



# Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 09:20 pm BST

PDB ID : 4NMA  
Title : Crystal structure of proline utilization A (PutA) from *Geobacter sulfurreducens* PCA in complex with L-tetrahydro-2-furoic acid  
Authors : Singh, H.; Tanner, J.J.  
Deposited on : 2013-11-14  
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.

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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

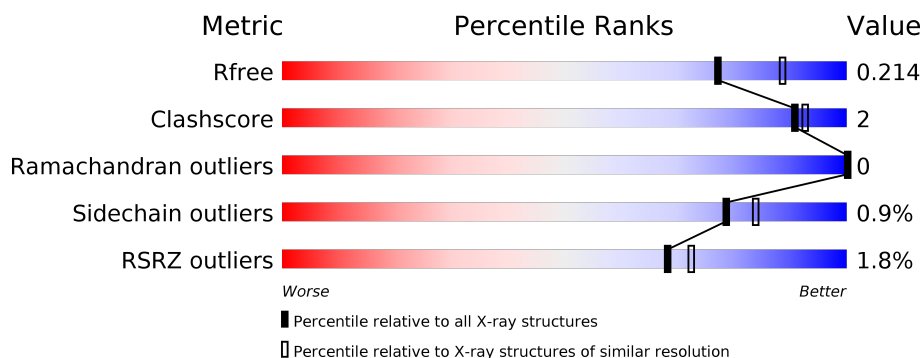
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 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 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	1005	<div> <div>2%</div> <div> <div></div> <div>92%</div> <div>5%</div> <div></div> </div> <div></div> </div>
1	B	1005	<div> <div>%</div> <div> <div></div> <div>92%</div> <div>5%</div> <div></div> </div> <div></div> </div>

2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 16069 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.

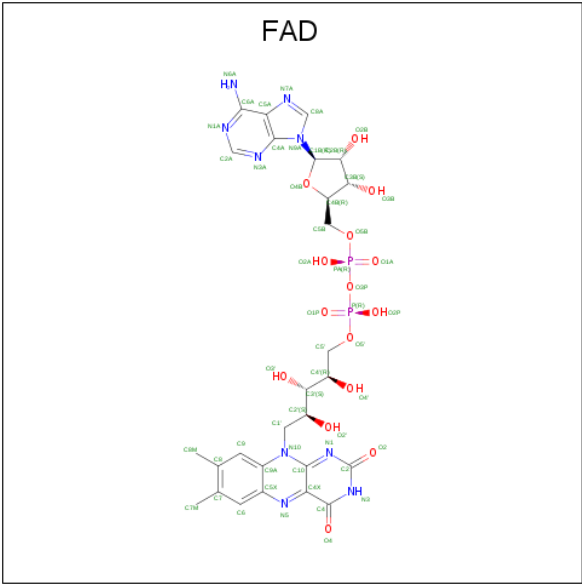
- Molecule 1 is a protein called Proline dehydrogenase and Delta-1-pyrroline-5-carboxylate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	977	Total	C	N	O	S	0	0	0
			7563	4833	1314	1378	38			
1	B	979	Total	C	N	O	S	0	0	0
			7566	4830	1315	1383	38			

There are 2 discrepancies between the modelled and reference sequences:

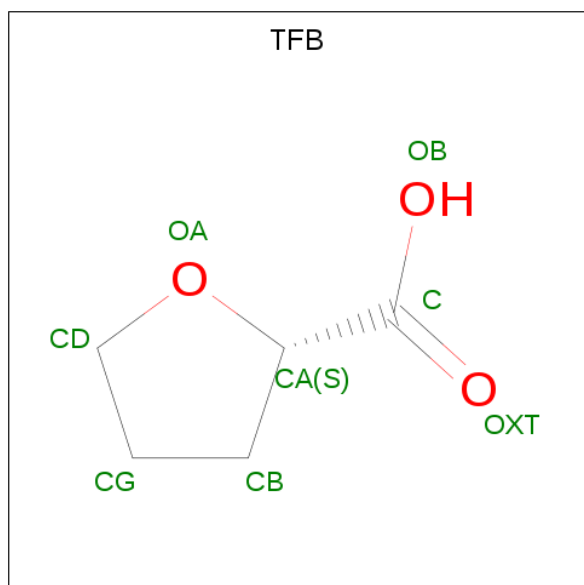
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP Q746X3
B	0	SER	-	EXPRESSION TAG	UNP Q746X3

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C<sub>27</sub>H<sub>33</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
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		

- Molecule 3 is TETRAHYDROFURAN-2-CARBOXYLIC ACID (three-letter code: TFB) (formula: C<sub>5</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	5	3		
3	B	1	Total	C	O	0	0
			8	5	3		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

