



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 09:00 PM UTC

PDB ID : 5L46 / pdb_00005l46
Title : Crystal structure of human dimethylglycine-dehydrogenase
Authors : Hromic, A.; Pavkov-Keller, T.; Gruber, K.
Deposited on : 2016-05-25
Resolution : 3.09 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 ⓘ 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

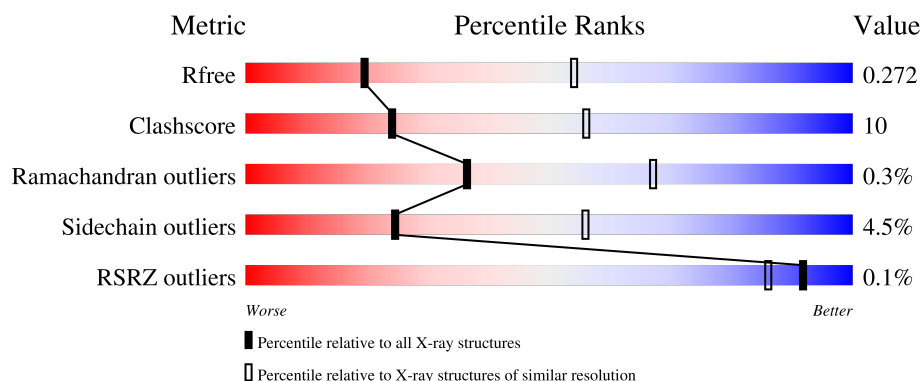
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.09 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}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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 $\leq 5\%$. 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	841	 71% 24% . .
1	B	841	 68% 26% . .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12894 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.

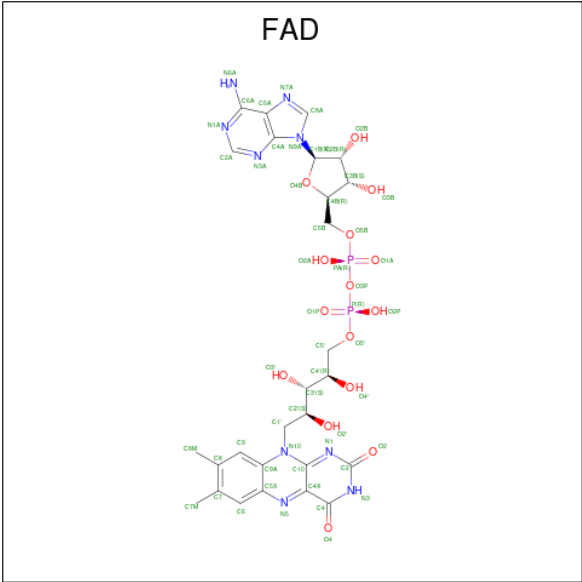
- Molecule 1 is a protein called Dimethylglycine dehydrogenase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	809	Total	C	N	O	S	0	0	0
			6398	4099	1090	1186	23			
1	B	808	Total	C	N	O	S	0	0	0
			6384	4088	1088	1185	23			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	MET	-	initiating methionine	UNP Q9UI17
A	279	PRO	SER	conflict	UNP Q9UI17
A	867	ARG	-	expression tag	UNP Q9UI17
A	868	PRO	-	expression tag	UNP Q9UI17
B	28	MET	-	initiating methionine	UNP Q9UI17
B	279	PRO	SER	conflict	UNP Q9UI17
B	867	ARG	-	expression tag	UNP Q9UI17
B	868	PRO	-	expression tag	UNP Q9UI17

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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 water.

