



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 18, 2023 – 04:38 PM EDT

PDB ID : 1FX1
Title : A CRYSTALLOGRAPHIC STRUCTURAL STUDY OF THE OXIDATION STATES OF DESULFOVIBRIO VULGARIS FLAVODOXIN
Authors : Watenpaugh, K.D.; Sieker, L.C.; Jensen, L.H.
Deposited on : 1984-10-15
Resolution : 2.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.34
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.34

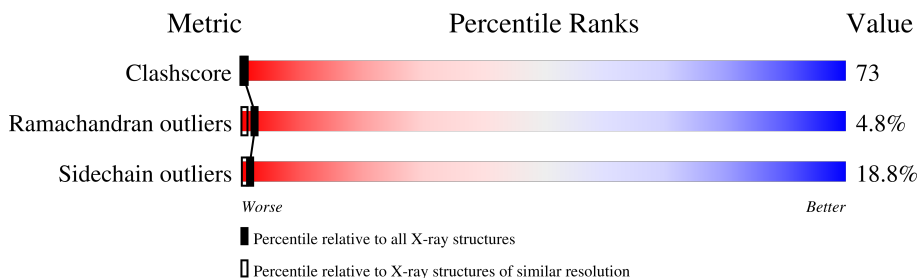
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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

Mol	Chain	Length	Quality of chain
1	A	148	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1135 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.

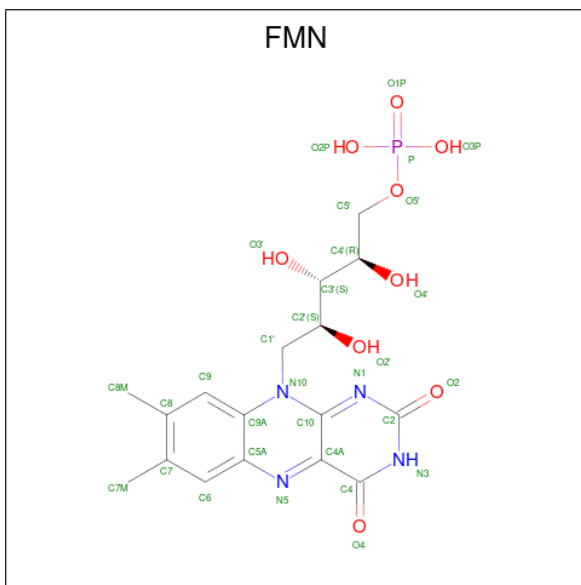
- Molecule 1 is a protein called FLAVODOXIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	147	1104	686	183	231	4	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	GLN	GLU	conflict	UNP P00323
A	28	ASN	ASP	conflict	UNP P00323

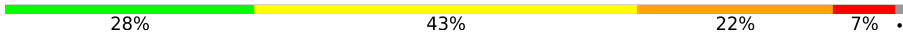
- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P).

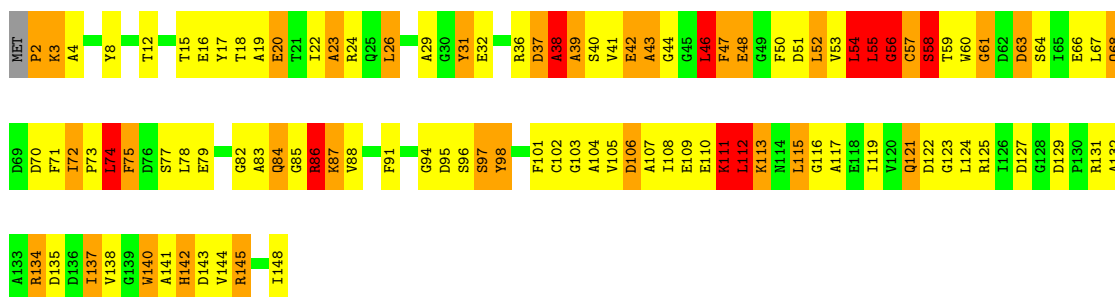


3 Residue-property plots [i](#)

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.

