



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 07:31 AM UTC

PDB ID : 7VJI / pdb_00007vji

Title : class II photolyase MmCPDII semiquinone to fully reduced TR-SFX studies (10 us time-point)

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Deposited on : 2021-09-28

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

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)

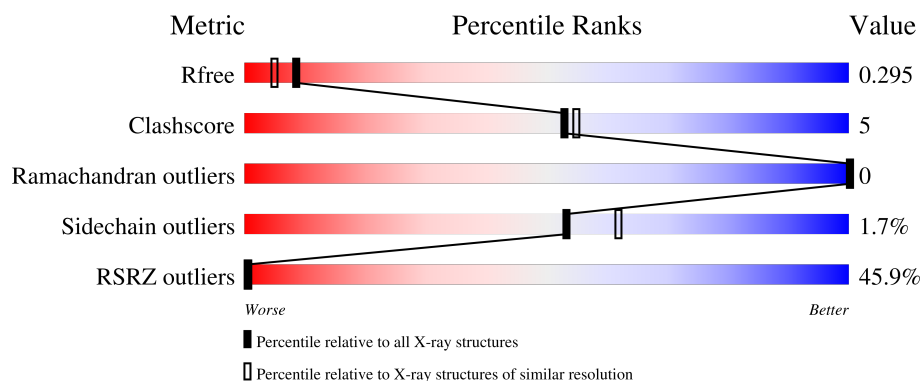
1 Overall quality at a glance

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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	482	

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

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3813 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.

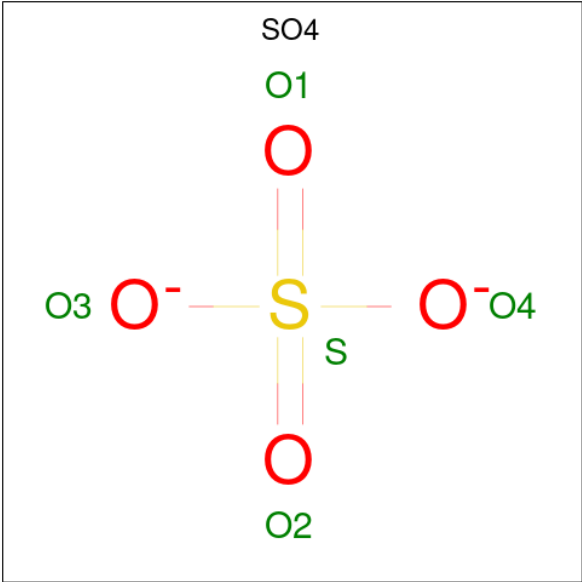
- Molecule 1 is a protein called DNA photolyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	453	Total	C	N	O	S	0	7	0
			3577	2318	585	658	16			

There are 21 discrepancies between the modelled and reference sequences:

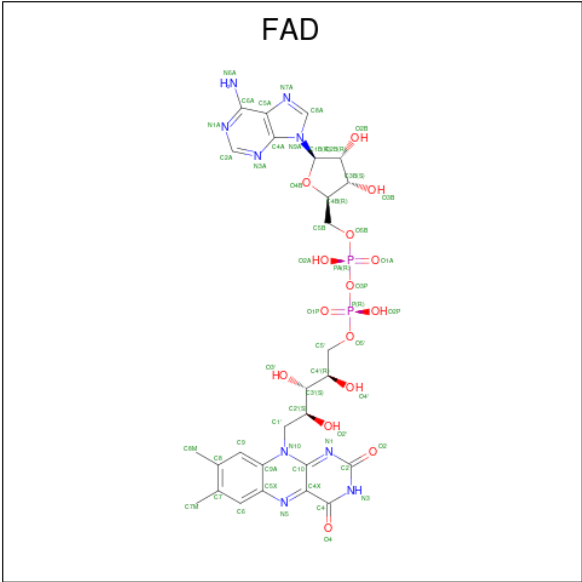
Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	initiating methionine	UNP Q8PYK9
A	-16	GLY	-	expression tag	UNP Q8PYK9
A	-15	SER	-	expression tag	UNP Q8PYK9
A	-14	SER	-	expression tag	UNP Q8PYK9
A	-13	HIS	-	expression tag	UNP Q8PYK9
A	-12	HIS	-	expression tag	UNP Q8PYK9
A	-11	HIS	-	expression tag	UNP Q8PYK9
A	-10	HIS	-	expression tag	UNP Q8PYK9
A	-9	HIS	-	expression tag	UNP Q8PYK9
A	-8	HIS	-	expression tag	UNP Q8PYK9
A	-7	SER	-	expression tag	UNP Q8PYK9
A	-6	SER	-	expression tag	UNP Q8PYK9
A	-5	GLY	-	expression tag	UNP Q8PYK9
A	-4	LEU	-	expression tag	UNP Q8PYK9
A	-3	VAL	-	expression tag	UNP Q8PYK9
A	-2	PRO	-	expression tag	UNP Q8PYK9
A	-1	ARG	-	expression tag	UNP Q8PYK9
A	0	GLY	-	expression tag	UNP Q8PYK9
A	1	SER	-	expression tag	UNP Q8PYK9
A	2	HIS	-	expression tag	UNP Q8PYK9
A	377	THR	MET	engineered mutation	UNP Q8PYK9

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



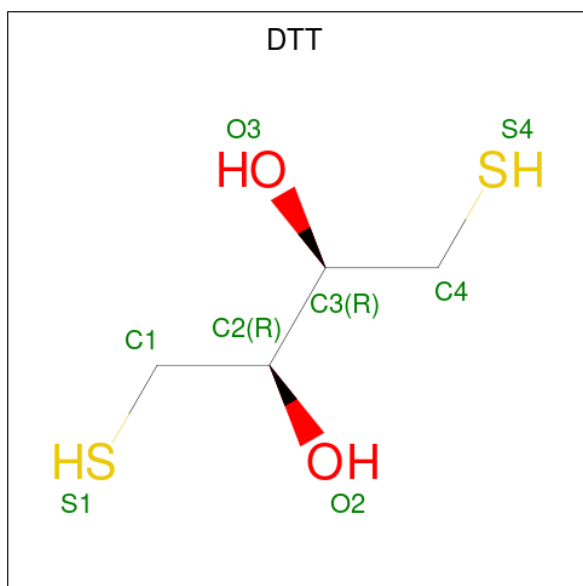
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (CCD ID: DTT) (formula: $C_4H_{10}O_2S_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	S	0	0
			8	4	2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	160	Total	O	0	0
			160	160		

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	70.52Å 70.52Å 246.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.68 – 2.10 31.68 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (31.68-2.10) 100.0 (31.68-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 1.95Å)	Xtriage
Refinement program	PHENIX (1.19_4092: ???)	Depositor
R, R_{free}	0.214 , 0.240 0.278 , 0.295	Depositor DCC
R_{free} test set	2254 reflections (1.99%)	wwPDB-VP
Wilson B-factor (Å ²)	13.8	Xtriage
Anisotropy	0.212	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	3813	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.34% 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: FAD, DTT, SO4

