



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 29, 2021 – 12:21 PM EDT

PDB ID : 7LJU  
Title : Porcine Dihydropyrimidine Dehydrogenase (DPD) crosslinked with 5-Ethynyluracil (5EU)  
Authors : Butrin, A.; Forouzesh, D.; Beaupre, B.; Wawrzak, Z.; Liu, D.; Moran, G.  
Deposited on : 2021-01-30  
Resolution : 1.87 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.18  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.18

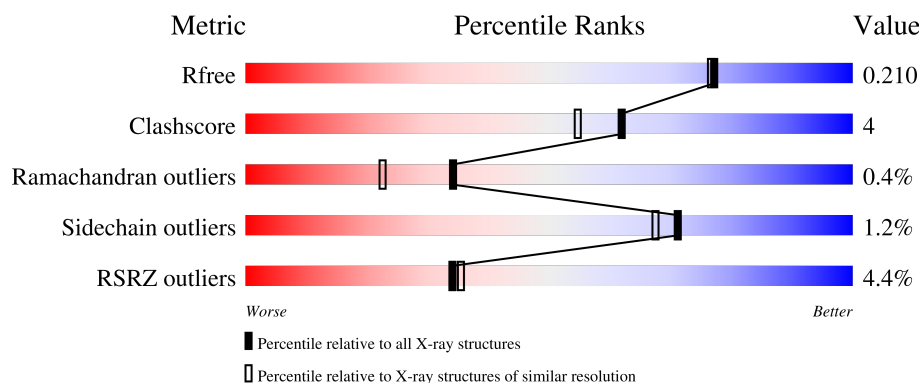
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.87 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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  $\geq 3$ , 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	1025	<div> <div>4%</div> <div>91%</div> <div>8%</div> <div>.</div> </div>
1	B	1025	<div> <div>5%</div> <div>89%</div> <div>9%</div> <div>..</div> </div>
1	C	1025	<div> <div>4%</div> <div>89%</div> <div>9%</div> <div>.</div> </div>
1	D	1025	<div> <div>4%</div> <div>88%</div> <div>10%</div> <div>..</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	FNR	A	1108	X	-	-	-
6	FNR	B	1107	X	-	-	-
6	FNR	C	1107	X	-	-	-
6	FNR	D	1108	X	-	-	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 34870 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.

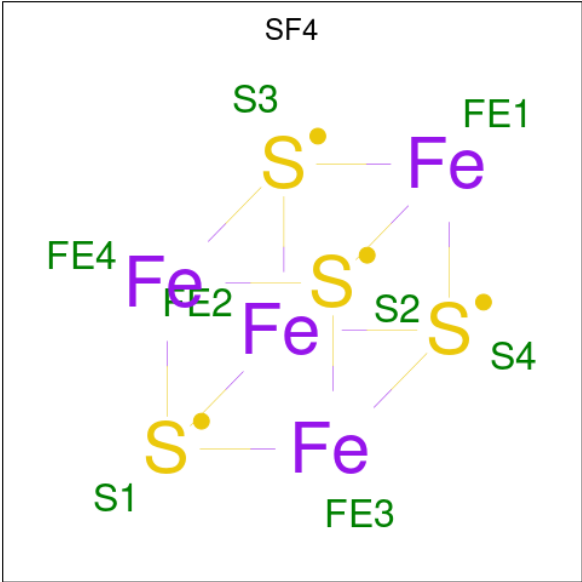
- Molecule 1 is a protein called Dihydropyrimidine dehydrogenase [NADP(+)].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1016	Total	C	N	O	S	66	0	0
			7727	4900	1306	1465	56			
1	C	1004	Total	C	N	O	S	0	0	0
			7656	4859	1295	1450	52			
1	D	1017	Total	C	N	O	S	43	0	0
			7746	4914	1314	1462	56			
1	B	1004	Total	C	N	O	S	0	0	0
			7656	4859	1295	1450	52			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	60	ASP	GLY	conflict	UNP Q28943
C	60	ASP	GLY	conflict	UNP Q28943
D	60	ASP	GLY	conflict	UNP Q28943
B	60	ASP	GLY	conflict	UNP Q28943

- Molecule 2 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



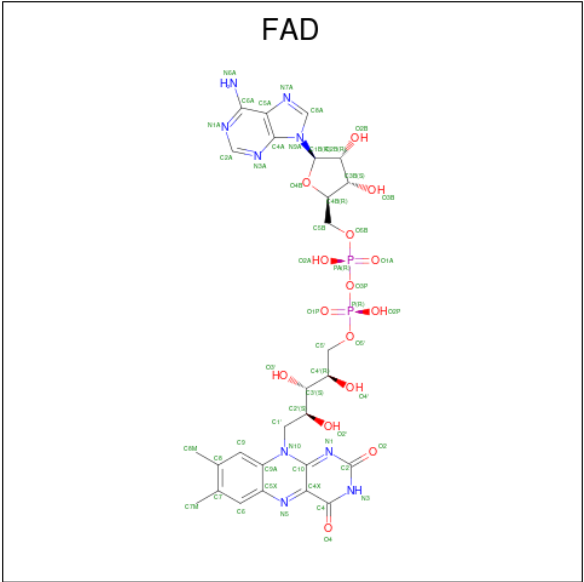
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			8	4	4		
2	A	1	Total	Fe	S	0	0
			8	4	4		
2	A	1	Total	Fe	S	0	0
			8	4	4		
2	A	1	Total	Fe	S	0	0
			8	4	4		
2	C	1	Total	Fe	S	0	0
			8	4	4		
2	C	1	Total	Fe	S	0	0
			8	4	4		
2	C	1	Total	Fe	S	0	0
			8	4	4		
2	D	1	Total	Fe	S	0	0
			8	4	4		
2	D	1	Total	Fe	S	0	0
			8	4	4		
2	D	1	Total	Fe	S	0	0
			8	4	4		
2	D	1	Total	Fe	S	0	0
			8	4	4		
2	B	1	Total	Fe	S	0	0
			8	4	4		
2	B	1	Total	Fe	S	0	0
			8	4	4		

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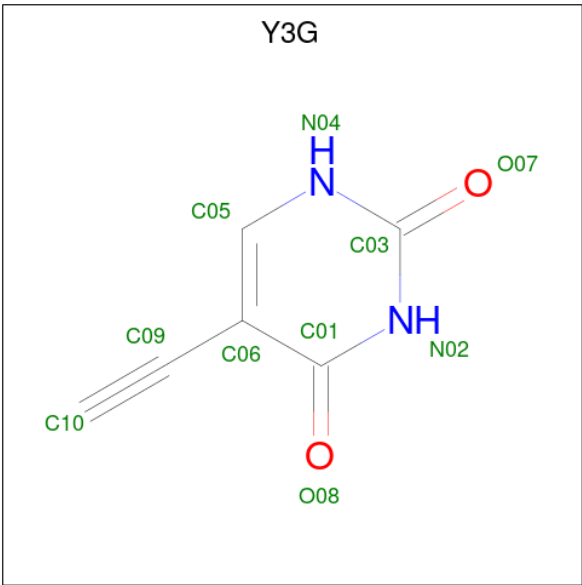
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	Fe	S	0	0
			8	4	4		
2	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C<sub>27</sub>H<sub>33</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



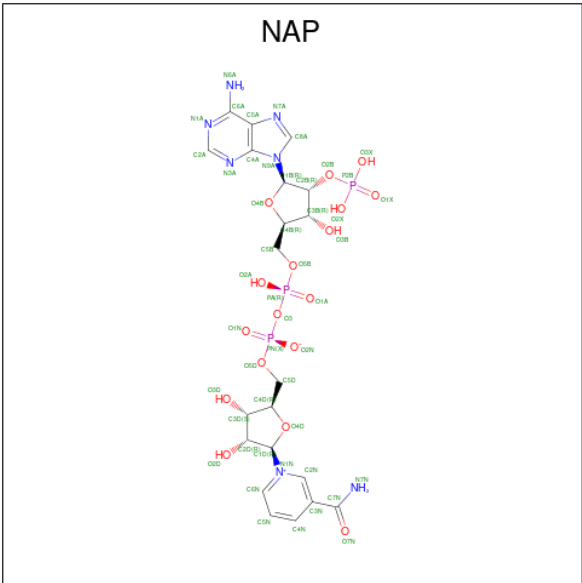
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is 5-ethynylpyrimidine-2,4(1H,3H)-dione (three-letter code: Y3G) (formula: C<sub>6</sub>H<sub>4</sub>N<sub>2</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



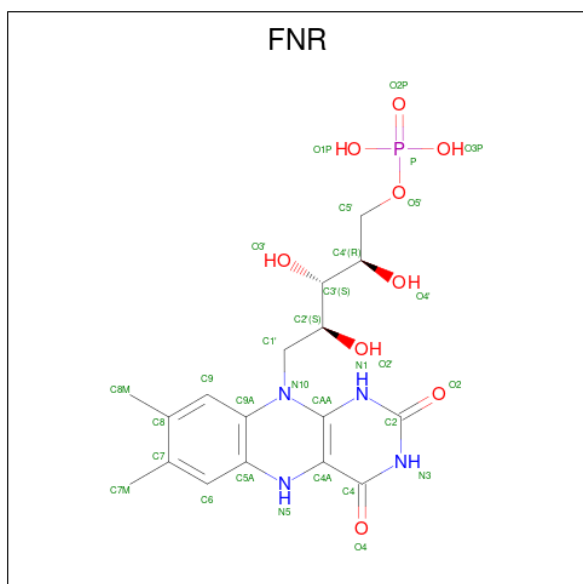
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			10	6	2	2		
4	C	1	Total	C	N	O	0	0
			10	6	2	2		
4	D	1	Total	C	N	O	0	0
			10	6	2	2		
4	B	1	Total	C	N	O	0	0
			10	6	2	2		

- Molecule 5 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
5	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
5	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
5	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 6 is 1-DEOXY-1-(7,8-DIMETHYL-2,4-DIOXO-3,4-DIHYDRO-2H-BENZO[G]P  
TERIDIN-1-ID-10(5H)-YL)-5-O-PHOSPHONATO-D-RIBITOL (three-letter code: FNR)  
(formula:  $C_{17}H_{23}N_4O_9P$ ) (labeled as "Ligand of Interest" by depositor).





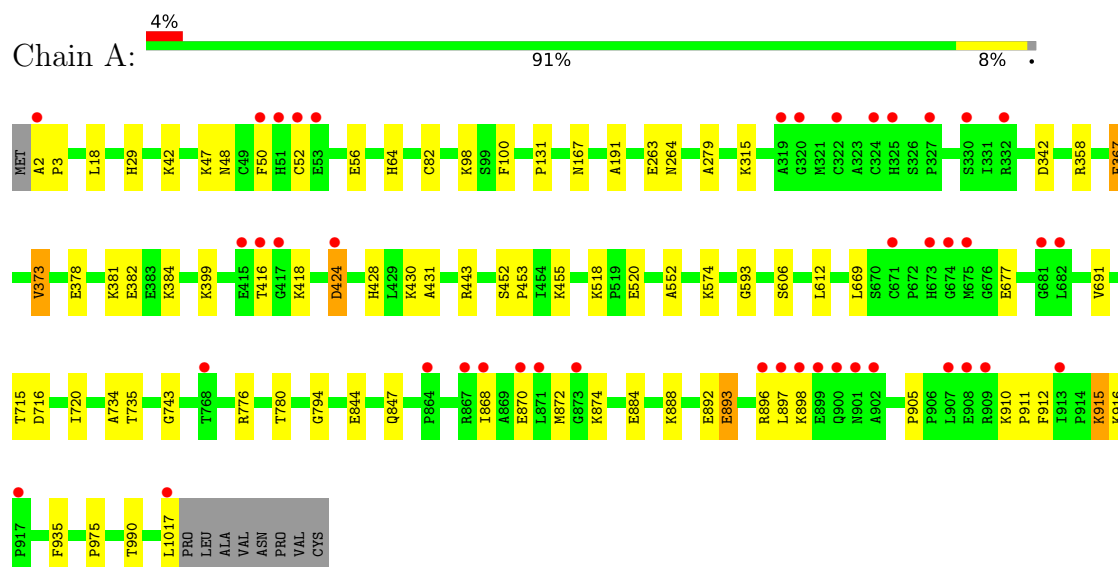
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	861	Total 861	O 861	0	0
7	D	891	Total 891	O 891	0	0
7	B	770	Total 770	O 770	0	0

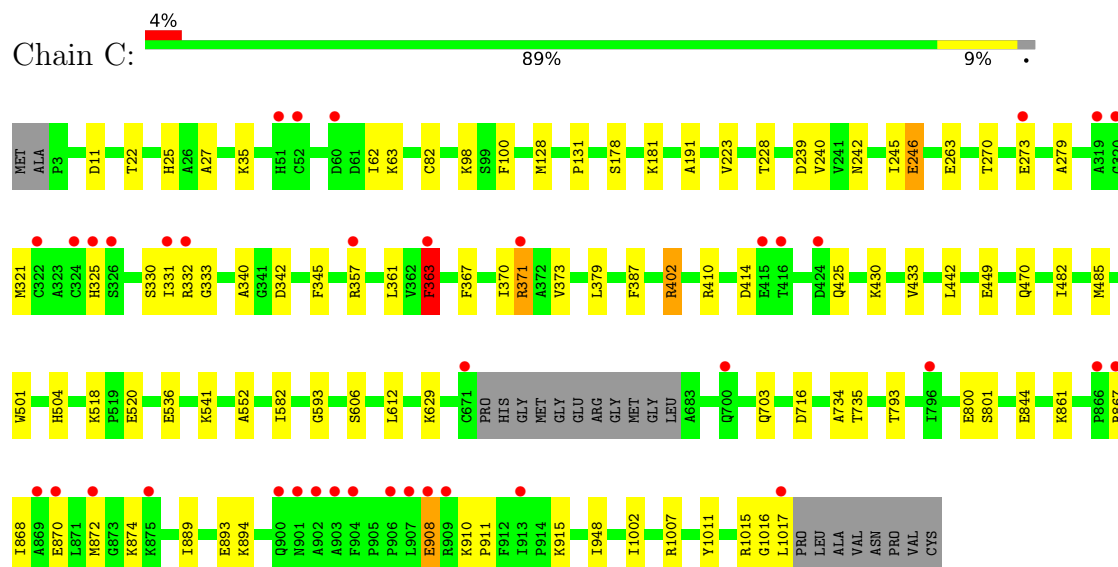
### 3 Residue-property plots [i](#)

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

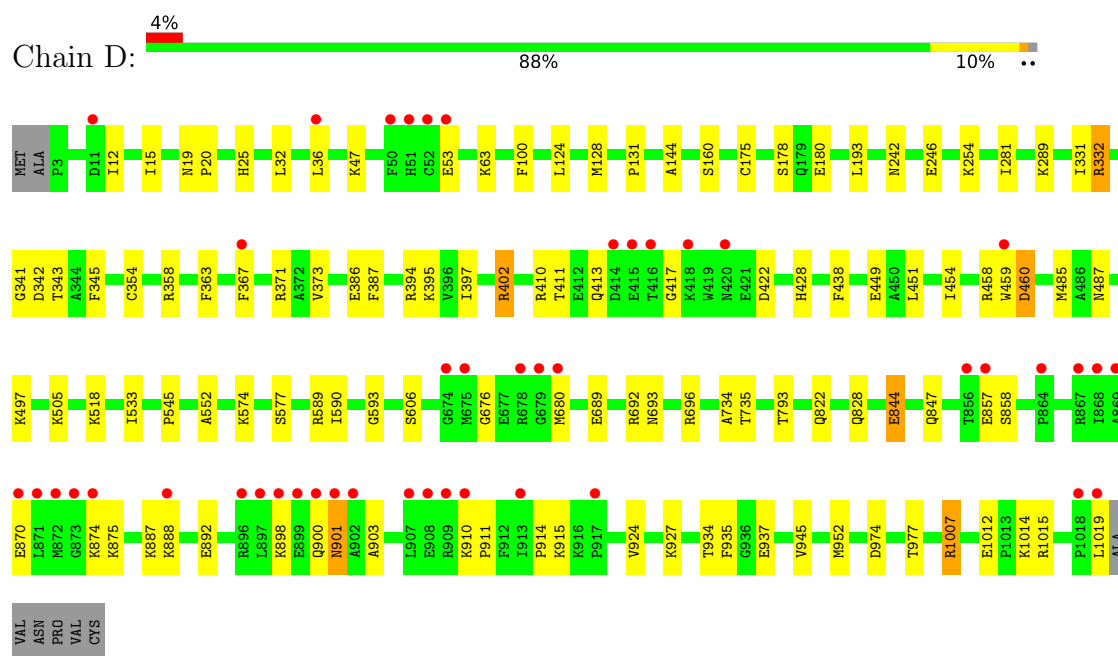
- Molecule 1: Dihydropyrimidine dehydrogenase [NADP(+)]



