



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 14, 2023 – 03:54 AM JST

PDB ID : 7YEJ

Title : TR-SFX MmCPDII-DNA complex: 100 ns time-point collected in SACLA.
Includes 100 ns, dark, and extrapolated structure factors

Authors : Maestre-Reyna, M.; Wang, P.-H.; Nango, E.; Hosokawa, Y.; Saft, M.; Furrer, A.; Yang, C.-H.; Ngura Putu, E.P.G.; Wu, W.-J.; Emmerich, H.-J.; Engilberge, S.; Caramello, N.; Wranik, M.; Glover, H.L.; Franz-Badur, S.; Wu, H.-Y.; Lee, C.-C.; Huang, W.-C.; Huang, K.-F.; Chang, Y.-K.; Liao, J.-H.; Weng, J.-H.; Gad, W.; Chang, C.-W.; Pang, A.H.; Gashi, D.; Beale, E.; Ozerov, D.; Milne, C.; Cirelli, C.; Bacellar, C.; Sugahara, M.; Owada, S.; Joti, Y.; Yamashita, A.; Tanaka, R.; Tanaka, T.; Luo, F.J.; Tono, K.; Kiontke, S.; Spadaccini, R.; Royant, A.; Yamamoto, J.; Iwata, S.; Standfuss, J.; Essen, L.-O.; Bessho, Y.; Tsai, M.-D.

Deposited on : 2022-07-05

Resolution : 2.55 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13

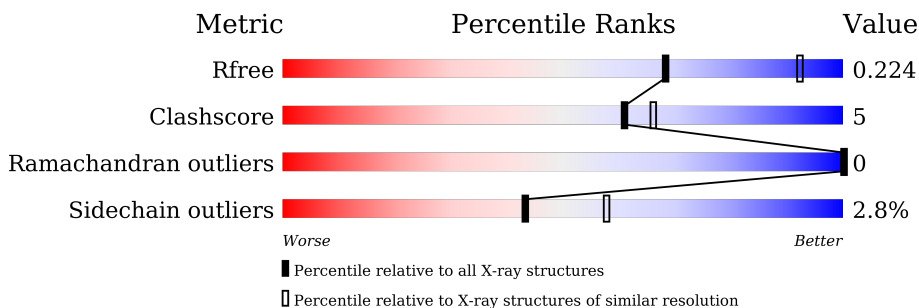
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)


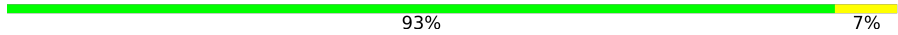

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	482	84% 10% • 5%
1	B	482	80% 9% • 10%
2	C	13	62% 31% 8%

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EDS : 2.36
 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

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Mol	Chain	Length	Quality of chain
2	E	13	 62% 38%
3	D	14	 93% 7%
3	F	14	 36% 64%

2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 8548 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 Deoxyribodipyrimidine photo-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	456	3635	2344	600	677	14	0	6	0
1	B	432	3455	2225	575	640	15	0	6	0

