Full wwPDB X-ray Structure Validation Report ⓘ

Apr 28, 2024 – 05:06 am BST

PDB ID	:	6FN0
Title	:	The animal-like Cryptochrome from Chlamydomonas reinhardtii in complex with 6-4 DNA
Authors	:	Franz, S.; Ignatz, E.; Wenzel, S.; Zielosko, H.; Yamamoto, J.; Mittag, M.; Essen, L.-O.
Deposited on	:	2018-02-02
Resolution	:	2.90 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:

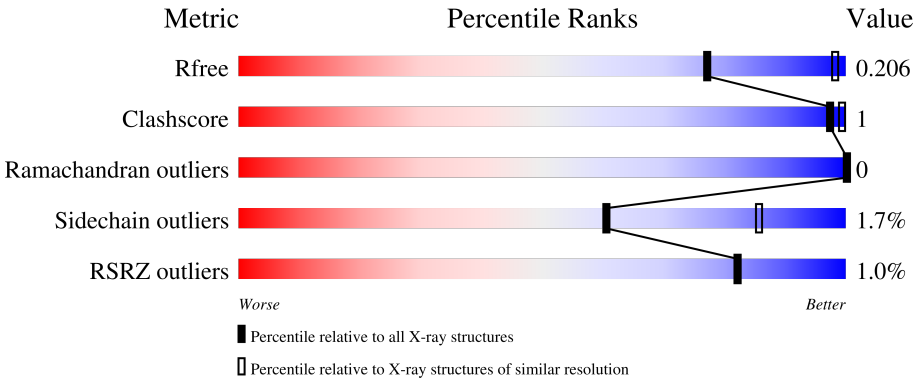
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 <=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	499	% 96%
2	C	14	86% 14%
3	D	14	86% 14%

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 4750 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 Cryptochrome photoreceptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	496	Total	C	N	O	S	0	1	0
			3981	2572	695	696	18			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	497	LYS	-	expression tag	UNP A8J8W0
A	498	LEU	-	expression tag	UNP A8J8W0
A	499	ALA	-	expression tag	UNP A8J8W0

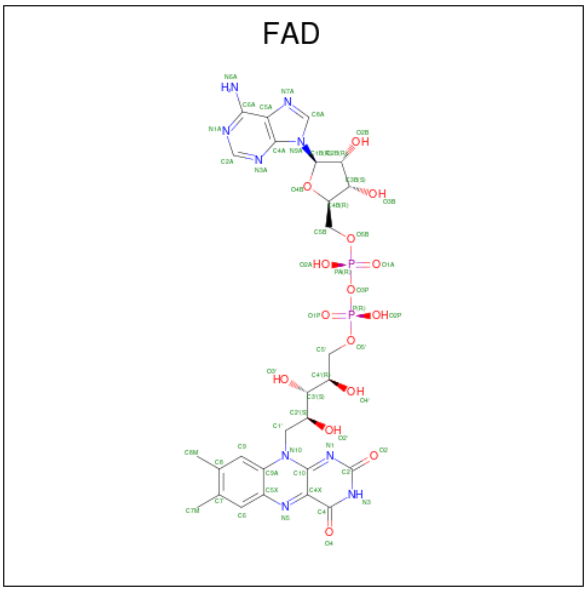
- Molecule 2 is a DNA chain called DNA (5'-D(*CP*AP*GP*CP*GP*GP*(64T)P*(5PY)P*GP*CP*CP*GP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	14	Total	C	N	O	P	0	0	0
			286	136	53	84	13			

- Molecule 3 is a DNA chain called DNA (5'-D(*CP*AP*CP*GP*GP*CP*AP*AP*CP*CP*GP*CP*TP*G)-3').