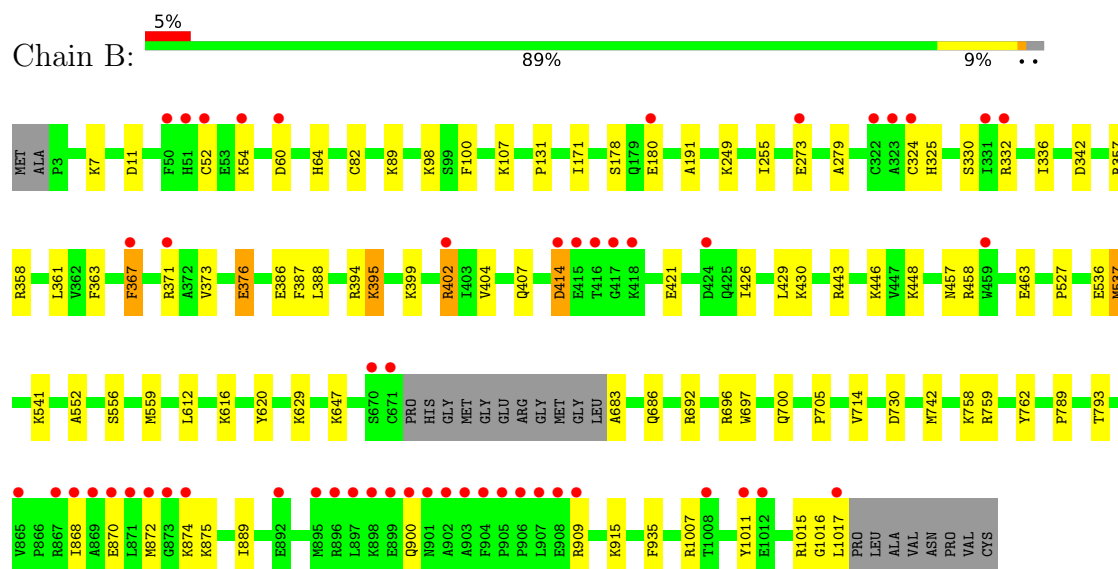
- Molecule 1: Dihydropyrimidine dehydrogenase [NADP(+)]



- Molecule 1: Dihydropyrimidine dehydrogenase [NADP(+)]



- Molecule 1: Dihydropyrimidine dehydrogenase [NADP(+)]



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.06Å 158.94Å 163.21Å 90.00° 96.03° 90.00°	Depositor
Resolution (Å)	40.59 – 1.87 45.46 – 1.87	Depositor EDS
% Data completeness (in resolution range)	98.2 (40.59-1.87) 98.3 (45.46-1.87)	Depositor EDS
$R_{merge}$	0.21	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.32 (at 1.87Å)	Xtriage
Refinement program	PHENIX 1.19_4092	Depositor
R, $R_{free}$	0.172 , 0.211 0.172 , 0.210	Depositor DCC
$R_{free}$ test set	16922 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.4	Xtriage
Anisotropy	0.372	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 41.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	34870	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.65% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: SF4, FNR, FAD, Y3G, NAP

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	0.42	1/7887 (0.0%)	0.64	3/10691 (0.0%)
1	B	0.42	2/7813 (0.0%)	0.86	8/10590 (0.1%)
1	C	0.42	1/7813 (0.0%)	0.67	6/10590 (0.1%)
1	D	0.42	0/7908	0.75	4/10719 (0.0%)
All	All	0.42	4/31421 (0.0%)	0.73	21/42590 (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	A	0	2
1	B	0	1
1	C	0	1
1	D	0	2
All	All	0	6

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	367	PHE	CB-CG	-7.49	1.38	1.51
1	A	367	PHE	CB-CG	-6.73	1.40	1.51
1	C	246	GLU	CB-CG	-6.26	1.40	1.52
1	B	395	LYS	CB-CG	-5.28	1.38	1.52

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	536	GLU	OE1-CD-OE2	-33.12	83.55	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	376	GLU	OE1-CD-OE2	-32.35	84.48	123.30
1	D	844	GLU	OE1-CD-OE2	-31.96	84.94	123.30
1	B	536	GLU	CG-CD-OE1	23.64	165.57	118.30
1	B	376	GLU	CG-CD-OE1	20.64	159.57	118.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	424	ASP	Sidechain
1	A	50	PHE	Peptide
1	C	363	PHE	Sidechain
1	D	332	ARG	Sidechain
1	D	844	GLU	Sidechain

## 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	7727	0	7737	58	0
1	B	7656	0	7677	69	0
1	C	7656	0	7677	77	0
1	D	7746	0	7769	80	0
2	A	32	0	0	0	0
2	B	32	0	0	0	0
2	C	32	0	0	0	0
2	D	32	0	0	0	0
3	A	53	0	30	2	0
3	B	53	0	30	2	0
3	C	53	0	30	2	0
3	D	53	0	31	3	0
4	A	10	0	0	0	0
4	B	10	0	0	0	0
4	C	10	0	0	0	0
4	D	10	0	0	0	0
5	A	48	0	25	6	0
5	B	48	0	25	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	48	0	25	5	0
5	D	48	0	25	7	0
6	A	31	0	21	3	0
6	B	31	0	21	1	0
6	C	31	0	21	1	0
6	D	31	0	21	3	0
7	A	867	0	0	15	3
7	B	770	0	0	19	3
7	C	861	0	0	14	2
7	D	891	0	0	22	1
All	All	34870	0	31165	275	5

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 4.

The worst 5 of 275 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:D:875:LYS:NZ	7:D:1201:HOH:O	1.84	1.06
1:C:340:ALA:HB2	1:C:363:PHE:HD2	1.17	1.02
1:D:332:ARG:NH1	7:D:1202:HOH:O	1.93	0.99
1:B:909:ARG:NH2	7:B:1201:HOH:O	1.99	0.96
1:C:340:ALA:HB2	1:C:363:PHE:CD2	2.04	0.92

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1879:HOH:O	7:C:1910:HOH:O[1_556]	2.12	0.08
7:C:1752:HOH:O	7:B:1791:HOH:O[2_655]	2.13	0.07
7:A:1980:HOH:O	7:B:1963:HOH:O[1_455]	2.15	0.05
7:D:2031:HOH:O	7:B:1949:HOH:O[2_656]	2.18	0.02
7:A:1778:HOH:O	7:A:2028:HOH:O[1_455]	2.19	0.01

## 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	1014/1025 (99%)	974 (96%)	36 (4%)	4 (0%)	34	22
1	B	1000/1025 (98%)	964 (96%)	32 (3%)	4 (0%)	34	22
1	C	1000/1025 (98%)	967 (97%)	30 (3%)	3 (0%)	41	30
1	D	1015/1025 (99%)	973 (96%)	37 (4%)	5 (0%)	29	17
All	All	4029/4100 (98%)	3878 (96%)	135 (3%)	16 (0%)	34	22

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	905	PRO
1	C	325	HIS
1	B	414	ASP
1	C	1016	GLY
1	D	676	GLY

### 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	841/854 (98%)	834 (99%)	7 (1%)	81	80
1	B	834/854 (98%)	820 (98%)	14 (2%)	60	54
1	C	834/854 (98%)	826 (99%)	8 (1%)	76	73
1	D	844/854 (99%)	833 (99%)	11 (1%)	69	64
All	All	3353/3416 (98%)	3313 (99%)	40 (1%)	71	67



5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	64	HIS
1	B	402	ARG
1	B	100	PHE
1	B	332	ARG
1	B	537	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	407	GLN
1	B	487	ASN
1	D	23	GLN
1	D	25	HIS
1	D	428	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

32 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
5	NAP	D	1107	-	45,52,52	2.31	12 (26%)	56,80,80	1.97	14 (25%)
2	SF4	B	1101	1	0,12,12	0.00	-	-		
3	FAD	A	1105	-	51,58,58	4.56	20 (39%)	60,89,89	2.35	13 (21%)
2	SF4	D	1101	1	0,12,12	0.00	-	-		
2	SF4	A	1104	1	0,12,12	0.00	-	-		
5	NAP	B	1106	-	45,52,52	2.64	16 (35%)	56,80,80	1.90	15 (26%)
4	Y3G	D	1106	-	9,10,10	2.30	5 (55%)	6,13,13	5.89	5 (83%)
6	FNR	C	1107	-	31,33,33	3.87	13 (41%)	40,50,50	2.54	12 (30%)
5	NAP	A	1107	-	45,52,52	2.69	11 (24%)	56,80,80	1.93	13 (23%)
2	SF4	A	1101	1	0,12,12	0.00	-	-		
4	Y3G	C	1108	1	9,10,10	2.61	4 (44%)	6,13,13	8.99	6 (100%)
6	FNR	A	1108	-	31,33,33	3.82	15 (48%)	40,50,50	2.36	11 (27%)
2	SF4	D	1102	1	0,12,12	0.00	-	-		
2	SF4	A	1102	1	0,12,12	0.00	-	-		
2	SF4	B	1104	1	0,12,12	0.00	-	-		
2	SF4	D	1103	1	0,12,12	0.00	-	-		
4	Y3G	B	1108	1	9,10,10	2.56	4 (44%)	6,13,13	8.72	5 (83%)
2	SF4	C	1102	1	0,12,12	0.00	-	-		
3	FAD	D	1105	-	51,58,58	4.50	22 (43%)	60,89,89	2.44	12 (20%)
4	Y3G	A	1106	-	9,10,10	2.11	2 (22%)	6,13,13	5.69	5 (83%)
2	SF4	D	1104	1	0,12,12	0.00	-	-		
5	NAP	C	1106	-	45,52,52	2.41	14 (31%)	56,80,80	1.88	14 (25%)
2	SF4	C	1103	1	0,12,12	0.00	-	-		
3	FAD	C	1105	-	51,58,58	4.56	21 (41%)	60,89,89	2.40	15 (25%)
2	SF4	C	1101	1	0,12,12	0.00	-	-		
6	FNR	B	1107	-	31,33,33	3.94	14 (45%)	40,50,50	2.02	9 (22%)
2	SF4	B	1102	1	0,12,12	0.00	-	-		
2	SF4	B	1103	1	0,12,12	0.00	-	-		
3	FAD	B	1105	-	51,58,58	4.62	20 (39%)	60,89,89	2.49	12 (20%)
2	SF4	C	1104	1	0,12,12	0.00	-	-		
6	FNR	D	1108	-	31,33,33	3.74	13 (41%)	40,50,50	2.22	9 (22%)
2	SF4	A	1103	1	0,12,12	0.00	-	-		

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
5	NAP	D	1107	-	-	6/31/67/67	0/5/5/5
3	FAD	A	1105	-	-	2/30/50/50	0/6/6/6
2	SF4	B	1101	1	-	-	0/6/5/5
2	SF4	D	1101	1	-	-	0/6/5/5
2	SF4	A	1104	1	-	-	0/6/5/5
5	NAP	B	1106	-	-	5/31/67/67	0/5/5/5
4	Y3G	D	1106	-	-	0/0/2/2	0/1/1/1
6	FNR	C	1107	-	1/1/4/4	7/18/18/18	0/3/3/3
5	NAP	A	1107	-	-	3/31/67/67	0/5/5/5
2	SF4	A	1101	1	-	-	0/6/5/5
4	Y3G	C	1108	1	-	0/0/2/2	0/1/1/1
6	FNR	A	1108	-	1/1/4/4	7/18/18/18	0/3/3/3
2	SF4	D	1102	1	-	-	0/6/5/5
2	SF4	A	1102	1	-	-	0/6/5/5
2	SF4	B	1104	1	-	-	0/6/5/5
2	SF4	D	1103	1	-	-	0/6/5/5
4	Y3G	B	1108	1	-	0/0/2/2	0/1/1/1
3	FAD	D	1105	-	-	2/30/50/50	0/6/6/6
2	SF4	C	1102	1	-	-	0/6/5/5
4	Y3G	A	1106	-	-	0/0/2/2	0/1/1/1
5	NAP	C	1106	-	-	1/31/67/67	0/5/5/5
2	SF4	D	1104	1	-	-	0/6/5/5
2	SF4	C	1103	1	-	-	0/6/5/5
3	FAD	C	1105	-	-	1/30/50/50	0/6/6/6
2	SF4	C	1101	1	-	-	0/6/5/5
6	FNR	B	1107	-	1/1/4/4	8/18/18/18	0/3/3/3
2	SF4	B	1102	1	-	-	0/6/5/5
2	SF4	B	1103	1	-	-	0/6/5/5
3	FAD	B	1105	-	-	1/30/50/50	0/6/6/6
2	SF4	C	1104	1	-	-	0/6/5/5
6	FNR	D	1108	-	1/1/4/4	7/18/18/18	0/3/3/3
2	SF4	A	1103	1	-	-	0/6/5/5

The worst 5 of 206 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1105	FAD	O4B-C1B	14.26	1.61	1.41
3	A	1105	FAD	O4B-C1B	14.23	1.60	1.41
3	B	1105	FAD	C2B-C1B	-14.17	1.32	1.53
3	C	1105	FAD	O4B-C1B	14.08	1.60	1.41
3	D	1105	FAD	O4B-C1B	13.65	1.60	1.41

The worst 5 of 170 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1108	Y3G	C06-C09-C10	-16.31	123.85	176.48
4	B	1108	Y3G	C06-C09-C10	-15.83	125.42	176.48
4	D	1106	Y3G	N04-C03-N02	-10.58	120.02	128.43
4	A	1106	Y3G	N04-C03-N02	-10.50	120.08	128.43
4	C	1108	Y3G	N04-C03-N02	-9.67	120.74	128.43

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	1108	FNR	C4'
6	C	1107	FNR	C4'
6	D	1108	FNR	C4'
6	B	1107	FNR	C4'

5 of 50 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	1107	NAP	C5D-O5D-PN-O3
5	B	1106	NAP	C5D-O5D-PN-O3
6	A	1108	FNR	C3'-C4'-C5'-O5'
6	A	1108	FNR	O4'-C4'-C5'-O5'
6	C	1107	FNR	O3'-C3'-C4'-O4'

