



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:28 AM UTC

PDB ID : 2FX2 / pdb_00002fx2
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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (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

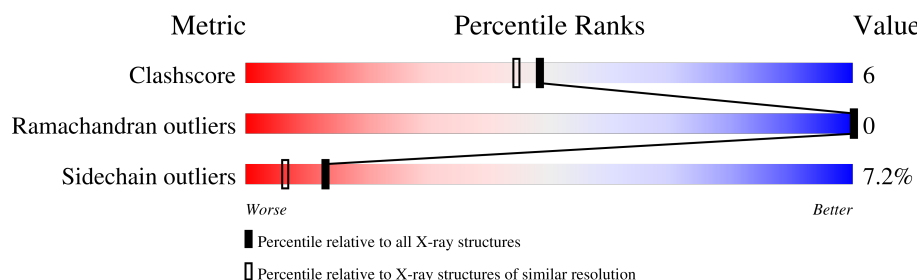
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	147	

2 Entry composition [i](#)

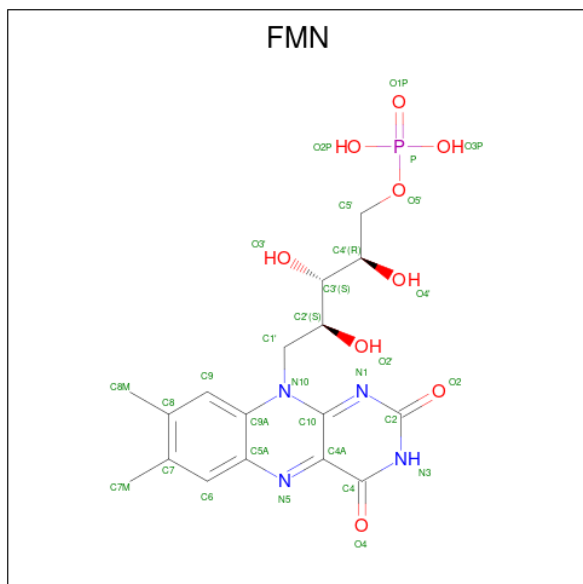
There are 3 unique types of molecules in this entry. The entry contains 1263 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
1	A	147	Total	C	N	O	S	0	0	0
			1102	684	181	233	4			

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

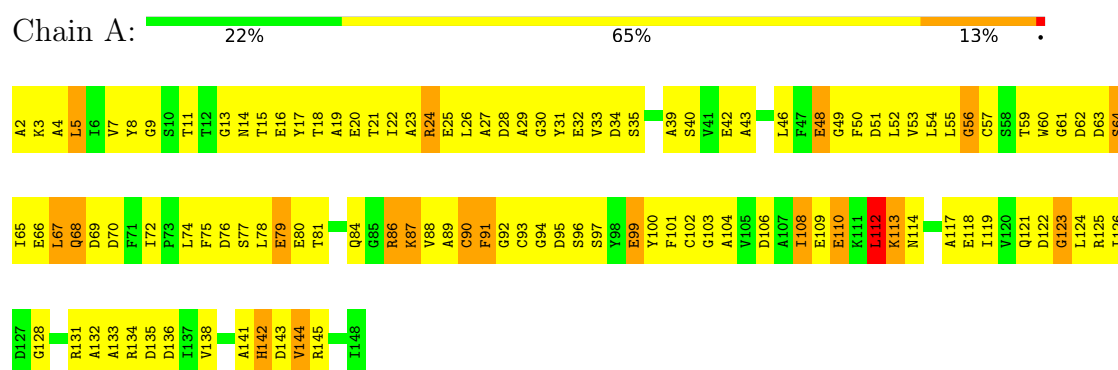


3 Residue-property plots [i](#)

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



4 Data and refinement statistics

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	51.96Å 51.96Å 139.86Å 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}	0.170 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1263	wwPDB-VP
Average B, all atoms (Å ²)	21.0	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	2.75	94/1119 (8.4%)	3.22	169/1514 (11.2%)

