



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:32 PM UTC

PDB ID : 2FZN / pdb_00002fzn
Title : Structure of the E. coli PutA proline dehydrogenase domain reduced by dithionite and complexed with proline
Authors : Tanner, J.J.
Deposited on : 2006-02-09
Resolution : 2.00 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 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

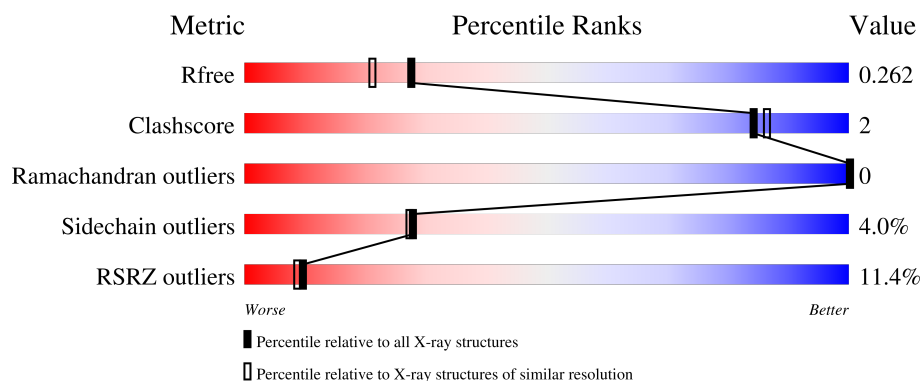
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	602	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FAD	A	2001	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3704 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.

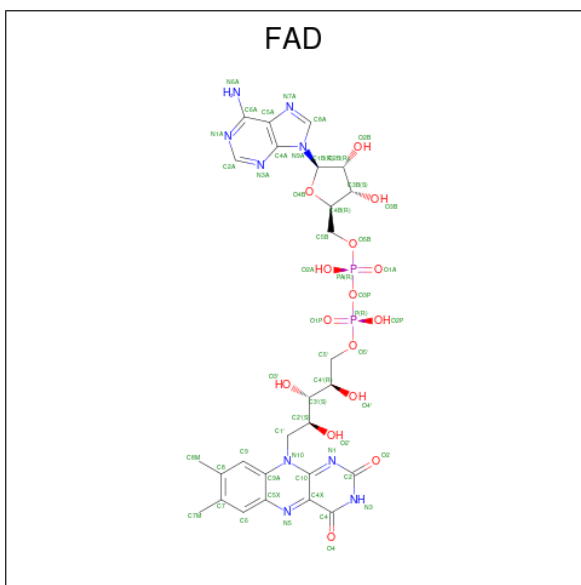
- Molecule 1 is a protein called Bifunctional protein putA, Proline dehydrogenase (EC 1.5.99.8) (Proline oxidase).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	449	Total	C	N	O	S	0	0	0
			3460	2198	608	637	17			

There are 18 discrepancies between the modelled and reference sequences:

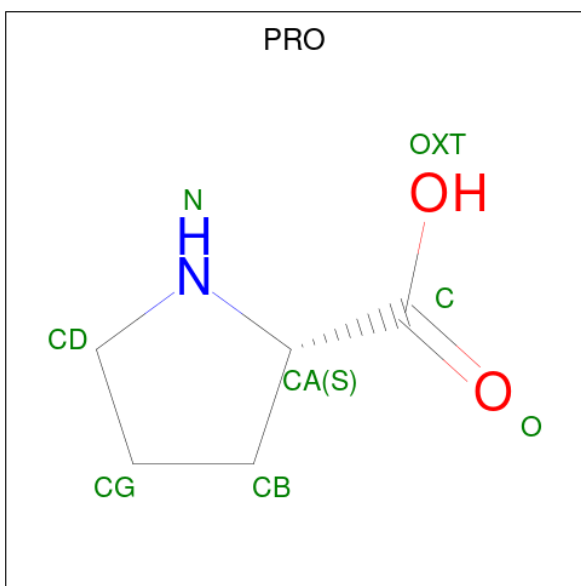
Chain	Residue	Modelled	Actual	Comment	Reference
A	670	SER	-	cloning artifact	UNP P09546
A	671	SER	-	cloning artifact	UNP P09546
A	672	SER	-	cloning artifact	UNP P09546
A	673	VAL	-	cloning artifact	UNP P09546
A	674	ASP	-	cloning artifact	UNP P09546
A	675	LYS	-	cloning artifact	UNP P09546
A	676	LEU	-	cloning artifact	UNP P09546
A	677	ALA	-	cloning artifact	UNP P09546
A	678	ALA	-	cloning artifact	UNP P09546
A	679	ALA	-	cloning artifact	UNP P09546
A	680	LEU	-	cloning artifact	UNP P09546
A	681	GLU	-	cloning artifact	UNP P09546
A	682	HIS	-	expression tag	UNP P09546
A	683	HIS	-	expression tag	UNP P09546
A	684	HIS	-	expression tag	UNP P09546
A	685	HIS	-	expression tag	UNP P09546
A	686	HIS	-	expression tag	UNP P09546
A	687	HIS	-	expression tag	UNP P09546