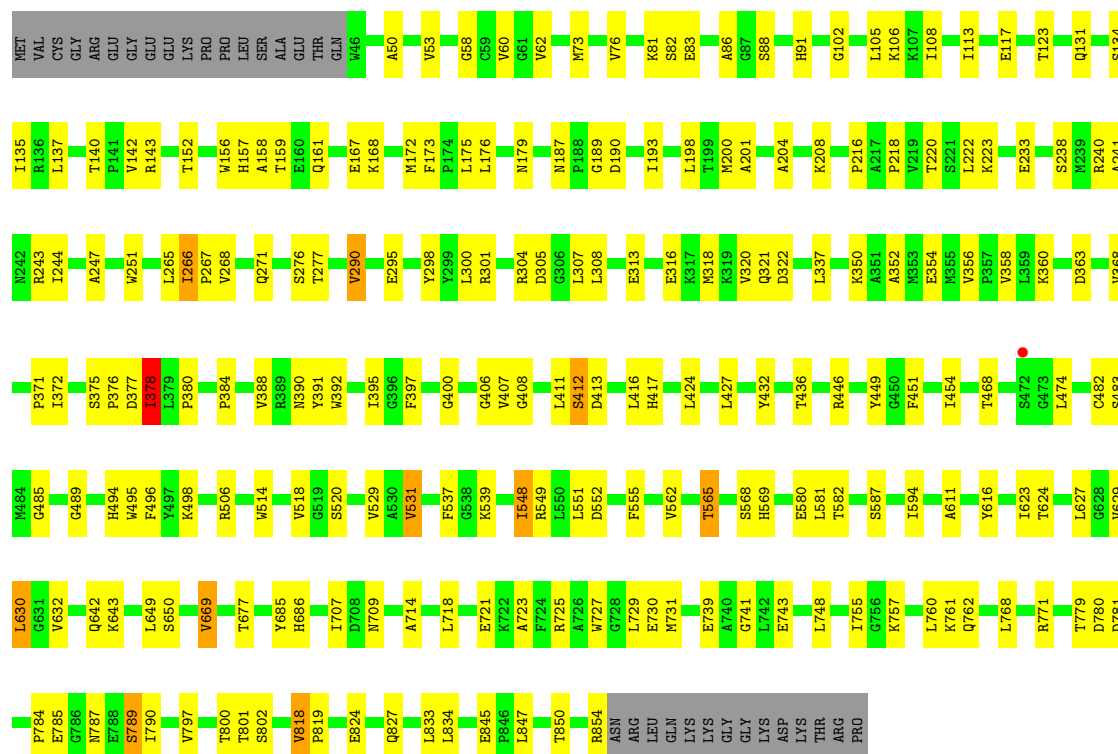
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	O	0	0
			4	4		
3	B	2	Total	O	0	0
			2	2		

3 Residue-property plots

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.

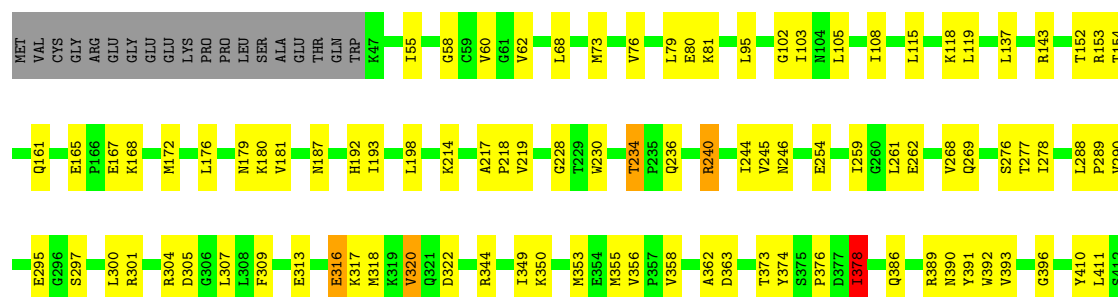
- Molecule 1: Dimethylglycine dehydrogenase, mitochondrial

Chain A: 



- Molecule 1: Dimethylglycine dehydrogenase, mitochondrial

Chain B: 



LYS	D780	D413	G538	V664
ASP	D781	L416	K539	I667
LYS	P784	H417	F540	P668
THR		G418	N541	V669
ARG	N787	E419	I542	I672
PRO	E788	D423	L548	
	S789	L424	L551	W682
	I790	Y432	F555	
		T436	I559	Y685
	N793	R446	V562	H686
	G794	E447	T565	R687
	K795	S448	N566	R688
	V796	Y449	I567	E689
	V797	G450	S568	D690
		N451		S691
	T800	N452		F710
	T801	N453		
	S802	I454		N716
		Y457		
	V818	R462		R719
	P819	R466		L720
	V820	C482		E721
	G821	G485		K722
	L822	F486		
	S823	H487		R725
	E824	E491		A726
		Q492		W727
	Q827	P493		
		H494		E730
	E830	W495		M731
	V831	F496		N732
	E832	P507		C733
	L833	R511		
	L834	T512		L738
	G835	N513		E739
	K836	W514		
	N837	Q524		F745
		V525		V746
	I842	M526		
	E845	V529		N749
	P846	A530		
	L847	V531		Q758
	V848	T532		A759
	L849	F537		L760
	T850			K761
	E851			Q762
	P852			
	T853			A765
	R854			
	ASN			L768
	ARG			K769
	LEU			
	GLN			L772
	LYS			
	LYS			L775
	GLY			T776
	GLY			K660
				L777