- Molecule 1: FLAVODOXIN

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	51.60Å 51.60Å 139.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.00 10.02 – 2.01	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-2.00) 86.0 (10.02-2.01)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtrriage
Refinement program	unknown	Depositor
R, R_{free}	(Not available) , (Not available) 0.497 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	25.8	Xtrriage
Anisotropy	0.353	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 37.8	EDS
L-test for twinning ¹	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.38$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.71	EDS
Total number of atoms	1135	wwPDB-VP
Average B, all atoms (Å ²)	0.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.63% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

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	2.58	33/1122 (2.9%)	1.79	29/1518 (1.9%)

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	4

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	3	LYS	CE-NZ	38.76	2.46	1.49
1	A	48	GLU	CA-C	26.76	2.22	1.52
1	A	38	ALA	N-CA	25.62	1.97	1.46
1	A	47	PHE	N-CA	15.96	1.78	1.46
1	A	46	LEU	CA-C	14.64	1.91	1.52
1	A	106	ASP	N-CA	-11.31	1.23	1.46
1	A	55	LEU	CA-C	-11.29	1.23	1.52
1	A	50	PHE	CA-CB	-10.31	1.31	1.53
1	A	47	PHE	CA-CB	-9.17	1.33	1.53
1	A	112	LEU	N-CA	8.45	1.63	1.46
1	A	112	LEU	CA-CB	8.13	1.72	1.53
1	A	56	GLY	C-N	8.12	1.52	1.34
1	A	56	GLY	N-CA	7.82	1.57	1.46
1	A	58	SER	N-CA	7.45	1.61	1.46
1	A	57	CYS	C-N	7.25	1.50	1.34
1	A	142	HIS	N-CA	-7.21	1.31	1.46
1	A	50	PHE	CA-C	6.92	1.71	1.52
1	A	75	PHE	N-CA	-6.30	1.33	1.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	39	ALA	N-CA	-6.25	1.33	1.46
1	A	137	ILE	N-CA	6.20	1.58	1.46
1	A	142	HIS	CB-CG	-5.98	1.39	1.50
1	A	61	GLY	N-CA	5.98	1.55	1.46
1	A	141	ALA	C-N	-5.93	1.20	1.34
1	A	142	HIS	CA-CB	-5.70	1.41	1.53
1	A	113	LYS	CA-C	-5.59	1.38	1.52
1	A	38	ALA	C-N	-5.51	1.21	1.34
1	A	57	CYS	N-CA	-5.50	1.35	1.46
1	A	37	ASP	CA-C	-5.26	1.39	1.52
1	A	83	ALA	C-N	-5.25	1.22	1.34
1	A	74	LEU	CA-C	-5.24	1.39	1.52
1	A	55	LEU	CA-CB	-5.18	1.41	1.53
1	A	140	TRP	CB-CG	5.14	1.59	1.50
1	A	12	THR	N-CA	5.00	1.56	1.46

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	48	GLU	CB-CA-C	-15.96	78.49	110.40
1	A	37	ASP	C-N-CA	-14.89	84.47	121.70
1	A	2	PRO	CA-N-CD	-14.77	90.82	111.50
1	A	3	LYS	CD-CE-NZ	-11.04	86.30	111.70
1	A	38	ALA	N-CA-CB	10.19	124.36	110.10
1	A	46	LEU	CB-CA-C	-10.07	91.07	110.20
1	A	112	LEU	CB-CA-C	-9.11	92.89	110.20
1	A	47	PHE	CB-CA-C	8.80	128.00	110.40
1	A	23	ALA	O-C-N	-8.64	108.88	122.70
1	A	24	ARG	NE-CZ-NH2	8.43	124.51	120.30
1	A	36	ARG	NE-CZ-NH2	7.94	124.27	120.30
1	A	125	ARG	NE-CZ-NH2	7.92	124.26	120.30
1	A	134	ARG	NE-CZ-NH2	7.89	124.25	120.30
1	A	56	GLY	C-N-CA	-7.86	102.06	121.70
1	A	86	ARG	NE-CZ-NH2	7.58	124.09	120.30
1	A	145	ARG	NE-CZ-NH2	7.44	124.02	120.30
1	A	57	CYS	CA-C-N	7.42	133.53	117.20
1	A	112	LEU	N-CA-CB	-7.13	96.14	110.40
1	A	38	ALA	N-CA-C	-7.00	92.09	111.00
1	A	31	TYR	CB-CG-CD1	-6.78	116.93	121.00
1	A	131	ARG	NE-CZ-NH2	6.69	123.64	120.30
1	A	48	GLU	CA-CB-CG	-6.62	98.83	113.40
1	A	107	ALA	N-CA-CB	-6.56	100.91	110.10

