



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 01:26 PM EDT

PDB ID : 2PGO  
Title : The crystal structure of FAD and ThDP dependent Cyclohexane-1,2-dione Hydrolase (Cdh) from Azoarcus sp. strain 22Lin  
Authors : Steinbach, A.K.; Warkentin, E.; Kroneck, P.M.H.; Ermler, U.  
Deposited on : 2007-04-10  
Resolution : 1.26 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.

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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
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)	:	2.36.2

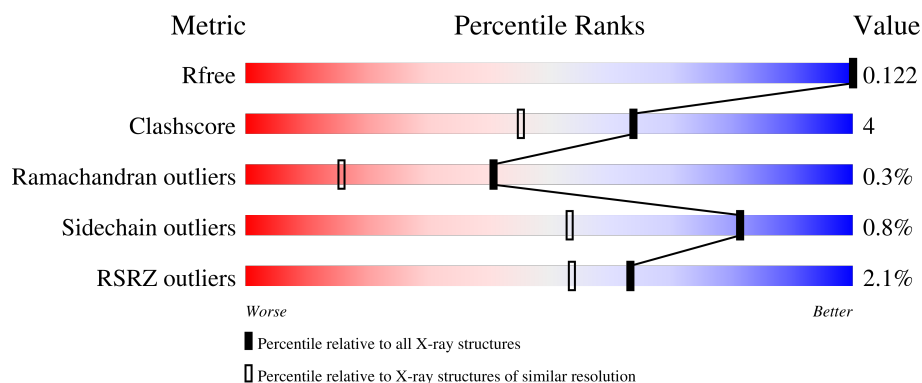
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.26 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	1023 (1.28-1.24)
Clashscore	141614	1060 (1.28-1.24)
Ramachandran outliers	138981	1029 (1.28-1.24)
Sidechain outliers	138945	1028 (1.28-1.24)
RSRZ outliers	127900	1004 (1.28-1.24)

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	589	
1	B	589	

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 10640 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 Cyclohexane-1,2-dione Hydrolase (Cdh).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	587	Total	C	N	O	S	0	46	0
			4643	2947	817	855	24			
1	B	587	Total	C	N	O	S	0	39	0
			4602	2922	815	843	22			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

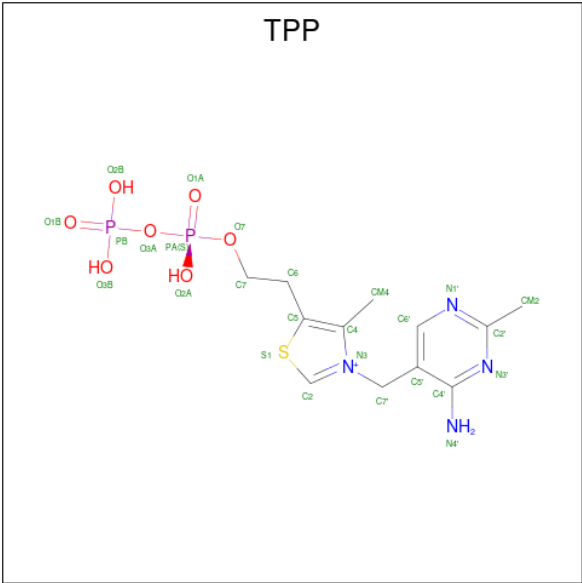
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		
3	B	1	Total	Cl	0	0
			1	1		

- Molecule 4 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>).



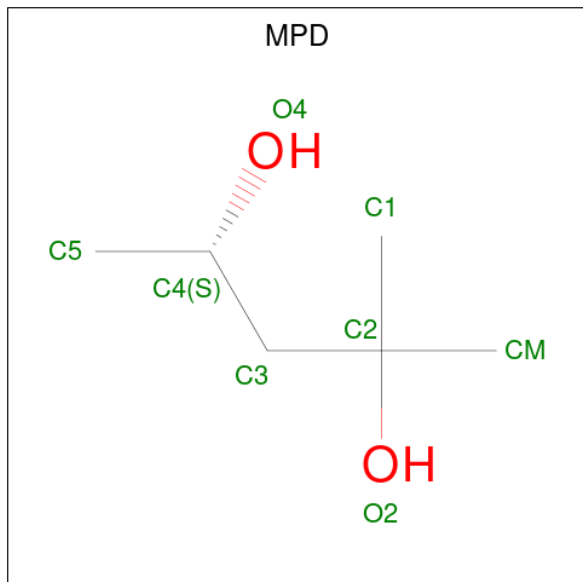
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
4	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 5 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: C<sub>12</sub>H<sub>19</sub>N<sub>4</sub>O<sub>7</sub>P<sub>2</sub>S).