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	0.16	0/3699	0.26	1/5029 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	378	ARG	CB-CG-CD	5.23	123.32	111.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3577	0	3359	34	0
2	A	15	0	0	1	0
3	A	53	0	28	1	0
4	A	8	0	10	0	0
5	A	160	0	0	5	0
All	All	3813	0	3397	35	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 (35) 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:373:MET:O	1:A:378:ARG:HD2	1.91	0.71
1:A:218:LEU:HD12	1:A:220:ASN:H	1.58	0.68
1:A:68:GLN:NE2	5:A:602:HOH:O	2.33	0.61
1:A:199:THR:HG22	1:A:201:SER:H	1.66	0.60
1:A:266:ASN:HA	1:A:372:LYS:HE3	1.81	0.60
1:A:18:ASP:OD1	1:A:109:ASN:ND2	2.36	0.58
1:A:129:LYS:NZ	5:A:611:HOH:O	2.40	0.55
1:A:52:VAL:HG12	1:A:89:PRO:HG2	1.88	0.55
1:A:251:SER:HB3	1:A:255:LEU:HD13	1.88	0.54
1:A:105:VAL:HG13	1:A:110:ALA:HB3	1.90	0.54
1:A:245:ILE:HD12	1:A:249:LEU:HD22	1.91	0.52
1:A:92:PHE:O	1:A:197:VAL:N	2.43	0.51
1:A:357:ASP:OD2	1:A:380:TYR:OH	2.23	0.49
1:A:373:MET:HE1	1:A:381:TRP:CG	2.47	0.49
1:A:66:ILE:HD12	1:A:215:ARG:HG3	1.95	0.48
1:A:238:LYS:O	1:A:242:GLU:HG3	2.14	0.47
1:A:215:ARG:NH1	5:A:621:HOH:O	2.49	0.46
3:A:503:FAD:H8A	3:A:503:FAD:O5B	2.15	0.46
1:A:4:ASN:ND2	5:A:622:HOH:O	2.49	0.45
1:A:259:PRO:HA	1:A:374:HIS:CD2	2.52	0.45
1:A:67:ARG:NE	2:A:501:SO4:O3	2.50	0.45
1:A:366:GLU:OE1	1:A:457:TYR:OH	2.18	0.45
1:A:28:ASP:HA	1:A:274:GLY:HA3	1.99	0.44
1:A:345:TYR:HB2	1:A:350:PHE:CZ	2.53	0.44
1:A:435:GLU:O	1:A:437:THR:N	2.47	0.43
1:A:49:VAL:HG22	1:A:50:PRO:HD2	2.01	0.41
1:A:337:ARG:NH2	1:A:393:GLU:OE2	2.27	0.41
1:A:403:ASN:ND2	1:A:403:ASN:C	2.79	0.41
1:A:345:TYR:OH	1:A:356:HIS:ND1	2.44	0.41
1:A:171:LEU:HD23	1:A:171:LEU:HA	1.89	0.41
1:A:411:ARG:NE	5:A:626:HOH:O	2.50	0.41
1:A:167:LEU:HD23	1:A:304:ILE:HD13	2.03	0.40
1:A:334:ASN:HA	1:A:337:ARG:HG3	2.04	0.40
1:A:22:VAL:HA	1:A:52:VAL:HG23	2.03	0.40
1:A:268:SER:OG	1:A:269:PRO:HD3	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	456/482 (95%)	443 (97%)	13 (3%)	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	359/416 (86%)	353 (98%)	6 (2%)	53	62

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ARG
1	A	49	VAL
1	A	79	LEU
1	A	155	LYS
1	A	403	ASN
1	A	456	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	403	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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	DTT	A	505	-	7,7,7	0.67	0	4,8,8	1.24	0
2	SO4	A	502	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	A	504	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	A	501	-	4,4,4	0.23	0	6,6,6	0.07	0
3	FAD	A	503	-	58,58,58	3.54	28 (48%)	85,89,89	2.09	24 (28%)

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
3	FAD	A	503	-	-	3/34/50/50	0/6/6/6
4	DTT	A	505	-	-	6/8/8/8	-

