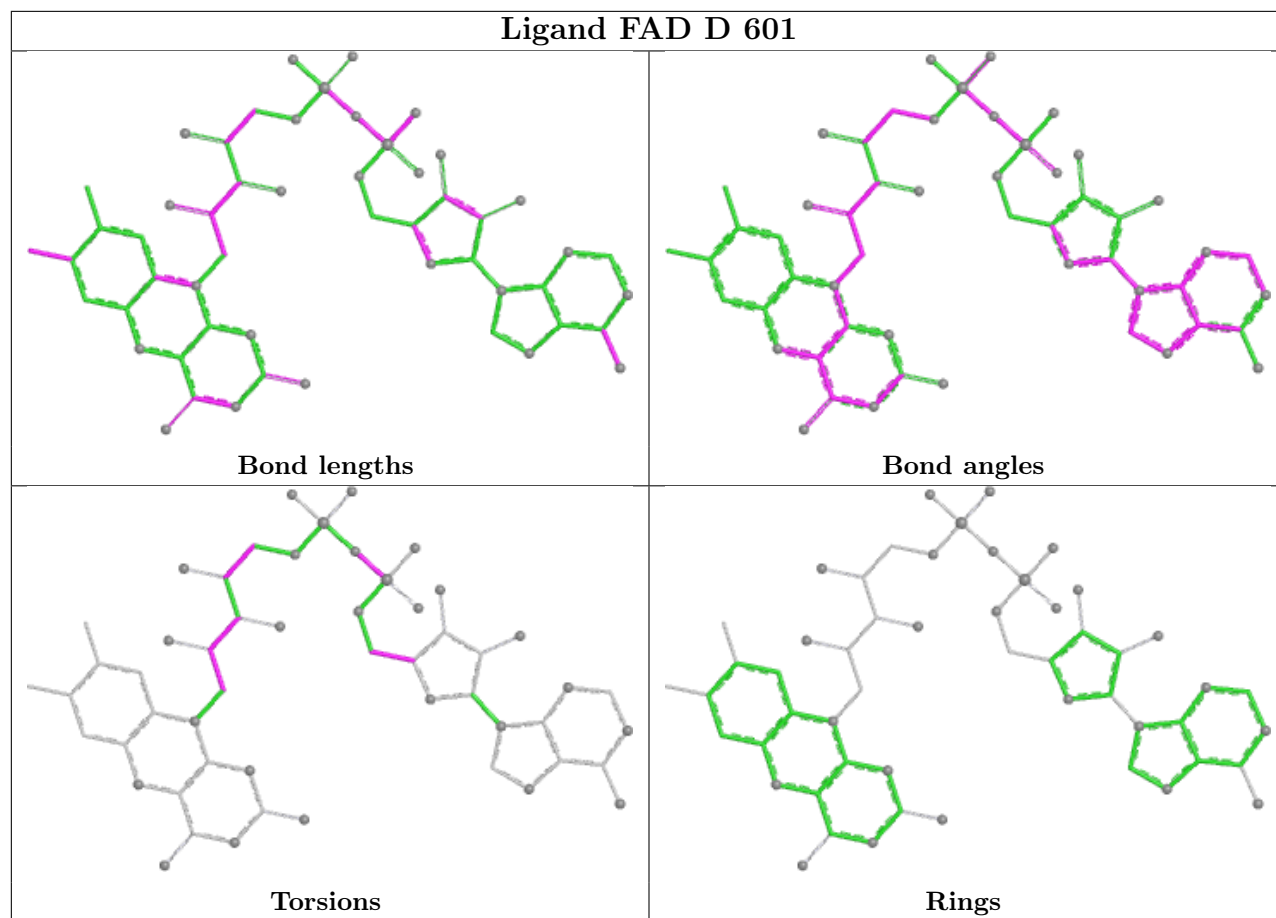


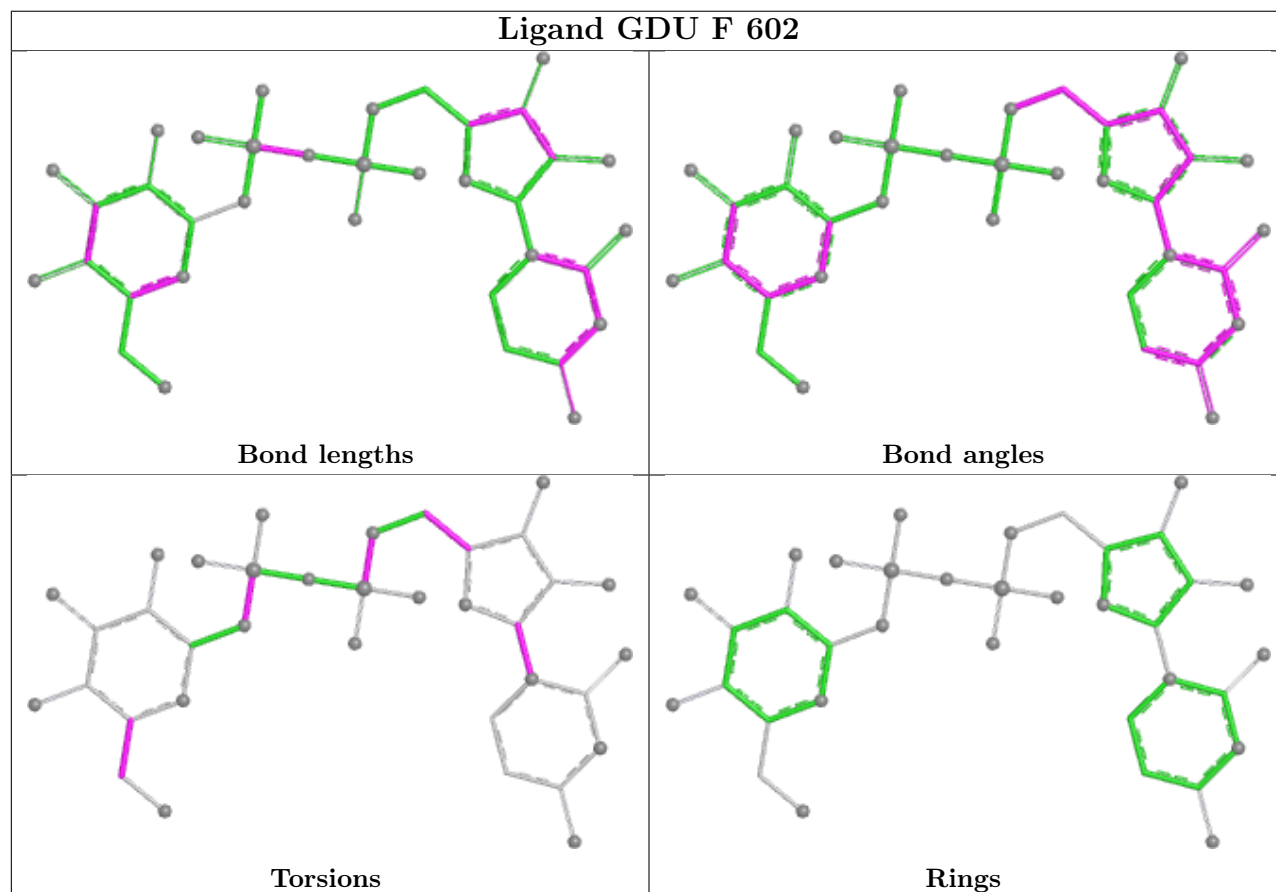