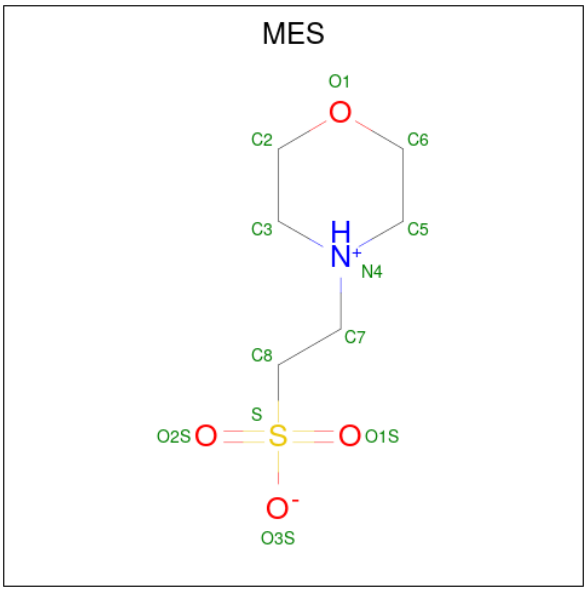
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	14	Total	C	N	O	P	0	0	0
			282	134	55	80	13			

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



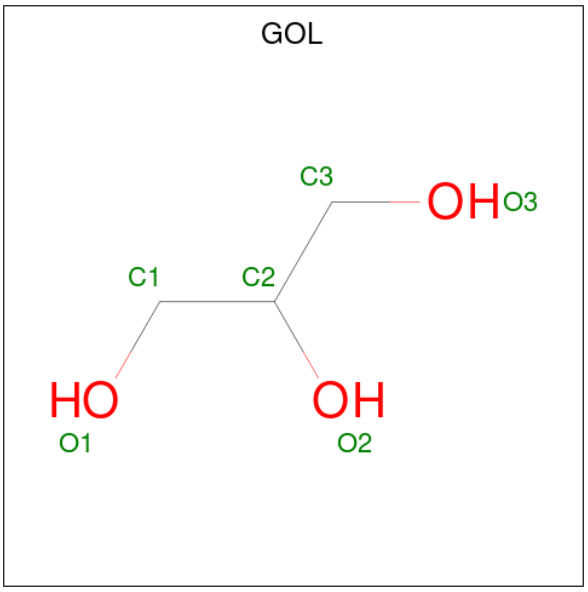
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 5 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 6 3 3	0	0

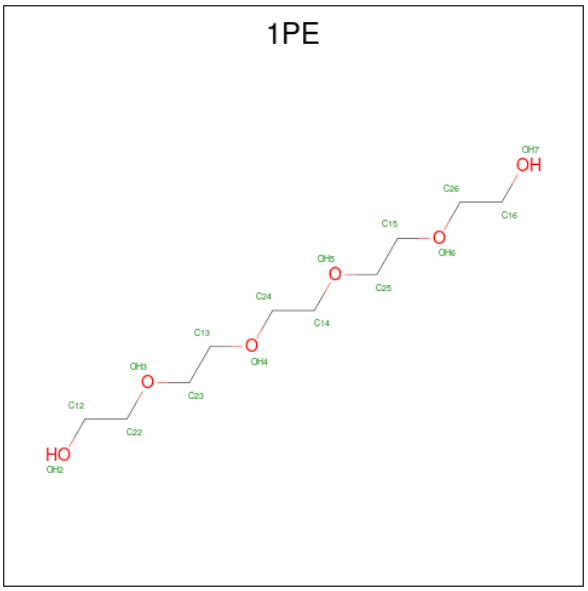
- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	2	Total Mg 2 2	0	0

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	D	1	Total Cl 1 1	0	0

- Molecule 9 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	D	1	Total C O 16 10 6	0	0

- Molecule 10 is water.

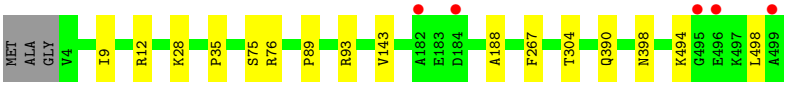
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	101	Total O 101 101	0	0
10	C	7	Total O 7 7	0	0
10	D	3	Total O 3 3	0	0

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.