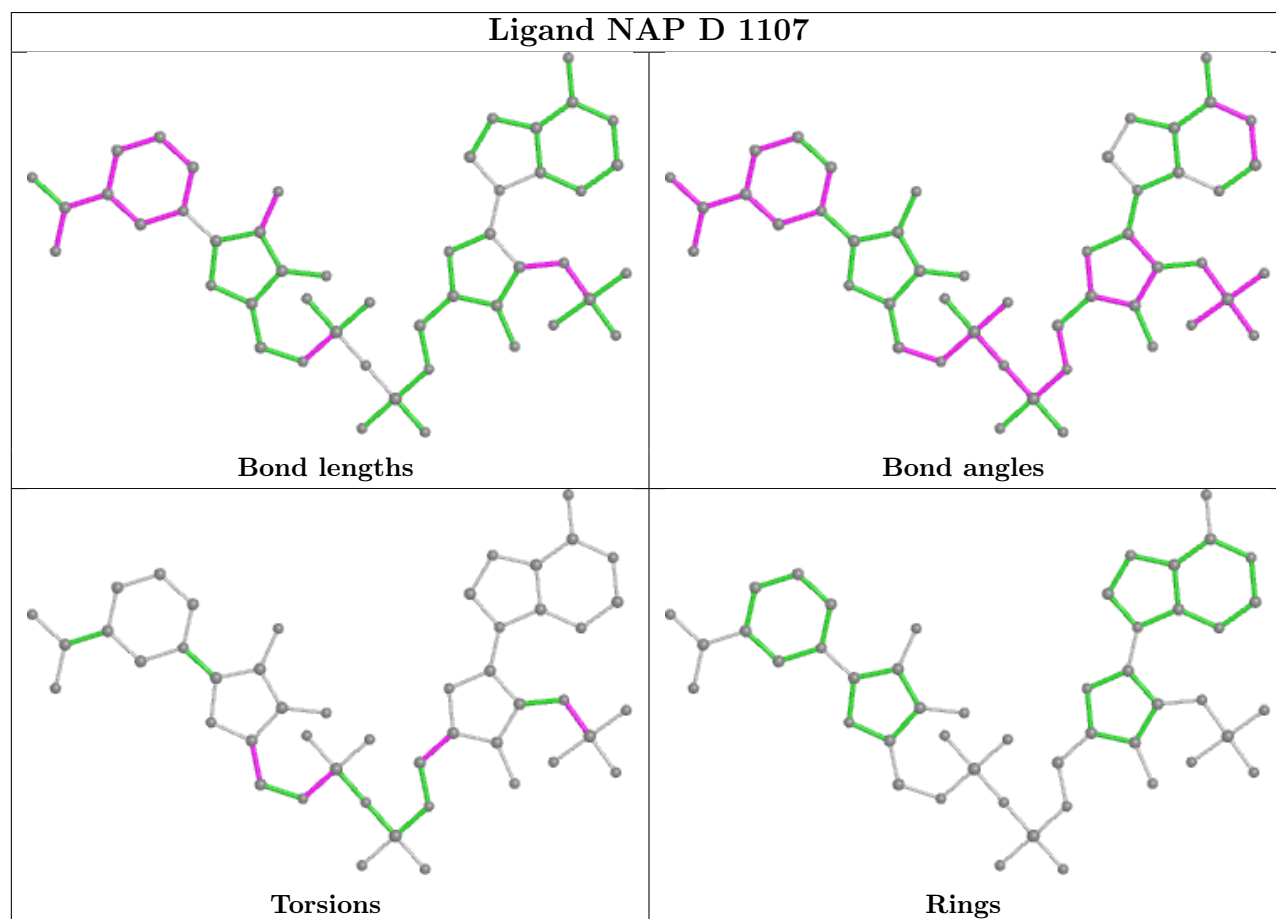
There are no ring outliers.

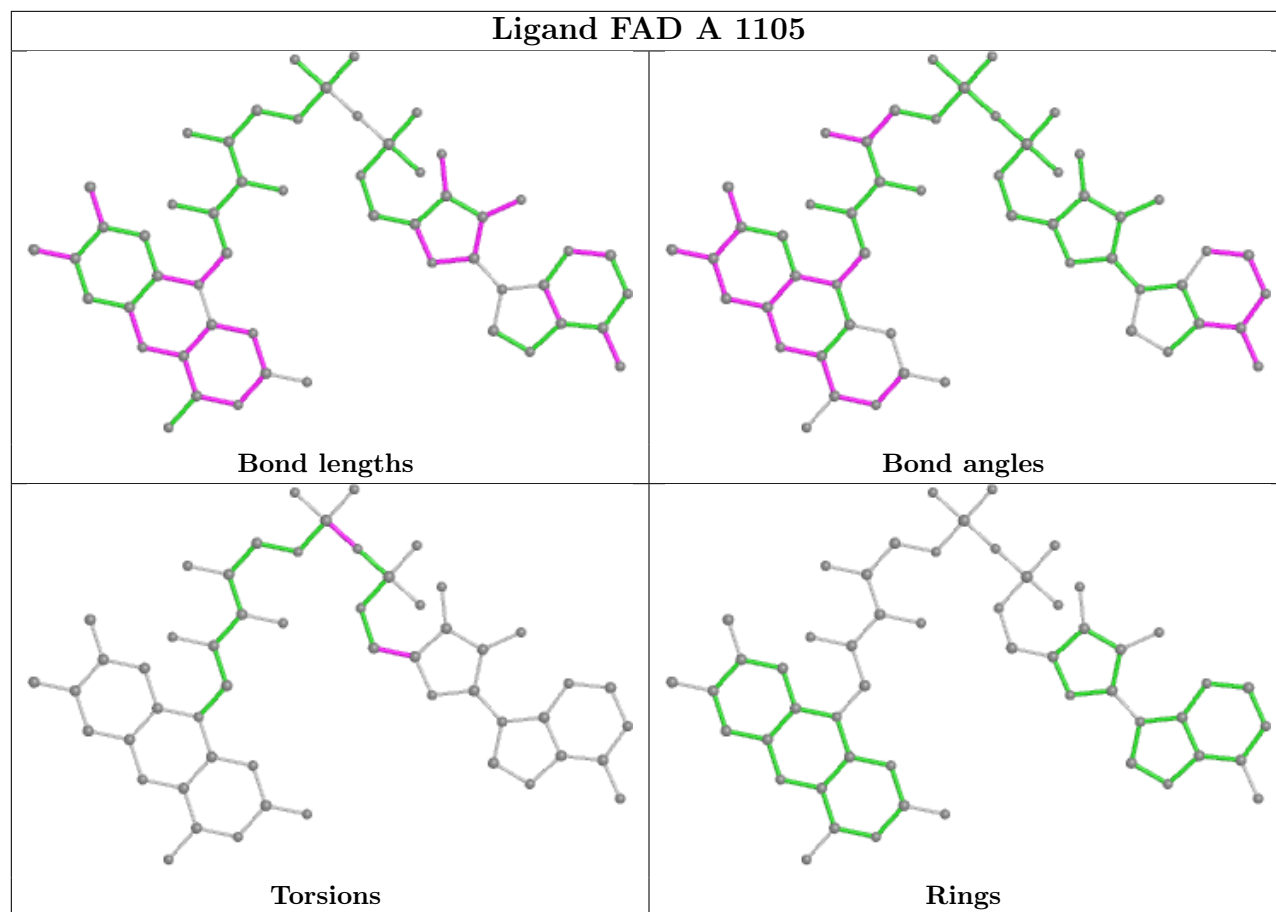
12 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	1107	NAP	7	0
3	A	1105	FAD	2	0
5	B	1106	NAP	7	0
6	C	1107	FNR	1	0
5	A	1107	NAP	6	0
6	A	1108	FNR	3	0
3	D	1105	FAD	3	0
5	C	1106	NAP	5	0
3	C	1105	FAD	2	0
6	B	1107	FNR	1	0
3	B	1105	FAD	2	0
6	D	1108	FNR	3	0

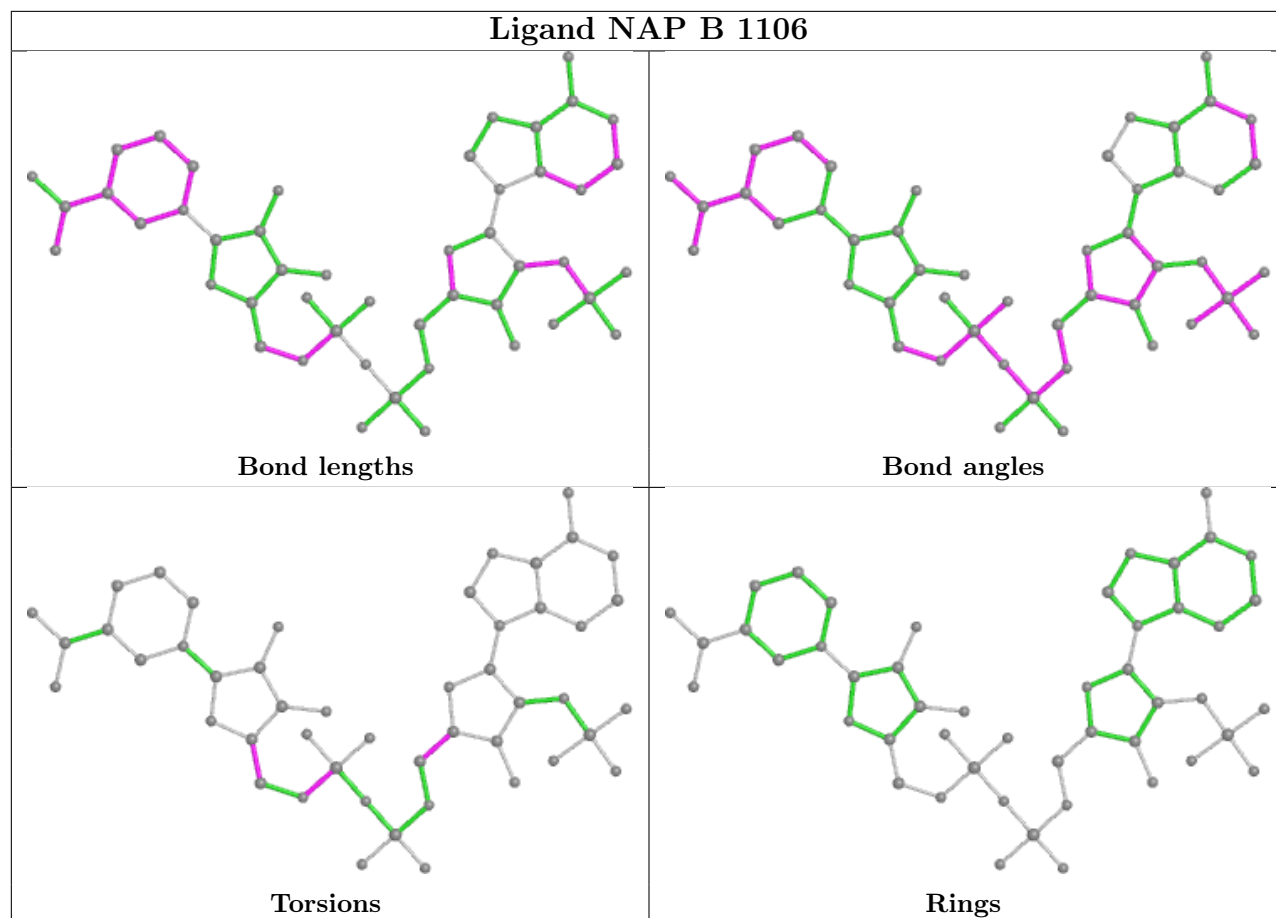
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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.