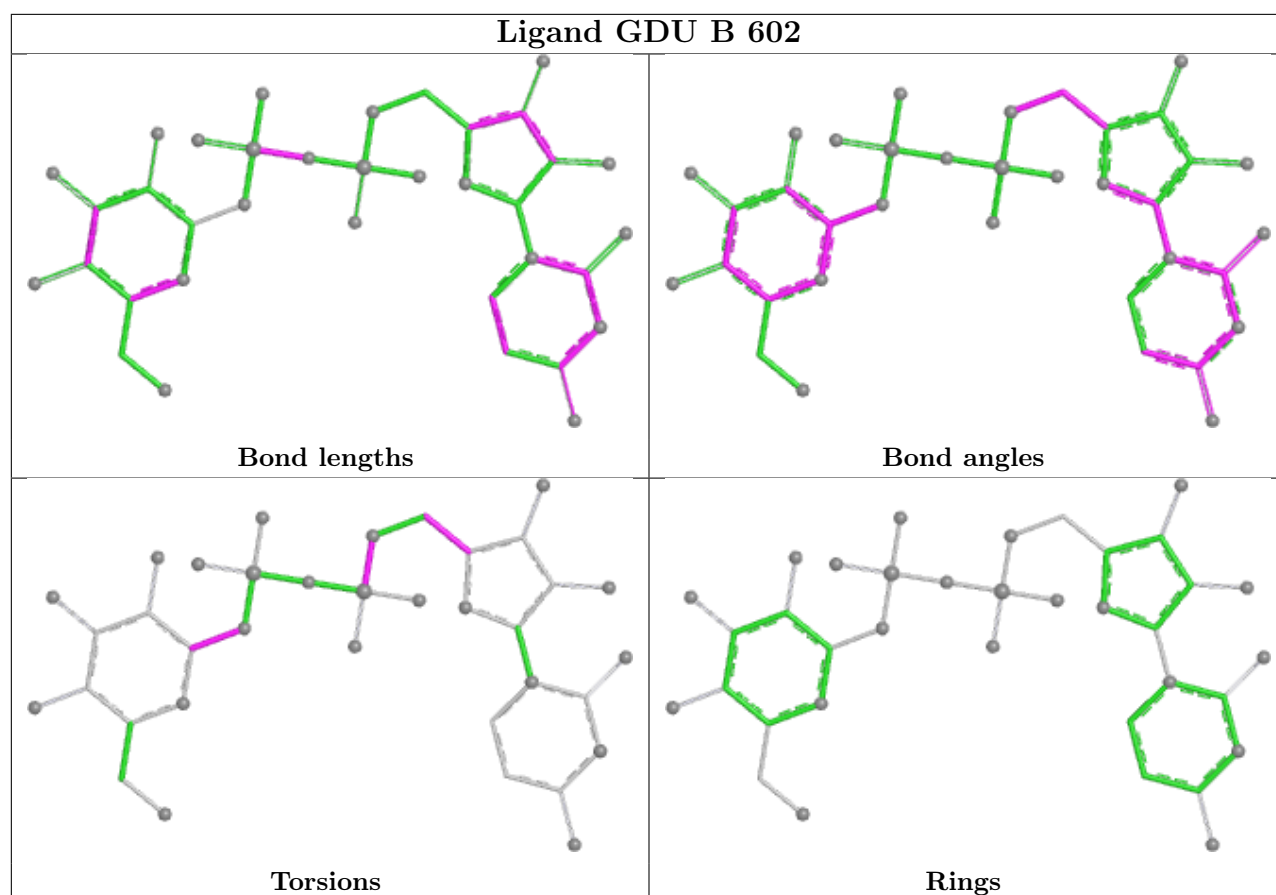


