



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 02:13 am BST

PDB ID : 5O8P
Title : The crystal structure of DfoA bound to FAD, the desferrioxamine biosynthetic pathway cadaverine monooxygenase from the fire blight disease pathogen *Erwinia amylovora*
Authors : Salomone-Stagni, M.; Bartho, J.D.; Polsinelli, I.; Bellini, D.; Walsh, M.A.; Demitri, N.; Benini, S.
Deposited on : 2017-06-14
Resolution : 2.75 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

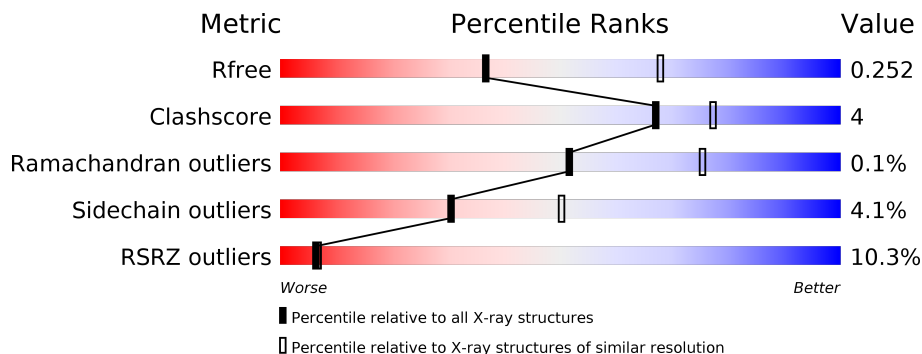
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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 ≥ 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	433	 12% 86% 11% ..
1	B	433	 8% 89% 9% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7130 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 L-lysine 6-monooxygenase involved in desferrioxamine biosynthesis.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	427	3530	2254	604	658	14	0	1	0
1	B	428	3526	2250	604	657	15	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP D4I246
A	-1	ALA	-	expression tag	UNP D4I246
A	0	MET	-	expression tag	UNP D4I246
A	1	ALA	-	expression tag	UNP D4I246
B	-2	GLY	-	expression tag	UNP D4I246
B	-1	ALA	-	expression tag	UNP D4I246
B	0	MET	-	expression tag	UNP D4I246
B	1	ALA	-	expression tag	UNP D4I246

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



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

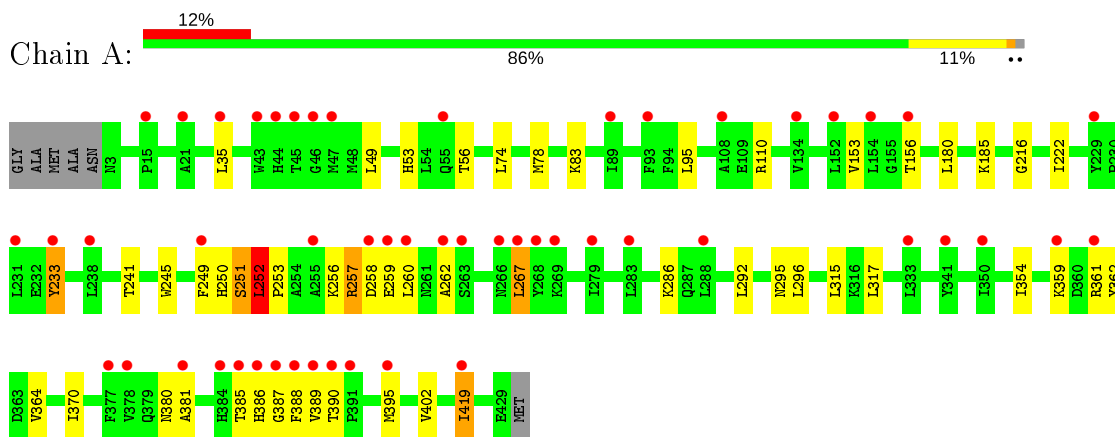
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	12	Total 12 O	0	0
3	B	9	Total 9 O	0	0

