Full wwPDB X-ray Structure Validation Report ⓘ

Jun 13, 2024 – 10:12 AM EDT

PDB ID	:	4FX2
Title	:	COMPARISON OF THE CRYSTAL STRUCTURES OF A FLAVODOXIN IN ITS THREE OXIDATION STATES AT CRYOGENIC TEMPERATURES
Authors	:	Watt, W.; Watenpaugh, K.D.
Deposited on	:	1991-10-17
Resolution	:	1.90 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:

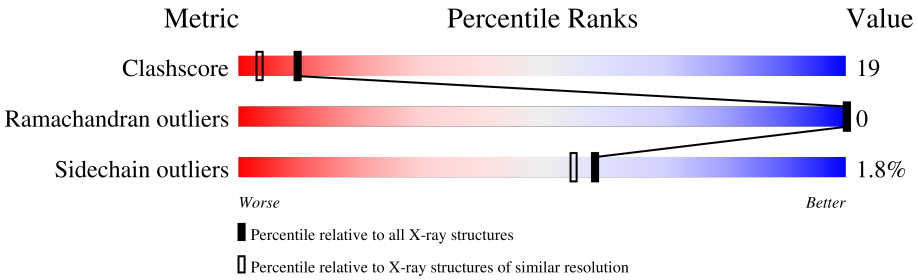
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 1.90 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))
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	147	37% 44% 16% .

2 Entry composition

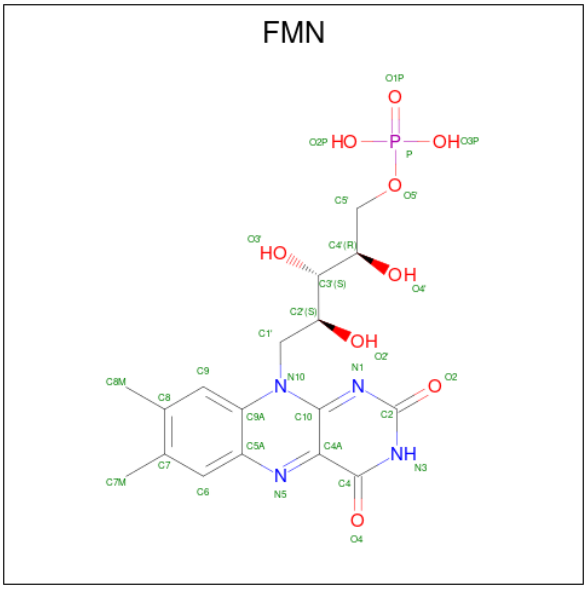
There are 3 unique types of molecules in this entry. The entry contains 1359 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FLAVODOXIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	147	1102	684	181	233	4	0	0	0

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	226	226	226	0	0

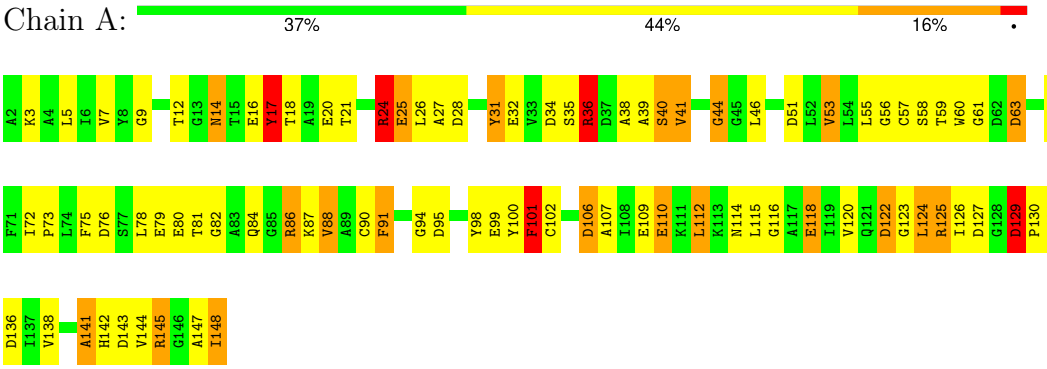
3 Residue-property plots (i)

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. 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.

