



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 03:01 AM UTC

PDB ID : 2FPY / pdb_00002fpy
Title : Dual binding mode of a novel series of DHODH inhibitors
Authors : Baumgartner, R.; Leban, J.
Deposited on : 2006-01-17
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)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

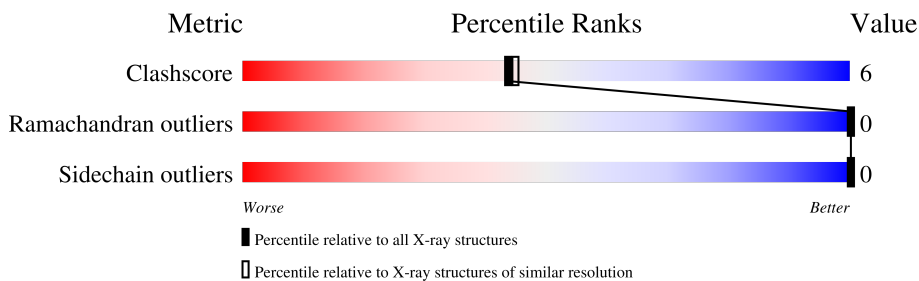
1 Overall quality at a glance

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))
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	395	 78% 14% 8%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 3177 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 Dihydroorotate dehydrogenase, mitochondrial precursor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	364	2785	1746	517	518	4	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

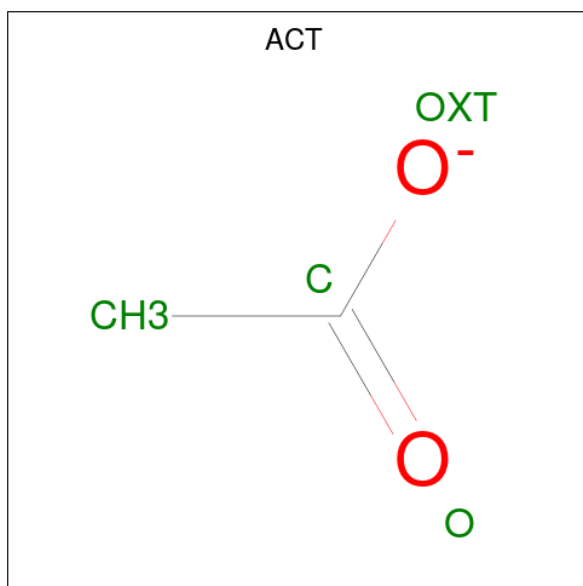
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	MET	-	cloning artifact	UNP Q02127
A	3	GLY	-	cloning artifact	UNP Q02127
A	4	HIS	-	expression tag	UNP Q02127
A	5	HIS	-	expression tag	UNP Q02127
A	6	HIS	-	expression tag	UNP Q02127
A	7	HIS	-	expression tag	UNP Q02127
A	8	HIS	-	expression tag	UNP Q02127
A	9	HIS	-	expression tag	UNP Q02127
A	10	HIS	-	expression tag	UNP Q02127
A	11	HIS	-	expression tag	UNP Q02127
A	12	HIS	-	expression tag	UNP Q02127
A	13	HIS	-	expression tag	UNP Q02127
A	14	SER	-	cloning artifact	UNP Q02127
A	15	SER	-	cloning artifact	UNP Q02127
A	16	GLY	-	cloning artifact	UNP Q02127
A	17	HIS	-	cloning artifact	UNP Q02127
A	18	ILE	-	cloning artifact	UNP Q02127
A	19	ASP	-	cloning artifact	UNP Q02127
A	20	ASP	-	cloning artifact	UNP Q02127
A	21	ASP	-	cloning artifact	UNP Q02127
A	22	ASP	-	cloning artifact	UNP Q02127
A	23	LYS	-	cloning artifact	UNP Q02127
A	24	HIS	-	cloning artifact	UNP Q02127
A	25	MET	-	cloning artifact	UNP Q02127
A	26	LEU	-	cloning artifact	UNP Q02127
A	27	GLU	-	cloning artifact	UNP Q02127
A	28	ASP	-	cloning artifact	UNP Q02127