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	503	FAD	PA-O3P	8.21	1.68	1.59
3	A	503	FAD	P-O3P	7.48	1.67	1.59
3	A	503	FAD	O2'-C2'	-7.43	1.27	1.43
3	A	503	FAD	O4'-C4'	-6.89	1.28	1.43
3	A	503	FAD	C3B-C4B	-6.77	1.35	1.53
3	A	503	FAD	C4'-C3'	-6.62	1.41	1.53
3	A	503	FAD	C9A-N10	-6.36	1.30	1.41
3	A	503	FAD	C2'-C3'	-5.90	1.43	1.53
3	A	503	FAD	O4-C4	5.89	1.34	1.23
3	A	503	FAD	C2B-C1B	-5.79	1.35	1.53
3	A	503	FAD	C2B-C3B	-5.76	1.37	1.53
3	A	503	FAD	C8A-N9A	-5.62	1.28	1.37
3	A	503	FAD	O2-C2	5.50	1.35	1.24
3	A	503	FAD	C6A-N6A	4.52	1.45	1.34
3	A	503	FAD	C4-N3	-4.21	1.31	1.38
3	A	503	FAD	O3'-C3'	-3.56	1.34	1.43
3	A	503	FAD	C4A-N9A	-3.53	1.30	1.37
3	A	503	FAD	C1B-N9A	-3.40	1.36	1.46
3	A	503	FAD	P-O5'	2.89	1.70	1.59
3	A	503	FAD	C5B-C4B	-2.89	1.42	1.51
3	A	503	FAD	C2-N3	-2.70	1.33	1.39
3	A	503	FAD	C10-N10	-2.64	1.31	1.37
3	A	503	FAD	PA-O2A	2.54	1.67	1.55
3	A	503	FAD	PA-O5B	2.48	1.69	1.59
3	A	503	FAD	C8M-C8	2.46	1.55	1.51
3	A	503	FAD	P-O2P	2.33	1.66	1.55
3	A	503	FAD	C5A-C4A	2.22	1.43	1.39
3	A	503	FAD	C5X-N5	-2.14	1.35	1.39

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	503	FAD	C4A-N9A-C8A	8.22	114.37	105.74
3	A	503	FAD	C5A-C4A-N3A	-5.65	118.94	126.72
3	A	503	FAD	N3A-C4A-N9A	5.55	136.60	127.17
3	A	503	FAD	C4A-C5A-N7A	-4.59	105.34	110.58
3	A	503	FAD	N3A-C2A-N1A	-4.14	122.32	128.58
3	A	503	FAD	N9A-C8A-N7A	-3.85	108.47	113.94
3	A	503	FAD	C5X-N5-C4X	-3.74	112.04	118.09
3	A	503	FAD	C5'-C4'-C3'	-3.63	105.38	112.22
3	A	503	FAD	C4X-C10-N1	-3.44	116.16	124.59
3	A	503	FAD	C2A-N3A-C4A	3.38	120.10	111.83
3	A	503	FAD	C4X-C10-N10	3.19	121.05	116.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	503	FAD	C4-N3-C2	-3.01	120.30	125.64
3	A	503	FAD	C4X-C4-N3	3.00	120.88	113.25
3	A	503	FAD	C4B-O4B-C1B	-2.87	103.13	109.47
3	A	503	FAD	C4-C4X-N5	-2.64	114.56	118.21
3	A	503	FAD	C5A-N7A-C8A	2.49	107.36	103.45
3	A	503	FAD	C6A-C5A-N7A	2.46	136.83	132.09
3	A	503	FAD	O4-C4-C4X	-2.43	120.11	126.53
3	A	503	FAD	C5X-C9A-N10	2.43	120.16	117.97
3	A	503	FAD	C3B-C2B-C1B	2.18	105.60	101.46
3	A	503	FAD	C10-N1-C2	2.16	121.52	116.85
3	A	503	FAD	C9A-N10-C10	-2.15	117.47	120.75
3	A	503	FAD	C4A-N9A-C1B	-2.10	121.73	126.63
3	A	503	FAD	C4-C4X-C10	2.05	120.45	116.93

