



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 10:03 am BST

PDB ID : 5FXF  
Title : Crystal structure of eugenol oxidase in complex with benzoate  
Authors : Nguyen, Q.-T.; de Gonzalo, G.; Binda, C.; Martinez, A.R.; Mattevi, A.; Fraaije, M.W.  
Deposited on : 2016-03-01  
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 2.11  
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) : 2.11

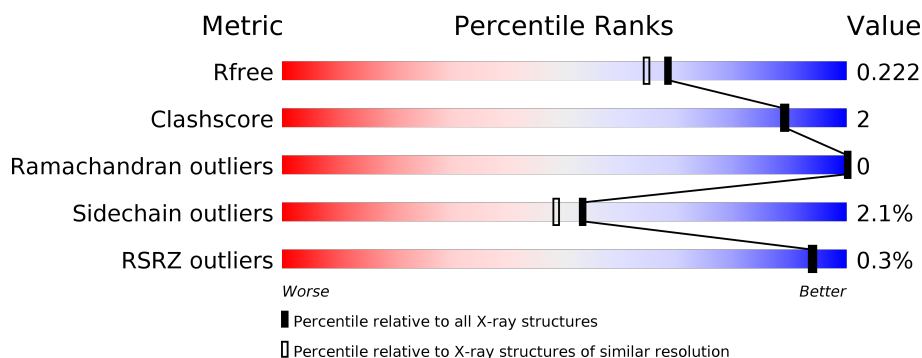
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 on 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	526	<div> <div style="width: 93%;"></div> <div style="width: 6%;"></div> <div style="width: 1%;"></div> </div> <div>93% 6% .</div>
1	B	526	<div> <div style="width: 92%;"></div> <div style="width: 7%;"></div> <div style="width: 1%;"></div> </div> <div>92% 7%</div>

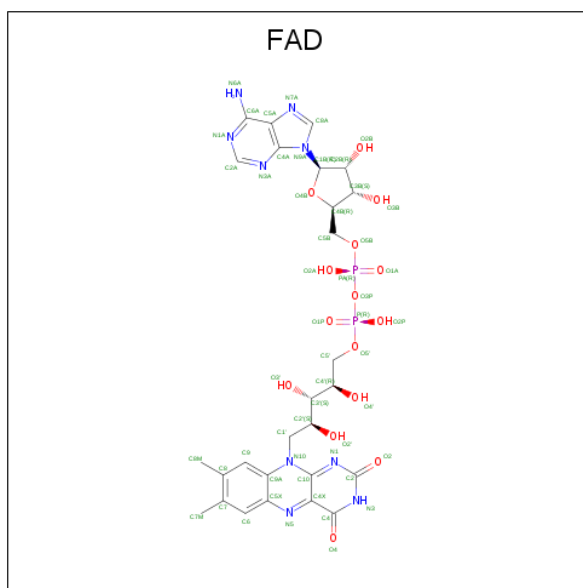


In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called EUGENOL OXIDASE.

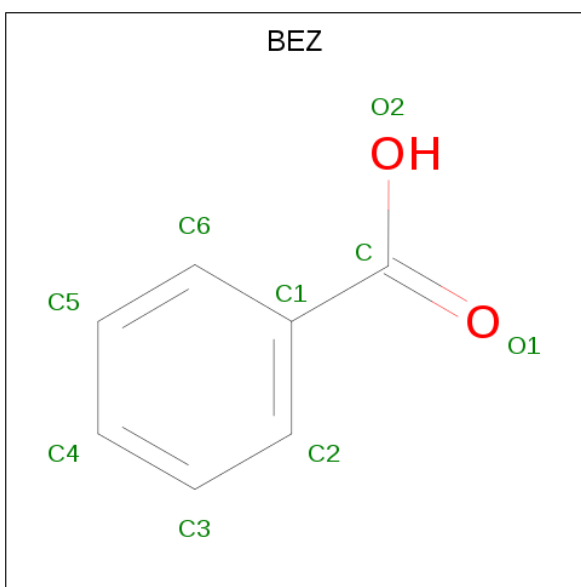
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	525	Total 4122	C 2626	N 701	O 772	S 23	0	0	0
1	B	525	Total 4110	C 2622	N 700	O 765	S 23	0	0	0

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$ ).