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	initiating methionine	UNP A0A0F8I5V2
A	-16	GLY	-	expression tag	UNP A0A0F8I5V2
A	-15	SER	-	expression tag	UNP A0A0F8I5V2
A	-14	SER	-	expression tag	UNP A0A0F8I5V2
A	-13	HIS	-	expression tag	UNP A0A0F8I5V2
A	-12	HIS	-	expression tag	UNP A0A0F8I5V2
A	-11	HIS	-	expression tag	UNP A0A0F8I5V2
A	-10	HIS	-	expression tag	UNP A0A0F8I5V2
A	-9	HIS	-	expression tag	UNP A0A0F8I5V2
A	-8	HIS	-	expression tag	UNP A0A0F8I5V2
A	-7	SER	-	expression tag	UNP A0A0F8I5V2
A	-6	SER	-	expression tag	UNP A0A0F8I5V2
A	-5	GLY	-	expression tag	UNP A0A0F8I5V2
A	-4	LEU	-	expression tag	UNP A0A0F8I5V2
A	-3	VAL	-	expression tag	UNP A0A0F8I5V2
A	-2	PRO	-	expression tag	UNP A0A0F8I5V2
A	-1	ARG	-	expression tag	UNP A0A0F8I5V2
A	0	GLY	-	expression tag	UNP A0A0F8I5V2
A	1	SER	-	expression tag	UNP A0A0F8I5V2
A	2	HIS	-	expression tag	UNP A0A0F8I5V2
A	377	THR	MET	engineered mutation	UNP A0A0F8I5V2
A	463	ALA	-	expression tag	UNP A0A0F8I5V2
A	464	LEU	-	expression tag	UNP A0A0F8I5V2
B	-17	MET	-	initiating methionine	UNP A0A0F8I5V2
B	-16	GLY	-	expression tag	UNP A0A0F8I5V2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	SER	-	expression tag	UNP A0A0F8I5V2
B	-14	SER	-	expression tag	UNP A0A0F8I5V2
B	-13	HIS	-	expression tag	UNP A0A0F8I5V2
B	-12	HIS	-	expression tag	UNP A0A0F8I5V2
B	-11	HIS	-	expression tag	UNP A0A0F8I5V2
B	-10	HIS	-	expression tag	UNP A0A0F8I5V2
B	-9	HIS	-	expression tag	UNP A0A0F8I5V2
B	-8	HIS	-	expression tag	UNP A0A0F8I5V2
B	-7	SER	-	expression tag	UNP A0A0F8I5V2
B	-6	SER	-	expression tag	UNP A0A0F8I5V2
B	-5	GLY	-	expression tag	UNP A0A0F8I5V2
B	-4	LEU	-	expression tag	UNP A0A0F8I5V2
B	-3	VAL	-	expression tag	UNP A0A0F8I5V2
B	-2	PRO	-	expression tag	UNP A0A0F8I5V2
B	-1	ARG	-	expression tag	UNP A0A0F8I5V2
B	0	GLY	-	expression tag	UNP A0A0F8I5V2
B	1	SER	-	expression tag	UNP A0A0F8I5V2
B	2	HIS	-	expression tag	UNP A0A0F8I5V2
B	377	THR	MET	engineered mutation	UNP A0A0F8I5V2
B	463	ALA	-	expression tag	UNP A0A0F8I5V2
B	464	LEU	-	expression tag	UNP A0A0F8I5V2

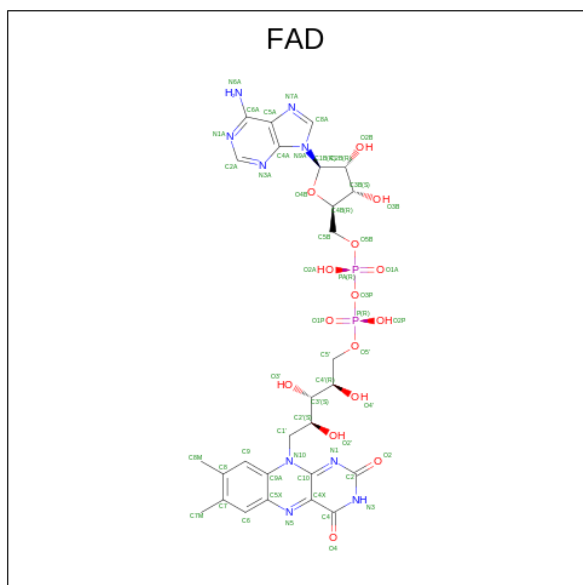
- Molecule 2 is a DNA chain called CPD photolesion containing DNA after repair.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	13	Total	C	N	O	P	0	0	0
			264	125	46	80	13			
2	E	13	Total	C	N	O	P	0	0	0
			264	125	46	80	13			

- Molecule 3 is a DNA chain called complementary oligonucleotide to the CPD containing DNA.

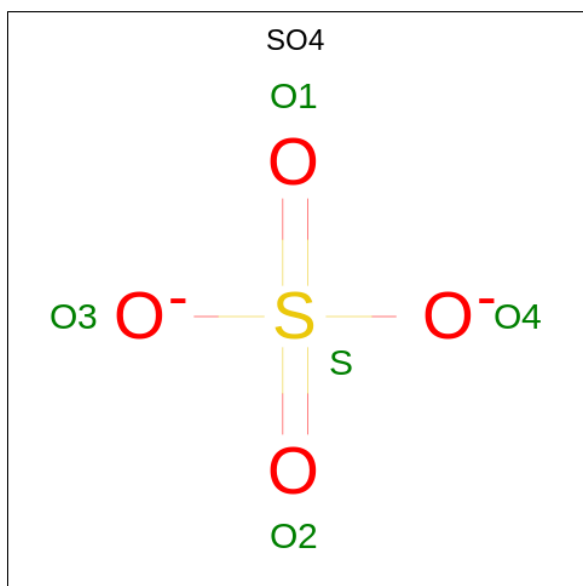
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	14	Total	C	N	O	P	0	0	0
			286	136	56	81	13			
3	F	14	Total	C	N	O	P	0	0	0
			286	136	56	81	13			

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
			Total	O			S
5	A	1	5	4	1	0	0


- Molecule 6 is water.

