wwPDB X-ray Structure Validation Summary Report (i)

Aug 28, 2023 – 09:44 PM EDT

PDB ID	:	3N0B
Title	:	TM0449 mutant crystals grown in loops/micromounts
Authors	:	Mathews, I.I.
Deposited on	:	2010-05-13
Resolution	:	2.30 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 (i) 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 (i)) were used in the production of this report:

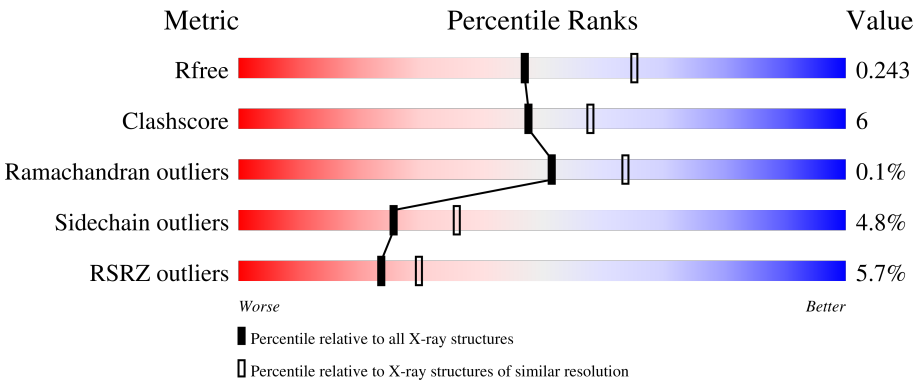
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 <=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	232	5% 78% 15% • 7%
1	B	232	7% 78% 16% • 5%
1	C	232	4% 74% 17% • 7%
1	D	232	5% 75% 14% • 9%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7464 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 Thymidylate synthase thyX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	216	1778	1153	307	312	6	0	0	0
			Total	C	N	O	S			
1	B	220	1821	1180	313	322	6	0	0	0
			Total	C	N	O	S			
1	C	216	1793	1162	308	318	5	0	0	0
			Total	C	N	O	S			
1	D	210	1741	1128	300	308	5	0	0	0

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	expression tag	UNP Q9WYT0
A	-10	GLY	-	expression tag	UNP Q9WYT0
A	-9	SER	-	expression tag	UNP Q9WYT0
A	-8	ASP	-	expression tag	UNP Q9WYT0
A	-7	LYS	-	expression tag	UNP Q9WYT0
A	-6	ILE	-	expression tag	UNP Q9WYT0
A	-5	HIS	-	expression tag	UNP Q9WYT0
A	-4	HIS	-	expression tag	UNP Q9WYT0
A	-3	HIS	-	expression tag	UNP Q9WYT0
A	-2	HIS	-	expression tag	UNP Q9WYT0
A	-1	HIS	-	expression tag	UNP Q9WYT0
A	0	HIS	-	expression tag	UNP Q9WYT0
A	158	ALA	PHE	engineered mutation	UNP Q9WYT0
A	160	ALA	TRP	engineered mutation	UNP Q9WYT0
B	-11	MET	-	expression tag	UNP Q9WYT0
B	-10	GLY	-	expression tag	UNP Q9WYT0
B	-9	SER	-	expression tag	UNP Q9WYT0
B	-8	ASP	-	expression tag	UNP Q9WYT0
B	-7	LYS	-	expression tag	UNP Q9WYT0
B	-6	ILE	-	expression tag	UNP Q9WYT0
B	-5	HIS	-	expression tag	UNP Q9WYT0

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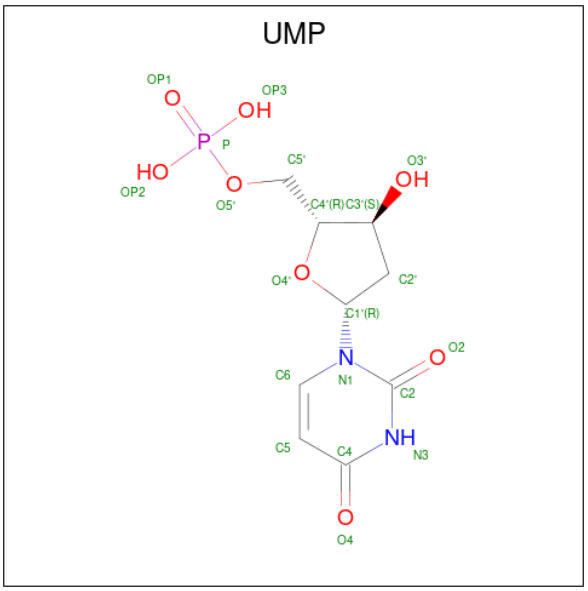
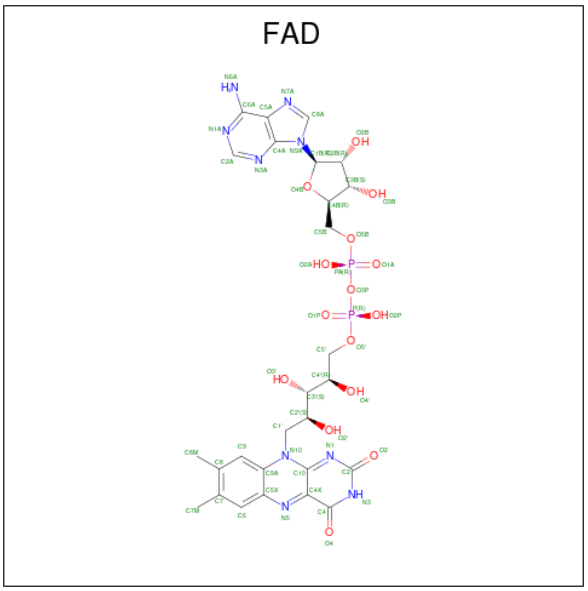
Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	HIS	-	expression tag	UNP Q9WYT0
B	-3	HIS	-	expression tag	UNP Q9WYT0
B	-2	HIS	-	expression tag	UNP Q9WYT0
B	-1	HIS	-	expression tag	UNP Q9WYT0
B	0	HIS	-	expression tag	UNP Q9WYT0
B	158	ALA	PHE	engineered mutation	UNP Q9WYT0
B	160	ALA	TRP	engineered mutation	UNP Q9WYT0
C	-11	MET	-	expression tag	UNP Q9WYT0
C	-10	GLY	-	expression tag	UNP Q9WYT0
C	-9	SER	-	expression tag	UNP Q9WYT0
C	-8	ASP	-	expression tag	UNP Q9WYT0
C	-7	LYS	-	expression tag	UNP Q9WYT0
C	-6	ILE	-	expression tag	UNP Q9WYT0
C	-5	HIS	-	expression tag	UNP Q9WYT0
C	-4	HIS	-	expression tag	UNP Q9WYT0
C	-3	HIS	-	expression tag	UNP Q9WYT0
C	-2	HIS	-	expression tag	UNP Q9WYT0
C	-1	HIS	-	expression tag	UNP Q9WYT0
C	0	HIS	-	expression tag	UNP Q9WYT0
C	158	ALA	PHE	engineered mutation	UNP Q9WYT0
C	160	ALA	TRP	engineered mutation	UNP Q9WYT0
D	-11	MET	-	expression tag	UNP Q9WYT0
D	-10	GLY	-	expression tag	UNP Q9WYT0
D	-9	SER	-	expression tag	UNP Q9WYT0
D	-8	ASP	-	expression tag	UNP Q9WYT0
D	-7	LYS	-	expression tag	UNP Q9WYT0
D	-6	ILE	-	expression tag	UNP Q9WYT0
D	-5	HIS	-	expression tag	UNP Q9WYT0
D	-4	HIS	-	expression tag	UNP Q9WYT0
D	-3	HIS	-	expression tag	UNP Q9WYT0
D	-2	HIS	-	expression tag	UNP Q9WYT0
D	-1	HIS	-	expression tag	UNP Q9WYT0
D	0	HIS	-	expression tag	UNP Q9WYT0
D	158	ALA	PHE	engineered mutation	UNP Q9WYT0
D	160	ALA	TRP	engineered mutation	UNP Q9WYT0

- Molecule 2 is 2'-DEOXYURIDINE 5'-MONOPHOSPHATE (three-letter code: UMP) (formula: $C_9H_{13}N_2O_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	20	9	2	8	1	0	0
			Total	C	N	O	P		
2	B	1	20	9	2	8	1	0	0
			Total	C	N	O	P		
2	C	1	20	9	2	8	1	0	0
			Total	C	N	O	P		
2	D	1	20	9	2	8	1	0	0

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

- Molecule 4 is water.