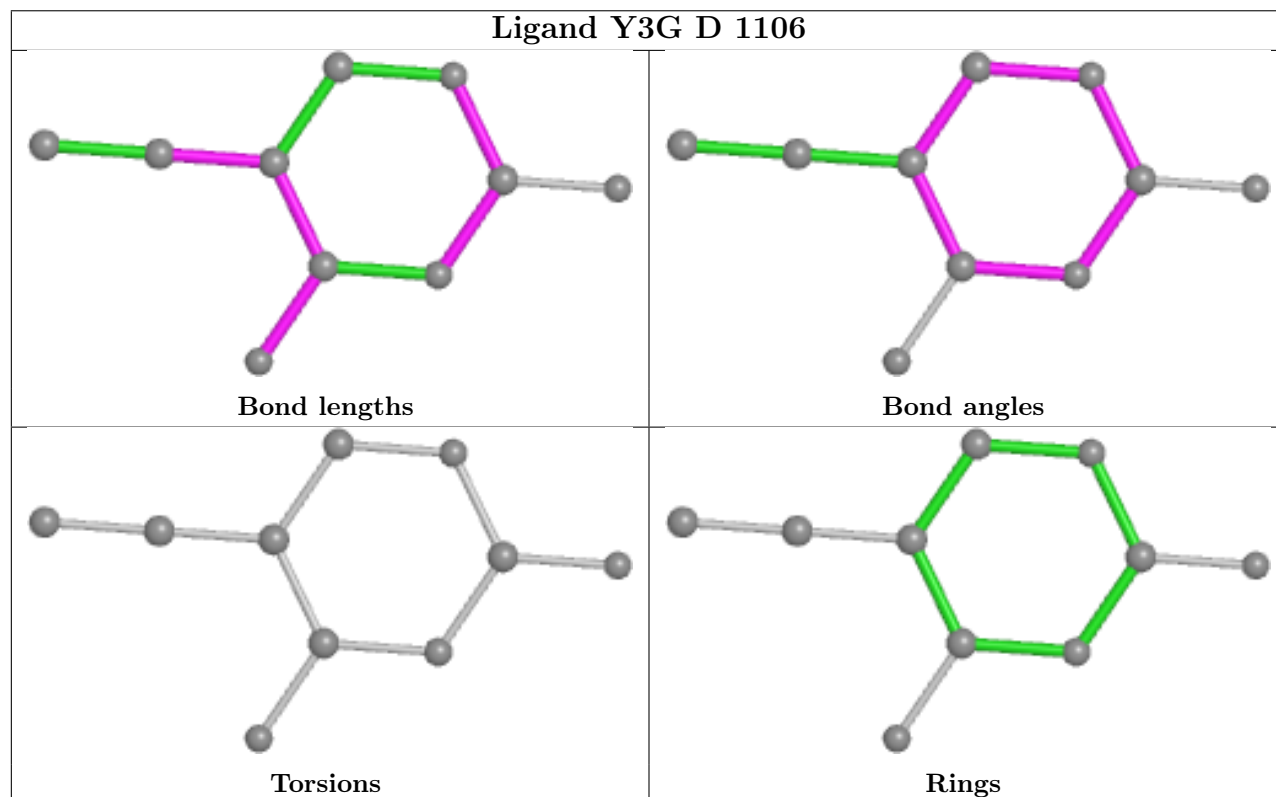




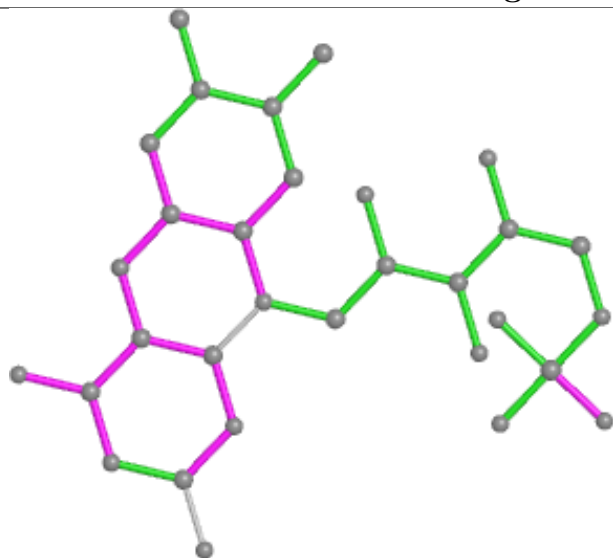
## Ligand NAP B 1106



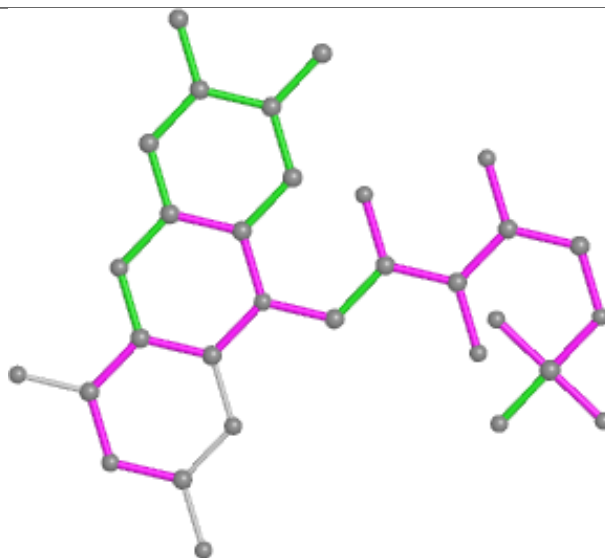
## Ligand Y3G D 1106



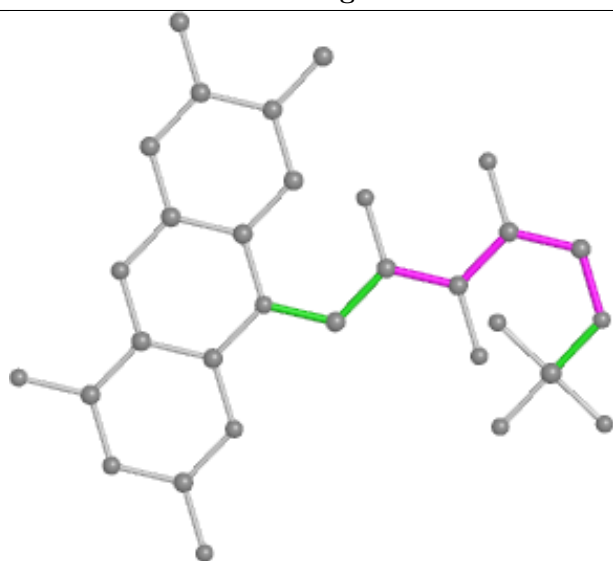
## Ligand FNR C 1107



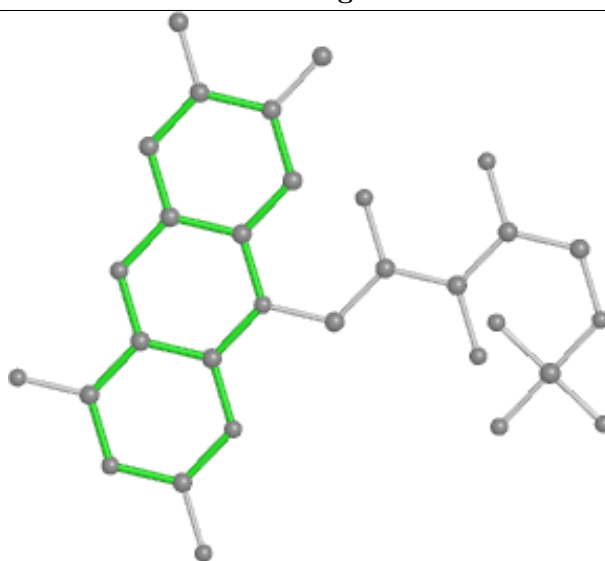
Bond lengths



Bond angles



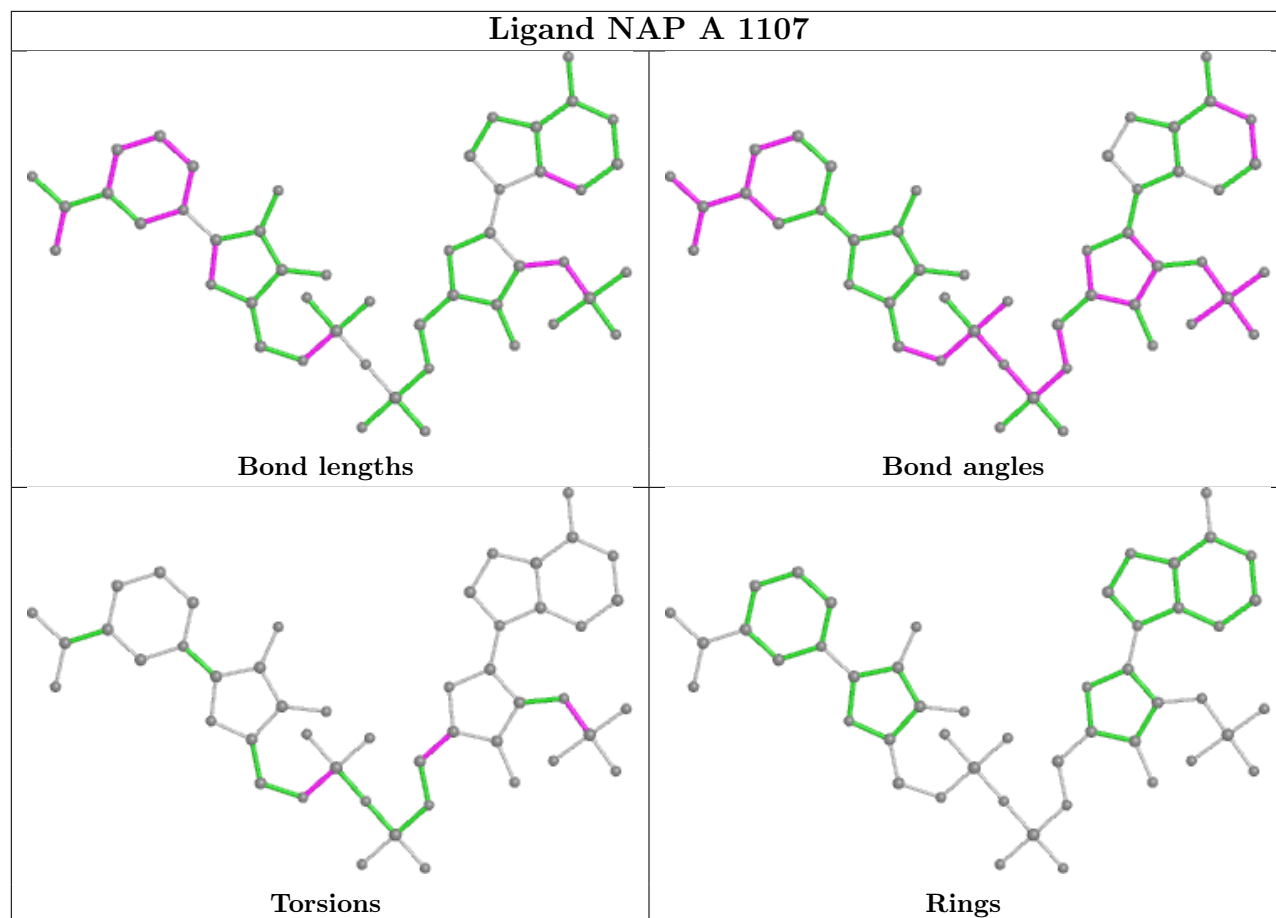
Torsions



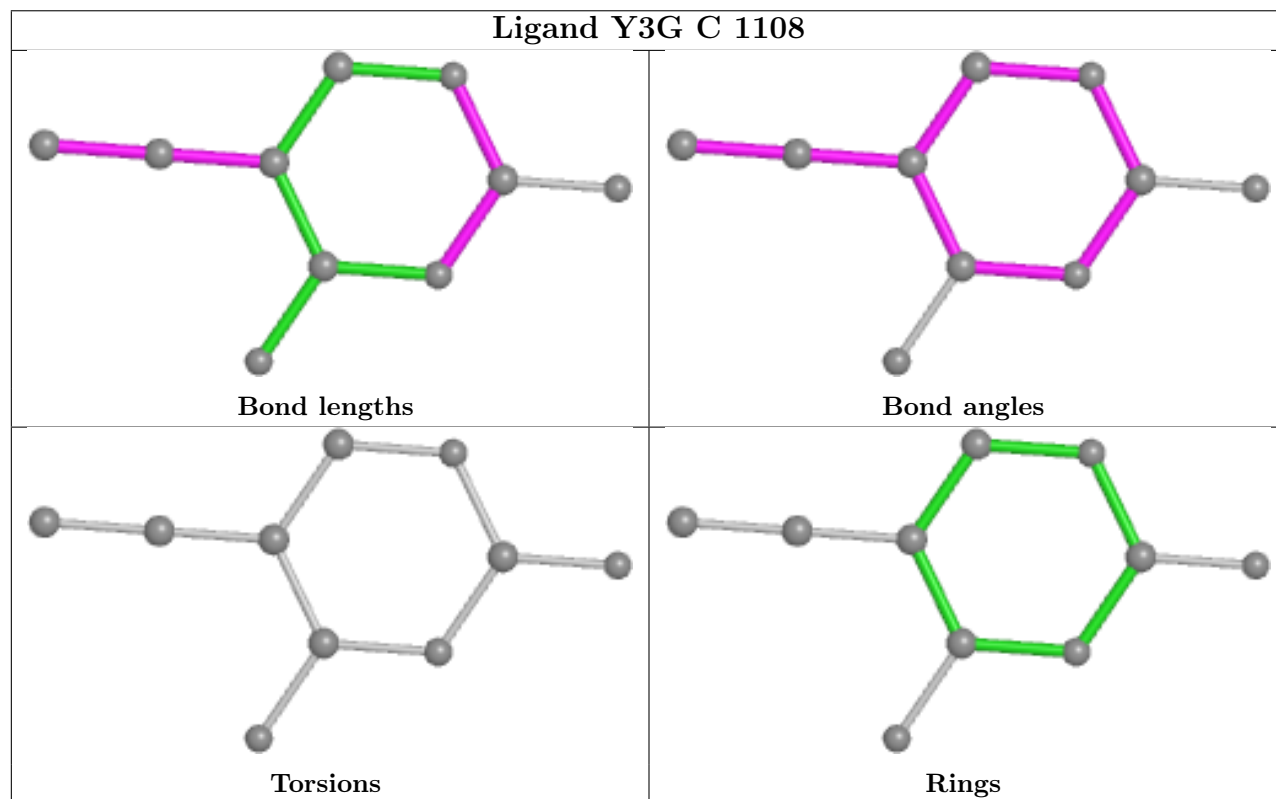
Rings