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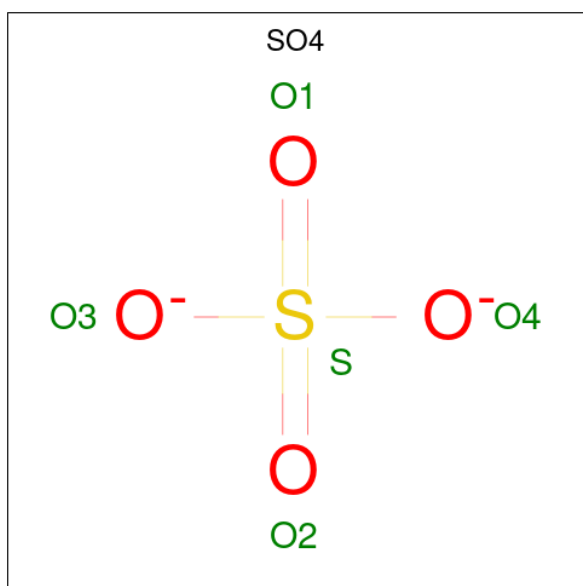
Chain	Residue	Modelled	Actual	Comment	Reference
A	29	PRO	-	cloning artifact	UNP Q02127

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



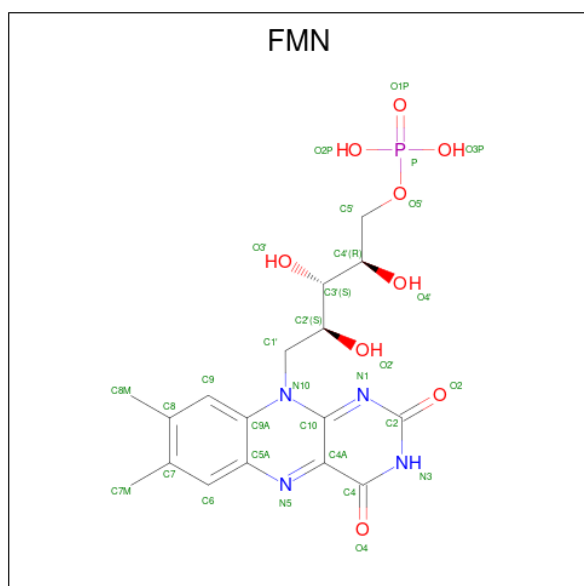
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	4	2	2	0	0

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



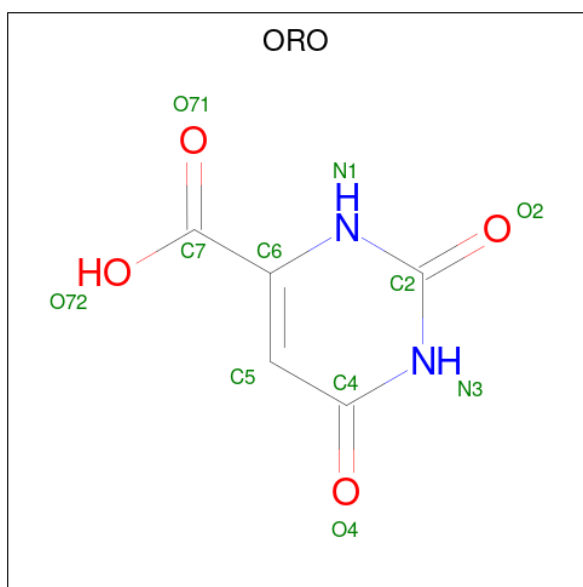
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0

- Molecule 4 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



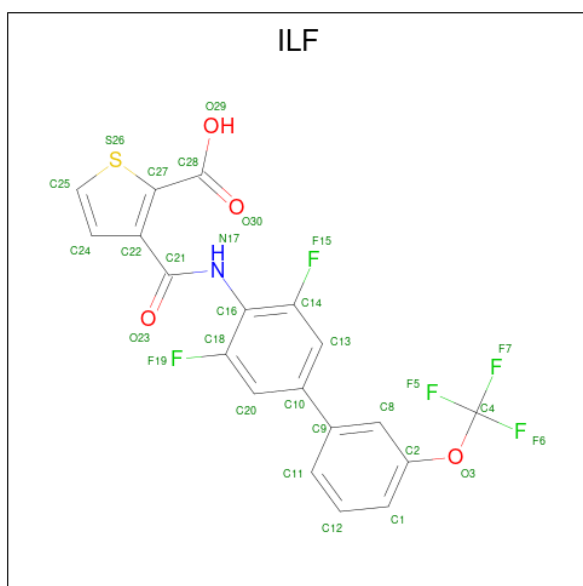
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O P 31 17 4 9 1	0	0