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	503	FAD	O4'-C4'-C5'-O5'
4	A	505	DTT	C1-C2-C3-O3
4	A	505	DTT	C1-C2-C3-C4
4	A	505	DTT	O2-C2-C3-O3
4	A	505	DTT	O2-C2-C3-C4
4	A	505	DTT	C2-C3-C4-S4
4	A	505	DTT	O3-C3-C4-S4
3	A	503	FAD	C4'-C5'-O5'-P
3	A	503	FAD	P-O3P-PA-O1A

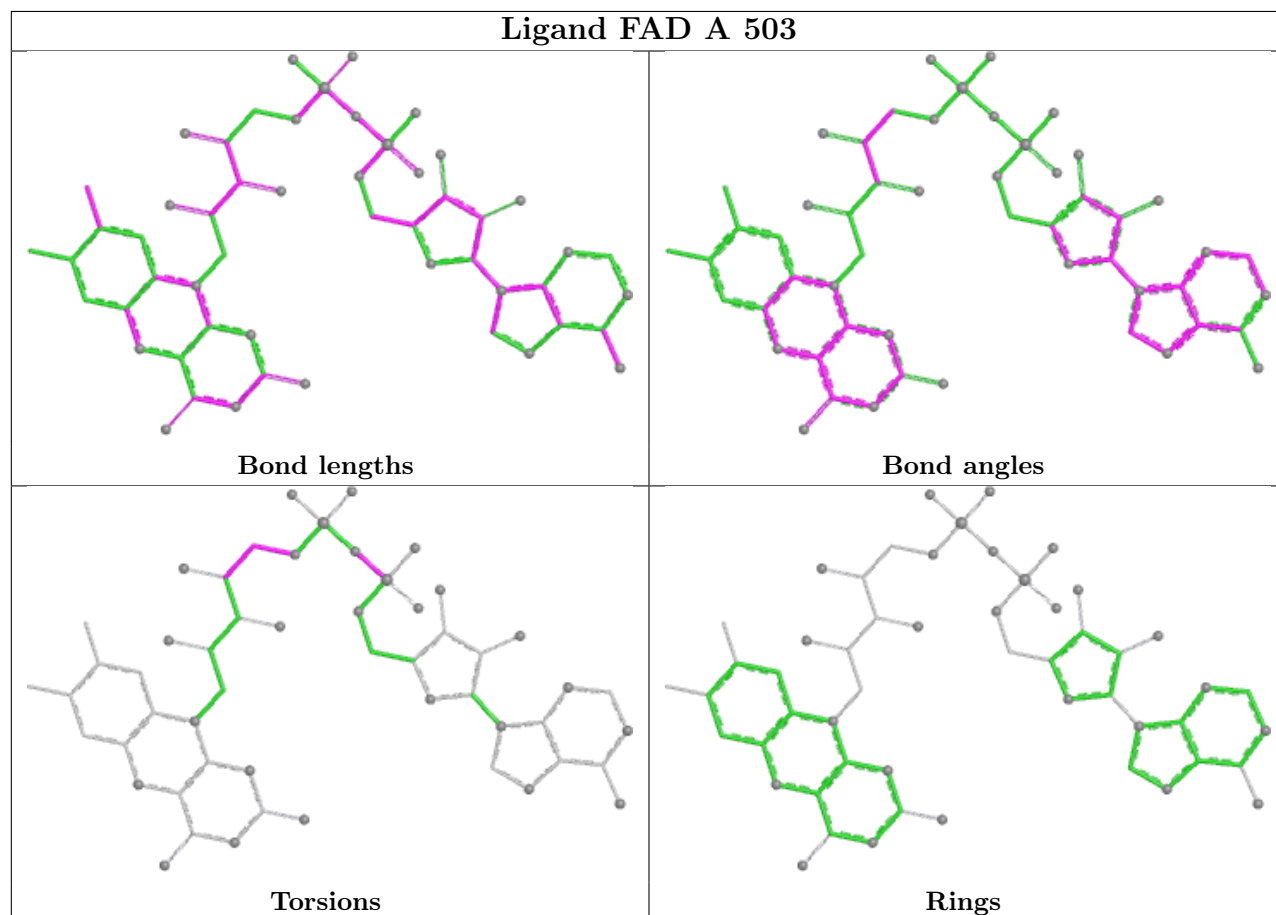
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	SO4	1	0
3	A	503	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 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	453/482 (93%)	2.04	208 (45%) 0 0	17, 36, 56, 86	10 (2%)