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



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

- Molecule 3 is PROLINE (CCD ID: PRO) (formula: $\text{C}_5\text{H}_9\text{NO}_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	5	1	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	183	Total 183	O 183	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	73.11Å 143.22Å 145.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	22.70 – 2.00 22.70 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (22.70-2.00) 96.3 (22.70-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 1.99Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.214 , 0.251 0.222 , 0.262	Depositor DCC
R_{free} test set	2538 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	30.2	Xtriage
Anisotropy	0.773	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 50.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3704	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.89% 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	0.88	1/3524 (0.0%)	0.92	2/4776 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	485	ALA	CA-CB	-5.58	1.45	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	524	VAL	N-CA-C	5.43	116.59	111.48
1	A	92	ARG	N-CA-C	5.24	116.99	111.28

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	3460	0	3450	16	0
2	A	53	0	30	1	0
3	A	8	0	7	1	0
4	A	183	0	0	2	0
All	All	3704	0	3487	16	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 (16) 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:99:TYR:HA	1:A:409:ARG:HD2	1.86	0.56
1:A:409:ARG:CD	4:A:2004:HOH:O	2.54	0.55
1:A:261:THR:HG21	1:A:541:ALA:HB1	1.88	0.54
1:A:396:TRP:O	1:A:426:ARG:NH1	2.42	0.53
1:A:92:ARG:NH2	1:A:382:ASP:OD2	2.35	0.52
1:A:409:ARG:HD2	4:A:2004:HOH:O	2.09	0.51
1:A:540:TYR:CZ	3:A:2002:PRO:HD2	2.46	0.50
1:A:503:TYR:OH	1:A:505:PRO:HA	2.12	0.49
1:A:261:THR:HG21	1:A:541:ALA:CB	2.43	0.47
1:A:261:THR:HG22	1:A:514:HIS:CD2	2.50	0.46
1:A:101:ARG:NH1	1:A:109:MET:HE1	2.31	0.45
1:A:111:LEU:HD22	1:A:585:VAL:HG13	1.98	0.44
1:A:98:ALA:O	1:A:99:TYR:C	2.61	0.43
1:A:540:TYR:HB2	2:A:2001:FAD:HM72	1.99	0.43
1:A:410:CYS:HB3	1:A:411:PRO:HD3	2.00	0.43
1:A:101:ARG:HD3	1:A:105:GLU:HG2	2.00	0.43

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	443/602 (74%)	435 (98%)	8 (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	345/490 (70%)	331 (96%)	14 (4%)	27	26

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

Mol	Chain	Res	Type
1	A	101	ARG
1	A	111	LEU
1	A	135	LEU
1	A	168	LEU
1	A	184	LEU
1	A	254	LEU
1	A	263	GLU
1	A	341	GLN
1	A	361	ARG
1	A	384	LEU
1	A	406	TYR
1	A	409	ARG
1	A	547	GLU
1	A	563	ASN