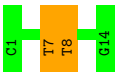
• Molecule 1: Cryptochrome photoreceptor

Chain A:



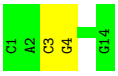
• Molecule 2: DNA (5'-D(*CP*AP*GP*CP*GP*GP*(64T)P*(5PY)P*GP*CP*CP*GP*TP*G)-3')

Chain C:



• Molecule 3: DNA (5'-D(*CP*AP*CP*GP*GP*CP*AP*AP*CP*CP*GP*CP*TP*G)-3')

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α, β, γ	146.24Å 146.24Å 67.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	61.20 – 2.90 65.40 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (61.20-2.90) 99.8 (65.40-2.90)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.47 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.8.0123	Depositor
R, R_{free}	0.157 , 0.212 0.165 , 0.206	Depositor DCC
R_{free} test set	536 reflections (3.20%)	wwPDB-VP
Wilson B-factor (Å^2)	61.7	Xtriage
Anisotropy	0.179	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 30.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4750	wwPDB-VP
Average B, all atoms (Å^2)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MES, GOL, 1PE, 5PY, MG, CL, FAD, 64T

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	0.53	0/4115	0.73	0/5609
2	C	0.43	0/275	0.93	0/421
3	D	0.43	0/316	0.91	0/485
All	All	0.52	0/4706	0.76	0/6515

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	3981	0	3901	5	0
2	C	286	0	159	1	0
3	D	282	0	157	1	0
4	A	53	0	31	1	0
5	A	12	0	13	0	0
6	A	6	0	8	0	0
7	C	2	0	0	0	0
8	D	1	0	0	0	0
9	D	16	0	22	0	0
10	A	101	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	C	7	0	0	0	0
10	D	3	0	0	0	0
All	All	4750	0	4291	7	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 (7) 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)
3:D:3:DC:H2'	3:D:4:DG:C8	2.38	0.57
2:C:7:64T:H2"	2:C:8:5PY:C4	2.37	0.54
1:A:76:ARG:NH2	1:A:188:ALA:O	2.46	0.49
1:A:398:ASN:HB3	4:A:501:FAD:C8	2.47	0.45
1:A:9:ILE:HG23	1:A:35:PRO:HA	2.01	0.42
1:A:143:VAL:HG21	1:A:304:THR:HG21	2.01	0.42
1:A:89:PRO:O	1:A:93:ARG:HG3	2.21	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	495/499 (99%)	474 (96%)	21 (4%)	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	415/416 (100%)	408 (98%)	7 (2%)	60 86

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	ARG
1	A	28	LYS
1	A	75	SER
1	A	267	PHE
1	A	390	GLN
1	A	494	LYS
1	A	498	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	227	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)

2 non-standard protein/DNA/RNA residues 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	64T	C	7	2	17,22,23	1.55	4 (23%)	24,33,36	1.51	5 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	5PY	C	8	2	15,20,21	0.94	1 (6%)	21,28,31	2.12	7 (33%)

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	64T	C	7	2	-	1/7/40/41	0/2/2/2
2	5PY	C	8	2	-	4/7/21/22	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	7	64T	C6-N1	3.52	1.50	1.46
2	C	7	64T	C1'-N1	3.28	1.50	1.45
2	C	7	64T	C2-N3	-2.24	1.34	1.38
2	C	7	64T	C4-N3	-2.15	1.34	1.37
2	C	8	5PY	C6-N1	-2.03	1.34	1.38

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	8	5PY	O4'-C1'-N1	-6.48	96.28	107.86
2	C	7	64T	N3-C2-N1	3.73	120.60	116.65
2	C	8	5PY	C2'-C1'-N1	3.32	121.41	113.77
2	C	8	5PY	C6-C5-C4	-2.58	115.52	118.09
2	C	7	64T	O4'-C1'-N1	2.55	111.66	108.41
2	C	7	64T	O2-C2-N3	-2.54	116.77	121.50
2	C	8	5PY	C5-C4-N3	-2.25	121.18	125.03
2	C	7	64T	C5M-C5-C4	-2.25	105.56	108.85
2	C	8	5PY	O4'-C1'-C2'	-2.24	102.02	106.25
2	C	8	5PY	C3'-C2'-C1'	2.24	108.14	102.54
2	C	7	64T	O5-C5-C4	2.16	113.48	109.63
2	C	8	5PY	C4'-O4'-C1'	2.14	114.63	109.45