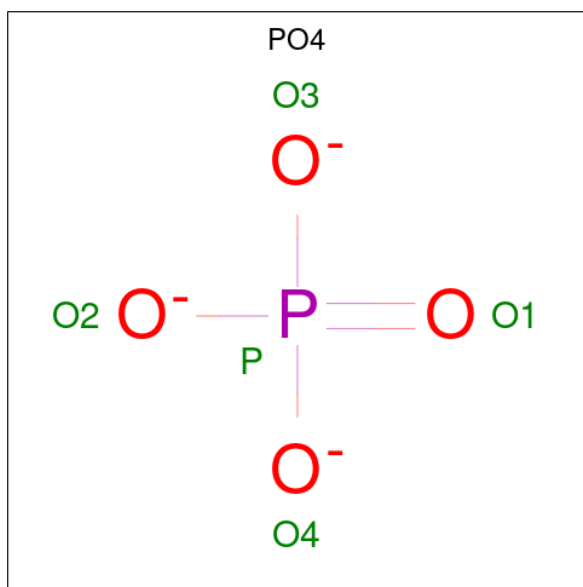
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
5	A	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
5	B	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		

- Molecule 6 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula:  $C_6H_{14}O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			8	6	2		
6	A	1	Total	C	O	0	0
			8	6	2		

- Molecule 7 is PHOSPHATE ION (three-letter code: PO4) (formula:  $O_4P$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	O	P	0	0
			5	4	1		

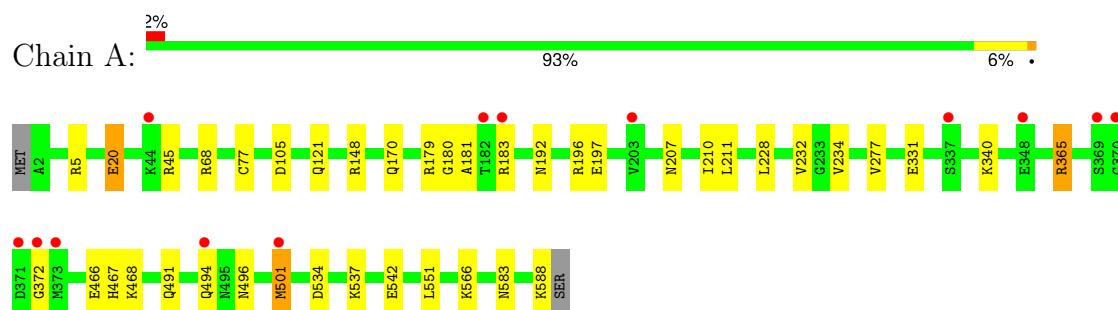
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	588	Total	O	0	0
			588	588		
8	B	624	Total	O	0	1
			624	624		

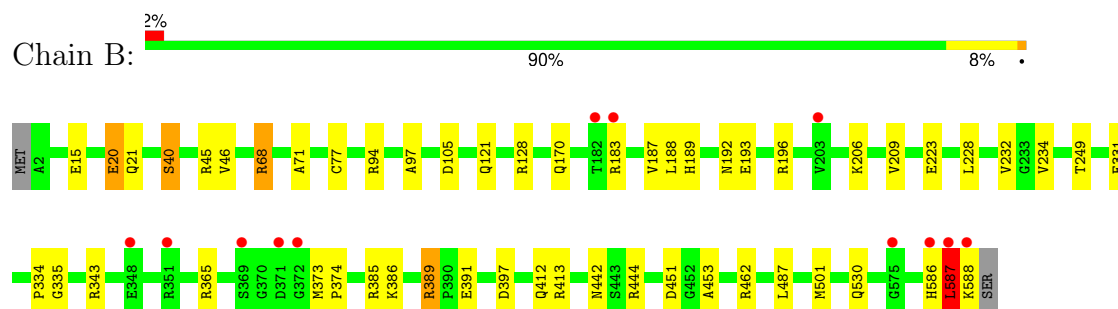
### 3 Residue-property plots [i](#)

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: Cyclohexane-1,2-dione Hydrolase (Cdh)



- Molecule 1: Cyclohexane-1,2-dione Hydrolase (Cdh)



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	123.60Å 123.60Å 144.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	5.00 – 1.26 19.89 – 1.26	Depositor EDS
% Data completeness (in resolution range)	93.2 (5.00-1.26) 93.3 (19.89-1.26)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.86 (at 1.26Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.097 , 0.120 0.101 , 0.122	Depositor DCC
$R_{free}$ test set	13765 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	7.3	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 57.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	10640	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	9.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.75% 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: MG, TPP, CL, FAD, PO4, MPD

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	0.89	6/4915 (0.1%)	0.93	13/6662 (0.2%)
1	B	0.92	10/4860 (0.2%)	0.96	20/6591 (0.3%)
All	All	0.90	16/9775 (0.2%)	0.94	33/13253 (0.2%)

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	1
1	B	0	1
All	All	0	2

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	179	ARG	CG-CD	-7.51	1.33	1.51
1	B	223	GLU	CD-OE2	7.31	1.33	1.25
1	A	20	GLU	CD-OE2	7.21	1.33	1.25
1	B	40[A]	SER	CB-OG	6.50	1.50	1.42
1	B	40[B]	SER	CB-OG	6.50	1.50	1.42