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

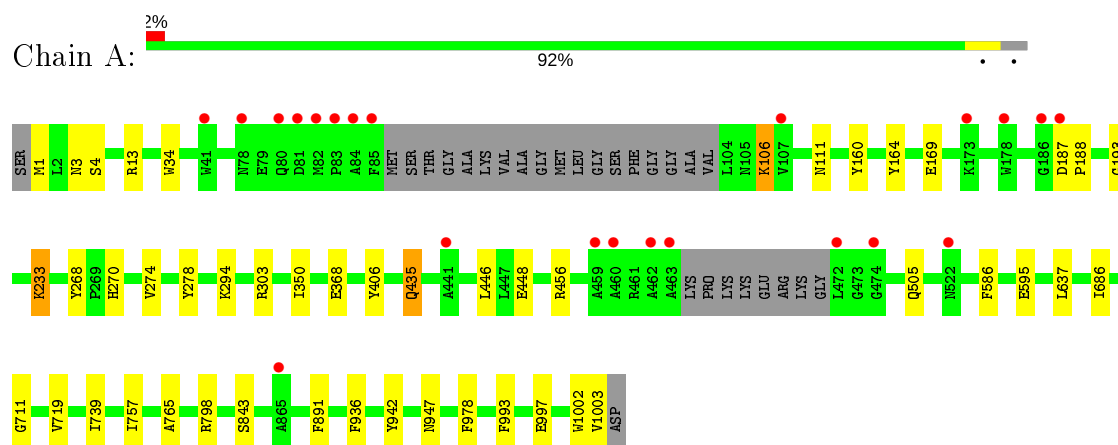
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	377	Total 377	O 377	0	0
5	B	361	Total 361	O 361	0	0

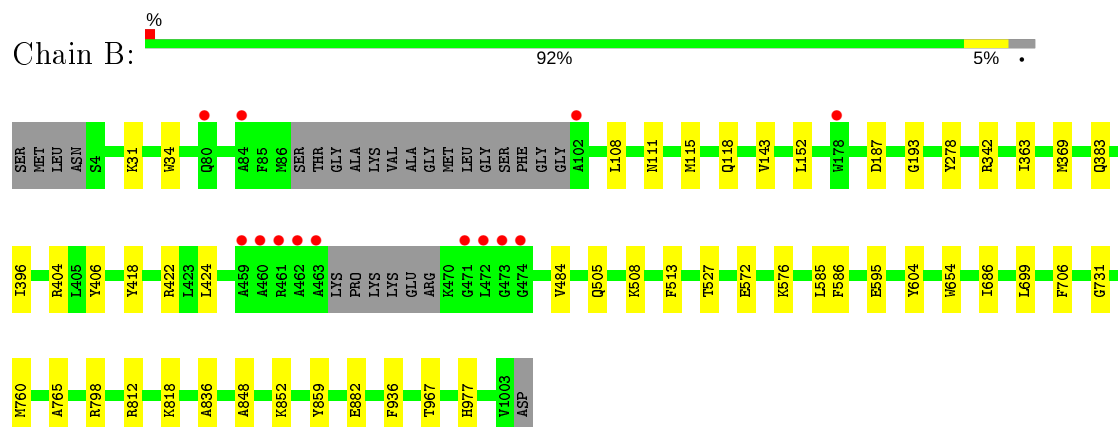
### 3 Residue-property plots [i](#)

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: Proline dehydrogenase and Delta-1-pyrroline-5-carboxylate dehydrogenase



- Molecule 1: Proline dehydrogenase and Delta-1-pyrroline-5-carboxylate dehydrogenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.62Å 151.74Å 176.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.14 – 2.10 47.53 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.1 (46.14-2.10) 98.1 (47.53-2.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.03 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.8_1069	Depositor
R, $R_{free}$	0.173 , 0.213 0.173 , 0.214	Depositor DCC
$R_{free}$ test set	7343 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.4	Xtriage
Anisotropy	0.501	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 50.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	16069	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.23% 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: EDO, FAD, TFB

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	0.38	0/7734	0.51	0/10483
1	B	0.37	0/7737	0.50	0/10489
All	All	0.37	0/15471	0.51	0/20972