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	8	5PY	C2'-C1'-N1-C6

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Mol	Chain	Res	Type	Atoms
2	C	8	5PY	C2'-C1'-N1-C2
2	C	8	5PY	O4'-C1'-N1-C6
2	C	8	5PY	O4'-C1'-N1-C2
2	C	7	64T	C3'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	7	64T	1	0
2	C	8	5PY	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 3 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	$\#\|Z\| > 2$
4	FAD	A	501	-	53,58,58	1.43	9 (16%)	68,89,89	1.43	12 (17%)
6	GOL	A	503	-	5,5,5	0.40	0	5,5,5	0.44	0
5	MES	A	502	-	12,12,12	2.23	1 (8%)	14,16,16	1.14	1 (7%)
9	1PE	D	102	-	15,15,15	0.55	0	14,14,14	0.42	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	FAD	A	501	-	-	2/30/50/50	0/6/6/6
6	GOL	A	503	-	-	0/4/4/4	-
5	MES	A	502	-	-	1/6/14/14	0/1/1/1
9	1PE	D	102	-	-	7/13/13/13	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	502	MES	C8-S	-7.38	1.67	1.77
4	A	501	FAD	C9A-C5X	5.13	1.49	1.41
4	A	501	FAD	C5A-C4A	2.83	1.48	1.40
4	A	501	FAD	C5X-N5	-2.77	1.34	1.39
4	A	501	FAD	C8-C7	2.75	1.47	1.40
4	A	501	FAD	C1'-C2'	-2.40	1.49	1.52
4	A	501	FAD	C2A-N3A	2.32	1.35	1.32
4	A	501	FAD	O4B-C1B	2.24	1.44	1.41
4	A	501	FAD	C10-N10	2.10	1.41	1.37
4	A	501	FAD	C9A-N10	2.05	1.44	1.41

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	501	FAD	C4'-C3'-C2'	-3.14	106.83	113.36
4	A	501	FAD	O2-C2-N1	-2.91	117.01	121.83
4	A	501	FAD	C4A-C5A-N7A	-2.89	106.39	109.40
4	A	501	FAD	N3A-C2A-N1A	-2.78	124.33	128.68
4	A	501	FAD	C4X-C10-N1	-2.47	119.00	124.73
4	A	501	FAD	O4-C4-C4X	-2.41	120.19	126.60
4	A	501	FAD	C9A-N10-C10	-2.27	117.23	120.77
5	A	502	MES	O1S-S-C8	2.12	109.47	106.92
4	A	501	FAD	O2'-C2'-C3'	2.09	114.17	109.10
4	A	501	FAD	O3'-C3'-C2'	2.08	113.83	108.81
4	A	501	FAD	C10-N1-C2	2.05	121.01	116.90
4	A	501	FAD	C4-C4X-N5	2.05	121.14	118.23
4	A	501	FAD	C5'-C4'-C3'	-2.04	108.26	112.20

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	D	102	1PE	OH4-C13-C23-OH3
9	D	102	1PE	OH5-C14-C24-OH4

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Mol	Chain	Res	Type	Atoms
9	D	102	1PE	C24-C14-OH5-C25
9	D	102	1PE	OH2-C12-C22-OH3
4	A	501	FAD	C4'-C5'-O5'-P
9	D	102	1PE	C23-C13-OH4-C24
4	A	501	FAD	P-O3P-PA-O1A
5	A	502	MES	N4-C7-C8-S
9	D	102	1PE	C25-C15-OH6-C26
9	D	102	1PE	C13-C23-OH3-C22

