



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:24 PM UTC

PDB ID : 1C7E / pdb_00001c7e
Title : D95E HYDROQUINONE FLAVODOXIN MUTANT FROM D. VULGARIS
Authors : McCarthy, A.; Walsh, M.; Higgins, T.; D'Arcy, D.
Deposited on : 2000-02-16
Resolution : 2.25 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

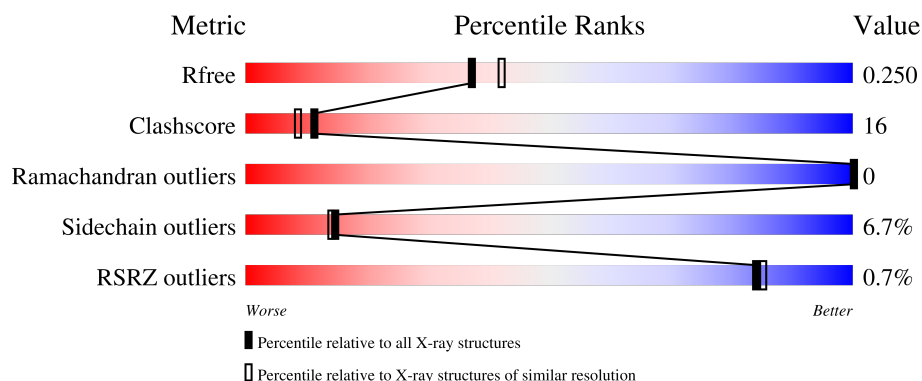
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	147	% 44% 37% 19%
1	B	147	46% 39% 12% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FMN	A	1149	-	X	-	-
2	FMN	B	2149	-	X	-	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2350 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.

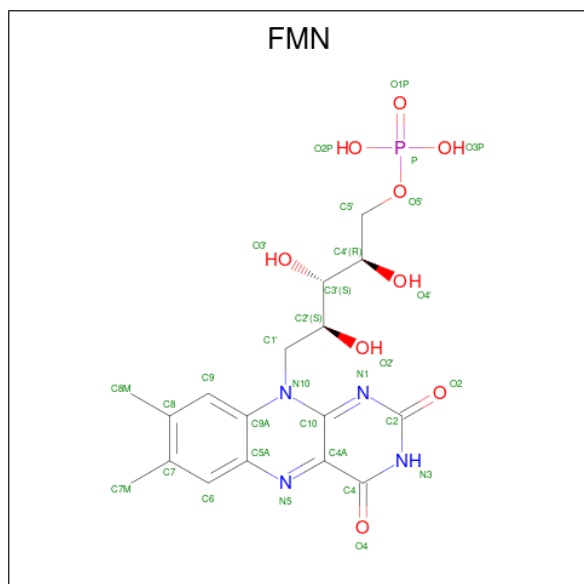
- Molecule 1 is a protein called FLAVODOXIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	147	Total	C	N	O	S	0	0	0
			1105	687	181	233	4			
1	B	147	Total	C	N	O	S	0	0	0
			1105	687	181	233	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	95	GLU	ASP	engineered mutation	UNP P00323
B	95	GLU	ASP	engineered mutation	UNP P00323

- Molecule 2 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: C₁₇H₂₁N₄O₉P).



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

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

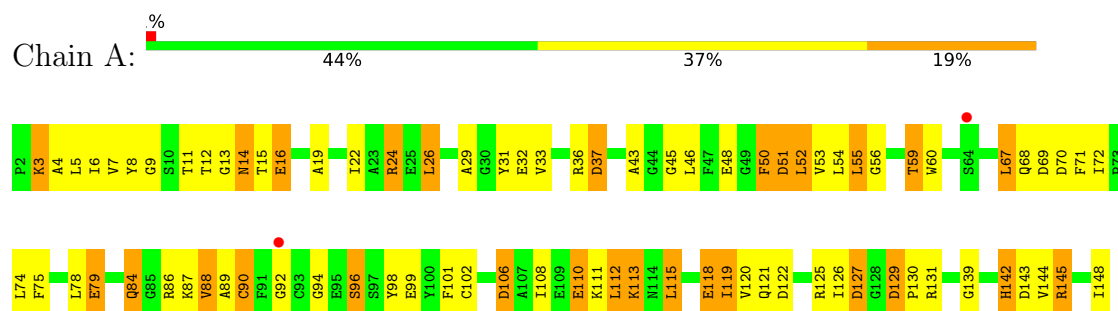
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	31	Total	O	0	0
			31	31		
3	B	47	Total	O	0	0
			47	47		

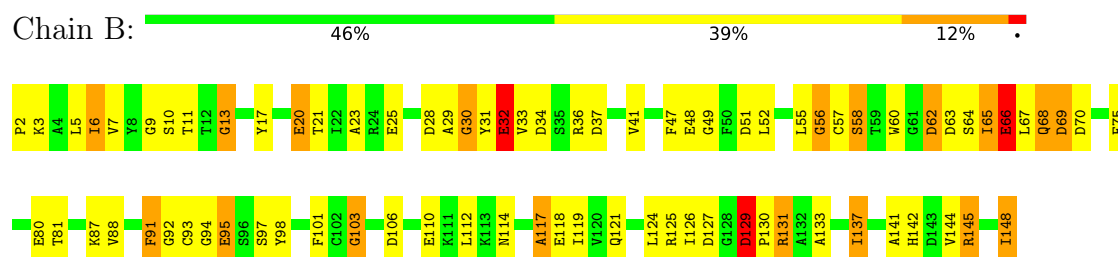
3 Residue-property plots

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

• Molecule 1: FLAVODOXIN



• Molecule 1: FLAVODOXIN



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	93.04Å 61.51Å 75.56Å 90.00° 127.06° 90.00°	Depositor
Resolution (Å)	19.76 – 2.25 19.76 – 2.25	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.76-2.25) 95.2 (19.76-2.25)	Depositor EDS
R_{merge}	0.66	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.73 (at 2.26Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.227 , 0.297 0.200 , 0.250	Depositor DCC
R_{free} test set	484 reflections (3.12%)	wwPDB-VP
Wilson B-factor (Å ²)	37.0	Xtriage
Anisotropy	0.196	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 48.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.017 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2350	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.71% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