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	111	LYS	C-N-CA	-5.47	108.03	121.70
1	A	137	ILE	CB-CA-C	-5.45	100.69	111.60
1	A	123	GLY	O-C-N	5.38	131.32	122.70
1	A	56	GLY	O-C-N	-5.34	114.15	122.70
1	A	46	LEU	CA-CB-CG	-5.08	103.61	115.30
1	A	57	CYS	N-CA-CB	5.06	119.70	110.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	23	ALA	Mainchain
1	A	31	TYR	Mainchain
1	A	54	LEU	Mainchain
1	A	56	GLY	Mainchain

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	1104	0	1034	160	6
2	A	31	0	19	4	0
All	All	1135	0	1053	160	6

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 73.

All (160) 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:47:PHE:N	1:A:47:PHE:CA	1.78	1.45
1:A:46:LEU:CA	1:A:46:LEU:C	1.91	1.39
1:A:52:LEU:HD23	1:A:53:VAL:N	1.47	1.30
1:A:37:ASP:O	1:A:38:ALA:CB	1.78	1.29
1:A:38:ALA:N	1:A:38:ALA:CA	1.97	1.27

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:VAL:CG1	1:A:46:LEU:HD11	1.68	1.24
1:A:37:ASP:O	1:A:38:ALA:HB2	1.49	1.11
1:A:37:ASP:O	1:A:38:ALA:CA	1.99	1.10
1:A:48:GLU:CA	1:A:48:GLU:C	2.22	1.07
1:A:37:ASP:C	1:A:38:ALA:CA	2.24	1.05
1:A:52:LEU:HD21	1:A:54:LEU:CD2	1.86	1.05
1:A:52:LEU:CD2	1:A:53:VAL:N	2.24	1.00
1:A:41:VAL:HG11	1:A:46:LEU:CD1	1.92	0.99
1:A:41:VAL:HG11	1:A:46:LEU:HD11	0.99	0.99
1:A:68:GLN:HE22	1:A:70:ASP:HB2	1.25	0.99
1:A:104:ALA:O	1:A:108:ILE:HG13	1.64	0.97
1:A:52:LEU:CD2	1:A:54:LEU:CD2	2.42	0.97
1:A:52:LEU:HD21	1:A:54:LEU:HD21	1.44	0.95
1:A:52:LEU:CD2	1:A:54:LEU:HD23	1.99	0.92
1:A:110:GLU:HA	1:A:113:LYS:HE2	1.52	0.91
1:A:52:LEU:HD23	1:A:53:VAL:H	1.16	0.91
1:A:53:VAL:C	1:A:54:LEU:HD23	1.92	0.91
1:A:41:VAL:CG1	1:A:46:LEU:CD1	2.49	0.89
1:A:52:LEU:CD2	1:A:54:LEU:HD21	2.04	0.87
1:A:97:SER:O	1:A:98:TYR:O	1.92	0.86
1:A:48:GLU:C	1:A:48:GLU:CB	2.48	0.81
1:A:46:LEU:C	1:A:46:LEU:CB	2.51	0.79
1:A:48:GLU:C	1:A:48:GLU:HB3	2.03	0.79
1:A:56:GLY:CA	1:A:91:PHE:O	2.30	0.79
1:A:3:LYS:CE	1:A:3:LYS:NZ	2.46	0.78
1:A:38:ALA:N	1:A:39:ALA:N	2.31	0.78
1:A:67:LEU:CD2	1:A:75:PHE:CD1	2.66	0.78
1:A:121:GLN:NE2	1:A:144:VAL:CG2	2.47	0.77
1:A:121:GLN:HE21	1:A:144:VAL:HG22	1.50	0.77
1:A:47:PHE:N	1:A:47:PHE:CB	2.48	0.76
1:A:78:LEU:HD13	1:A:112:LEU:HD21	1.68	0.76
1:A:52:LEU:CD2	1:A:52:LEU:C	2.54	0.76
1:A:112:LEU:N	1:A:112:LEU:HD23	2.02	0.74
1:A:56:GLY:HA2	1:A:91:PHE:O	1.88	0.74
1:A:2:PRO:O	1:A:32:GLU:HB2	1.88	0.73
1:A:142:HIS:O	1:A:142:HIS:CD2	2.41	0.73
1:A:94:GLY:HA3	2:A:149:FMN:O2	1.89	0.73
1:A:71:PHE:CE1	1:A:108:ILE:HD13	2.24	0.71