All (208) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	186	VAL	7.1
1	A	197	VAL	7.0
1	A	218	LEU	5.7
1	A	462	SER	5.5
1	A	220	ASN	5.3
1	A	16	GLN	5.2
1	A	233	GLY	5.2
1	A	49	VAL	4.9
1	A	86	LYS	4.9
1	A	203	VAL	4.9
1	A	84	SER	4.8
1	A	291	ASN	4.8
1	A	431	TRP	4.7
1	A	39	PHE	4.7
1	A	198	GLU	4.6
1	A	343	HIS	4.5
1	A	13	SER	4.5
1	A	189	GLU	4.5
1	A	205	GLU	4.5
1	A	18	ASP	4.4
1	A	294	SER	4.3
1	A	251	SER	4.3
1	A	219	LYS	4.2
1	A	132	SER	4.2
1	A	108	TYR	4.2
1	A	202	ASP	4.1
1	A	342	SER	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	19	GLY	4.1
1	A	104	PHE	4.0
1	A	201	SER	4.0
1	A	42	ALA	4.0
1	A	217	LEU	3.9
1	A	52	VAL	3.9
1	A	158	TYR	3.8
1	A	362	ALA	3.8
1	A	188	PRO	3.8
1	A	17	GLY	3.7
1	A	185	SER	3.7
1	A	168	TYR	3.7
1	A	199	THR	3.7
1	A	43	ILE	3.7
1	A	350	PHE	3.6
1	A	187	THR	3.6
1	A	204	LEU	3.6
1	A	20	PRO	3.5
1	A	454	VAL	3.5
1	A	262	ASN	3.5
1	A	61	PHE	3.4
1	A	208	VAL	3.4
1	A	344	ILE	3.4
1	A	87	LYS	3.4
1	A	167	LEU	3.4
1	A	50	PRO	3.3
1	A	88	ILE	3.3
1	A	83	LEU	3.3
1	A	3	MET	3.3
1	A	45	LYS	3.2
1	A	381	TRP	3.2
1	A	340	VAL	3.2
1	A	47	ALA	3.2
1	A	290	SER	3.2
1	A	212	LEU	3.1
1	A	161	HIS	3.1
1	A	221	LYS	3.1
1	A	182	GLU	3.1
1	A	164	ARG	3.1
1	A	449	LYS	3.1
1	A	174	PHE	3.1
1	A	53	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	81	VAL	3.1
1	A	105	VAL	3.1
1	A	200	LEU	3.1
1	A	109	ASN	3.0
1	A	184	ASN	3.0
1	A	91	PHE	3.0
1	A	48	ASN	3.0
1	A	438	GLY	3.0
1	A	356	HIS	3.0
1	A	82	SER	3.0
1	A	335	ALA	3.0
1	A	21	VAL	3.0
1	A	54	VAL	3.0
1	A	456	LEU	2.9
1	A	101	ILE	2.9
1	A	388	TRP	2.9
1	A	216	ALA	2.9
1	A	170	LEU	2.9
1	A	98	GLY	2.9
1	A	432	GLY	2.9
1	A	136	ILE	2.9
1	A	437	THR	2.9
1	A	46	GLU	2.9
1	A	44	ALA	2.9
1	A	110	ALA	2.9
1	A	255	LEU	2.9
1	A	102	SER	2.9
1	A	85	ARG	2.8
1	A	440	ILE	2.8
1	A	135	SER	2.8
1	A	457	TYR	2.8
1	A	222	ASP	2.8
1	A	303	LEU	2.8
1	A	215	ARG	2.8
1	A	348	GLU	2.8
1	A	181	LEU	2.8