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

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	7563	0	7417	26	0
1	B	7566	0	7401	26	0
2	A	53	0	31	2	0
2	B	53	0	31	1	0
3	A	8	0	7	0	0
3	B	8	0	7	0	0
4	A	44	0	66	3	0
4	B	36	0	54	3	0
5	A	377	0	0	0	0
5	B	361	0	0	0	0
All	All	16069	0	15014	52	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 (52) 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:586:PHE:HB2	4:A:2010:EDO:H22	1.71	0.71
1:A:448:GLU:OE2	1:A:456:ARG:NH1	2.26	0.67
1:B:586:PHE:HB2	4:B:2011:EDO:H12	1.76	0.67
1:A:1:MET:HE2	1:A:3:ASN:HB2	1.79	0.63
1:A:637:LEU:HD21	1:A:997:GLU:HG3	1.80	0.62
1:B:383:GLN:HG2	1:B:404:ARG:HB3	1.89	0.54
1:A:169:GLU:OE1	1:A:233:LYS:NZ	2.43	0.52
1:A:268:TYR:CE2	1:A:270:HIS:HB2	2.46	0.51
1:A:406:TYR:HB2	2:A:2001:FAD:HM72	1.95	0.48
1:B:406:TYR:HB2	2:B:2001:FAD:HM72	1.93	0.48
1:B:505:GLN:OE1	1:B:508:LYS:NZ	2.42	0.48
1:B:699:LEU:O	4:B:2010:EDO:H21	2.14	0.48
1:A:435:GLN:HB3	1:A:446:LEU:HD21	1.95	0.47
1:B:765:ALA:HA	1:B:798:ARG:O	2.14	0.47
1:A:719:VAL:HG21	1:A:739:ILE:HG12	1.95	0.47
1:B:115:MET:O	1:B:118:GLN:HB3	2.15	0.47
1:A:1:MET:HB3	1:A:4:SER:H	1.79	0.46
1:A:711:GLY:H	4:A:2011:EDO:H11	1.80	0.46
1:A:13:ARG:NE	1:A:368:GLU:OE2	2.36	0.46
1:A:765:ALA:HA	1:A:798:ARG:O	2.16	0.46
1:B:699:LEU:HD23	4:B:2010:EDO:H11	1.97	0.46
1:B:152:LEU:HD12	1:B:812:ARG:CZ	2.46	0.45
1:B:967:THR:HG22	1:B:977:HIS:CE1	2.52	0.44
1:A:1002:TRP:CG	1:A:1003:VAL:N	2.86	0.44
1:A:595:GLU:OE1	1:A:686:ILE:HG12	2.18	0.44
1:A:294:LYS:HE3	1:A:350:ILE:HD13	2.00	0.44
1:B:143:VAL:HG13	1:B:406:TYR:HA	2.00	0.44
1:B:418:TYR:O	1:B:422:ARG:HG2	2.17	0.44
1:B:595:GLU:OE1	1:B:686:ILE:HG12	2.18	0.44
1:B:187:ASP:O	1:B:193:GLY:HA2	2.18	0.43
1:B:818:LYS:HG2	1:B:859:TYR:CE1	2.53	0.43
1:B:654:TRP:CZ3	1:B:836:ALA:HB2	2.54	0.43
1:A:757:ILE:HD13	1:A:978:PHE:CZ	2.54	0.42
1:B:731:GLY:O	1:B:760:MET:HA	2.19	0.42
1:B:363:ILE:HD13	1:B:396:ILE:HD11	2.02	0.42
1:A:187:ASP:O	1:A:193:GLY:HA2	2.20	0.42
1:A:34:TRP:CE3	1:A:111:ASN:HB3	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:LYS:HE3	1:A:106:LYS:HB3	1.94	0.42
1:A:187:ASP:HA	1:A:188:PRO:HD2	1.95	0.42
1:A:993:PHE:HB3	1:B:424:LEU:HD11	2.02	0.42
1:A:274:VAL:HG22	1:A:303:ARG:HB3	2.02	0.41
1:A:942:TYR:CD1	1:A:947:ASN:HA	2.54	0.41
1:A:160:TYR:CZ	1:A:164:TYR:HE2	2.39	0.41
1:B:342:ARG:HB2	1:B:369:MET:SD	2.60	0.41
1:A:711:GLY:H	4:A:2011:EDO:C1	2.34	0.41
1:B:848:ALA:O	1:B:852:LYS:HG3	2.21	0.41
1:B:484:VAL:HB	1:B:604:TYR:CG	2.55	0.41
2:A:2001:FAD:H9	2:A:2001:FAD:H1'1	1.90	0.40
1:B:572:GLU:HG3	1:B:576:LYS:HE2	2.03	0.40
1:B:34:TRP:CE3	1:B:111:ASN:HB3	2.56	0.40
1:B:108:LEU:HD12	1:B:108:LEU:HA	1.93	0.40
1:B:513:PHE:HB3	1:B:706:PHE:HB3	2.04	0.40

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	971/1005 (97%)	951 (98%)	20 (2%)	0	100	100
1	B	973/1005 (97%)	954 (98%)	19 (2%)	0	100	100
All	All	1944/2010 (97%)	1905 (98%)	39 (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	763/821 (93%)	755 (99%)	8 (1%)	76	82
1	B	763/821 (93%)	757 (99%)	6 (1%)	81	86
All	All	1526/1642 (93%)	1512 (99%)	14 (1%)	78	84

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	LYS
1	A	233	LYS
1	A	278	TYR
1	A	435	GLN
1	A	505	GLN
1	A	843	SER
1	A	891	PHE
1	A	936	PHE
1	B	31	LYS
1	B	278	TYR
1	B	527	THR
1	B	585	LEU
1	B	882	GLU
1	B	936	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