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	3

All (94) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	5	LEU	CA-C	10.60	1.65	1.52
1	A	56	GLY	CA-C	10.18	1.60	1.52
1	A	72	ILE	CA-CB	10.16	1.59	1.54
1	A	62	ASP	N-CA	-9.50	1.33	1.46
1	A	145	ARG	CD-NE	-9.21	1.33	1.46
1	A	109	GLU	C-O	8.80	1.34	1.24
1	A	100	TYR	C-N	-8.65	1.21	1.33
1	A	29	ALA	C-N	-8.60	1.20	1.33
1	A	52	LEU	N-CA	8.54	1.56	1.46
1	A	4	ALA	N-CA	8.33	1.56	1.46
1	A	124	LEU	CA-C	8.02	1.62	1.52
1	A	32	GLU	CA-C	7.96	1.62	1.52
1	A	66	GLU	CA-C	7.87	1.61	1.52
1	A	22	ILE	C-O	7.85	1.33	1.24
1	A	3	LYS	CA-C	7.83	1.62	1.52
1	A	110	GLU	C-O	7.53	1.32	1.24
1	A	11	THR	CA-CB	7.49	1.65	1.53
1	A	65	ILE	CA-CB	7.40	1.63	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	52	LEU	C-N	7.33	1.43	1.33
1	A	89	ALA	CA-C	7.33	1.61	1.52
1	A	65	ILE	N-CA	7.29	1.55	1.46
1	A	9	GLY	C-N	-7.15	1.24	1.33
1	A	65	ILE	CA-C	-7.13	1.44	1.52
1	A	112	LEU	C-N	-6.97	1.24	1.33
1	A	66	GLU	N-CA	-6.89	1.37	1.46
1	A	18	THR	N-CA	-6.84	1.38	1.46
1	A	51	ASP	CA-CB	6.80	1.64	1.53
1	A	68	GLN	CD-NE2	-6.79	1.19	1.33
1	A	65	ILE	C-O	6.74	1.32	1.24
1	A	145	ARG	NE-CZ	-6.61	1.25	1.33
1	A	91	PHE	CA-C	6.59	1.60	1.52
1	A	144	VAL	CA-C	6.59	1.61	1.52
1	A	18	THR	C-N	-6.58	1.25	1.33
1	A	30	GLY	C-N	6.53	1.42	1.33
1	A	23	ALA	N-CA	-6.47	1.38	1.46
1	A	22	ILE	C-N	-6.47	1.25	1.33
1	A	122	ASP	C-N	-6.32	1.25	1.33
1	A	17	TYR	C-O	6.26	1.31	1.24
1	A	131	ARG	NE-CZ	6.24	1.40	1.33
1	A	54	LEU	CA-C	6.24	1.60	1.52
1	A	14	ASN	CA-C	6.21	1.60	1.52
1	A	102	CYS	CA-CB	6.16	1.62	1.53
1	A	117	ALA	CA-C	-6.14	1.44	1.53
1	A	108	ILE	CA-C	6.13	1.60	1.52
1	A	65	ILE	C-N	-6.12	1.25	1.33
1	A	94	GLY	N-CA	6.05	1.51	1.44
1	A	18	THR	C-O	6.05	1.31	1.24
1	A	60	TRP	N-CA	6.04	1.54	1.46
1	A	88	VAL	CA-CB	6.04	1.65	1.55
1	A	59	THR	CA-C	6.03	1.59	1.52
1	A	81	THR	CA-CB	5.97	1.63	1.53
1	A	69	ASP	CG-OD2	5.96	1.36	1.25
1	A	99	GLU	C-N	-5.95	1.26	1.33
1	A	16	GLU	CA-C	5.94	1.60	1.52
1	A	104	ALA	CA-C	5.89	1.60	1.52
1	A	18	THR	CB-OG1	5.89	1.53	1.43
1	A	18	THR	CA-C	5.84	1.60	1.52
1	A	25	GLU	C-O	5.82	1.30	1.24
1	A	40	SER	C-N	-5.81	1.27	1.33
1	A	60	TRP	NE1-CE2	5.72	1.43	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	92	GLY	N-CA	5.72	1.54	1.45
1	A	27	ALA	C-N	-5.70	1.26	1.34
1	A	126	ILE	CB-CG1	5.66	1.64	1.53
1	A	24	ARG	C-N	-5.64	1.26	1.33
1	A	88	VAL	CA-C	-5.63	1.46	1.52
1	A	53	VAL	CA-C	5.62	1.59	1.52
1	A	27	ALA	CA-C	5.56	1.59	1.52
1	A	51	ASP	N-CA	-5.51	1.39	1.46
1	A	64	SER	CA-CB	-5.51	1.45	1.53
1	A	24	ARG	CA-CB	-5.50	1.44	1.53
1	A	67	LEU	N-CA	5.49	1.52	1.45
1	A	95	ASP	N-CA	5.48	1.52	1.46
1	A	75	PHE	N-CA	-5.45	1.39	1.46
1	A	29	ALA	C-O	5.44	1.31	1.24
1	A	138	VAL	C-N	-5.42	1.27	1.33
1	A	8	TYR	N-CA	5.41	1.52	1.45
1	A	59	THR	CB-OG1	5.41	1.52	1.43
1	A	121	GLN	CD-NE2	-5.34	1.22	1.33
1	A	122	ASP	N-CA	5.33	1.52	1.46
1	A	24	ARG	CZ-NH2	5.30	1.40	1.33
1	A	88	VAL	N-CA	5.25	1.51	1.46
1	A	125	ARG	CA-CB	5.24	1.61	1.53
1	A	123	GLY	CA-C	5.22	1.57	1.52
1	A	72	ILE	C-O	5.16	1.28	1.24
1	A	74	LEU	CA-CB	5.16	1.61	1.53
1	A	93	CYS	N-CA	5.16	1.51	1.45
1	A	31	TYR	C-N	-5.14	1.26	1.33
1	A	66	GLU	C-O	-5.12	1.17	1.24
1	A	7	VAL	N-CA	5.10	1.52	1.46
1	A	48	GLU	N-CA	5.10	1.52	1.46
1	A	67	LEU	CA-CB	5.06	1.61	1.53
1	A	100	TYR	N-CA	5.04	1.53	1.46
1	A	119	ILE	CA-CB	5.03	1.59	1.53
1	A	142	HIS	C-O	-5.01	1.18	1.24