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	1.28	6/1123 (0.5%)	2.57	92/1519 (6.1%)
1	B	1.16	3/1123 (0.3%)	2.46	85/1519 (5.6%)
All	All	1.22	9/2246 (0.4%)	2.51	177/3038 (5.8%)

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	7
1	B	0	14
All	All	0	21

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	46	LEU	CA-C	-7.64	1.43	1.52
1	A	74	LEU	N-CA	-6.56	1.38	1.46
1	B	32	GLU	CA-C	6.33	1.60	1.52
1	A	72	ILE	N-CA	-6.22	1.39	1.46
1	B	56	GLY	CA-C	6.12	1.56	1.52
1	B	60	TRP	CA-CB	6.04	1.62	1.53
1	A	9	GLY	CA-C	5.48	1.59	1.51
1	A	5	LEU	N-CA	-5.30	1.39	1.46
1	A	67	LEU	C-O	-5.14	1.17	1.23

All (177) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	24	ARG	CD-NE-CZ	18.97	150.95	124.40
1	A	50	PHE	CA-C-O	-13.30	105.58	121.28
1	B	95	GLU	CA-CB-CG	12.63	139.37	114.10
1	A	4	ALA	CA-C-N	12.01	140.17	123.11
1	A	4	ALA	C-N-CA	12.01	140.17	123.11
1	B	145	ARG	CD-NE-CZ	10.46	139.05	124.40
1	A	14	ASN	CA-C-O	9.96	130.96	120.70
1	A	84	GLN	CA-C-O	-9.43	110.61	120.80
1	B	127	ASP	CA-C-O	-9.42	110.72	120.71
1	A	13	GLY	CA-C-O	9.37	131.25	119.25
1	B	129	ASP	CA-C-O	8.97	128.37	119.49
1	A	3	LYS	CA-CB-CG	8.95	131.99	114.10
1	B	48	GLU	CB-CG-CD	8.84	127.64	112.60
1	A	119	ILE	N-CA-CB	8.76	120.84	111.46
1	B	133	ALA	CA-C-O	8.65	129.14	120.32
1	B	30	GLY	CA-C-O	-8.54	108.31	119.25
1	B	34	ASP	N-CA-CB	8.43	124.16	110.42
1	A	98	TYR	CB-CG-CD2	8.16	133.03	120.80
1	B	145	ARG	CA-C-N	7.90	128.88	120.03
1	B	145	ARG	C-N-CA	7.90	128.88	120.03
1	B	47	PHE	CA-CB-CG	7.79	121.59	113.80
1	A	13	GLY	N-CA-C	7.78	126.51	115.30
1	A	33	VAL	CA-C-N	7.74	133.78	122.41
1	A	33	VAL	C-N-CA	7.74	133.78	122.41
1	B	60	TRP	CA-CB-CG	-7.66	99.04	113.60
1	B	92	GLY	CA-C-O	7.48	128.68	121.49
1	A	46	LEU	CA-C-O	-7.48	112.49	120.42
1	A	52	LEU	CA-C-N	7.47	133.27	123.11
1	A	52	LEU	C-N-CA	7.47	133.27	123.11
1	B	6	ILE	O-C-N	-7.43	115.04	122.99
1	B	34	ASP	CA-CB-CG	7.41	120.01	112.60
1	A	75	PHE	CA-CB-CG	7.41	121.21	113.80
1	A	48	GLU	CA-C-N	7.37	135.40	122.05
1	A	48	GLU	C-N-CA	7.37	135.40	122.05
1	B	129	ASP	O-C-N	-7.37	114.33	121.18
1	A	60	TRP	CA-CB-CG	-7.23	99.87	113.60
1	A	126	ILE	N-CA-CB	7.15	118.51	110.72
1	B	23	ALA	CA-C-O	7.15	128.55	120.90
1	B	117	ALA	CA-C-O	-7.08	114.57	122.01
1	B	87	LYS	CA-C-N	7.06	132.40	122.23
1	B	87	LYS	C-N-CA	7.06	132.40	122.23
1	A	71	PHE	CA-C-N	6.92	127.07	120.43
1	A	71	PHE	C-N-CA	6.92	127.07	120.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	5	LEU	CA-C-N	-6.88	114.66	123.19
1	A	5	LEU	C-N-CA	-6.88	114.66	123.19
1	B	65	ILE	CB-CA-C	-6.88	102.21	111.15
1	B	37	ASP	CA-CB-CG	6.86	119.46	112.60
1	A	59	THR	CA-C-N	6.81	131.15	122.16
1	A	59	THR	C-N-CA	6.81	131.15	122.16
1	A	14	ASN	O-C-N	-6.80	114.74	122.09
1	B	106	ASP	CA-C-O	6.79	127.62	120.42
1	A	24	ARG	CG-CD-NE	6.79	126.94	112.00
1	A	37	ASP	CA-CB-CG	6.79	119.39	112.60
1	A	118	GLU	CA-C-O	6.78	128.16	120.84
1	B	5	LEU	CA-C-N	6.78	132.21	123.13
1	B	5	LEU	C-N-CA	6.78	132.21	123.13
1	A	98	TYR	O-C-N	-6.77	115.31	122.96
1	B	75	PHE	CA-C-O	-6.75	112.48	120.10
1	A	72	ILE	CA-C-N	6.74	126.20	118.85
1	A	72	ILE	C-N-CA	6.74	126.20	118.85
1	B	118	GLU	CA-C-O	6.72	129.04	120.57
1	B	94	GLY	CA-C-N	-6.71	111.05	122.33
1	B	94	GLY	C-N-CA	-6.71	111.05	122.33
1	A	142	HIS	CA-C-N	6.63	129.71	120.29
1	A	142	HIS	C-N-CA	6.63	129.71	120.29
1	A	5	LEU	N-CA-CB	6.63	121.48	110.47
1	B	58	SER	CA-C-O	6.62	129.56	121.94
1	B	66	GLU	N-CA-CB	6.59	122.36	111.08
1	B	97	SER	CA-C-O	-6.57	110.70	119.11
1	A	71	PHE	CA-CB-CG	6.55	120.35	113.80
1	B	13	GLY	O-C-N	-6.54	115.49	122.56
1	A	98	TYR	CB-CG-CD1	-6.50	111.05	120.80
1	B	119	ILE	N-CA-CB	6.50	118.41	111.46
1	A	45	GLY	O-C-N	-6.47	114.44	122.34
1	B	103	GLY	CA-C-N	-6.46	111.62	120.28
1	B	103	GLY	C-N-CA	-6.46	111.62	120.28
1	A	33	VAL	CA-C-O	6.43	127.55	120.48
1	A	4	ALA	O-C-N	-6.39	114.92	123.23
1	B	21	THR	CA-C-N	6.37	128.71	120.56
1	B	21	THR	C-N-CA	6.37	128.71	120.56
1	A	9	GLY	N-CA-C	-6.36	98.11	113.18