24 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
4	EDO	A	2007	-	3,3,3	0.57	0	2,2,2	0.38	0
4	EDO	A	2010	-	3,3,3	0.60	0	2,2,2	0.29	0
4	EDO	B	2010	-	3,3,3	0.55	0	2,2,2	0.39	0
4	EDO	A	2006	-	3,3,3	0.57	0	2,2,2	0.39	0
2	FAD	A	2001	-	51,58,58	2.19	19 (37%)	60,89,89	1.63	11 (18%)
4	EDO	A	2009	-	3,3,3	0.68	0	2,2,2	0.49	0
4	EDO	A	2012	-	3,3,3	0.51	0	2,2,2	0.18	0
4	EDO	A	2004	-	3,3,3	0.63	0	2,2,2	0.44	0
4	EDO	B	2007	-	3,3,3	0.53	0	2,2,2	0.27	0
2	FAD	B	2001	-	51,58,58	2.26	20 (39%)	60,89,89	1.70	10 (16%)
4	EDO	B	2011	-	3,3,3	0.52	0	2,2,2	0.11	0
4	EDO	B	2005	-	3,3,3	0.58	0	2,2,2	0.36	0
4	EDO	A	2008	-	3,3,3	0.57	0	2,2,2	0.14	0
4	EDO	A	2003	-	3,3,3	0.51	0	2,2,2	0.26	0
4	EDO	A	2013	-	3,3,3	0.57	0	2,2,2	0.25	0
3	TFB	B	2002	-	5,8,8	2.22	1 (20%)	2,10,10	0.35	0
4	EDO	B	2009	-	3,3,3	0.54	0	2,2,2	0.36	0
4	EDO	B	2004	-	3,3,3	0.52	0	2,2,2	0.30	0
4	EDO	A	2005	-	3,3,3	0.54	0	2,2,2	0.25	0
4	EDO	A	2011	-	3,3,3	0.54	0	2,2,2	0.53	0
3	TFB	A	2002	-	5,8,8	2.41	1 (20%)	2,10,10	0.45	0
4	EDO	B	2003	-	3,3,3	0.53	0	2,2,2	0.40	0
4	EDO	B	2006	-	3,3,3	0.58	0	2,2,2	0.42	0
4	EDO	B	2008	-	3,3,3	0.54	0	2,2,2	0.33	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	2007	-	-	0/1/1/1	-
4	EDO	A	2010	-	-	1/1/1/1	-
4	EDO	B	2010	-	-	0/1/1/1	-
4	EDO	A	2006	-	-	0/1/1/1	-
2	FAD	A	2001	-	-	7/30/50/50	0/6/6/6
4	EDO	A	2009	-	-	1/1/1/1	-
4	EDO	A	2012	-	-	1/1/1/1	-
4	EDO	A	2004	-	-	1/1/1/1	-
4	EDO	B	2007	-	-	1/1/1/1	-
2	FAD	B	2001	-	-	8/30/50/50	0/6/6/6
4	EDO	B	2011	-	-	1/1/1/1	-
4	EDO	B	2005	-	-	1/1/1/1	-
4	EDO	A	2008	-	-	0/1/1/1	-
4	EDO	A	2003	-	-	0/1/1/1	-
4	EDO	A	2013	-	-	0/1/1/1	-
3	TFB	B	2002	-	-	0/0/11/11	0/1/1/1
4	EDO	B	2009	-	-	0/1/1/1	-
4	EDO	B	2004	-	-	1/1/1/1	-
4	EDO	A	2005	-	-	0/1/1/1	-
4	EDO	A	2011	-	-	0/1/1/1	-
3	TFB	A	2002	-	-	0/0/11/11	0/1/1/1
4	EDO	B	2003	-	-	1/1/1/1	-
4	EDO	B	2006	-	-	1/1/1/1	-
4	EDO	B	2008	-	-	0/1/1/1	-

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2001	FAD	O4-C4	5.55	1.38	1.24
2	B	2001	FAD	C4X-C10	5.42	1.44	1.38
2	A	2001	FAD	C4X-C10	5.19	1.44	1.38
2	B	2001	FAD	C4-C4X	5.15	1.50	1.41
2	A	2001	FAD	O4-C4	5.05	1.37	1.24
3	A	2002	TFB	CB-CA	-5.05	1.45	1.53
2	A	2001	FAD	C10-N1	4.75	1.39	1.33
2	B	2001	FAD	C4X-N5	4.74	1.40	1.33
3	B	2002	TFB	CB-CA	-4.55	1.46	1.53
2	B	2001	FAD	C10-N1	4.55	1.39	1.33
2	B	2001	FAD	C9A-N10	4.50	1.44	1.38
2	A	2001	FAD	C9A-N10	4.39	1.44	1.38
2	A	2001	FAD	C4-C4X	4.25	1.48	1.41
2	A	2001	FAD	C4X-N5	4.21	1.39	1.33
2	B	2001	FAD	C2B-C1B	-3.29	1.48	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2001	FAD	C2B-C1B	-3.28	1.48	1.53
2	A	2001	FAD	C4-N3	3.14	1.38	1.33
2	B	2001	FAD	C2-N1	3.13	1.44	1.38
2	B	2001	FAD	C4-N3	3.07	1.38	1.33
2	B	2001	FAD	C6A-N6A	2.98	1.44	1.34
2	A	2001	FAD	C2-N1	2.98	1.44	1.38
2	A	2001	FAD	C6A-N6A	2.93	1.44	1.34
2	A	2001	FAD	C5X-N5	2.72	1.39	1.35
2	B	2001	FAD	C2A-N3A	2.71	1.36	1.32
2	A	2001	FAD	C2A-N3A	2.67	1.36	1.32
2	A	2001	FAD	PA-O5B	-2.60	1.48	1.59
2	A	2001	FAD	O2'-C2'	-2.58	1.37	1.43
2	B	2001	FAD	C5X-N5	2.55	1.39	1.35
2	B	2001	FAD	O2'-C2'	-2.52	1.38	1.43
2	B	2001	FAD	PA-O5B	-2.39	1.49	1.59
2	A	2001	FAD	PA-O2A	-2.28	1.44	1.55
2	B	2001	FAD	O4'-C4'	-2.26	1.38	1.43
2	A	2001	FAD	O4'-C4'	-2.24	1.38	1.43
2	B	2001	FAD	PA-O2A	-2.23	1.44	1.55
2	B	2001	FAD	O2B-C2B	-2.22	1.37	1.43
2	B	2001	FAD	O3'-C3'	-2.22	1.37	1.43
2	A	2001	FAD	O2B-C2B	-2.20	1.37	1.43
2	B	2001	FAD	P-O1P	2.13	1.58	1.50
2	A	2001	FAD	O3'-C3'	-2.08	1.38	1.43
2	B	2001	FAD	O4B-C4B	-2.08	1.40	1.45
2	A	2001	FAD	O3B-C3B	-2.05	1.38	1.43