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

- Molecule 3 is BENZOIC ACID (three-letter code: BEZ) (formula:  $\text{C}_7\text{H}_6\text{O}_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			9	7	2		
3	B	1	Total	C	O	0	0
			9	7	2		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

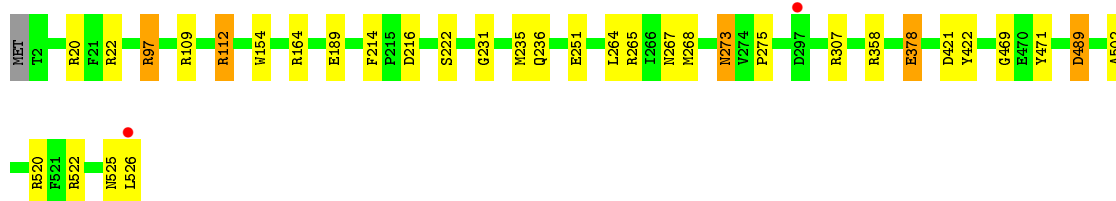
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	190	Total	O	0	0
			190	190		
5	B	113	Total	O	0	0
			113	113		

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

These plots are drawn for all protein, RNA and DNA 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.

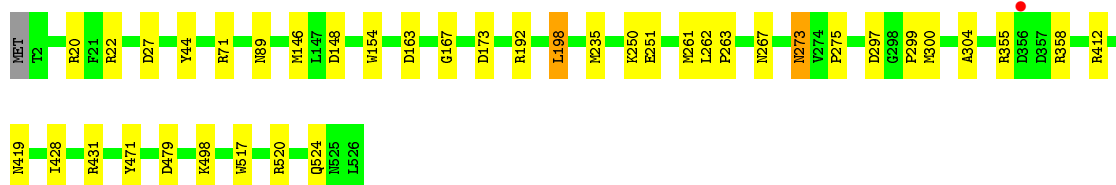
#### • Molecule 1: EUGENOL OXIDASE

Chain A:  93% 6%



#### • Molecule 1: EUGENOL OXIDASE

Chain B:  92% 7%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.29 Å 96.87 Å 179.66 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	89.83 – 1.90 65.87 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.3 (89.83-1.90) 99.3 (65.87-1.90)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.50 (at 1.90 Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.165 , 0.212 0.176 , 0.222	Depositor DCC
$R_{free}$ test set	3858 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.2	Xtriage
Anisotropy	0.033	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 42.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8689	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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: BEZ, GOL, 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	0.99	4/4229 (0.1%)	1.06	19/5738 (0.3%)
1	B	0.93	0/4217	0.97	11/5722 (0.2%)
All	All	0.96	4/8446 (0.0%)	1.01	30/11460 (0.3%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	231	GLY	C-O	5.33	1.32	1.23
1	A	222	SER	CB-OG	-5.26	1.35	1.42
1	A	489	ASP	CB-CG	-5.19	1.40	1.51
1	A	109	ARG	CD-NE	-5.12	1.37	1.46

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	109	ARG	NE-CZ-NH1	14.72	127.66	120.30
1	A	109	ARG	NE-CZ-NH2	-13.57	113.51	120.30
1	B	520	ARG	NE-CZ-NH2	-12.87	113.87	120.30
1	A	112	ARG	NE-CZ-NH1	11.58	126.09	120.30
1	B	520	ARG	NE-CZ-NH1	11.44	126.02	120.30
1	A	522	ARG	NE-CZ-NH1	7.79	124.20	120.30
1	A	358	ARG	NE-CZ-NH1	7.42	124.01	120.30
1	A	235	MET	CG-SD-CE	-7.11	88.83	100.20
1	A	112	ARG	CG-CD-NE	6.98	126.45	111.80
1	A	112	ARG	CD-NE-CZ	6.97	133.36	123.60
1	A	265	ARG	NE-CZ-NH2	-6.66	116.97	120.30
1	A	522	ARG	NE-CZ-NH2	-6.61	116.99	120.30
1	A	20	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	A	97	ARG	NE-CZ-NH2	-6.30	117.15	120.30
1	A	421	ASP	CB-CG-OD1	6.18	123.86	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	173	ASP	CB-CG-OD1	6.09	123.78	118.30
1	B	20	ARG	NE-CZ-NH1	6.06	123.33	120.30
1	B	479	ASP	CB-CG-OD1	5.89	123.60	118.30
1	B	71	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	A	112	ARG	NE-CZ-NH2	-5.52	117.54	120.30
1	B	431	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	B	22	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	A	489	ASP	CB-CG-OD1	-5.18	113.64	118.30
1	A	520	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	B	355	ARG	NE-CZ-NH1	5.13	122.86	120.30
1	B	192	ARG	NE-CZ-NH2	-5.07	117.77	120.30
1	A	22	ARG	NE-CZ-NH1	5.05	122.83	120.30
1	A	164	ARG	NE-CZ-NH1	5.05	122.83	120.30
1	B	358	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	A	307	ARG	NE-CZ-NH1	5.01	122.81	120.30

