



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 16, 2023 – 04:38 PM EDT

PDB ID : 1ZP3  
Title : E. coli Methylenetetrahydrofolate Reductase (oxidized)  
Authors : Pejchal, R.; Sargeant, R.; Ludwig, M.L.  
Deposited on : 2005-05-16  
Resolution : 1.85 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>.

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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 : 2.35  
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

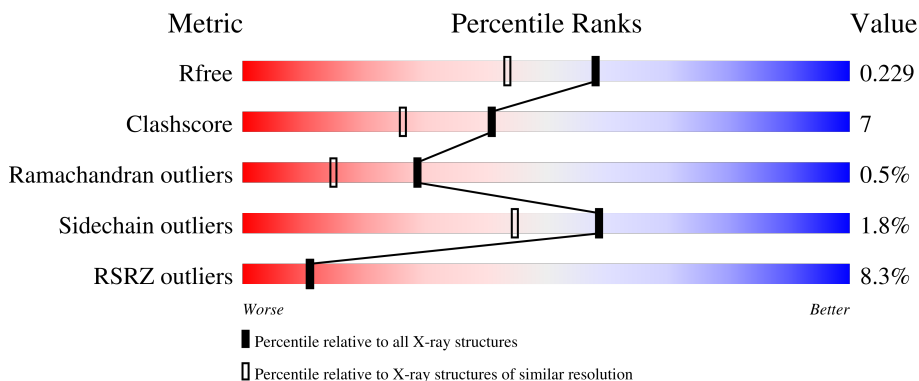
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.85 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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	304	
1	B	304	
1	C	304	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7110 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 5,10-methylenetetrahydrofolate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	284	2157	1368	376	402	11	4	0	0
1	B	290	2242	1418	391	422	11	4	0	0
1	C	267	2073	1315	363	384	11	3	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	297	LEU	-	cloning artifact	UNP P00394
A	298	GLU	-	cloning artifact	UNP P00394
A	299	HIS	-	expression tag	UNP P00394
A	300	HIS	-	expression tag	UNP P00394
A	301	HIS	-	expression tag	UNP P00394
A	302	HIS	-	expression tag	UNP P00394
A	303	HIS	-	expression tag	UNP P00394
A	304	HIS	-	expression tag	UNP P00394
B	297	LEU	-	cloning artifact	UNP P00394
B	298	GLU	-	cloning artifact	UNP P00394
B	299	HIS	-	expression tag	UNP P00394
B	300	HIS	-	expression tag	UNP P00394
B	301	HIS	-	expression tag	UNP P00394
B	302	HIS	-	expression tag	UNP P00394
B	303	HIS	-	expression tag	UNP P00394
B	304	HIS	-	expression tag	UNP P00394
C	297	LEU	-	cloning artifact	UNP P00394
C	298	GLU	-	cloning artifact	UNP P00394
C	299	HIS	-	expression tag	UNP P00394
C	300	HIS	-	expression tag	UNP P00394
C	301	HIS	-	expression tag	UNP P00394
C	302	HIS	-	expression tag	UNP P00394
C	303	HIS	-	expression tag	UNP P00394

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Chain	Residue	Modelled	Actual	Comment	Reference
C	304	HIS	-	expression tag	UNP P00394

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



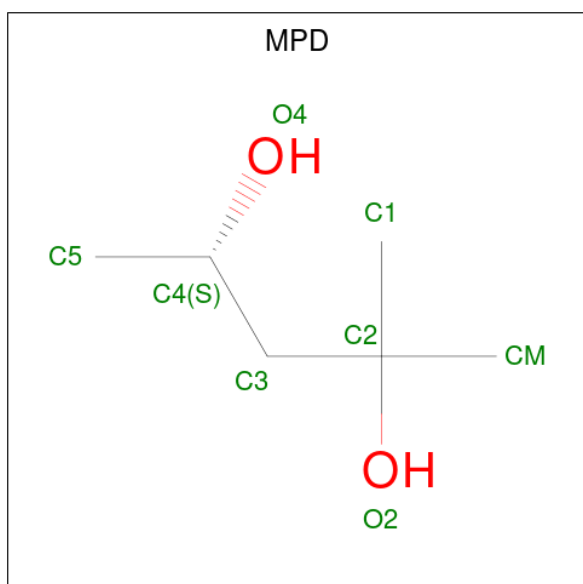
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0
2	B	1	5	4	1	0	0
2	C	1	5	4	1	0	0

- 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>).