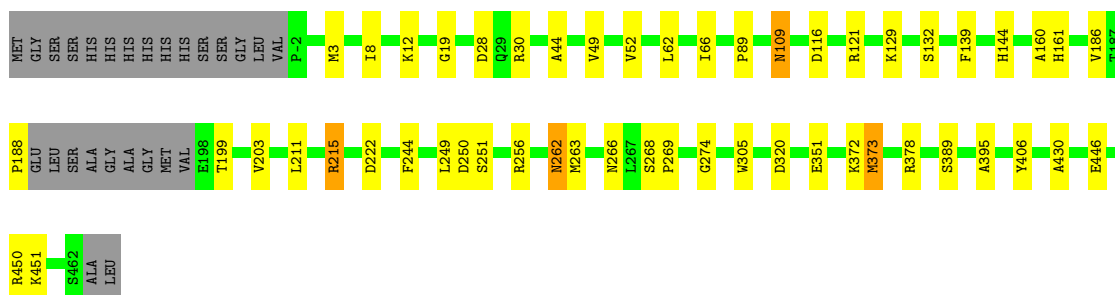
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	149	Total O 149 149	0	0
6	B	83	Total O 83 83	0	0
6	C	7	Total O 7 7	0	0
6	D	2	Total O 2 2	0	0
6	E	2	Total O 2 2	0	0
6	F	4	Total O 4 4	0	0

3 Residue-property plots


These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

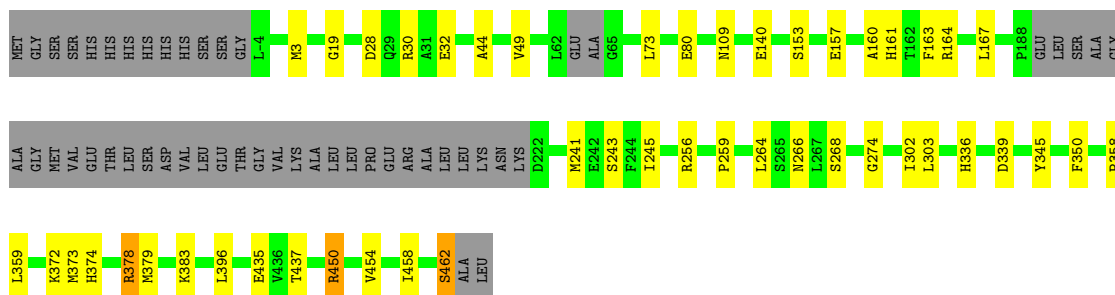
- Molecule 1: Deoxyribodipyrimidine photo-lyase

Chain A: 



- Molecule 1: Deoxyribodipyrimidine photo-lyase

Chain B: 



- Molecule 2: CPD photolesion containing DNA after repair

Chain C: 



- Molecule 2: CPD photolesion containing DNA after repair

Chain E: 



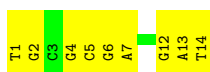
- Molecule 3: complementary oligonucleotide to the CPD containing DNA

Chain D:
93% 7%



- Molecule 3: complementary oligonucleotide to the CPD containing DNA

Chain F:
36% 64%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.53Å 115.71Å 169.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.05 – 2.55 34.05 – 2.24	Depositor EDS
% Data completeness (in resolution range)	99.9 (34.05-2.55) 100.0 (34.05-2.24)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.39 (at 2.24Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.203 , 0.224 0.204 , 0.224	Depositor DCC
R_{free} test set	3391 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8548	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.08% 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 i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, 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	0.24	0/3754	0.44	0/5093
1	B	0.24	0/3570	0.44	0/4847
2	C	1.98	6/294 (2.0%)	1.70	9/451 (2.0%)
2	E	0.52	0/294	0.94	0/451
3	D	0.46	0/321	0.80	0/494
3	F	0.44	0/321	0.73	0/494
All	All	0.46	6/8554 (0.1%)	0.60	9/11830 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	8	DT	C5-C6	26.82	1.53	1.34
2	C	8	DT	N1-C6	13.95	1.48	1.38
2	C	8	DT	C4-C5	6.76	1.51	1.45
2	C	8	DT	N3-C4	-6.49	1.33	1.38
2	C	8	DT	C2-N3	-6.12	1.32	1.37
2	C	8	DT	N1-C2	5.20	1.42	1.38