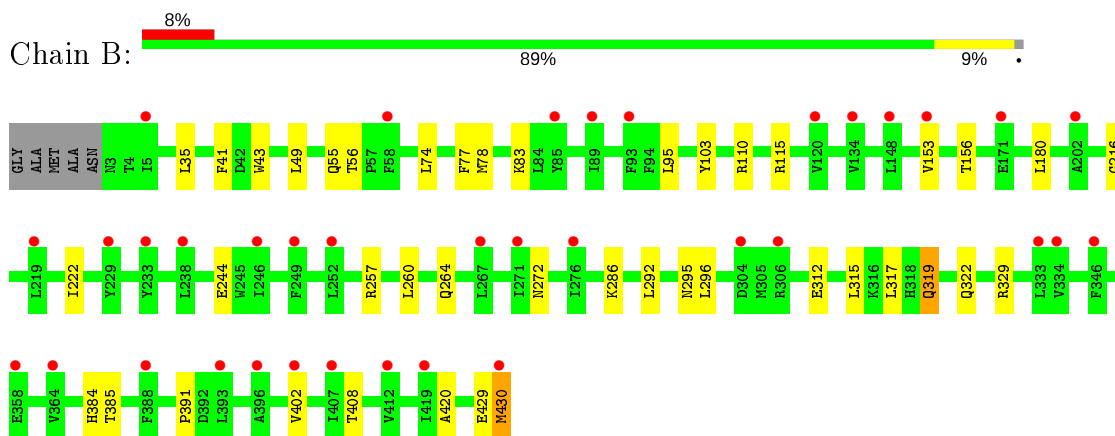
3 Residue-property plots [i](#)

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: L-lysine 6-monooxygenase involved in desferrioxamine biosynthesis



- Molecule 1: L-lysine 6-monooxygenase involved in desferrioxamine biosynthesis



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	164.09Å 164.09Å 168.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	117.57 – 2.75 117.57 – 2.75	Depositor EDS
% Data completeness (in resolution range)	100.0 (117.57-2.75) 100.0 (117.57-2.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.200 , 0.224 0.227 , 0.252	Depositor DCC
R_{free} test set	3071 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	62.3	Xtriage
Anisotropy	0.402	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 22.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.022 for -h,l,k 0.003 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7130	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.21% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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

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	0.50	0/3624	0.74	1/4916 (0.0%)
1	B	0.49	0/3619	0.72	0/4908
All	All	0.50	0/7243	0.73	1/9824 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	252	LEU	C-N-CD	6.36	141.76	128.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	216	GLY	Peptide
1	B	216	GLY	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	3530	0	3397	38	0
1	B	3526	0	3398	16	0
2	B	53	0	31	0	0
3	A	12	0	0	0	0
3	B	9	0	0	0	0
All	All	7130	0	6826	54	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 4.