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2001	FAD	C4-N3-C2	6.04	120.24	115.14
2	A	2001	FAD	C4-N3-C2	5.93	120.15	115.14
2	B	2001	FAD	N3A-C2A-N1A	-5.25	120.47	128.68
2	A	2001	FAD	N3A-C2A-N1A	-5.19	120.56	128.68
2	B	2001	FAD	C4X-N5-C5X	4.00	120.77	116.77
2	A	2001	FAD	C4-C4X-C10	-3.67	117.52	119.95
2	B	2001	FAD	C4-C4X-C10	-3.25	117.80	119.95
2	A	2001	FAD	C4X-N5-C5X	3.09	119.86	116.77
2	B	2001	FAD	C4-C4X-N5	2.93	121.95	118.60
2	A	2001	FAD	C5X-C9A-N10	2.68	119.66	117.72
2	B	2001	FAD	C5X-C9A-N10	2.68	119.66	117.72
2	A	2001	FAD	O2P-P-O5'	-2.53	96.02	107.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2001	FAD	C1'-N10-C9A	2.51	120.27	118.29
2	B	2001	FAD	O5'-P-O1P	2.38	118.36	109.07
2	A	2001	FAD	C4-C4X-N5	2.37	121.31	118.60
2	B	2001	FAD	C1'-N10-C9A	2.28	120.09	118.29
2	B	2001	FAD	C4X-C4-N3	-2.27	120.33	123.43
2	A	2001	FAD	O5'-P-O1P	2.22	117.73	109.07
2	A	2001	FAD	O5B-PA-O1A	2.22	117.73	109.07
2	B	2001	FAD	C4A-C5A-N7A	-2.13	107.18	109.40
2	A	2001	FAD	C4X-C4-N3	-2.12	120.54	123.43

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2001	FAD	P-O3P-PA-O5B
2	A	2001	FAD	N10-C1'-C2'-O2'
2	A	2001	FAD	N10-C1'-C2'-C3'
2	A	2001	FAD	C1'-C2'-C3'-C4'
2	B	2001	FAD	N10-C1'-C2'-O2'
2	B	2001	FAD	N10-C1'-C2'-C3'
2	B	2001	FAD	C5'-O5'-P-O2P
2	B	2001	FAD	C3B-C4B-C5B-O5B
4	A	2010	EDO	O1-C1-C2-O2
4	B	2011	EDO	O1-C1-C2-O2
4	B	2004	EDO	O1-C1-C2-O2
2	B	2001	FAD	P-O3P-PA-O5B
2	B	2001	FAD	C5B-O5B-PA-O3P
2	B	2001	FAD	C5'-O5'-P-O1P
2	A	2001	FAD	C3B-C4B-C5B-O5B
2	B	2001	FAD	O4B-C4B-C5B-O5B
4	A	2012	EDO	O1-C1-C2-O2
2	A	2001	FAD	O2'-C2'-C3'-O3'
2	A	2001	FAD	O2'-C2'-C3'-C4'
4	A	2009	EDO	O1-C1-C2-O2
4	A	2004	EDO	O1-C1-C2-O2
4	B	2007	EDO	O1-C1-C2-O2
4	B	2005	EDO	O1-C1-C2-O2
4	B	2003	EDO	O1-C1-C2-O2
4	B	2006	EDO	O1-C1-C2-O2

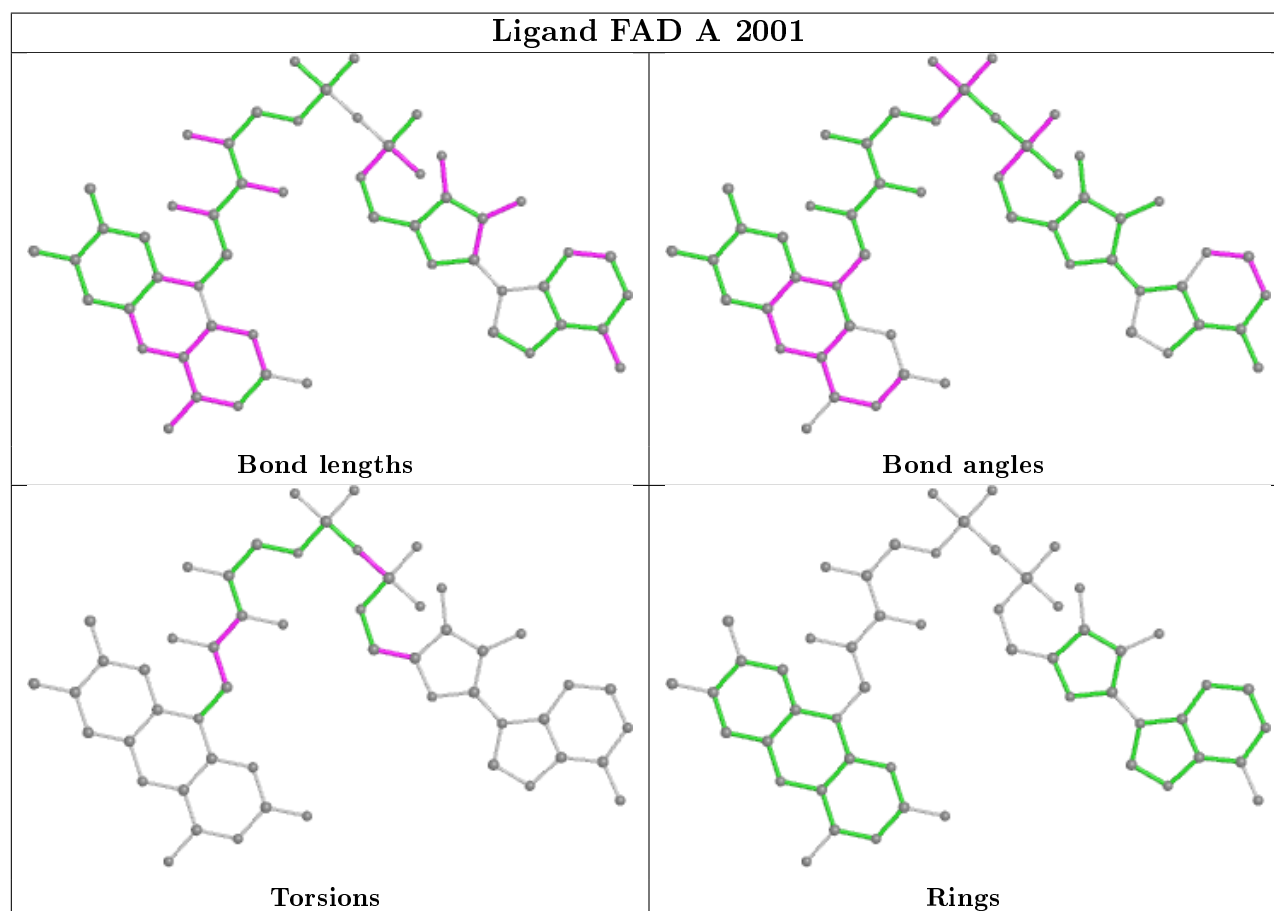
There are no ring outliers.