There are no chirality outliers.

There are no planarity outliers.

## 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	4122	0	3993	17	0
1	B	4110	0	3983	15	0
2	A	53	0	30	1	0
2	B	53	0	30	1	0
3	A	9	0	5	0	0
3	B	9	0	5	0	0
4	A	12	0	16	1	0
4	B	18	0	24	2	0
5	A	190	0	0	4	0
5	B	113	0	0	0	0
All	All	8689	0	8086	31	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 2.

All (31) 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:97:ARG:HH22	1:A:526:LEU:HD11	1.20	1.05
1:A:268:MET:SD	5:A:2128:HOH:O	2.34	0.84
1:B:299:PRO:HD3	1:B:419:ASN:OD1	1.96	0.65
1:B:524:GLN:O	4:B:1529:GOL:H2	2.03	0.57
1:A:526:LEU:HD23	5:A:2045:HOH:O	2.04	0.57
2:A:600:FAD:H8A	2:A:600:FAD:O5B	2.08	0.54
1:A:97:ARG:NH2	1:A:526:LEU:HD11	2.05	0.52
1:A:273:ASN:O	1:A:275:PRO:HD3	2.10	0.52
1:A:97:ARG:HH12	1:A:526:LEU:HD21	1.75	0.52
2:B:600:FAD:H8A	2:B:600:FAD:O5B	2.10	0.51
1:A:378:GLU:HG2	5:A:2131:HOH:O	2.11	0.51
1:B:251:GLU:OE2	1:B:412:ARG:NH1	2.40	0.49
1:A:97:ARG:HH12	1:A:526:LEU:CG	2.25	0.49
1:B:44:TYR:CE2	1:B:89:ASN:HB3	2.48	0.49
1:A:502:ALA:O	1:B:498:LYS:HE2	2.14	0.48
1:B:148:ASP:OD1	1:B:167:GLY:HA3	2.14	0.46
1:A:97:ARG:HH12	1:A:526:LEU:CD2	2.28	0.46
1:B:262:LEU:HB3	1:B:263:PRO:HD3	1.97	0.46
1:B:273:ASN:O	1:B:275:PRO:HD3	2.16	0.46
1:A:525:ASN:O	1:A:526:LEU:HB2	2.16	0.45
1:A:236:GLN:HB2	1:B:267:ASN:HD21	1.82	0.45
1:A:469:GLY:HA3	1:B:198:LEU:HD13	1.99	0.44
1:B:146:MET:SD	1:B:235:MET:HE2	2.58	0.44
1:B:300:MET:HG2	1:B:304:ALA:HB3	2.00	0.43
1:A:97:ARG:HH12	1:A:526:LEU:HG	1.82	0.43
1:A:526:LEU:N	1:A:526:LEU:HD12	2.33	0.43
1:B:261:MET:SD	1:B:428:ILE:HG21	2.58	0.43
1:B:297:ASP:O	1:B:419:ASN:ND2	2.52	0.42
1:A:267:ASN:HB2	5:A:2125:HOH:O	2.20	0.42
1:B:517:TRP:NE1	4:B:1529:GOL:H31	2.34	0.42
1:A:214:PHE:HZ	4:A:1527:GOL:O3	2.03	0.41

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	523/526 (99%)	512 (98%)	11 (2%)	0	100	100
1	B	523/526 (99%)	510 (98%)	13 (2%)	0	100	100
All	All	1046/1052 (99%)	1022 (98%)	24 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	432/434 (100%)	421 (98%)	11 (2%)	47	41
1	B	428/434 (99%)	421 (98%)	7 (2%)	62	60
All	All	860/868 (99%)	842 (98%)	18 (2%)	53	48