All (54) 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:251:SER:CB	1:A:253:PRO:HD3	2.02	0.89
1:A:251:SER:HB2	1:A:253:PRO:HD3	1.56	0.88
1:A:253:PRO:O	1:A:257:ARG:HD3	1.80	0.80
1:A:250:HIS:HA	1:A:257:ARG:HH22	1.51	0.76
1:A:354:ILE:HG23	1:A:370:ILE:HG22	1.73	0.70
1:A:252:LEU:H	1:A:257:ARG:NH2	1.89	0.69
1:B:244:GLU:OE1	1:B:420:ALA:HB3	1.95	0.67
1:A:389:VAL:CG1	1:A:395:MET:HG3	2.25	0.66
1:A:251:SER:O	1:A:252:LEU:HB3	1.98	0.64
1:A:362:TYR:HB3	1:A:370:ILE:HD12	1.79	0.63
1:B:55:GLN:OE1	1:B:272:ASN:HB2	1.98	0.63
1:A:251:SER:C	1:A:253:PRO:HD3	2.20	0.59
1:A:385:THR:HG23	1:A:386:HIS:HD2	1.67	0.58
1:A:251:SER:HB2	1:A:253:PRO:CD	2.32	0.58
1:A:286:LYS:HB3	1:A:292:LEU:HD21	1.87	0.56
1:A:364:VAL:HB	1:A:385:THR:HG21	1.91	0.53
1:A:49:LEU:HD23	1:A:180:LEU:HD21	1.90	0.53
1:B:286:LYS:HB3	1:B:292:LEU:HD21	1.91	0.52
1:A:252:LEU:N	1:A:253:PRO:HD3	2.24	0.52
1:A:222:ILE:HD13	1:A:317:LEU:HD11	1.90	0.52
1:A:380:ASN:O	1:A:381:ALA:HB3	2.09	0.52
1:A:354:ILE:HG23	1:A:370:ILE:CG2	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:319:GLN:HG3	1:B:322:GLN:HB3	1.93	0.51
1:B:49:LEU:HD23	1:B:180:LEU:HD21	1.92	0.51
1:A:387:GLY:O	1:A:390:THR:HG23	2.12	0.49
1:A:419:ILE:HD13	1:A:419:ILE:H	1.76	0.49
1:A:256:LYS:HA	1:A:259:GLU:HG2	1.93	0.49
1:A:245:TRP:CH2	1:A:249:PHE:CD1	3.01	0.49
1:B:74:LEU:HG	1:B:95:LEU:HD11	1.95	0.48
1:B:222:ILE:HD13	1:B:317:LEU:HD11	1.95	0.48
1:A:233[B]:TYR:N	1:A:233[B]:TYR:CD1	2.78	0.46
1:A:74:LEU:HG	1:A:95:LEU:HD11	1.98	0.46
1:A:250:HIS:HA	1:A:257:ARG:NH2	2.26	0.46
1:A:252:LEU:N	1:A:253:PRO:CD	2.80	0.44
1:B:260:LEU:HD12	1:B:264:GLN:NE2	2.33	0.44
1:B:286:LYS:CB	1:B:292:LEU:HD21	2.47	0.44
1:A:286:LYS:CB	1:A:292:LEU:HD21	2.48	0.43
1:A:364:VAL:HB	1:A:385:THR:CG2	2.48	0.43
1:B:384:HIS:CD2	1:B:385:THR:HG23	2.53	0.43
1:A:251:SER:OG	1:A:253:PRO:HD3	2.19	0.43
1:B:295:ASN:C	1:B:296:LEU:HD12	2.38	0.43
1:A:241:THR:O	1:A:241:THR:OG1	2.37	0.43
1:B:429:GLU:O	1:B:430:MET:HG2	2.18	0.43
1:A:295:ASN:C	1:A:296:LEU:HD12	2.38	0.42
1:B:78:MET:HG3	1:B:83:LYS:HG3	2.01	0.42
1:B:312:GLU:OE1	1:B:329:ARG:NH1	2.53	0.41
1:B:77:PHE:CE2	1:B:103:TYR:HA	2.56	0.41
1:A:259:GLU:O	1:A:262:ALA:O	2.38	0.41
1:A:252:LEU:O	1:A:252:LEU:HG	2.20	0.41
1:A:249:PHE:CZ	1:A:257:ARG:HG3	2.56	0.41
1:A:251:SER:CB	1:A:253:PRO:CD	2.85	0.41
1:B:41:PHE:CE2	1:B:43:TRP:HB2	2.56	0.41
1:A:267:LEU:HB3	1:A:388:PHE:CD2	2.56	0.40
1:A:78:MET:HG3	1:A:83:LYS:HG3	2.02	0.40

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	426/433 (98%)	406 (95%)	19 (4%)	1 (0%)	47	69
1	B	426/433 (98%)	410 (96%)	16 (4%)	0	100	100
All	All	852/866 (98%)	816 (96%)	35 (4%)	1 (0%)	51	75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	252	LEU

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	379/381 (100%)	360 (95%)	19 (5%)	24	42
1	B	379/381 (100%)	366 (97%)	13 (3%)	37	58
All	All	758/762 (100%)	726 (96%)	32 (4%)	30	49

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	LEU
1	A	53	HIS
1	A	56	THR
1	A	110	ARG
1	A	153	VAL
1	A	156	THR
1	A	185	LYS
1	A	233[A]	TYR
1	A	233[B]	TYR
1	A	251	SER
1	A	257	ARG

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Mol	Chain	Res	Type
1	A	258	ASP
1	A	260	LEU
1	A	267	LEU
1	A	315	LEU
1	A	359	LYS
1	A	361	ARG
1	A	402	VAL
1	A	419	ILE
1	B	35	LEU
1	B	56	THR
1	B	110	ARG
1	B	115	ARG
1	B	153	VAL
1	B	156	THR
1	B	257	ARG
1	B	315	LEU
1	B	319	GLN
1	B	391	PRO
1	B	402	VAL
1	B	408	THR
1	B	430	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	117	ASN
1	A	342	GLN
1	A	380	ASN
1	A	386	HIS
1	B	31	ASN
1	B	117	ASN
1	B	128	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](#)