All (169) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	145	ARG	CD-NE-CZ	33.39	171.15	124.40
1	A	114	ASN	OD1-CG-ND2	-13.21	109.39	122.60
1	A	125	ARG	CD-NE-CZ	11.72	140.81	124.40
1	A	17	TYR	CA-C-N	11.55	135.89	120.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	17	TYR	C-N-CA	11.55	135.89	120.65
1	A	117	ALA	O-C-N	-11.43	109.76	122.79
1	A	114	ASN	CB-CG-ND2	10.52	132.18	116.40
1	A	69	ASP	CA-CB-CG	10.27	122.87	112.60
1	A	104	ALA	N-CA-CB	9.13	123.25	110.01
1	A	122	ASP	CA-C-N	9.12	129.00	120.34
1	A	122	ASP	C-N-CA	9.12	129.00	120.34
1	A	18	THR	N-CA-CB	8.95	122.98	109.91
1	A	118	GLU	CA-C-O	-8.93	110.91	120.46
1	A	43	ALA	N-CA-C	8.84	121.00	111.36
1	A	138	VAL	CA-C-N	8.83	129.74	119.94
1	A	138	VAL	C-N-CA	8.83	129.74	119.94
1	A	142	HIS	CA-C-O	-8.69	111.75	120.70
1	A	117	ALA	CA-C-O	8.53	131.76	121.87
1	A	40	SER	CA-C-O	-8.48	109.95	119.95
1	A	101	PHE	CA-CB-CG	-8.33	105.47	113.80
1	A	7	VAL	O-C-N	8.29	131.99	123.20
1	A	35	SER	CA-C-O	-8.22	111.51	120.30
1	A	20	GLU	CA-C-N	7.92	131.21	120.44
1	A	20	GLU	C-N-CA	7.92	131.21	120.44
1	A	51	ASP	CA-CB-CG	-7.90	104.70	112.60
1	A	39	ALA	CA-C-O	7.87	128.99	120.10
1	A	5	LEU	O-C-N	7.83	133.41	123.23
1	A	65	ILE	CA-C-N	7.80	133.99	122.99
1	A	65	ILE	C-N-CA	7.80	133.99	122.99
1	A	27	ALA	N-CA-CB	7.75	121.25	110.01
1	A	34	ASP	CA-C-O	-7.75	111.80	120.32
1	A	143	ASP	CA-C-O	-7.69	112.40	120.55
1	A	67	LEU	O-C-N	-7.61	114.18	122.85
1	A	99	GLU	CA-C-O	-7.57	112.39	120.42
1	A	103	GLY	CA-C-N	7.55	130.26	120.44
1	A	103	GLY	C-N-CA	7.55	130.26	120.44
1	A	66	GLU	O-C-N	7.55	132.28	123.30
1	A	95	ASP	CB-CA-C	7.55	122.63	109.80
1	A	5	LEU	CA-C-N	-7.52	113.29	123.14
1	A	5	LEU	C-N-CA	-7.52	113.29	123.14
1	A	66	GLU	N-CA-CB	7.52	123.31	110.68
1	A	97	SER	N-CA-C	-7.51	104.11	113.28
1	A	125	ARG	NE-CZ-NH1	7.47	128.97	121.50
1	A	63	ASP	CB-CG-OD2	7.36	135.34	118.40
1	A	87	LYS	O-C-N	7.36	132.07	123.02
1	A	22	ILE	CA-C-O	-7.27	113.39	120.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	32	GLU	CA-C-O	-7.22	112.35	120.43
1	A	66	GLU	OE1-CD-OE2	7.17	140.11	122.90
1	A	66	GLU	CA-CB-CG	-7.13	99.84	114.10
1	A	64	SER	CA-C-N	-7.12	113.18	122.37
1	A	64	SER	C-N-CA	-7.12	113.18	122.37
1	A	61	GLY	CA-C-N	7.08	135.06	121.54
1	A	61	GLY	C-N-CA	7.08	135.06	121.54
1	A	144	VAL	N-CA-CB	7.03	120.10	110.54