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112	ARG
1	A	154	TRP
1	A	189	GLU
1	A	216	ASP
1	A	251	GLU
1	A	264	LEU
1	A	273	ASN
1	A	378	GLU

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Mol	Chain	Res	Type
1	A	422	TYR
1	A	471	TYR
1	A	489	ASP
1	B	27	ASP
1	B	154	TRP
1	B	163	ASP
1	B	198	LEU
1	B	250	LYS
1	B	273	ASN
1	B	471	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	236	GLN
1	B	267	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

9 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	FAD	A	600	1	51,58,58	2.10	12 (23%)	60,89,89	2.59	11 (18%)
4	GOL	B	1528	-	5,5,5	0.42	0	5,5,5	0.37	0
4	GOL	A	1527	-	5,5,5	0.86	0	5,5,5	1.40	1 (20%)
3	BEZ	B	601	-	7,9,9	1.08	1 (14%)	8,11,11	1.25	1 (12%)
4	GOL	A	1528	-	5,5,5	0.62	0	5,5,5	0.52	0
3	BEZ	A	601	-	7,9,9	1.35	2 (28%)	8,11,11	1.43	2 (25%)
4	GOL	B	1527	-	5,5,5	1.00	0	5,5,5	1.53	1 (20%)
2	FAD	B	600	1	51,58,58	2.10	9 (17%)	60,89,89	2.55	11 (18%)
4	GOL	B	1529	-	5,5,5	0.45	0	5,5,5	0.79	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
2	FAD	A	600	1	-	7/30/50/50	0/6/6/6
4	GOL	B	1528	-	-	2/4/4/4	-
4	GOL	A	1527	-	-	2/4/4/4	-
3	BEZ	B	601	-	-	0/0/4/4	0/1/1/1
4	GOL	A	1528	-	-	2/4/4/4	-
3	BEZ	A	601	-	-	0/0/4/4	0/1/1/1
4	GOL	B	1527	-	-	2/4/4/4	-
2	FAD	B	600	1	-	3/30/50/50	0/6/6/6
4	GOL	B	1529	-	-	2/4/4/4	-

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	600	FAD	C4X-C10	8.74	1.47	1.38
2	A	600	FAD	C4X-C10	6.92	1.45	1.38
2	A	600	FAD	C9A-N10	5.88	1.46	1.38
2	B	600	FAD	C9A-N10	5.43	1.45	1.38
2	A	600	FAD	C4-C4X	4.04	1.48	1.41
2	B	600	FAD	C4-C4X	4.03	1.48	1.41
2	B	600	FAD	C8-C7	3.93	1.50	1.40
2	A	600	FAD	C5'-C4'	3.52	1.56	1.51
2	B	600	FAD	C8M-C8	3.50	1.58	1.51
2	A	600	FAD	C8M-C8	3.40	1.57	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	600	FAD	C9A-C5X	3.30	1.49	1.42
2	A	600	FAD	C9A-C5X	3.29	1.49	1.42
2	A	600	FAD	C10-N1	3.20	1.37	1.33
2	A	600	FAD	C2-N3	-3.17	1.31	1.38
2	A	600	FAD	C8-C7	3.05	1.48	1.40
2	B	600	FAD	C10-N1	2.95	1.37	1.33
2	A	600	FAD	C5X-N5	2.60	1.39	1.35
2	A	600	FAD	C2B-C1B	-2.53	1.49	1.53
3	B	601	BEZ	C1-C	2.51	1.49	1.47
2	B	600	FAD	O4B-C1B	2.45	1.44	1.41
2	B	600	FAD	C2B-C1B	-2.08	1.50	1.53
2	A	600	FAD	C2'-C3'	2.07	1.57	1.53
3	A	601	BEZ	C5-C6	2.07	1.43	1.38
3	A	601	BEZ	C1-C	2.02	1.49	1.47