1 ligand is 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	B	501	-	51,58,58	2.11	8 (15%)	60,89,89	2.03	10 (16%)

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	B	501	-	-	8/30/50/50	0/6/6/6

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	FAD	C4X-C10	10.78	1.49	1.38
2	B	501	FAD	C9A-C5X	4.39	1.51	1.42
2	B	501	FAD	C4-C4X	4.38	1.48	1.41
2	B	501	FAD	C9A-N10	4.12	1.44	1.38
2	B	501	FAD	C8-C7	3.50	1.49	1.40
2	B	501	FAD	C5A-C4A	2.48	1.47	1.40
2	B	501	FAD	C10-N1	2.36	1.36	1.33
2	B	501	FAD	O4B-C1B	2.04	1.43	1.41

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	FAD	C4-N3-C2	8.05	121.94	115.14
2	B	501	FAD	C1'-N10-C9A	7.19	123.95	118.29
2	B	501	FAD	C4-C4X-C10	-5.09	116.58	119.95
2	B	501	FAD	N3A-C2A-N1A	-3.78	122.78	128.68
2	B	501	FAD	C4X-N5-C5X	3.68	120.45	116.77
2	B	501	FAD	C9A-N10-C10	-3.46	117.38	121.91
2	B	501	FAD	C4X-C4-N3	-3.22	119.03	123.43
2	B	501	FAD	C4A-C5A-N7A	-3.03	106.24	109.40
2	B	501	FAD	C4-C4X-N5	2.92	121.94	118.60
2	B	501	FAD	C1B-N9A-C4A	-2.61	122.06	126.64

There are no chirality outliers.

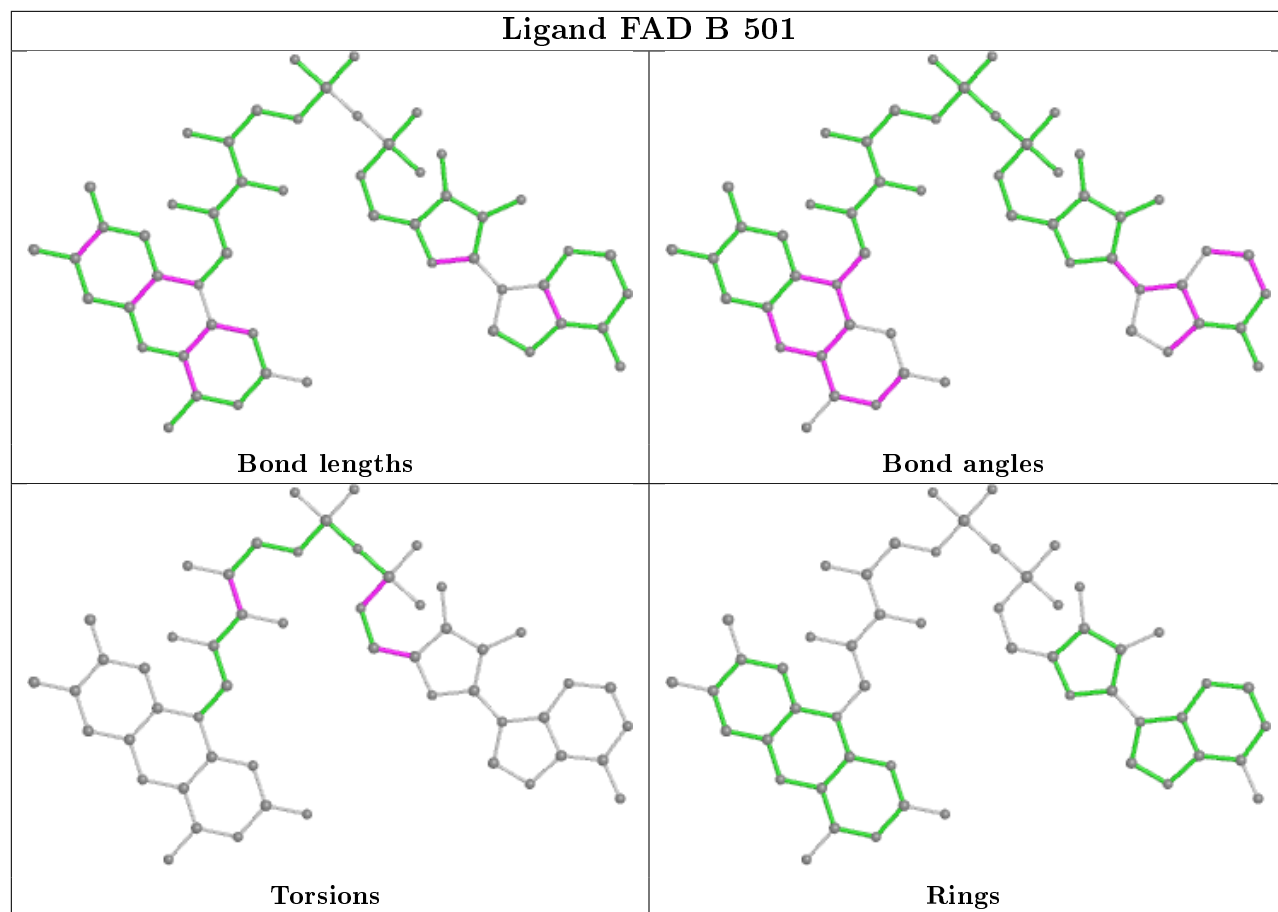
All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	FAD	C5B-O5B-PA-O1A
2	B	501	FAD	C5B-O5B-PA-O2A
2	B	501	FAD	C2'-C3'-C4'-O4'
2	B	501	FAD	C2'-C3'-C4'-C5'
2	B	501	FAD	O4B-C4B-C5B-O5B
2	B	501	FAD	O3'-C3'-C4'-O4'
2	B	501	FAD	C3B-C4B-C5B-O5B
2	B	501	FAD	C5B-O5B-PA-O3P

