



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:45 PM UTC

PDB ID : 4FX2 / pdb_00004fx2
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

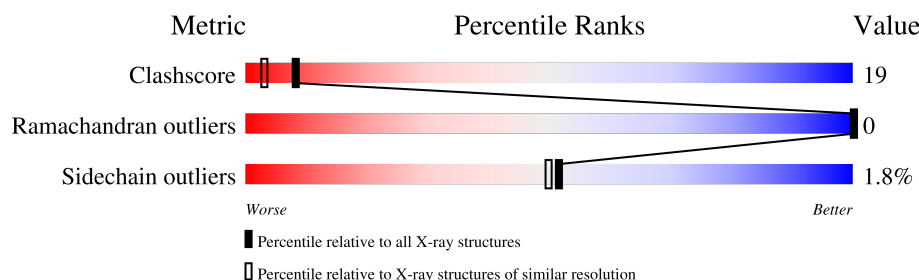
1 Overall quality at a glance

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 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
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: $C_{17}H_{21}N_4O_9P$).

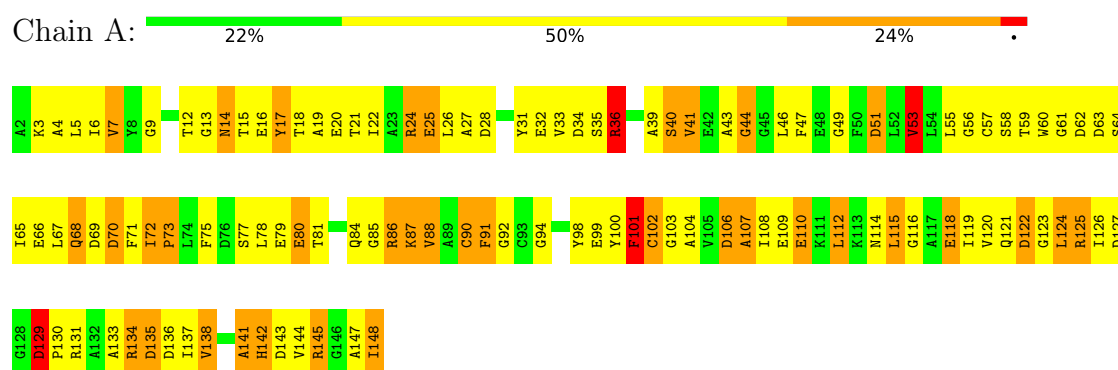


3 Residue-property plots

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	51.44Å 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	2.30	52/1119 (4.6%)	3.48	206/1514 (13.6%)

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 (52) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	94	GLY	N-CA	10.57	1.55	1.45
1	A	122	ASP	CA-C	7.32	1.62	1.52
1	A	69	ASP	C-O	7.29	1.32	1.24
1	A	18	THR	N-CA	-7.29	1.37	1.46
1	A	34	ASP	N-CA	7.12	1.54	1.46
1	A	66	GLU	C-N	-7.08	1.23	1.33
1	A	44	GLY	N-CA	7.06	1.54	1.45
1	A	61	GLY	N-CA	7.04	1.52	1.45
1	A	122	ASP	N-CA	6.97	1.54	1.46
1	A	124	LEU	CA-C	6.82	1.61	1.52
1	A	44	GLY	C-O	6.78	1.30	1.24
1	A	90	CYS	C-N	6.63	1.41	1.33
1	A	138	VAL	CA-C	-6.60	1.44	1.52
1	A	81	THR	C-N	-6.51	1.24	1.33
1	A	67	LEU	N-CA	6.50	1.54	1.45
1	A	92	GLY	CA-C	-6.49	1.44	1.51
1	A	122	ASP	C-N	-6.37	1.27	1.33
1	A	7	VAL	N-CA	6.33	1.53	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	68	GLN	C-O	-6.33	1.16	1.23
1	A	143	ASP	CG-OD2	6.22	1.37	1.25
1	A	126	ILE	C-O	-6.21	1.17	1.24
1	A	72	ILE	CA-CB	5.93	1.61	1.54
1	A	14	ASN	N-CA	-5.88	1.39	1.46
1	A	120	VAL	CA-C	-5.82	1.44	1.52
1	A	9	GLY	N-CA	5.81	1.53	1.45
1	A	116	GLY	C-O	5.80	1.31	1.24
1	A	19	ALA	C-O	5.79	1.30	1.24
1	A	16	GLU	C-O	5.65	1.30	1.24
1	A	20	GLU	C-N	-5.64	1.26	1.33
1	A	61	GLY	CA-C	-5.60	1.45	1.52
1	A	67	LEU	CB-CG	-5.58	1.42	1.53
1	A	134	ARG	N-CA	-5.58	1.39	1.46
1	A	5	LEU	CB-CG	5.56	1.64	1.53
1	A	81	THR	N-CA	-5.54	1.39	1.46
1	A	104	ALA	C-N	-5.45	1.27	1.33
1	A	147	ALA	C-O	5.45	1.31	1.24
1	A	144	VAL	C-N	-5.38	1.27	1.33
1	A	6	ILE	CB-CG1	5.36	1.64	1.53
1	A	145	ARG	CZ-NH2	-5.27	1.26	1.33
1	A	106	ASP	N-CA	5.21	1.52	1.46
1	A	102	CYS	C-O	5.20	1.30	1.24
1	A	33	VAL	CA-CB	5.19	1.60	1.54
1	A	145	ARG	C-O	5.14	1.30	1.24
1	A	25	GLU	C-N	-5.13	1.27	1.33
1	A	121	GLN	CD-NE2	-5.11	1.22	1.33
1	A	26	LEU	C-N	-5.11	1.27	1.33
1	A	18	THR	C-N	-5.09	1.27	1.33
1	A	119	ILE	N-CA	-5.08	1.40	1.46
1	A	137	ILE	N-CA	-5.08	1.40	1.46
1	A	100	TYR	N-CA	5.08	1.53	1.46
1	A	115	LEU	C-N	-5.07	1.26	1.33
1	A	14	ASN	C-O	-5.02	1.18	1.24