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	413	ARG	NE-CZ-NH1	-11.80	114.40	120.30
1	B	68	ARG	NE-CZ-NH1	-9.70	115.45	120.30
1	B	343	ARG	NE-CZ-NH1	9.03	124.81	120.30
1	B	389	ARG	NE-CZ-NH2	-8.69	115.95	120.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	94	ARG	NE-CZ-NH1	8.43	124.52	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	372	GLY	Peptide
1	B	587	LEU	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	4643	0	4599	37	2
1	B	4602	0	4582	40	2
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	1	0
3	B	1	0	0	1	0
4	A	53	0	31	0	0
4	B	53	0	31	0	0
5	A	26	0	16	1	0
5	B	26	0	16	1	0
6	A	16	0	28	6	0
7	B	5	0	0	0	0
8	A	588	0	0	16	0
8	B	624	0	0	22	2
All	All	10640	0	9303	79	3

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 79 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:B:442[B]:ASN:ND2	8:B:830:HOH:O	1.79	1.04

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:331[B]:GLU:OE1	8:A:1169:HOH:O	1.78	1.00
1:B:331[A]:GLU:OE2	8:B:1219:HOH:O	1.79	0.99
1:B:192[A]:ASN:OD1	1:B:196[A]:ARG:NH1	1.96	0.98
1:B:45:ARG:C	8:B:1221:HOH:O	2.04	0.95

All (3) 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)
1:A:121:GLN:NE2	1:B:121[A]:GLN:NE2[8_665]	1.59	0.61
1:A:180[B]:GLY:O	8:B:1089:HOH:O[6_455]	1.80	0.40
1:B:442[B]:ASN:OD1	8:B:988:HOH:O[4_554]	2.00	0.20

## 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	631/589 (107%)	621 (98%)	9 (1%)	1 (0%)	47	18
1	B	624/589 (106%)	613 (98%)	9 (1%)	2 (0%)	41	16
All	All	1255/1178 (106%)	1234 (98%)	18 (1%)	3 (0%)	41	18

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	77	CYS
1	B	77	CYS
1	B	587	LEU

### 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	493/453 (109%)	488 (99%)	5 (1%)	76	42
1	B	487/453 (108%)	481 (99%)	6 (1%)	71	35
All	All	980/906 (108%)	969 (99%)	11 (1%)	81	39

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	206[A]	LYS
1	B	206[B]	LYS
1	B	530[B]	GLN
1	B	530[A]	GLN
1	A	583	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	583	ASN
1	B	491	GLN
1	B	189	HIS
1	A	583	ASN
1	B	484	ASN

### 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 [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 4 are monoatomic - leaving 7 for Mogul analysis.

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	TPP	A	614	-	23,27,27	1.34	5 (21%)	30,40,40	1.15	1 (3%)
4	FAD	A	612	-	54,58,58	1.03	4 (7%)	71,89,89	0.92	3 (4%)
6	MPD	A	620	-	7,7,7	0.46	0	9,10,10	0.73	0
7	PO4	B	625	-	4,4,4	0.23	0	6,6,6	0.91	0
5	TPP	B	615	-	23,27,27	1.42	3 (13%)	30,40,40	1.19	2 (6%)
6	MPD	A	621	-	7,7,7	0.64	0	9,10,10	1.21	1 (11%)
4	FAD	B	613	-	54,58,58	1.10	5 (9%)	71,89,89	0.96	2 (2%)

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	TPP	A	614	-	-	0/16/17/17	0/2/2/2
4	FAD	A	612	-	-	2/30/50/50	0/6/6/6
6	MPD	A	620	-	-	0/5/5/5	-
5	TPP	B	615	-	-	0/16/17/17	0/2/2/2
6	MPD	A	621	-	-	1/5/5/5	-
4	FAD	B	613	-	-	3/30/50/50	0/6/6/6

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	612	FAD	PA-O3P	3.96	1.63	1.59

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	613	FAD	P-O3P	3.71	1.63	1.59
4	B	613	FAD	PA-O3P	3.46	1.63	1.59
5	B	615	TPP	C4-N3	-3.09	1.37	1.39
5	A	614	TPP	C2-N3	-3.08	1.29	1.36

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	614	TPP	C5-C4-N3	3.19	113.95	107.57
5	B	615	TPP	C5-C4-N3	2.84	113.25	107.57
4	A	612	FAD	C5A-C6A-N6A	2.59	124.26	120.31
5	B	615	TPP	CM2-C2'-N1'	2.50	119.86	117.20
6	A	621	MPD	O2-C2-CM	2.45	115.63	107.99

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	612	FAD	PA-O3P-P-O5'
6	A	621	MPD	C2-C3-C4-C5
4	B	613	FAD	PA-O3P-P-O5'
4	A	612	FAD	C4B-C5B-O5B-PA
4	B	613	FAD	C4B-C5B-O5B-PA