1	A	122	ASP	CA-CB-CG	-6.30	106.30	112.60
1	A	139	GLY	O-C-N	6.21	128.22	122.19
1	A	99	GLU	N-CA-CB	-6.21	100.69	109.94
1	B	62	ASP	CA-CB-CG	6.17	118.77	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	75	PHE	CA-CB-CG	6.15	119.95	113.80
1	B	64	SER	N-CA-CB	-6.12	101.69	111.43
1	B	95	GLU	CA-C-O	-6.11	112.76	120.28
1	A	13	GLY	O-C-N	-6.10	114.23	122.35
1	A	115	LEU	N-CA-C	-6.10	105.12	113.30
1	A	52	LEU	O-C-N	-6.07	116.16	123.27
1	A	98	TYR	CA-C-O	6.07	128.45	121.47
1	A	129	ASP	CA-CB-CG	6.07	118.67	112.60
1	B	29	ALA	CA-C-O	6.04	128.47	121.34
1	B	137	ILE	N-CA-C	-6.03	104.43	111.00
1	A	72	ILE	O-C-N	-6.01	116.57	120.42
1	A	106	ASP	N-CA-CB	5.99	119.03	110.16
1	B	41	VAL	CA-C-O	-5.99	114.91	121.92
1	A	99	GLU	CA-C-O	5.97	127.28	120.90
1	B	20	GLU	O-C-N	-5.96	115.80	122.12
1	B	91	PHE	O-C-N	-5.96	116.46	123.25
1	A	50	PHE	N-CA-CB	-5.94	100.95	110.63
1	B	28	ASP	CA-CB-CG	5.94	118.54	112.60
1	B	32	GLU	N-CA-C	-5.90	99.58	108.96
1	B	32	GLU	N-CA-CB	5.87	120.03	110.17
1	A	52	LEU	CA-C-O	-5.84	114.05	120.24
1	A	6	ILE	O-C-N	-5.83	117.06	123.18
1	A	16	GLU	N-CA-C	-5.82	105.01	111.36
1	A	101	PHE	CA-CB-CG	-5.81	107.99	113.80
1	B	117	ALA	N-CA-C	-5.80	103.00	110.19
1	A	3	LYS	N-CA-CB	-5.79	101.45	110.55
1	A	119	ILE	CB-CA-C	-5.78	105.05	111.35
1	A	102	CYS	CA-C-N	5.75	132.68	121.41
1	A	102	CYS	C-N-CA	5.75	132.68	121.41
1	A	89	ALA	CA-C-N	5.71	131.98	122.73
1	A	89	ALA	C-N-CA	5.71	131.98	122.73
1	A	129	ASP	CA-C-N	5.70	125.23	119.19
1	A	129	ASP	C-N-CA	5.70	125.23	119.19
1	B	6	ILE	CA-C-N	5.68	130.51	123.12
1	B	6	ILE	C-N-CA	5.68	130.51	123.12
1	B	29	ALA	N-CA-CB	-5.67	103.03	111.43
1	B	51	ASP	CA-CB-CG	-5.67	106.93	112.60
1	A	19	ALA	CA-C-O	5.65	126.76	120.82
1	B	80	GLU	O-C-N	5.65	129.40	122.34
1	A	79	GLU	CB-CG-CD	5.64	122.19	112.60
1	B	127	ASP	O-C-N	5.63	130.36	123.21
1	A	122	ASP	CA-C-O	-5.62	115.01	121.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	37	ASP	N-CA-C	-5.60	101.98	110.28
1	B	145	ARG	CA-C-O	5.59	126.35	120.42
1	B	33	VAL	N-CA-C	5.53	115.75	107.51
1	B	145	ARG	NE-CZ-NH2	-5.53	114.22	119.20
1	B	94	GLY	CA-C-O	-5.53	114.81	121.33
1	A	127	ASP	CA-C-O	-5.52	114.41	120.43
1	A	69	ASP	CA-C-O	-5.52	112.62	120.51
1	B	66	GLU	CA-C-O	-5.51	114.88	121.11
1	B	69	ASP	N-CA-C	5.51	119.50	112.34
1	B	63	ASP	CA-C-O	5.50	126.14	119.31
1	B	127	ASP	CA-CB-CG	5.50	118.10	112.60
1	A	16	GLU	CB-CA-C	5.49	120.18	110.85
1	B	118	GLU	N-CA-CB	-5.47	101.66	110.69
1	A	22	ILE	N-CA-C	-5.47	105.39	110.53
1	B	69	ASP	CA-C-O	-5.46	113.17	119.61
1	A	43	ALA	N-CA-C	5.44	118.71	111.75
1	A	32	GLU	N-CA-C	-5.44	99.87	108.73
1	B	125	ARG	CD-NE-CZ	-5.44	116.79	124.40
1	B	9	GLY	N-CA-C	-5.43	100.30	113.18
1	A	55	LEU	CA-C-O	-5.43	114.77	120.80
1	B	129	ASP	CA-C-N	5.42	125.24	119.28
1	B	129	ASP	C-N-CA	5.42	125.24	119.28
1	B	75	PHE	N-CA-CB	5.39	118.53	110.22
1	A	113	LYS	N-CA-C	-5.35	105.34	111.07
1	A	119	ILE	CA-C-O	-5.35	113.95	120.69
1	A	16	GLU	CB-CG-CD	5.34	121.69	112.60
1	A	29	ALA	N-CA-CB	-5.29	103.14	110.65
1	A	90	CYS	N-CA-C	5.25	118.00	109.24
1	A	53	VAL	CA-C-O	-5.23	114.54	120.66
1	A	139	GLY	N-CA-C	-5.23	106.08	112.77
1	A	145	ARG	NE-CZ-NH1	5.22	126.72	121.50
1	B	80	GLU	CA-C-N	-5.22	111.41	121.58
1	B	80	GLU	C-N-CA	-5.22	111.41	121.58
1	A	108	ILE	CA-CB-CG1	-5.21	101.53	110.40
1	B	11	THR	N-CA-C	-5.14	105.84	112.68
1	B	62	ASP	N-CA-CB	-5.14	101.81	110.49
1	B	106	ASP	CA-C-N	-5.12	113.02	120.29
1	B	106	ASP	C-N-CA	-5.12	113.02	120.29
1	B	57	CYS	CA-CB-SG	5.12	126.16	114.40
1	A	144	VAL	CA-C-O	-5.10	115.44	120.85
1	B	63	ASP	CA-C-N	5.09	131.38	122.82
1	B	63	ASP	C-N-CA	5.09	131.38	122.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	93	CYS	CA-C-O	-5.07	115.33	120.71
1	B	34	ASP	CB-CA-C	-5.06	101.99	110.19
1	A	52	LEU	N-CA-C	5.04	116.61	108.34
1	A	145	ARG	O-C-N	-5.04	116.79	122.03
1	B	81	THR	N-CA-C	5.03	119.27	113.18
1	B	25	GLU	N-CA-C	-5.02	105.90	112.23
1	A	54	LEU	CA-C-N	-5.00	115.19	122.65
1	A	54	LEU	C-N-CA	-5.00	115.19	122.65