All (206) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	145	ARG	NE-CZ-NH2	27.37	143.83	119.20
1	A	122	ASP	CA-CB-CG	13.54	126.14	112.60
1	A	145	ARG	NE-CZ-NH1	-12.89	108.61	121.50
1	A	86	ARG	CA-C-N	12.23	138.68	122.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	86	ARG	C-N-CA	12.23	138.68	122.42
1	A	127	ASP	CA-C-O	-11.83	108.06	120.84
1	A	145	ARG	NH1-CZ-NH2	-11.58	104.25	119.30
1	A	18	THR	CA-C-N	11.28	135.40	120.28
1	A	18	THR	C-N-CA	11.28	135.40	120.28
1	A	81	THR	CA-C-N	11.18	143.32	121.41
1	A	81	THR	C-N-CA	11.18	143.32	121.41
1	A	41	VAL	CB-CA-C	11.02	123.72	111.59
1	A	43	ALA	N-CA-C	10.90	123.25	111.36
1	A	104	ALA	CA-C-N	10.82	133.93	120.72
1	A	104	ALA	C-N-CA	10.82	133.93	120.72
1	A	109	GLU	CB-CG-CD	10.73	130.84	112.60
1	A	109	GLU	N-CA-CB	10.13	124.70	109.91
1	A	84	GLN	CG-CD-NE2	9.89	131.24	116.40
1	A	137	ILE	CA-C-N	9.72	132.81	120.56
1	A	137	ILE	C-N-CA	9.72	132.81	120.56
1	A	134	ARG	NE-CZ-NH2	-9.54	110.61	119.20
1	A	17	TYR	CA-C-N	9.30	133.09	120.54
1	A	17	TYR	C-N-CA	9.30	133.09	120.54
1	A	125	ARG	CD-NE-CZ	9.27	137.37	124.40
1	A	136	ASP	CA-C-N	9.10	132.02	120.56
1	A	136	ASP	C-N-CA	9.10	132.02	120.56
1	A	34	ASP	CB-CA-C	9.09	125.10	110.19
1	A	80	GLU	CA-C-N	8.98	132.50	120.65
1	A	80	GLU	C-N-CA	8.98	132.50	120.65
1	A	69	ASP	CB-CA-C	8.88	124.83	110.88
1	A	27	ALA	O-C-N	-8.81	112.78	122.12
1	A	145	ARG	CD-NE-CZ	-8.80	112.08	124.40
1	A	134	ARG	N-CA-CB	8.76	124.05	109.78
1	A	61	GLY	CA-C-O	-8.62	116.28	122.23
1	A	40	SER	CA-C-O	-8.61	109.07	119.32
1	A	125	ARG	NE-CZ-NH1	8.58	130.08	121.50
1	A	112	LEU	O-C-N	8.57	131.01	122.09
1	A	141	ALA	CA-C-N	8.57	132.10	120.44
1	A	141	ALA	C-N-CA	8.57	132.10	120.44
1	A	34	ASP	CA-CB-CG	8.51	121.11	112.60
1	A	109	GLU	CG-CD-OE1	8.47	137.89	118.40
1	A	129	ASP	CA-CB-CG	-8.40	104.20	112.60
1	A	138	VAL	O-C-N	-8.38	113.70	121.91
1	A	39	ALA	O-C-N	-8.33	111.51	122.59
1	A	71	PHE	N-CA-C	8.27	120.38	111.36
1	A	126	ILE	O-C-N	8.27	132.09	122.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	108	ILE	CA-C-N	8.27	131.56	120.65
1	A	108	ILE	C-N-CA	8.27	131.56	120.65
1	A	69	ASP	N-CA-C	8.21	119.85	111.07