- Molecule 5 is OROTIC ACID (CCD ID: ORO) (formula: $C_5H_4N_2O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	11	5	2	4	0	0

- Molecule 6 is 3-({[3,5-DIFLUORO-3'-(TRIFLUOROMETHOXY)BIPHENYL-4-YL]AMINO}CARBONYL)THIOPHENE-2-CARBOXYLIC ACID (CCD ID: ILF) (formula: C₁₉H₁₀F₅NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	F	N	O			S
6	A	1	30	19	5	1	4	1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	291	Total 291	O 291	0	0

4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	90.30Å 90.30Å 122.69Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	17.22 – 2.00	Depositor
% Data completeness (in resolution range)	98.5 (17.22-2.00)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS, CNX 2002	Depositor
R, R_{free}	0.181 , 0.200	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	3177	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

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: FMN, ORO, ILF, ACT, 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	0.34	0/2831	0.89	11/3824 (0.3%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	LEU	CA-C-N	5.51	124.97	119.24
1	A	137	LEU	C-N-CA	5.51	124.97	119.24
1	A	364	PRO	N-CA-C	5.51	117.42	110.70
1	A	363	GLY	CA-C-N	5.42	125.96	120.38
1	A	363	GLY	C-N-CA	5.42	125.96	120.38
1	A	207	ASP	N-CA-C	-5.28	105.58	112.23
1	A	251	ALA	N-CA-C	-5.22	102.75	110.48
1	A	150	ASN	N-CA-C	-5.13	102.05	109.59
1	A	176	LEU	CA-C-N	5.01	124.99	120.03
1	A	176	LEU	C-N-CA	5.01	124.99	120.03
1	A	278	ASP	N-CA-C	5.00	117.62	111.82

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	2785	0	2849	35	0
2	A	4	0	3	0	0
3	A	25	0	0	0	0
4	A	31	0	19	0	0
5	A	11	0	3	0	0
6	A	30	0	9	0	0
7	A	291	0	0	2	0
All	All	3177	0	2883	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 6.

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:89:ARG:HD2	1:A:176:LEU:HD21	1.66	0.77
1:A:52:PRO:HB2	1:A:134:VAL:HG13	1.68	0.76
1:A:215:SER:HB3	1:A:221:LEU:HD23	1.77	0.66
1:A:33:GLY:HA3	1:A:69:PRO:HB2	1.81	0.63
1:A:57:ARG:HH21	1:A:61:ARG:HH22	1.50	0.60
1:A:89:ARG:CD	1:A:176:LEU:HD21	2.31	0.59
1:A:52:PRO:HG3	1:A:136:ARG:HG3	1.85	0.58
1:A:184:LYS:HE3	1:A:221:LEU:HD13	1.87	0.57
1:A:241:ARG:HD2	1:A:241:ARG:C	2.30	0.57
1:A:195:TYR:OH	1:A:221:LEU:HD11	2.12	0.49
1:A:80:GLU:OE2	1:A:87:LYS:HD2	2.13	0.49
1:A:43:MET:HB2	1:A:44:PRO:HD3	1.94	0.48
1:A:83:VAL:HG22	1:A:84:LEU:N	2.30	0.47
1:A:282:VAL:HG13	1:A:283:THR:HG22	1.96	0.46
1:A:222:ARG:O	1:A:225:GLN:HB2	2.15	0.46
1:A:123:PRO:HA	1:A:154:LEU:CD1	2.45	0.46
1:A:282:VAL:HA	1:A:283:THR:HA	1.74	0.46
1:A:227:LYS:HE2	1:A:231:ARG:NH2	2.30	0.46
1:A:356:TYR:C	1:A:356:TYR:CD2	2.93	0.45
1:A:123:PRO:HA	1:A:154:LEU:HG	1.99	0.45
1:A:154:LEU:HD21	7:A:582:HOH:O	2.17	0.45
1:A:215:SER:HB3	1:A:221:LEU:CD2	2.45	0.44
1:A:247:VAL:HG23	1:A:248:HIS:CD2	2.53	0.43
1:A:393:ASP:O	1:A:396:ARG:HG2	2.19	0.43
1:A:189:VAL:O	1:A:189:VAL:HG12	2.19	0.43
1:A:203:GLY:N	1:A:204:PRO:CD	2.82	0.43
1:A:355:LEU:HD12	1:A:355:LEU:C	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:VAL:HG13	1:A:277:ILE:HB	2.00	0.43
1:A:159:HIS:HD2	7:A:618:HOH:O	2.01	0.42
1:A:42:LEU:C	1:A:42:LEU:HD23	2.44	0.42
1:A:136:ARG:C	1:A:138:PRO:HD3	2.45	0.42
1:A:260:LEU:HB3	1:A:264:ASP:HB2	2.01	0.42
1:A:282:VAL:CG1	1:A:283:THR:HG22	2.50	0.41
1:A:68:LEU:HD22	1:A:111:MET:HE2	2.02	0.41
1:A:56:HIS:HE1	1:A:98:PHE:O	2.05	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	362/395 (92%)	352 (97%)	10 (3%)	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	294/322 (91%)	294 (100%)	0	100 100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	HIS
1	A	141	GLN
1	A	159	HIS
1	A	239	GLN
1	A	381	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](#)