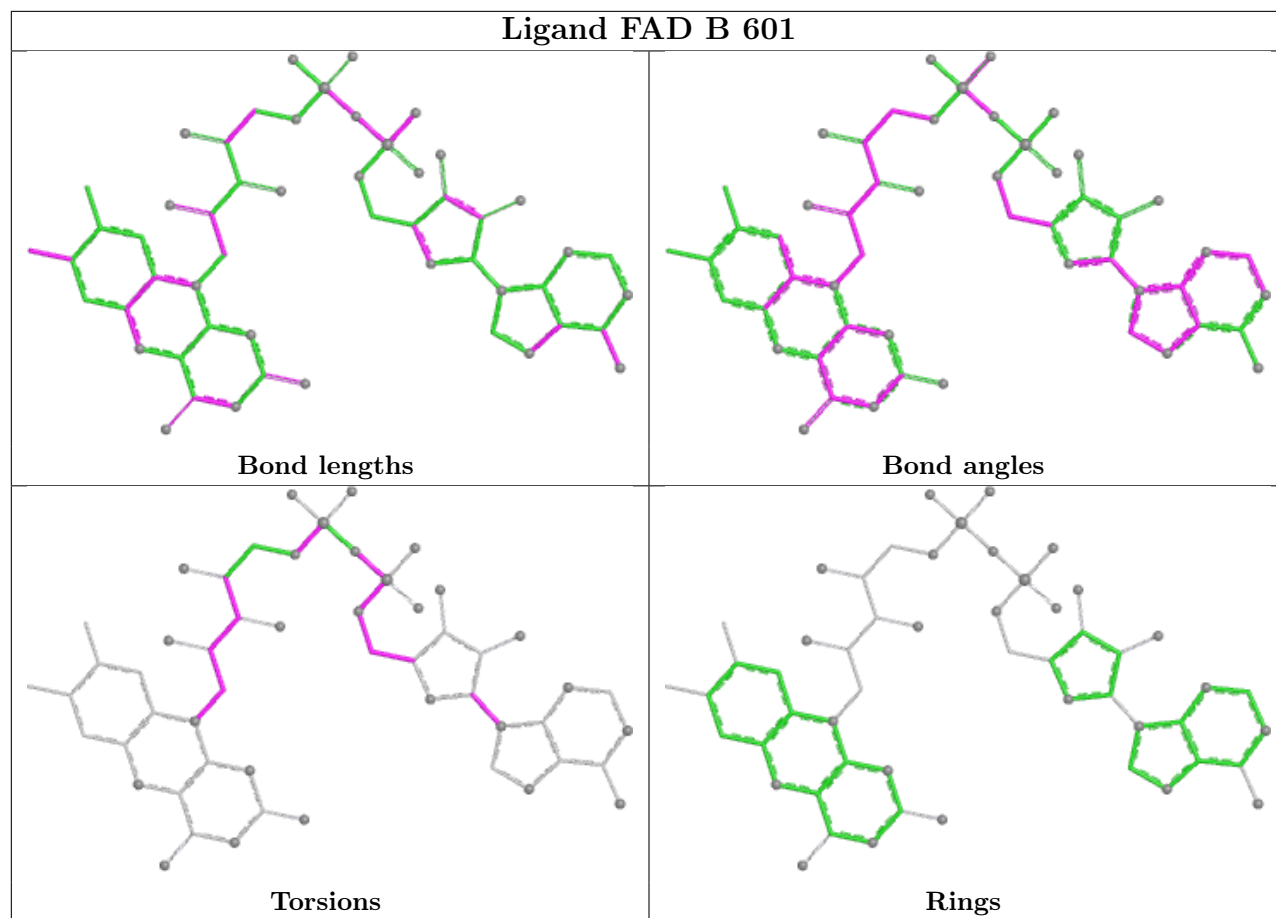


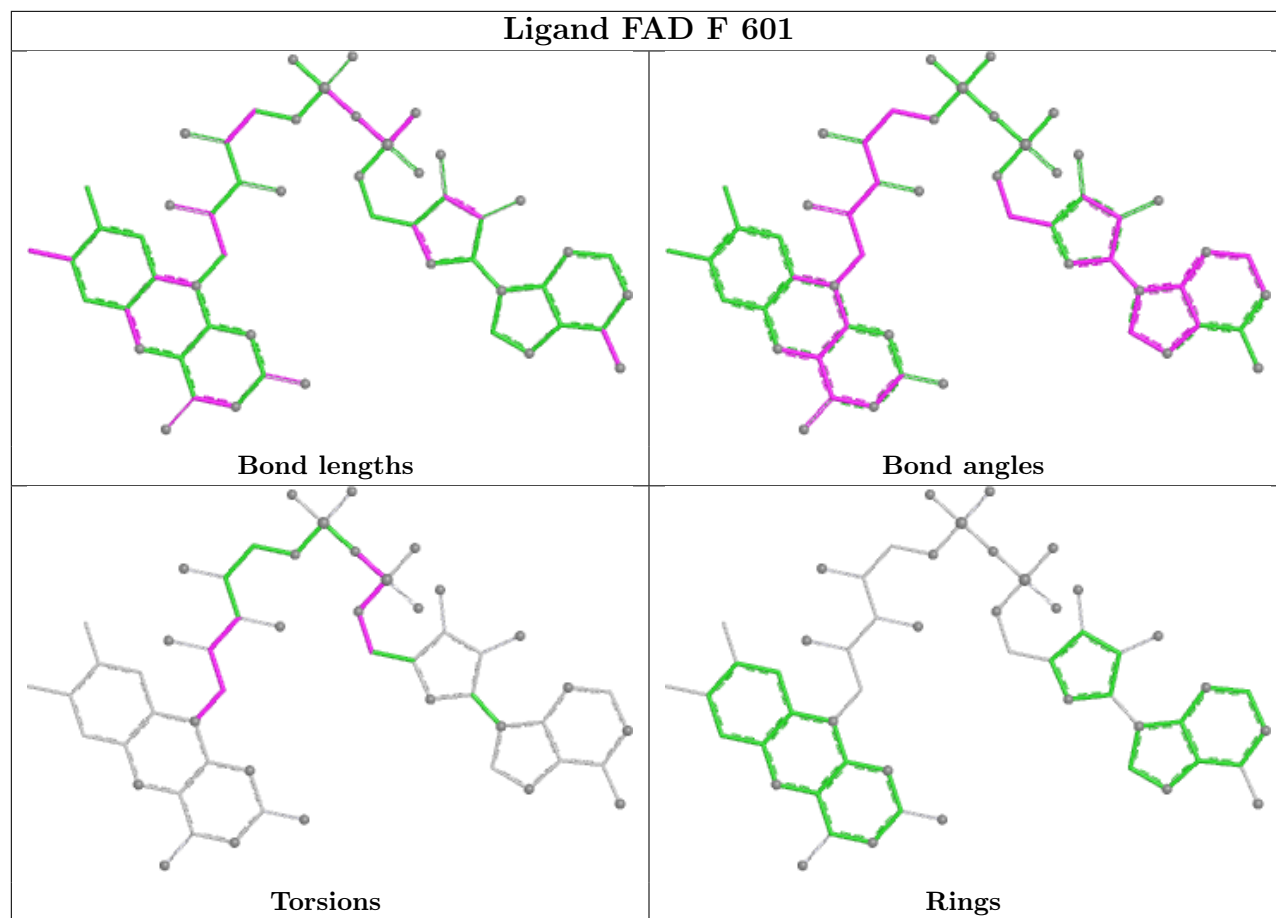


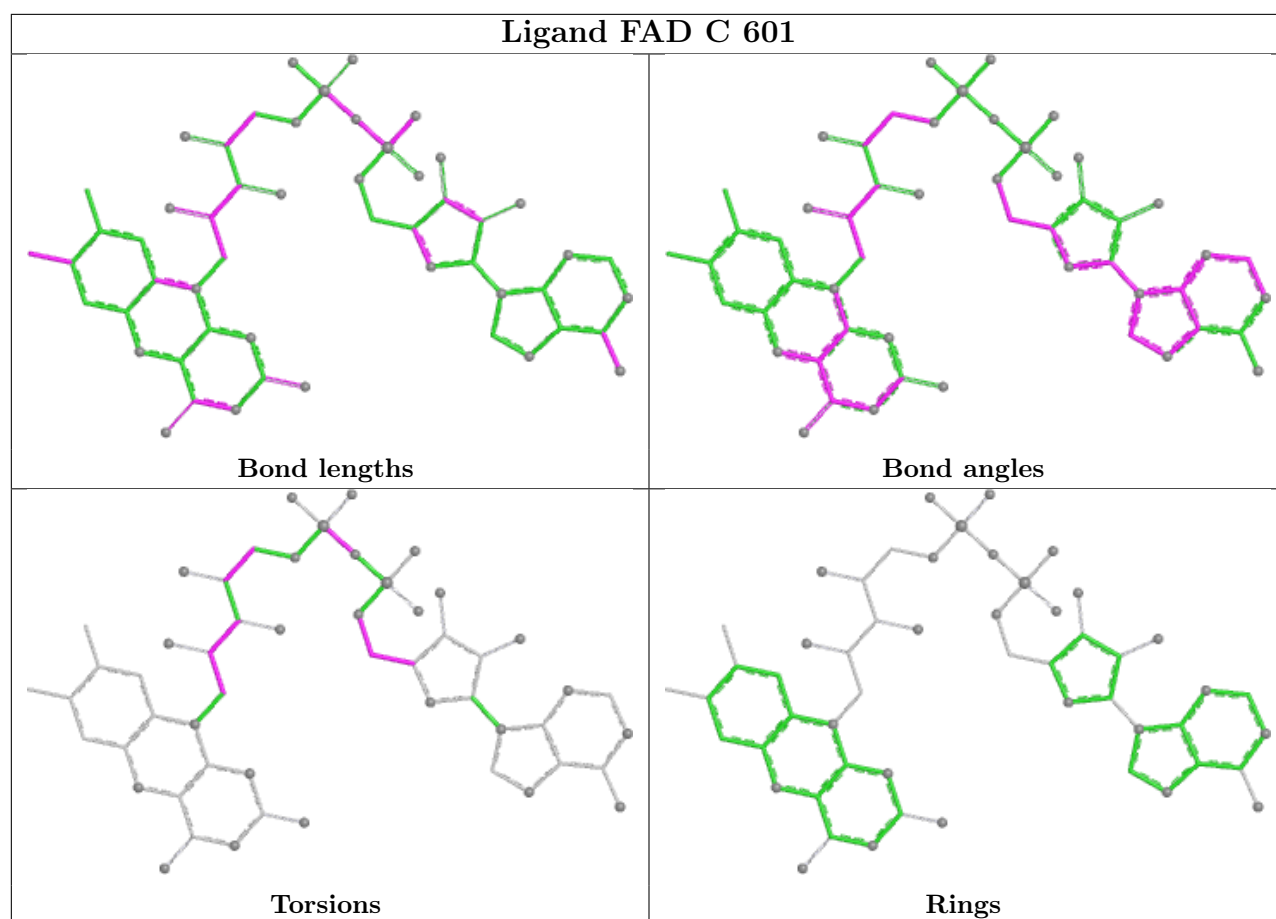












5.7 Other polymers [i](#)

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	509/509 (100%)	-1.63	0 100 100	22, 64, 110, 167	0
1	B	509/509 (100%)	-1.61	0 100 100	24, 64, 106, 166	0
1	C	509/509 (100%)	-1.61	0 100 100	29, 65, 108, 170	0
1	D	509/509 (100%)	-1.62	0 100 100	27, 65, 109, 172	0
1	E	509/509 (100%)	-1.67	0 100 100	22, 62, 99, 156	0
1	F	509/509 (100%)	-1.66	0 100 100	23, 59, 99, 151	0
1	G	509/509 (100%)	-1.68	0 100 100	14, 61, 93, 126	0
1	H	509/509 (100%)	-1.67	0 100 100	22, 63, 94, 132	1 (0%)
All	All	4072/4072 (100%)	-1.64	0 100 100	14, 63, 104, 172	1 (0%)

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates [i](#)