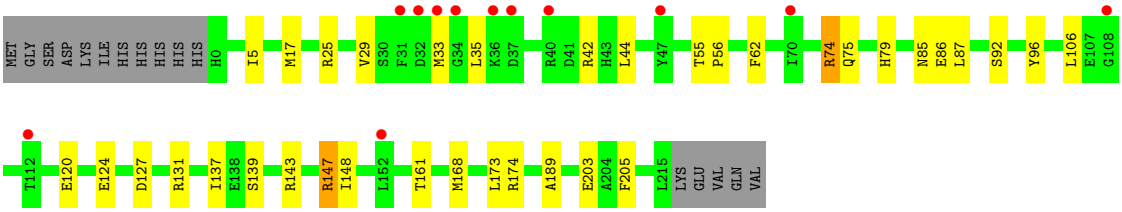
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	13	13	13	0	0
4	B	10	10	10	0	0
4	C	9	9	9	0	0
4	D	7	7	7	0	0

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.

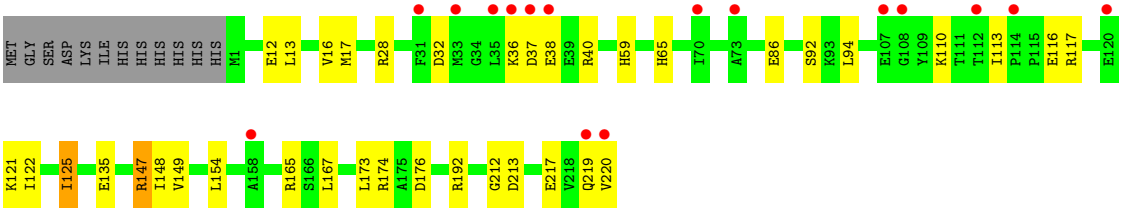
• Molecule 1: Thymidylate synthase thyX

Chain A:



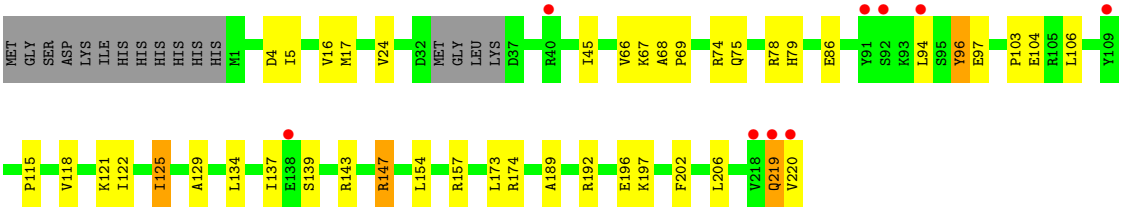
• Molecule 1: Thymidylate synthase thyX

Chain B:



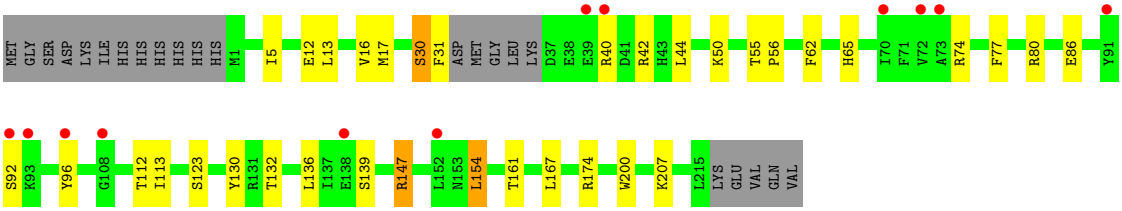
• Molecule 1: Thymidylate synthase thyX

Chain C:



• Molecule 1: Thymidylate synthase thyX

Chain D:


MET
GLY
SER
ASP
LYS
ILE
HIS
HIS
HIS
HIS
HIS
HIS
M1
I5
E12
L13
V16
M17
S30
F31
ASP
MET
GLY
LEU
LYS
D37
E38
E39
R40
D41
R42
H43
L44
K50
T55
P56
F62
H65
I70
F71
V72
A73
R74
F77
R80
E86
Y91
S92
K93
Y96
G108
T112
I113
S123
Y130
R131
T132
L136
I137
E138
S139
R147
L152
N153
L154
T161
L167
R174
W200
K207
L215
LYS
GLU
VAL
GLN
VAL

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	54.52Å 116.75Å 141.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.30 29.98 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (30.00-2.30) 99.8 (29.98-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.22 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.198 , 0.249 0.193 , 0.243	Depositor DCC
R_{free} test set	2046 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	40.9	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 40.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7464	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.39% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: UMP, 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	0.83	0/1824	0.78	1/2465 (0.0%)
1	B	0.77	0/1867	0.79	1/2522 (0.0%)
1	C	0.81	0/1838	0.79	1/2483 (0.0%)
1	D	0.79	0/1785	0.78	1/2414 (0.0%)
All	All	0.80	0/7314	0.79	4/9884 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	74	ARG	NE-CZ-NH2	-8.29	116.16	120.30
1	B	213	ASP	CB-CG-OD1	5.91	123.62	118.30
1	C	134	LEU	CA-CB-CG	5.25	127.38	115.30
1	D	154	LEU	CA-CB-CG	5.13	127.11	115.30

There are no chirality outliers.

There are no planarity outliers.

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	1778	0	1776	20	0
1	B	1821	0	1825	28	0
1	C	1793	0	1790	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1741	0	1737	18	0
2	A	20	0	11	1	0
2	B	20	0	11	3	0
2	C	20	0	11	3	0
2	D	20	0	11	2	0
3	A	53	0	31	0	0
3	B	53	0	31	2	0
3	C	53	0	31	1	0
3	D	53	0	31	2	0
4	A	13	0	0	0	0
4	B	10	0	0	0	0
4	C	9	0	0	0	0
4	D	7	0	0	0	0
All	All	7464	0	7296	89	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 6.

The worst 5 of 89 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:C:17:MET:HB2	1:D:17:MET:HB2	1.39	1.02
2:A:303:UMP:HN3	1:D:174:ARG:HH12	1.08	1.00
1:B:174:ARG:HH12	2:C:313:UMP:HN3	1.15	0.92
2:B:308:UMP:HN3	1:C:174:ARG:HH12	1.17	0.86
1:B:122:ILE:O	1:B:125:ILE:HD12	1.76	0.86

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	214/232 (92%)	207 (97%)	7 (3%)	0	100	100
1	B	218/232 (94%)	209 (96%)	9 (4%)	0	100	100
1	C	212/232 (91%)	204 (96%)	7 (3%)	1 (0%)	29	35
1	D	206/232 (89%)	198 (96%)	8 (4%)	0	100	100
All	All	850/928 (92%)	818 (96%)	31 (4%)	1 (0%)	51	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	96	TYR

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	187/205 (91%)	179 (96%)	8 (4%)	29	40
1	B	193/205 (94%)	183 (95%)	10 (5%)	23	32
1	C	190/205 (93%)	184 (97%)	6 (3%)	39	54
1	D	184/205 (90%)	172 (94%)	12 (6%)	17	23
All	All	754/820 (92%)	718 (95%)	36 (5%)	25	36

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	50	LYS
1	D	207	LYS
1	D	92	SER
1	D	139	SER
1	B	113	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	219	GLN
1	C	219	GLN
1	D	75	GLN
1	A	169	ASN
1	A	85	ASN

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)