Note EDS was not executed.

• Molecule 1: FLAVODOXIN

Chain A:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	51.44Å 51.44Å 139.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.90	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.203 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1359	wwPDB-VP
Average B, all atoms (Å^2)	14.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMN

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	1.77	14/1119 (1.3%)	3.29	122/1514 (8.1%)

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
1	A	0	11

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	20	GLU	CD-OE2	-7.56	1.17	1.25
1	A	17	TYR	CG-CD1	-6.98	1.30	1.39
1	A	20	GLU	CD-OE1	-6.21	1.18	1.25
1	A	25	GLU	CD-OE1	6.12	1.32	1.25
1	A	94	GLY	N-CA	5.99	1.55	1.46
1	A	35	SER	CB-OG	-5.80	1.34	1.42
1	A	16	GLU	CG-CD	-5.61	1.43	1.51
1	A	44	GLY	N-CA	5.60	1.54	1.46
1	A	109	GLU	CG-CD	-5.57	1.43	1.51
1	A	116	GLY	C-O	5.20	1.31	1.23
1	A	9	GLY	N-CA	5.17	1.53	1.46
1	A	143	ASP	CG-OD2	5.13	1.37	1.25
1	A	82	GLY	N-CA	-5.11	1.38	1.46
1	A	81	THR	C-N	-5.03	1.24	1.33