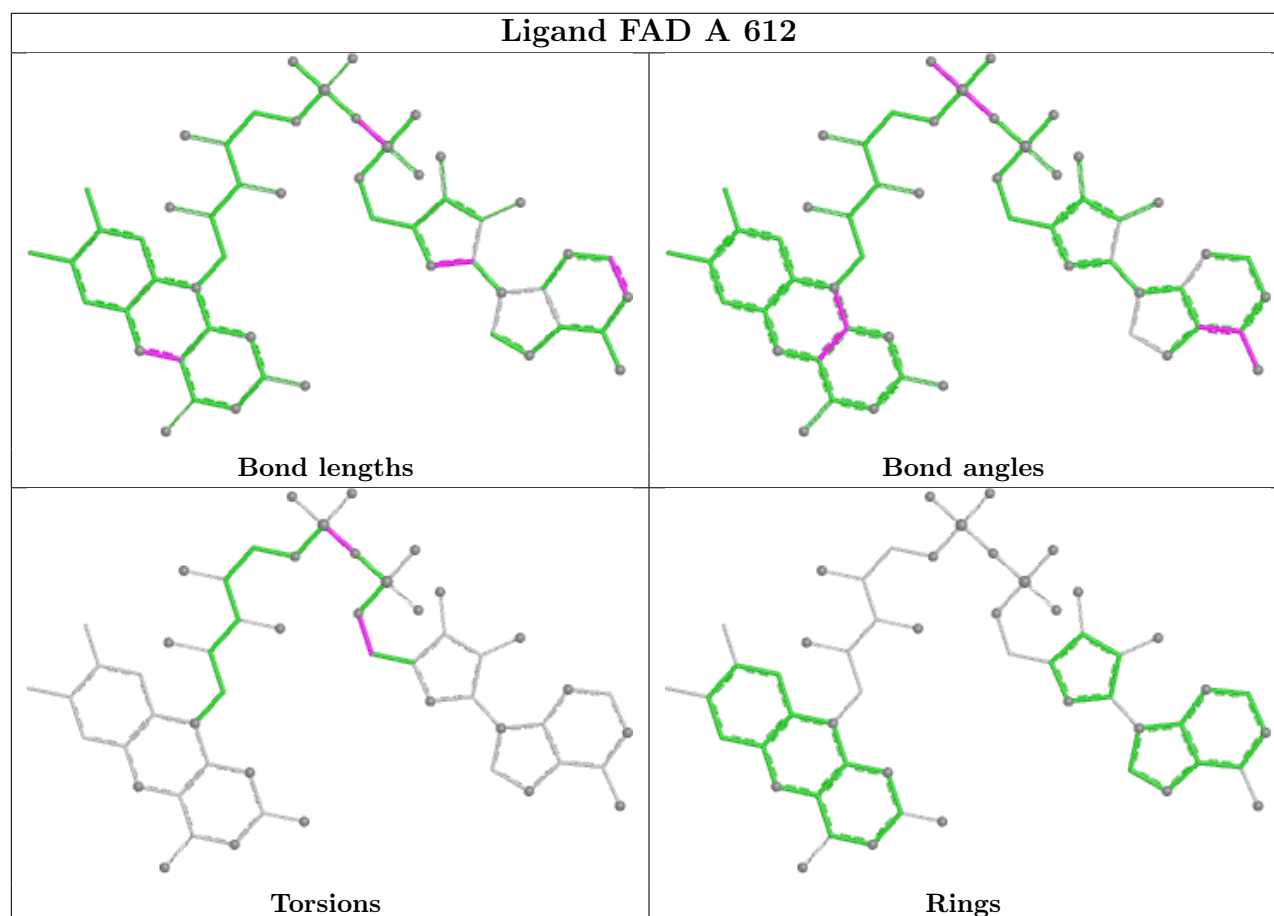
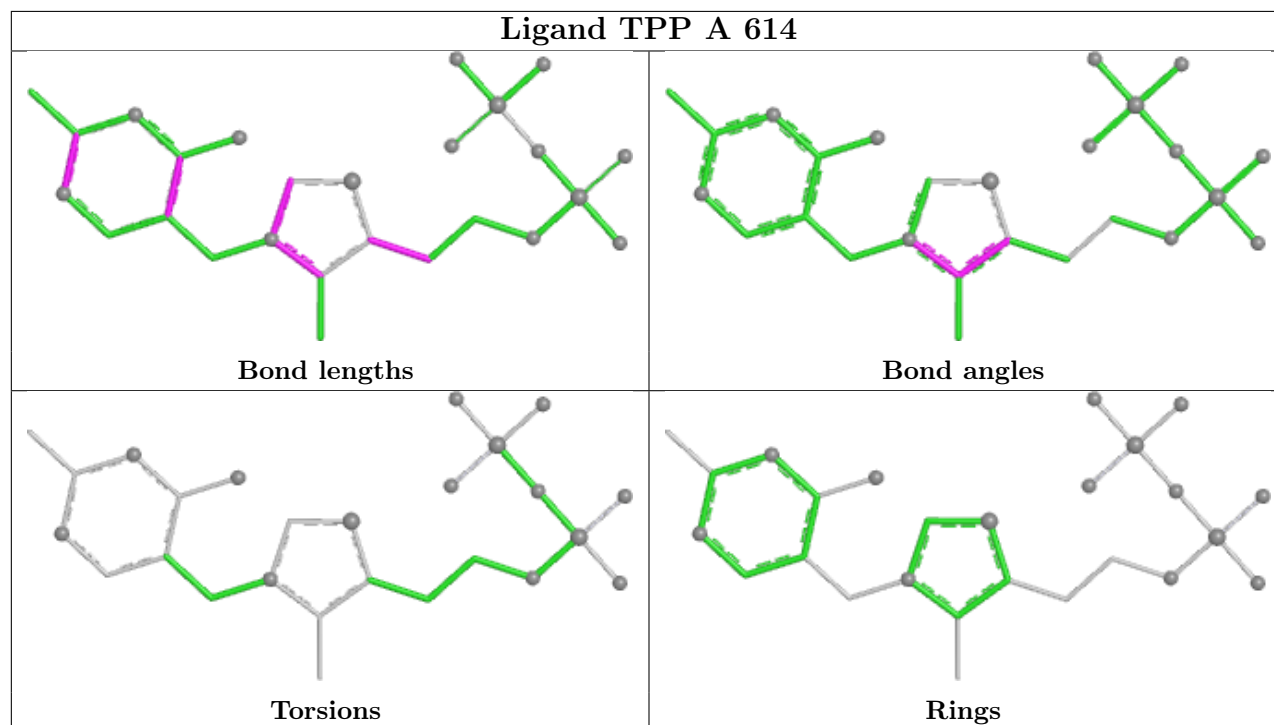
There are no ring outliers.