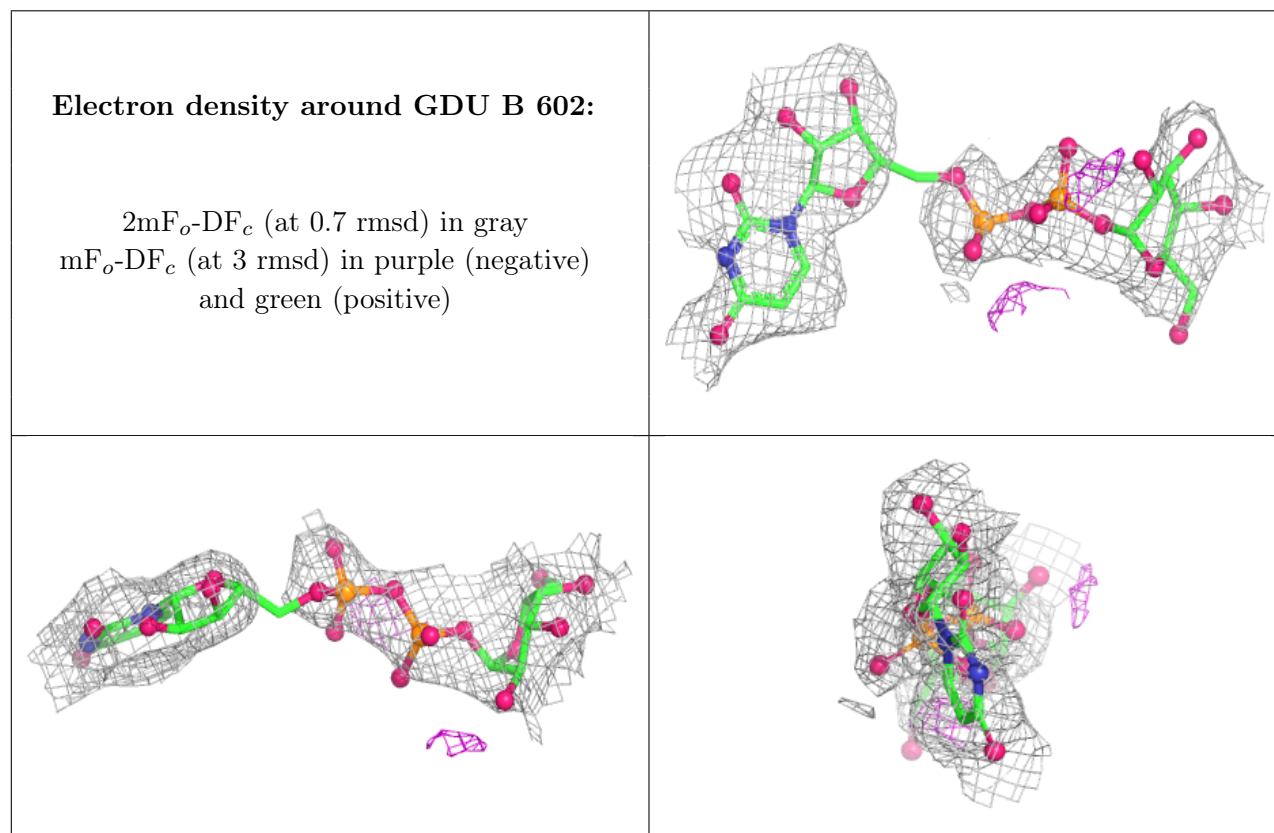
There are no oligosaccharides in this entry.

6.4 Ligands [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.

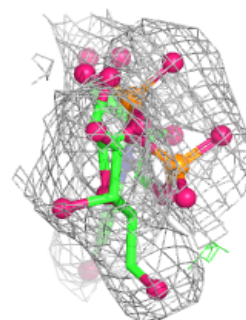
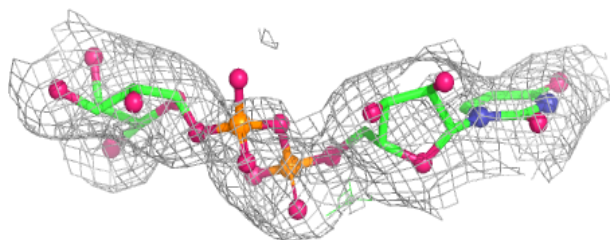
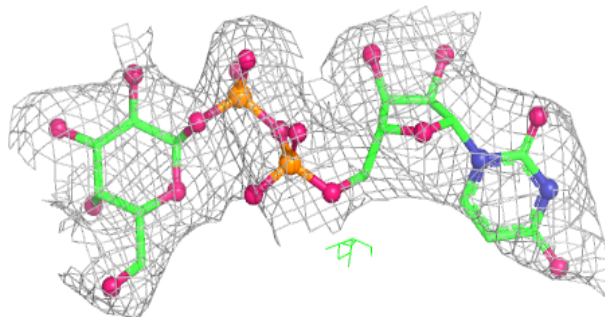
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GDU	B	602	36/36	0.98	0.04	42,114,153,160	0
3	GDU	A	602	36/36	0.99	0.04	30,108,162,203	0
2	FAD	B	601	53/53	0.99	0.03	18,64,87,92	0
3	GDU	C	602	36/36	0.99	0.03	25,103,142,180	0
3	GDU	D	602	36/36	0.99	0.03	35,99,135,179	0
3	GDU	E	602	36/36	0.99	0.04	22,92,139,142	0
3	GDU	F	602	36/36	0.99	0.03	28,101,153,194	0
2	FAD	H	601	53/53	1.00	0.03	20,79,102,111	0
2	FAD	A	601	53/53	1.00	0.02	6,57,87,95	0
2	FAD	C	601	53/53	1.00	0.03	0,49,83,94	0
2	FAD	D	601	53/53	1.00	0.02	0,57,88,102	0
2	FAD	E	601	53/53	1.00	0.03	14,57,97,102	0
2	FAD	F	601	53/53	1.00	0.03	12,67,90,107	0
2	FAD	G	601	53/53	1.00	0.03	0,57,86,102	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.

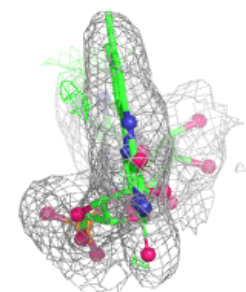
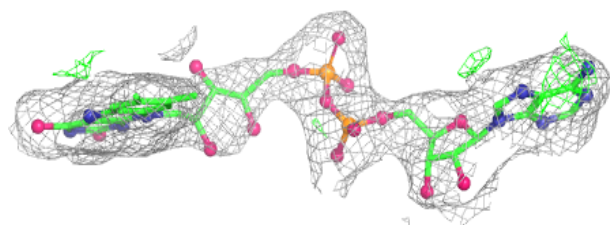
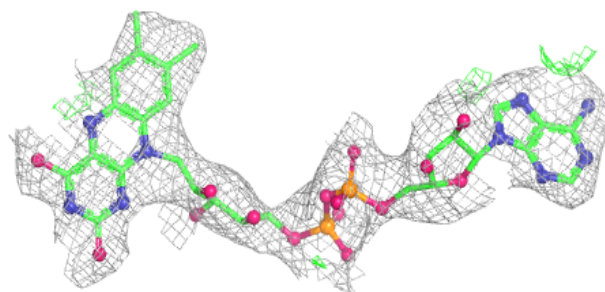


Electron density around GDU A 602:

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

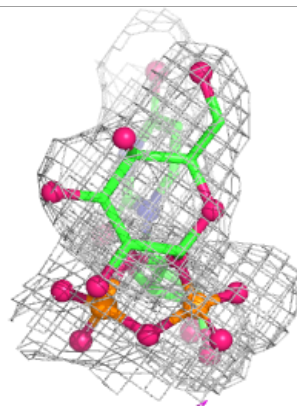
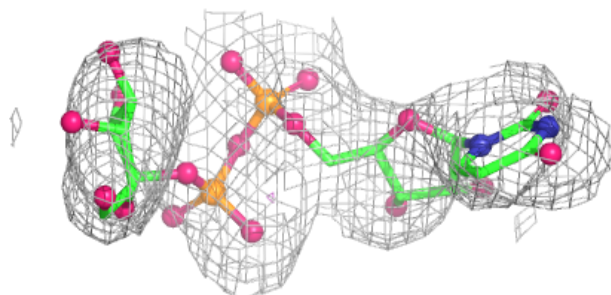
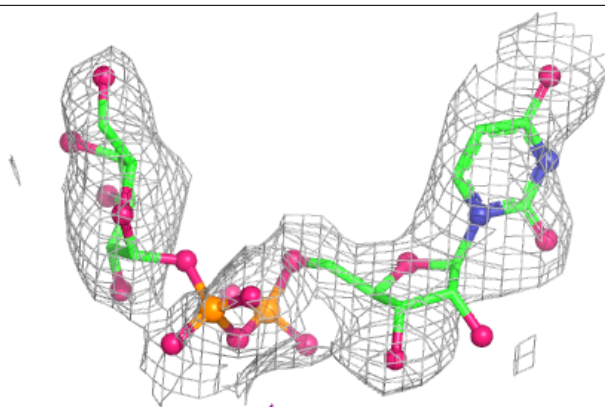
**Electron density around FAD B 601:**

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

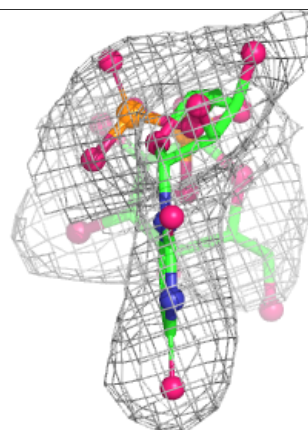
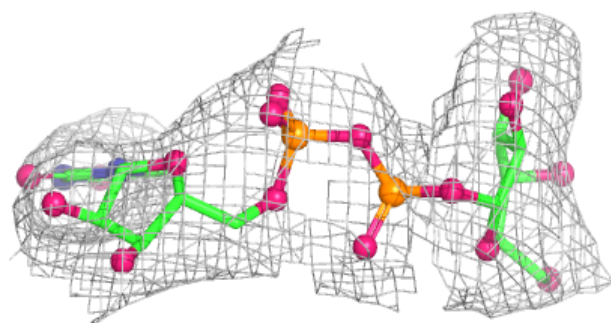
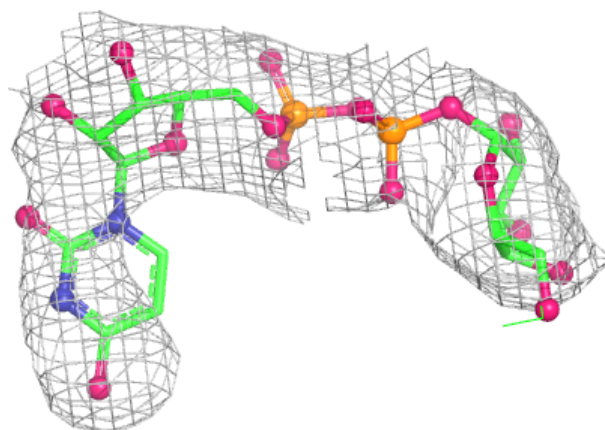


Electron density around GDU C 602:

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

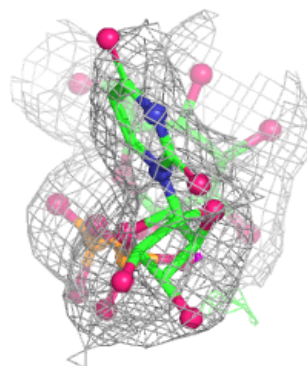
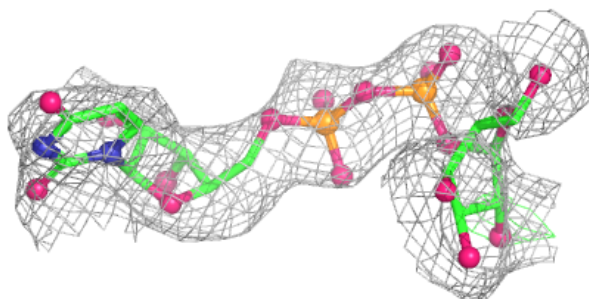
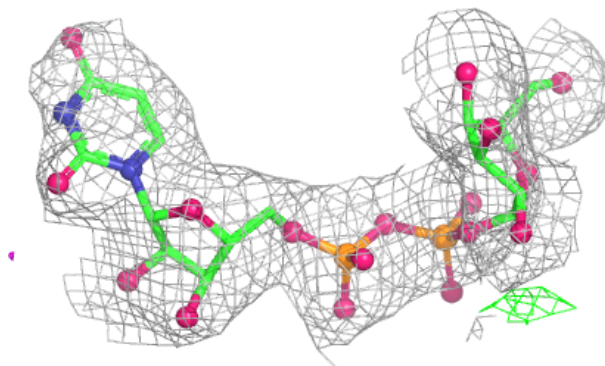
**Electron density around GDU D 602:**