1:A:53:VAL:O	1:A:54:LEU:HD23	1.89	0.71
1:A:52:LEU:HD22	1:A:54:LEU:CD2	2.20	0.71
1:A:111:LYS:HD2	1:A:111:LYS:O	1.90	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:ALA:N	1:A:39:ALA:H	1.89	0.70
1:A:57:CYS:HB2	1:A:108:ILE:CD1	2.22	0.69
1:A:110:GLU:HA	1:A:113:LYS:CE	2.22	0.69
1:A:8:TYR:O	1:A:38:ALA:HB2	1.93	0.69
1:A:38:ALA:N	1:A:38:ALA:C	2.47	0.69
1:A:134:ARG:O	1:A:138:VAL:HG23	1.94	0.68
1:A:52:LEU:HD22	1:A:54:LEU:HD23	1.74	0.67
1:A:68:GLN:HE22	1:A:70:ASP:CB	2.06	0.67
1:A:109:GLU:O	1:A:113:LYS:HG2	1.94	0.66
1:A:47:PHE:HB3	1:A:86:ARG:HD3	1.79	0.65
1:A:71:PHE:O	1:A:72:ILE:C	2.32	0.65
1:A:121:GLN:NE2	1:A:144:VAL:HG22	2.09	0.64
1:A:121:GLN:NE2	1:A:144:VAL:HG23	2.12	0.64
1:A:74:LEU:HD12	1:A:74:LEU:O	1.98	0.63
1:A:142:HIS:CD2	1:A:142:HIS:C	2.70	0.63
1:A:67:LEU:HD21	1:A:75:PHE:CD1	2.33	0.63
1:A:71:PHE:HE1	1:A:108:ILE:HD13	1.64	0.62
1:A:135:ASP:O	1:A:135:ASP:OD2	2.17	0.62
1:A:47:PHE:N	1:A:47:PHE:C	2.53	0.62
1:A:148:ILE:HG13	1:A:148:ILE:O	2.00	0.60
1:A:57:CYS:HB2	1:A:108:ILE:HD11	1.82	0.59
1:A:142:HIS:ND1	1:A:145:ARG:NH2	2.50	0.59
1:A:22:ILE:CD1	1:A:91:PHE:CE2	2.85	0.59
1:A:142:HIS:O	1:A:142:HIS:HD2	1.86	0.59
1:A:46:LEU:C	1:A:46:LEU:HB3	2.24	0.57
1:A:148:ILE:O	1:A:148:ILE:CG1	2.52	0.57
1:A:37:ASP:O	1:A:38:ALA:HB3	1.92	0.57
1:A:47:PHE:HZ	1:A:55:LEU:HD11	1.69	0.57
1:A:57:CYS:CB	1:A:108:ILE:HD11	2.35	0.57
1:A:16:GLU:O	1:A:20:GLU:HG2	2.06	0.56
1:A:26:LEU:O	1:A:29:ALA:HB3	2.06	0.56
1:A:75:PHE:HD2	1:A:78:LEU:HD12	1.70	0.56
1:A:84:GLN:OE1	1:A:116:GLY:HA3	2.05	0.56
1:A:58:SER:HG	1:A:60:TRP:HE1	1.54	0.55
1:A:71:PHE:CE1	1:A:108:ILE:CD1	2.89	0.55
1:A:112:LEU:HB3	1:A:117:ALA:HB3	1.88	0.55
1:A:111:LYS:O	1:A:115:LEU:HB2	2.07	0.55
1:A:37:ASP:C	1:A:37:ASP:OD1	2.42	0.55
1:A:53:VAL:CG1	1:A:88:VAL:HG22	2.36	0.55
1:A:88:VAL:HG11	1:A:112:LEU:HD12	1.87	0.55
1:A:101:PHE:O	1:A:102:CYS:HB2	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:VAL:HG12	1:A:88:VAL:HG22	1.90	0.54
1:A:47:PHE:CZ	1:A:55:LEU:CD1	2.90	0.54
1:A:94:GLY:CA	2:A:149:FMN:O2	2.56	0.54
1:A:79:GLU:HA	1:A:115:LEU:HD21	1.90	0.54
1:A:4:ALA:HA	1:A:52:LEU:O	2.08	0.53
1:A:52:LEU:HD11	1:A:144:VAL:HG11	1.89	0.53
1:A:43:ALA:O	1:A:46:LEU:HB2	2.09	0.53
1:A:57:CYS:HB2	1:A:108:ILE:HD12	1.90	0.53
1:A:119:ILE:HD13	1:A:119:ILE:N	2.22	0.53
1:A:52:LEU:HD11	1:A:144:VAL:CG1	2.39	0.52
1:A:68:GLN:NE2	1:A:70:ASP:H	2.08	0.52
1:A:78:LEU:HD13	1:A:112:LEU:CD2	2.37	0.51
1:A:72:ILE:HB	1:A:73:PRO:CD	2.40	0.51
1:A:19:ALA:HA	1:A:22:ILE:HD12	1.93	0.51