There are no ring outliers.

No monomer is involved in short contacts.

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

6.1 Protein, DNA and RNA chains

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	427/433 (98%)	1.22	52 (12%) 4 4	24, 39, 98, 136	0
1	B	428/433 (98%)	1.06	36 (8%) 11 13	29, 42, 63, 87	0
All	All	855/866 (98%)	1.14	88 (10%) 6 7	24, 41, 78, 136	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	389	VAL	10.4
1	A	46	GLY	7.1
1	A	385	THR	7.0
1	A	45	THR	6.8
1	A	390	THR	6.3
1	A	388	PHE	6.0
1	A	384	HIS	5.5
1	A	263	SER	5.2
1	A	259	GLU	4.9
1	A	381	ALA	4.5
1	A	386	HIS	4.5
1	A	156	THR	4.1
1	A	255	ALA	3.6
1	B	171	GLU	3.4
1	A	44	HIS	3.4
1	A	269	LYS	3.4
1	A	233[A]	TYR	3.4
1	A	249	PHE	3.3
1	A	341	TYR	3.2
1	A	267	LEU	3.2
1	A	268	TYR	3.1
1	A	258	ASP	3.1
1	B	364	VAL	3.0
1	A	152	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	233	TYR	3.0
1	A	260	LEU	3.0
1	B	430	MET	3.0
1	A	229	TYR	2.9
1	A	47	MET	2.8
1	B	333	LEU	2.7
1	A	359	LYS	2.7
1	B	85	TYR	2.7
1	B	153	VAL	2.7
1	A	55	GLN	2.6
1	A	387	GLY	2.6
1	B	358	GLU	2.6
1	A	134	VAL	2.6
1	A	21	ALA	2.5
1	A	43	TRP	2.5
1	A	154	LEU	2.5
1	B	246	ILE	2.5
1	B	412	VAL	2.4
1	B	306	ARG	2.4
1	A	333	LEU	2.4
1	A	350	ILE	2.4
1	B	396	ALA	2.3
1	A	419	ILE	2.3
1	B	419	ILE	2.3
1	B	148	LEU	2.3
1	B	267	LEU	2.3
1	B	276	ILE	2.3
1	A	361	ARG	2.3
1	B	249	PHE	2.3
1	A	108	ALA	2.2
1	B	89	ILE	2.2
1	A	15	PRO	2.2
1	B	219	LEU	2.2
1	A	262	ALA	2.2
1	A	279	ILE	2.2
1	B	407	ILE	2.2
1	A	377	PHE	2.2
1	B	252	LEU	2.2
1	B	393	LEU	2.2
1	A	231	LEU	2.2
1	B	58	PHE	2.2
1	A	266	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	346	PHE	2.1
1	B	5	ILE	2.1
1	B	229	TYR	2.1
1	A	283	LEU	2.1
1	B	238	LEU	2.1
1	A	89	ILE	2.1
1	B	134	VAL	2.1
1	A	395	MET	2.1
1	A	93	PHE	2.1
1	B	388	PHE	2.1
1	B	120	VAL	2.1
1	A	391	PRO	2.1
1	B	304	ASP	2.1
1	A	35	LEU	2.0
1	A	288	LEU	2.0
1	B	271	ILE	2.0
1	B	202	ALA	2.0
1	B	402	VAL	2.0
1	B	93	PHE	2.0
1	A	238	LEU	2.0
1	A	378	VAL	2.0
1	B	334	VAL	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](#)