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	8	DT	C5-C6-N1	-14.91	114.76	123.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	8	DT	N1-C2-N3	14.87	123.52	114.60
2	C	8	DT	O4'-C1'-N1	14.38	118.06	108.00
2	C	8	DT	N1-C2-O2	-9.39	115.59	123.10
2	C	8	DT	C1'-O4'-C4'	-7.23	102.87	110.10
2	C	8	DT	N3-C4-C5	6.74	119.25	115.20
2	C	8	DT	C5-C4-O4	-6.63	120.26	124.90
2	C	8	DT	C6-N1-C2	-6.45	118.08	121.30
2	C	8	DT	C6-C5-C7	-5.10	119.84	122.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	8	DT	Sidechain

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	3635	0	3445	32	0
1	B	3455	0	3235	27	0
2	C	264	0	147	5	0
2	E	264	0	147	3	0
3	D	286	0	158	1	0
3	F	286	0	158	6	0
4	A	53	0	31	2	0
4	B	53	0	31	2	0
5	A	5	0	0	0	0
6	A	149	0	0	2	0
6	B	83	0	0	0	0
6	C	7	0	0	0	0
6	D	2	0	0	0	0
6	E	2	0	0	0	0
6	F	4	0	0	0	0
All	All	8548	0	7352	69	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 5.

All (69) 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:302:ILE:HG23	1:B:303:LEU:HD12	1.79	0.65
1:A:161:HIS:HB3	2:C:7:DT:OP2	1.99	0.63
1:A:451:LYS:NZ	2:C:10:DG:OP2	2.31	0.62
1:B:153:SER:OG	1:B:157:GLU:OE2	2.15	0.62
1:B:373:MET:HB3	1:B:378:ARG:HD2	1.82	0.60
1:A:305:TRP:CE3	2:C:7:DT:H72	2.37	0.59
1:B:359:LEU:HD13	1:B:454:VAL:HG13	1.85	0.59
1:A:66:ILE:HD12	1:A:215:ARG:HD2	1.83	0.59
1:A:378:ARG:HH21	4:A:501:FAD:C4X	2.16	0.58
3:F:4:DG:H2''	3:F:5:DC:H5''	1.85	0.58
1:B:28:ASP:HA	1:B:274:GLY:HA3	1.86	0.57
1:A:28:ASP:HA	1:A:274:GLY:HA3	1.87	0.57
1:A:450:ARG:NE	6:A:608:HOH:O	2.38	0.55
1:B:462:SER:O	1:B:462:SER:OG	2.25	0.55
3:F:1:DT:H2''	3:F:2:DG:OP1	2.07	0.55
1:A:262:ASN:ND2	6:A:613:HOH:O	2.41	0.53
1:B:256:ARG:HG3	1:B:256:ARG:NH1	2.24	0.53
1:A:28:ASP:HB3	1:A:30:ARG:NH1	2.24	0.52
1:B:259:PRO:HA	1:B:374:HIS:CD2	2.45	0.52
1:B:379:MET:O	1:B:383:LYS:HG3	2.11	0.51
1:A:262:ASN:HD21	1:A:266:ASN:HD21	1.58	0.51
1:A:351:GLU:OE2	1:A:406:TYR:OH	2.20	0.51
1:A:266:ASN:HA	1:A:372:LYS:HE3	1.92	0.51
1:B:435:GLU:O	1:B:437:THR:N	2.43	0.51
1:A:52:VAL:HG12	1:A:89:PRO:HG2	1.92	0.50
2:E:11:DC:H2''	2:E:12:DG:C8	2.47	0.50
1:B:256:ARG:HG3	1:B:256:ARG:HH11	1.76	0.50
1:B:358:PRO:HB2	1:B:458:ILE:HD13	1.95	0.49
1:A:251:SER:HB2	1:A:263:MET:HE2	1.94	0.49
1:A:8:ILE:HD11	1:A:139:PHE:HB3	1.95	0.49
1:A:186:VAL:HG12	1:A:188:PRO:HD2	1.95	0.49
1:B:160:ALA:O	1:B:164:ARG:N	2.43	0.48
1:A:262:ASN:C	1:A:262:ASN:HD22	2.17	0.48
1:A:62:LEU:HA	1:A:211:LEU:HD21	1.96	0.47
1:A:28:ASP:OD1	1:A:144:HIS:ND1	2.44	0.46
1:B:163:PHE:CE2	1:B:167:LEU:HD22	2.50	0.46
1:B:32:GLU:HA	1:B:32:GLU:OE1	2.15	0.45
1:A:160:ALA:HB2	1:A:305:TRP:CH2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:450[A]:ARG:H	1:B:450[A]:ARG:HG2	1.49	0.45
1:B:336:HIS:ND1	1:B:339:ASP:OD2	2.40	0.45
1:B:19:GLY:HA3	1:B:109:ASN:O	2.18	0.44
1:A:19:GLY:HA3	1:A:109:ASN:O	2.17	0.44
1:B:161:HIS:HB3	2:E:7:DT:OP2	2.18	0.44
1:A:430:ALA:HB3	3:D:8:DA:H2''	2.00	0.44
3:F:6:DG:H2''	3:F:7:DA:C8	2.52	0.43
1:A:129:LYS:HA	1:A:129:LYS:HD3	1.87	0.43
1:A:305:TRP:CD2	2:C:7:DT:H72	2.52	0.43
1:B:266:ASN:HA	1:B:372:LYS:HE3	2.00	0.43
1:A:446:GLU:H	1:A:446:GLU:CD	2.22	0.43
3:F:13:DA:H2'	3:F:14:DT:C6	2.53	0.42
1:B:28:ASP:HB3	1:B:30:ARG:NH1	2.33	0.42
1:B:241:MET:O	1:B:245:ILE:HG12	2.19	0.42
1:A:268:SER:OG	1:A:269:PRO:HD3	2.19	0.42
3:F:1:DT:H2'	3:F:2:DG:C8	2.54	0.42
1:B:345:TYR:HB2	1:B:350:PHE:CZ	2.55	0.42
2:C:11:DC:H2''	2:C:12:DG:C8	2.55	0.42
1:B:268:SER:HB3	4:B:501:FAD:H5'2	2.01	0.42
1:A:199:THR:O	1:A:203:VAL:HG23	2.20	0.42
1:A:44:ALA:HB1	1:A:49:VAL:O	2.20	0.41
1:A:244:PHE:O	1:A:249:LEU:N	2.51	0.41
1:A:121[A]:ARG:NH2	1:A:320:ASP:OD1	2.52	0.41
1:A:373:MET:O	1:A:378:ARG:HD2	2.20	0.41
1:B:378:ARG:HH21	4:B:501:FAD:C4X	2.34	0.41
1:B:44:ALA:HB1	1:B:49:VAL:O	2.21	0.41
1:B:264:LEU:HD11	1:B:374:HIS:NE2	2.35	0.41
4:A:501:FAD:H2'	4:A:501:FAD:C5A	2.51	0.41
3:F:12:DG:H2''	3:F:13:DA:H5''	2.02	0.40
1:A:389[A]:SER:OG	1:A:395:ALA:HB2	2.21	0.40
2:E:4:DG:H4'	2:E:5:DG:OP1	2.21	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	458/482 (95%)	452 (99%)	6 (1%)	0	100	100
1	B	432/482 (90%)	431 (100%)	1 (0%)	0	100	100
All	All	890/964 (92%)	883 (99%)	7 (1%)	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	371/416 (89%)	359 (97%)	12 (3%)	39	53
1	B	352/416 (85%)	341 (97%)	11 (3%)	40	54
All	All	723/832 (87%)	700 (97%)	23 (3%)	43	53