1	A	142	HIS	CB-CA-C	-7.01	99.82	110.90
1	A	22	ILE	CA-C-N	7.01	130.01	120.54
1	A	22	ILE	C-N-CA	7.01	130.01	120.54
1	A	108	ILE	CA-C-O	-6.94	113.73	120.95
1	A	118	GLU	O-C-N	6.89	131.81	123.13
1	A	133	ALA	CA-C-O	-6.83	111.85	119.78
1	A	67	LEU	N-CA-CB	-6.83	100.07	110.45
1	A	49	GLY	CA-C-O	-6.81	111.61	118.96
1	A	86	ARG	CA-CB-CG	6.80	127.70	114.10
1	A	34	ASP	CA-CB-CG	-6.77	105.83	112.60
1	A	113	LYS	CA-C-N	6.67	130.45	120.31
1	A	113	LYS	C-N-CA	6.67	130.45	120.31
1	A	43	ALA	CA-C-O	-6.66	113.36	120.42
1	A	46	LEU	CA-C-O	-6.62	113.53	120.55
1	A	143	ASP	N-CA-CB	6.61	119.83	110.12
1	A	126	ILE	O-C-N	6.60	130.36	123.03
1	A	50	PHE	CA-C-O	-6.56	113.70	121.11
1	A	19	ALA	CA-C-N	6.48	129.49	120.29
1	A	19	ALA	C-N-CA	6.48	129.49	120.29
1	A	112	LEU	CA-C-O	-6.45	114.04	120.82
1	A	69	ASP	N-CA-C	6.43	117.95	111.07
1	A	135	ASP	CA-C-N	6.43	128.90	120.28
1	A	135	ASP	C-N-CA	6.43	128.90	120.28
1	A	14	ASN	O-C-N	6.36	128.96	122.09
1	A	21	THR	CA-C-O	-6.35	114.16	120.70
1	A	34	ASP	CA-C-N	-6.32	114.08	123.00
1	A	34	ASP	C-N-CA	-6.32	114.08	123.00
1	A	42	GLU	CA-C-O	-6.31	113.54	120.36
1	A	17	TYR	O-C-N	-6.29	115.45	122.12
1	A	34	ASP	N-CA-CB	-6.29	100.67	110.55
1	A	2	ALA	CB-CA-C	6.29	119.93	110.50
1	A	24	ARG	CA-CB-CG	6.28	126.65	114.10
1	A	13	GLY	CA-C-N	6.27	128.96	120.44
1	A	13	GLY	C-N-CA	6.27	128.96	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	87	LYS	CA-CB-CG	-6.26	101.59	114.10
1	A	121	GLN	CA-C-O	-6.21	114.03	120.99
1	A	121	GLN	N-CA-CB	-6.16	100.06	111.52
1	A	131	ARG	NE-CZ-NH2	-6.16	113.66	119.20
1	A	108	ILE	O-C-N	6.07	127.76	121.87
1	A	80	GLU	CA-CB-CG	6.04	126.19	114.10
1	A	65	ILE	O-C-N	-6.03	116.08	122.95
1	A	15	THR	N-CA-C	-6.02	104.80	111.36
1	A	49	GLY	CA-C-N	-5.88	113.57	122.81
1	A	49	GLY	C-N-CA	-5.88	113.57	122.81
1	A	26	LEU	CA-C-N	5.86	128.06	120.44
1	A	26	LEU	C-N-CA	5.86	128.06	120.44
1	A	57	CYS	N-CA-CB	-5.83	100.72	110.57
1	A	66	GLU	CA-C-N	-5.82	109.09	121.32
1	A	66	GLU	C-N-CA	-5.82	109.09	121.32
1	A	18	THR	CA-C-O	-5.80	114.91	121.00
1	A	96	SER	N-CA-C	5.80	120.09	113.19
1	A	136	ASP	CA-CB-CG	5.77	118.37	112.60
1	A	29	ALA	CA-C-N	5.76	131.70	122.25
1	A	29	ALA	C-N-CA	5.76	131.70	122.25
1	A	87	LYS	CA-C-O	-5.76	113.81	120.49
1	A	104	ALA	O-C-N	5.75	127.99	122.07
1	A	84	GLN	CG-CD-NE2	5.72	124.99	116.40
1	A	18	THR	CA-C-N	5.72	127.94	120.28
