



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 26, 2023 – 01:30 PM EDT

PDB ID : 6BZT  
Title : Crystal structure of halogenase PltM L111Y mutant in complex with FAD  
Authors : Pang, A.H.; Garneau-Tsodikova, S.; Tsodikov, O.V.  
Deposited on : 2017-12-26  
Resolution : 2.10 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.

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 : 2.35.1  
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

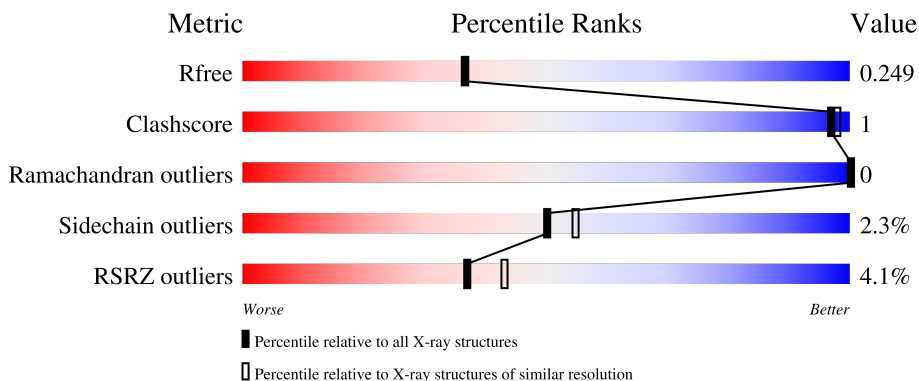
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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  $\geq 3$ , 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	522	 92%
1	B	522	 92%
1	C	522	 92%
1	D	522	 94%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 17070 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 Halogenase PltM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	501	3969	2533	700	725	11	0	1	0
1	B	501	3977	2537	702	727	11	0	2	0
1	C	501	3983	2540	703	729	11	0	3	0
1	D	501	3970	2534	700	725	11	0	1	0

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q4KCZ3
A	-18	GLY	-	expression tag	UNP Q4KCZ3
A	-17	SER	-	expression tag	UNP Q4KCZ3
A	-16	SER	-	expression tag	UNP Q4KCZ3
A	-15	HIS	-	expression tag	UNP Q4KCZ3
A	-14	HIS	-	expression tag	UNP Q4KCZ3
A	-13	HIS	-	expression tag	UNP Q4KCZ3
A	-12	HIS	-	expression tag	UNP Q4KCZ3
A	-11	HIS	-	expression tag	UNP Q4KCZ3
A	-10	HIS	-	expression tag	UNP Q4KCZ3
A	-9	SER	-	expression tag	UNP Q4KCZ3
A	-8	SER	-	expression tag	UNP Q4KCZ3
A	-7	GLY	-	expression tag	UNP Q4KCZ3
A	-6	LEU	-	expression tag	UNP Q4KCZ3
A	-5	VAL	-	expression tag	UNP Q4KCZ3
A	-4	PRO	-	expression tag	UNP Q4KCZ3
A	-3	ARG	-	expression tag	UNP Q4KCZ3
A	-2	GLY	-	expression tag	UNP Q4KCZ3
A	-1	SER	-	expression tag	UNP Q4KCZ3
A	0	HIS	-	expression tag	UNP Q4KCZ3
A	111	TYR	LEU	engineered mutation	UNP Q4KCZ3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	initiating methionine	UNP Q4KCZ3
B	-18	GLY	-	expression tag	UNP Q4KCZ3
B	-17	SER	-	expression tag	UNP Q4KCZ3
B	-16	SER	-	expression tag	UNP Q4KCZ3
B	-15	HIS	-	expression tag	UNP Q4KCZ3
B	-14	HIS	-	expression tag	UNP Q4KCZ3
B	-13	HIS	-	expression tag	UNP Q4KCZ3
B	-12	HIS	-	expression tag	UNP Q4KCZ3
B	-11	HIS	-	expression tag	UNP Q4KCZ3
B	-10	HIS	-	expression tag	UNP Q4KCZ3
B	-9	SER	-	expression tag	UNP Q4KCZ3
B	-8	SER	-	expression tag	UNP Q4KCZ3
B	-7	GLY	-	expression tag	UNP Q4KCZ3
B	-6	LEU	-	expression tag	UNP Q4KCZ3
B	-5	VAL	-	expression tag	UNP Q4KCZ3
B	-4	PRO	-	expression tag	UNP Q4KCZ3
B	-3	ARG	-	expression tag	UNP Q4KCZ3
B	-2	GLY	-	expression tag	UNP Q4KCZ3
B	-1	SER	-	expression tag	UNP Q4KCZ3
B	0	HIS	-	expression tag	UNP Q4KCZ3
B	111	TYR	LEU	engineered mutation	UNP Q4KCZ3
C	-19	MET	-	initiating methionine	UNP Q4KCZ3
C	-18	GLY	-	expression tag	UNP Q4KCZ3
C	-17	SER	-	expression tag	UNP Q4KCZ3
C	-16	SER	-	expression tag	UNP Q4KCZ3
C	-15	HIS	-	expression tag	UNP Q4KCZ3
C	-14	HIS	-	expression tag	UNP Q4KCZ3
C	-13	HIS	-	expression tag	UNP Q4KCZ3
C	-12	HIS	-	expression tag	UNP Q4KCZ3
C	-11	HIS	-	expression tag	UNP Q4KCZ3
C	-10	HIS	-	expression tag	UNP Q4KCZ3
C	-9	SER	-	expression tag	UNP Q4KCZ3
C	-8	SER	-	expression tag	UNP Q4KCZ3
C	-7	GLY	-	expression tag	UNP Q4KCZ3
C	-6	LEU	-	expression tag	UNP Q4KCZ3
C	-5	VAL	-	expression tag	UNP Q4KCZ3
C	-4	PRO	-	expression tag	UNP Q4KCZ3
C	-3	ARG	-	expression tag	UNP Q4KCZ3
C	-2	GLY	-	expression tag	UNP Q4KCZ3
C	-1	SER	-	expression tag	UNP Q4KCZ3
C	0	HIS	-	expression tag	UNP Q4KCZ3
C	111	TYR	LEU	engineered mutation	UNP Q4KCZ3

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

- 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		
3	C	1	Total	Cl	0	0
			1	1		
3	D	2	Total	Cl	0	0
			2	2		

- Molecule 4 is BROMIDE ION (three-letter code: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	Br	0	0
			4	4		
4	B	2	Total	Br	0	0
			2	2		
4	C	2	Total	Br	0	0
			2	2		
4	D	1	Total	Br	0	0
			1	1		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		
5	B	1	Total	Ca	0	0
			1	1		