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

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	75	Total O 75 75	0	0
5	B	186	Total O 186 186	0	0
5	C	174	Total O 174 174	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.24Å 127.79Å 97.70Å 90.00° 121.55° 90.00°	Depositor
Resolution (Å)	19.91 – 1.85 19.91 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.4 (19.91-1.85) 99.3 (19.91-1.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.40 (at 1.80Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.214 , 0.237 0.206 , 0.229	Depositor DCC
$R_{free}$ test set	9117 reflections (9.22%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.8	Xtrriage
Anisotropy	0.218	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 48.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.011 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7110	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.51% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FAD, MPD, SO4

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	0.30	0/2200	0.51	0/2990
1	B	0.35	0/2289	0.58	1/3108 (0.0%)
1	C	0.36	0/2115	0.60	1/2866 (0.0%)
All	All	0.34	0/6604	0.56	2/8964 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	146	ASP	N-CA-C	-5.80	95.34	111.00
1	B	146	ASP	N-CA-C	-5.36	96.54	111.00

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	2157	0	2071	44	0
1	B	2242	0	2168	27	0
1	C	2073	0	2027	24	0
2	A	10	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	53	0	31	0	0
3	B	53	0	31	0	0
3	C	53	0	31	0	0
4	A	8	0	13	0	0
4	B	8	0	13	1	0
4	C	8	0	14	1	0
5	A	75	0	0	1	0
5	B	186	0	0	6	0
5	C	174	0	0	3	0
All	All	7110	0	6399	92	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 7.

The worst 5 of 92 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:A:100:ARG:HG2	1:A:138:LEU:HD11	1.42	0.99
1:B:179:ARG:NH1	5:B:677:HOH:O	2.20	0.74
1:A:100:ARG:CG	1:A:138:LEU:HD11	2.20	0.72
1:B:16:LEU:O	1:B:19:VAL:HG22	1.90	0.71
1:A:9:ARG:HD2	1:C:263:ILE:CD1	2.21	0.71

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	280/304 (92%)	271 (97%)	7 (2%)	2 (1%)	22 9
1	B	286/304 (94%)	282 (99%)	3 (1%)	1 (0%)	41 26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	263/304 (86%)	259 (98%)	3 (1%)	1 (0%)	34	19
All	All	829/912 (91%)	812 (98%)	13 (2%)	4 (0%)	29	15

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	155	VAL
1	A	155	VAL
1	B	155	VAL
1	A	22	GLN

### 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	218/258 (84%)	213 (98%)	5 (2%)	50	34
1	B	234/258 (91%)	228 (97%)	6 (3%)	46	30
1	C	216/258 (84%)	215 (100%)	1 (0%)	88	86
All	All	668/774 (86%)	656 (98%)	12 (2%)	59	45

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	75	LYS
1	B	206	GLU
1	C	54	LYS
1	B	228	ASN
1	A	193	ARG

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	A	168	ASN

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Mol	Chain	Res	Type
1	B	168	ASN
1	C	228	ASN
1	A	39	GLN
1	A	14	GLN

### 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](#)

10 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	A	401	-	4,4,4	0.28	0	6,6,6	0.08	0
4	MPD	C	497	-	7,7,7	1.23	1 (14%)	9,10,10	0.39	0
4	MPD	B	496	-	7,7,7	1.27	1 (14%)	9,10,10	0.40	0
3	FAD	A	395	-	53,58,58	1.78	11 (20%)	68,89,89	1.56	12 (17%)
3	FAD	C	397	-	53,58,58	1.62	8 (15%)	68,89,89	1.28	8 (11%)
2	SO4	C	402	-	4,4,4	0.24	0	6,6,6	0.10	0
2	SO4	B	399	-	4,4,4	0.26	0	6,6,6	0.08	0
3	FAD	B	396	-	53,58,58	1.71	10 (18%)	68,89,89	1.38	15 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	MPD	A	495	-	7,7,7	1.32	1 (14%)	9,10,10	0.41	0
2	SO4	A	400	-	4,4,4	0.25	0	6,6,6	0.04	0