1	A	18	THR	C-N-CA	5.72	127.94	120.28
1	A	123	GLY	O-C-N	5.70	130.00	122.76
1	A	79	GLU	CA-C-N	5.70	131.95	122.54
1	A	79	GLU	C-N-CA	5.70	131.95	122.54
1	A	53	VAL	CA-CB-CG1	-5.63	100.82	110.40
1	A	28	ASP	CB-CG-OD2	-5.63	105.45	118.40
1	A	27	ALA	CA-C-O	-5.63	114.91	120.82
1	A	63	ASP	OD1-CG-OD2	-5.62	109.40	122.90
1	A	108	ILE	CB-CG1-CD1	-5.58	102.08	113.80
1	A	24	ARG	NE-CZ-NH1	-5.57	115.93	121.50
1	A	75	PHE	O-C-N	5.57	128.02	122.12
1	A	20	GLU	N-CA-CB	5.53	118.34	110.16
1	A	49	GLY	O-C-N	5.51	128.62	122.50
1	A	32	GLU	N-CA-C	-5.50	100.21	108.96
1	A	7	VAL	CA-C-N	-5.50	113.96	122.59
1	A	7	VAL	C-N-CA	-5.50	113.96	122.59
1	A	141	ALA	CA-C-N	5.49	127.91	120.44
1	A	141	ALA	C-N-CA	5.49	127.91	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	64	SER	CA-C-O	-5.48	115.31	121.40
1	A	122	ASP	N-CA-C	-5.44	102.34	110.23
1	A	21	THR	CA-CB-OG1	-5.42	101.48	109.60
1	A	14	ASN	N-CA-CB	5.42	117.92	110.07
1	A	56	GLY	O-C-N	5.40	128.56	123.48
1	A	32	GLU	O-C-N	5.39	129.33	123.13
1	A	76	ASP	O-C-N	5.35	127.79	122.12
1	A	96	SER	CA-CB-OG	-5.34	100.42	111.10
1	A	3	LYS	CA-C-N	-5.33	114.95	122.94
1	A	3	LYS	C-N-CA	-5.33	114.95	122.94
1	A	90	CYS	CA-C-N	-5.33	113.14	121.87
1	A	90	CYS	C-N-CA	-5.33	113.14	121.87
1	A	63	ASP	CA-CB-CG	-5.32	107.28	112.60
1	A	77	SER	CA-C-O	-5.30	113.47	119.78
1	A	3	LYS	N-CA-CB	5.29	118.87	110.57
1	A	144	VAL	CA-C-N	5.27	127.30	120.44
1	A	144	VAL	C-N-CA	5.27	127.30	120.44
1	A	3	LYS	N-CA-C	-5.26	100.60	109.07
1	A	27	ALA	CA-C-N	5.26	127.85	120.28
1	A	27	ALA	C-N-CA	5.26	127.85	120.28
1	A	126	ILE	CA-C-N	-5.24	115.80	122.77
1	A	126	ILE	C-N-CA	-5.24	115.80	122.77
1	A	128	GLY	O-C-N	5.21	127.20	122.88
1	A	99	GLU	CA-CB-CG	5.20	124.50	114.10
1	A	117	ALA	N-CA-C	-5.19	103.68	110.53
1	A	81	THR	N-CA-C	5.17	118.05	111.69
1	A	110	GLU	CA-C-N	5.16	127.14	120.44
1	A	110	GLU	C-N-CA	5.16	127.14	120.44
1	A	84	GLN	CG-CD-OE1	-5.14	110.53	120.80
1	A	69	ASP	OD1-CG-OD2	-5.13	110.58	122.90
1	A	132	ALA	O-C-N	-5.11	115.33	122.37
1	A	32	GLU	CG-CD-OE1	-5.09	106.69	118.40
1	A	69	ASP	CB-CG-OD1	5.07	130.07	118.40
1	A	33	VAL	CA-C-O	-5.06	115.07	120.39
1	A	136	ASP	CB-CG-OD1	5.06	130.04	118.40
1	A	106	ASP	CA-CB-CG	5.04	117.64	112.60
1	A	99	GLU	OE1-CD-OE2	5.01	134.94	122.90
1	A	68	GLN	CA-C-N	5.01	126.95	120.44
1	A	68	GLN	C-N-CA	5.01	126.95	120.44