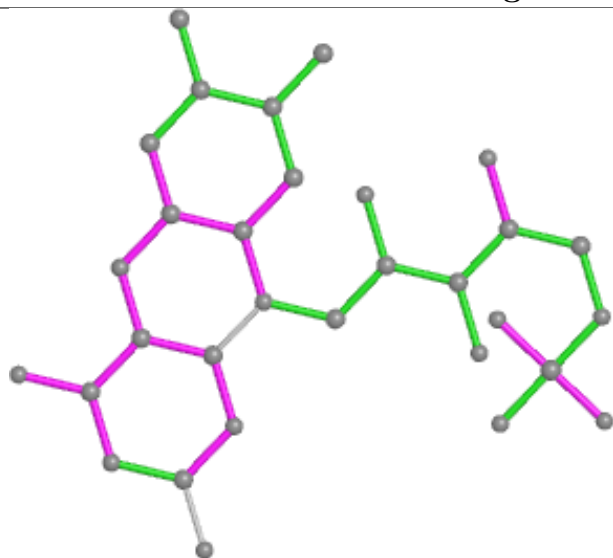
## Ligand NAP A 1107



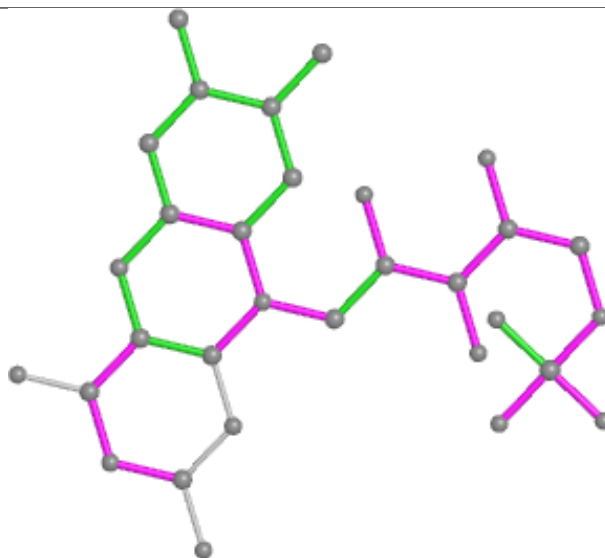
## Ligand Y3G C 1108



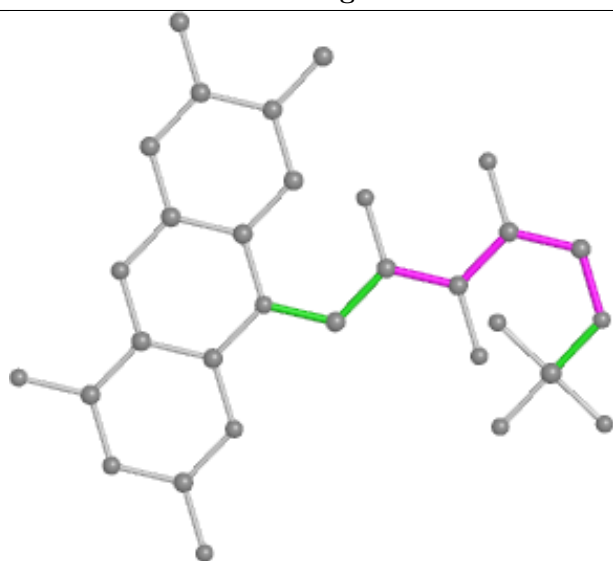
## Ligand FNR A 1108



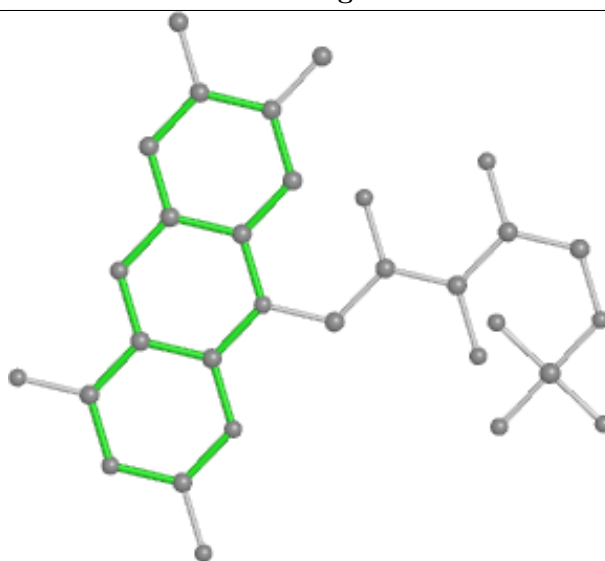
Bond lengths



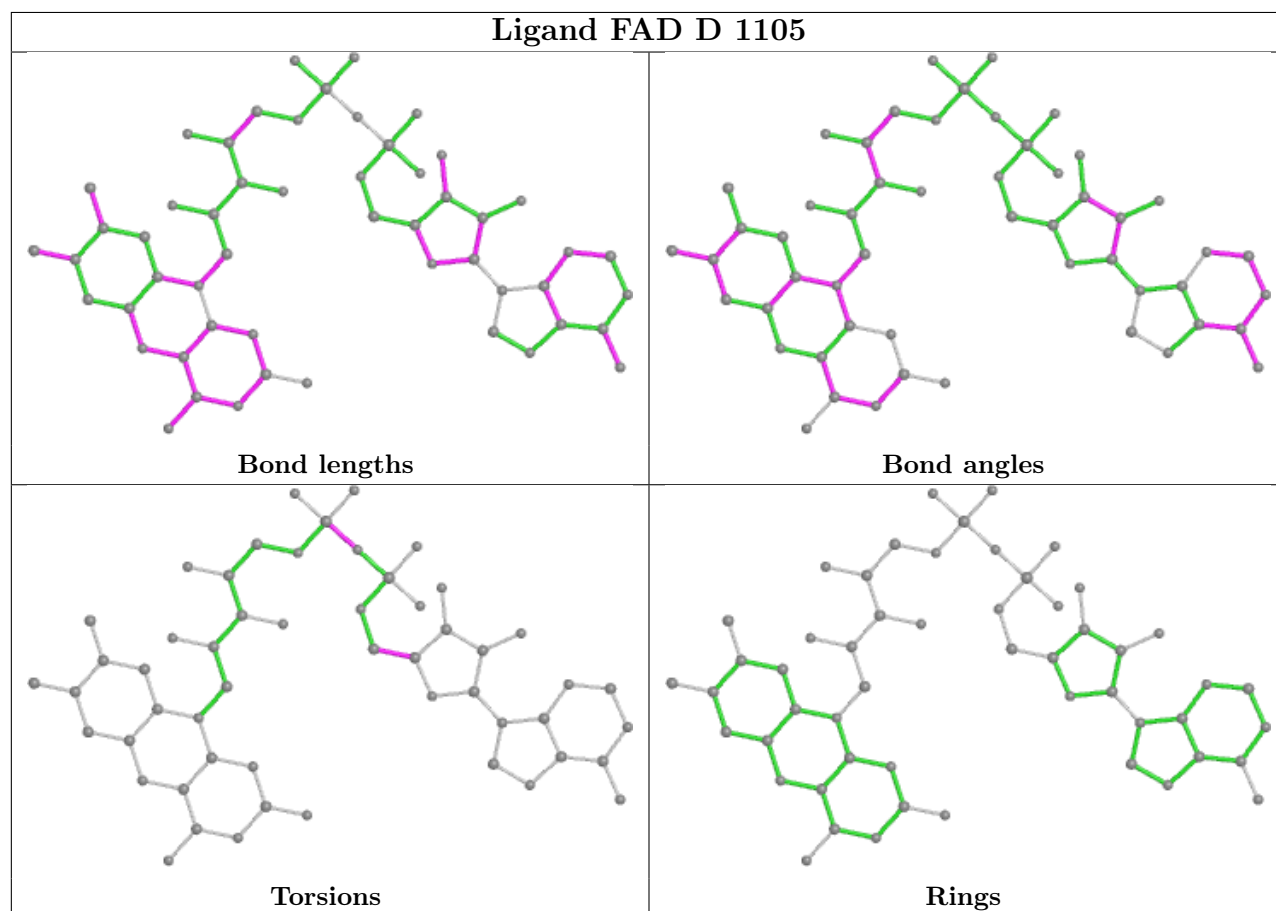
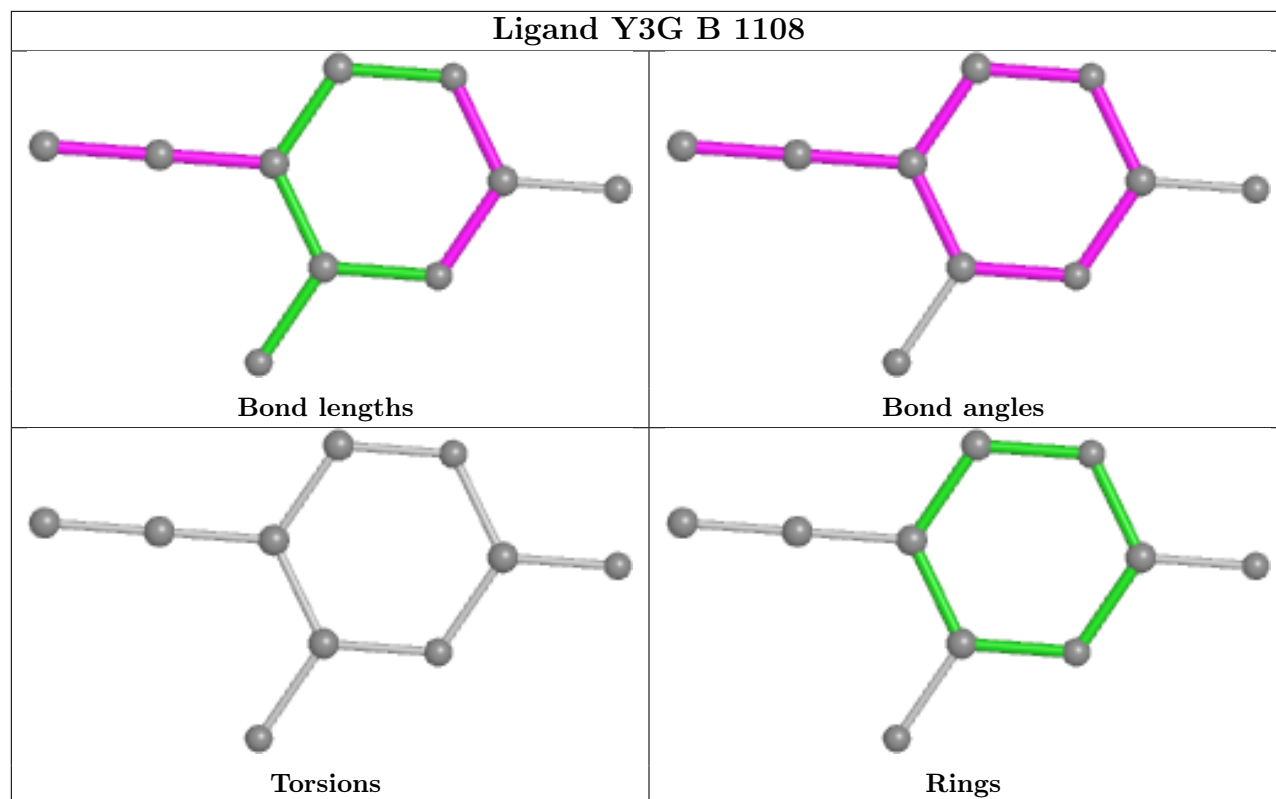
Bond angles

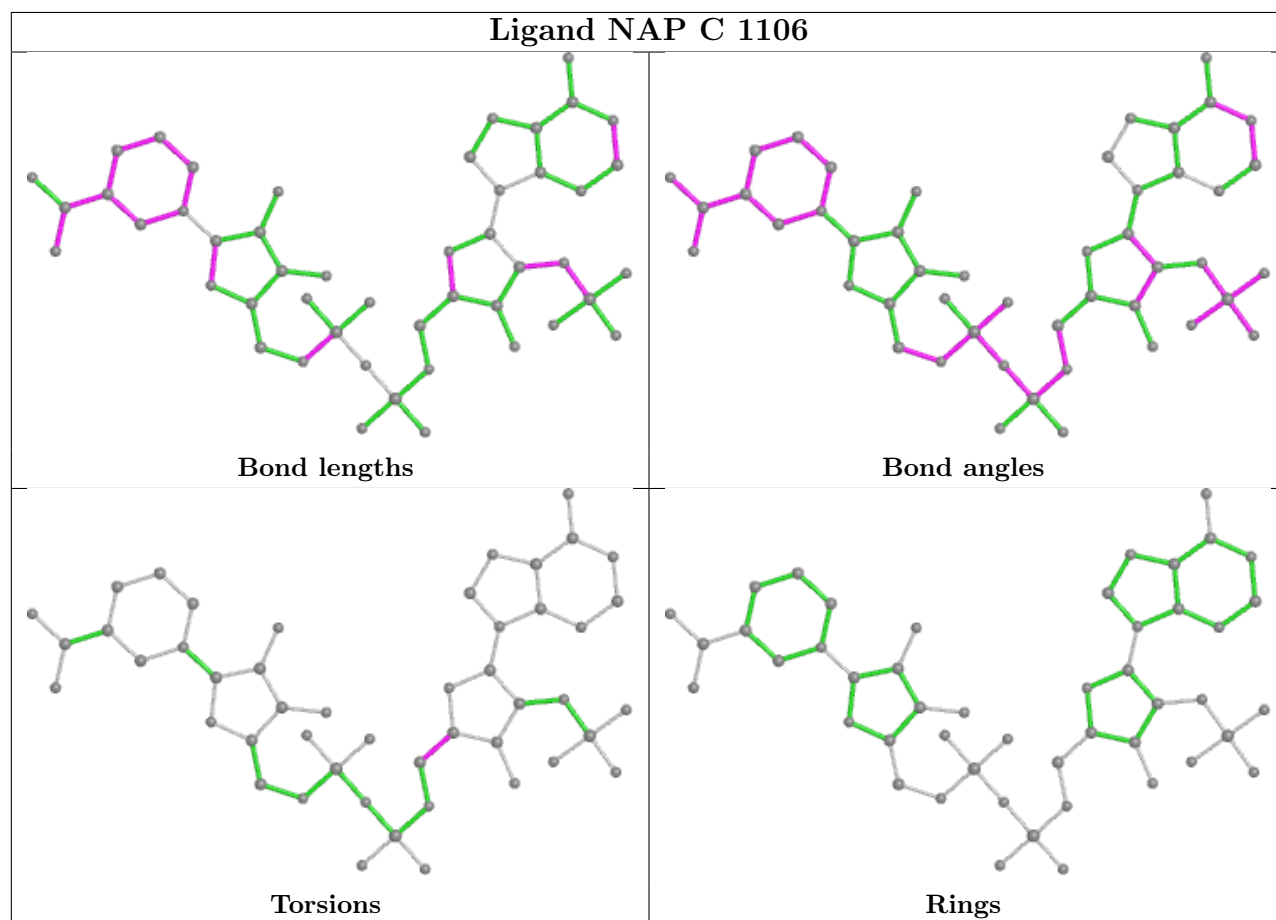
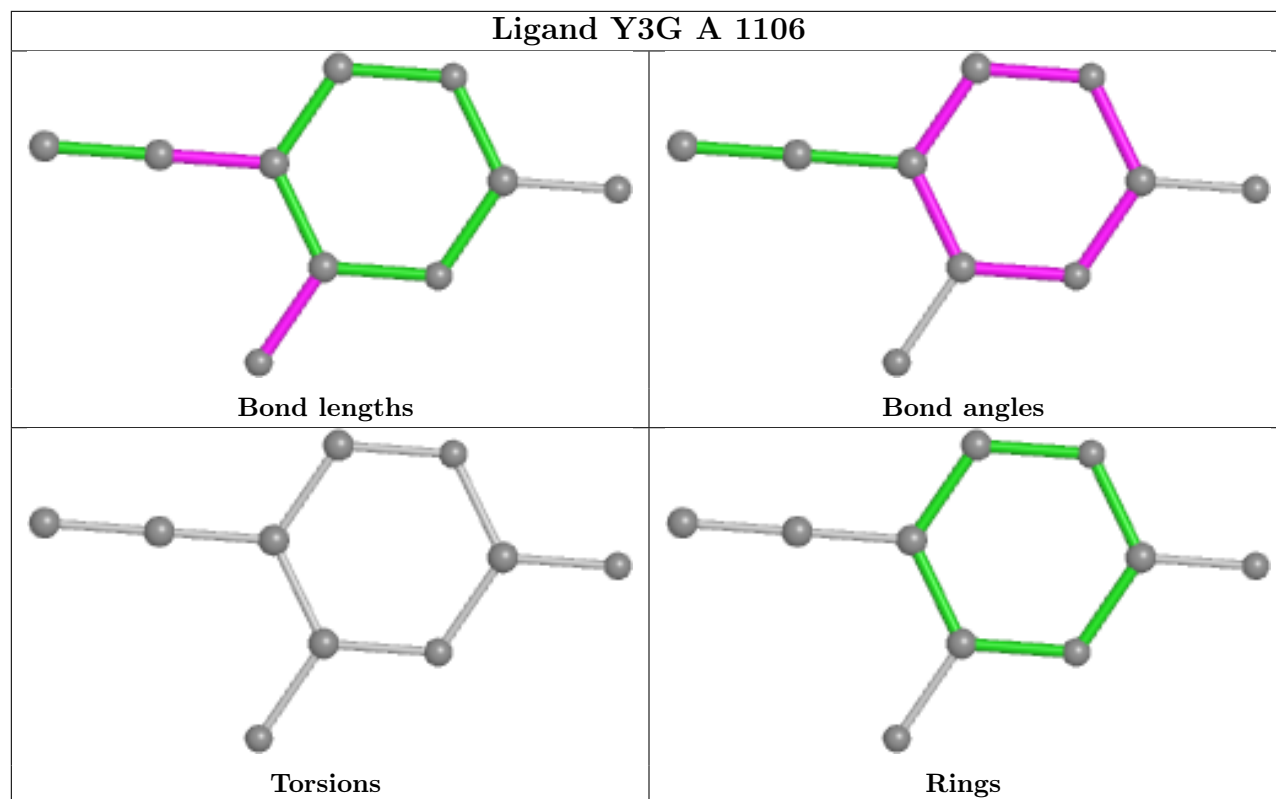