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
4	MPD	C	497	-	-	0/5/5/5	-
4	MPD	B	496	-	-	3/5/5/5	-
3	FAD	C	397	-	-	1/30/50/50	0/6/6/6
3	FAD	A	395	-	-	7/30/50/50	0/6/6/6
3	FAD	B	396	-	-	2/30/50/50	0/6/6/6
4	MPD	A	495	-	-	0/5/5/5	-

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	397	FAD	C4X-N5	5.45	1.41	1.30
3	A	395	FAD	C4X-N5	5.13	1.40	1.30
3	B	396	FAD	C4X-N5	4.97	1.40	1.30
3	A	395	FAD	C10-N10	4.90	1.48	1.37
3	C	397	FAD	C10-N10	4.75	1.47	1.37

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	395	FAD	C5'-C4'-C3'	3.98	119.89	112.20
3	A	395	FAD	C9-C9A-N10	3.46	126.52	121.84
3	A	395	FAD	C9A-C5X-N5	3.42	126.15	122.43
3	A	395	FAD	C5X-C9A-N10	-3.41	114.43	117.95
3	C	397	FAD	O5'-C5'-C4'	3.21	117.94	109.36

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	395	FAD	O2'-C2'-C3'-C4'
3	B	396	FAD	O2'-C2'-C3'-C4'
3	A	395	FAD	O4'-C4'-C5'-O5'

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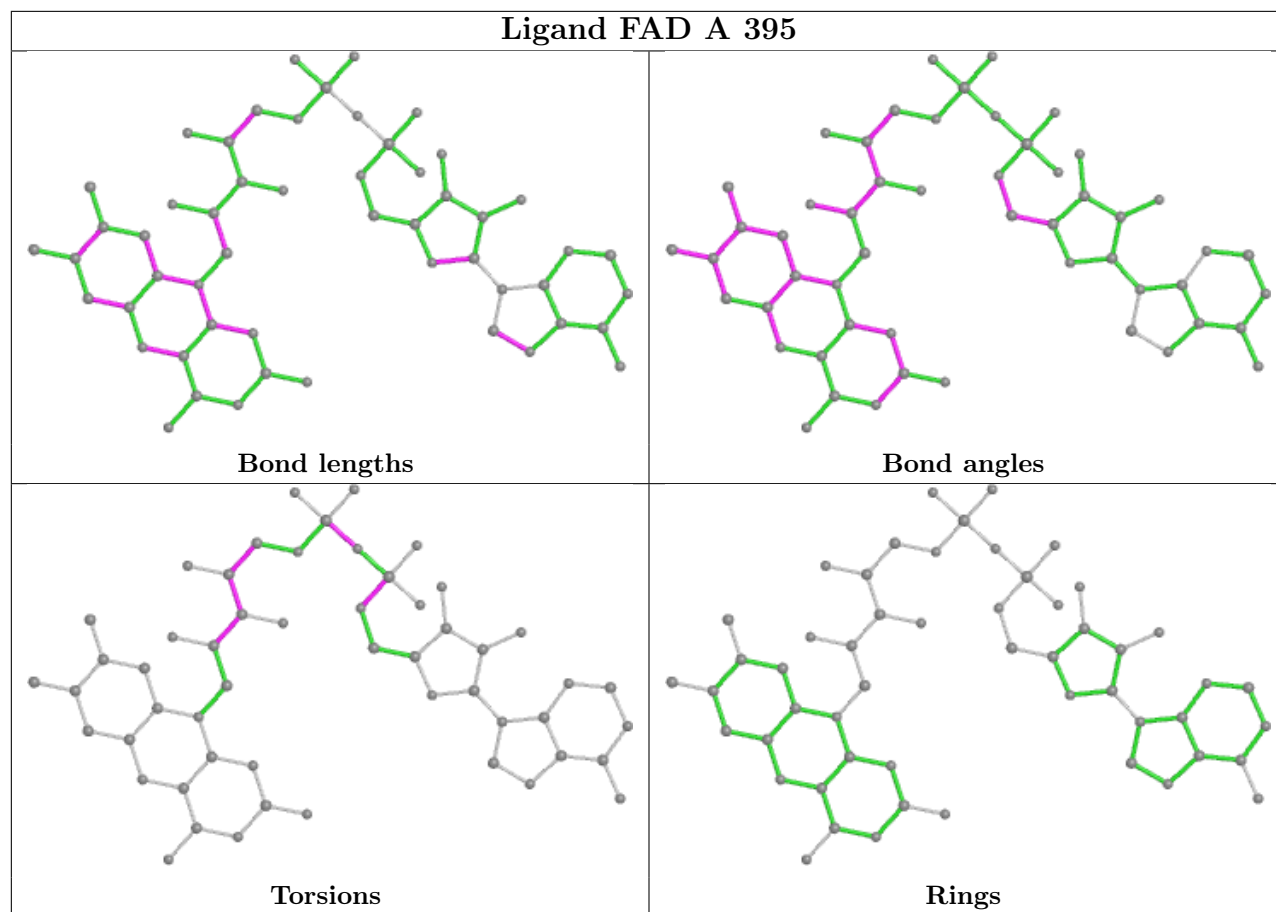
Mol	Chain	Res	Type	Atoms
3	A	395	FAD	C5B-O5B-PA-O1A
4	B	496	MPD	C1-C2-C3-C4