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	134	ARG	Sidechain
1	A	24	ARG	Sidechain
1	A	86	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1102	0	1029	11	0
2	A	31	0	19	1	0
3	A	130	0	0	5	0
All	All	1263	0	1048	12	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 (12) 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:64:SER:HB2	3:A:252:HOH:O	1.99	0.63
1:A:79:GLU:OE1	3:A:274:HOH:O	2.17	0.55
1:A:110:GLU:OE1	1:A:113:LYS:HE3	2.10	0.52
1:A:56:GLY:HA2	1:A:91:PHE:O	2.12	0.50
1:A:108:ILE:HG22	1:A:112:LEU:HD22	1.95	0.48
1:A:68:GLN:HE22	1:A:70:ASP:HB2	1.78	0.47
1:A:79:GLU:HG2	3:A:273:HOH:O	2.13	0.47
2:A:149:FMN:H1'2	2:A:149:FMN:H9	1.57	0.45
1:A:87:LYS:HD2	3:A:254:HOH:O	2.19	0.43
1:A:67:LEU:O	1:A:68:GLN:C	2.63	0.41
1:A:64:SER:CB	3:A:252:HOH:O	2.64	0.41
1:A:90:CYS:O	1:A:123:GLY:HA2	2.21	0.41

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	145/147 (99%)	141 (97%)	4 (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	111/111 (100%)	103 (93%)	8 (7%)	13	6