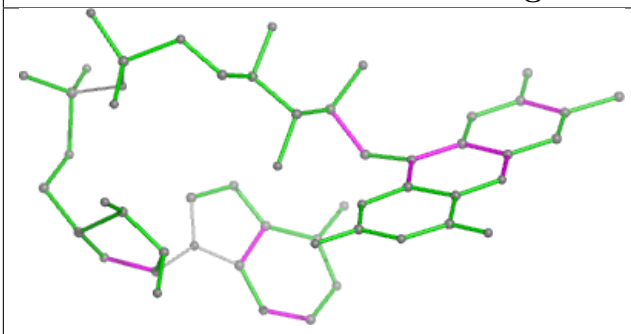
There are no ring outliers.

1 monomer is involved in 1 short contact:

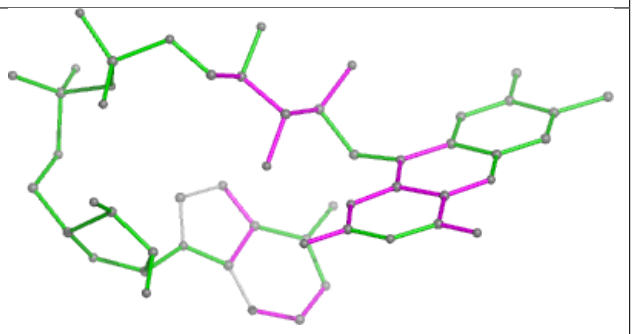
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	501	FAD	1	0

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 then 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.

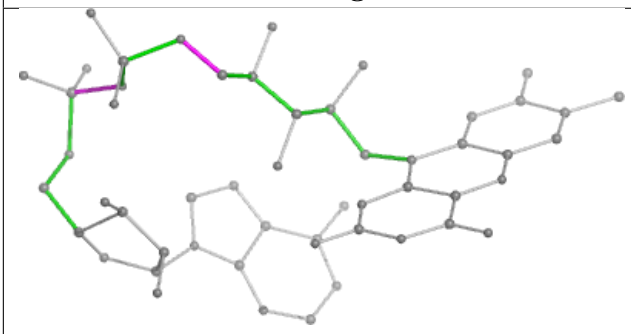
Ligand FAD A 501



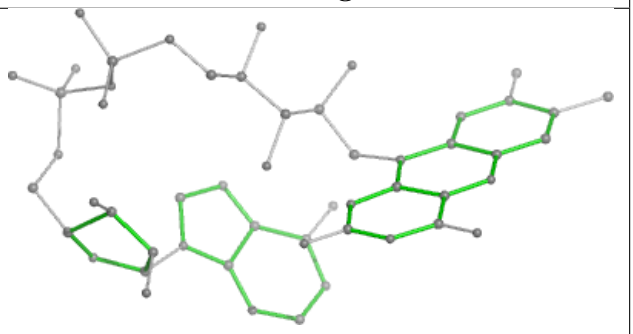
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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^{th} 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	496/499 (99%)	-0.22	5 (1%) 82 82	38, 60, 97, 129	0
2	C	12/14 (85%)	-0.51	0 100 100	53, 71, 104, 124	0
3	D	14/14 (100%)	-0.49	0 100 100	59, 75, 90, 107	0
All	All	522/527 (99%)	-0.23	5 (0%) 82 82	38, 61, 99, 129	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	495	GLY	2.7
1	A	499	ALA	2.5
1	A	496	GLU	2.4
1	A	184	ASP	2.3
1	A	182	ALA	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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^{th} 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	5PY	C	8	19/20	0.98	0.15	44,46,49,50	0
2	64T	C	7	21/22	0.99	0.14	45,48,49,51	0

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands (i)