1:A:112:LEU:HA	1:A:115:LEU:HB2	1.93	0.50
1:A:18:THR:HA	1:A:137:ILE:CD1	2.41	0.50
1:A:52:LEU:HD21	1:A:54:LEU:HD23	1.69	0.50
1:A:61:GLY:O	1:A:63:ASP:OD2	2.30	0.50
1:A:96:SER:HB3	1:A:127:ASP:OD2	2.12	0.49
1:A:17:TYR:OH	1:A:134:ARG:HG3	2.12	0.49
1:A:68:GLN:NE2	1:A:70:ASP:HB2	2.10	0.49
1:A:78:LEU:CD1	1:A:112:LEU:HD21	2.41	0.49
1:A:95:ASP:O	1:A:97:SER:O	2.31	0.49
1:A:47:PHE:CZ	1:A:55:LEU:HD11	2.47	0.49
1:A:124:LEU:HG	1:A:140:TRP:CG	2.47	0.49
1:A:59:THR:HG22	2:A:149:FMN:C4	2.43	0.48
1:A:121:GLN:HE21	1:A:144:VAL:CG2	2.13	0.48
1:A:67:LEU:HD21	1:A:75:PHE:CE1	2.48	0.48
1:A:129:ASP:O	1:A:132:ALA:HB3	2.12	0.48
1:A:67:LEU:HD22	1:A:75:PHE:CD1	2.46	0.48
1:A:72:ILE:HB	1:A:73:PRO:HD2	1.96	0.48
1:A:68:GLN:O	1:A:71:PHE:N	2.39	0.47
1:A:75:PHE:CD2	1:A:78:LEU:HD12	2.48	0.47
1:A:54:LEU:HD23	1:A:54:LEU:N	2.26	0.47
1:A:8:TYR:O	1:A:37:ASP:O	2.32	0.47
1:A:18:THR:O	1:A:22:ILE:HG13	2.16	0.46
1:A:56:GLY:HA3	1:A:91:PHE:O	2.15	0.46
1:A:82:GLY:O	1:A:86:ARG:HD2	2.16	0.46
1:A:42:GLU:O	1:A:43:ALA:C	2.53	0.46
1:A:121:GLN:HE22	1:A:144:VAL:HG23	1.79	0.46
1:A:103:GLY:O	1:A:106:ASP:HB2	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:LYS:NZ	1:A:3:LYS:HD3	2.32	0.45
1:A:77:SER:C	1:A:79:GLU:H	2.20	0.45
1:A:18:THR:HA	1:A:137:ILE:HD11	1.97	0.45
1:A:41:VAL:HG13	1:A:46:LEU:HD21	1.98	0.45
1:A:72:ILE:CB	1:A:73:PRO:CD	2.95	0.44
1:A:55:LEU:CD2	1:A:71:PHE:HZ	2.30	0.44
1:A:22:ILE:HD13	1:A:91:PHE:CE2	2.53	0.44
1:A:91:PHE:CD1	1:A:91:PHE:C	2.91	0.44
1:A:47:PHE:N	1:A:48:GLU:N	2.65	0.44
1:A:72:ILE:HG22	1:A:73:PRO:HD3	1.99	0.44
1:A:22:ILE:HG13	1:A:137:ILE:HG21	2.00	0.43
1:A:22:ILE:HD12	1:A:91:PHE:CE2	2.52	0.43
1:A:140:TRP:O	1:A:143:ASP:N	2.51	0.43
1:A:72:ILE:O	1:A:75:PHE:HB3	2.17	0.43
1:A:77:SER:C	1:A:79:GLU:N	2.71	0.43
1:A:140:TRP:O	1:A:143:ASP:HB2	2.19	0.43
1:A:142:HIS:CE1	1:A:145:ARG:HH12	2.36	0.43
1:A:3:LYS:NZ	1:A:3:LYS:CD	2.82	0.42
1:A:15:THR:HB	2:A:149:FMN:O2P	2.19	0.42
1:A:87:LYS:HZ1	1:A:148:ILE:HA	1.83	0.42
1:A:137:ILE:HG21	1:A:137:ILE:HD13	1.73	0.42
1:A:121:GLN:HE22	1:A:144:VAL:N	2.18	0.42
1:A:124:LEU:HD11	1:A:137:ILE:HA	2.02	0.42
1:A:84:GLN:HG3	1:A:85:GLY:N	2.34	0.42
1:A:46:LEU:C	1:A:47:PHE:CA	2.72	0.41
1:A:71:PHE:O	1:A:72:ILE:O	2.37	0.41
1:A:96:SER:CB	1:A:127:ASP:OD2	2.69	0.41
1:A:22:ILE:CD1	1:A:91:PHE:CD2	3.04	0.41
1:A:91:PHE:HB2	1:A:124:LEU:HB2	2.03	0.41
1:A:103:GLY:C	1:A:105:VAL:N	2.72	0.41
1:A:2:PRO:HB3	1:A:51:ASP:OD1	2.20	0.40
1:A:112:LEU:HB3	1:A:117:ALA:CB	2.51	0.40