There are no chirality outliers.

All (21) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	112	LEU	Mainchain
1	A	37	ASP	Mainchain
1	A	50	PHE	Mainchain
1	A	55	LEU	Mainchain
1	A	86	ARG	Mainchain
1	A	90	CYS	Mainchain
1	A	92	GLY	Mainchain
1	B	10	SER	Mainchain
1	B	101	PHE	Mainchain
1	B	117	ALA	Mainchain
1	B	121	GLN	Mainchain
1	B	126	ILE	Mainchain
1	B	129	ASP	Mainchain
1	B	13	GLY	Mainchain
1	B	131	ARG	Mainchain
1	B	141	ALA	Mainchain
1	B	20	GLU	Mainchain
1	B	30	GLY	Mainchain
1	B	49	GLY	Mainchain
1	B	6	ILE	Mainchain
1	B	66	GLU	Mainchain

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	1105	0	1034	43	0
1	B	1105	0	1034	28	0
2	A	31	0	19	8	0
2	B	31	0	19	3	0
3	A	31	0	0	3	0
3	B	47	0	0	1	0
All	All	2350	0	2106	71	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 16.

All (71) 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:14:ASN:HB2	2:A:1149:FMN:P	1.99	1.02
1:A:113:LYS:HE2	1:A:119:ILE:HG13	1.55	0.89
1:A:120:VAL:HG11	1:A:148:ILE:HG22	1.56	0.86
1:B:88:VAL:HG11	1:B:112:LEU:HD13	1.61	0.83
1:B:114:ASN:HB3	3:B:2167:HOH:O	1.80	0.80
1:B:68:GLN:NE2	1:B:70:ASP:H	1.80	0.79
1:A:14:ASN:HB2	2:A:1149:FMN:O3P	1.85	0.76
1:A:88:VAL:HG11	1:A:112:LEU:HD13	1.68	0.75
1:A:88:VAL:HG12	1:A:119:ILE:HD13	1.68	0.74
1:B:3:LYS:HG2	1:B:32:GLU:HG3	1.68	0.74
1:B:95:GLU:HG2	2:B:2149:FMN:H1'	1.69	0.73
1:A:15:THR:N	2:A:1149:FMN:O2P	2.21	0.71
1:B:144:VAL:O	1:B:148:ILE:HG23	1.92	0.69
1:A:79:GLU:HG3	1:A:115:LEU:HD21	1.75	0.67
1:A:68:GLN:NE2	1:A:70:ASP:H	1.94	0.66
1:B:52:LEU:HD13	1:B:148:ILE:HG21	1.76	0.66
1:B:68:GLN:HE22	1:B:70:ASP:H	1.46	0.64
1:A:31:TYR:OH	1:A:148:ILE:HD11	1.97	0.64
1:A:88:VAL:CG1	1:A:112:LEU:HD13	2.29	0.63
1:B:95:GLU:HG2	2:B:2149:FMN:C1'	2.28	0.62
1:A:8:TYR:HA	1:A:56:GLY:O	2.02	0.60
1:B:142:HIS:HA	1:B:145:ARG:NH2	2.17	0.59
1:B:17:TYR:CZ	1:B:131:ARG:HG2	2.37	0.59
1:B:95:GLU:HG3	1:B:98:TYR:HE1	1.68	0.59
1:A:14:ASN:HB2	2:A:1149:FMN:O2P	2.02	0.58
1:A:87:LYS:HZ2	1:A:118:GLU:CD	2.13	0.56
1:A:14:ASN:CB	2:A:1149:FMN:O3P	2.54	0.55
1:A:94:GLY:HA2	2:A:1149:FMN:H4'	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:88:VAL:CG1	1:B:112:LEU:HD13	2.37	0.53
1:A:96:SER:OG	1:A:127:ASP:OD2	2.26	0.52
1:B:124:LEU:HD21	1:B:137:ILE:HG12	1.92	0.52
1:A:68:GLN:HE22	1:A:70:ASP:HB2	1.74	0.52
1:A:79:GLU:HB2	3:A:1157:HOH:O	2.10	0.52
1:B:65:ILE:HD12	1:B:103:GLY:HA3	1.91	0.52
1:A:106:ASP:O	1:A:110:GLU:HB2	2.11	0.51
1:A:79:GLU:HG3	1:A:115:LEU:CD2	2.42	0.50
1:A:106:ASP:OD1	1:A:125:ARG:NH2	2.35	0.49
1:A:26:LEU:HD12	1:A:145:ARG:HG3	1.94	0.49
1:B:7:VAL:HA	1:B:36:ARG:O	2.12	0.49
1:A:142:HIS:ND1	1:A:145:ARG:NH2	2.61	0.49
1:B:2:PRO:HG2	1:B:31:TYR:CD2	2.48	0.48
1:A:121:GLN:NE2	1:A:143:ASP:HB3	2.28	0.48
1:A:68:GLN:HE22	1:A:70:ASP:H	1.62	0.48
1:A:88:VAL:CG1	1:A:119:ILE:HD13	2.42	0.48
1:A:68:GLN:NE2	1:A:70:ASP:N	2.63	0.47
1:A:7:VAL:HA	1:A:36:ARG:O	2.15	0.47
1:A:120:VAL:HG21	1:A:148:ILE:CG2	2.44	0.46
1:A:68:GLN:HE22	1:A:70:ASP:CB	2.30	0.45
1:A:12:THR:OG1	2:A:1149:FMN:O3P	2.29	0.45
1:A:131:ARG:HD3	3:A:1156:HOH:O	2.16	0.45
1:B:17:TYR:CE1	1:B:131:ARG:HG2	2.51	0.45
1:B:56:GLY:HA2	1:B:91:PHE:O	2.16	0.45
1:B:3:LYS:HG2	1:B:32:GLU:CG	2.43	0.44