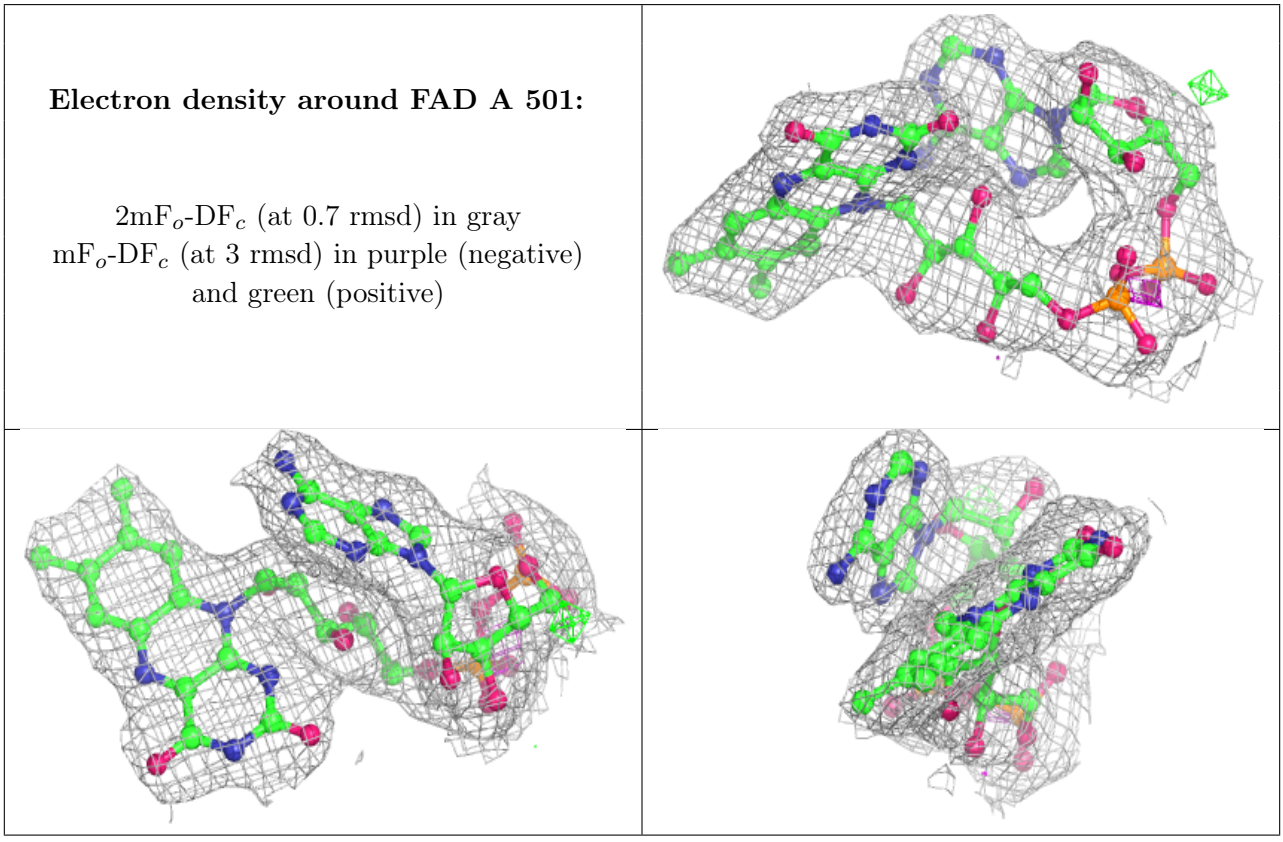
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
9	1PE	D	102	16/16	0.83	0.15	81,95,101,103	0
6	GOL	A	503	6/6	0.89	0.23	74,76,77,79	0
5	MES	A	502	12/12	0.90	0.25	84,97,104,106	0
8	CL	D	101	1/1	0.94	0.13	68,68,68,68	0
7	MG	C	101	1/1	0.96	0.18	62,62,62,62	0
7	MG	C	102	1/1	0.96	0.17	75,75,75,75	0
4	FAD	A	501	53/53	0.99	0.16	40,42,45,47	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 A 501:

$2mF_o$-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.