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](#)

9 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	$\# Z > 2$
3	SO4	A	406	-	4,4,4	0.37	0	6,6,6	0.06	0
4	FMN	A	398	-	33,33,33	1.44	5 (15%)	48,50,50	1.28	5 (10%)
6	ILF	A	407	-	32,32,32	3.13	21 (65%)	44,47,47	2.48	14 (31%)
5	ORO	A	399	-	11,11,11	1.23	1 (9%)	14,15,15	1.42	4 (28%)
3	SO4	A	402	-	4,4,4	0.36	0	6,6,6	0.05	0
2	ACT	A	401	-	3,3,3	1.04	0	3,3,3	1.34	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	A	405	-	4,4,4	0.37	0	6,6,6	0.06	0
3	SO4	A	403	-	4,4,4	0.37	0	6,6,6	0.08	0
3	SO4	A	404	-	4,4,4	0.37	0	6,6,6	0.08	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
5	ORO	A	399	-	-	2/4/4/4	0/1/1/1
4	FMN	A	398	-	-	5/18/18/18	0/3/3/3
6	ILF	A	407	-	-	4/21/21/21	0/3/3/3

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	407	ILF	C16-C14	5.91	1.47	1.38
6	A	407	ILF	C8-C2	5.80	1.48	1.39
6	A	407	ILF	O30-C28	5.33	1.35	1.22
6	A	407	ILF	C13-C10	5.08	1.48	1.39
6	A	407	ILF	C1-C2	4.49	1.47	1.38
4	A	398	FMN	C6-C5A	4.29	1.46	1.40
6	A	407	ILF	C16-C18	4.19	1.44	1.38
6	A	407	ILF	C20-C10	3.94	1.46	1.39
6	A	407	ILF	C20-C18	3.83	1.44	1.37
6	A	407	ILF	C21-N17	3.76	1.43	1.35
6	A	407	ILF	C11-C9	3.69	1.46	1.39
6	A	407	ILF	C28-C27	-3.63	1.42	1.48
6	A	407	ILF	C8-C9	3.45	1.45	1.39
6	A	407	ILF	C12-C11	3.15	1.44	1.38
4	A	398	FMN	C9A-C5A	3.12	1.46	1.41
6	A	407	ILF	C13-C14	3.03	1.42	1.37
6	A	407	ILF	C22-C27	3.01	1.43	1.38
6	A	407	ILF	O3-C4	2.68	1.45	1.31
6	A	407	ILF	C12-C1	2.57	1.43	1.38
4	A	398	FMN	C8-C7	2.41	1.46	1.40
6	A	407	ILF	C27-S26	-2.36	1.68	1.72
6	A	407	ILF	O29-C28	-2.30	1.24	1.30
4	A	398	FMN	C2-N3	2.30	1.44	1.39
6	A	407	ILF	O23-C21	2.21	1.27	1.23
5	A	399	ORO	C5-C4	2.10	1.47	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	398	FMN	C4A-C10	2.03	1.50	1.44
6	A	407	ILF	C22-C21	-2.00	1.43	1.49