1	A	16	GLU	CB-CG-CD	7.99	126.19	112.60
1	A	57	CYS	N-CA-C	7.93	121.33	108.32
1	A	72	ILE	CA-C-N	7.85	127.76	119.05
1	A	72	ILE	C-N-CA	7.85	127.76	119.05
1	A	118	GLU	CB-CA-C	-7.82	97.53	110.19
1	A	86	ARG	CA-C-O	7.73	129.69	121.19
1	A	24	ARG	CA-C-N	7.72	136.29	121.54
1	A	24	ARG	C-N-CA	7.72	136.29	121.54
1	A	134	ARG	O-C-N	7.69	130.95	122.11
1	A	13	GLY	CA-C-N	7.67	133.52	120.71
1	A	13	GLY	C-N-CA	7.67	133.52	120.71
1	A	135	ASP	CA-CB-CG	7.59	120.19	112.60
1	A	14	ASN	O-C-N	7.50	131.25	122.17
1	A	84	GLN	CG-CD-OE1	-7.45	105.90	120.80
1	A	141	ALA	CA-C-O	7.44	128.43	120.55
1	A	81	THR	N-CA-C	7.43	119.06	110.97
1	A	141	ALA	O-C-N	-7.42	114.26	122.12
1	A	62	ASP	O-C-N	7.36	130.56	121.95
1	A	101	PHE	CA-C-O	-7.31	112.99	120.96
1	A	136	ASP	CA-C-O	-7.27	112.84	120.55
1	A	86	ARG	O-C-N	-7.24	113.97	122.87
1	A	144	VAL	CA-C-O	-7.23	113.50	121.17
1	A	138	VAL	CB-CA-C	7.21	121.19	111.97
1	A	3	LYS	CG-CD-CE	7.20	127.86	111.30
1	A	145	ARG	CA-CB-CG	7.15	128.41	114.10
1	A	21	THR	CA-CB-OG1	-7.14	98.89	109.60
1	A	61	GLY	O-C-N	-7.12	114.38	122.64
1	A	12	THR	CA-C-N	7.12	134.11	120.66
1	A	12	THR	C-N-CA	7.12	134.11	120.66
1	A	24	ARG	CD-NE-CZ	7.11	134.35	124.40
1	A	33	VAL	CA-C-N	-7.09	113.13	123.05
1	A	33	VAL	C-N-CA	-7.09	113.13	123.05
1	A	86	ARG	CA-CB-CG	7.06	128.22	114.10
1	A	20	GLU	CA-C-N	7.06	129.96	120.65
1	A	20	GLU	C-N-CA	7.06	129.96	120.65
1	A	16	GLU	CA-C-N	7.04	129.59	120.44
1	A	16	GLU	C-N-CA	7.04	129.59	120.44
1	A	27	ALA	CA-C-O	7.04	128.01	120.55
1	A	145	ARG	CA-C-O	7.01	128.18	120.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	41	VAL	CA-CB-CG1	6.97	122.26	110.40
1	A	33	VAL	N-CA-C	6.97	117.92	107.75
1	A	26	LEU	O-C-N	-6.93	114.88	122.09
1	A	24	ARG	NE-CZ-NH1	6.92	128.42	121.50
1	A	28	ASP	CB-CG-OD2	-6.89	102.55	118.40
1	A	84	GLN	O-C-N	-6.88	113.86	123.01
1	A	133	ALA	CA-C-O	6.87	126.83	119.34
1	A	148	ILE	N-CA-CB	6.85	123.15	111.50
1	A	109	GLU	CA-CB-CG	6.84	127.78	114.10
1	A	21	THR	CA-CB-CG2	6.82	122.10	110.50
1	A	35	SER	CA-C-O	-6.77	113.00	120.38
1	A	64	SER	CA-C-O	6.77	128.76	121.11
1	A	94	GLY	CA-C-N	6.75	132.52	121.58
1	A	94	GLY	C-N-CA	6.75	132.52	121.58