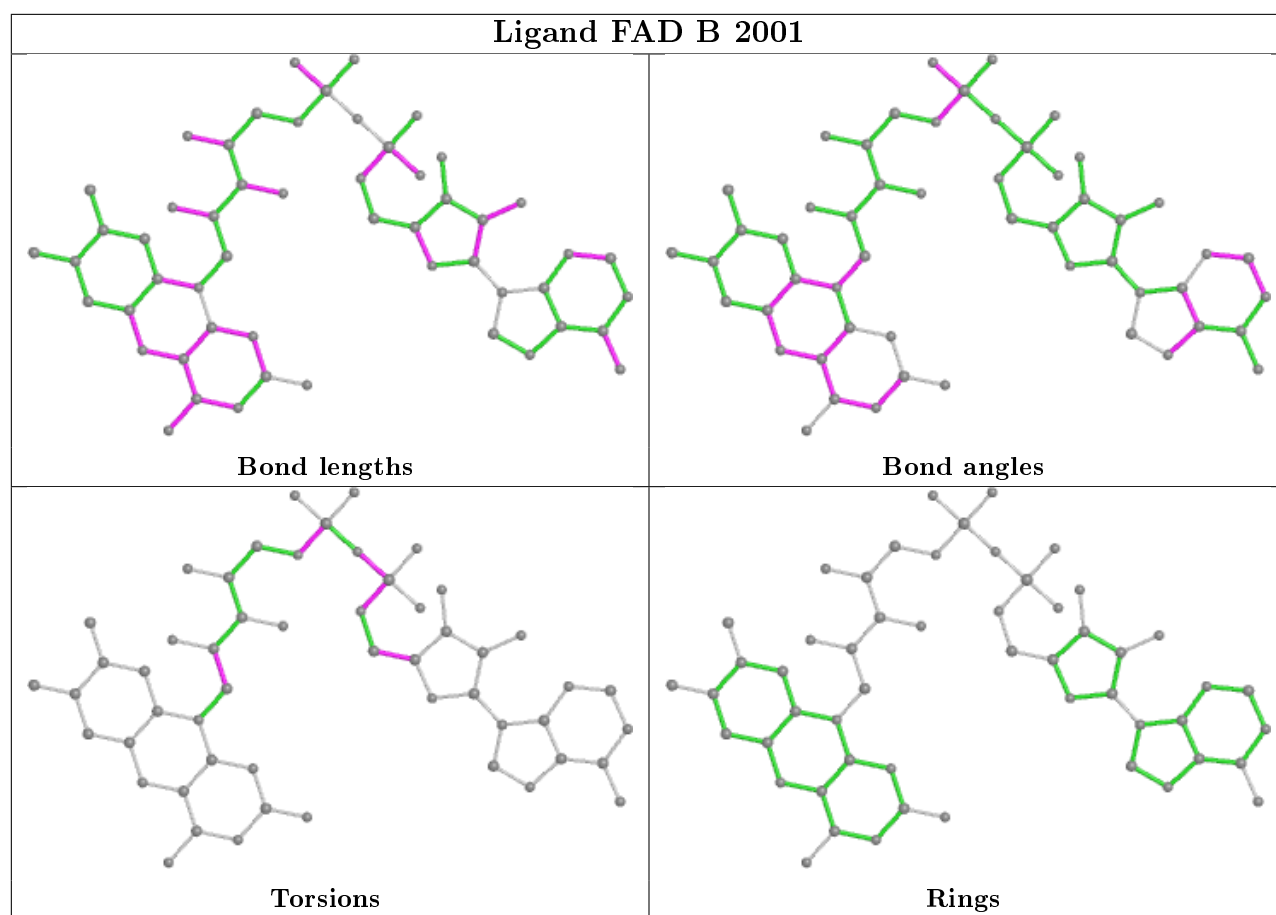
6 monomers are involved in 9 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	2010	EDO	1	0
4	B	2010	EDO	2	0
2	A	2001	FAD	2	0
2	B	2001	FAD	1	0
4	B	2011	EDO	1	0
4	A	2011	EDO	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 ⓘ