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	600	FAD	C4-N3-C2	11.71	125.03	115.14
2	A	600	FAD	C4-N3-C2	10.39	123.91	115.14
2	A	600	FAD	C1'-N10-C9A	9.76	125.98	118.29
2	A	600	FAD	C4-C4X-C10	-8.00	114.66	119.95
2	B	600	FAD	C1'-N10-C9A	6.76	123.61	118.29
2	B	600	FAD	C4X-N5-C5X	6.26	123.03	116.77
2	B	600	FAD	C4X-C4-N3	-6.26	114.87	123.43
2	A	600	FAD	O2'-C2'-C3'	-5.32	96.17	109.10
2	B	600	FAD	O2'-C2'-C3'	-4.61	97.89	109.10
2	A	600	FAD	C9A-N10-C10	-4.00	116.67	121.91
2	A	600	FAD	C4X-C4-N3	-3.73	118.33	123.43
2	B	600	FAD	N3A-C2A-N1A	-3.66	122.96	128.68
2	B	600	FAD	C9A-N10-C10	-3.13	117.81	121.91
2	A	600	FAD	C10-C4X-N5	3.09	123.39	121.26
4	B	1527	GOL	O1-C1-C2	2.93	124.23	110.20
2	A	600	FAD	P-O3P-PA	-2.87	122.97	132.83
2	B	600	FAD	C1'-C2'-C3'	2.82	117.67	109.79
2	A	600	FAD	C4-C4X-N5	2.82	121.82	118.60
4	A	1527	GOL	O3-C3-C2	2.66	122.97	110.20
3	A	601	BEZ	C3-C2-C1	-2.61	117.28	120.56
2	A	600	FAD	N6A-C6A-N1A	2.60	123.97	118.57
2	B	600	FAD	C9A-C5X-N5	-2.47	118.50	122.36
2	B	600	FAD	C5X-C9A-N10	2.34	119.41	117.72
2	A	600	FAD	O2P-P-O1P	2.18	123.00	112.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	600	FAD	P-O3P-PA	-2.16	125.43	132.83
3	A	601	BEZ	C6-C1-C2	2.11	121.80	117.59
3	B	601	BEZ	C5-C6-C1	-2.08	117.95	120.56

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	600	FAD	N10-C1'-C2'-O2'
4	B	1527	GOL	O1-C1-C2-C3
4	B	1529	GOL	O1-C1-C2-C3
2	A	600	FAD	O4'-C4'-C5'-O5'
2	B	600	FAD	O4'-C4'-C5'-O5'
4	A	1527	GOL	O1-C1-C2-O2
4	B	1527	GOL	O1-C1-C2-O2
2	A	600	FAD	C3'-C4'-C5'-O5'
2	B	600	FAD	C3'-C4'-C5'-O5'
4	B	1529	GOL	O1-C1-C2-O2
2	A	600	FAD	C4'-C5'-O5'-P
2	B	600	FAD	C4'-C5'-O5'-P
4	B	1528	GOL	O2-C2-C3-O3
4	B	1528	GOL	C1-C2-C3-O3
4	A	1527	GOL	O1-C1-C2-C3
2	A	600	FAD	N10-C1'-C2'-C3'
4	A	1528	GOL	O1-C1-C2-O2
2	A	600	FAD	C2'-C3'-C4'-O4'
4	A	1528	GOL	O1-C1-C2-C3
2	A	600	FAD	O2'-C2'-C3'-O3'