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	407	ILF	C25-S26-C27	8.02	99.59	91.38
6	A	407	ILF	C22-C21-N17	7.32	125.92	115.61
6	A	407	ILF	C22-C27-S26	-4.67	106.35	111.94
6	A	407	ILF	F15-C14-C16	3.75	121.53	117.64
6	A	407	ILF	C24-C25-S26	-3.70	106.24	112.86
6	A	407	ILF	F19-C18-C16	3.57	121.34	117.64
6	A	407	ILF	C18-C16-C14	3.49	119.48	115.70
6	A	407	ILF	O23-C21-N17	-3.15	116.41	123.89
6	A	407	ILF	O29-C28-C27	2.70	123.75	115.22
4	A	398	FMN	C4-C4A-N5	2.67	121.90	118.21
4	A	398	FMN	C10-N1-C2	2.66	122.62	116.85
6	A	407	ILF	O29-C28-O30	-2.65	117.59	123.90
4	A	398	FMN	C9A-C9-C8	2.53	124.31	119.22
6	A	407	ILF	C1-C2-C8	-2.50	117.14	120.50
5	A	399	ORO	C5-C6-N1	2.46	123.75	120.87
5	A	399	ORO	C6-N1-C2	-2.44	120.04	122.65
5	A	399	ORO	O72-C7-O71	2.24	129.22	123.90
6	A	407	ILF	C13-C14-C16	-2.23	120.28	123.39
6	A	407	ILF	C20-C18-C16	-2.15	120.39	123.39
6	A	407	ILF	C18-C16-N17	-2.13	119.44	122.12
4	A	398	FMN	C6-C5A-N5	2.09	121.91	118.44
5	A	399	ORO	O72-C7-C6	-2.08	109.78	114.27
4	A	398	FMN	C9-C9A-N10	2.06	124.63	121.85

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	399	ORO	N1-C6-C7-O71
5	A	399	ORO	N1-C6-C7-O72
6	A	407	ILF	N17-C21-C22-C24
6	A	407	ILF	O23-C21-C22-C24
4	A	398	FMN	O3'-C3'-C4'-C5'
4	A	398	FMN	C2'-C3'-C4'-C5'
4	A	398	FMN	O3'-C3'-C4'-O4'
4	A	398	FMN	C2'-C3'-C4'-O4'