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

Mol	Chain	Res	Type
1	A	113	GLN
1	A	123	GLN
1	A	305	GLN
1	A	316	ASN
1	A	483	GLN
1	A	497	GLN
1	A	507	GLN
1	A	534	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	A	2001	-	58,58,58	1.55	11 (18%)	85,89,89	1.69	20 (23%)
3	PRO	A	2002	-	8,8,8	0.87	0	10,10,10	1.17	1 (10%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FAD	A	2001	-	1/1/9/9	6/34/50/50	0/6/6/6
3	PRO	A	2002	-	-	1/4/11/11	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2001	FAD	C4X-N5	5.26	1.42	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2001	FAD	PA-O3P	3.53	1.63	1.59
2	A	2001	FAD	C2A-N1A	3.19	1.39	1.33
2	A	2001	FAD	O4B-C4B	-3.08	1.38	1.45
2	A	2001	FAD	C5A-N7A	-2.75	1.34	1.39
2	A	2001	FAD	C2-N3	-2.72	1.33	1.39
2	A	2001	FAD	C10-N1	2.64	1.38	1.33
2	A	2001	FAD	P-O3P	2.57	1.62	1.59
2	A	2001	FAD	O4B-C1B	2.53	1.47	1.42
2	A	2001	FAD	C4A-N9A	-2.24	1.33	1.37
2	A	2001	FAD	C1'-N10	2.19	1.53	1.47

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2001	FAD	O4B-C4B-C5B	5.24	126.11	109.33
2	A	2001	FAD	N3A-C2A-N1A	-4.80	121.32	128.58
2	A	2001	FAD	N9A-C8A-N7A	-3.54	108.92	113.94
2	A	2001	FAD	C4X-C10-N10	3.49	121.48	116.48
2	A	2001	FAD	O4B-C4B-C3B	3.32	111.74	105.15
2	A	2001	FAD	C4-C4X-N5	3.00	122.36	118.21
2	A	2001	FAD	O2A-PA-O3P	2.85	114.97	107.27
2	A	2001	FAD	C2A-N3A-C4A	2.79	118.64	111.83
2	A	2001	FAD	C5A-N7A-C8A	2.71	107.71	103.45
2	A	2001	FAD	C5A-C4A-N3A	-2.66	123.05	126.72
2	A	2001	FAD	C4A-C5A-N7A	-2.57	107.65	110.58
2	A	2001	FAD	C7M-C7-C6	-2.40	115.35	119.57
2	A	2001	FAD	O2P-P-O3P	-2.35	100.91	107.27
2	A	2001	FAD	C4A-N9A-C8A	2.35	108.20	105.74
2	A	2001	FAD	C2A-N1A-C6A	2.32	122.54	118.73
2	A	2001	FAD	C4X-C4-N3	2.25	118.98	113.25
3	A	2002	PRO	CB-CA-C	-2.23	106.97	112.72
2	A	2001	FAD	C10-N1-C2	2.20	121.62	116.85
2	A	2001	FAD	C10-C4X-N5	-2.11	120.51	124.81
2	A	2001	FAD	C4A-N9A-C1B	-2.08	121.78	126.63
2	A	2001	FAD	C5X-C9A-N10	2.04	119.81	117.97

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	2001	FAD	C4B

All (7) torsion outliers are listed below:

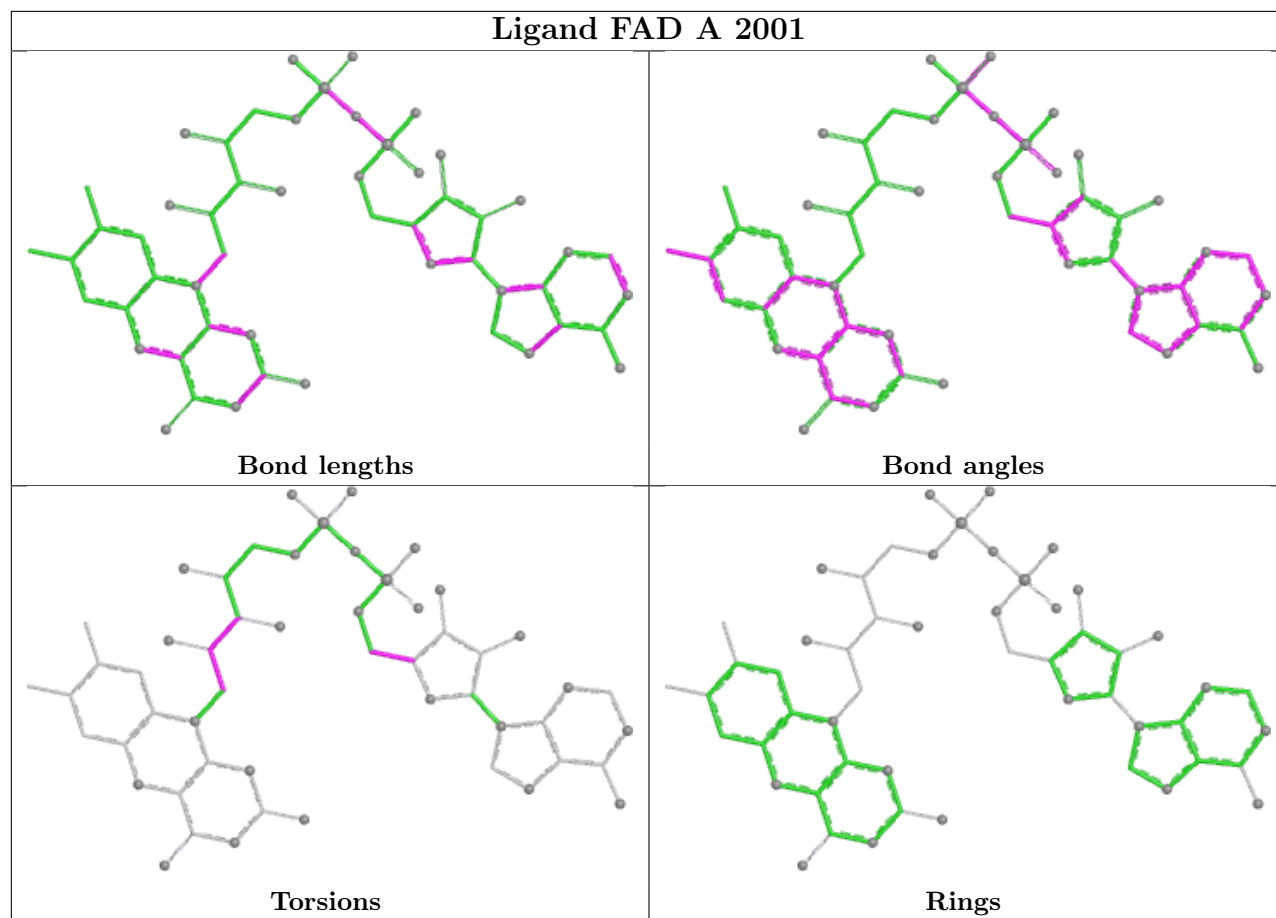
Mol	Chain	Res	Type	Atoms
2	A	2001	FAD	N10-C1'-C2'-O2'
2	A	2001	FAD	N10-C1'-C2'-C3'
2	A	2001	FAD	C1'-C2'-C3'-C4'
2	A	2001	FAD	O4B-C4B-C5B-O5B
2	A	2001	FAD	O2'-C2'-C3'-C4'
2	A	2001	FAD	O2'-C2'-C3'-O3'
3	A	2002	PRO	OXT-C-CA-CB

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2001	FAD	1	0
3	A	2002	PRO	1	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, 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	449/602 (74%)	0.70	51 (11%) 10 9	15, 24, 58, 73	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	146	GLY	9.5
1	A	140	ASN	7.7
1	A	141	ALA	6.1
1	A	164	ALA	5.2
1	A	138	GLN	5.0
1	A	143	GLY	4.9
1	A	245	ARG	4.9
1	A	145	ALA	4.6
1	A	165	LEU	4.2
1	A	167	CYS	4.1
1	A	142	SER	4.0
1	A	574	SER	3.9
1	A	244	ILE	3.7
1	A	246	LYS	3.7
1	A	184	LEU	3.5
1	A	253	ARG	3.5
1	A	179	ALA	3.4
1	A	447	MET	3.4
1	A	139	LYS	3.4
1	A	163	VAL	3.4
1	A	183	ALA	3.2
1	A	177	ASP	3.1
1	A	137	ASN	2.8
1	A	182	ASP	2.8
1	A	180	THR	2.8
1	A	272	ALA	2.7
1	A	172	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	251	ALA	2.7
1	A	263	GLU	2.6
1	A	268	ALA	2.6
1	A	271	ASN	2.6
1	A	144	ARG	2.6
1	A	169	ALA	2.5
1	A	166	MET	2.5
1	A	162	GLY	2.5
1	A	547	GLU	2.4
1	A	175	ILE	2.4
1	A	97	ALA	2.3
1	A	298	GLN	2.2
1	A	546	HIS	2.2
1	A	573	THR	2.2
1	A	572	ASP	2.2
1	A	134	LYS	2.2
1	A	297	ALA	2.1
1	A	355	SER	2.1
1	A	440	SER	2.1
1	A	249	ASP	2.1
1	A	109	MET	2.1
1	A	362	GLN	2.1
1	A	296	ASP	2.1
1	A	120	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](#)