1	A	245	ILE	2.8
1	A	107	ASP	2.7
1	A	89	PRO	2.7
1	A	240	VAL	2.7
1	A	106	LYS	2.7
1	A	297	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	69	TYR	2.7
1	A	134	ILE	2.7
1	A	40	SER	2.7
1	A	169	ALA	2.7
1	A	236	ALA	2.7
1	A	299	LEU	2.7
1	A	183	PRO	2.7
1	A	228	TRP	2.7
1	A	62	LEU	2.6
1	A	445	TYR	2.6
1	A	57	LEU	2.6
1	A	359	LEU	2.6
1	A	345	TYR	2.6
1	A	77	GLN	2.6
1	A	452	PHE	2.6
1	A	56[A]	CYS	2.6
1	A	339	ASP	2.6
1	A	126[A]	TRP	2.6
1	A	249	LEU	2.6
1	A	305	TRP	2.6
1	A	298	PHE	2.5
1	A	214	GLU	2.5
1	A	8	ILE	2.5
1	A	163	PHE	2.5
1	A	177	GLU	2.5
1	A	435	GLU	2.5
1	A	260	THR	2.5
1	A	327	SER	2.5
1	A	246	ALA	2.5
1	A	292	PRO	2.5
1	A	211	LEU	2.5
1	A	55	PHE	2.5
1	A	443	MET	2.4
1	A	176	GLU	2.4
1	A	23	TYR	2.4
1	A	162	THR	2.4
1	A	206	THR	2.4
1	A	6	LYS	2.4
1	A	99	GLU	2.4
1	A	322	PHE	2.4
1	A	357	ASP	2.4
1	A	254	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	38	LEU	2.4
1	A	267	LEU	2.4
1	A	293	GLY	2.4
1	A	448	CYS	2.4
1	A	349	GLU	2.3
1	A	76	LEU	2.3
1	A	128	GLU	2.3
1	A	289	GLU	2.3
1	A	402	LEU	2.3
1	A	434	ARG	2.3
1	A	458	ILE	2.3
1	A	97	PRO	2.3
1	A	237	ALA	2.3
1	A	417	ALA	2.3
1	A	14	GLY	2.3
1	A	171	LEU	2.3
1	A	256	ARG	2.3
1	A	451	LYS	2.3
1	A	265	SER	2.3
1	A	281	VAL	2.3
1	A	338	ASN	2.3
1	A	96	ASP	2.3
1	A	263	MET	2.3
1	A	22	VAL	2.2
1	A	111	GLY	2.2
1	A	241	MET	2.2
1	A	421	TRP	2.2
1	A	264	LEU	2.2
1	A	24	TRP	2.2
1	A	436	VAL	2.2
1	A	80	GLU	2.2
1	A	378	ARG	2.2
1	A	92	PHE	2.1
1	A	32	GLU	2.1
1	A	70	GLU	2.1
1	A	5	PRO	2.1
1	A	360	TRP	2.1
1	A	426	VAL	2.1
1	A	79	LEU	2.1
1	A	137	PRO	2.1
1	A	346	THR	2.1
1	A	328	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	352	ALA	2.1
1	A	430	ALA	2.1
1	A	175	LEU	2.1
1	A	283	LEU	2.1
1	A	397	GLU	2.1
1	A	442	TYR	2.1
1	A	287	LYS	2.1
1	A	210	ALA	2.1
1	A	224	LEU	2.0
1	A	361	ASN	2.0
1	A	59	ASP	2.0
1	A	252	TYR	2.0
1	A	444	SER	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](#)