All (122) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	145	ARG	NE-CZ-NH2	47.06	143.83	120.30
1	A	145	ARG	NE-CZ-NH1	-23.38	108.61	120.30
1	A	125	ARG	NE-CZ-NH1	19.57	130.08	120.30
1	A	134	ARG	NE-CZ-NH2	-19.37	110.61	120.30
1	A	28	ASP	CB-CG-OD2	-17.50	102.55	118.30
1	A	24	ARG	NE-CZ-NH1	16.24	128.42	120.30
1	A	134	ARG	NE-CZ-NH1	15.60	128.10	120.30
1	A	86	ARG	NE-CZ-NH1	15.53	128.07	120.30
1	A	17	TYR	CB-CG-CD1	15.12	130.07	121.00
1	A	145	ARG	NH1-CZ-NH2	-13.78	104.25	119.40
1	A	70	ASP	CB-CG-OD1	-13.64	106.02	118.30
1	A	16	GLU	OE1-CD-OE2	-13.60	106.98	123.30
1	A	135	ASP	CB-CG-OD2	-13.12	106.49	118.30
1	A	24	ARG	NE-CZ-NH2	-12.23	114.18	120.30
1	A	98	TYR	CB-CG-CD2	-11.98	113.81	121.00
1	A	76	ASP	CB-CG-OD1	11.66	128.79	118.30
1	A	69	ASP	CB-CG-OD2	-11.29	108.14	118.30
1	A	100	TYR	CB-CG-CD2	-11.17	114.30	121.00
1	A	122	ASP	CB-CG-OD1	10.93	128.13	118.30
1	A	95	ASP	CB-CG-OD2	10.44	127.70	118.30
1	A	17	TYR	CB-CG-CD2	-10.40	114.76	121.00
1	A	109	GLU	OE1-CD-OE2	-10.05	111.23	123.30
1	A	81	THR	C-N-CA	10.01	143.32	122.30
1	A	125	ARG	CD-NE-CZ	9.84	137.37	123.60
1	A	109	GLU	CG-CD-OE1	9.80	137.89	118.30
1	A	131	ARG	NE-CZ-NH2	-8.73	115.93	120.30
1	A	63	ASP	CB-CG-OD2	-8.61	110.56	118.30
1	A	145	ARG	CD-NE-CZ	-8.23	112.08	123.60
1	A	100	TYR	CB-CG-CD1	7.96	125.78	121.00
1	A	84	GLN	CG-CD-OE1	-7.85	105.90	121.60
1	A	109	GLU	N-CA-CB	7.83	124.70	110.60
1	A	67	LEU	CB-CG-CD1	7.76	124.20	111.00
1	A	136	ASP	CB-CG-OD2	7.72	125.25	118.30
1	A	24	ARG	CD-NE-CZ	7.68	134.35	123.60
1	A	135	ASP	CB-CG-OD1	7.67	125.20	118.30
1	A	41	VAL	CA-CB-CG1	7.57	122.26	110.90
1	A	99	GLU	OE1-CD-OE2	7.50	132.30	123.30
1	A	134	ARG	N-CA-CB	7.47	124.05	110.60
1	A	34	ASP	CB-CA-C	7.35	125.10	110.40
1	A	98	TYR	CB-CG-CD1	7.25	125.35	121.00
1	A	69	ASP	CB-CA-C	7.21	124.83	110.40
1	A	17	TYR	CG-CD1-CE1	7.12	127.00	121.30
1	A	120	VAL	CA-CB-CG2	7.08	121.52	110.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	39	ALA	O-C-N	-6.99	111.51	122.70
1	A	21	THR	CA-CB-CG2	6.93	122.10	112.40
1	A	145	ARG	CA-CB-CG	6.82	128.41	113.40
1	A	86	ARG	C-N-CA	6.79	138.68	121.70
1	A	110	GLU	OE1-CD-OE2	6.75	131.39	123.30
1	A	86	ARG	CA-CB-CG	6.74	128.22	113.40
1	A	86	ARG	NE-CZ-NH2	-6.71	116.95	120.30
1	A	58	SER	N-CA-CB	6.67	120.50	110.50
1	A	5	LEU	CB-CG-CD2	-6.62	99.74	111.00
1	A	109	GLU	CA-CB-CG	6.54	127.78	113.40
1	A	99	GLU	CG-CD-OE2	-6.51	105.27	118.30
1	A	36	ARG	NH1-CZ-NH2	-6.50	112.25	119.40
1	A	32	GLU	OE1-CD-OE2	-6.49	115.52	123.30
1	A	41	VAL	CB-CA-C	6.48	123.72	111.40
1	A	118	GLU	CB-CA-C	-6.43	97.53	110.40
1	A	147	ALA	CB-CA-C	6.43	119.74	110.10