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

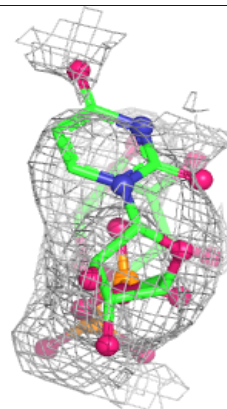
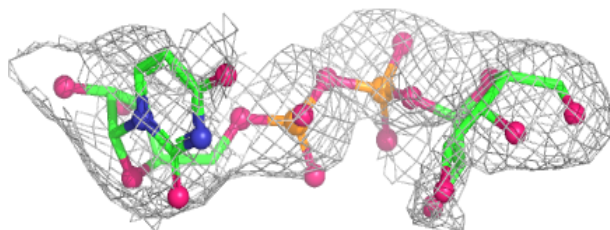
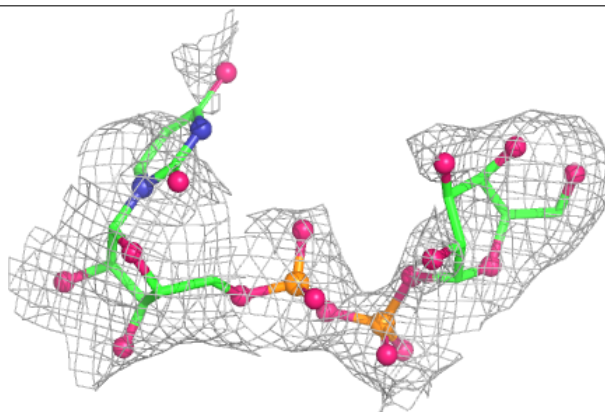


Electron density around GDU E 602:

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

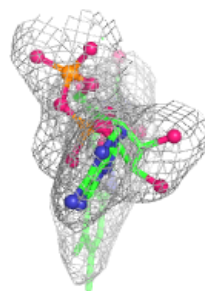
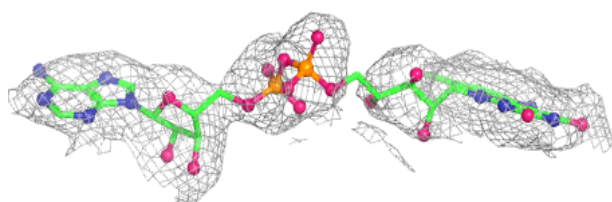
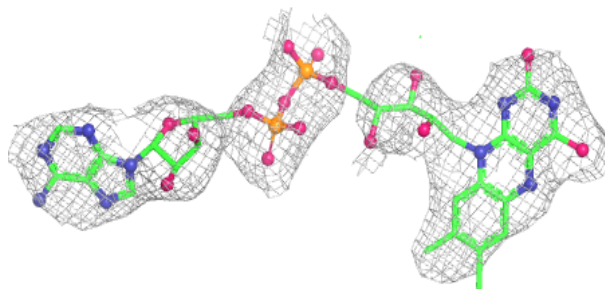
**Electron density around GDU F 602:**

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

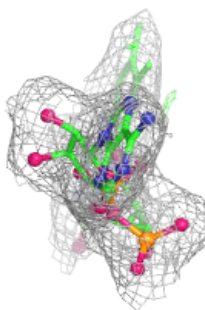
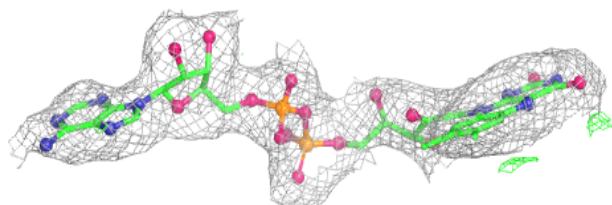
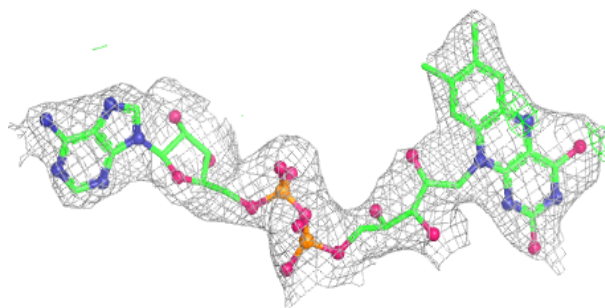


Electron density around FAD H 601:

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

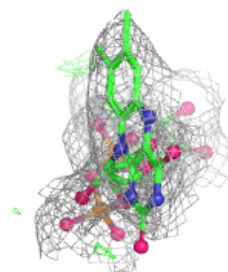
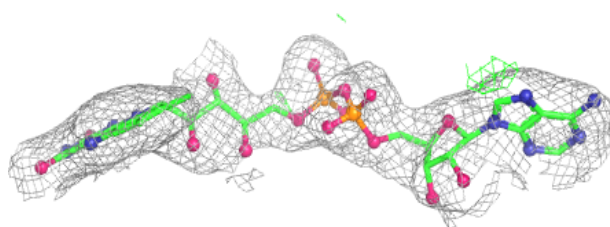
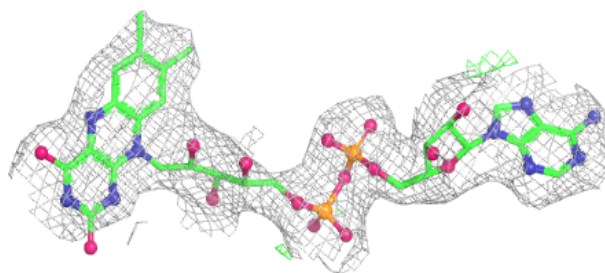
**Electron density around FAD A 601:**

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

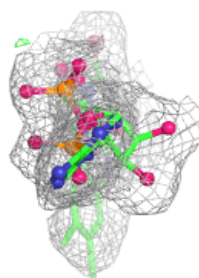
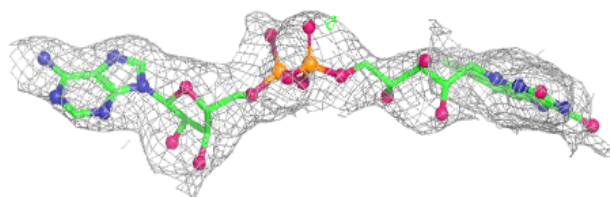
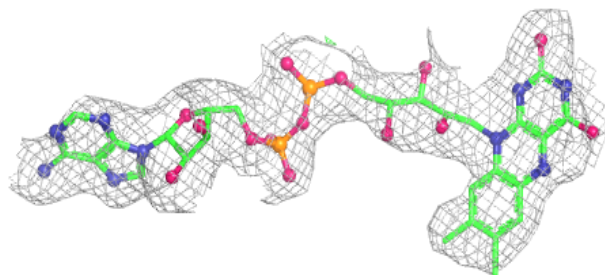