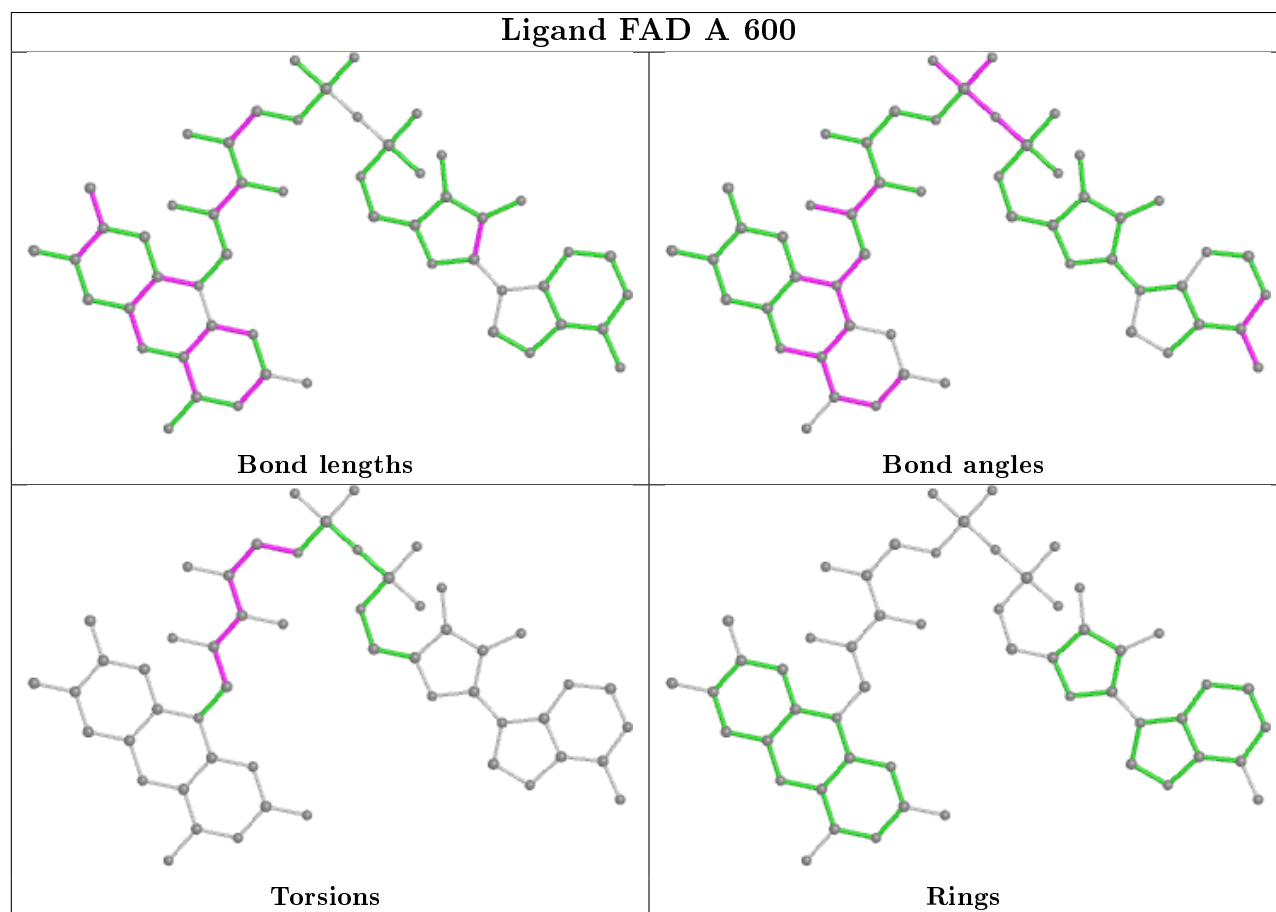
There are no ring outliers.

4 monomers are involved in 5 short contacts:

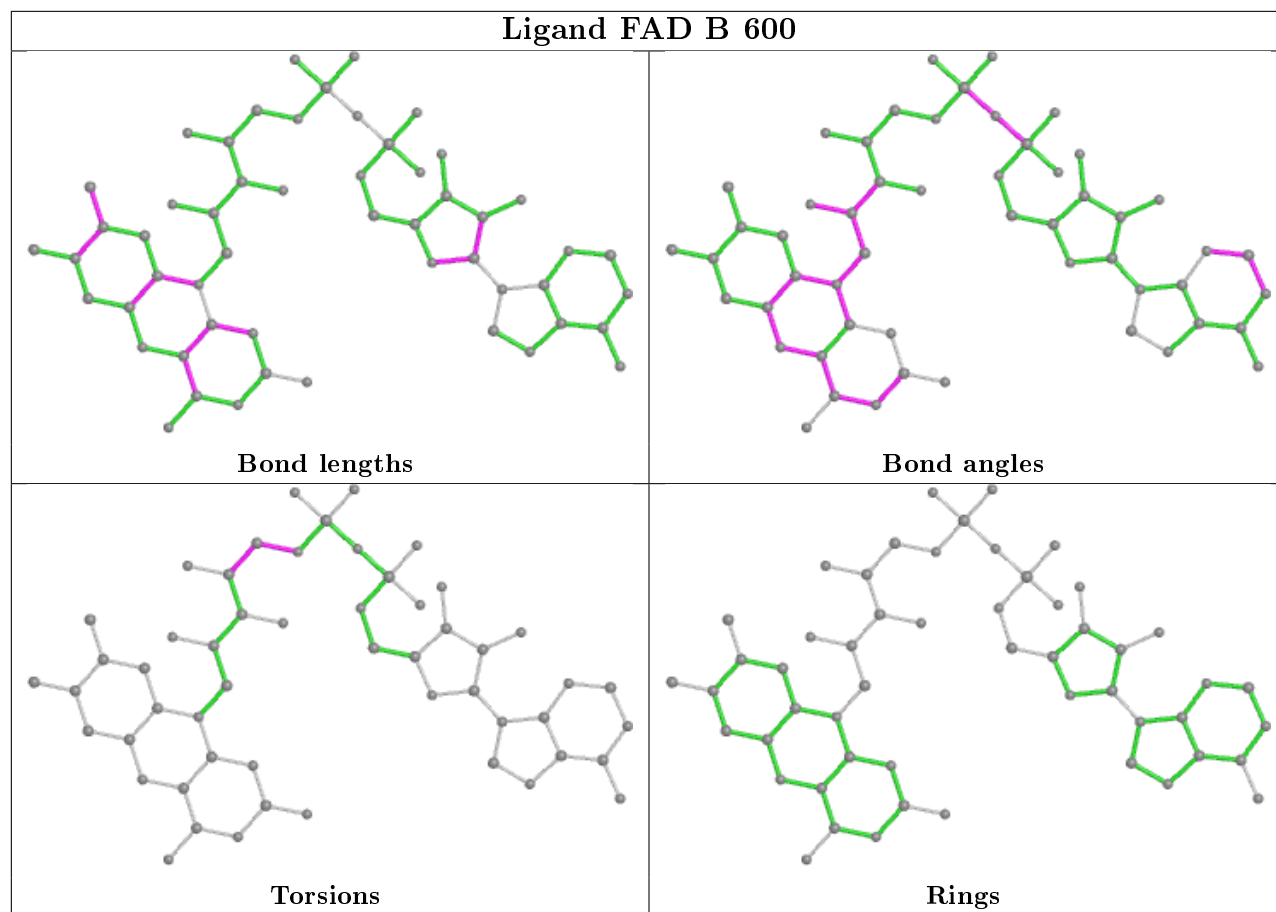
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	600	FAD	1	0
4	A	1527	GOL	1	0
2	B	600	FAD	1	0
4	B	1529	GOL	2	0

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.







## 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	525/526 (99%)	-0.48	2 (0%) 92 93	10, 17, 33, 51	0
1	B	525/526 (99%)	-0.32	1 (0%) 95 95	13, 23, 41, 55	0
All	All	1050/1052 (99%)	-0.40	3 (0%) 94 94	10, 20, 39, 55	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	356	ASP	2.8
1	A	526	LEU	2.5
1	A	297	ASP	2.0

### 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 carbohydrates 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(Å <sup>2</sup> )	Q<0.9
4	GOL	B	1527	6/6	0.73	0.21	33,41,41,42	0
4	GOL	A	1527	6/6	0.80	0.25	32,39,41,42	0