All (6) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:ASP:OD1	1:A:111:LYS:CE[6_455]	1.56	0.64
1:A:95:ASP:CG	1:A:111:LYS:CE[6_455]	1.87	0.33
1:A:95:ASP:OD2	1:A:111:LYS:CE[6_455]	1.90	0.30

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:ASP:OD1	1:A:111:LYS:NZ[6_455]	1.95	0.25
1:A:48:GLU:OE1	1:A:48:GLU:OE1[7_555]	1.97	0.23
1:A:95:ASP:OD1	1:A:111:LYS:CD[6_455]	2.09	0.11

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	145/148 (98%)	125 (86%)	13 (9%)	7 (5%)	2 0

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	44	GLY
1	A	74	LEU
1	A	98	TYR
1	A	38	ALA
1	A	43	ALA
1	A	72	ILE
1	A	97	SER

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	112/113 (99%)	91 (81%)	21 (19%)	1 0

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	GLU
1	A	26	LEU
1	A	40	SER
1	A	42	GLU
1	A	46	LEU
1	A	52	LEU
1	A	54	LEU
1	A	55	LEU
1	A	58	SER
1	A	63	ASP
1	A	64	SER
1	A	66	GLU
1	A	68	GLN
1	A	84	GLN
1	A	86	ARG
1	A	87	LYS
1	A	111	LYS
1	A	112	LEU
1	A	115	LEU
1	A	121	GLN
1	A	122	ASP

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	68	GLN
1	A	121	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 monosaccharides in this entry.

5.6 Ligand geometry

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	3.40	12 (36%)	48,50,50	1.27	8 (16%)

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	-	-	8/18/18/18	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	O4-C4	8.87	1.40	1.23
2	A	149	FMN	O2-C2	8.63	1.40	1.24
2	A	149	FMN	P-O1P	6.09	1.70	1.50
2	A	149	FMN	C5'-C4'	-5.93	1.43	1.51
2	A	149	FMN	C8M-C8	-5.24	1.40	1.51
2	A	149	FMN	C7M-C7	-5.16	1.40	1.51
2	A	149	FMN	C4A-N5	4.97	1.40	1.30
2	A	149	FMN	P-O3P	4.14	1.70	1.54
2	A	149	FMN	P-O2P	3.93	1.70	1.54
2	A	149	FMN	C10-N1	3.50	1.40	1.33
2	A	149	FMN	C1'-N10	-3.26	1.39	1.48
2	A	149	FMN	P-O5'	3.22	1.70	1.60

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	149	FMN	P-O5'-C5'	-3.11	109.74	118.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	149	FMN	C4-N3-C2	-2.93	120.23	125.64
2	A	149	FMN	C4A-C4-N3	2.67	119.96	113.19
2	A	149	FMN	O4-C4-C4A	-2.55	119.82	126.60
2	A	149	FMN	C5A-C9A-N10	2.36	120.39	117.95
2	A	149	FMN	C4A-C10-N10	2.32	119.87	116.48
2	A	149	FMN	C9A-C5A-N5	-2.28	119.95	122.43
2	A	149	FMN	C10-C4A-N5	-2.08	120.45	124.86

There are no chirality outliers.