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.38Å 119.87Å 86.47Å 90.00° 92.58° 90.00°	Depositor
Resolution (Å)	58.65 – 3.09 58.65 – 3.09	Depositor EDS
% Data completeness (in resolution range)	97.7 (58.65-3.09) 97.7 (58.65-3.09)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 3.07Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.179 , 0.269 0.186 , 0.272	Depositor DCC
R_{free} test set	1525 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	47.0	Xtriage
Anisotropy	0.706	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.003 for l,k,-h 0.068 for h,-k,-l 0.030 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12894	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: 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	0.62	0/6558	0.97	8/8895 (0.1%)
1	B	0.62	0/6542	0.98	10/8872 (0.1%)
All	All	0.62	0/13100	0.97	18/17767 (0.1%)

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	234	THR	CA-C-N	-7.13	112.29	119.56
1	B	234	THR	C-N-CA	-7.13	112.29	119.56
1	B	559	ILE	CA-C-N	6.43	126.35	119.85
1	B	559	ILE	C-N-CA	6.43	126.35	119.85
1	B	179	ASN	N-CA-C	5.45	117.30	111.36

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	6398	0	6352	121	0
1	B	6384	0	6342	138	0
2	A	53	0	30	6	0
2	B	53	0	30	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	4	0	0	0	0
3	B	2	0	0	0	0
All	All	12894	0	12754	257	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 10.

The worst 5 of 257 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:290:VAL:HG13	1:B:301:ARG:HB3	1.54	0.90
1:B:487:HIS:CD2	1:B:492:GLN:HE21	2.01	0.78
1:A:290:VAL:HG13	1:A:301:ARG:HB3	1.66	0.76
1:A:755:ILE:HD11	1:B:793:ASN:HD21	1.53	0.74
1:B:115:LEU:HA	1:B:118:LYS:HE2	1.71	0.72

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	807/841 (96%)	765 (95%)	39 (5%)	3 (0%)	30	61
1	B	806/841 (96%)	756 (94%)	48 (6%)	2 (0%)	43	73
All	All	1613/1682 (96%)	1521 (94%)	87 (5%)	5 (0%)	36	67

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	378	ILE
1	B	378	ILE

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Mol	Chain	Res	Type
1	A	537	PHE
1	B	102	GLY
1	A	102	GLY

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	682/709 (96%)	652 (96%)	30 (4%)	25	56
1	B	681/709 (96%)	650 (95%)	31 (5%)	24	55
All	All	1363/1418 (96%)	1302 (96%)	61 (4%)	24	56

5 of 61 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	818	VAL
1	B	797	VAL
1	B	320	VAL
1	B	790	ILE
1	B	830	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	787	ASN
1	B	125	GLN
1	B	793	ASN
1	B	492	GLN
1	B	622	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	B	901	1	58,58,58	1.63	9 (15%)	85,89,89	1.81	19 (22%)
2	FAD	A	901	1	58,58,58	1.65	12 (20%)	85,89,89	2.00	21 (24%)

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	901	1	-	6/34/50/50	0/6/6/6
2	FAD	A	901	1	-	19/34/50/50	0/6/6/6

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	FAD	C9A-C5X	5.95	1.50	1.41
2	B	901	FAD	C5A-C4A	5.43	1.48	1.39
2	A	901	FAD	C9A-C5X	5.06	1.49	1.41
2	A	901	FAD	PA-O3P	4.28	1.64	1.59
2	A	901	FAD	C5A-C4A	3.94	1.46	1.39

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	FAD	C5A-C4A-N3A	-6.15	118.24	126.72
2	B	901	FAD	C5A-C4A-N3A	-6.13	118.28	126.72
2	A	901	FAD	C1'-N10-C9A	-5.66	109.63	120.63
2	B	901	FAD	N3A-C4A-N9A	5.51	136.54	127.17
2	B	901	FAD	O4B-C1B-N9A	5.28	118.23	108.09