1	A	126	ILE	CA-CB-CG1	-6.74	98.94	110.40
1	A	58	SER	N-CA-CB	6.72	120.50	110.29
1	A	26	LEU	CA-C-N	6.71	129.27	120.28
1	A	26	LEU	C-N-CA	6.71	129.27	120.28
1	A	16	GLU	OE1-CD-OE2	-6.63	106.98	122.90
1	A	65	ILE	CA-C-N	-6.62	111.69	122.81
1	A	65	ILE	C-N-CA	-6.62	111.69	122.81
1	A	134	ARG	NE-CZ-NH1	6.60	128.10	121.50
1	A	69	ASP	CA-C-N	6.60	129.12	120.28
1	A	69	ASP	C-N-CA	6.60	129.12	120.28
1	A	68	GLN	CB-CG-CD	6.57	123.78	112.60
1	A	86	ARG	NE-CZ-NH1	6.57	128.07	121.50
1	A	120	VAL	CA-CB-CG2	6.54	121.52	110.40
1	A	68	GLN	CA-C-N	6.54	128.94	120.44
1	A	68	GLN	C-N-CA	6.54	128.94	120.44
1	A	138	VAL	CA-C-O	6.52	128.08	121.17
1	A	19	ALA	CA-C-N	6.45	128.83	120.44
1	A	19	ALA	C-N-CA	6.45	128.83	120.44
1	A	142	HIS	N-CA-CB	6.41	119.37	110.07
1	A	144	VAL	CA-C-N	6.35	128.70	120.44
1	A	144	VAL	C-N-CA	6.35	128.70	120.44
1	A	25	GLU	N-CA-CB	6.29	121.12	110.49
1	A	81	THR	N-CA-CB	6.27	119.06	109.91
1	A	68	GLN	N-CA-C	-6.26	101.41	110.24
1	A	14	ASN	N-CA-CB	6.23	119.35	110.13
1	A	43	ALA	CA-C-O	-6.21	113.83	120.42
1	A	142	HIS	N-CA-C	-6.21	104.44	111.14
1	A	17	TYR	CB-CG-CD1	6.18	130.07	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	15	THR	N-CA-C	-6.12	104.51	112.23
1	A	12	THR	CA-CB-OG1	-6.12	100.42	109.60
1	A	51	ASP	CA-CB-CG	6.05	118.65	112.60
1	A	67	LEU	CA-C-N	6.04	129.42	120.90
1	A	67	LEU	C-N-CA	6.04	129.42	120.90
1	A	118	GLU	CA-C-O	-6.04	113.90	120.36
1	A	39	ALA	CA-C-O	6.02	129.11	120.51
1	A	148	ILE	CA-CB-CG1	6.02	120.63	110.40
1	A	145	ARG	O-C-N	-6.01	115.88	122.07
1	A	18	THR	N-CA-CB	5.93	118.77	109.94
1	A	98	TYR	N-CA-CB	5.92	119.45	110.45
1	A	22	ILE	CA-C-O	-5.90	114.92	121.17
1	A	57	CYS	N-CA-CB	-5.89	100.61	110.57
1	A	47	PHE	CA-CB-CG	5.85	119.65	113.80
1	A	17	TYR	N-CA-CB	5.85	118.49	110.01
1	A	4	ALA	CA-C-O	-5.83	114.52	121.11
1	A	147	ALA	CB-CA-C	5.81	119.74	109.75
1	A	135	ASP	CA-C-O	-5.80	114.27	120.42
1	A	6	ILE	N-CA-CB	5.80	118.77	111.46
1	A	20	GLU	CB-CG-CD	5.80	122.46	112.60
1	A	116	GLY	CA-C-N	5.79	131.50	120.97
1	A	116	GLY	C-N-CA	5.79	131.50	120.97
1	A	144	VAL	CA-CB-CG1	5.78	120.23	110.40
1	A	66	GLU	CB-CG-CD	5.74	122.36	112.60