4 monomers are involved in 8 short contacts:

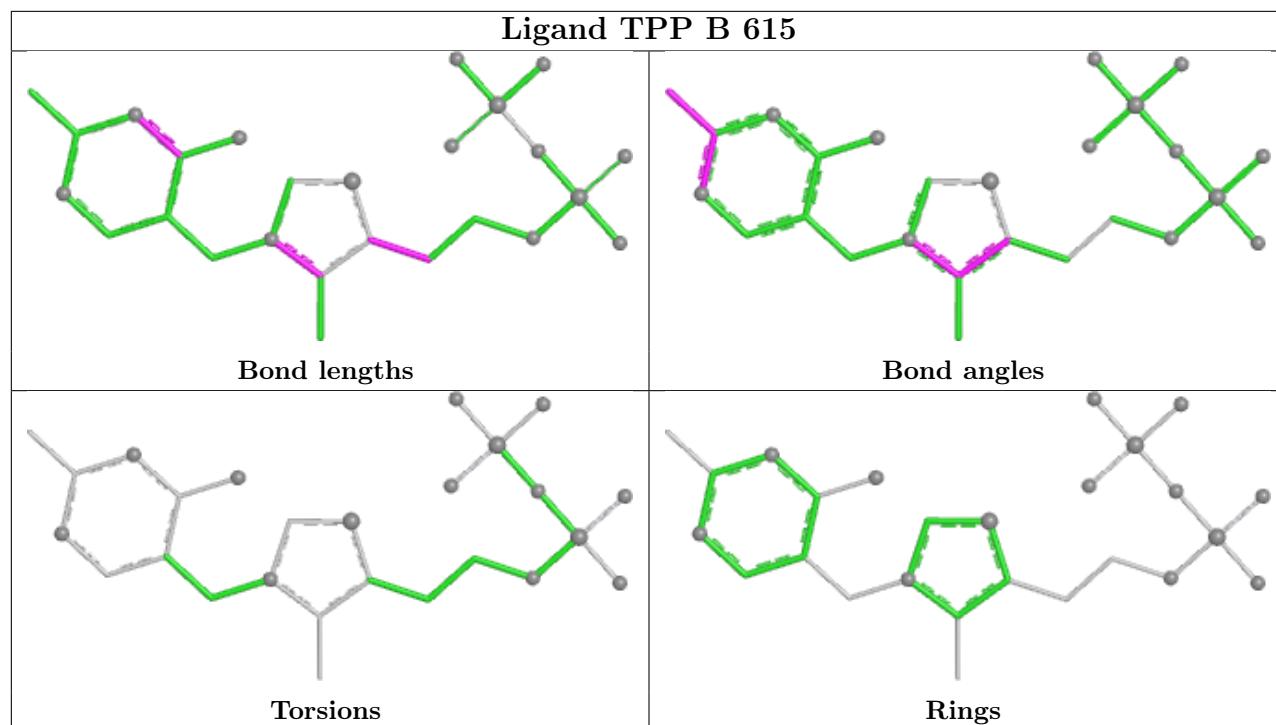
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	614	TPP	1	0
6	A	620	MPD	4	0
5	B	615	TPP	1	0
6	A	621	MPD	2	0