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	48	GLU
1	A	55	LEU
1	A	78	LEU
1	A	99	GLU
1	A	112	LEU
1	A	142	HIS
1	A	144	VAL

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	68	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](#)

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	2.96	16 (48%)	48,50,50	3.11	22 (45%)

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 (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	149	FMN	C1'-C2'	7.93	1.63	1.52
2	A	149	FMN	C4'-C3'	4.95	1.62	1.53
2	A	149	FMN	C5A-N5	-4.75	1.30	1.39
2	A	149	FMN	P-O5'	-4.71	1.45	1.60
2	A	149	FMN	C9A-C5A	4.69	1.48	1.41
2	A	149	FMN	C6-C7	-3.62	1.34	1.39
2	A	149	FMN	P-O1P	3.61	1.61	1.50
2	A	149	FMN	O4'-C4'	3.52	1.50	1.43
2	A	149	FMN	C7M-C7	3.49	1.57	1.51
2	A	149	FMN	C4A-C10	3.09	1.53	1.44
2	A	149	FMN	O2-C2	-2.93	1.18	1.24
2	A	149	FMN	C9-C9A	-2.84	1.35	1.39
2	A	149	FMN	C5'-C4'	-2.81	1.48	1.51
2	A	149	FMN	C9A-N10	2.78	1.46	1.41
2	A	149	FMN	C10-N1	2.68	1.38	1.33
2	A	149	FMN	C2-N1	-2.55	1.30	1.36

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	149	FMN	C1'-N10-C9A	-9.60	101.97	120.63
2	A	149	FMN	C4-C4A-N5	8.14	129.46	118.21
2	A	149	FMN	C5A-C9A-N10	-7.93	110.80	117.97
2	A	149	FMN	C9-C9A-N10	5.62	129.41	121.85
2	A	149	FMN	C6-C7-C8	4.64	126.50	119.69
2	A	149	FMN	O2P-P-O5'	4.61	118.70	106.67
2	A	149	FMN	C7M-C7-C8	-4.23	112.13	120.76
2	A	149	FMN	C5A-N5-C4A	3.99	124.54	118.09
2	A	149	FMN	O3P-P-O5'	3.65	116.19	106.67
2	A	149	FMN	C10-C4A-N5	-3.24	118.20	124.81
2	A	149	FMN	O4'-C4'-C5'	-3.21	102.90	109.99
2	A	149	FMN	C9-C8-C7	-3.06	115.19	119.69
2	A	149	FMN	C4A-C4-N3	2.96	120.80	113.25
2	A	149	FMN	O4-C4-N3	-2.72	115.00	120.11
2	A	149	FMN	C4-C4A-C10	-2.68	112.34	116.93
2	A	149	FMN	C5A-C6-C7	-2.39	116.40	120.83
2	A	149	FMN	O2'-C2'-C1'	2.31	119.71	110.20
2	A	149	FMN	O3'-C3'-C2'	-2.29	103.73	108.93
2	A	149	FMN	O3'-C3'-C4'	-2.19	103.95	108.93
2	A	149	FMN	O2P-P-O1P	-2.18	102.33	110.83
2	A	149	FMN	C9A-N10-C10	2.18	124.07	120.75
2	A	149	FMN	C1'-C2'-C3'	-2.17	103.79	109.66

There are no chirality outliers.