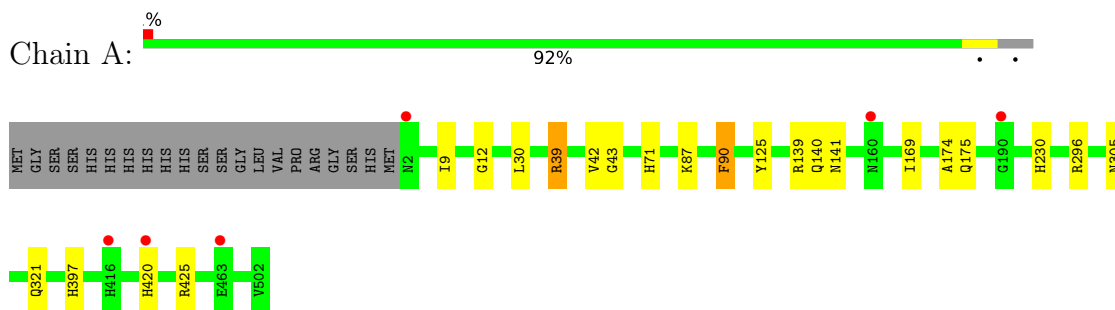
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	293	Total 293	O 293	0	0
6	B	244	Total 244	O 244	0	0
6	C	241	Total 241	O 241	0	0
6	D	165	Total 165	O 165	0	0

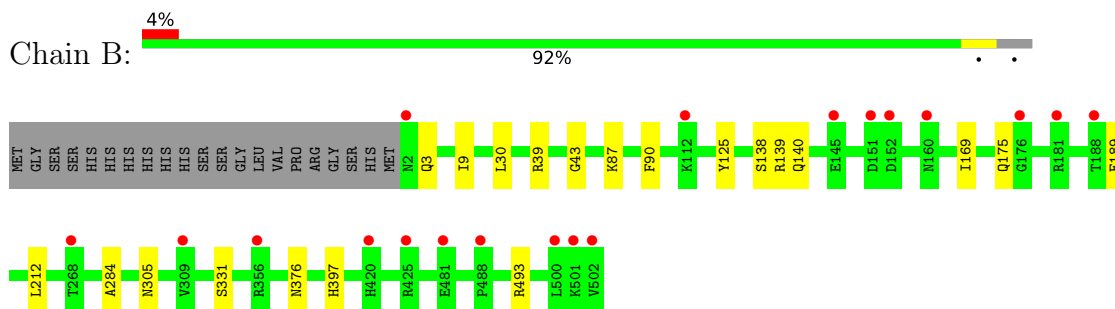
### 3 Residue-property plots [i](#)

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.

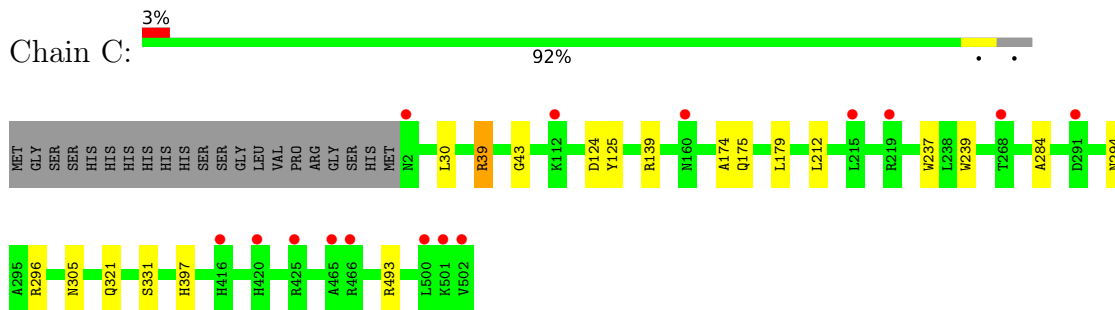
- Molecule 1: Halogenase PltM



- Molecule 1: Halogenase PltM



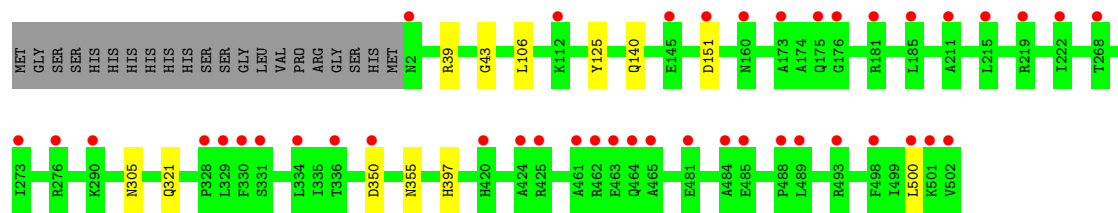
- Molecule 1: Halogenase PltM



- Molecule 1: Halogenase PltM







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.97Å 157.46Å 213.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.00 – 2.10 34.60 – 2.10	Depositor EDS
% Data completeness (in resolution range)	94.7 (35.00-2.10) 94.7 (34.60-2.10)	Depositor EDS
$R_{merge}$	0.20	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.52 (at 2.10Å)	Xtrriage
Refinement program	REFMAC 5.8.0107	Depositor
R, $R_{free}$	0.207 , 0.244 0.213 , 0.249	Depositor DCC
$R_{free}$ test set	5971 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.2	Xtrriage
Anisotropy	0.210	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 36.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	17070	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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: CL, FAD, BR, CA

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	0.37	0/4070	0.61	0/5527
1	B	0.37	0/4078	0.62	0/5538
1	C	0.36	0/4084	0.62	0/5546
1	D	0.37	0/4071	0.61	0/5528
All	All	0.37	0/16303	0.62	0/22139

There are no bond length outliers.

There are no bond angle outliers.

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	3969	0	3906	9	0
1	B	3977	0	3911	9	0
1	C	3983	0	3915	8	0
1	D	3970	0	3908	2	0
2	A	53	0	31	2	0
2	B	53	0	31	2	0
2	C	53	0	31	3	0
2	D	53	0	31	2	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	2	0	0	0	0
4	A	4	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	293	0	0	1	0
6	B	244	0	0	2	0
6	C	241	0	0	0	0
6	D	165	0	0	0	0
All	All	17070	0	15764	28	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 1.