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

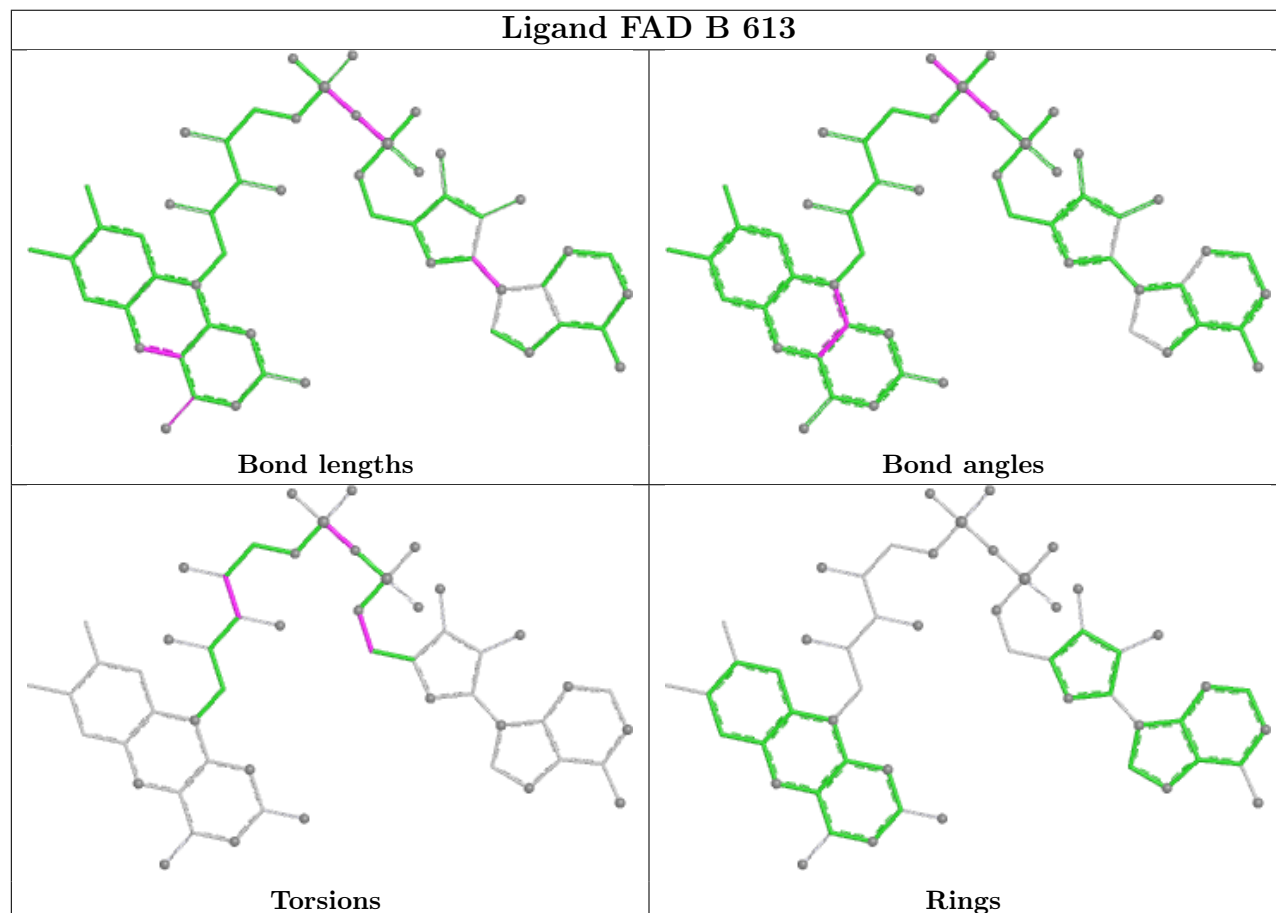
any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## Ligand TPP B 615



## Ligand FAD B 613





## 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	587/589 (99%)	-0.52	13 (2%)	62 52	3, 7, 17, 36	2 (0%)
1	B	587/589 (99%)	-0.51	12 (2%)	65 55	4, 7, 17, 44	3 (0%)
All	All	1174/1178 (99%)	-0.52	25 (2%)	63 54	3, 7, 17, 44	5 (0%)

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	587	LEU	9.4
1	B	588	LYS	8.1
1	A	371	ASP	7.6
1	A	370	GLY	6.0
1	A	369	SER	4.8