1:A:52:LEU:HB2	1:A:148:ILE:CD1	2.47	0.44
1:B:95:GLU:HB2	1:B:98:TYR:HD1	1.83	0.44
1:A:78:LEU:HD12	1:A:111:LYS:HG2	1.99	0.44
1:B:129:ASP:HA	1:B:130:PRO:HD2	1.59	0.43
1:A:120:VAL:HG21	1:A:148:ILE:HG23	2.00	0.43
1:A:11:THR:O	1:A:11:THR:HG22	2.16	0.43
1:A:84:GLN:NE2	3:A:1160:HOH:O	2.51	0.43
1:B:3:LYS:CG	1:B:32:GLU:HG3	2.44	0.43
1:A:129:ASP:HA	1:A:130:PRO:HD2	1.84	0.43
1:A:59:THR:HG22	2:A:1149:FMN:C4	2.49	0.42
1:B:55:LEU:HD12	1:B:112:LEU:HD11	2.00	0.42
1:B:95:GLU:HG3	1:B:98:TYR:CE1	2.53	0.42
1:A:3:LYS:N	1:A:51:ASP:OD2	2.44	0.42
1:A:87:LYS:NZ	1:A:118:GLU:OE1	2.53	0.42
1:B:68:GLN:NE2	1:B:70:ASP:N	2.59	0.42
1:B:58:SER:HB2	2:B:2149:FMN:H5'2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:TYR:CE1	1:A:16:GLU:HB2	2.57	0.40
1:B:3:LYS:HB3	1:B:3:LYS:HE2	1.91	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%)	138 (95%)	7 (5%)	0	100	100
1	B	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
All	All	290/294 (99%)	276 (95%)	14 (5%)	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	112/112 (100%)	105 (94%)	7 (6%)	16	16
1	B	112/112 (100%)	104 (93%)	8 (7%)	13	12
All	All	224/224 (100%)	209 (93%)	15 (7%)	15	14

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ARG
1	A	26	LEU
1	A	51	ASP
1	A	67	LEU
1	A	88	VAL
1	A	96	SER
1	A	110	GLU
1	B	32	GLU
1	B	62	ASP
1	B	66	GLU
1	B	67	LEU
1	B	68	GLN
1	B	69	ASP
1	B	110	GLU
1	B	148	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	GLN
1	A	84	GLN
1	A	121	GLN
1	B	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](#)

2 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
2	FMN	B	2149	-	33,33,33	3.13	17 (51%)	48,50,50	3.06	22 (45%)
2	FMN	A	1149	-	33,33,33	3.13	15 (45%)	48,50,50	3.54	25 (52%)

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	B	2149	-	-	4/18/18/18	0/3/3/3
2	FMN	A	1149	-	-	5/18/18/18	0/3/3/3

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1149	FMN	O4-C4	9.18	1.41	1.23
2	B	2149	FMN	O4-C4	7.48	1.37	1.23
2	A	1149	FMN	P-O3P	6.51	1.79	1.54
2	B	2149	FMN	C5'-C4'	-6.08	1.43	1.51
2	B	2149	FMN	P-O2P	5.82	1.76	1.54
2	B	2149	FMN	O2-C2	5.41	1.35	1.24
2	A	1149	FMN	O2-C2	5.03	1.34	1.24
2	B	2149	FMN	C4'-C3'	-5.00	1.44	1.53
2	B	2149	FMN	P-O5'	4.97	1.76	1.60
2	A	1149	FMN	C10-N10	4.44	1.46	1.37
2	A	1149	FMN	C4'-C3'	-4.29	1.45	1.53
2	A	1149	FMN	P-O1P	4.11	1.63	1.50
2	A	1149	FMN	C1'-N10	-3.87	1.38	1.47
2	B	2149	FMN	C8M-C8	-3.85	1.43	1.51
2	A	1149	FMN	C4A-N5	3.80	1.39	1.30
2	B	2149	FMN	C10-N1	3.78	1.40	1.33
2	B	2149	FMN	C4A-N5	3.63	1.38	1.30
2	A	1149	FMN	P-O2P	3.47	1.67	1.54
2	A	1149	FMN	C7M-C7	-3.43	1.44	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2149	FMN	C7M-C7	-3.35	1.44	1.51
2	A	1149	FMN	C5'-C4'	-3.27	1.47	1.51
2	A	1149	FMN	C4A-C10	-3.07	1.35	1.44
2	A	1149	FMN	C8M-C8	-3.03	1.45	1.51
2	B	2149	FMN	P-O1P	2.88	1.59	1.50
2	B	2149	FMN	C6-C5A	2.87	1.44	1.40
2	B	2149	FMN	P-O3P	2.65	1.64	1.54
2	B	2149	FMN	C1'-C2'	2.58	1.56	1.52
2	A	1149	FMN	C6-C5A	2.55	1.43	1.40
2	B	2149	FMN	C1'-N10	-2.53	1.41	1.47
2	A	1149	FMN	C4-N3	-2.22	1.34	1.38
2	B	2149	FMN	C9A-C5A	-2.05	1.38	1.41
2	B	2149	FMN	C4A-C10	-2.02	1.38	1.44