1	A	99	GLU	CG-CD-OE2	-5.71	105.27	118.40
1	A	49	GLY	CA-C-O	-5.64	112.31	119.19
1	A	60	TRP	N-CA-CB	-5.63	102.32	111.22
1	A	66	GLU	N-CA-C	-5.60	101.00	109.85
1	A	64	SER	O-C-N	-5.58	115.94	123.19
1	A	24	ARG	NE-CZ-NH2	-5.57	114.18	119.20
1	A	118	GLU	N-CA-CB	5.57	119.50	110.42
1	A	126	ILE	CA-C-O	-5.56	114.18	120.74
1	A	133	ALA	CA-C-N	5.56	129.16	120.82
1	A	133	ALA	C-N-CA	5.56	129.16	120.82
1	A	131	ARG	CA-C-O	-5.53	112.80	119.49
1	A	120	VAL	CB-CA-C	5.49	121.15	112.26
1	A	78	LEU	CA-C-O	5.44	126.07	119.38
1	A	55	LEU	CA-C-N	-5.43	118.37	122.33
1	A	55	LEU	C-N-CA	-5.43	118.37	122.33
1	A	36	ARG	NH1-CZ-NH2	-5.42	112.25	119.30
1	A	91	PHE	CA-C-O	5.41	127.17	121.33
1	A	88	VAL	CA-CB-CG1	5.40	119.59	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	107	ALA	CA-C-N	5.39	128.12	120.53
1	A	107	ALA	C-N-CA	5.39	128.12	120.53
1	A	70	ASP	CB-CG-OD1	-5.38	106.02	118.40
1	A	73	PRO	CA-C-N	5.37	127.74	120.44
1	A	73	PRO	C-N-CA	5.37	127.74	120.44
1	A	67	LEU	N-CA-CB	-5.35	101.69	110.41
1	A	87	LYS	CA-C-N	5.35	130.28	122.69
1	A	87	LYS	C-N-CA	5.35	130.28	122.69
1	A	98	TYR	CA-C-O	5.34	128.12	121.81
1	A	125	ARG	NH1-CZ-NH2	-5.34	112.36	119.30
1	A	85	GLY	CA-C-N	5.33	128.27	120.71
1	A	85	GLY	C-N-CA	5.33	128.27	120.71
1	A	92	GLY	N-CA-C	5.32	118.26	110.38
1	A	131	ARG	N-CA-C	-5.32	105.89	112.38
1	A	138	VAL	CA-C-N	5.28	125.69	119.94
1	A	138	VAL	C-N-CA	5.28	125.69	119.94
1	A	103	GLY	N-CA-C	-5.28	108.41	115.32
1	A	79	GLU	CG-CD-OE2	5.27	130.53	118.40
1	A	119	ILE	N-CA-CB	5.27	119.93	111.23
1	A	110	GLU	CG-CD-OE2	-5.26	106.30	118.40
1	A	122	ASP	CA-C-N	5.25	124.96	119.92
1	A	122	ASP	C-N-CA	5.25	124.96	119.92
1	A	60	TRP	CA-C-O	-5.25	115.40	121.49
1	A	16	GLU	O-C-N	-5.24	116.67	122.07
1	A	53	VAL	CB-CA-C	5.24	117.80	110.99
1	A	32	GLU	N-CA-C	-5.22	100.79	109.46
1	A	16	GLU	CG-CD-OE2	5.21	130.38	118.40
1	A	138	VAL	N-CA-CB	-5.19	104.48	110.55
1	A	135	ASP	CB-CG-OD2	-5.18	106.49	118.40
1	A	87	LYS	N-CA-CB	5.17	118.44	110.21
1	A	53	VAL	O-C-N	-5.16	117.47	122.99
1	A	12	THR	OG1-CB-CG2	5.15	119.60	109.30
1	A	68	GLN	N-CA-CB	5.08	117.77	109.69
1	A	79	GLU	CA-CB-CG	5.03	124.16	114.10