All (8) torsion outliers are listed below:

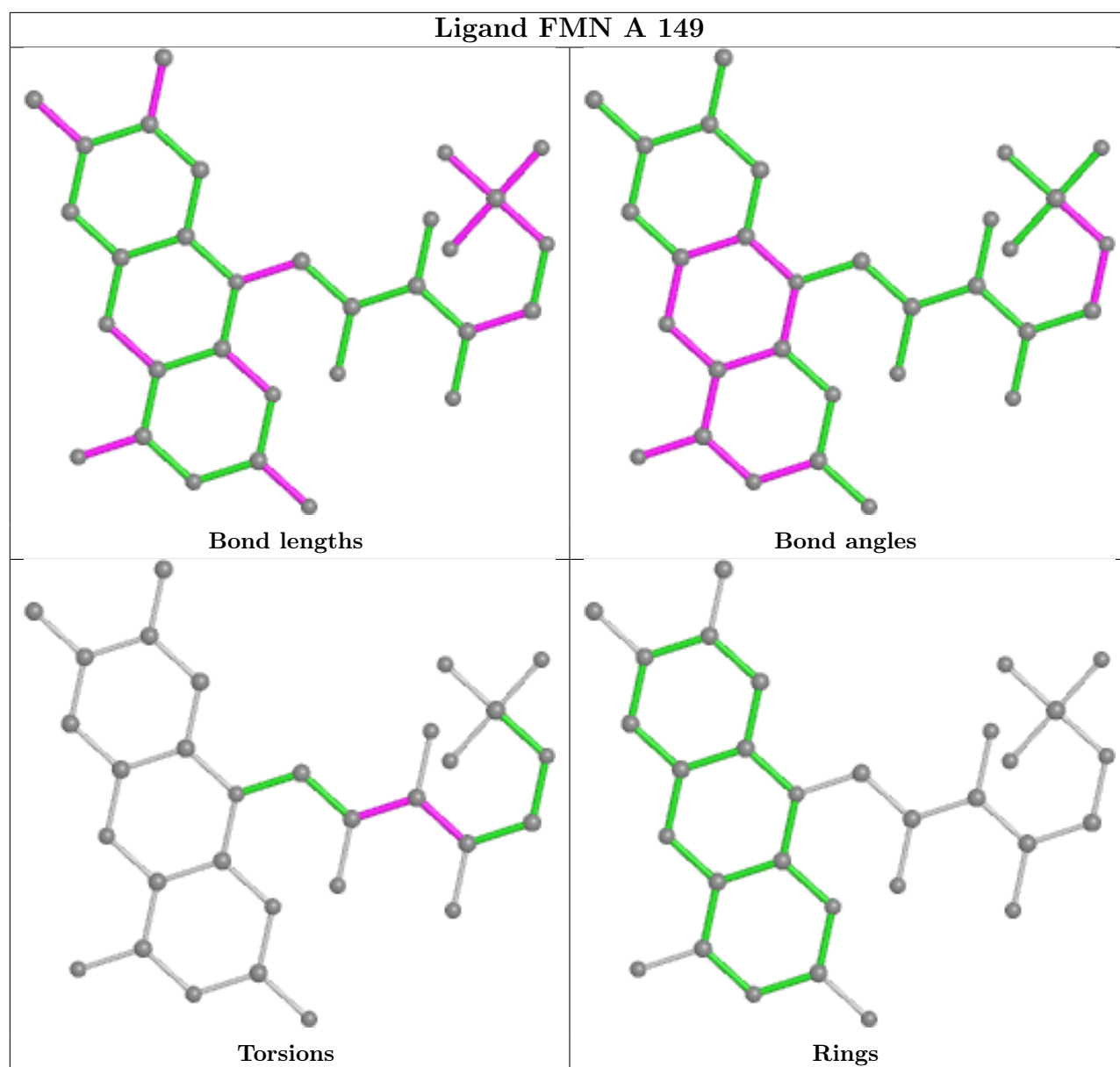
Mol	Chain	Res	Type	Atoms
2	A	149	FMN	C1'-C2'-C3'-O3'
2	A	149	FMN	C1'-C2'-C3'-C4'
2	A	149	FMN	O3'-C3'-C4'-C5'
2	A	149	FMN	O2'-C2'-C3'-O3'
2	A	149	FMN	O2'-C2'-C3'-C4'
2	A	149	FMN	C2'-C3'-C4'-C5'
2	A	149	FMN	C2'-C3'-C4'-O4'
2	A	149	FMN	O3'-C3'-C4'-O4'