### 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	977/1005 (97%)	-0.34	22 (2%) 60 65	11, 22, 46, 67	0
1	B	979/1005 (97%)	-0.49	13 (1%) 77 80	11, 20, 39, 62	0
All	All	1956/2010 (97%)	-0.42	35 (1%) 68 72	11, 21, 43, 67	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	84	ALA	5.5
1	A	462	ALA	5.0
1	B	471	GLY	4.5
1	B	461	ARG	4.2
1	A	78	ASN	3.8
1	B	473	GLY	3.4
1	A	83	PRO	3.3
1	B	102	ALA	3.2
1	A	80	GLN	3.0
1	A	85	PHE	3.0
1	A	463	ALA	3.0
1	A	81	ASP	2.9
1	B	462	ALA	2.9
1	A	41	TRP	2.8
1	A	186	GLY	2.6
1	B	459	ALA	2.6
1	A	474	GLY	2.6
1	A	460	ALA	2.6
1	B	474	GLY	2.6
1	A	187	ASP	2.5
1	A	472	LEU	2.5
1	B	463	ALA	2.5
1	A	82	MET	2.4
1	B	178	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	84	ALA	2.3
1	B	80	GLN	2.3
1	A	178	TRP	2.3
1	A	522	ASN	2.3
1	A	173	LYS	2.2
1	B	460	ALA	2.2
1	A	441	ALA	2.2
1	A	865	ALA	2.2
1	B	472	LEU	2.1
1	A	107	VAL	2.1
1	A	459	ALA	2.1

## 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.

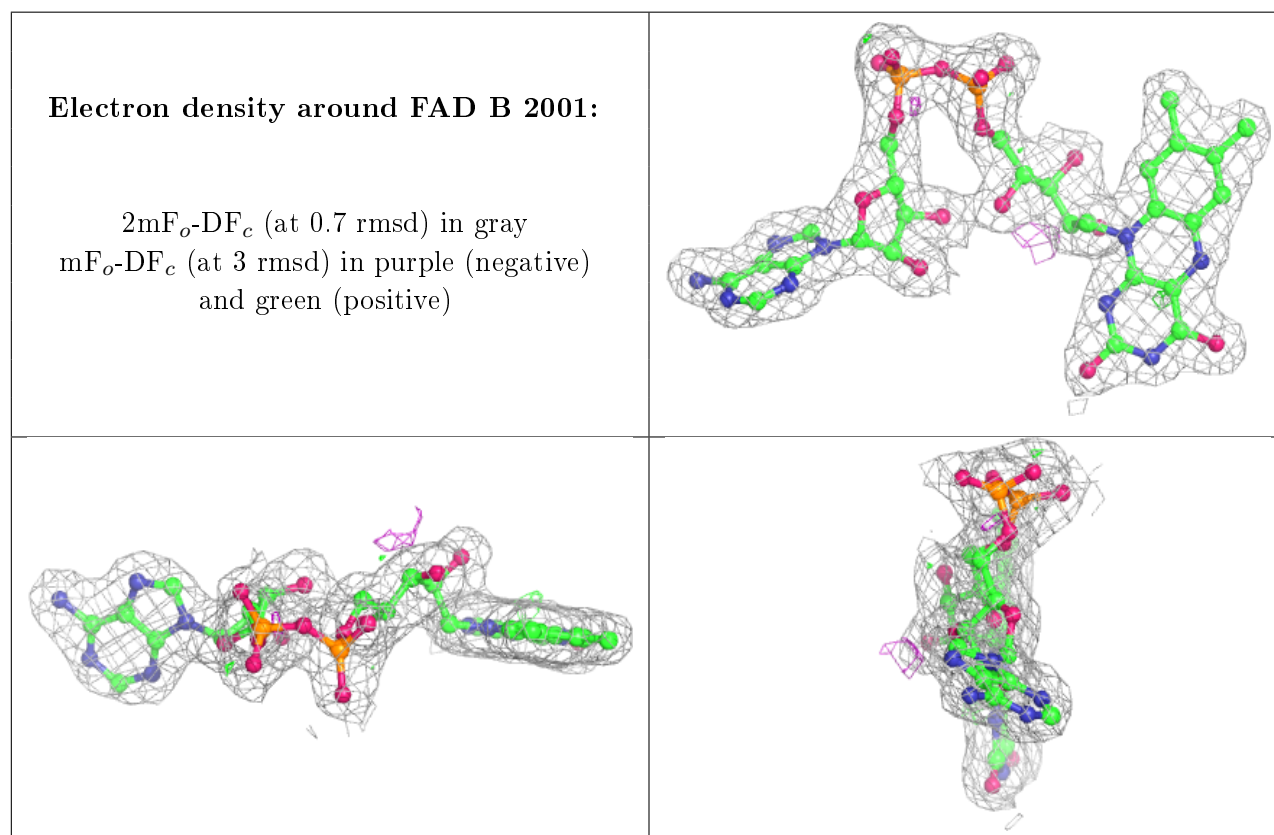
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	EDO	A	2005	4/4	0.86	0.14	38,40,41,44	0
4	EDO	B	2006	4/4	0.90	0.18	27,30,32,37	0
4	EDO	A	2012	4/4	0.91	0.15	31,32,33,43	0
4	EDO	A	2009	4/4	0.92	0.11	31,31,34,34	0
4	EDO	B	2007	4/4	0.92	0.10	36,37,38,39	0
4	EDO	A	2011	4/4	0.93	0.18	33,39,45,53	0
4	EDO	B	2011	4/4	0.93	0.13	28,30,31,32	0
4	EDO	A	2013	4/4	0.94	0.17	20,32,36,38	0
4	EDO	B	2004	4/4	0.95	0.12	26,28,32,35	0
4	EDO	A	2008	4/4	0.96	0.13	23,25,30,31	0
4	EDO	A	2010	4/4	0.96	0.12	23,31,32,33	0
4	EDO	B	2003	4/4	0.96	0.10	15,18,23,31	0