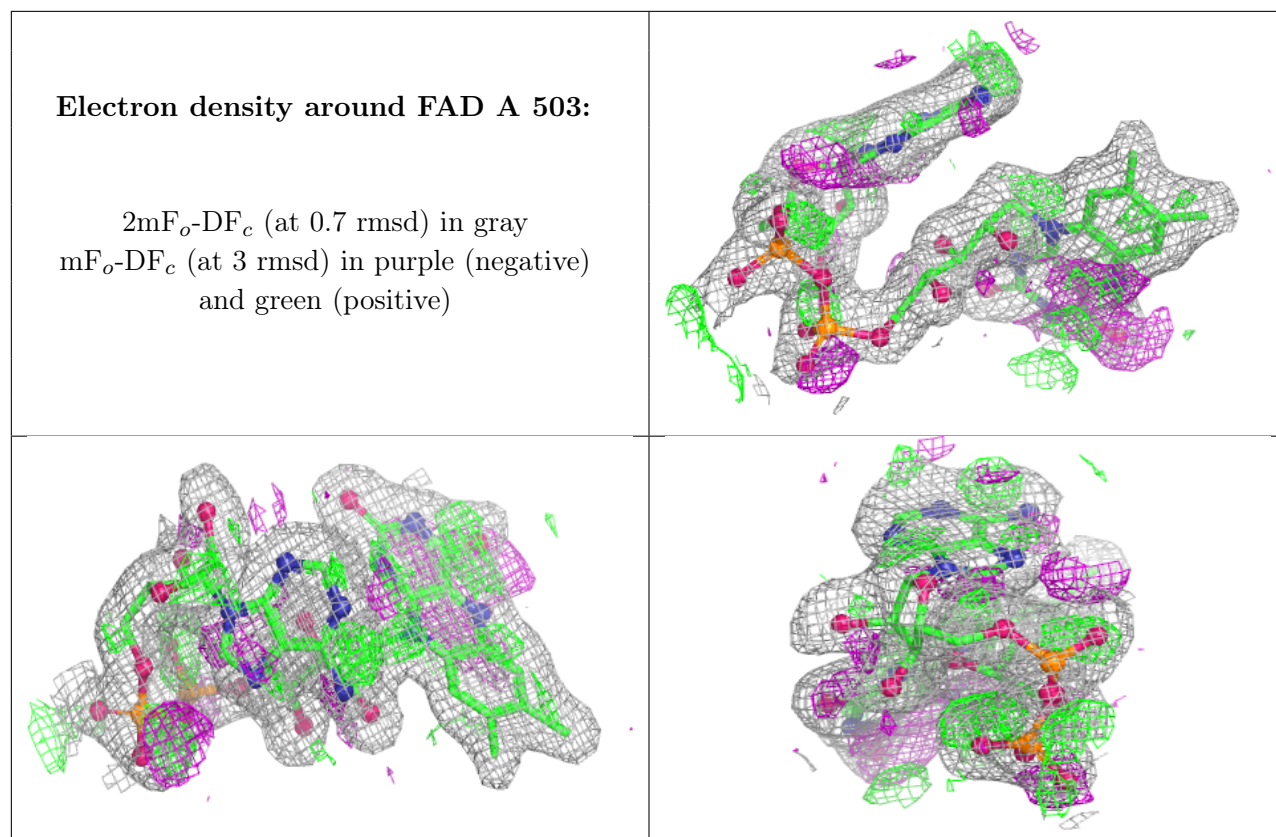
There are no oligosaccharides in this entry.

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
2	SO4	A	504	5/5	0.55	0.16	71,78,81,84	0
4	DTT	A	505	8/8	0.69	0.31	23,24,25,27	8
2	SO4	A	502	5/5	0.76	0.22	47,50,58,58	0
3	FAD	A	503	53/53	0.87	0.15	22,23,24,35	0
2	SO4	A	501	5/5	0.93	0.13	28,29,34,35	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.