All (28) 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:331:SER:OG	2:B:601:FAD:N3	2.37	0.57
1:B:493:ARG:NE	1:B:493:ARG:HA	2.20	0.56
1:B:376[B]:ASN:ND2	6:B:701:HOH:O	2.39	0.55
1:C:39:ARG:NH2	1:C:124:ASP:OD2	2.40	0.54
1:D:43:GLY:HA2	2:D:601:FAD:C4X	2.38	0.53
1:C:43:GLY:HA2	2:C:601:FAD:C4X	2.39	0.53
1:A:12:GLY:HA2	1:A:39:ARG:NH2	2.25	0.52
1:B:43:GLY:HA2	2:B:601:FAD:C4X	2.41	0.51
1:B:138:SER:HB3	6:B:804:HOH:O	2.12	0.50
1:C:30:LEU:HD11	1:C:139:ARG:HD3	1.93	0.50
1:A:174:ALA:HA	1:A:321:GLN:HB3	1.94	0.49
1:A:43:GLY:HA2	2:A:601:FAD:C4X	2.45	0.47
1:A:90:PHE:CD1	1:A:230:HIS:HE1	2.32	0.47
1:B:87:LYS:NZ	1:B:90:PHE:CE1	2.83	0.46
1:C:174:ALA:HA	1:C:321:GLN:HB3	1.97	0.46
1:D:321:GLN:HG3	2:D:601:FAD:H5'1	1.99	0.45
1:C:321:GLN:CG	2:C:601:FAD:H3'	2.47	0.44
1:B:9:ILE:HD11	1:B:169:ILE:HD11	2.00	0.43
1:C:237:TRP:CZ3	1:C:239:TRP:HB3	2.55	0.42
1:C:331[A]:SER:OG	2:C:601:FAD:N3	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:LEU:HD11	1:A:139:ARG:HD3	2.01	0.41
1:B:30:LEU:HD11	1:B:139:ARG:HD3	2.02	0.41
1:A:87:LYS:NZ	1:A:90:PHE:CE1	2.89	0.41
1:C:212:LEU:HD21	1:C:284:ALA:O	2.20	0.41
1:A:71:HIS:HE1	6:A:964:HOH:O	2.03	0.41
1:B:212:LEU:HD21	1:B:284:ALA:O	2.21	0.41
1:A:321:GLN:HG3	2:A:601:FAD:H5'1	2.04	0.40
1:A:9:ILE:HD11	1:A:169:ILE:HD11	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	500/522 (96%)	490 (98%)	10 (2%)	0	100	100
1	B	501/522 (96%)	491 (98%)	10 (2%)	0	100	100
1	C	502/522 (96%)	492 (98%)	10 (2%)	0	100	100
1	D	500/522 (96%)	489 (98%)	11 (2%)	0	100	100
All	All	2003/2088 (96%)	1962 (98%)	41 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	423/440 (96%)	411 (97%)	12 (3%)	43	47
1	B	424/440 (96%)	416 (98%)	8 (2%)	57	63
1	C	425/440 (97%)	416 (98%)	9 (2%)	53	59
1	D	423/440 (96%)	413 (98%)	10 (2%)	49	53
All	All	1695/1760 (96%)	1656 (98%)	39 (2%)	50	55

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	ARG
1	A	42	VAL
1	A	90	PHE
1	A	125	TYR
1	A	140	GLN
1	A	141	ASN
1	A	175	GLN
1	A	296	ARG
1	A	305	ASN
1	A	397	HIS
1	A	420	HIS
1	A	425	ARG
1	B	3	GLN
1	B	39	ARG
1	B	125	TYR
1	B	140	GLN
1	B	175	GLN
1	B	189	GLU
1	B	305	ASN
1	B	397	HIS
1	C	39	ARG
1	C	125	TYR
1	C	175	GLN
1	C	179	LEU
1	C	294	ASN
1	C	296	ARG
1	C	305	ASN
1	C	397	HIS
1	C	493	ARG
1	D	39	ARG
1	D	106	LEU
1	D	125	TYR
1	D	140	GLN

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Mol	Chain	Res	Type
1	D	151	ASP
1	D	305	ASN
1	D	350	ASP
1	D	355	ASN
1	D	397	HIS
1	D	500	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	HIS
1	A	98	ASN
1	A	175	GLN
1	A	321	GLN
1	A	405	ASN
1	B	160	ASN
1	B	246	HIS
1	B	321	GLN
1	B	405	ASN
1	C	230	HIS
1	C	294	ASN
1	C	321	GLN
1	C	405	ASN
1	C	426	GLN
1	D	98	ASN
1	D	321	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

Of 20 ligands modelled in this entry, 16 are monoatomic - leaving 4 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
2	FAD	B	601	-	53,58,58	1.41	7 (13%)	68,89,89	1.42	12 (17%)
2	FAD	D	601	-	53,58,58	1.41	7 (13%)	68,89,89	1.47	13 (19%)
2	FAD	A	601	-	53,58,58	1.42	7 (13%)	68,89,89	1.39	9 (13%)
2	FAD	C	601	-	53,58,58	1.39	7 (13%)	68,89,89	1.42	12 (17%)

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	601	-	-	1/30/50/50	0/6/6/6
2	FAD	D	601	-	-	5/30/50/50	0/6/6/6
2	FAD	A	601	-	-	2/30/50/50	0/6/6/6
2	FAD	C	601	-	-	2/30/50/50	0/6/6/6

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	FAD	C9A-C5X	5.60	1.50	1.41
2	D	601	FAD	C9A-C5X	5.56	1.50	1.41
2	C	601	FAD	C9A-C5X	5.56	1.50	1.41
2	B	601	FAD	C9A-C5X	5.53	1.50	1.41
2	A	601	FAD	C8-C7	3.72	1.50	1.40
2	B	601	FAD	C8-C7	3.67	1.50	1.40
2	D	601	FAD	C8-C7	3.66	1.50	1.40
2	C	601	FAD	C8-C7	3.57	1.49	1.40
2	D	601	FAD	C4X-N5	2.67	1.35	1.30
2	C	601	FAD	C4X-N5	2.66	1.35	1.30
2	D	601	FAD	C5A-C4A	2.62	1.47	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	FAD	C5A-C4A	2.60	1.47	1.40
2	B	601	FAD	C1'-C2'	2.58	1.56	1.52
2	C	601	FAD	C5A-C4A	2.56	1.47	1.40
2	A	601	FAD	C4-N3	-2.48	1.34	1.38
2	A	601	FAD	C4X-N5	2.47	1.35	1.30
2	B	601	FAD	C5A-C4A	2.46	1.47	1.40
2	B	601	FAD	C4-N3	-2.45	1.34	1.38
2	C	601	FAD	C2A-N3A	2.36	1.35	1.32
2	A	601	FAD	C2A-N3A	2.32	1.35	1.32
2	C	601	FAD	C4-N3	-2.31	1.34	1.38
2	D	601	FAD	C4-N3	-2.31	1.34	1.38
2	A	601	FAD	C10-N10	2.28	1.42	1.37
2	D	601	FAD	C2A-N3A	2.27	1.35	1.32
2	B	601	FAD	C2A-N3A	2.24	1.35	1.32
2	D	601	FAD	C10-N10	2.16	1.42	1.37
2	C	601	FAD	C10-N10	2.07	1.41	1.37
2	B	601	FAD	C4X-N5	2.05	1.34	1.30