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

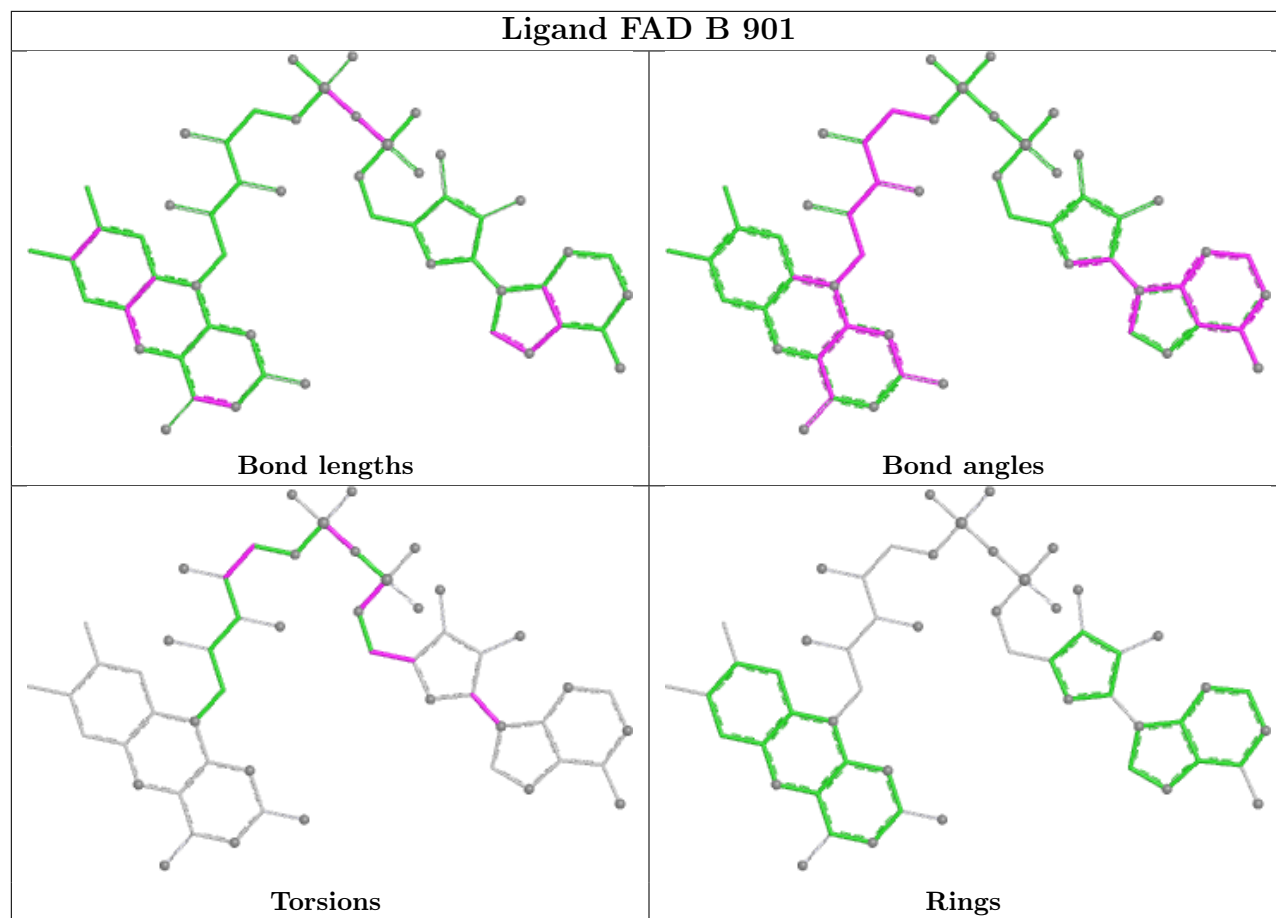
Mol	Chain	Res	Type	Atoms
2	A	901	FAD	C5B-O5B-PA-O1A
2	A	901	FAD	C5B-O5B-PA-O2A
2	A	901	FAD	C5B-O5B-PA-O3P
2	A	901	FAD	C2'-C1'-N10-C9A
2	A	901	FAD	C2'-C1'-N10-C10