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	MET
1	A	12	LYS
1	A	109	ASN
1	A	116	ASP
1	A	132[A]	SER
1	A	132[B]	SER
1	A	215	ARG
1	A	222	ASP
1	A	250	ASP
1	A	256	ARG
1	A	262	ASN
1	A	373	MET
1	B	3[A]	MET
1	B	3[B]	MET
1	B	73	LEU

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Mol	Chain	Res	Type
1	B	80	GLU
1	B	140	GLU
1	B	243	SER
1	B	378	ARG
1	B	396	LEU
1	B	450[A]	ARG
1	B	450[B]	ARG
1	B	462	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	GLN
1	A	262	ASN
1	A	266	ASN

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 [i](#)

3 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	FAD	B	501	-	53,58,58	0.46	0	68,89,89	0.53	2 (2%)
5	SO4	A	502	-	4,4,4	0.14	0	6,6,6	0.05	0
4	FAD	A	501	-	53,58,58	1.82	8 (15%)	68,89,89	1.43	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
4	FAD	B	501	-	-	6/30/50/50	0/6/6/6
4	FAD	A	501	-	-	4/30/50/50	0/6/6/6

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	501	FAD	C9A-N10	-6.23	1.30	1.41
4	A	501	FAD	O4-C4	5.84	1.34	1.23
4	A	501	FAD	O2-C2	5.54	1.34	1.24
4	A	501	FAD	C4-N3	-3.92	1.31	1.38
4	A	501	FAD	C2-N3	-2.90	1.32	1.39
4	A	501	FAD	C8M-C8	2.85	1.56	1.51
4	A	501	FAD	C10-N10	-2.71	1.31	1.37
4	A	501	FAD	C7M-C7	2.23	1.55	1.51