8 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	C	305	-	53,58,58	3.12	16 (30%)	68,89,89	1.85	15 (22%)
2	UMP	D	318	-	21,21,21	1.24	4 (19%)	31,31,31	1.54	6 (19%)
3	FAD	B	310	-	53,58,58	3.13	17 (32%)	68,89,89	1.74	13 (19%)
2	UMP	B	308	-	21,21,21	1.18	2 (9%)	31,31,31	1.75	8 (25%)
3	FAD	A	315	-	53,58,58	3.40	17 (32%)	68,89,89	2.17	18 (26%)
3	FAD	D	300	-	53,58,58	3.16	15 (28%)	68,89,89	1.74	14 (20%)
2	UMP	A	303	-	21,21,21	1.23	4 (19%)	31,31,31	1.60	5 (16%)
2	UMP	C	313	-	21,21,21	1.01	1 (4%)	31,31,31	1.79	7 (22%)

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	C	305	-	-	5/30/50/50	0/6/6/6
2	UMP	D	318	-	-	0/10/22/22	0/2/2/2
3	FAD	B	310	-	-	0/30/50/50	0/6/6/6
2	UMP	B	308	-	-	0/10/22/22	0/2/2/2
3	FAD	A	315	-	-	1/30/50/50	0/6/6/6
3	FAD	D	300	-	-	8/30/50/50	0/6/6/6
2	UMP	A	303	-	-	0/10/22/22	0/2/2/2
2	UMP	C	313	-	-	0/10/22/22	0/2/2/2

The worst 5 of 76 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	315	FAD	C6-C7	10.86	1.55	1.39
3	D	300	FAD	C6-C7	10.35	1.54	1.39
3	B	310	FAD	C6-C7	9.74	1.53	1.39
3	A	315	FAD	C6-C5X	9.52	1.54	1.40
3	C	305	FAD	C6-C7	9.40	1.53	1.39

The worst 5 of 86 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	315	FAD	C4-C4X-N5	6.66	127.70	118.23
3	A	315	FAD	C1'-N10-C9A	5.56	129.79	120.51
3	C	305	FAD	C1'-N10-C9A	5.54	129.75	120.51
2	C	313	UMP	O2-C2-N1	-5.44	115.56	122.79
3	C	305	FAD	C4X-C10-N1	-5.23	112.60	124.73

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	305	FAD	P-O3P-PA-O5B
3	C	305	FAD	C5'-O5'-P-O3P
3	A	315	FAD	O4'-C4'-C5'-O5'
3	D	300	FAD	O3'-C3'-C4'-C5'
3	D	300	FAD	O2'-C2'-C3'-C4'

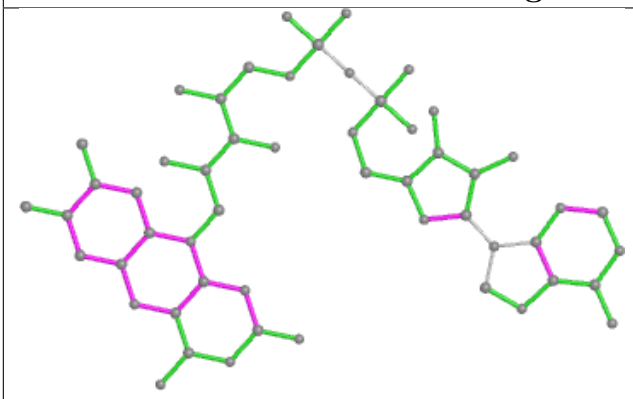
There are no ring outliers.

7 monomers are involved in 14 short contacts:

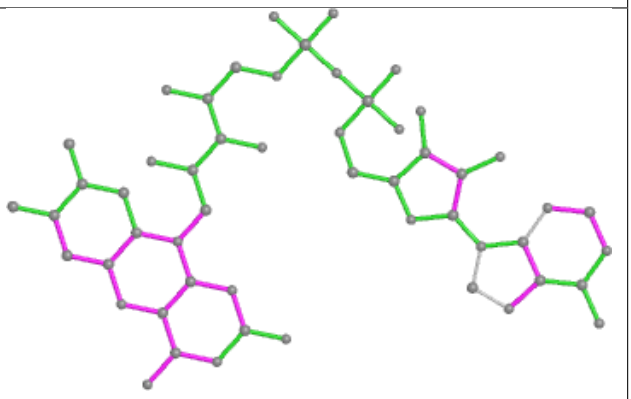
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	305	FAD	1	0
2	D	318	UMP	2	0
3	B	310	FAD	2	0
2	B	308	UMP	3	0
3	D	300	FAD	2	0
2	A	303	UMP	1	0
2	C	313	UMP	3	0