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

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Mol	Chain	Res	Type	Group
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	1028	41	0
2	A	31	0	18	1	0
3	A	226	0	0	11	0
All	All	1359	0	1046	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:101:PHE:O	1:A:102:CYS:C	2.59	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:17:TYR:OH	1:A:134:ARG:HD2	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	145/147 (99%)	134 (92%)	11 (8%)	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%)	109 (98%)	2 (2%)	51	50

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

Mol	Chain	Res	Type
1	A	77	SER
1	A	138	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	14	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	2.29	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(°)	Ideal(°)
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'

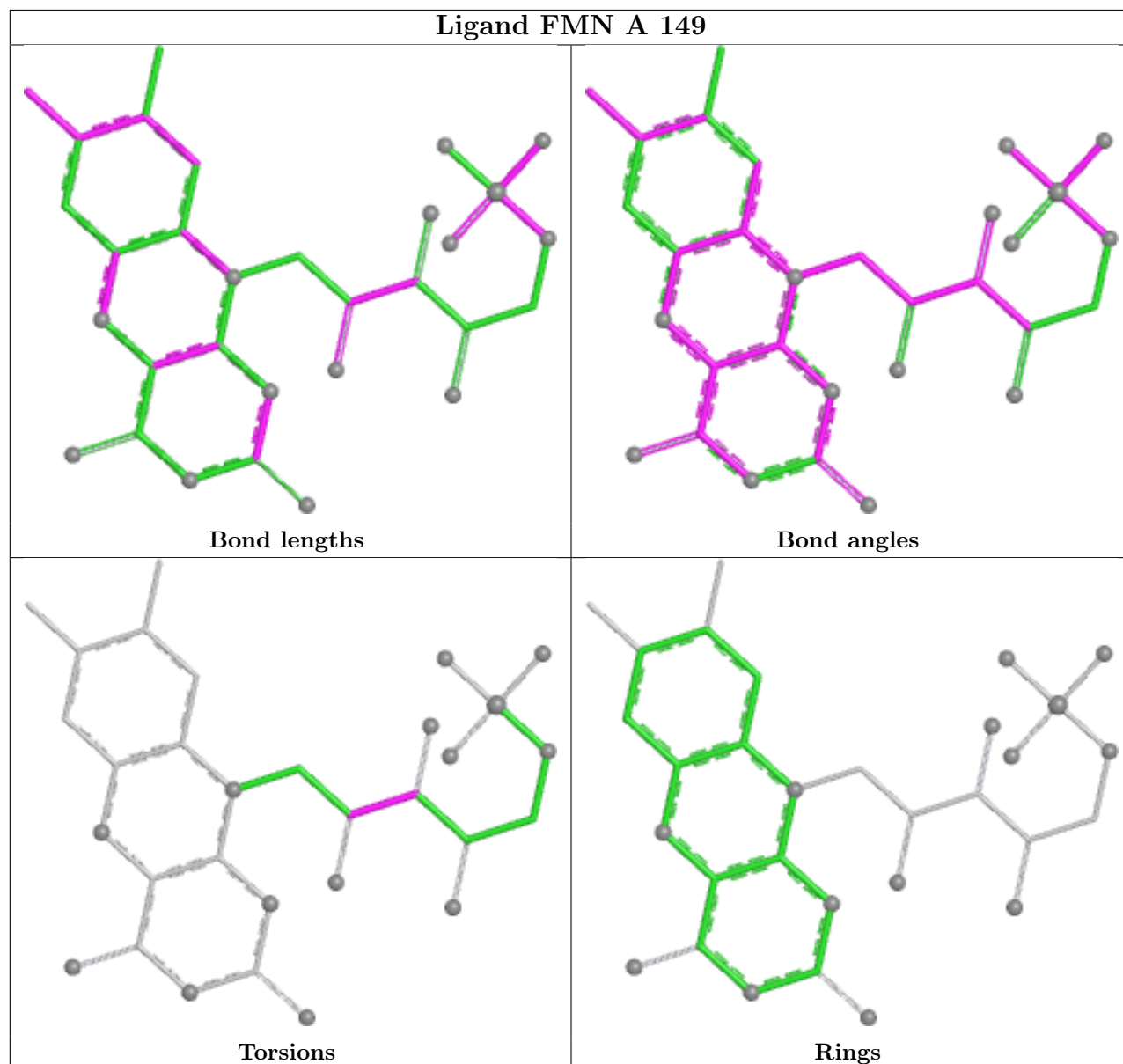
There are no ring outliers.

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 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.