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	501	FAD	C5X-N5-C4X	-4.48	110.63	118.07
4	A	501	FAD	C4X-C10-N10	3.69	121.88	116.48
4	A	501	FAD	C4X-C10-N1	-3.62	116.32	124.73
4	A	501	FAD	C4X-C4-N3	3.35	121.70	113.19
4	A	501	FAD	C4-N3-C2	-3.21	119.71	125.64
4	A	501	FAD	C9A-N10-C10	-3.16	115.84	120.77
4	B	501	FAD	P-O3P-PA	-2.62	123.82	132.83
4	A	501	FAD	C5X-C9A-N10	2.58	120.62	117.95
4	A	501	FAD	C10-N1-C2	2.47	121.84	116.90
4	B	501	FAD	C5A-C6A-N6A	2.28	123.81	120.35
4	A	501	FAD	C5A-C6A-N6A	2.28	123.81	120.35
4	A	501	FAD	O4-C4-N3	-2.24	115.82	120.12
4	A	501	FAD	P-O3P-PA	-2.22	125.19	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	501	FAD	C9-C9A-C5X	-2.02	116.29	120.11

There are no chirality outliers.

All (10) torsion outliers are listed below:

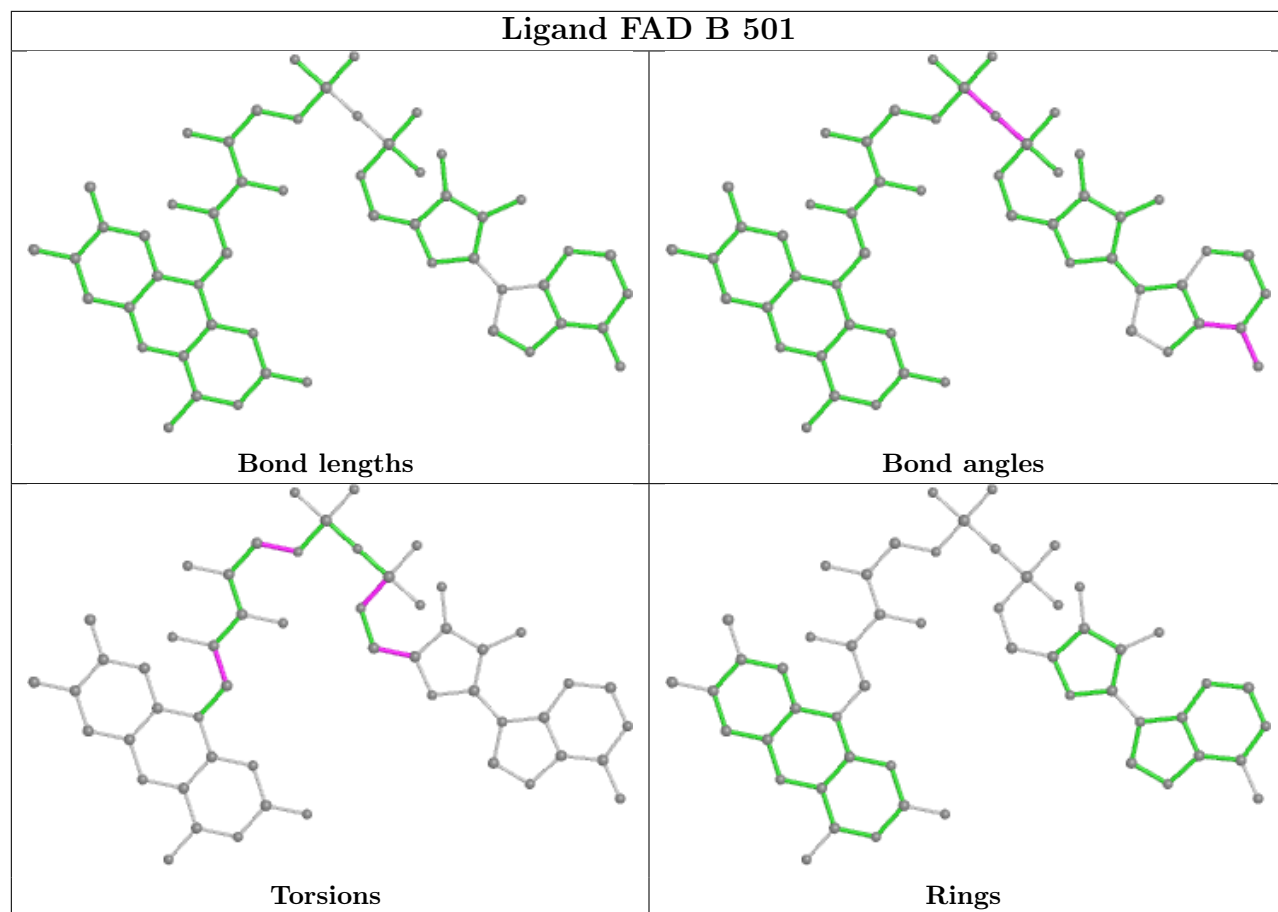
Mol	Chain	Res	Type	Atoms
4	A	501	FAD	C5B-O5B-PA-O1A
4	A	501	FAD	C5B-O5B-PA-O2A
4	B	501	FAD	C5B-O5B-PA-O2A
4	B	501	FAD	C5B-O5B-PA-O3P
4	B	501	FAD	N10-C1'-C2'-C3'
4	B	501	FAD	O4B-C4B-C5B-O5B
4	A	501	FAD	C4'-C5'-O5'-P
4	B	501	FAD	C4'-C5'-O5'-P
4	B	501	FAD	C3B-C4B-C5B-O5B
4	A	501	FAD	C5B-O5B-PA-O3P