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1149	FMN	O4-C4-C4A	-9.50	101.45	126.53
2	B	2149	FMN	C5A-C9A-N10	8.80	125.92	117.97
2	A	1149	FMN	O4-C4-N3	8.72	136.51	120.11
2	A	1149	FMN	O4'-C4'-C5'	-7.26	93.98	109.99
2	B	2149	FMN	O3P-P-O1P	7.07	138.39	110.83
2	B	2149	FMN	C4'-C3'-C2'	7.03	125.27	113.57
2	A	1149	FMN	C10-N1-C2	6.73	131.43	116.85
2	A	1149	FMN	C1'-N10-C9A	6.28	132.83	120.63
2	B	2149	FMN	C6-C5A-C9A	5.72	126.91	119.05
2	A	1149	FMN	O5'-C5'-C4'	-5.48	94.73	109.36
2	B	2149	FMN	C9A-N10-C10	-5.43	112.47	120.75
2	A	1149	FMN	O3P-P-O5'	5.43	120.82	106.67
2	A	1149	FMN	C5A-C9A-N10	4.90	122.40	117.97
2	B	2149	FMN	C5A-C6-C7	-4.56	112.38	120.83
2	B	2149	FMN	C9-C9A-N10	-4.52	115.77	121.85
2	B	2149	FMN	C4-C4A-N5	-4.14	112.49	118.21
2	A	1149	FMN	N3-C2-N1	-4.11	110.76	119.50
2	A	1149	FMN	C6-C5A-C9A	4.10	124.68	119.05
2	A	1149	FMN	C9-C9A-C5A	-4.01	112.94	120.03
2	B	2149	FMN	C1'-N10-C9A	3.94	128.29	120.63
2	A	1149	FMN	C8M-C8-C9	3.86	126.37	119.57
2	A	1149	FMN	C8M-C8-C7	-3.75	113.11	120.76
2	A	1149	FMN	O5'-P-O1P	3.58	116.12	106.44
2	B	2149	FMN	O2P-P-O5'	-3.53	97.45	106.67
2	A	1149	FMN	C4A-C4-N3	3.44	122.00	113.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2149	FMN	C4A-C10-N10	3.42	121.38	116.48
2	A	1149	FMN	O2-C2-N1	3.42	127.48	121.80
2	B	2149	FMN	O2-C2-N3	-3.38	112.10	118.58
2	B	2149	FMN	C6-C5A-N5	-3.30	112.96	118.44
2	A	1149	FMN	C9A-N10-C10	-3.30	115.72	120.75
2	A	1149	FMN	O3P-P-O1P	-3.26	98.11	110.83
2	B	2149	FMN	C4-C4A-C10	3.22	122.46	116.93
2	B	2149	FMN	C5A-N5-C4A	-3.22	112.88	118.09
2	A	1149	FMN	O4'-C4'-C3'	3.07	116.43	109.25
2	A	1149	FMN	C7M-C7-C6	2.99	124.83	119.57
2	B	2149	FMN	N3-C2-N1	2.83	125.52	119.50
2	A	1149	FMN	C4A-C10-N1	-2.76	117.82	124.59
2	A	1149	FMN	C6-C5A-N5	-2.53	114.25	118.44
2	B	2149	FMN	C9-C8-C7	2.44	123.26	119.69
2	B	2149	FMN	O3P-P-O5'	-2.41	100.39	106.67
2	A	1149	FMN	C5A-N5-C4A	-2.41	114.20	118.09
2	A	1149	FMN	C9A-C9-C8	2.34	123.92	119.22
2	B	2149	FMN	C9A-C5A-N5	-2.32	119.99	122.45
2	B	2149	FMN	O4-C4-N3	2.21	124.27	120.11
2	A	1149	FMN	C9-C9A-N10	2.07	124.64	121.85
2	B	2149	FMN	C10-N1-C2	-2.05	112.41	116.85
2	B	2149	FMN	O2P-P-O1P	-2.02	102.96	110.83

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1149	FMN	C1'-C2'-C3'-O3'
2	A	1149	FMN	C1'-C2'-C3'-C4'
2	A	1149	FMN	O2'-C2'-C3'-O3'
2	A	1149	FMN	O2'-C2'-C3'-C4'
2	B	2149	FMN	C5'-O5'-P-O2P
2	B	2149	FMN	C5'-O5'-P-O3P
2	B	2149	FMN	O2'-C2'-C3'-C4'
2	A	1149	FMN	C2'-C1'-N10-C10
2	B	2149	FMN	C2'-C3'-C4'-C5'