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	601	FAD	C4-C4X-N5	4.13	124.11	118.23
2	C	601	FAD	C4-C4X-N5	3.89	123.77	118.23
2	D	601	FAD	N3A-C2A-N1A	-3.86	122.65	128.68
2	A	601	FAD	N3A-C2A-N1A	-3.82	122.71	128.68
2	C	601	FAD	N3A-C2A-N1A	-3.73	122.85	128.68
2	B	601	FAD	C4-C4X-N5	3.45	123.14	118.23
2	B	601	FAD	N3A-C2A-N1A	-3.41	123.34	128.68
2	A	601	FAD	C4-C4X-N5	3.40	123.06	118.23
2	D	601	FAD	C4A-C5A-N7A	-3.09	106.17	109.40
2	B	601	FAD	C4X-C10-N10	3.02	120.90	116.48
2	A	601	FAD	C4X-C10-N1	-2.90	118.01	124.73
2	B	601	FAD	C4X-C10-N1	-2.83	118.16	124.73
2	D	601	FAD	C10-N1-C2	2.81	122.53	116.90
2	D	601	FAD	C4X-C10-N1	-2.79	118.25	124.73
2	B	601	FAD	C1'-C2'-C3'	2.73	117.42	109.79
2	A	601	FAD	C4A-C5A-N7A	-2.68	106.61	109.40
2	C	601	FAD	C4A-C5A-N7A	-2.65	106.64	109.40
2	C	601	FAD	P-O3P-PA	-2.65	123.74	132.83
2	C	601	FAD	C4X-C10-N1	-2.62	118.64	124.73
2	A	601	FAD	C10-N1-C2	2.57	122.05	116.90
2	B	601	FAD	P-O3P-PA	-2.49	124.29	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	FAD	C10-N1-C2	2.48	121.87	116.90
2	C	601	FAD	C10-N1-C2	2.46	121.81	116.90
2	B	601	FAD	C1'-N10-C9A	2.45	124.59	120.51
2	D	601	FAD	C4X-C4-N3	2.39	119.25	113.19
2	C	601	FAD	C4X-C10-N10	2.33	119.88	116.48
2	D	601	FAD	C4X-C10-N10	2.29	119.83	116.48
2	A	601	FAD	C4X-C4-N3	2.28	118.97	113.19
2	D	601	FAD	C5X-N5-C4X	2.27	121.85	118.07
2	B	601	FAD	C10-C4X-N5	-2.22	120.15	124.86
2	B	601	FAD	C4A-C5A-N7A	-2.21	107.10	109.40
2	D	601	FAD	P-O3P-PA	-2.21	125.25	132.83
2	C	601	FAD	C4X-C4-N3	2.21	118.80	113.19
2	D	601	FAD	C10-C4X-N5	-2.20	120.18	124.86
2	A	601	FAD	C4X-C10-N10	2.19	119.69	116.48
2	D	601	FAD	C5'-C4'-C3'	-2.19	107.97	112.20
2	C	601	FAD	C10-C4X-N5	-2.13	120.34	124.86
2	B	601	FAD	O2-C2-N1	-2.12	118.32	121.83
2	C	601	FAD	C1'-C2'-C3'	2.09	115.61	109.79
2	C	601	FAD	C5X-N5-C4X	2.08	121.53	118.07
2	D	601	FAD	C1'-N10-C9A	2.06	123.94	120.51
2	C	601	FAD	C2A-N1A-C6A	2.04	122.24	118.75
2	A	601	FAD	C5X-N5-C4X	2.03	121.45	118.07
2	D	601	FAD	C2A-N1A-C6A	2.02	122.22	118.75
2	A	601	FAD	P-O3P-PA	-2.01	125.91	132.83
2	B	601	FAD	O2P-P-O1P	2.01	122.17	112.24

There are no chirality outliers.

All (10) torsion outliers are listed below:

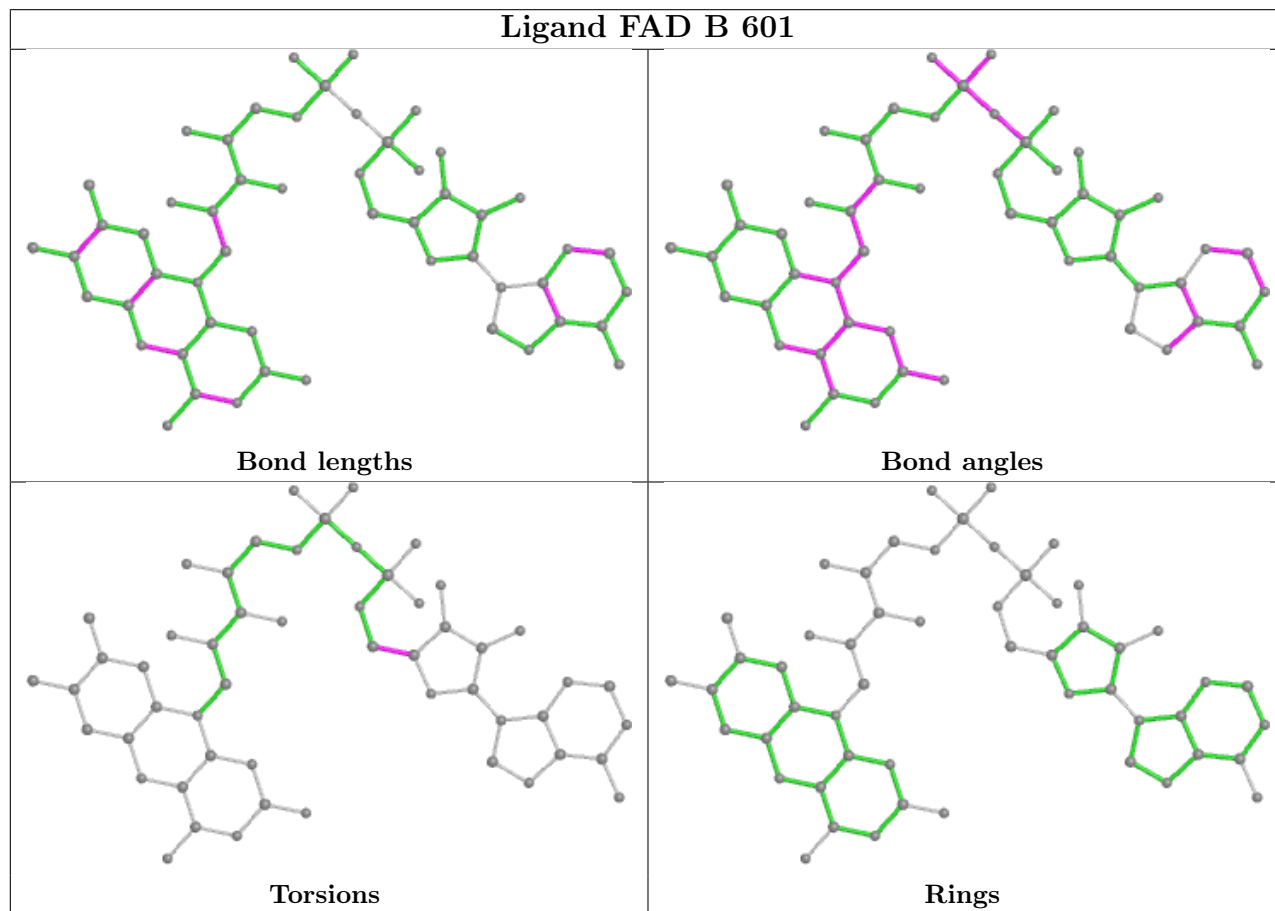
Mol	Chain	Res	Type	Atoms
2	D	601	FAD	C2'-C3'-C4'-C5'
2	D	601	FAD	C2'-C3'-C4'-O4'
2	D	601	FAD	O3'-C3'-C4'-C5'
2	D	601	FAD	O3'-C3'-C4'-O4'
2	A	601	FAD	O4B-C4B-C5B-O5B
2	A	601	FAD	C2'-C3'-C4'-O4'
2	D	601	FAD	O4B-C4B-C5B-O5B
2	C	601	FAD	C2'-C3'-C4'-O4'
2	B	601	FAD	O4B-C4B-C5B-O5B
2	C	601	FAD	O4B-C4B-C5B-O5B