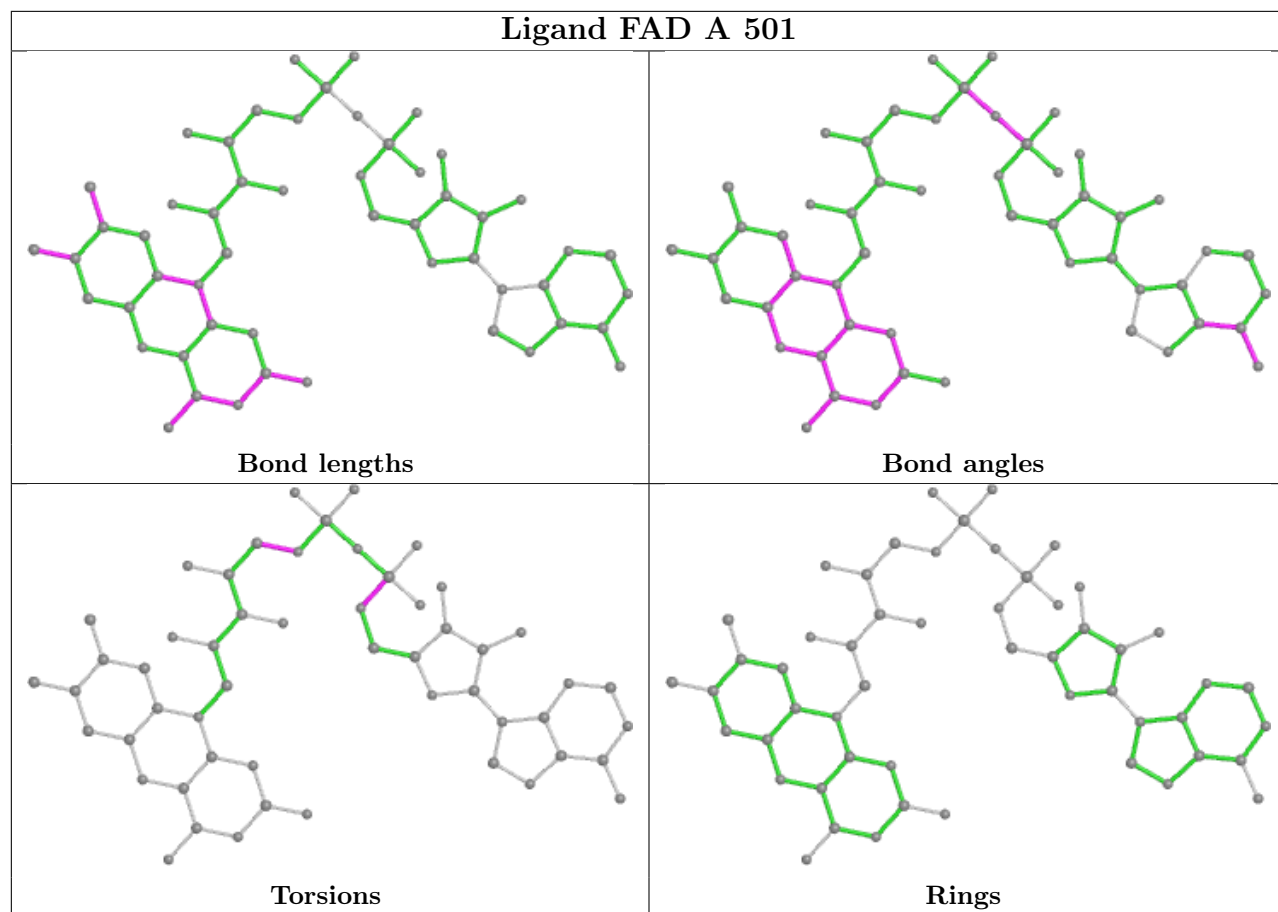
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	501	FAD	2	0
4	A	501	FAD	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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