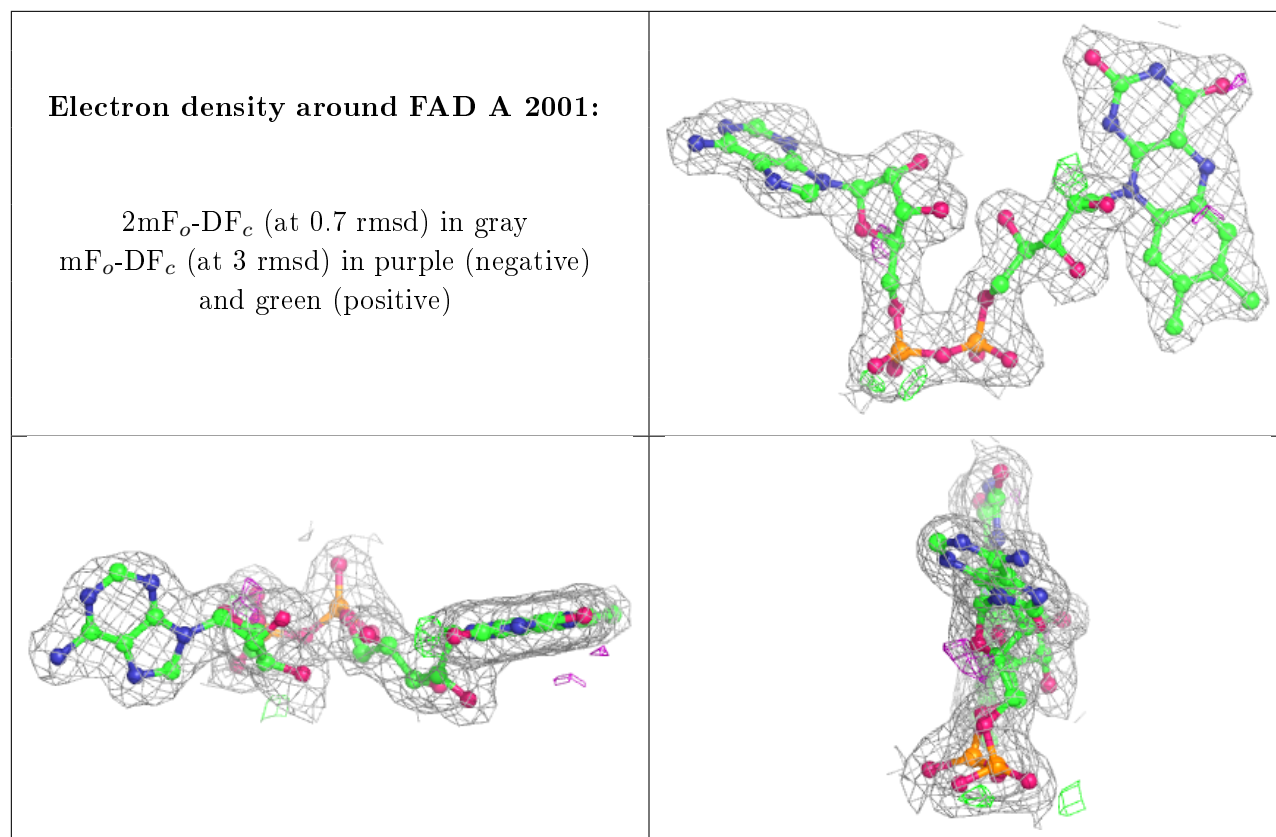
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	EDO	A	2004	4/4	0.96	0.18	23,29,30,34	0
4	EDO	B	2008	4/4	0.96	0.11	29,31,32,34	0
3	TFB	B	2002	8/8	0.97	0.09	14,18,20,22	0
4	EDO	B	2009	4/4	0.97	0.09	29,32,34,37	0
2	FAD	B	2001	53/53	0.97	0.09	10,16,19,25	0
4	EDO	A	2006	4/4	0.97	0.17	27,33,38,39	0
4	EDO	B	2005	4/4	0.97	0.07	28,30,32,32	0
2	FAD	A	2001	53/53	0.97	0.11	11,16,23,25	0
4	EDO	A	2003	4/4	0.97	0.09	20,24,27,32	0
4	EDO	A	2007	4/4	0.97	0.07	23,32,33,34	0
3	TFB	A	2002	8/8	0.98	0.12	12,17,22,24	0
4	EDO	B	2010	4/4	0.98	0.06	22,25,25,26	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.