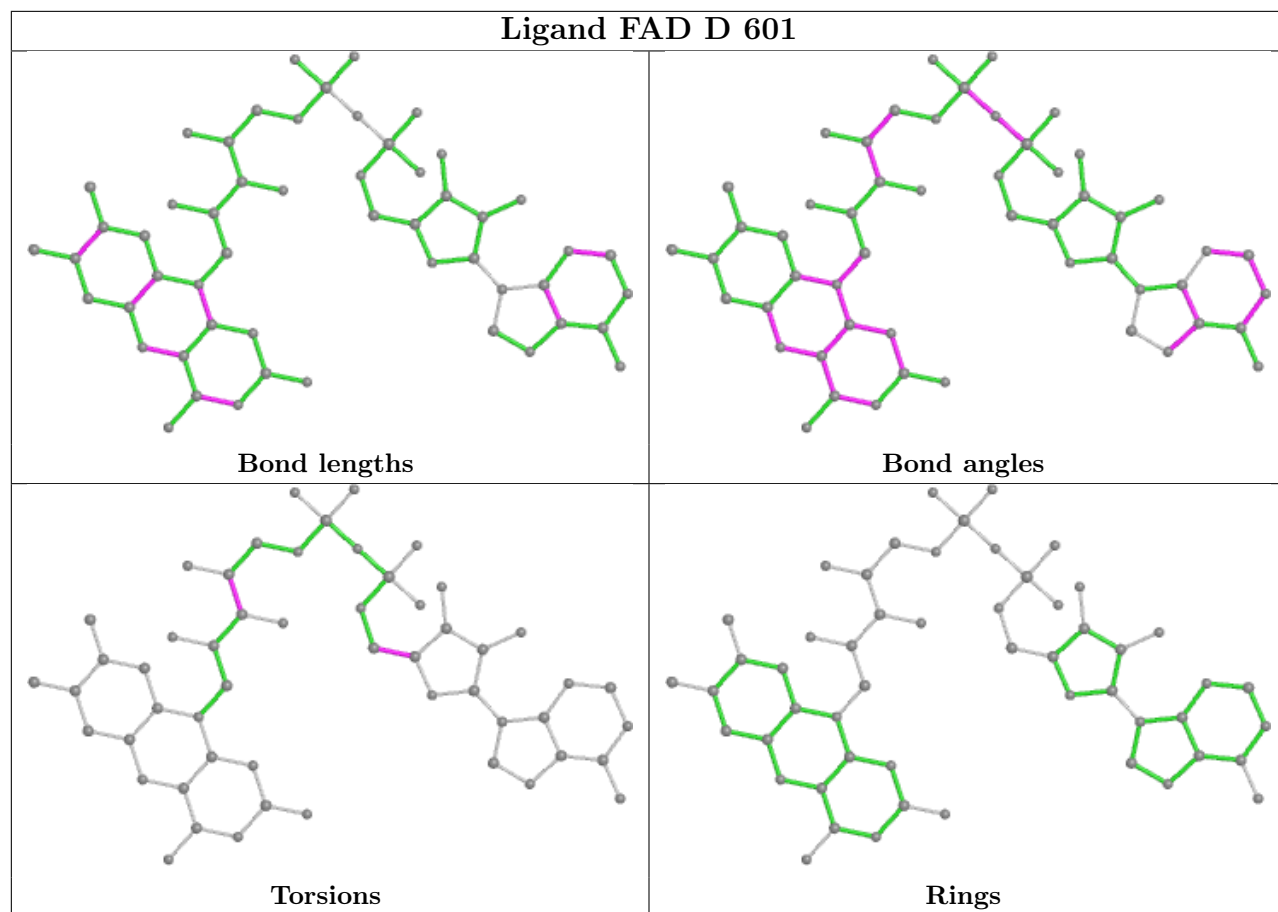
There are no ring outliers.

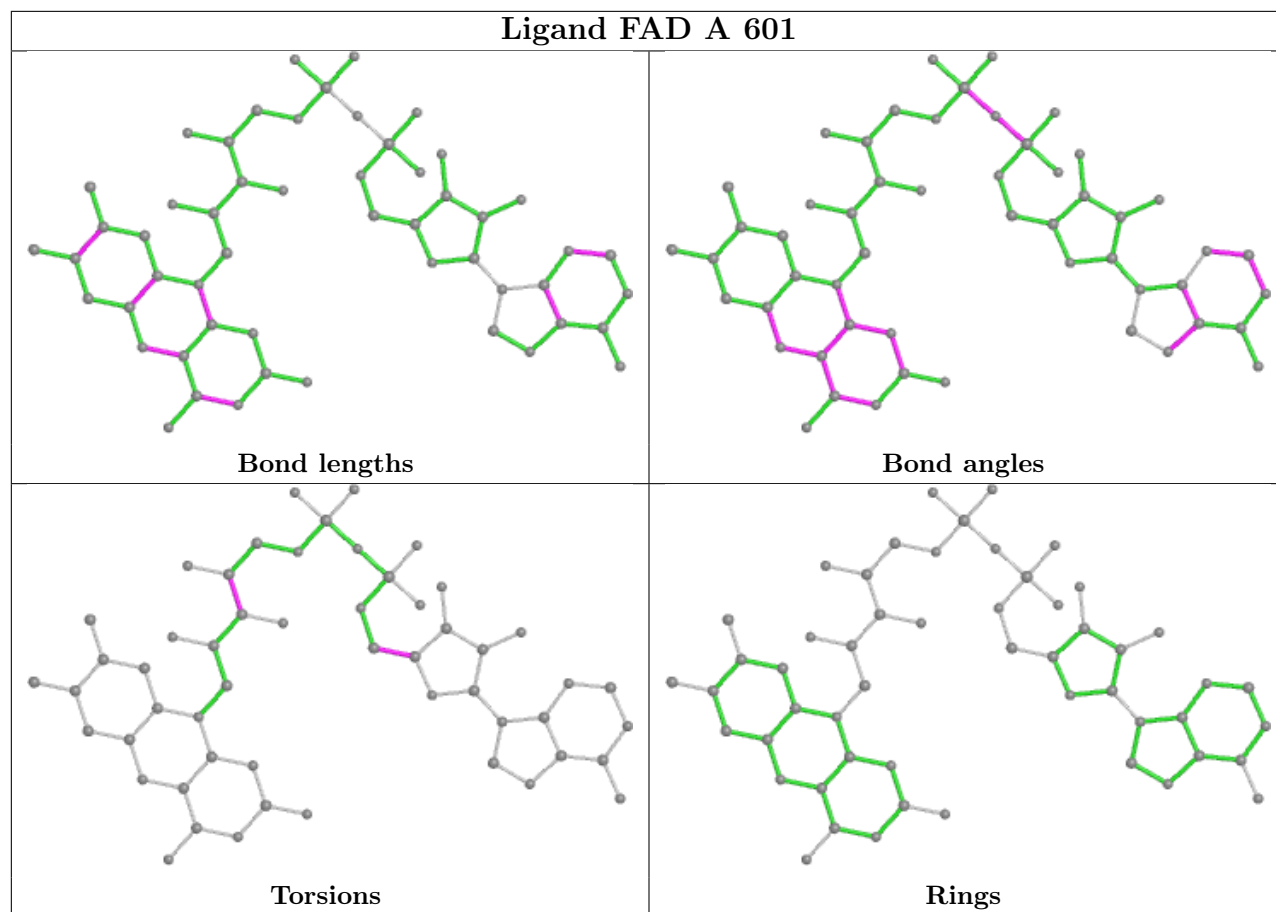
4 monomers are involved in 9 short contacts:

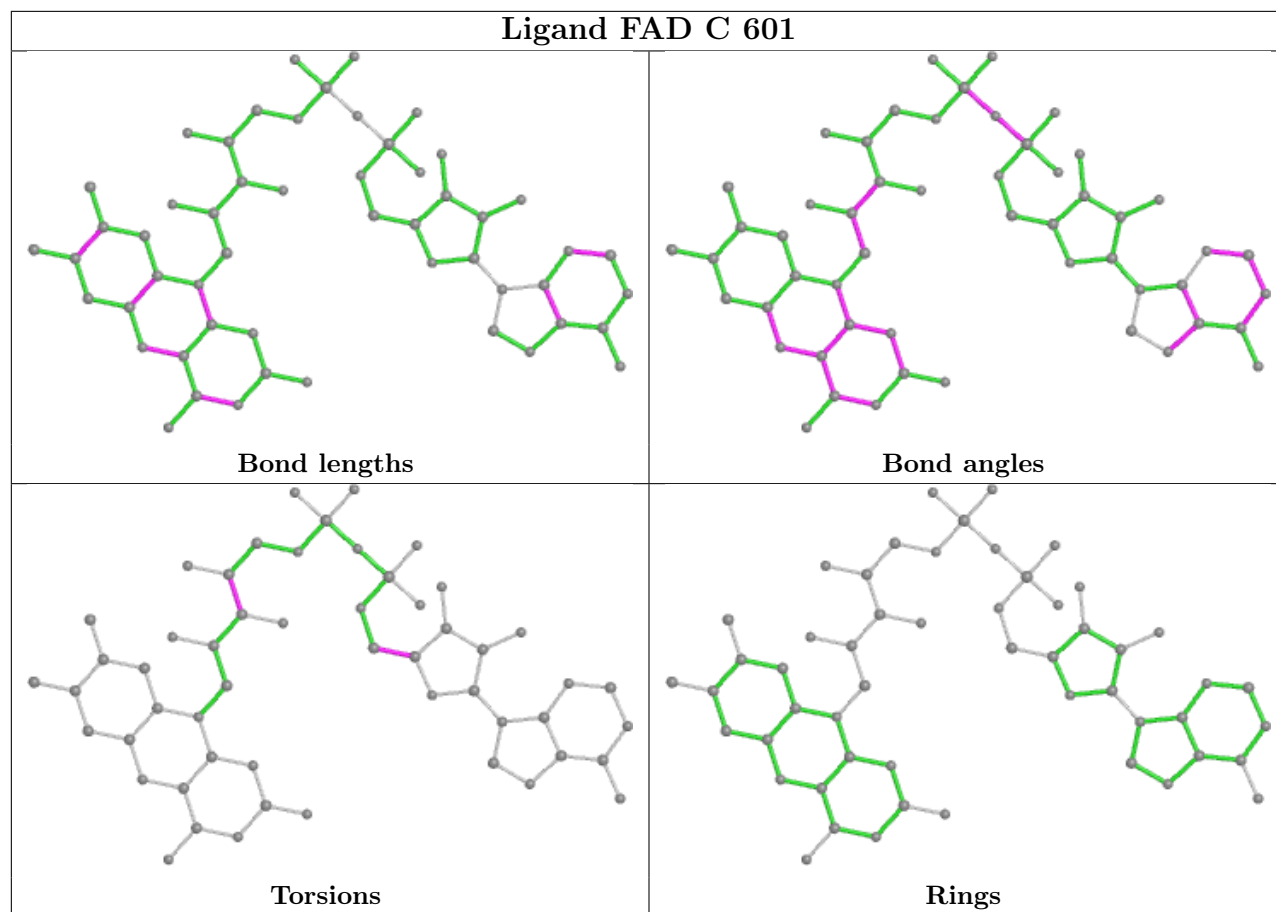
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	FAD	2	0
2	D	601	FAD	2	0
2	A	601	FAD	2	0
2	C	601	FAD	3	0