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

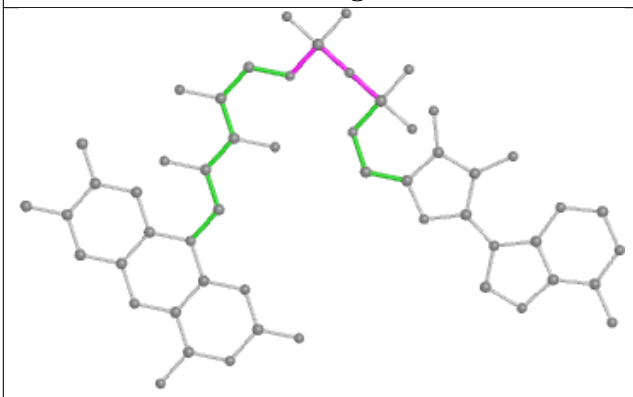
Ligand FAD C 305



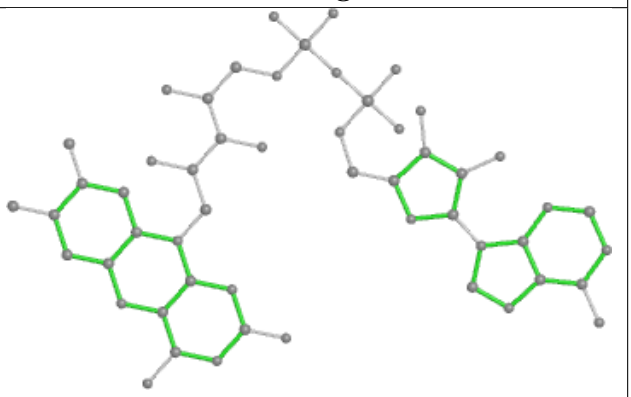
Bond lengths



Bond angles

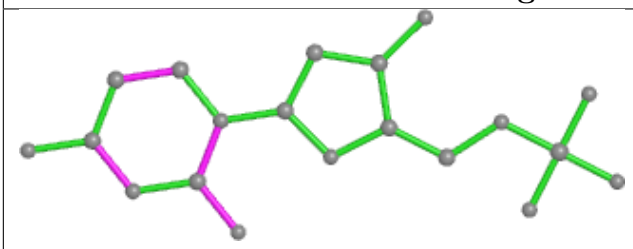


Torsions

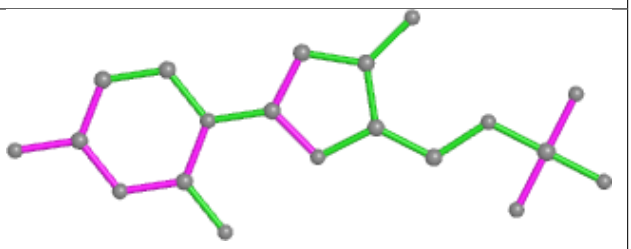


Rings

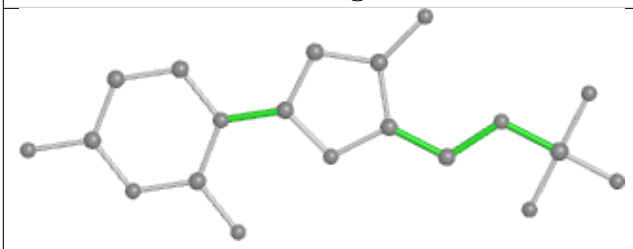
Ligand UMP D 318



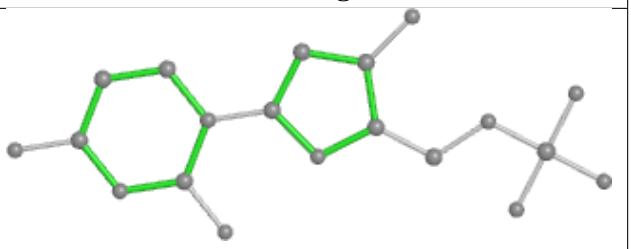
Bond lengths



Bond angles

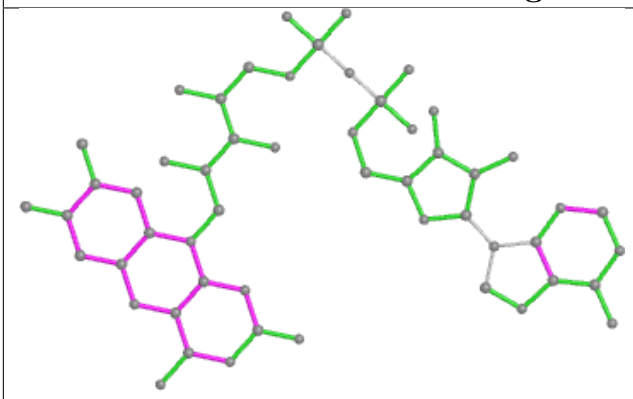


Torsions

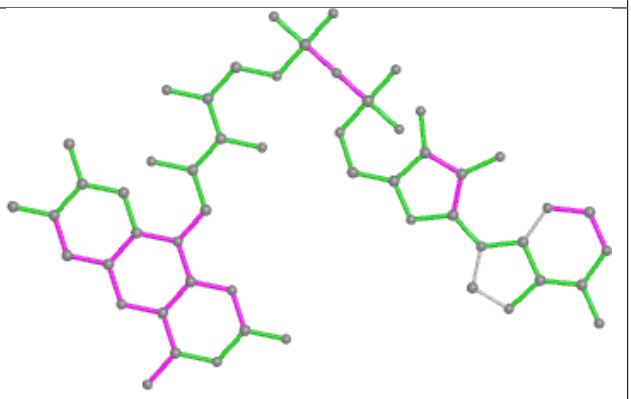


Rings

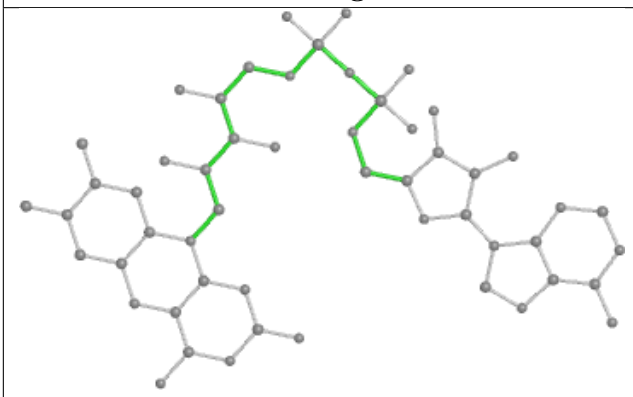
Ligand FAD B 310



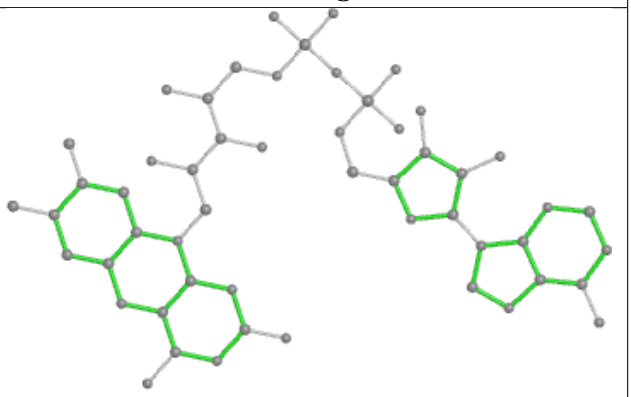
Bond lengths



Bond angles

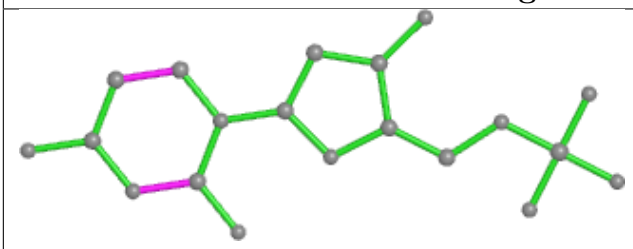


Torsions