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	149	FMN	4	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 [\(i\)](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	141:ALA	C	142:HIS	N	1.20

6 Fit of model and data

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

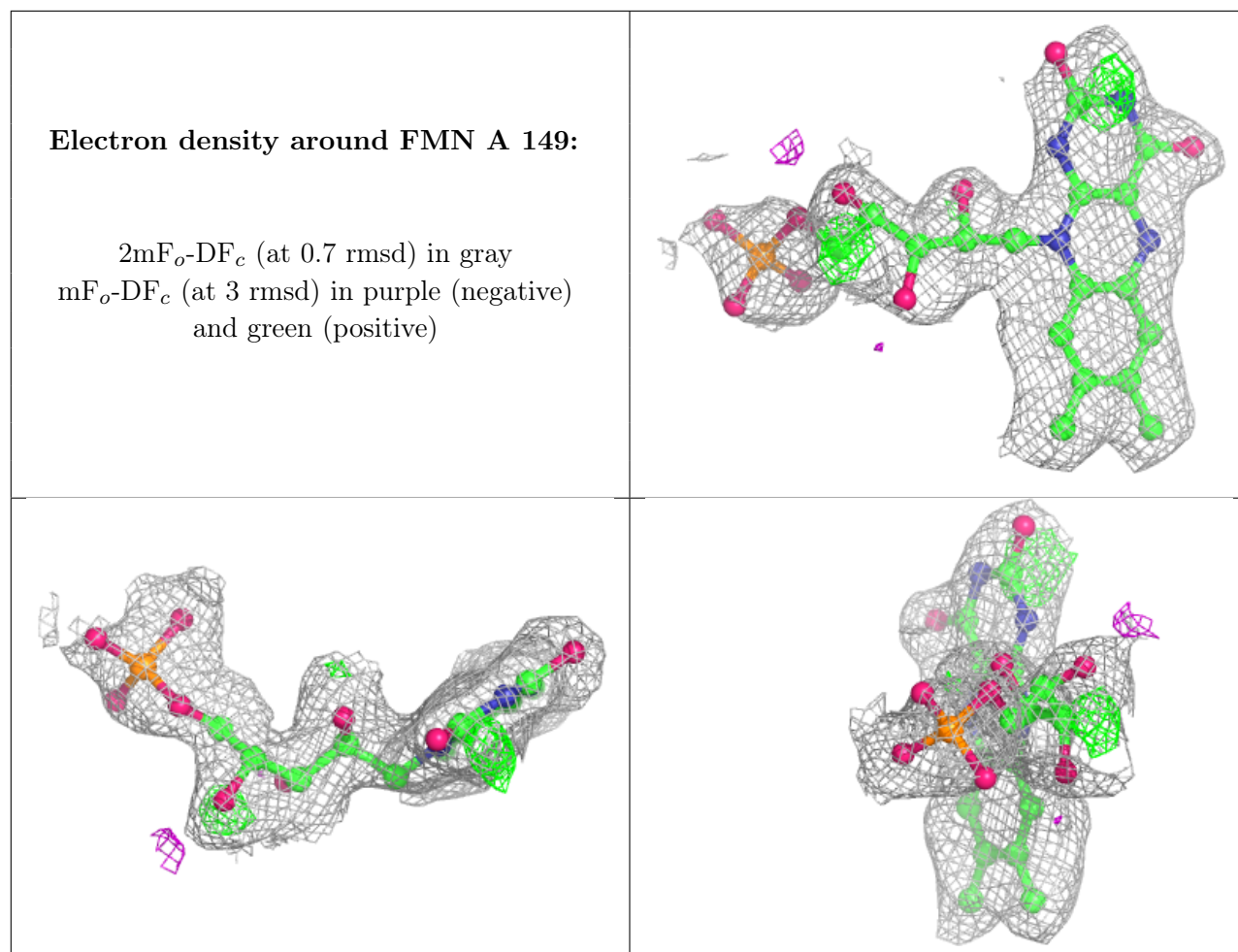
6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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.



6.5 Other polymers [i](#)

Unable to reproduce the depositor's R factor - this section is therefore empty.