All (1) torsion outliers are listed below:

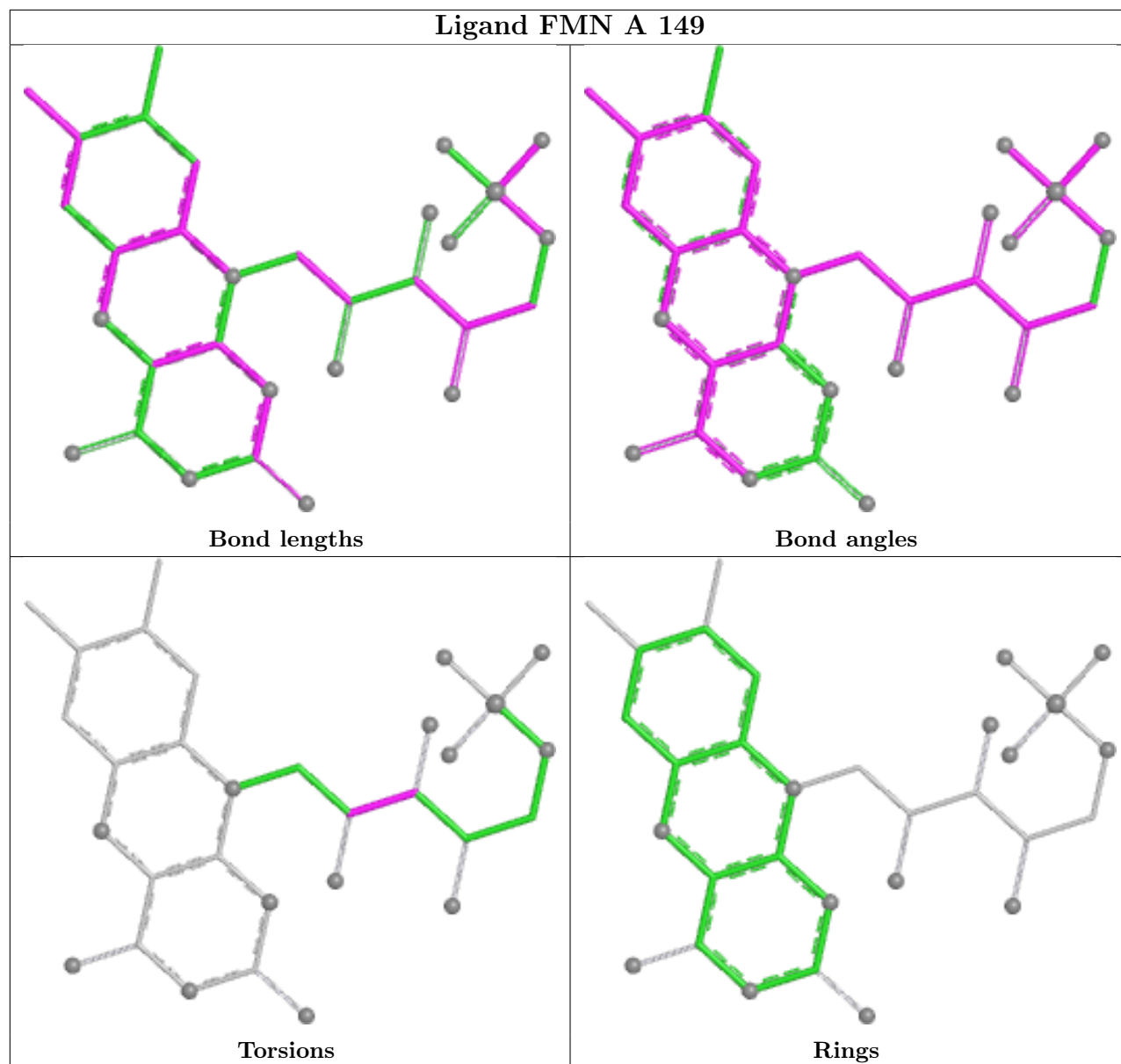
Mol	Chain	Res	Type	Atoms
2	A	149	FMN	O2'-C2'-C3'-O3'

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 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

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.