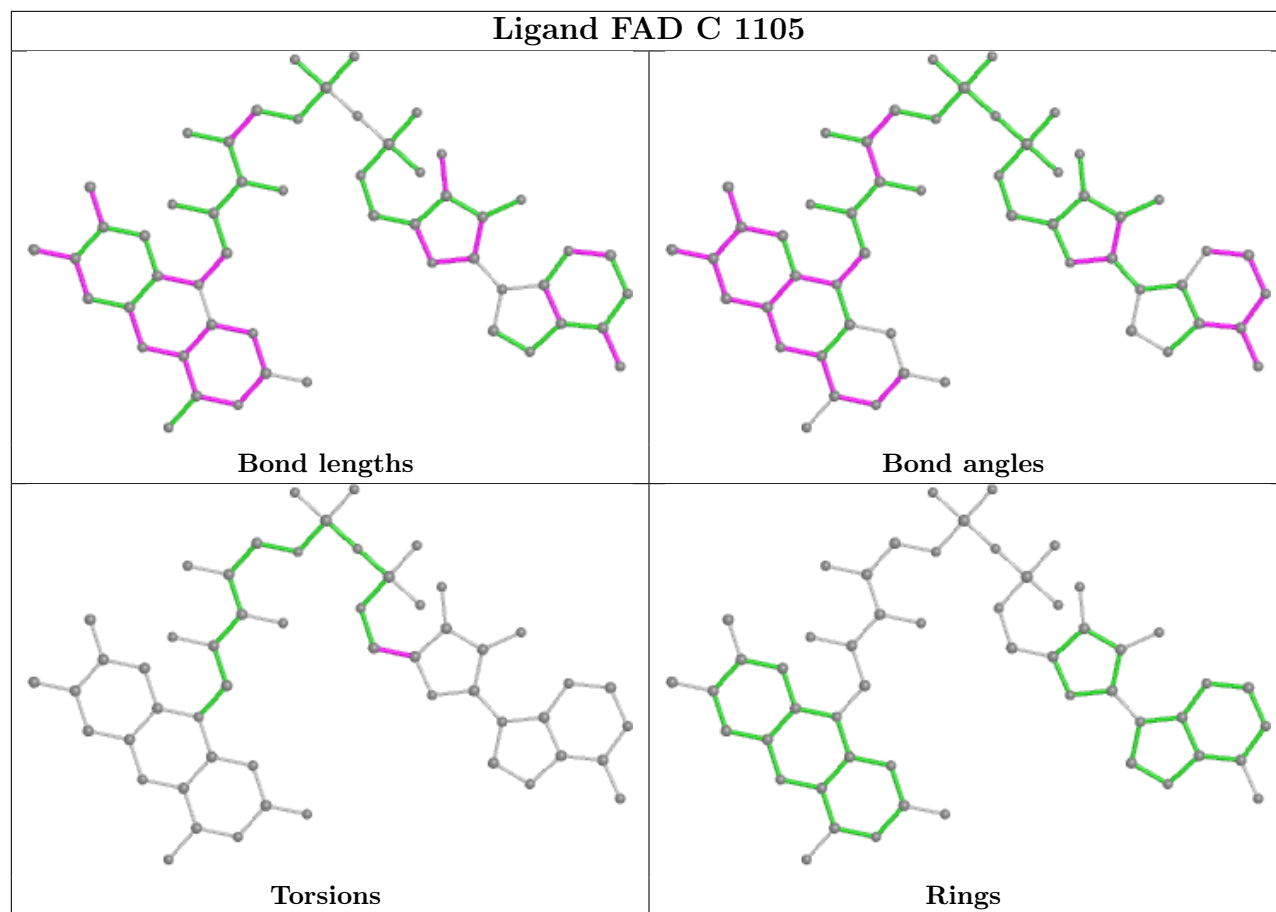
Torsions



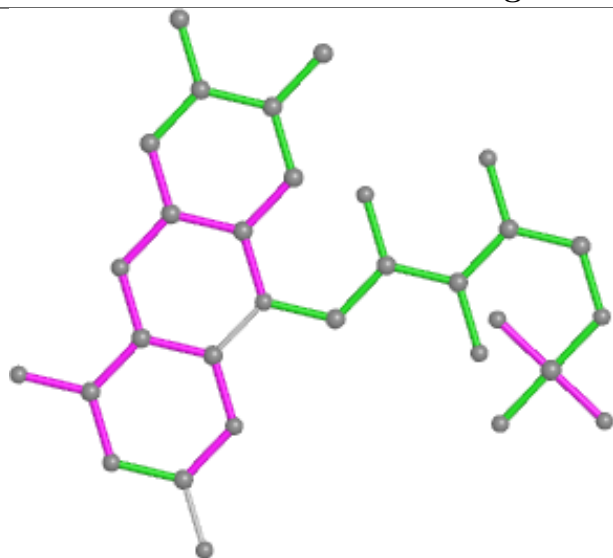
Rings



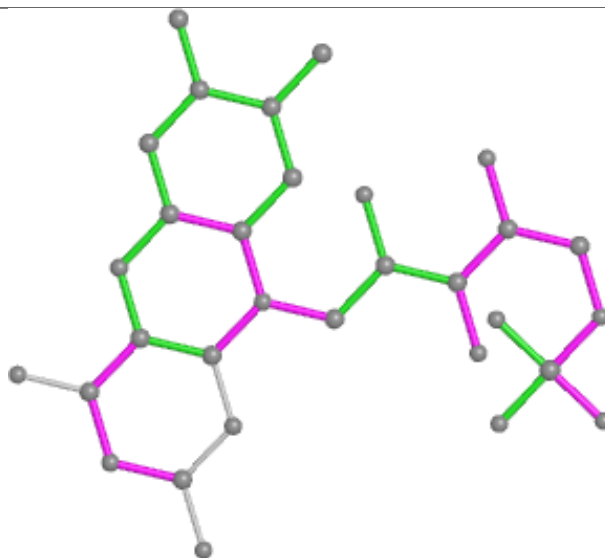




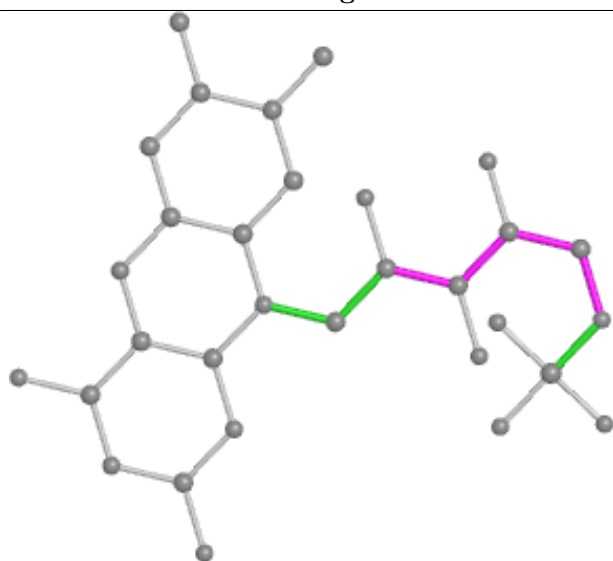
## Ligand FNR B 1107



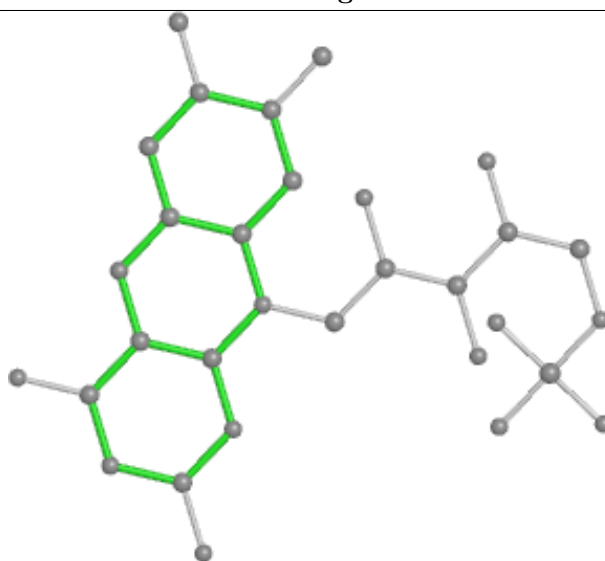
Bond lengths



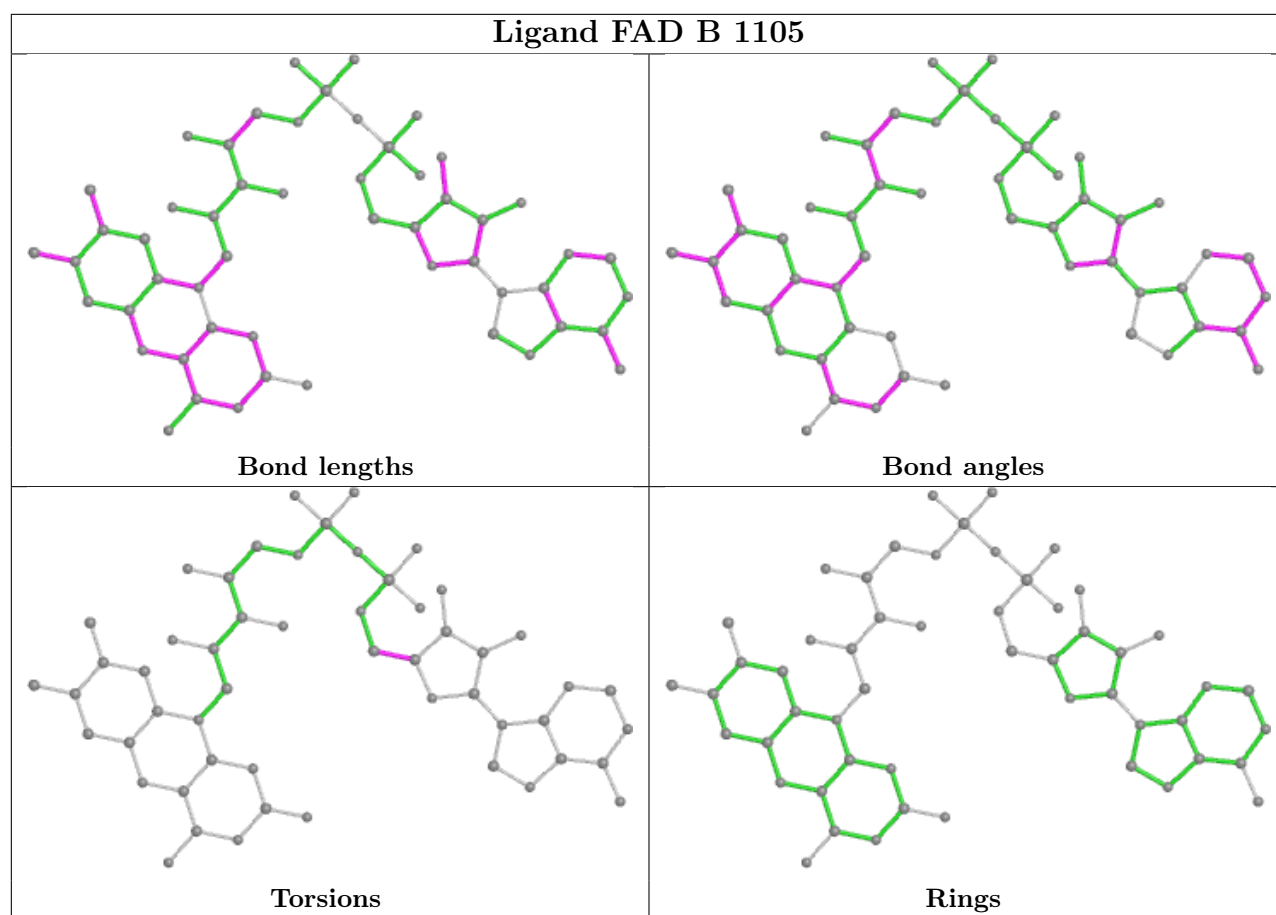
Bond angles

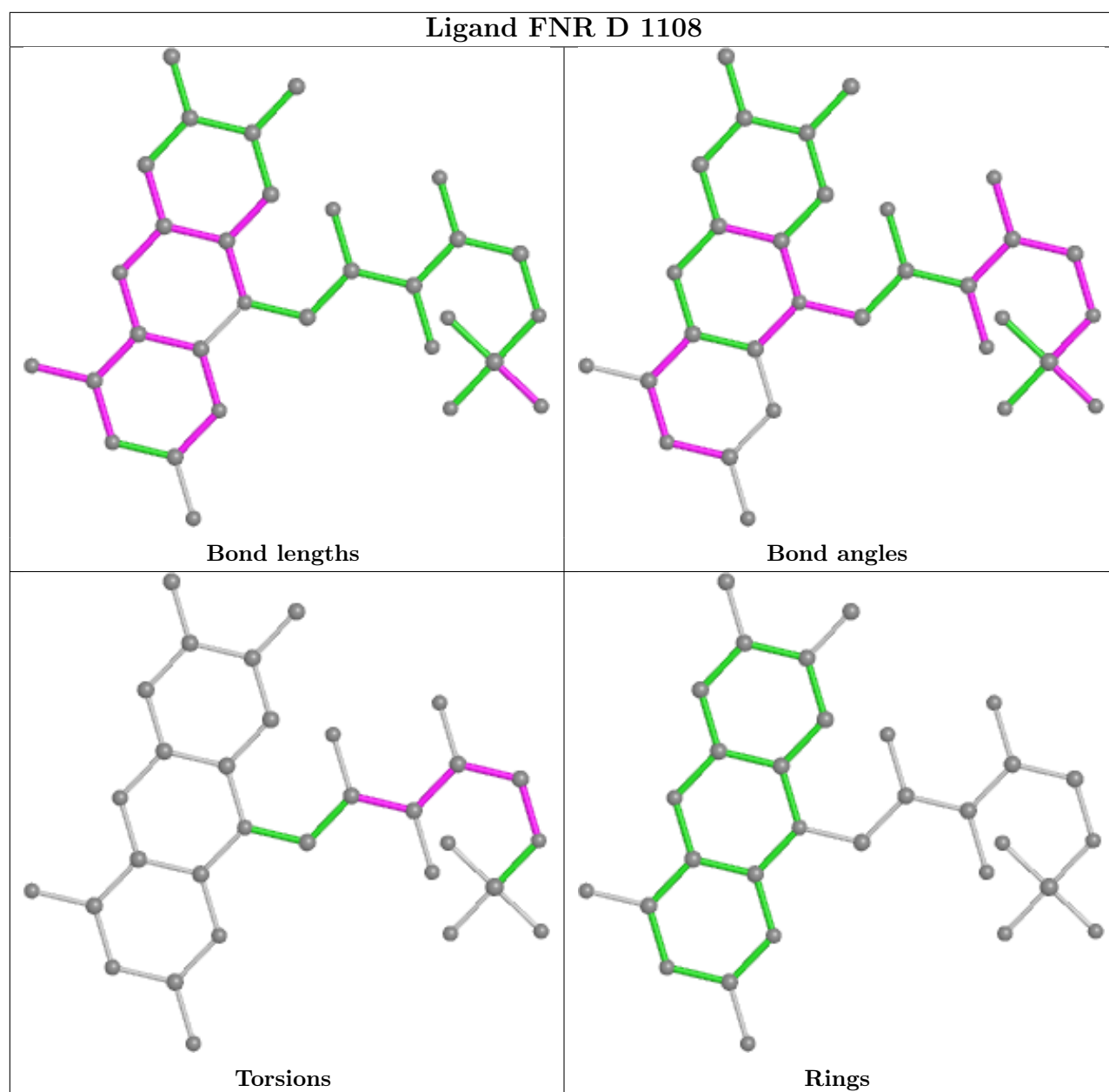


Torsions



Rings





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	1007/1025 (98%)	0.15	43 (4%)	35	36	15, 23, 45, 91	0
1	B	1004/1025 (97%)	0.17	53 (5%)	26	28	15, 23, 47, 108	0
1	C	1004/1025 (97%)	0.06	38 (3%)	40	42	15, 22, 42, 74	0
1	D	1011/1025 (98%)	0.12	45 (4%)	33	34	15, 23, 45, 80	0
All	All	4026/4100 (98%)	0.12	179 (4%)	34	35	15, 23, 45, 108	0

The worst 5 of 179 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	907	LEU	13.6
1	B	907	LEU	12.7
1	B	901	ASN	11.5
1	B	902	ALA	11.3
1	A	2	ALA	11.2