### 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](#)

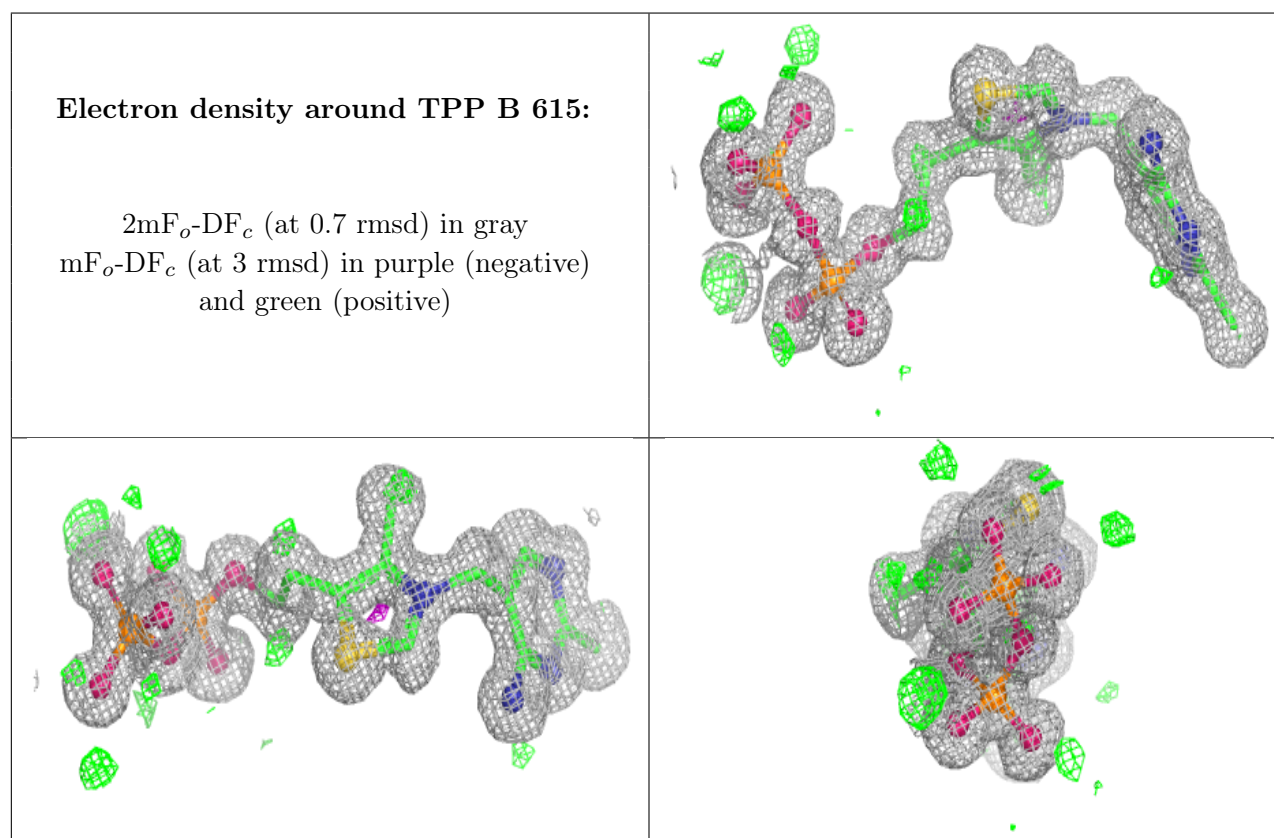
There are no monosaccharides in this entry.

### 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.

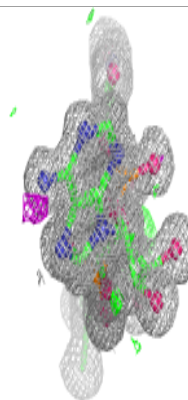
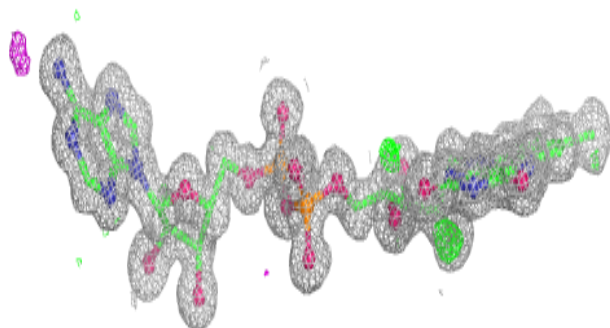
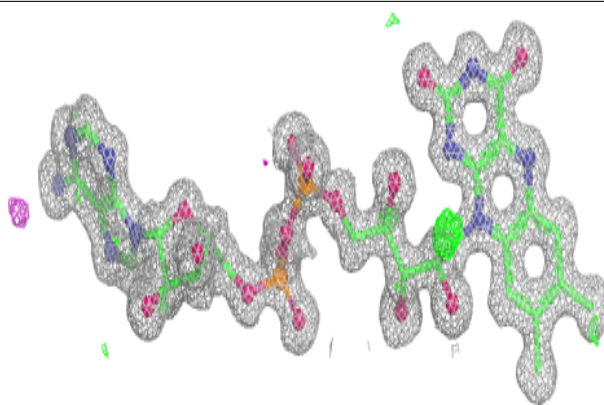
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
7	PO4	B	625	5/5	0.85	0.12	13,19,24,24	5
6	MPD	A	621	8/8	0.86	0.17	11,15,22,23	8
6	MPD	A	620	8/8	0.96	0.07	10,14,15,15	0
5	TPP	B	615	26/26	0.99	0.04	3,4,5,8	0
4	FAD	A	612	53/53	0.99	0.04	3,4,5,6	0
4	FAD	B	613	53/53	0.99	0.04	3,4,6,6	0
5	TPP	A	614	26/26	0.99	0.04	3,4,6,7	0
3	CL	B	610	1/1	1.00	0.01	5,5,5,5	0
2	MG	A	608	1/1	1.00	0.07	3,3,3,3	0
2	MG	B	609	1/1	1.00	0.07	2,2,2,2	0
3	CL	A	611	1/1	1.00	0.03	6,6,6,6	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.