Electron density around FAD C 601:

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

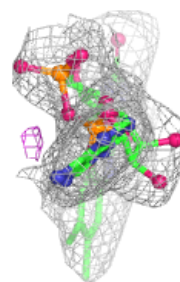
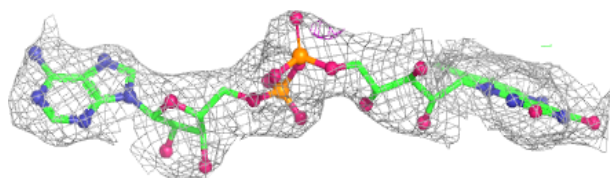
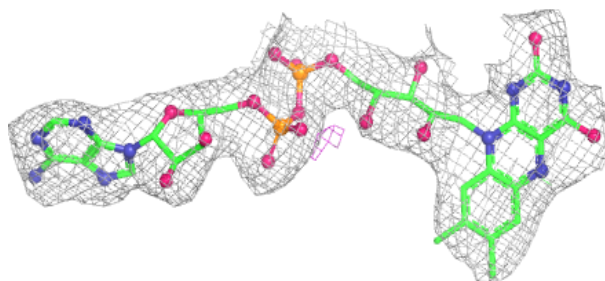
**Electron density around FAD D 601:**

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

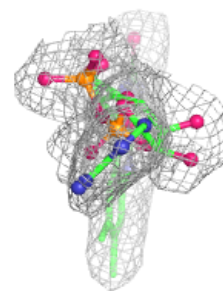
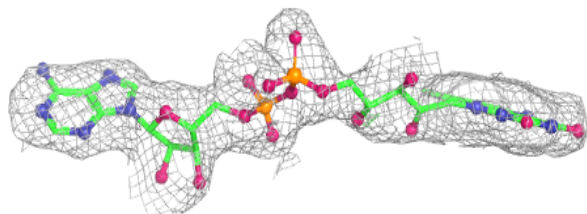
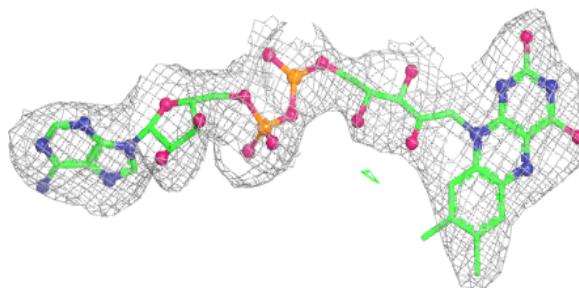


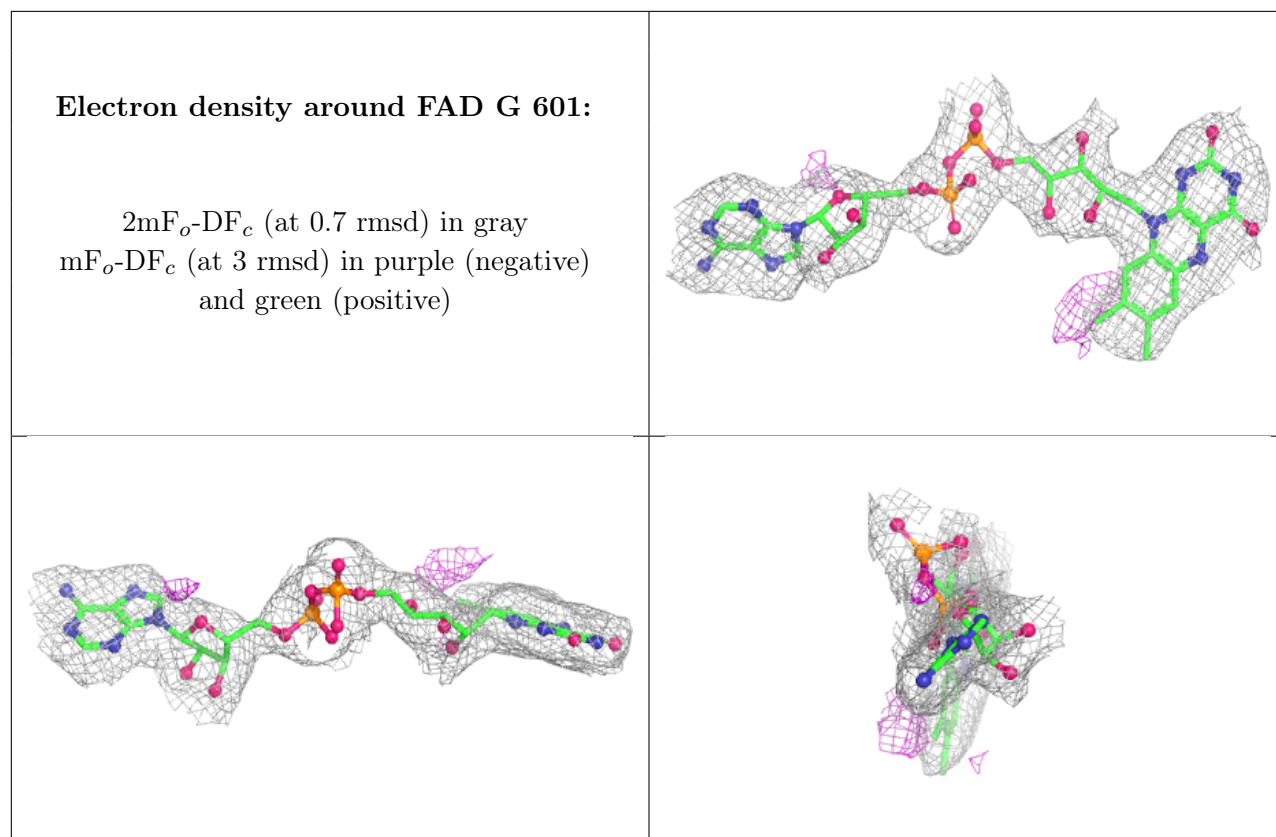
Electron density around FAD E 601:

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

**Electron density around FAD F 601:**

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





6.5 Other polymers [i](#)

There are no such residues in this entry.