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

### 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, 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	501/522 (95%)	-0.02	6 (1%) 79 82	12, 20, 32, 44	0
1	B	501/522 (95%)	0.12	19 (3%) 40 46	11, 21, 39, 64	0
1	C	501/522 (95%)	0.12	15 (2%) 50 56	12, 21, 37, 77	0
1	D	501/522 (95%)	0.53	43 (8%) 10 13	16, 29, 52, 89	0
All	All	2004/2088 (95%)	0.19	83 (4%) 37 43	11, 22, 44, 89	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	502	VAL	14.8
1	C	502	VAL	10.4
1	D	112	LYS	5.1
1	D	463	GLU	4.6
1	D	500	LEU	4.3
1	D	2	ASN	4.3
1	A	2	ASN	4.3
1	C	2	ASN	4.3
1	A	160	ASN	3.9
1	D	484	ALA	3.8
1	B	500	LEU	3.8
1	C	465	ALA	3.8
1	D	488	PRO	3.8
1	D	493	ARG	3.8
1	D	173	ALA	3.7
1	D	501	LYS	3.7
1	B	160	ASN	3.7
1	C	160	ASN	3.7
1	C	420	HIS	3.6
1	B	502	VAL	3.6
1	B	420	HIS	3.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	D	151	ASP	3.5
1	D	145	GLU	3.3
1	B	2	ASN	3.3
1	C	466	ARG	3.2
1	D	461	ALA	3.2
1	D	160	ASN	3.1
1	D	211	ALA	3.0
1	D	219	ARG	3.0
1	B	188	THR	3.0
1	C	112	LYS	3.0
1	D	350	ASP	3.0
1	D	425	ARG	2.9
1	D	181	ARG	2.9
1	C	501	LYS	2.9
1	B	425	ARG	2.9
1	A	420	HIS	2.8
1	D	268	THR	2.8
1	D	331	SER	2.8
1	D	465	ALA	2.8
1	D	329	LEU	2.8
1	B	488	PRO	2.7
1	D	276	ARG	2.7
1	B	181	ARG	2.7
1	D	176	GLY	2.6
1	D	185	LEU	2.6
1	B	151	ASP	2.6
1	C	425	ARG	2.6
1	A	190	GLY	2.6
1	D	222	ILE	2.4
1	D	464	GLN	2.4
1	D	420	HIS	2.4
1	B	112	LYS	2.4
1	B	268	THR	2.4
1	C	416	HIS	2.3
1	C	268	THR	2.3
1	C	219	ARG	2.3
1	A	416	HIS	2.3
1	D	328	PRO	2.3
1	C	291	ASP	2.2
1	D	462	ARG	2.2
1	B	501	LYS	2.2
1	D	485	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	463	GLU	2.2
1	D	273	ILE	2.2
1	C	500	LEU	2.2
1	D	215	LEU	2.2
1	D	330	PHE	2.2
1	D	489	LEU	2.2
1	D	481	GLU	2.1
1	D	424	ALA	2.1
1	C	215	LEU	2.1
1	B	481	GLU	2.1
1	B	145	GLU	2.1
1	D	334	LEU	2.1
1	B	309	VAL	2.1
1	D	498	PHE	2.1
1	D	175	GLN	2.1
1	D	290	LYS	2.0
1	B	152	ASP	2.0
1	D	336	THR	2.0
1	B	356	ARG	2.0
1	B	176	GLY	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 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.

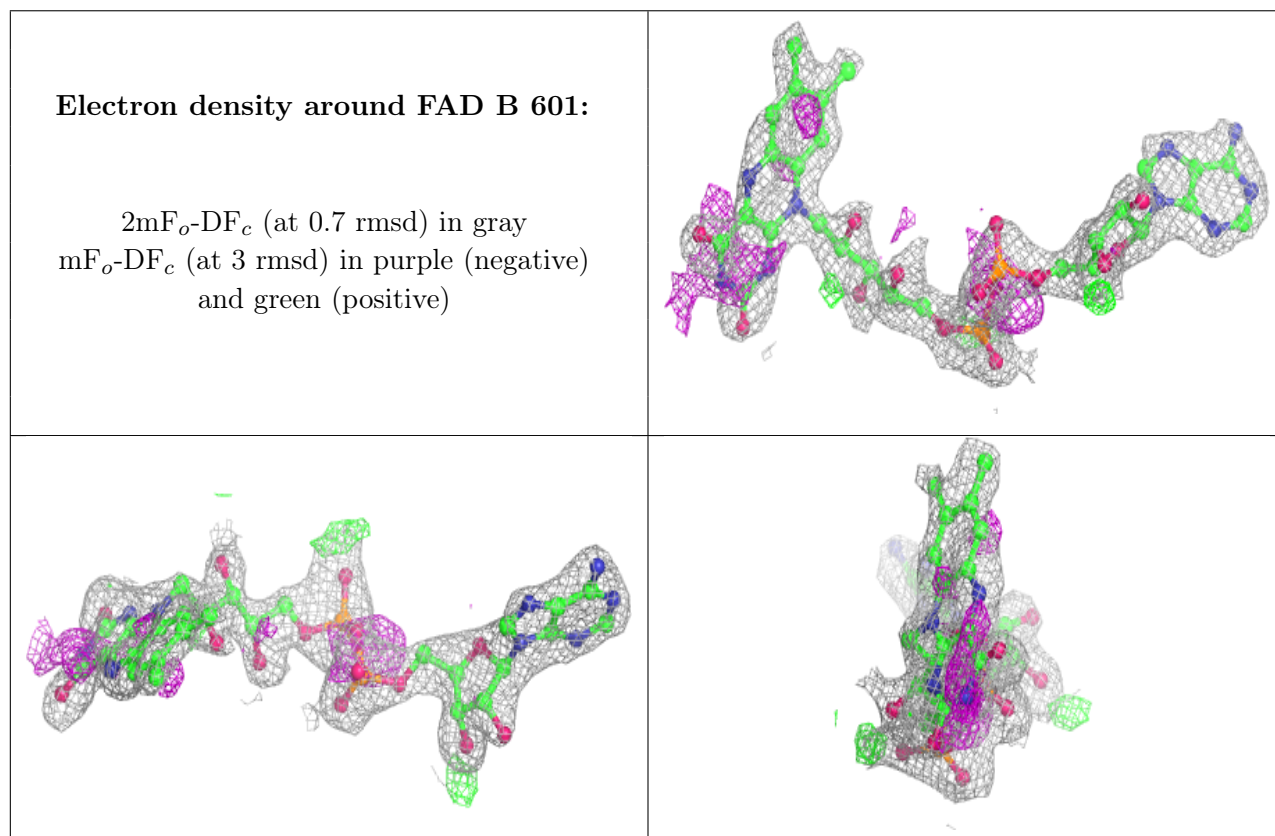
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	CL	C	602	1/1	0.77	0.19	44,44,44,44	0
4	BR	A	605	1/1	0.80	0.08	84,84,84,84	0
5	CA	B	605	1/1	0.80	0.22	37,37,37,37	0

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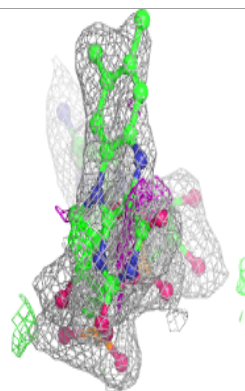
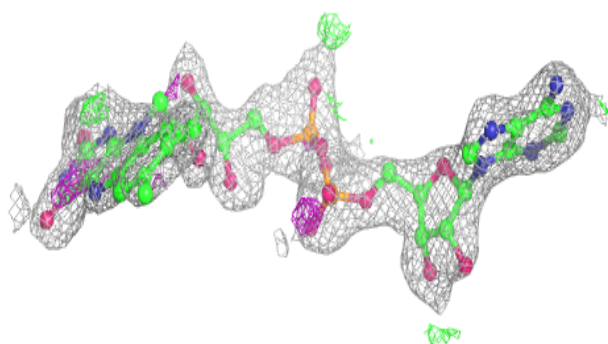
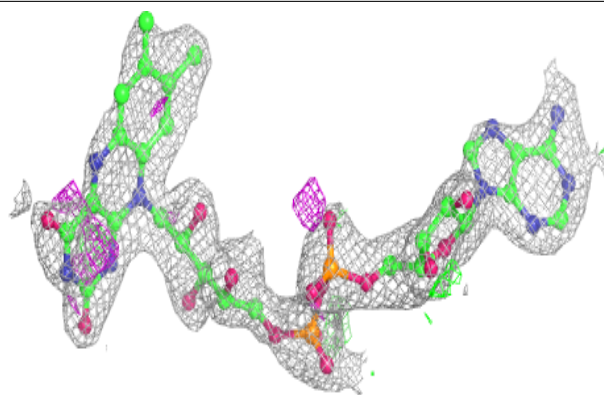
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	BR	B	603	1/1	0.81	0.08	76,76,76,76	0
2	FAD	B	601	53/53	0.82	0.19	37,41,44,44	0
2	FAD	D	601	53/53	0.84	0.17	36,39,42,42	0
5	CA	A	607	1/1	0.86	0.34	37,37,37,37	0
4	BR	B	604	1/1	0.86	0.15	78,78,78,78	0
2	FAD	C	601	53/53	0.88	0.14	27,29,30,30	0
3	CL	D	602	1/1	0.89	0.15	50,50,50,50	0
2	FAD	A	601	53/53	0.90	0.14	27,28,29,29	0
4	BR	D	604	1/1	0.92	0.17	78,78,78,78	0
4	BR	A	606	1/1	0.94	0.22	39,39,39,39	0
3	CL	A	602	1/1	0.94	0.35	58,58,58,58	0
3	CL	D	603	1/1	0.95	0.13	49,49,49,49	0
3	CL	B	602	1/1	0.95	0.34	48,48,48,48	0
4	BR	C	603	1/1	0.96	0.40	41,41,41,41	0
4	BR	C	604	1/1	0.97	0.28	37,37,37,37	0
4	BR	A	604	1/1	0.98	0.17	69,69,69,69	0
4	BR	A	603	1/1	0.99	0.04	30,30,30,30	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.