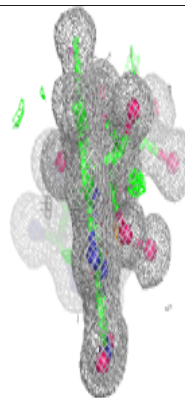
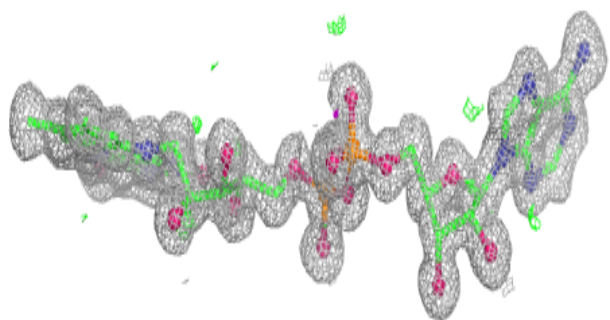
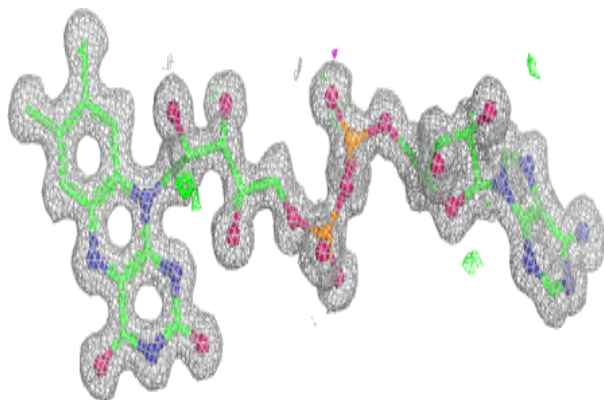


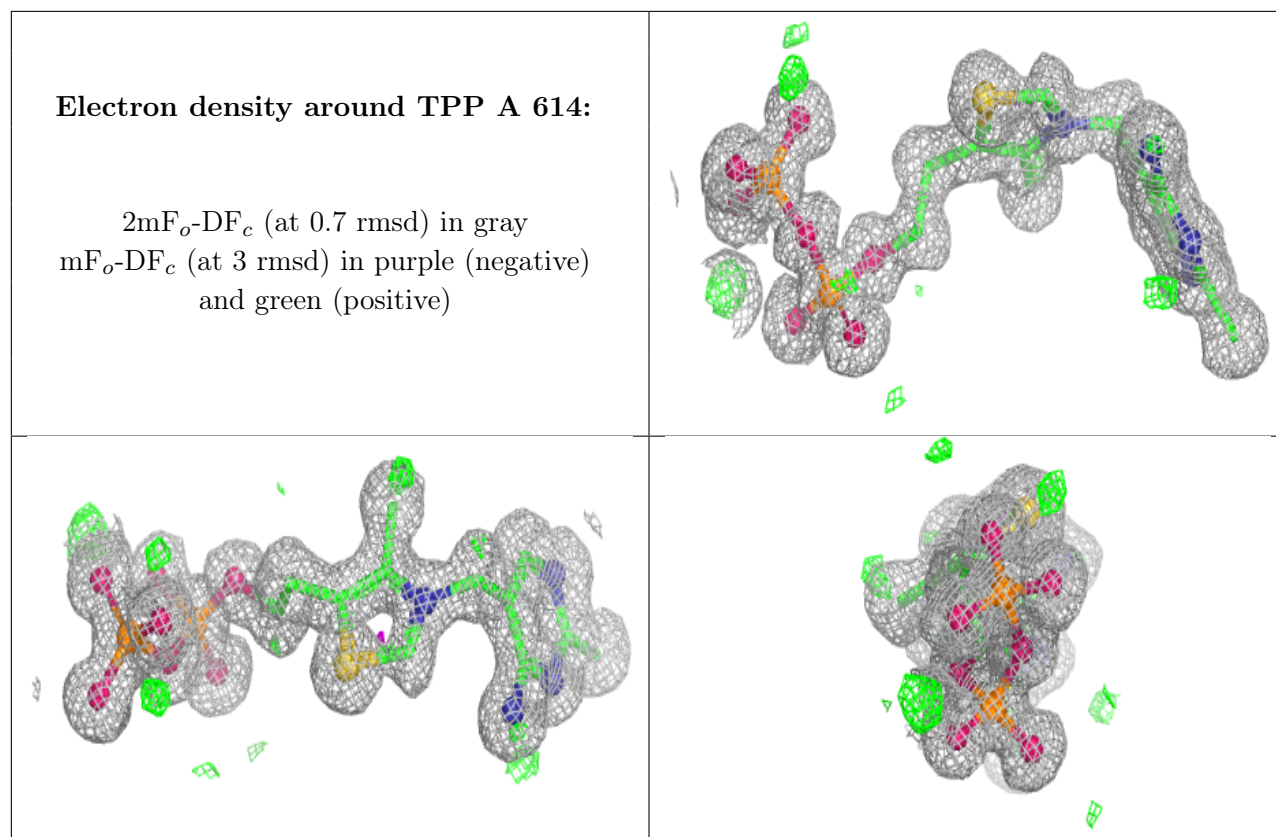
**Electron density around FAD A 612:**

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

**Electron density around FAD B 613:**

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





## 6.5 Other polymers ⓘ

There are no such residues in this entry.