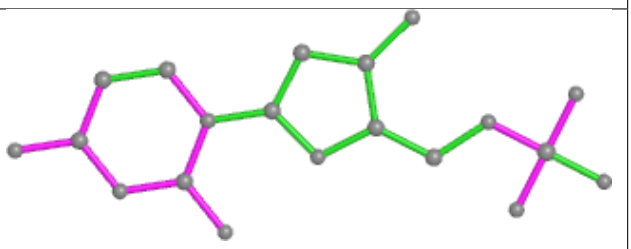


Rings

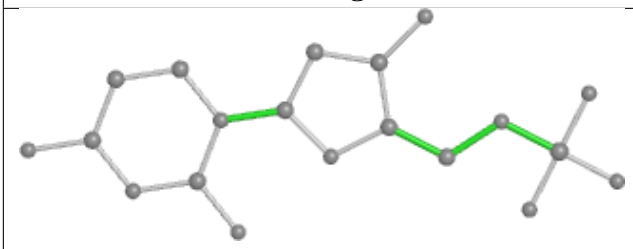
Ligand UMP B 308



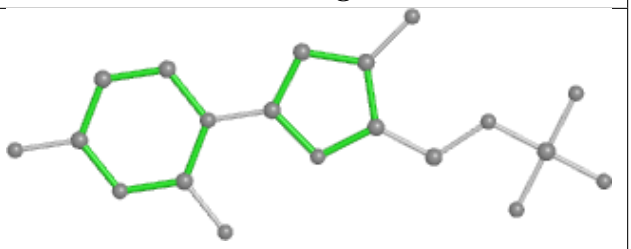
Bond lengths



Bond angles

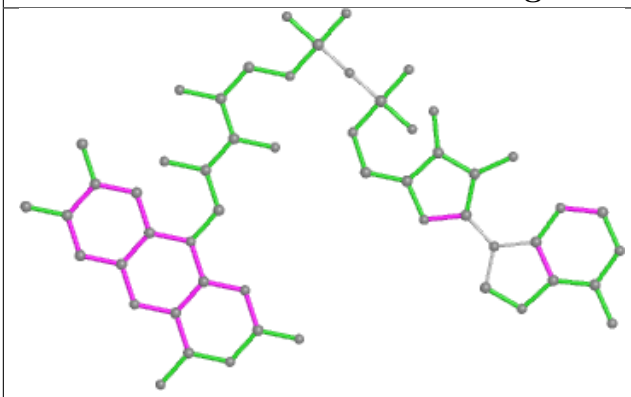


Torsions

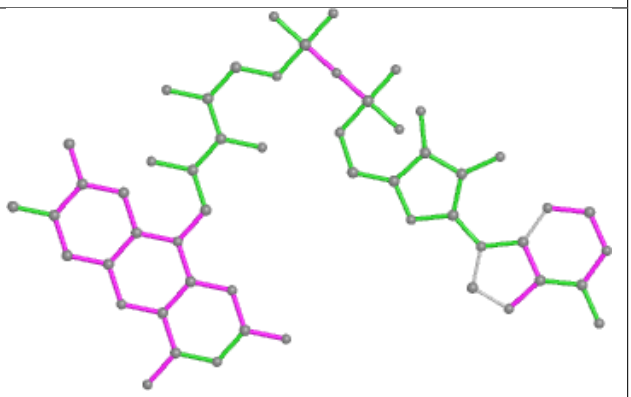


Rings

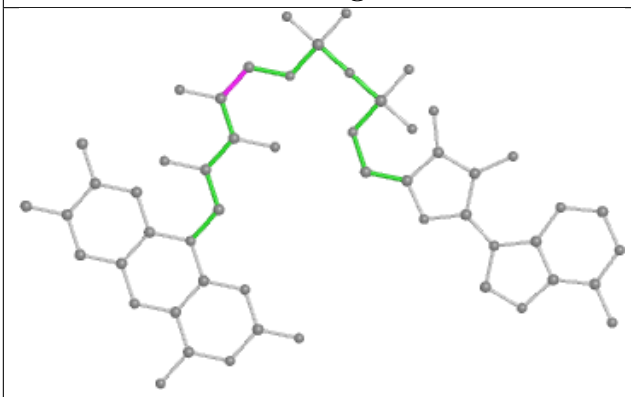
Ligand FAD A 315



Bond lengths



Bond angles



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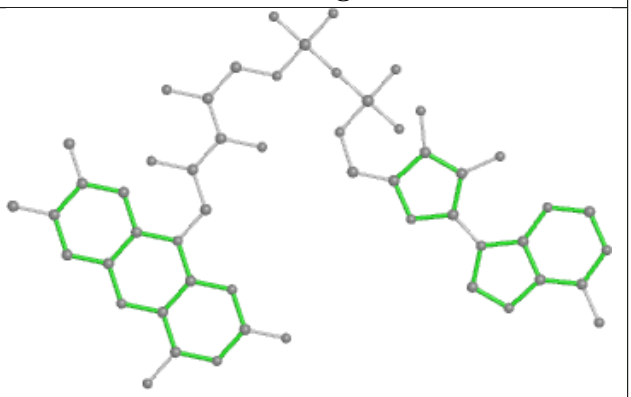
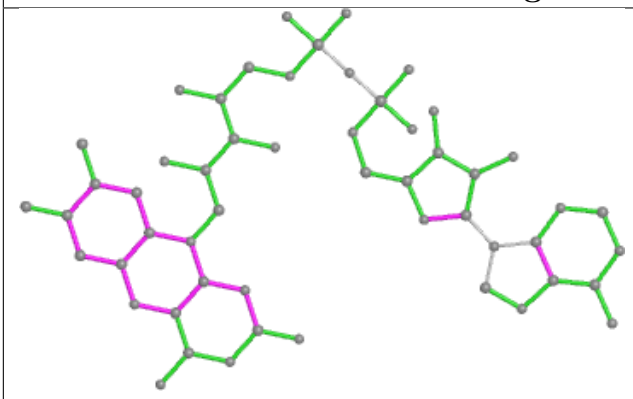


Rings

Ligand FAD D 300



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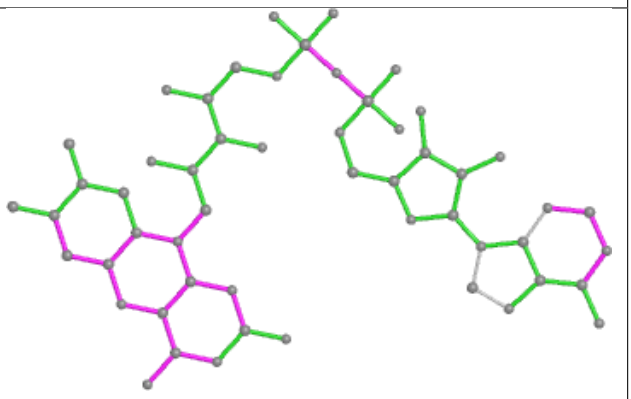
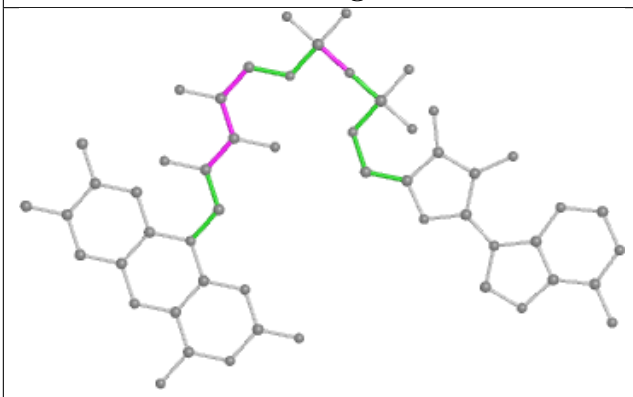
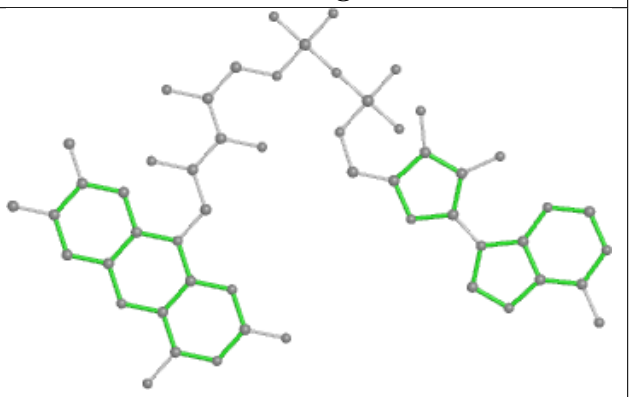