1	A	125	ARG	NH1-CZ-NH2	-6.40	112.36	119.40
1	A	126	ILE	CA-CB-CG1	-6.35	98.94	111.00
1	A	76	ASP	CB-CG-OD2	-6.33	112.61	118.30
1	A	28	ASP	CB-CG-OD1	6.31	123.98	118.30
1	A	144	VAL	CA-CB-CG1	6.22	120.23	110.90
1	A	67	LEU	CB-CG-CD2	-6.20	100.45	111.00
1	A	27	ALA	O-C-N	-6.20	112.78	122.70
1	A	109	GLU	CB-CG-CD	6.16	130.84	114.20
1	A	91	PHE	CB-CG-CD2	-6.12	116.52	120.80
1	A	79	GLU	CG-CD-OE2	6.12	130.53	118.30
1	A	127	ASP	CA-C-N	6.09	128.39	116.20
1	A	84	GLN	CG-CD-NE2	6.06	131.24	116.70
1	A	16	GLU	CG-CD-OE2	6.04	130.38	118.30
1	A	110	GLU	CG-CD-OE2	-6.00	106.30	118.30
1	A	129	ASP	CB-CG-OD1	5.96	123.66	118.30
1	A	31	TYR	CB-CG-CD1	5.92	124.55	121.00
1	A	126	ILE	O-C-N	5.87	132.09	122.70
1	A	26	LEU	CB-CG-CD2	5.87	120.97	111.00
1	A	38	ALA	CB-CA-C	5.87	118.90	110.10
1	A	101	PHE	CB-CG-CD1	5.85	124.90	120.80
1	A	25	GLU	N-CA-CB	5.84	121.12	110.60
1	A	24	ARG	C-N-CA	5.83	136.29	121.70
1	A	88	VAL	CA-CB-CG1	5.79	119.59	110.90
1	A	122	ASP	CA-CB-CG	5.79	126.14	113.40
1	A	55	LEU	CA-CB-CG	5.73	128.48	115.30
1	A	127	ASP	CA-C-O	-5.73	108.06	120.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	118	GLU	OE1-CD-OE2	5.68	130.11	123.30
1	A	12	THR	C-N-CA	5.62	134.11	122.30
1	A	138	VAL	O-C-N	-5.59	113.70	123.20
1	A	69	ASP	OD1-CG-OD2	5.55	133.85	123.30
1	A	57	CYS	N-CA-CB	-5.55	100.61	110.60
1	A	86	ARG	NH1-CZ-NH2	-5.53	113.31	119.40
1	A	70	ASP	CB-CG-OD2	5.53	123.28	118.30
1	A	125	ARG	NE-CZ-NH2	-5.53	117.54	120.30
1	A	129	ASP	OD1-CG-OD2	-5.52	112.81	123.30
1	A	143	ASP	CB-CG-OD1	5.51	123.26	118.30
1	A	60	TRP	CA-C-N	5.51	127.21	116.20
1	A	84	GLN	O-C-N	-5.50	113.86	123.20
1	A	18	THR	C-N-CA	5.48	135.40	121.70
1	A	86	ARG	O-C-N	-5.46	113.97	122.70
1	A	79	GLU	CG-CD-OE1	-5.42	107.47	118.30
1	A	148	ILE	N-CA-CB	5.37	123.15	110.80
1	A	98	TYR	CA-C-N	-5.35	105.42	117.20
1	A	26	LEU	CA-C-N	5.35	128.97	117.20
1	A	14	ASN	O-C-N	5.34	131.25	122.70
1	A	28	ASP	OD1-CG-OD2	5.33	133.43	123.30
1	A	3	LYS	CG-CD-CE	5.32	127.86	111.90
1	A	129	ASP	CB-CG-OD2	5.29	123.06	118.30
1	A	141	ALA	O-C-N	-5.28	114.26	122.70
1	A	40	SER	CA-C-O	-5.25	109.07	120.10
1	A	61	GLY	O-C-N	-5.20	114.38	122.70
1	A	27	ALA	CB-CA-C	5.19	117.89	110.10
1	A	112	LEU	O-C-N	5.19	131.01	122.70
1	A	134	ARG	O-C-N	5.16	130.95	122.70
1	A	78	LEU	CA-CB-CG	5.15	127.15	115.30
1	A	138	VAL	CB-CA-C	5.15	121.19	111.40
1	A	106	ASP	CB-CG-OD2	5.14	122.93	118.30
1	A	120	VAL	CB-CA-C	5.13	121.15	111.40
1	A	31	TYR	CB-CG-CD2	-5.08	117.95	121.00
1	A	148	ILE	CA-CB-CG1	5.07	120.63	111.00
1	A	78	LEU	CB-CA-C	5.06	119.81	110.20
1	A	124	LEU	CB-CG-CD1	-5.03	102.45	111.00
1	A	61	GLY	CA-C-N	5.02	128.25	117.20