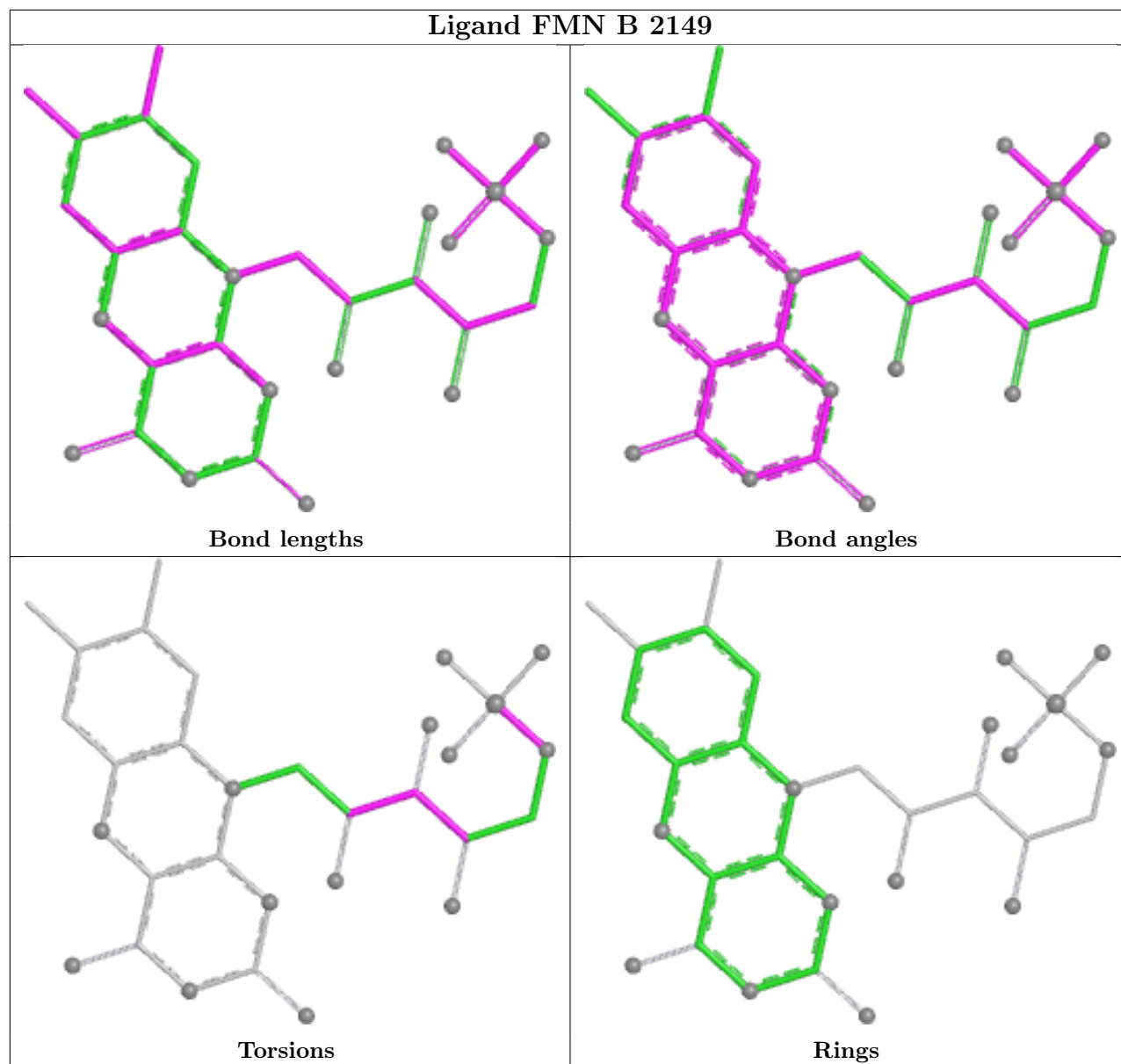
There are no ring outliers.

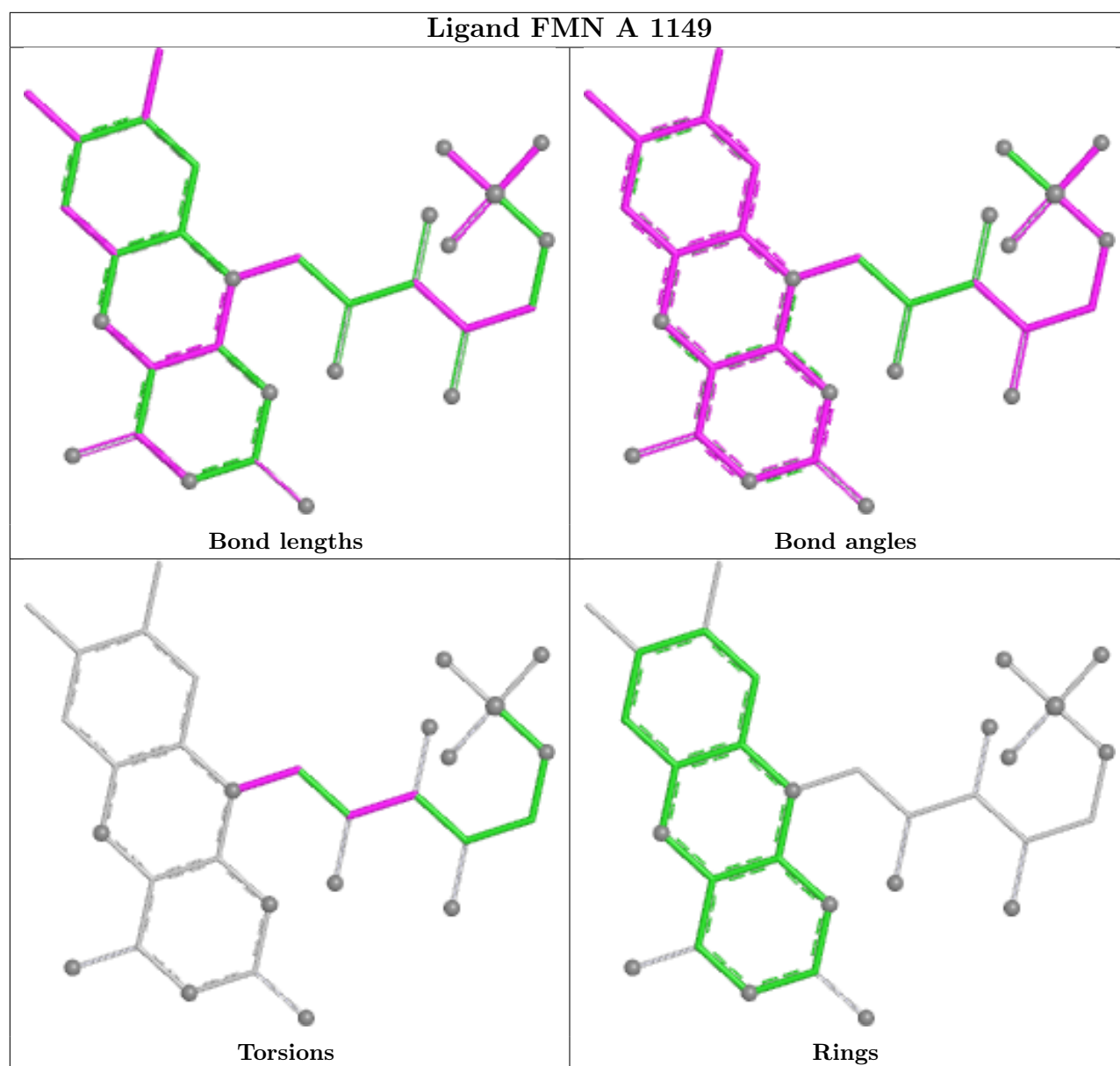
2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2149	FMN	3	0
2	A	1149	FMN	8	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.