Bond angles

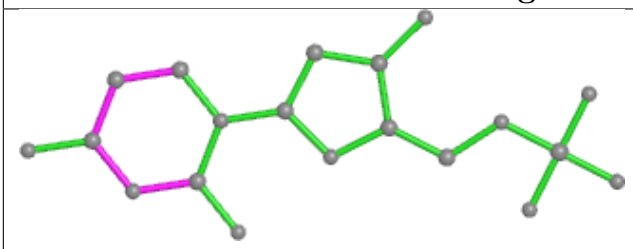


Torsions

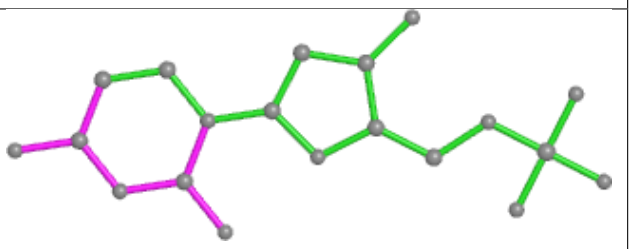


Rings

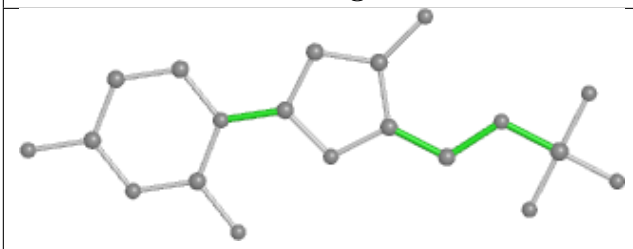
Ligand UMP A 303



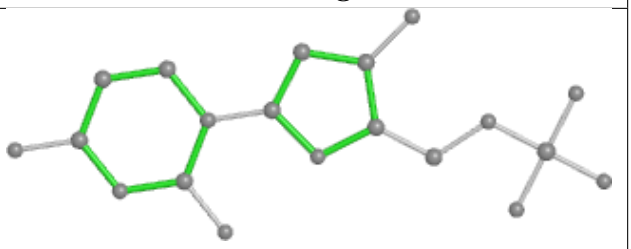
Bond lengths



Bond angles

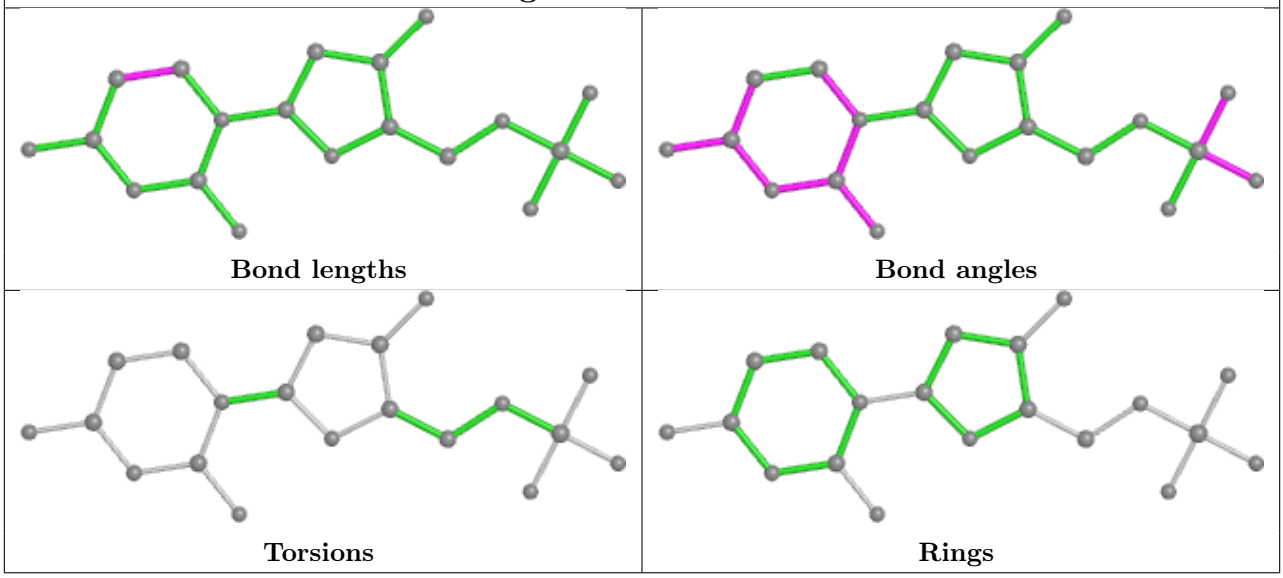


Torsions



Rings

Ligand UMP C 313



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	216/232 (93%)	0.07	12 (5%)	24	30	25, 36, 66, 72	0
1	B	220/232 (94%)	0.25	16 (7%)	15	20	24, 38, 71, 76	0
1	C	216/232 (93%)	0.03	9 (4%)	36	43	24, 34, 61, 69	0
1	D	210/232 (90%)	0.16	12 (5%)	23	30	23, 36, 62, 72	0
All	All	862/928 (92%)	0.13	49 (5%)	23	30	23, 36, 66, 76	0

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	96	TYR	4.8
1	A	36	LYS	4.8
1	D	91	TYR	4.7
1	B	35	LEU	4.6
1	D	108	GLY	4.5

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

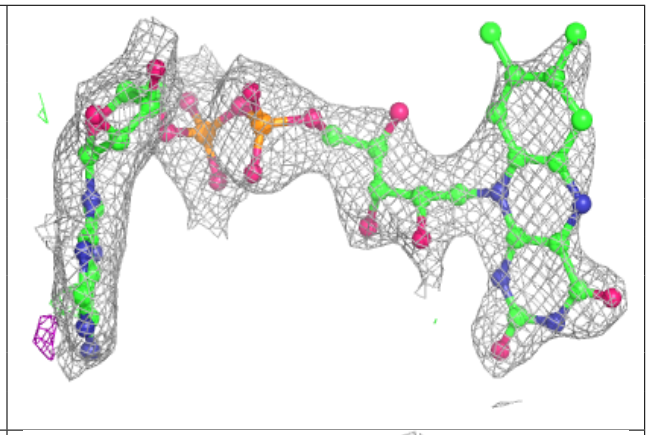
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

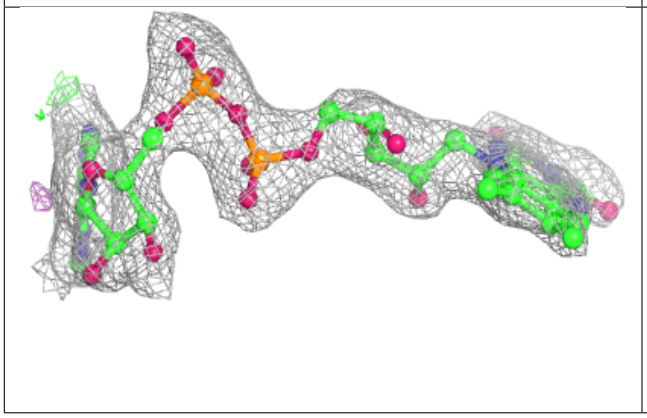
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	FAD	B	310	53/53	0.89	0.19	42,55,63,63	0
3	FAD	A	315	53/53	0.90	0.18	46,61,69,71	0
2	UMP	D	318	20/20	0.90	0.15	49,53,56,56	0
3	FAD	D	300	53/53	0.90	0.17	41,54,58,60	0
3	FAD	C	305	53/53	0.93	0.14	38,52,58,59	0
2	UMP	C	313	20/20	0.95	0.13	38,42,48,49	0
2	UMP	B	308	20/20	0.96	0.14	35,41,43,44	0
2	UMP	A	303	20/20	0.97	0.12	33,36,38,39	0

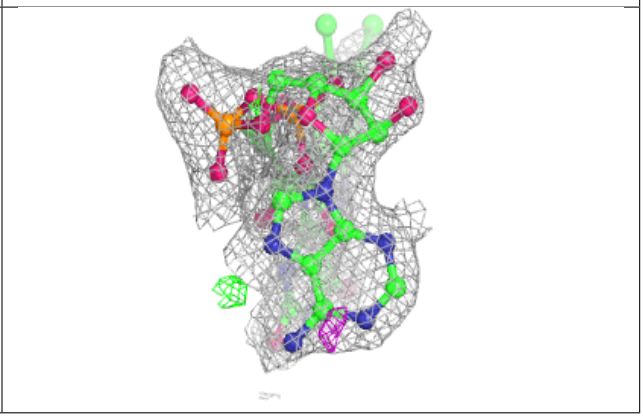
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FAD B 310:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

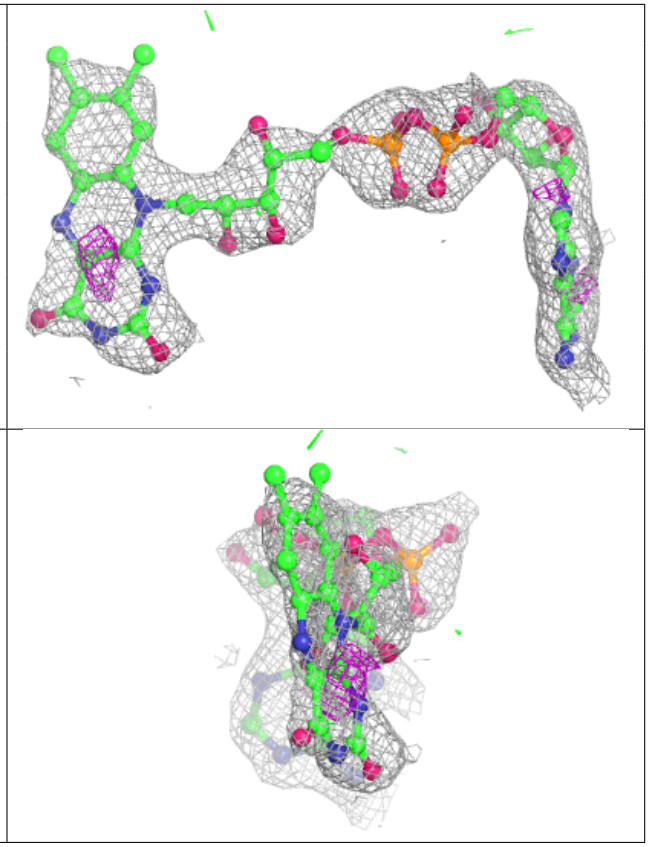






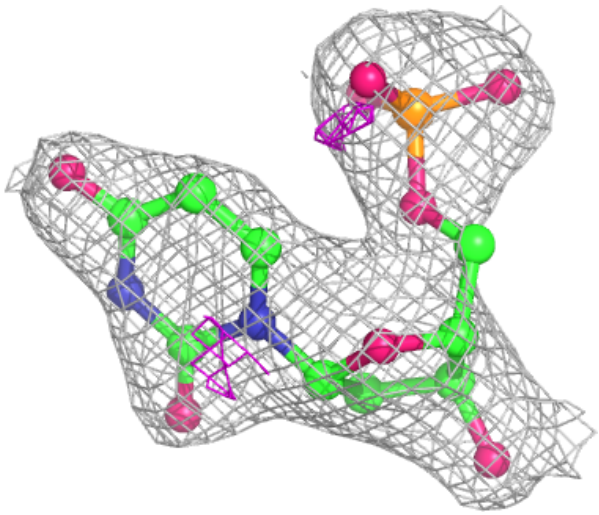
Electron density around FAD A 315:

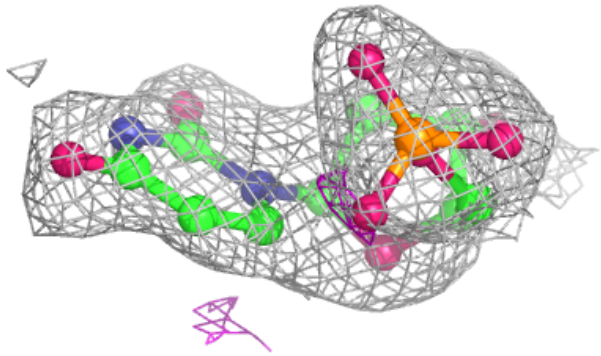
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

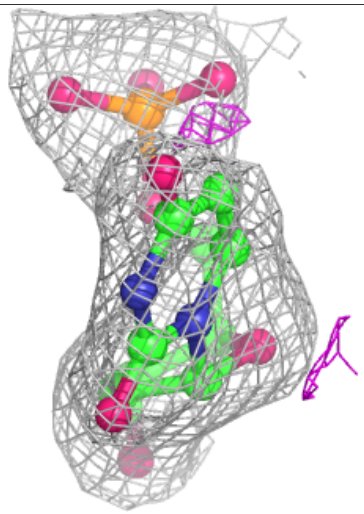


Electron density around UMP D 318:

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

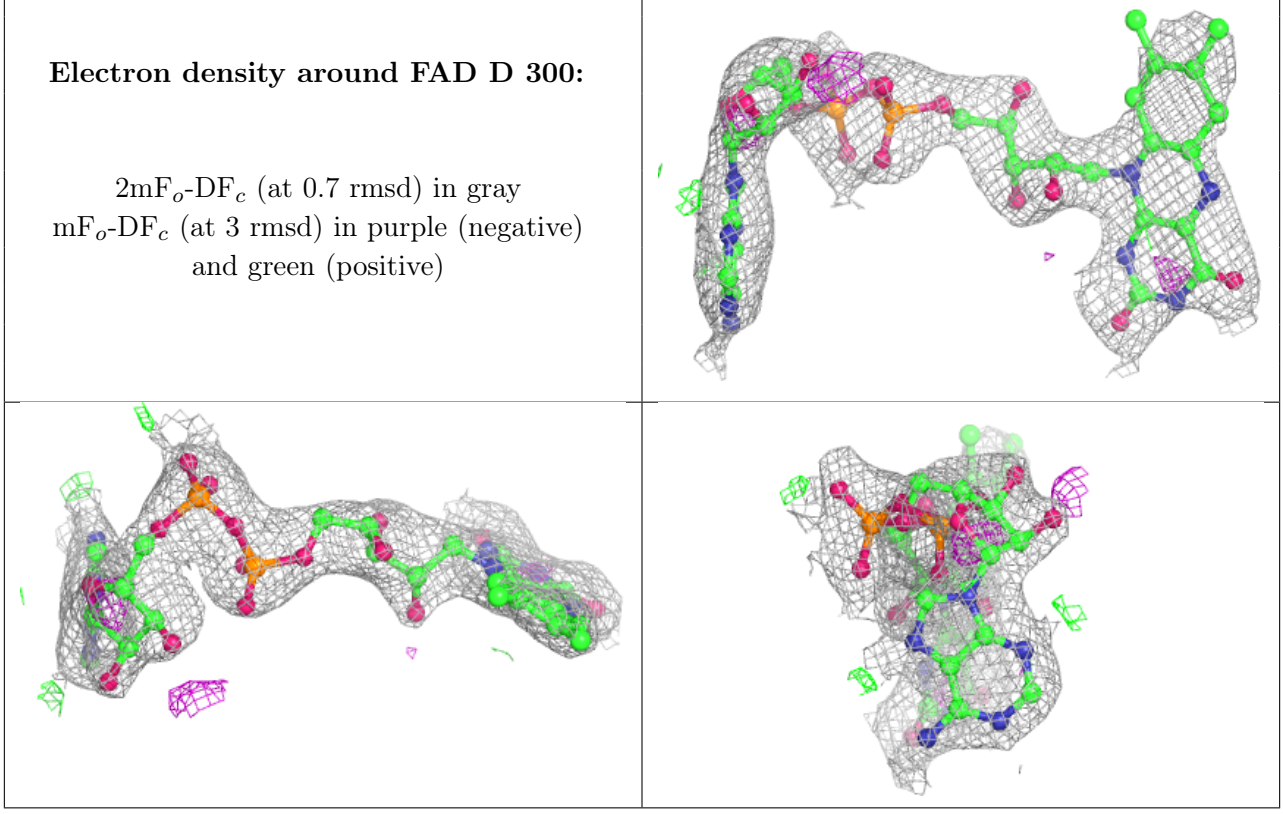






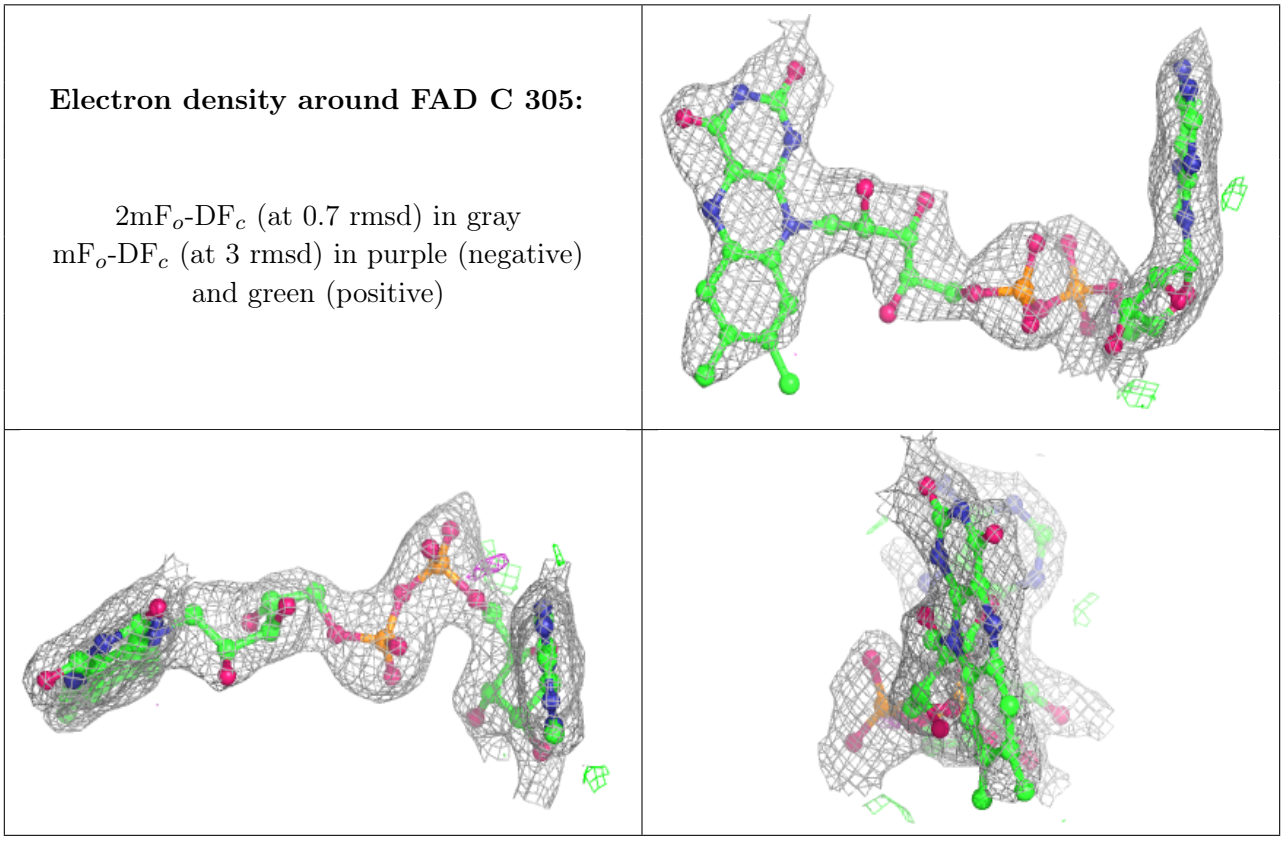
Electron density around FAD D 300:

$2mF_o$-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 305:

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



Electron density around UMP C 313:

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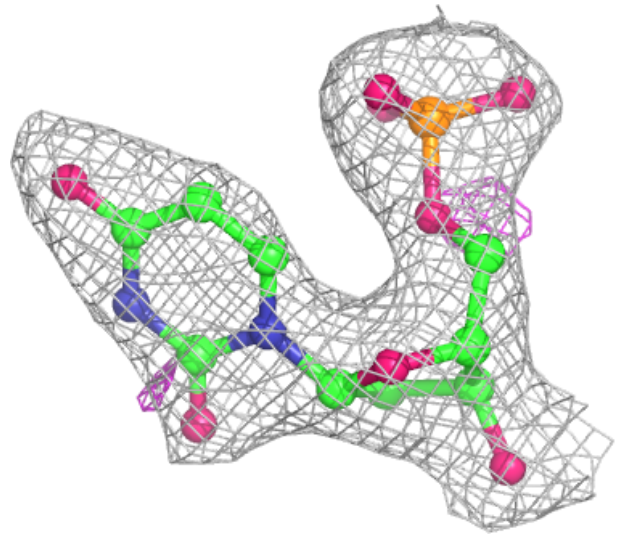
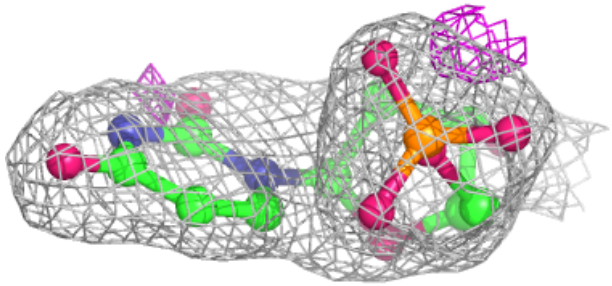
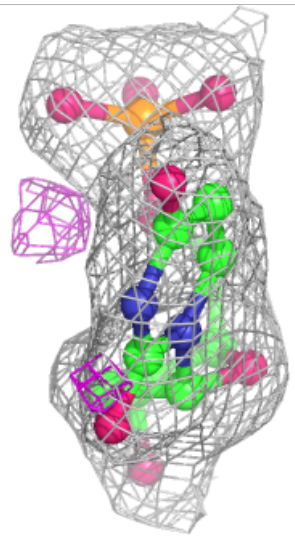
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

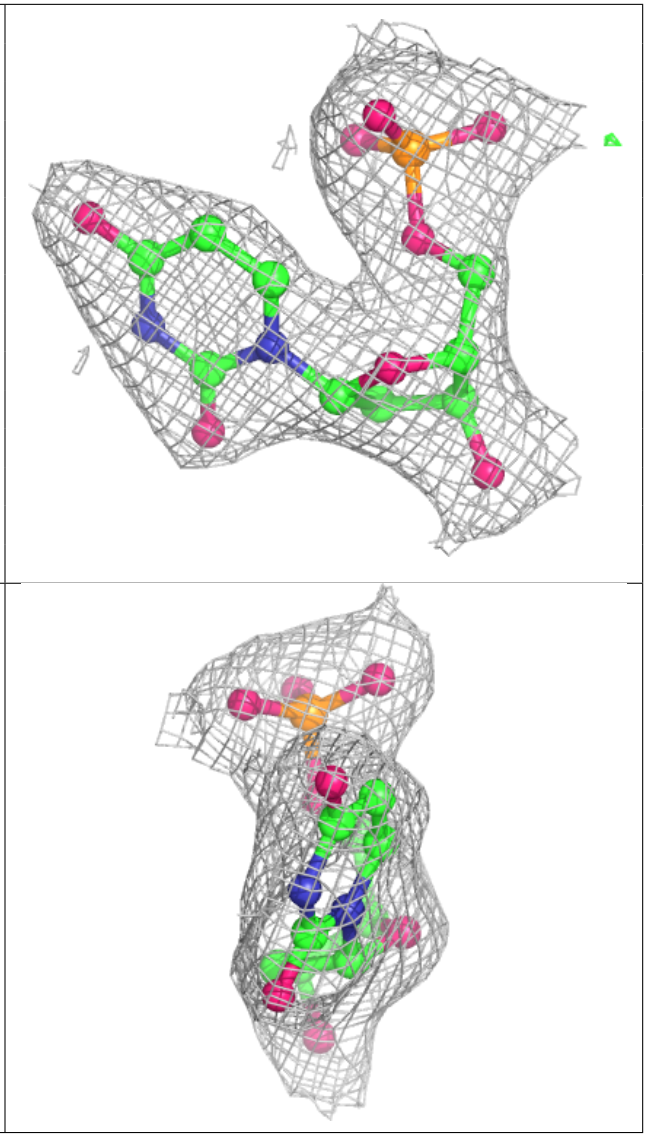






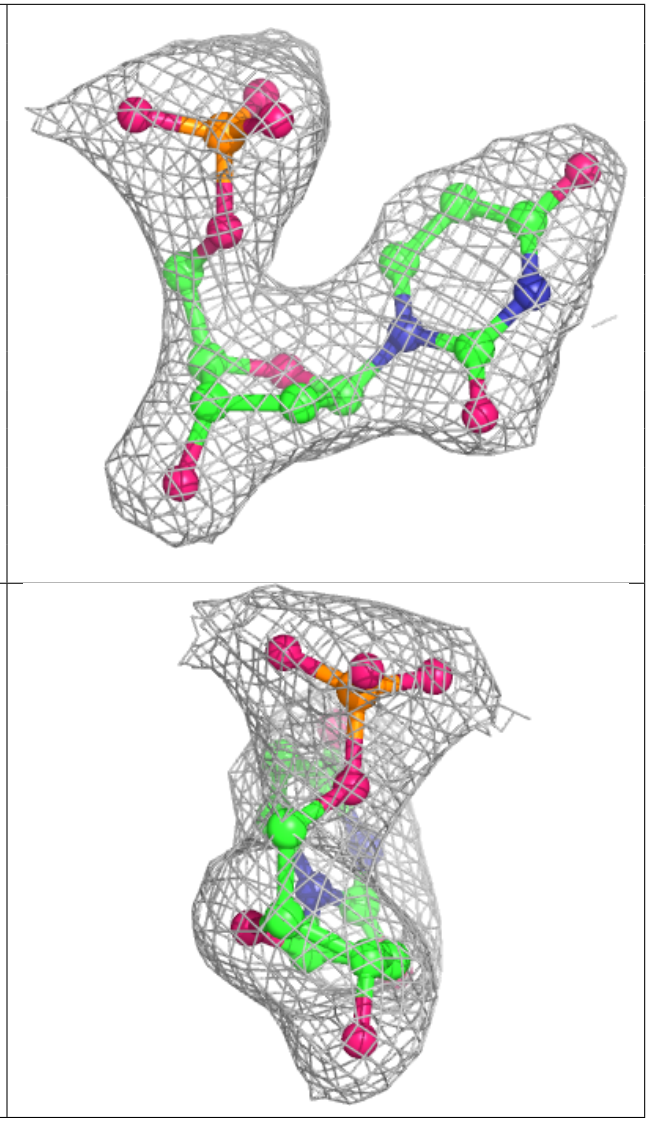
Electron density around UMP B 308:

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



Electron density around UMP A 303:

$2mF_o$-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.