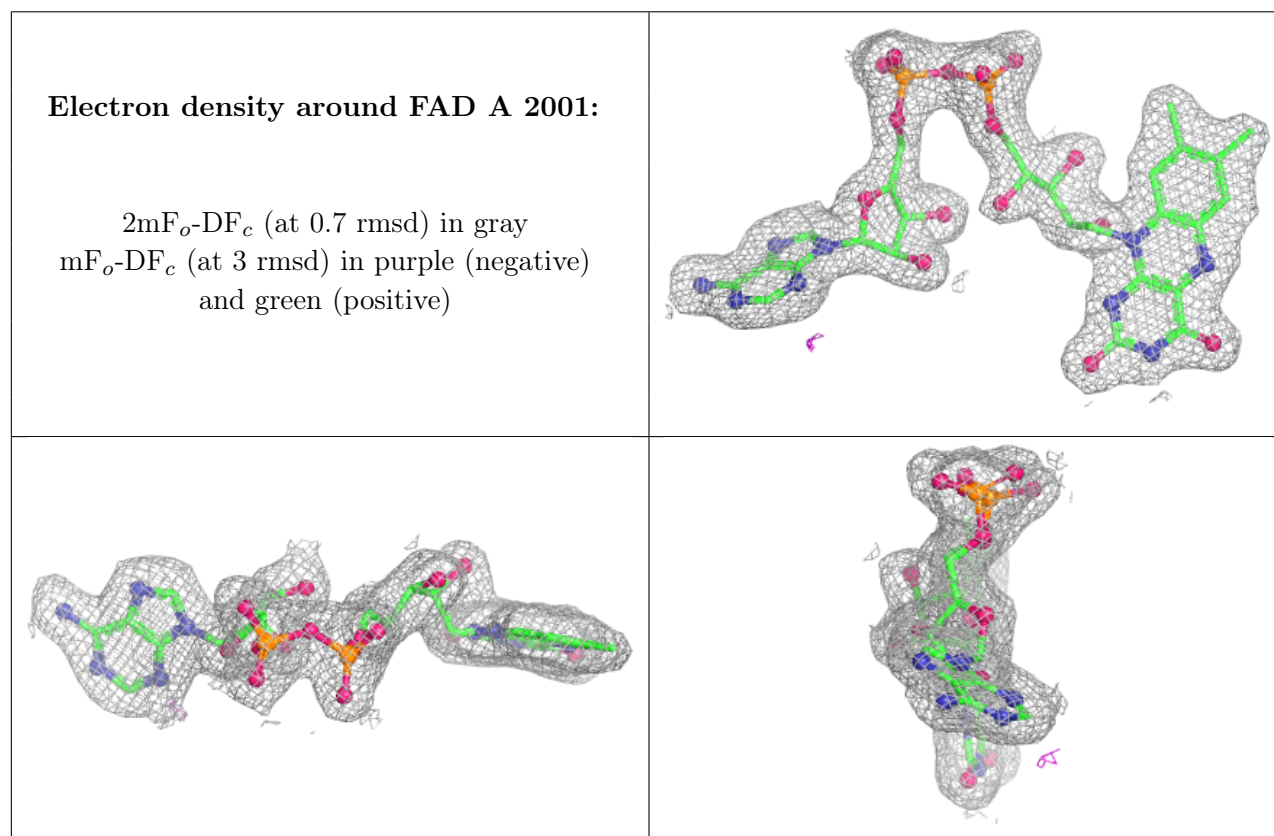
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
3	PRO	A	2002	8/8	0.94	0.08	35,36,37,38	0
2	FAD	A	2001	53/53	0.97	0.07	24,29,31,32	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.