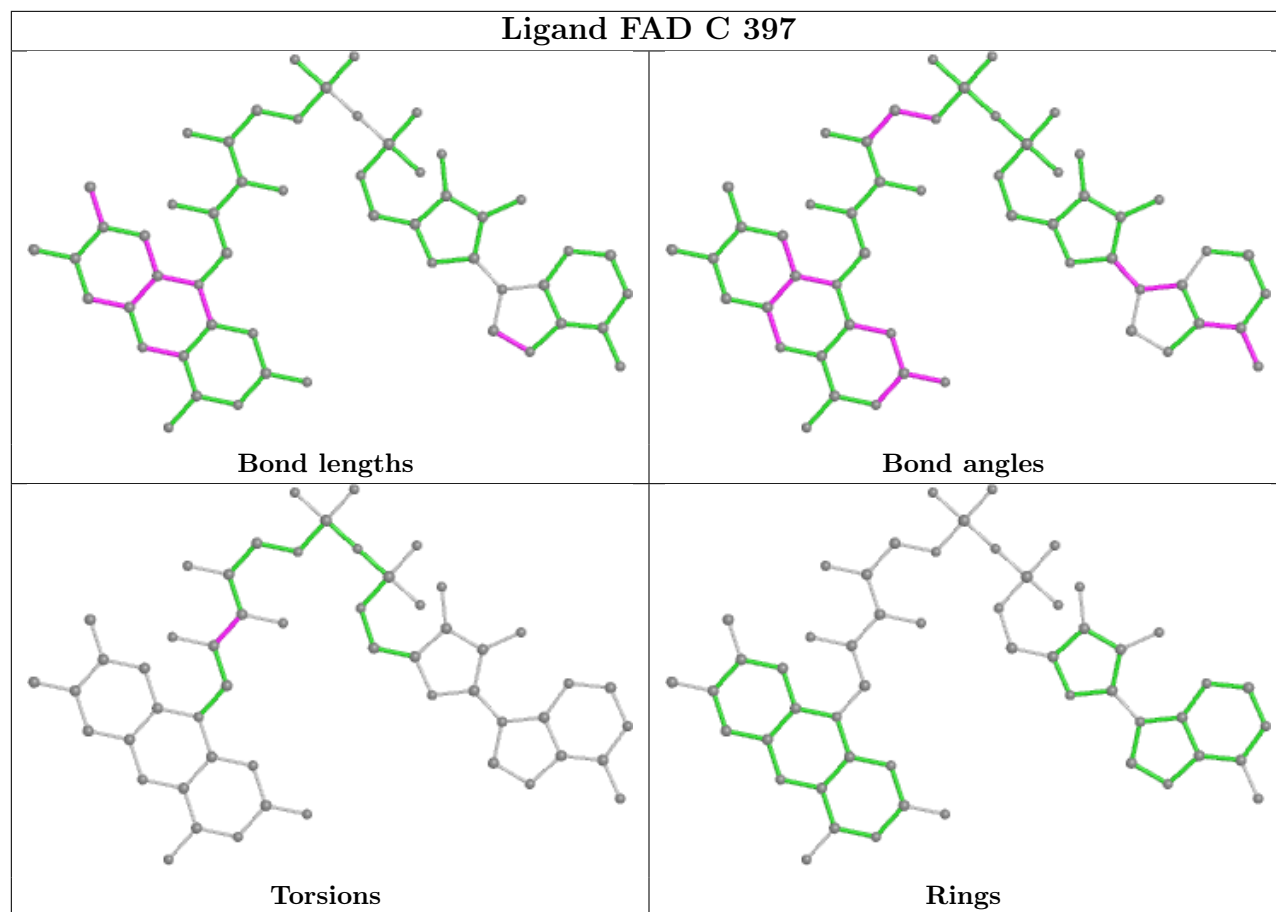
There are no ring outliers.