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

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

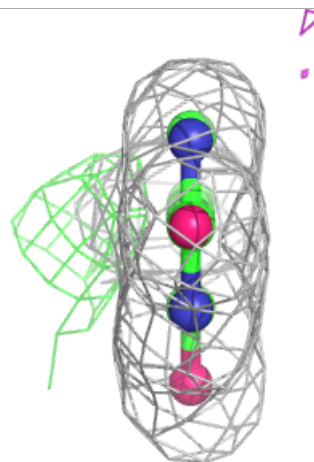
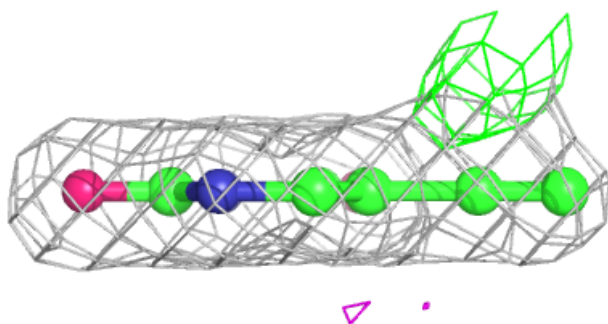
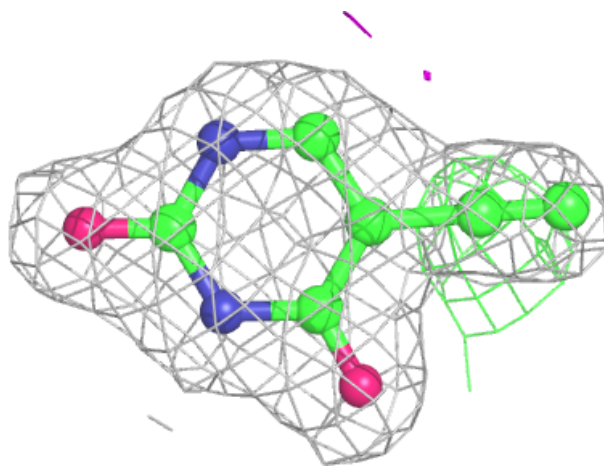
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 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
4	Y3G	A	1106	10/10	0.93	0.11	18,21,26,28	0
4	Y3G	B	1108	10/10	0.94	0.12	23,24,26,27	0
5	NAP	D	1107	48/48	0.95	0.15	22,27,40,46	0
5	NAP	B	1106	48/48	0.95	0.12	21,29,41,43	0
5	NAP	A	1107	48/48	0.96	0.12	19,26,35,36	0
4	Y3G	C	1108	10/10	0.96	0.09	18,20,24,25	0
3	FAD	B	1105	53/53	0.96	0.11	17,21,26,27	0
6	FNR	A	1108	31/31	0.96	0.14	16,19,21,23	0
6	FNR	C	1107	31/31	0.96	0.12	15,18,21,22	0
6	FNR	B	1107	31/31	0.96	0.10	15,20,24,27	0
3	FAD	C	1105	53/53	0.97	0.09	18,21,25,29	0
3	FAD	A	1105	53/53	0.97	0.10	15,19,25,27	0
5	NAP	C	1106	48/48	0.97	0.10	19,28,33,36	0
6	FNR	D	1108	31/31	0.97	0.13	16,18,21,24	0
4	Y3G	D	1106	10/10	0.97	0.09	17,20,26,26	0
3	FAD	D	1105	53/53	0.98	0.10	16,20,24,26	0
2	SF4	D	1104	8/8	0.98	0.07	16,17,18,18	0
2	SF4	A	1103	8/8	0.99	0.06	17,18,18,21	0
2	SF4	A	1104	8/8	0.99	0.06	18,20,20,21	0
2	SF4	C	1101	8/8	0.99	0.06	15,16,17,17	0
2	SF4	C	1102	8/8	0.99	0.06	15,17,18,18	0
2	SF4	C	1103	8/8	0.99	0.07	14,16,16,17	0
2	SF4	C	1104	8/8	0.99	0.07	17,18,18,18	0
2	SF4	D	1101	8/8	0.99	0.06	17,18,19,19	0
2	SF4	D	1102	8/8	0.99	0.06	17,18,18,18	0
2	SF4	D	1103	8/8	0.99	0.07	14,16,17,17	0
2	SF4	A	1101	8/8	0.99	0.06	17,18,20,21	0
2	SF4	B	1101	8/8	0.99	0.06	16,17,18,18	0
2	SF4	B	1102	8/8	0.99	0.06	16,18,19,19	0
2	SF4	B	1103	8/8	0.99	0.07	15,16,17,17	0
2	SF4	B	1104	8/8	0.99	0.07	16,17,18,19	0
2	SF4	A	1102	8/8	0.99	0.07	16,16,17,17	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.

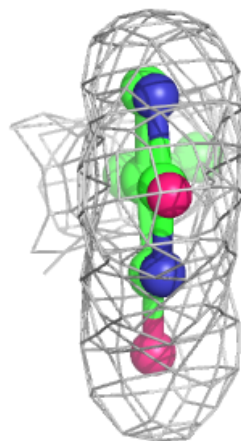
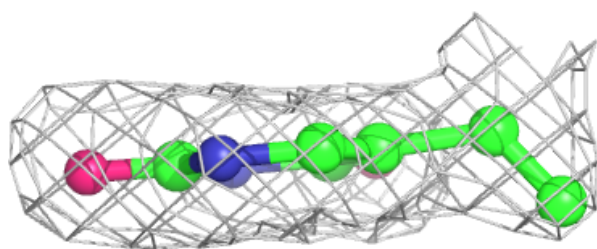
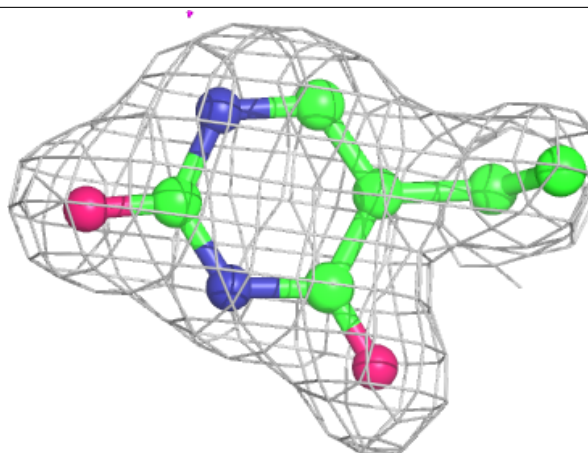
**Electron density around Y3G A 1106:**

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

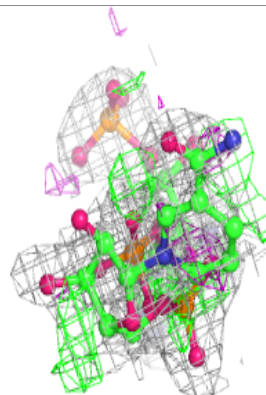
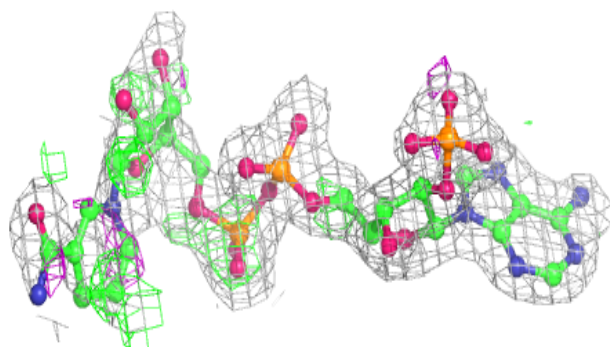
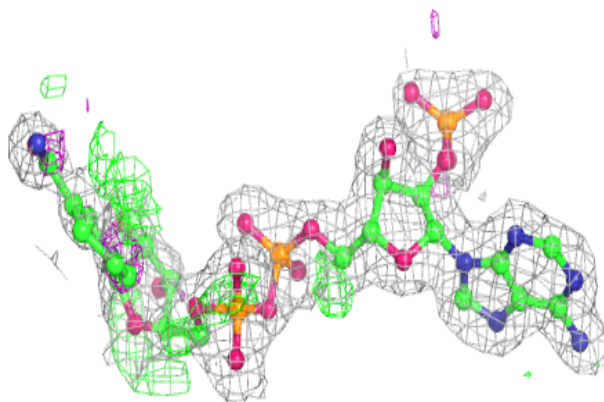


**Electron density around Y3G B 1108:**

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

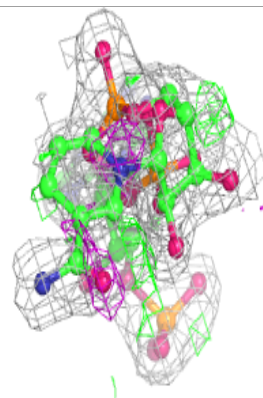
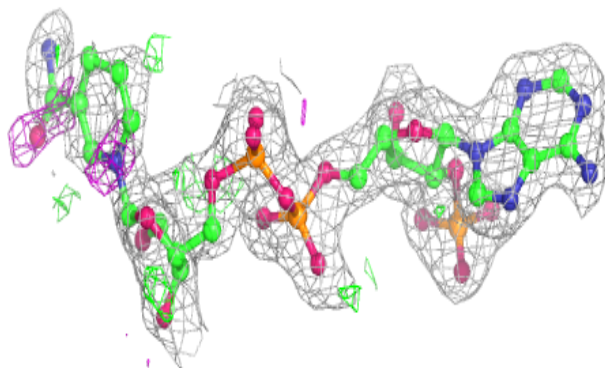
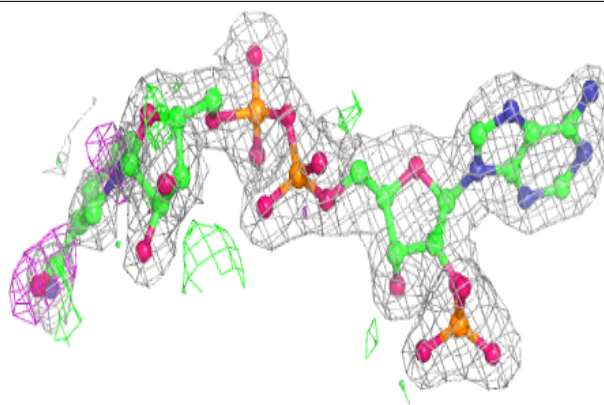
**Electron density around NAP D 1107:**

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

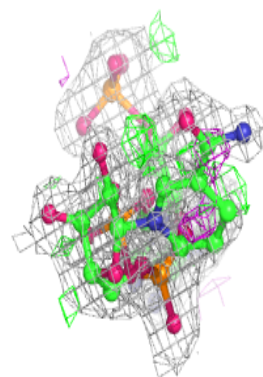
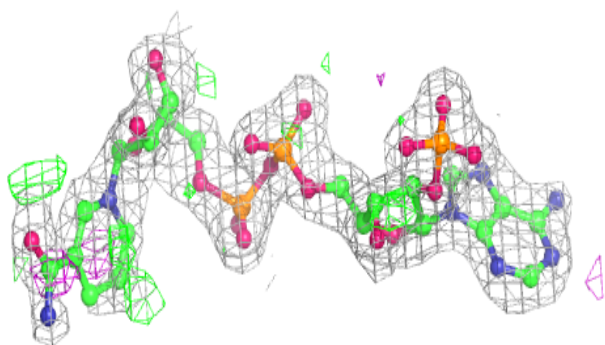
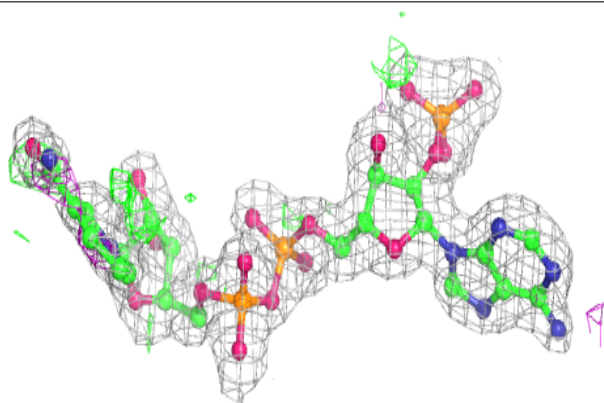


**Electron density around NAP B 1106:**

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

**Electron density around NAP A 1107:**

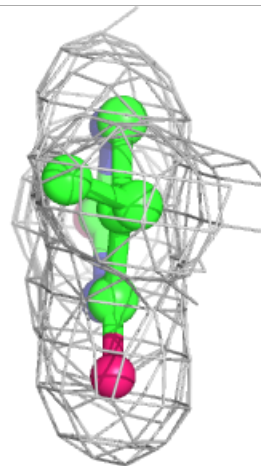
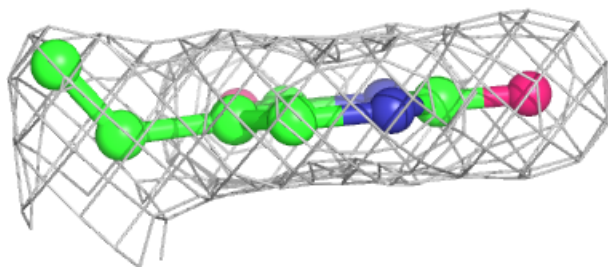
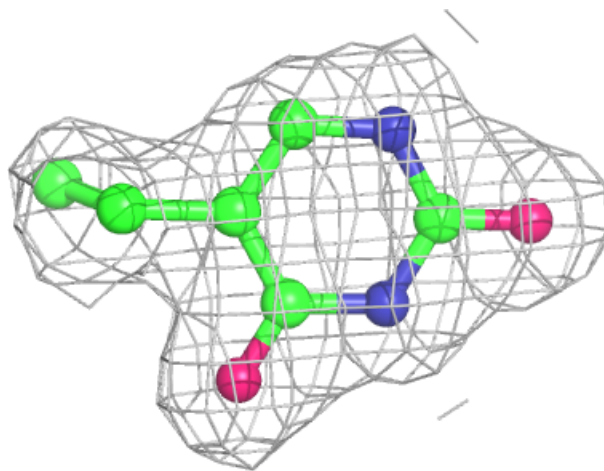
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





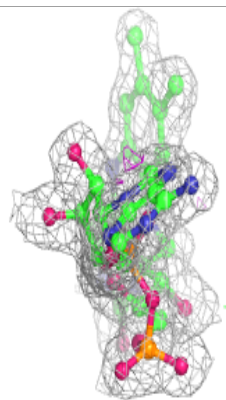
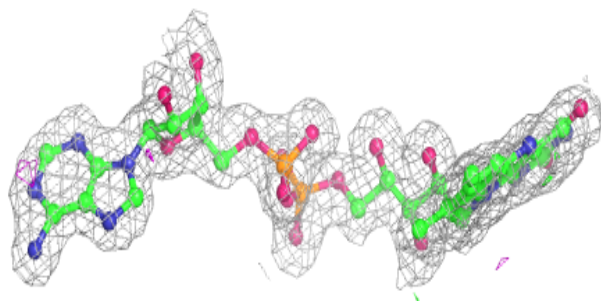
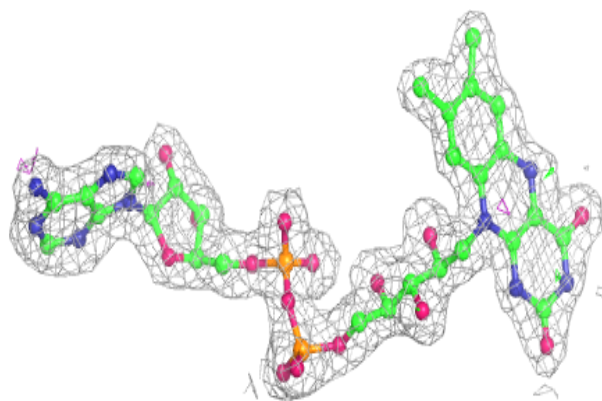
**Electron density around Y3G C 1108:**

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



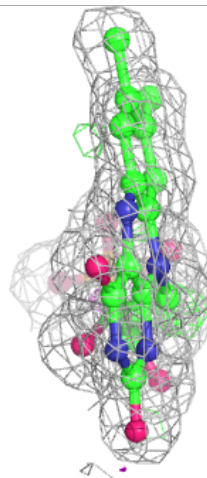
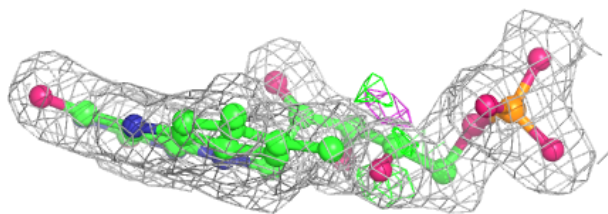
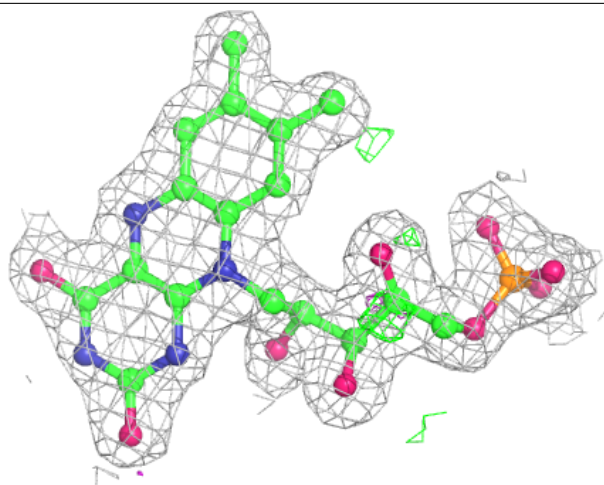
**Electron density around FAD B 1105:**