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	101	PHE	Mainchain
1	A	107	ALA	Mainchain
1	A	115	LEU	Mainchain
1	A	122	ASP	Mainchain
1	A	124	LEU	Mainchain
1	A	129	ASP	Mainchain
1	A	135	ASP	Mainchain
1	A	141	ALA	Mainchain
1	A	36	ARG	Sidechain
1	A	53	VAL	Mainchain
1	A	75	PHE	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	1102	0	1027	41	0
2	A	31	0	18	1	0
3	A	226	0	0	11	0
All	All	1359	0	1045	42	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 19.

All (42) 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:25:GLU:OE1	3:A:293:HOH:O	1.80	0.99
1:A:63:ASP:HB3	3:A:336:HOH:O	1.60	0.99
1:A:40:SER:HB2	3:A:240:HOH:O	1.82	0.80
1:A:24:ARG:HA	1:A:24:ARG:HE	1.48	0.76
1:A:25:GLU:HB3	3:A:293:HOH:O	1.84	0.76
1:A:31:TYR:OH	1:A:148:ILE:HD11	1.87	0.75
1:A:68:GLN:OE1	1:A:70:ASP:HB2	1.89	0.72
1:A:86:ARG:O	1:A:118:GLU:N	2.24	0.68
1:A:7:VAL:HA	1:A:36:ARG:O	1.95	0.67
1:A:51:ASP:OD1	3:A:213:HOH:O	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:CYS:O	1:A:123:GLY:HA2	1.96	0.65
1:A:72:ILE:HB	1:A:73:PRO:HD3	1.79	0.64
1:A:110:GLU:OE2	3:A:193:HOH:O	2.15	0.64
1:A:87:LYS:HD3	1:A:148:ILE:HG22	1.81	0.61
1:A:41:VAL:CG1	1:A:46:LEU:CD2	2.79	0.60
1:A:41:VAL:CG1	1:A:46:LEU:HD21	2.32	0.59
1:A:129:ASP:OD1	1:A:130:PRO:HD2	2.03	0.58
1:A:41:VAL:HG13	1:A:46:LEU:HD13	1.86	0.56
1:A:41:VAL:HG11	1:A:46:LEU:HD21	1.88	0.56
1:A:142:HIS:CD2	3:A:266:HOH:O	2.60	0.55
1:A:24:ARG:CD	3:A:289:HOH:O	2.55	0.54
1:A:44:GLY:HA2	1:A:80:GLU:O	2.08	0.54
1:A:41:VAL:HG13	1:A:46:LEU:CD1	2.40	0.51
1:A:106:ASP:OD1	1:A:125:ARG:NH2	2.42	0.50
1:A:134:ARG:HG2	1:A:134:ARG:HH11	1.76	0.49
1:A:24:ARG:HD3	3:A:289:HOH:O	2.13	0.48
1:A:59:THR:OG1	1:A:102:CYS:HA	2.15	0.47
1:A:24:ARG:HE	1:A:24:ARG:CA	2.20	0.47
1:A:53:VAL:O	1:A:88:VAL:HA	2.16	0.46
1:A:36:ARG:NH1	1:A:46:LEU:HD12	2.31	0.46
1:A:41:VAL:CG1	1:A:46:LEU:HD22	2.46	0.45
2:A:149:FMN:H1'2	2:A:149:FMN:H9	1.52	0.45
1:A:114:ASN:HB2	3:A:323:HOH:O	2.16	0.45
1:A:88:VAL:HG21	1:A:112:LEU:HD13	1.99	0.44
1:A:24:ARG:HD2	3:A:289:HOH:O	2.16	0.43
1:A:145:ARG:HH11	1:A:145:ARG:HD2	1.01	0.43
1:A:112:LEU:HD23	1:A:112:LEU:HA	1.91	0.43
1:A:72:ILE:CB	1:A:73:PRO:HD3	2.46	0.41
1:A:14:ASN:HD22	1:A:14:ASN:HA	1.66	0.41
1:A:56:GLY:HA2	1:A:91:PHE:O	2.21	0.41
1:A:101:PHE:O	1:A:102:CYS:C	2.59	0.41
1:A:17:TYR:OH	1:A:134:ARG:HD2	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	145/147 (99%)	134 (92%)	11 (8%)	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	111/111 (100%)	109 (98%)	2 (2%)	59 55