2 monomers are involved in 2 short contacts:

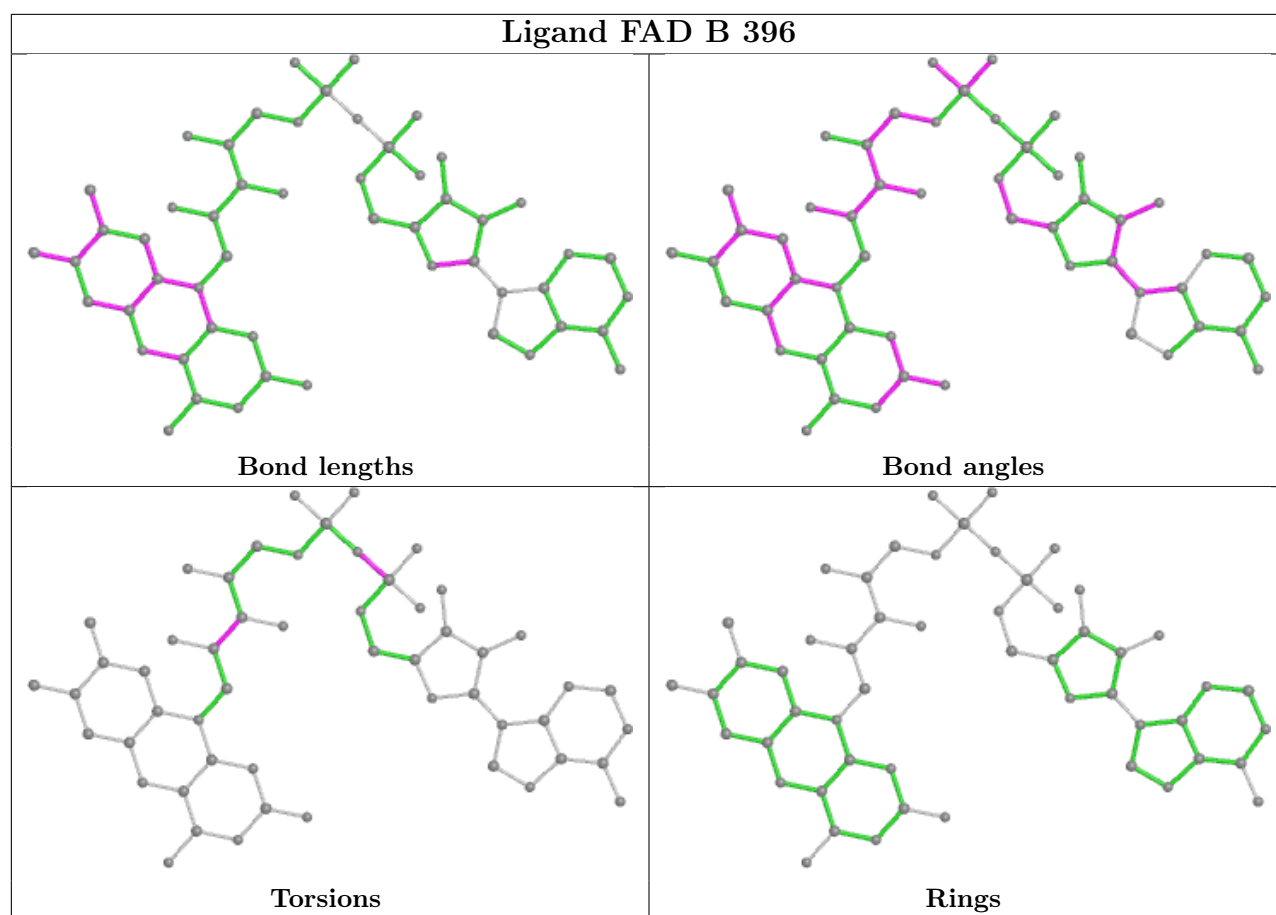
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	497	MPD	1	0
4	B	496	MPD	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	284/304 (93%)	1.05	53 (18%) <b>1</b> <b>1</b>	18, 41, 64, 73	1 (0%)
1	B	290/304 (95%)	0.05	9 (3%) 49 47	13, 23, 40, 56	1 (0%)
1	C	267/304 (87%)	-0.04	8 (2%) 50 48	14, 21, 35, 53	1 (0%)
All	All	841/912 (92%)	0.36	70 (8%) <b>11</b> <b>11</b>	13, 27, 57, 73	3 (0%)