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



**Electron density around FNR A 1108:**

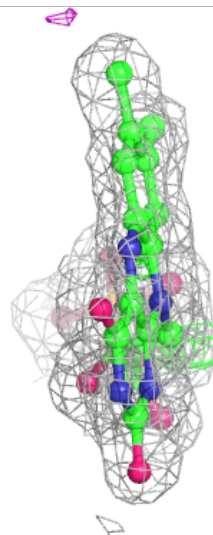
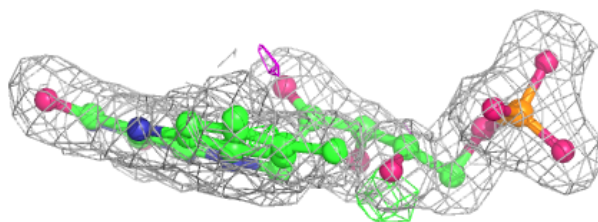
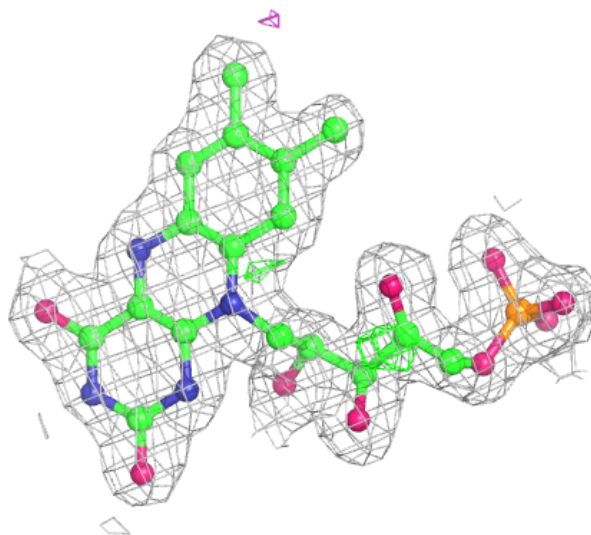
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





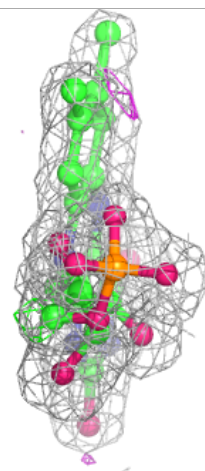
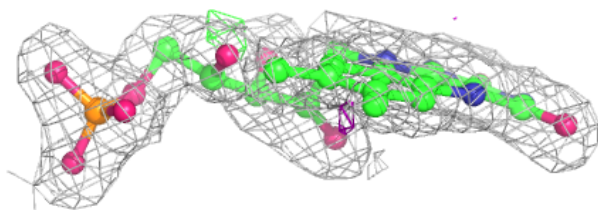
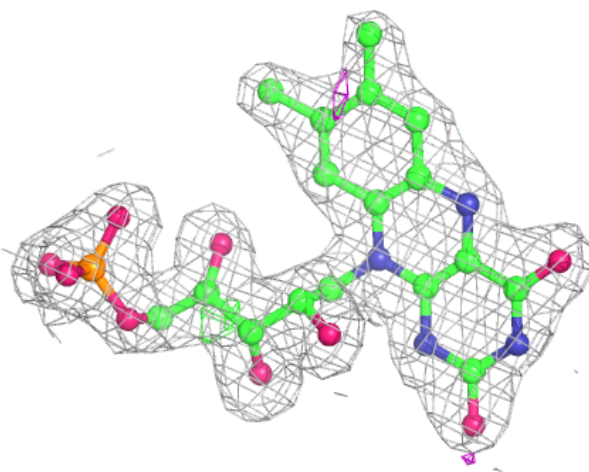
**Electron density around FNR C 1107:**

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



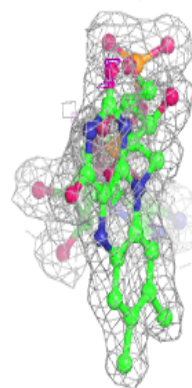
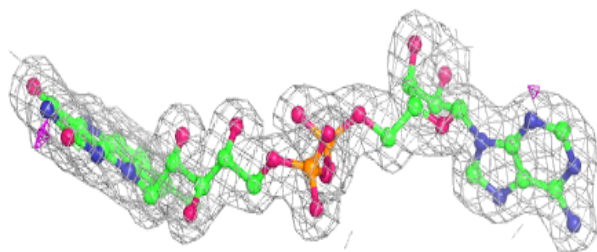
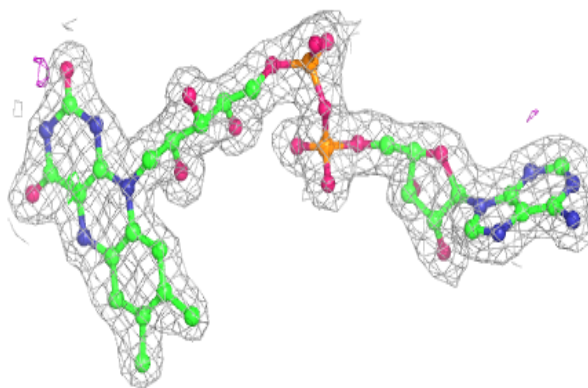
**Electron density around FNR B 1107:**

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

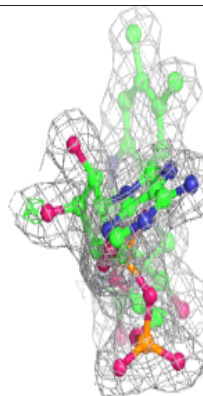
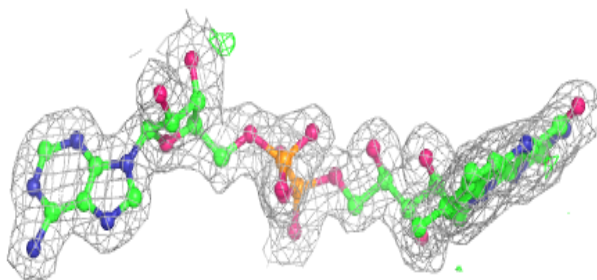
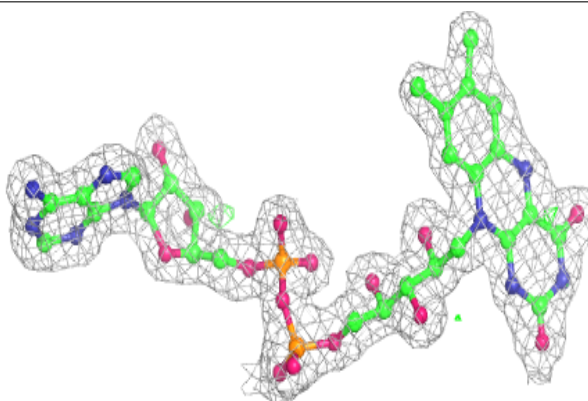


**Electron density around FAD C 1105:**

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

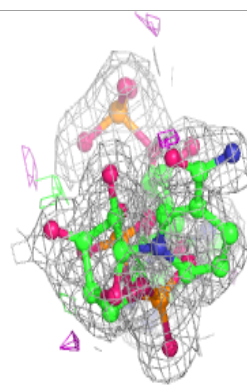
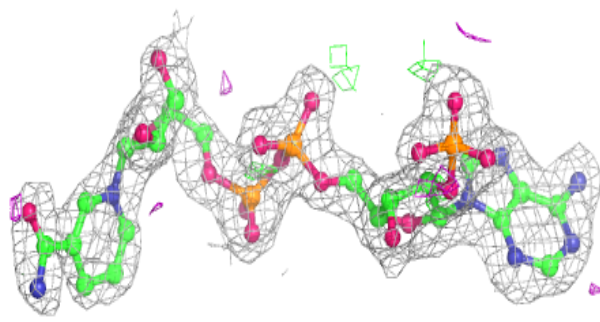
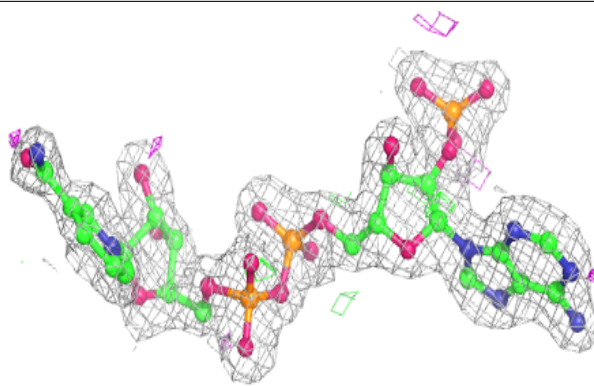
**Electron density around FAD A 1105:**

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

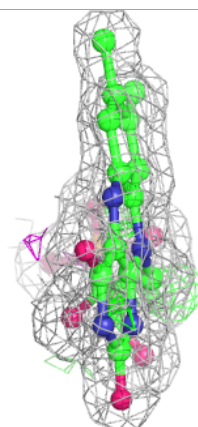
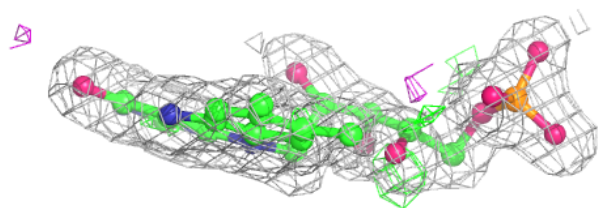
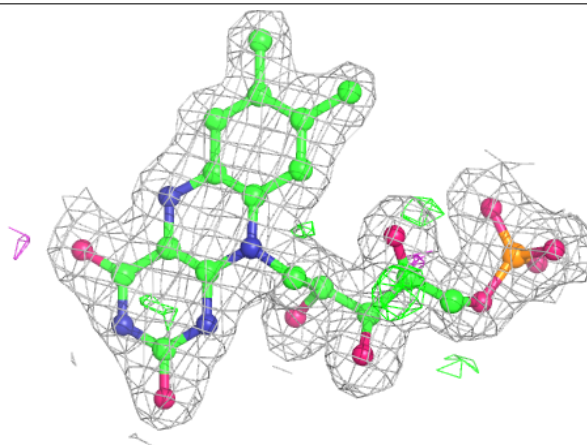


**Electron density around NAP C 1106:**

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

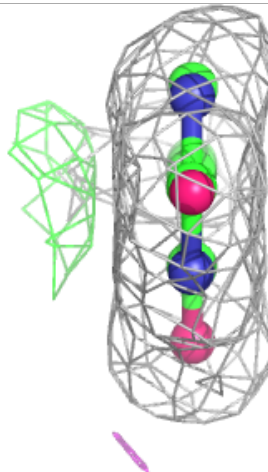
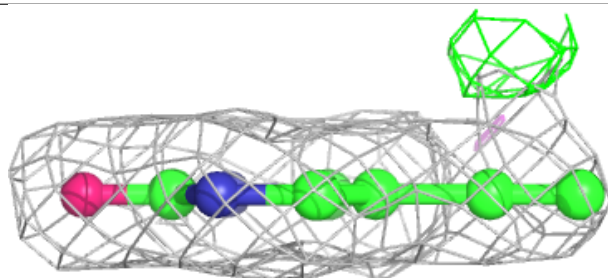
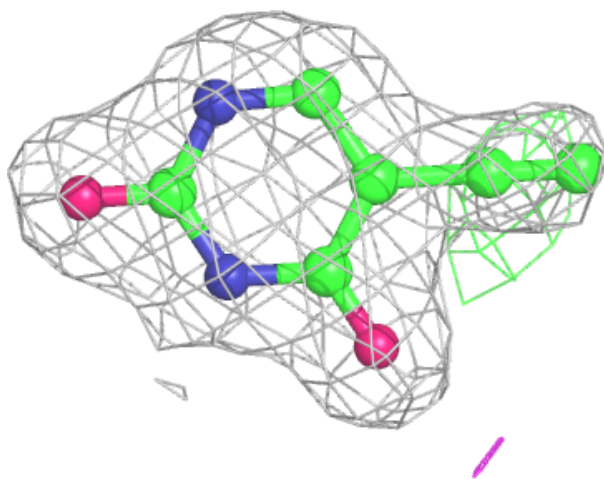
**Electron density around FNR D 1108:**

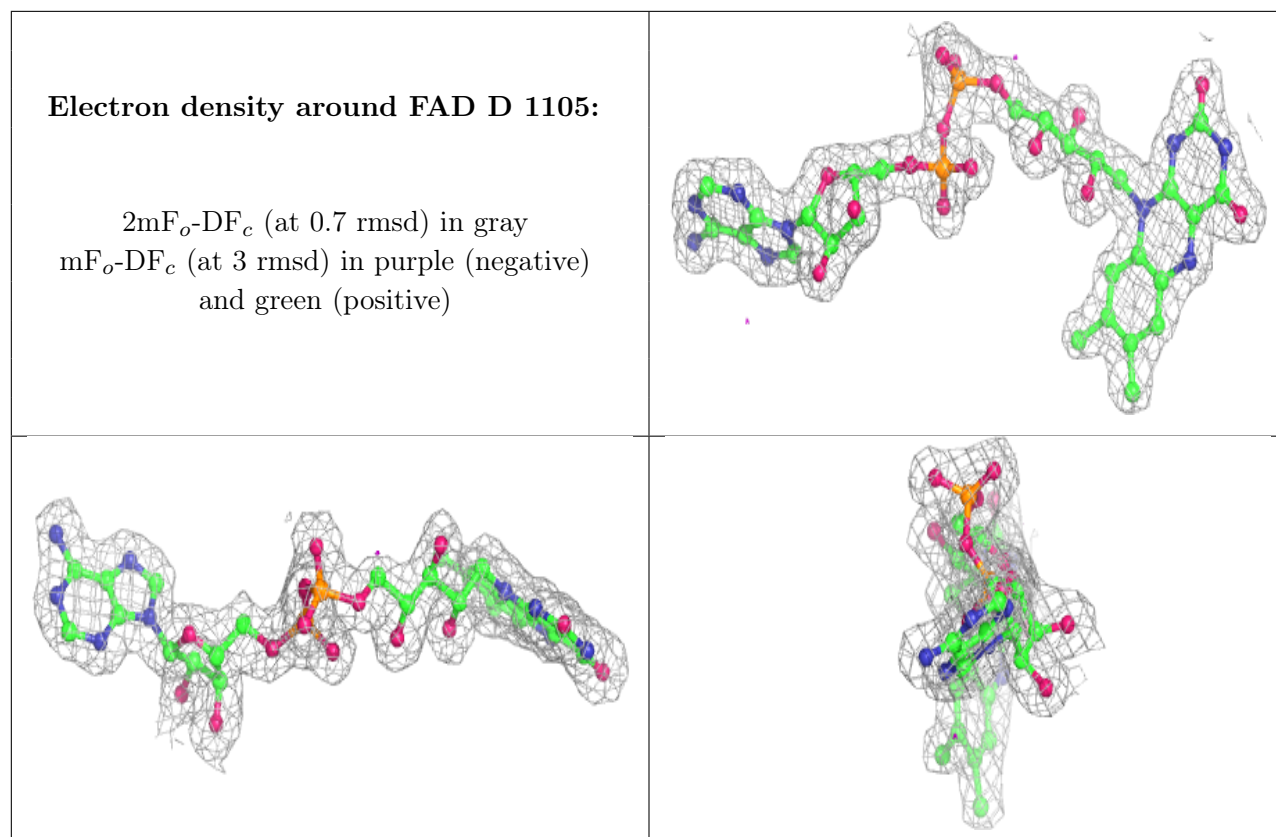
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Y3G D 1106:**

$2mF_o-DF_c$  (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.