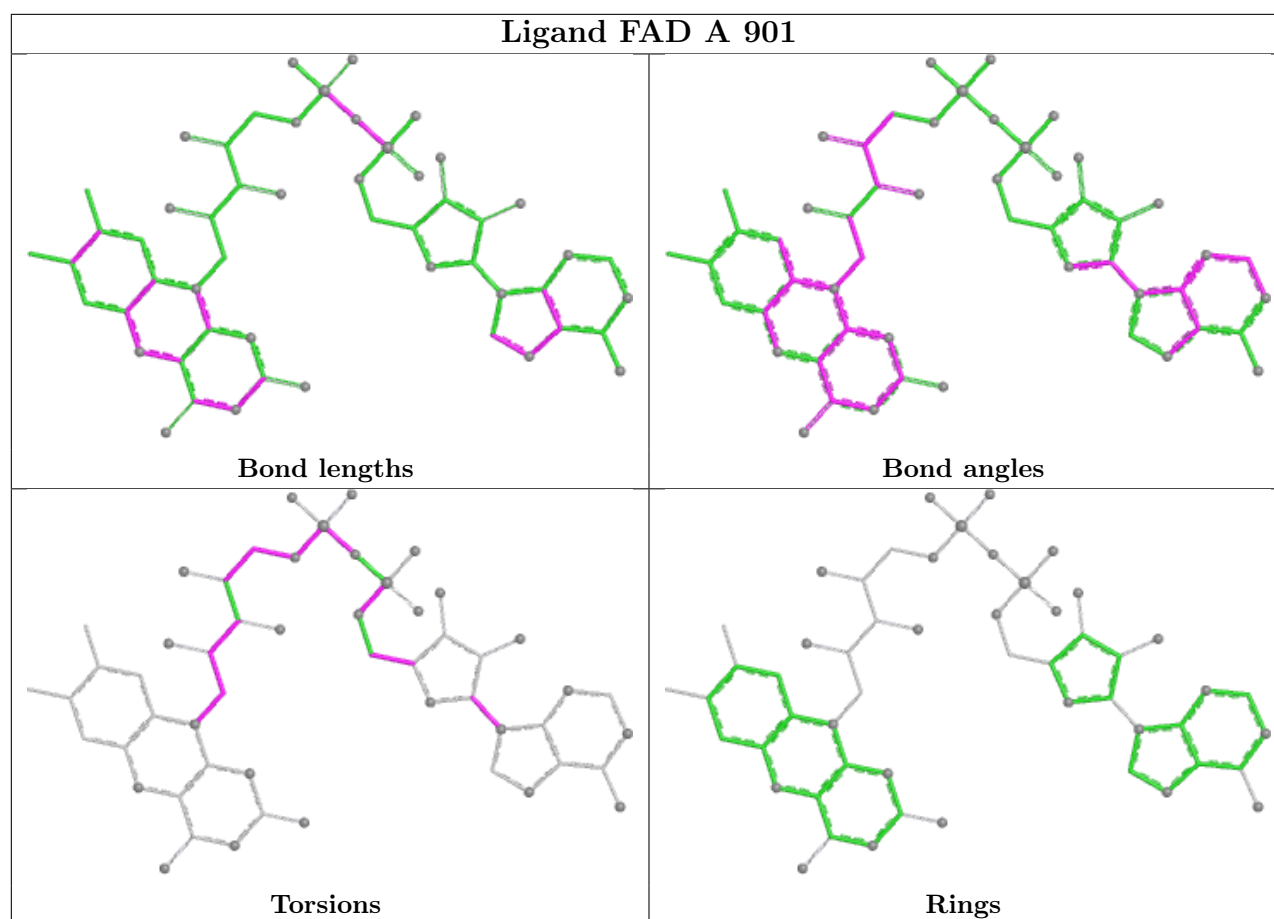
There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	901	FAD	3	0
2	A	901	FAD	6	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, 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	809/841 (96%)	-0.34	1 (0%) 92 86	7, 36, 61, 98	0
1	B	808/841 (96%)	-0.36	0 100 100	10, 36, 62, 105	0
All	All	1617/1682 (96%)	-0.35	1 (0%) 92 86	7, 36, 62, 105	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	472	SER	2.2

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 oligosaccharides 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.