The worst 5 of 70 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	21	GLY	8.5
1	A	121	LEU	8.4
1	C	121	LEU	7.7
1	C	21	GLY	6.0
1	A	65	GLY	5.7

### 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](#)

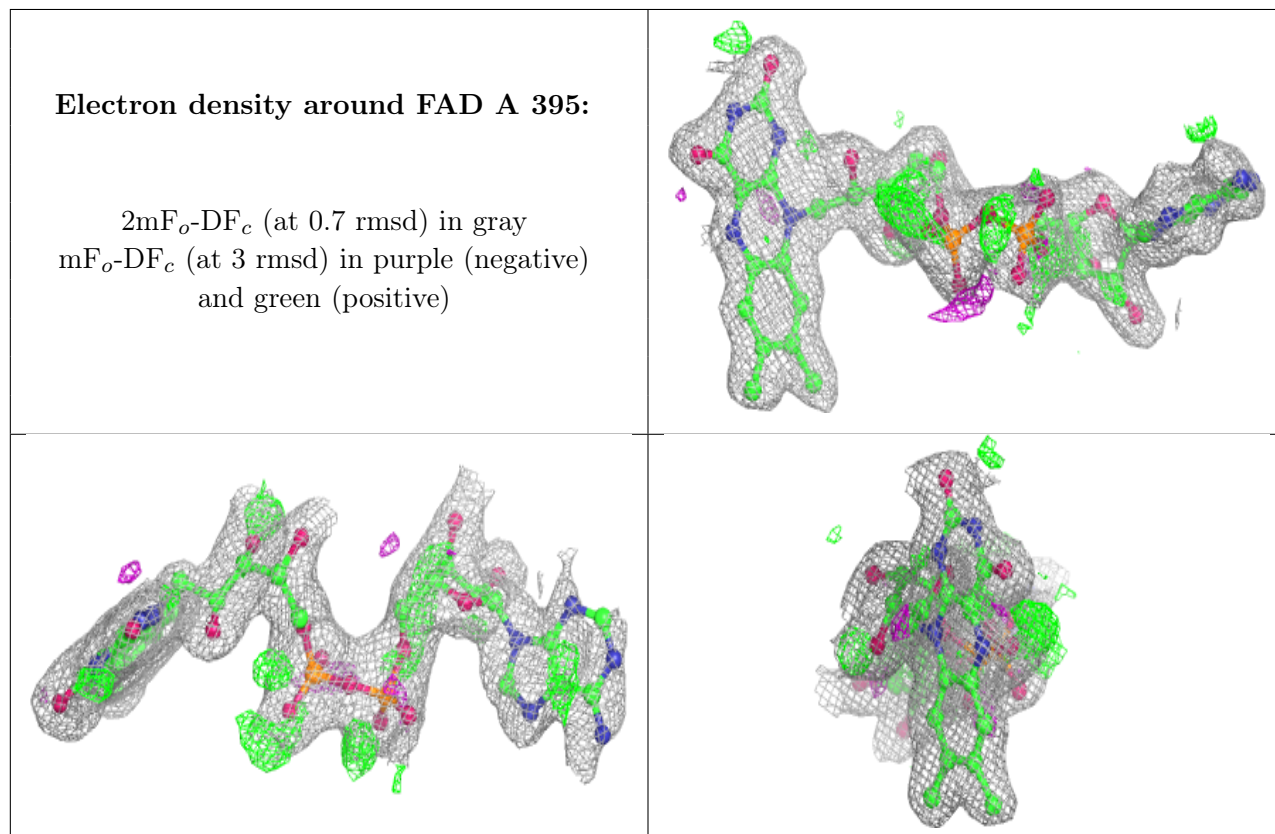
There are no monosaccharides in this entry.