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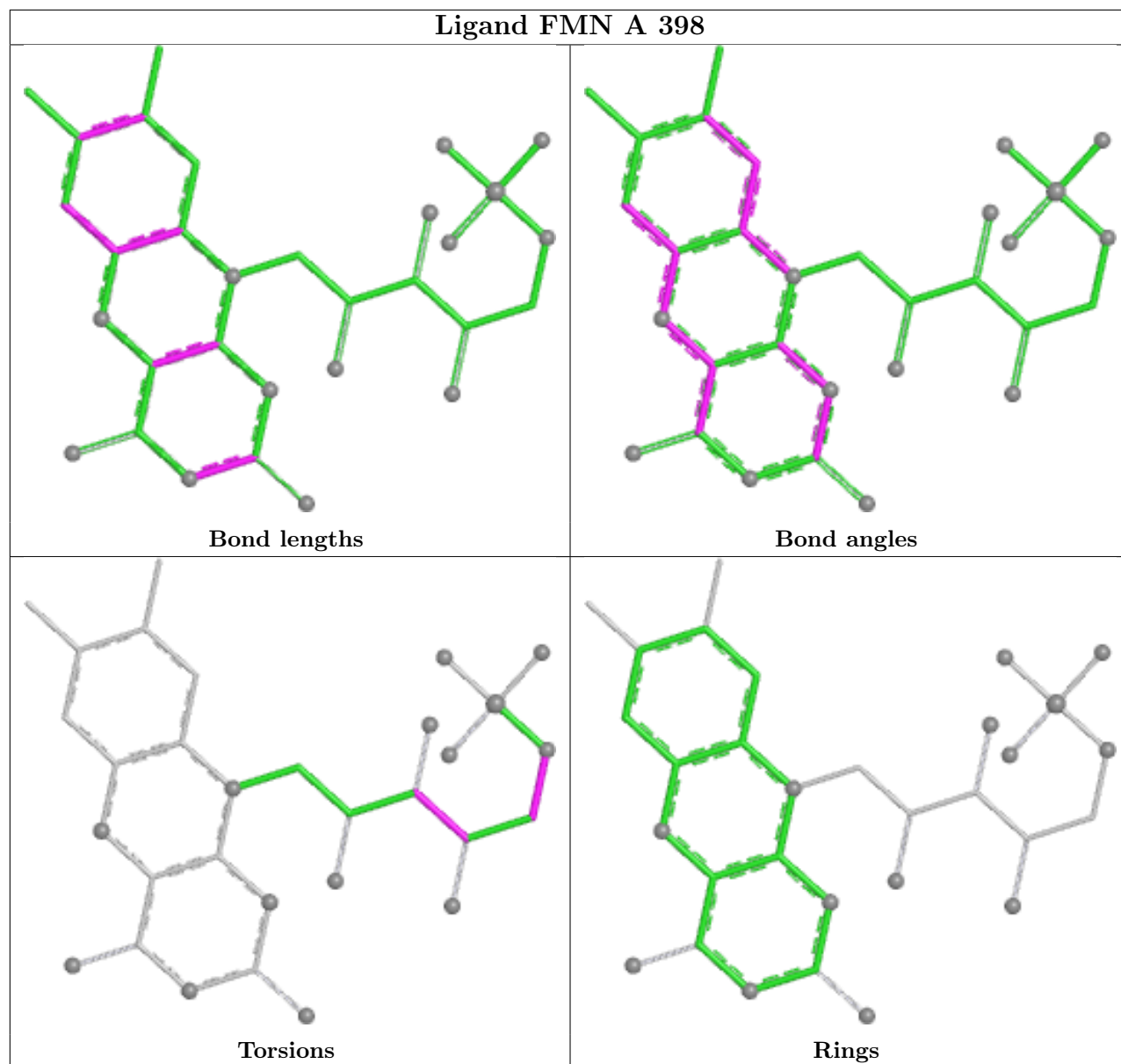
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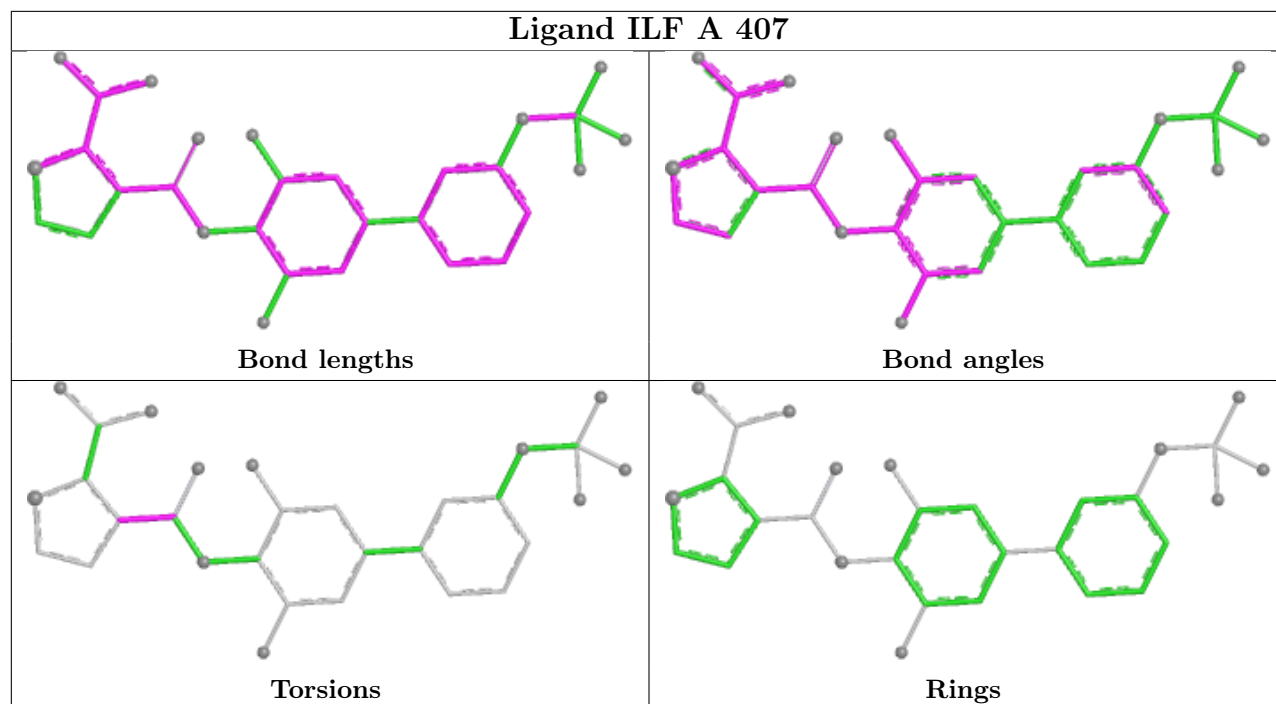
Mol	Chain	Res	Type	Atoms
6	A	407	ILF	O23-C21-C22-C27
6	A	407	ILF	N17-C21-C22-C27
4	A	398	FMN	C4'-C5'-O5'-P

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.