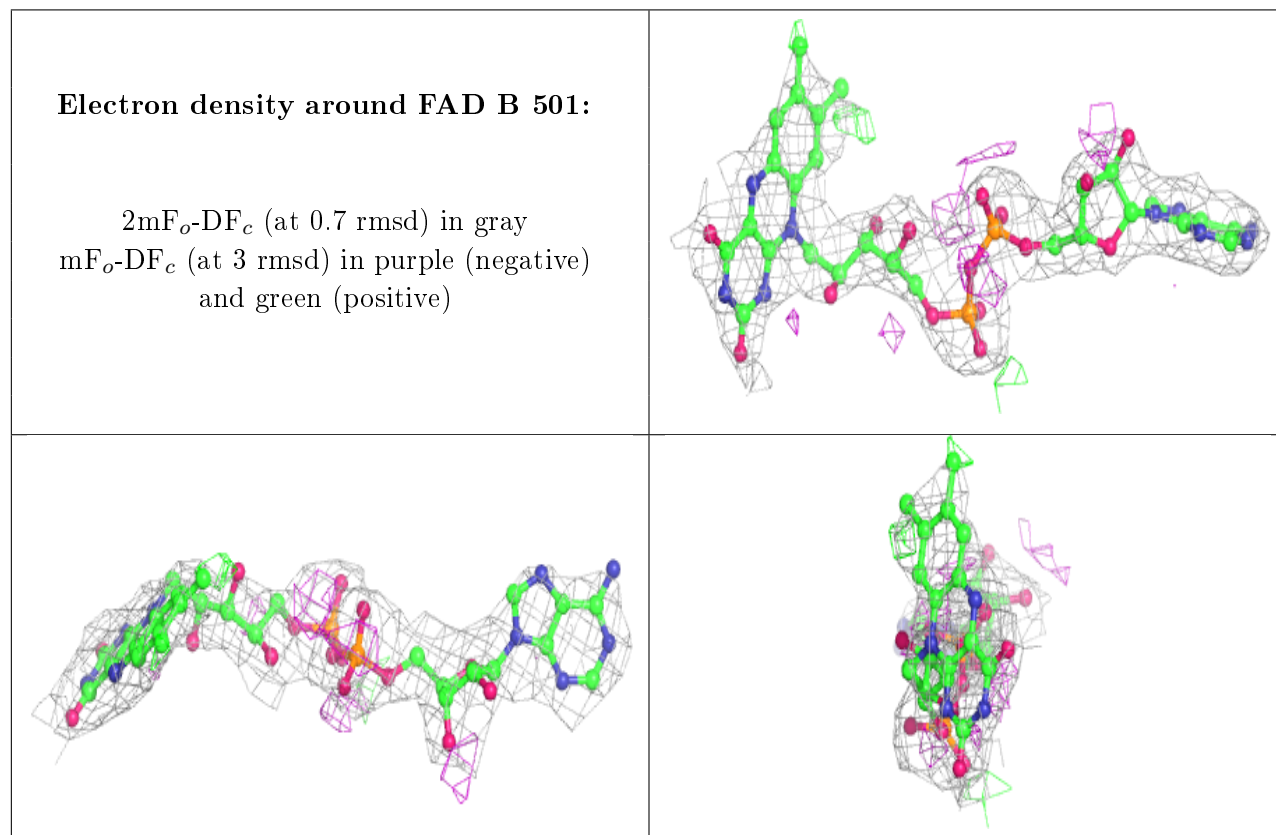
There are no carbohydrates in this entry.

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, 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
2	FAD	B	501	53/53	0.92	0.31	68,92,105,113	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.