### 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.

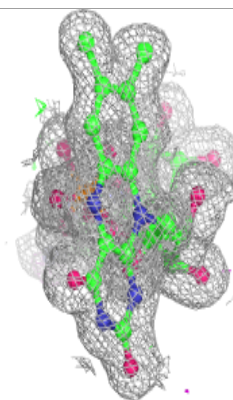
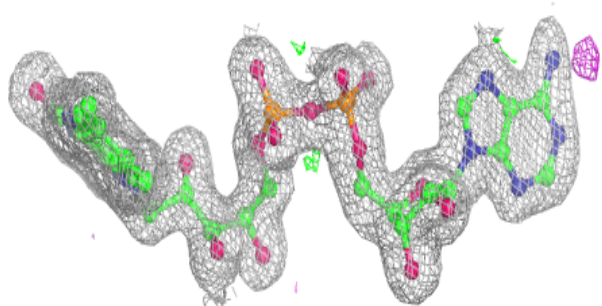
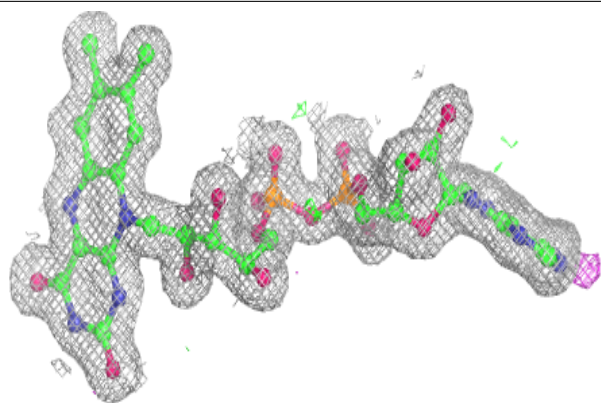
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	MPD	B	496	8/8	0.81	0.28	31,32,33,34	8
3	FAD	A	395	53/53	0.82	0.16	30,37,55,55	0
4	MPD	A	495	8/8	0.83	0.23	36,38,39,40	8
4	MPD	C	497	8/8	0.87	0.19	31,33,34,34	8
2	SO4	A	401	5/5	0.93	0.16	48,48,49,49	0
2	SO4	A	400	5/5	0.95	0.12	56,56,57,57	5
2	SO4	B	399	5/5	0.96	0.11	28,30,30,30	5
3	FAD	B	396	53/53	0.96	0.08	12,18,28,30	0
3	FAD	C	397	53/53	0.96	0.08	15,18,28,31	0
2	SO4	C	402	5/5	0.97	0.12	30,31,31,34	5

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.

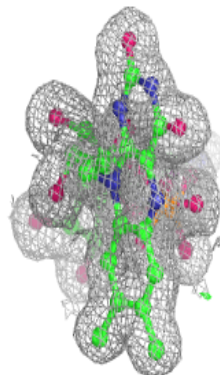
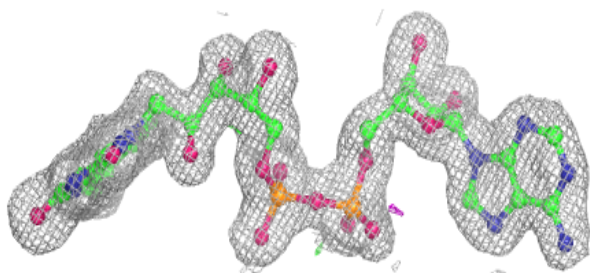


**Electron density around FAD B 396:**

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

**Electron density around FAD C 397:**

$2mF_o-DF_c$  (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.