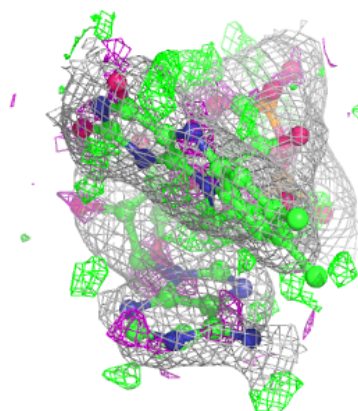
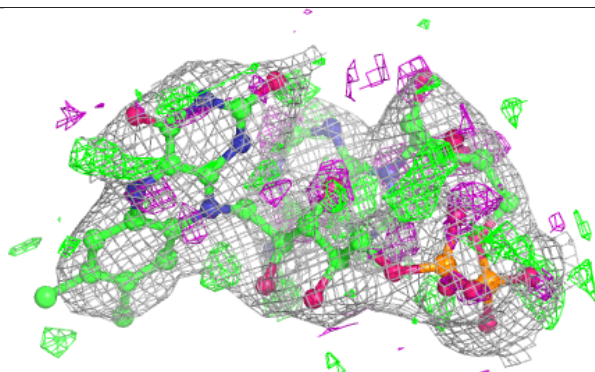
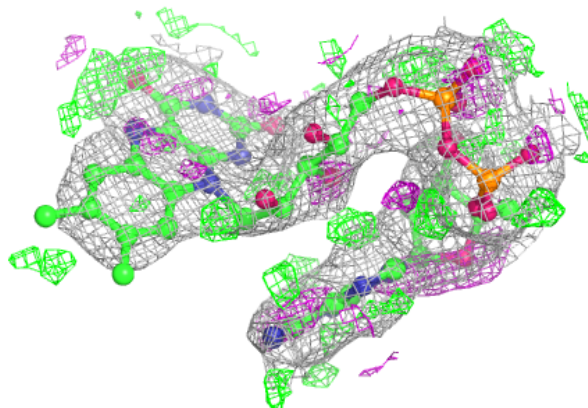
6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

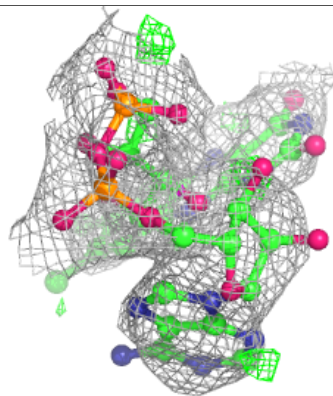
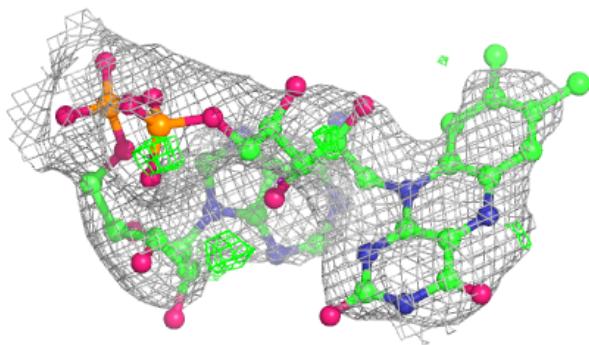
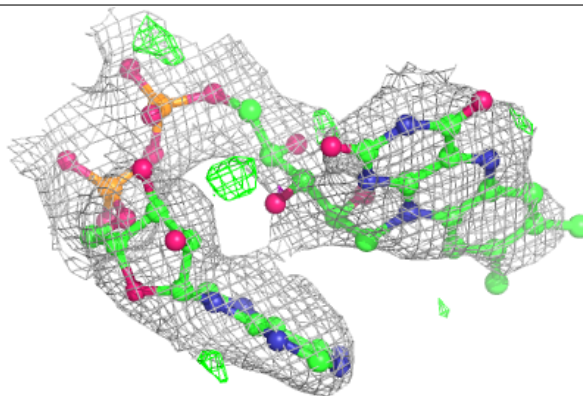
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation 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)

**Electron density around FAD B 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

Unable to reproduce the depositors R factor - this section is therefore empty.