Ligand FMN B 2149





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](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	147/147 (100%)	0.12	2 (1%) 73 74	32, 45, 71, 94	0
1	B	147/147 (100%)	0.00	0 100 100	31, 43, 71, 100	0
All	All	294/294 (100%)	0.06	2 (0%) 84 85	31, 44, 71, 100	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	92	GLY	2.3
1	A	64	SER	2.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

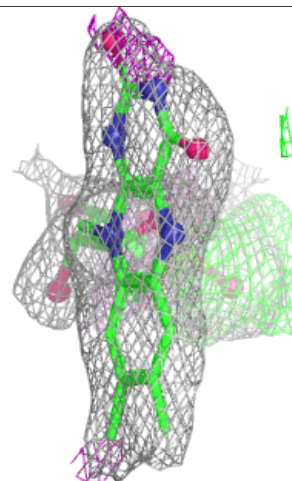
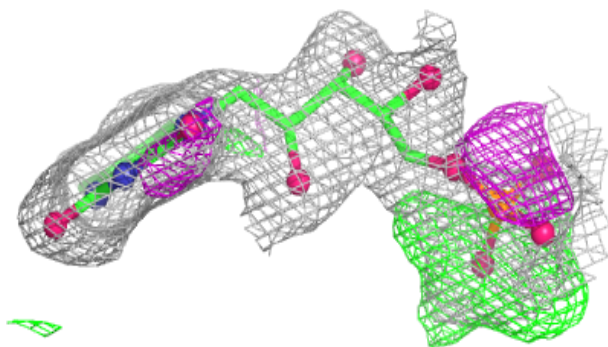
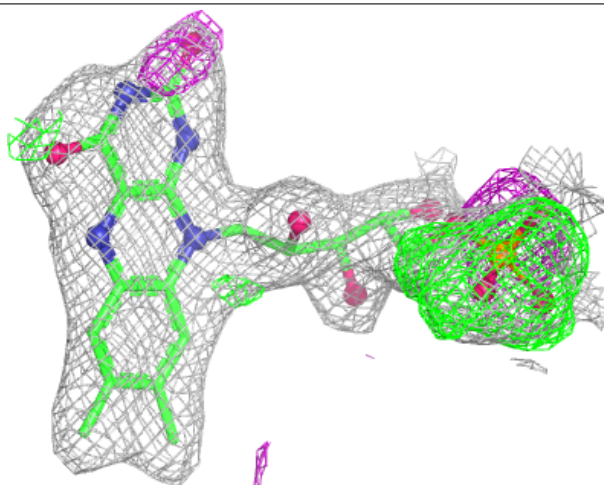
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FMN	A	1149	31/31	0.80	0.14	23,42,62,70	0
2	FMN	B	2149	31/31	0.95	0.10	24,40,53,59	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

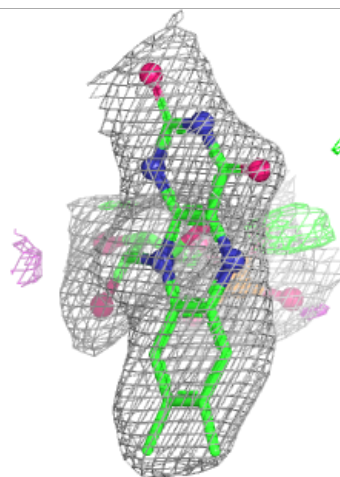
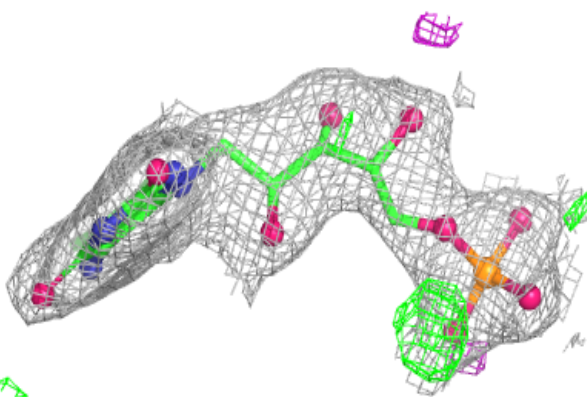
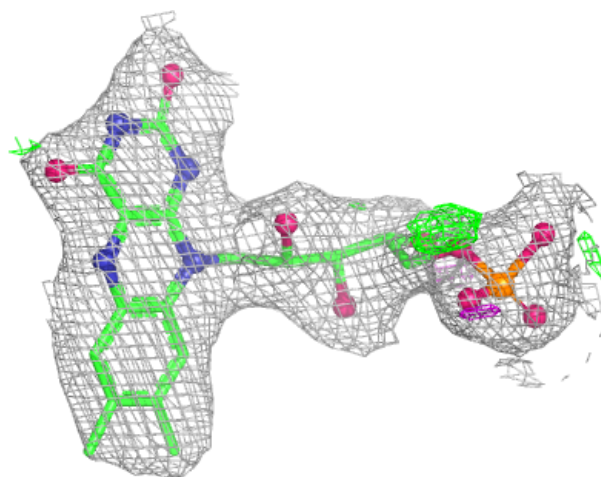
Electron density around FMN A 1149:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FMN B 2149:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.