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	TYR
1	A	24	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	ASN
1	A	142	HIS

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)

1 ligand is 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	FMN	A	149	-	33,33,33	2.29	12 (36%)	48,50,50	2.96	19 (39%)

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	FMN	A	149	-	-	1/18/18/18	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	149	FMN	P-O1P	5.57	1.67	1.50
2	A	149	FMN	C9A-N10	4.30	1.48	1.41
2	A	149	FMN	C2-N1	-3.79	1.28	1.36
2	A	149	FMN	C4A-C10	3.68	1.55	1.44
2	A	149	FMN	C7M-C7	3.63	1.57	1.51
2	A	149	FMN	O2'-C2'	-3.60	1.35	1.43
2	A	149	FMN	C5A-N5	-3.56	1.32	1.39
2	A	149	FMN	P-O3P	-3.21	1.42	1.54
2	A	149	FMN	C2'-C3'	-2.60	1.48	1.53
2	A	149	FMN	C9-C8	2.42	1.42	1.39
2	A	149	FMN	P-O5'	-2.39	1.52	1.60
2	A	149	FMN	C8-C7	2.01	1.45	1.40

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	149	FMN	C1'-N10-C9A	-9.81	101.56	120.63
2	A	149	FMN	C4-C4A-N5	7.12	128.05	118.21
2	A	149	FMN	C7M-C7-C8	-6.79	106.90	120.76
2	A	149	FMN	C4-C4A-C10	-5.32	107.82	116.93
2	A	149	FMN	C5A-C9A-N10	-5.23	113.24	117.97
2	A	149	FMN	C5A-N5-C4A	4.86	125.95	118.09
2	A	149	FMN	O2P-P-O5'	4.73	119.00	106.67
2	A	149	FMN	O5'-P-O1P	3.75	116.57	106.44
2	A	149	FMN	C10-C4A-N5	-3.57	117.52	124.81
2	A	149	FMN	O4-C4-C4A	-3.42	117.50	126.53
2	A	149	FMN	O2P-P-O1P	-3.04	99.00	110.83
2	A	149	FMN	O3'-C3'-C4'	2.95	115.64	108.93
2	A	149	FMN	O3'-C3'-C2'	2.54	114.71	108.93
2	A	149	FMN	C1'-C2'-C3'	-2.53	102.81	109.66
2	A	149	FMN	C9A-N10-C10	2.46	124.50	120.75
2	A	149	FMN	C4A-C4-N3	2.32	119.16	113.25
2	A	149	FMN	C9-C9A-N10	2.21	124.83	121.85
2	A	149	FMN	O2-C2-N1	-2.09	118.32	121.80
2	A	149	FMN	C10-N1-C2	2.02	121.22	116.85

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	149	FMN	O2'-C2'-C3'-C4'

There are no ring outliers.

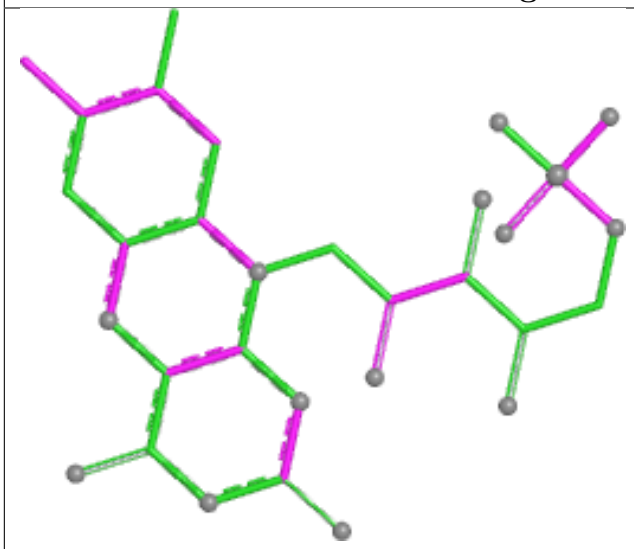
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	149	FMN	1	0