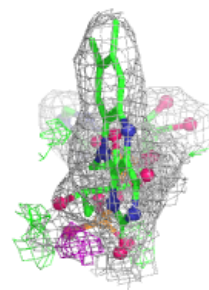
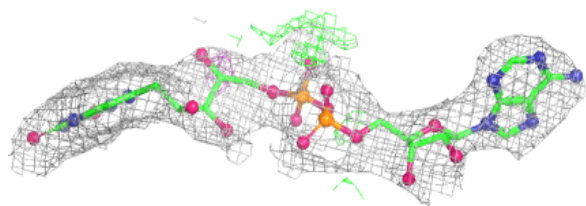
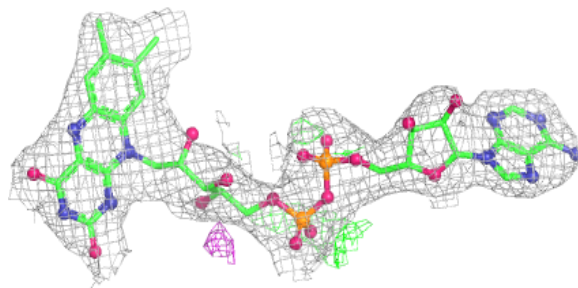
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FAD	B	901	53/53	0.93	0.10	34,34,34,34	0
2	FAD	A	901	53/53	0.94	0.08	25,25,25,25	0

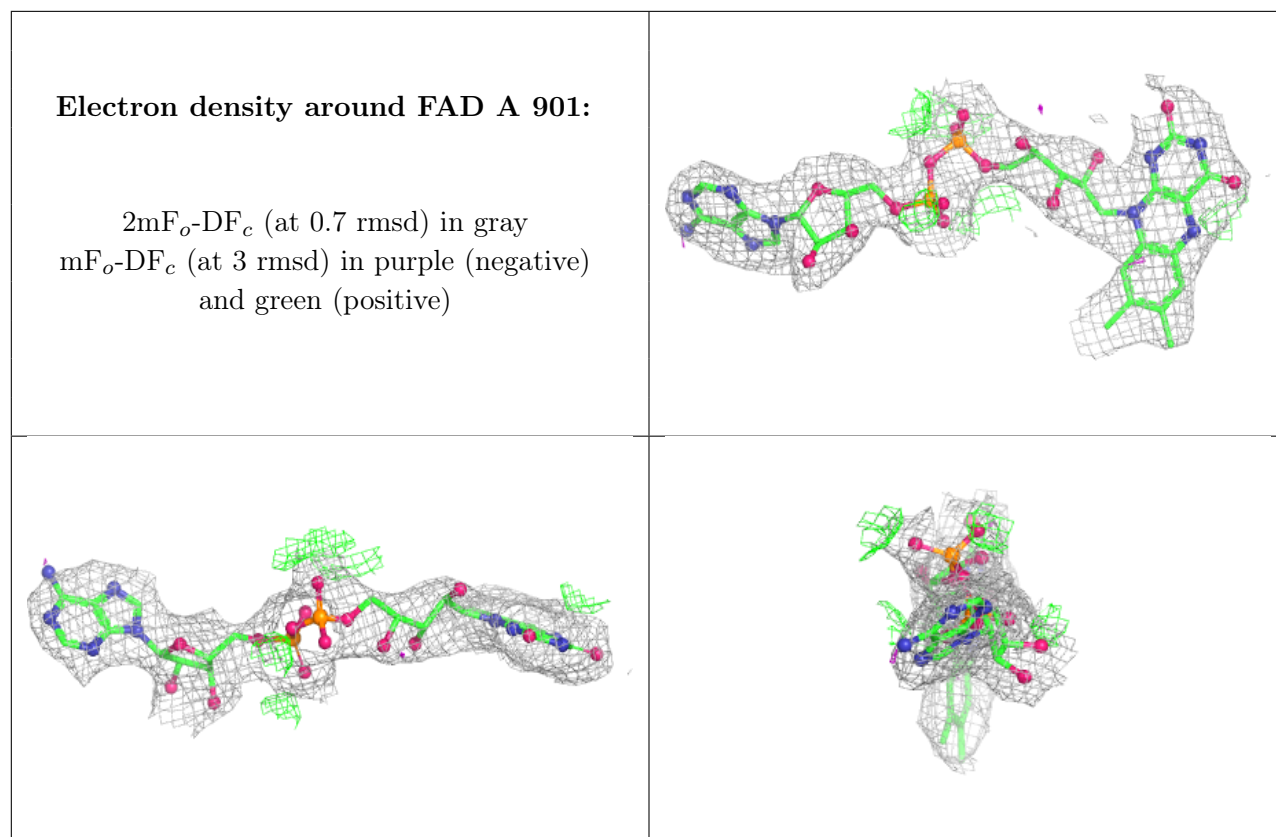
The following is a graphical depiction of the model fit to experimental electron density of all

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 901:

$2mF_o-DF_c$ (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.