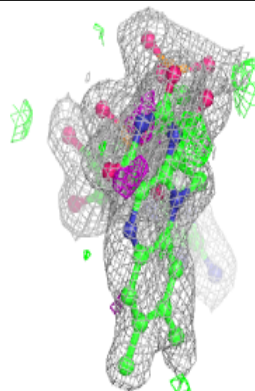
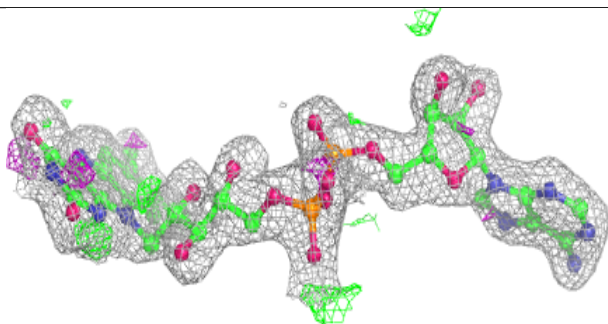
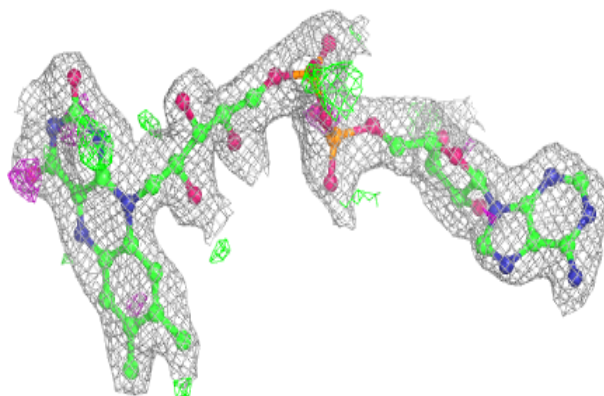


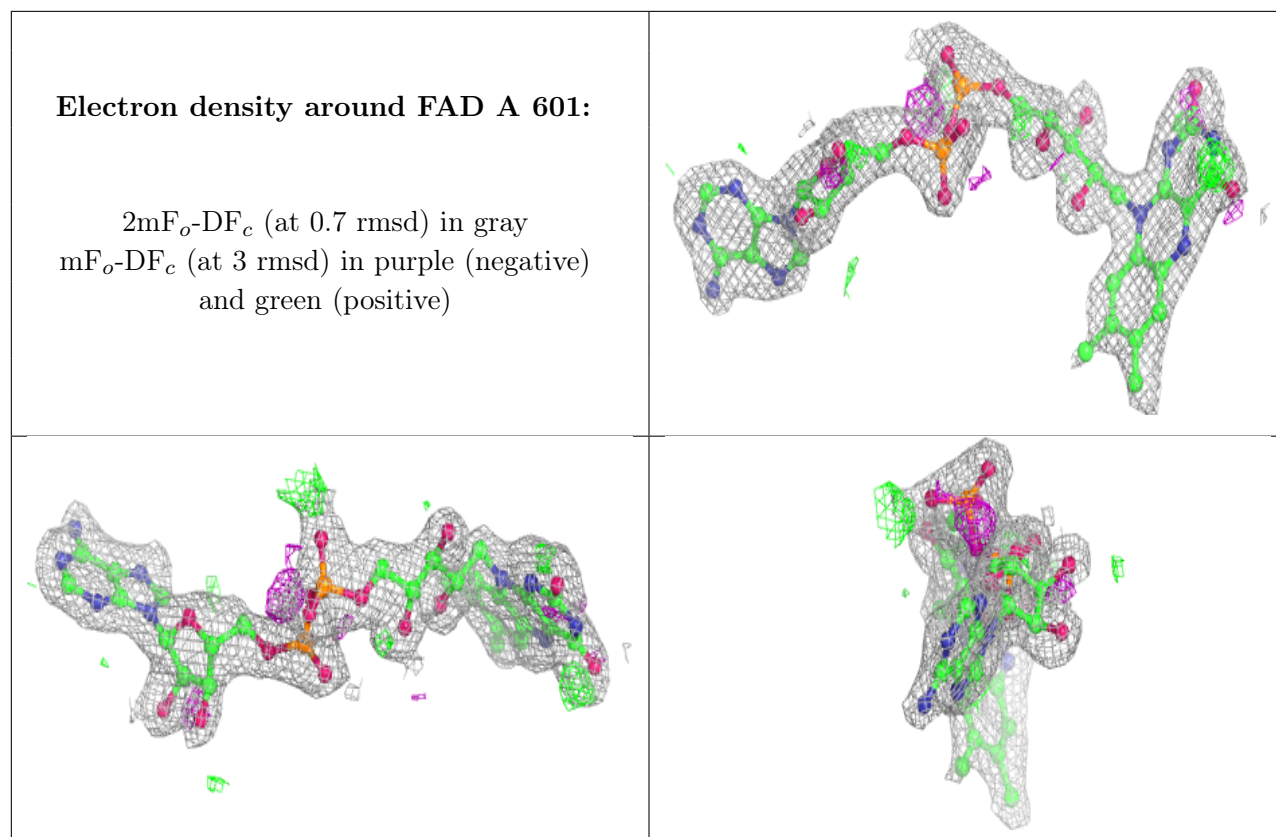
**Electron density around FAD D 601:**

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

**Electron density around FAD C 601:**

$2mF_o-DF_c$  (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.