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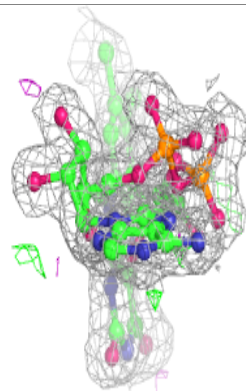
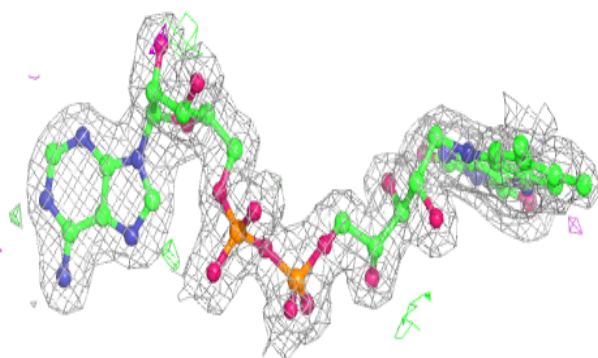
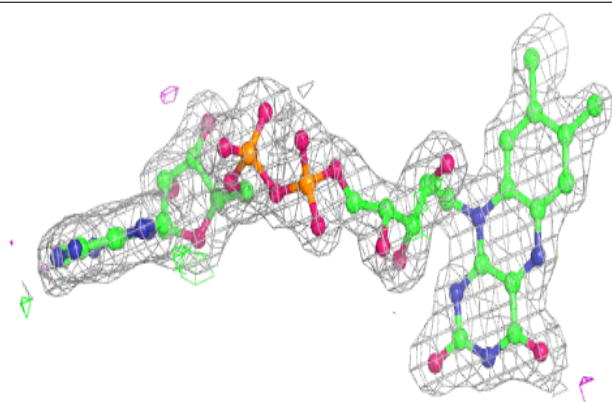
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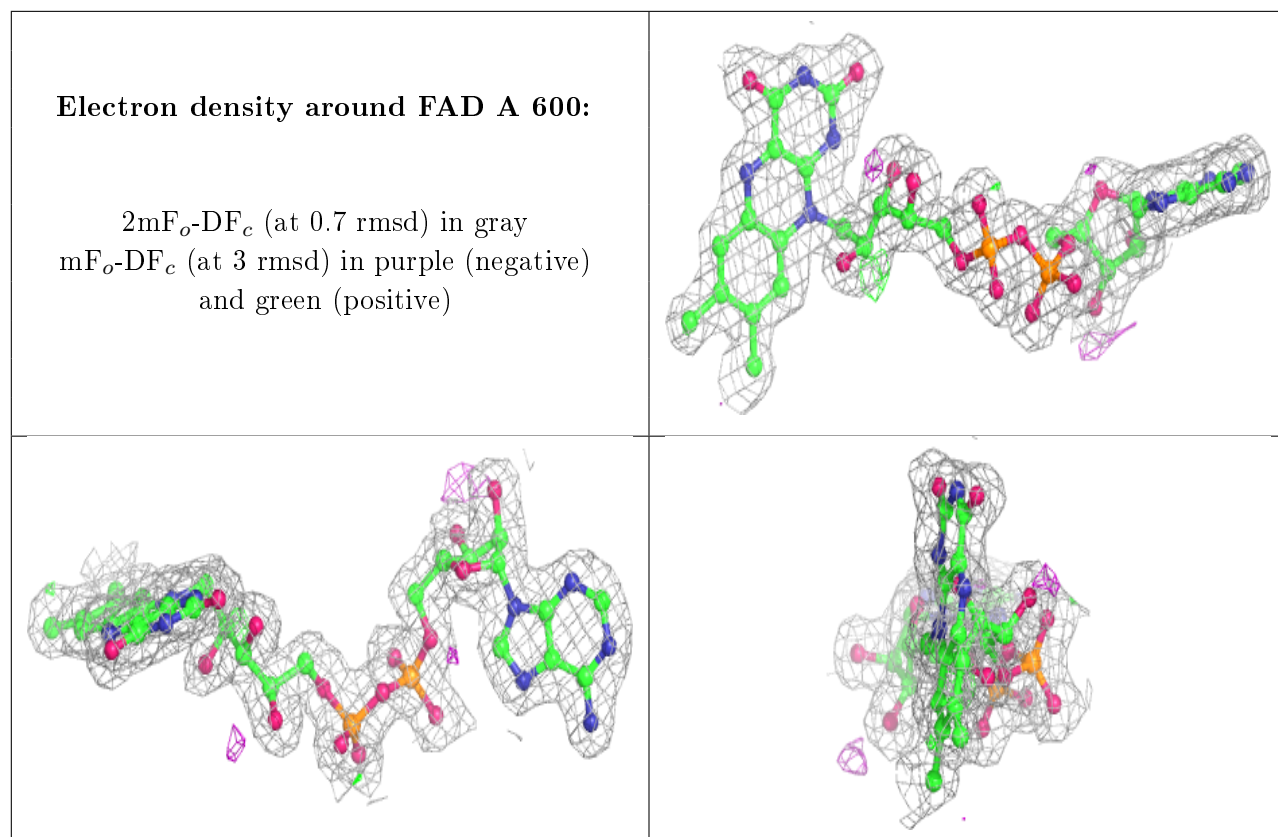
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GOL	B	1529	6/6	0.87	0.17	42,44,47,54	0
4	GOL	A	1528	6/6	0.88	0.27	33,39,40,43	0
3	BEZ	B	601	9/9	0.89	0.15	28,31,35,36	0
4	GOL	B	1528	6/6	0.89	0.16	36,42,42,44	0
3	BEZ	A	601	9/9	0.92	0.12	21,22,24,28	0
2	FAD	B	600	53/53	0.98	0.08	15,19,24,28	0
2	FAD	A	600	53/53	0.98	0.07	10,12,14,20	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 600:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.