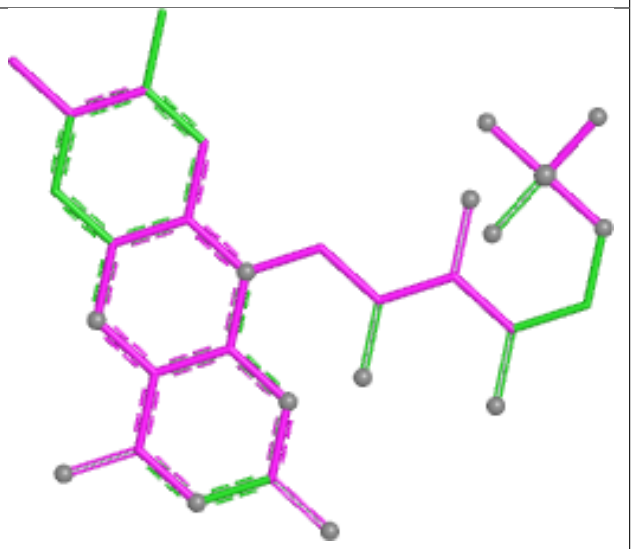
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

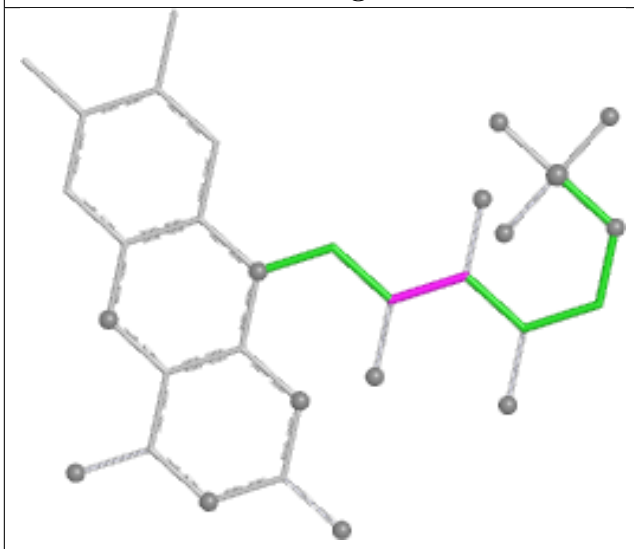
Ligand FMN A 149



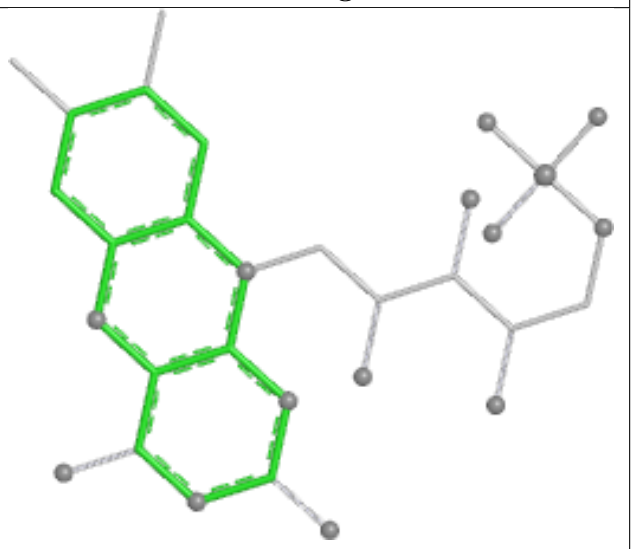
Bond lengths



Bond angles



Torsions



Rings

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.