



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:46 AM UTC

PDB ID : 2Z98 / pdb_00002z98
Title : The crystal structure of AzoR (azoreductase) from Escherichia coli: Oxidized AzoR in tetragonal crystals (The resolution has improved from 1.8 (1v4b) to 1.4 angstrom)
Authors : Ito, K.
Deposited on : 2007-09-18
Resolution : 1.40 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

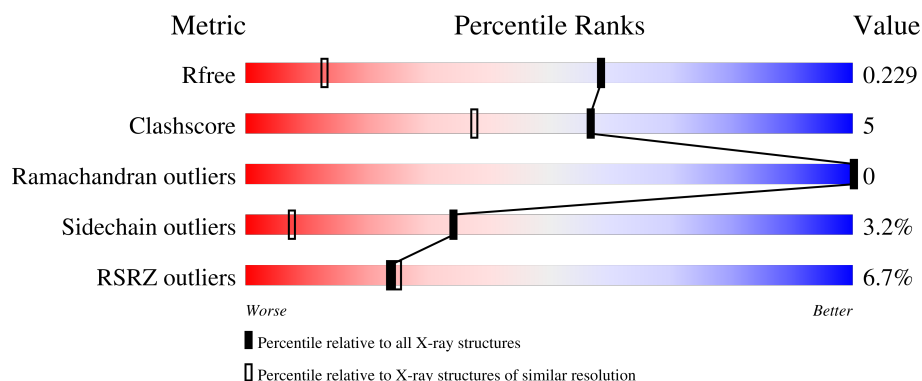
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 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	2563 (1.40-1.40)
Clashscore	190562	2660 (1.40-1.40)
Ramachandran outliers	187476	2611 (1.40-1.40)
Sidechain outliers	187428	2610 (1.40-1.40)
RSRZ outliers	180081	2561 (1.40-1.40)

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	200	6% 38% 52% 6%

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	201	-	X	-	-

2 Entry composition [i](#)

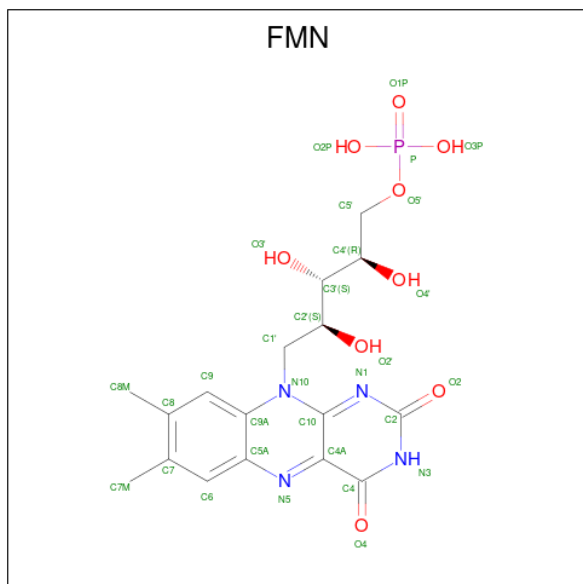
There are 4 unique types of molecules in this entry. The entry contains 1632 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FMN-dependent NADH-azoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	194	Total	C	N	O	S	2	0	0
			1476	945	243	286	2			

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



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

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

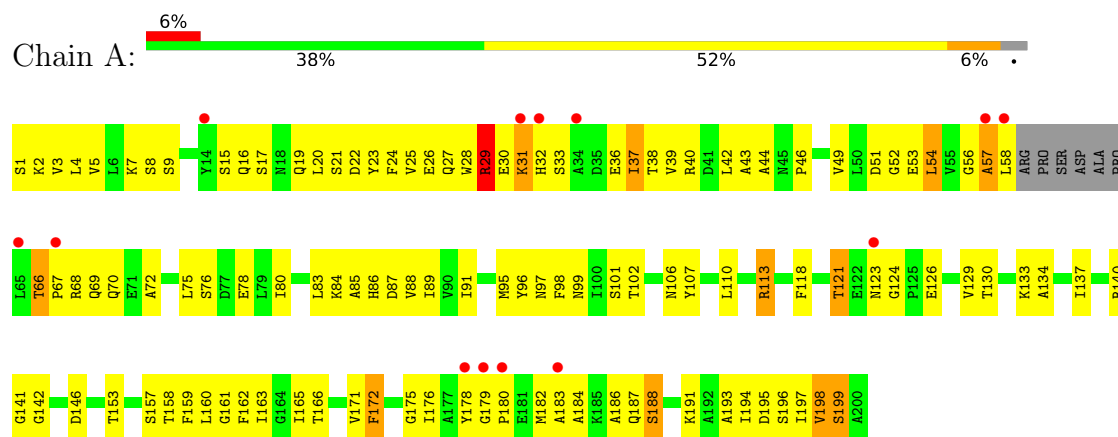
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	117	Total	O	0	0
			117	117		

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 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: FMN-dependent NADH-azoreductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 ₂ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	92.20Å 92.20Å 51.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.30 – 1.40 34.30 – 1.40	Depositor EDS
% Data completeness (in resolution range)	96.0 (34.30-1.40) 95.9 (34.30-1.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.52 (at 1.40Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.184 , 0.220 0.194 , 0.229	Depositor DCC
R_{free} test set	2155 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	13.1	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 36.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	1632	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.90% 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, EDO

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	2.80	113/1502 (7.5%)	2.39	98/2038 (4.8%)

All (113) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	15	SER	C-O	10.49	1.36	1.23
1	A	165	ILE	CA-C	-10.32	1.44	1.52
1	A	184	ALA	C-O	9.89	1.35	1.24
1	A	67	PRO	CA-CB	-9.76	1.40	1.53
1	A	184	ALA	CA-C	-9.25	1.41	1.52
1	A	102	THR	N-CA	-9.22	1.34	1.46
1	A	26	GLU	C-O	9.16	1.34	1.24
1	A	178	TYR	C-N	-8.74	1.20	1.33
1	A	15	SER	C-N	-8.72	1.22	1.33
1	A	197	ILE	CA-CB	8.68	1.65	1.54
1	A	19	GLN	C-O	8.56	1.34	1.24
1	A	57	ALA	N-CA	8.32	1.56	1.46
1	A	130	THR	CA-C	8.22	1.62	1.52
1	A	141	GLY	CA-C	-8.17	1.43	1.52
1	A	199	SER	N-CA	8.04	1.55	1.46
1	A	56	GLY	N-CA	7.91	1.56	1.45
1	A	178	TYR	CA-CB	-7.74	1.41	1.53
1	A	57	ALA	CA-CB	-7.73	1.40	1.53
1	A	171	VAL	CA-CB	-7.65	1.44	1.54
1	A	24	PHE	C-O	7.62	1.32	1.24
1	A	130	THR	CA-CB	7.62	1.66	1.53
1	A	83	LEU	CB-CG	-7.46	1.38	1.53
1	A	53	GLU	N-CA	7.30	1.55	1.46
1	A	188	SER	C-O	7.30	1.32	1.24
1	A	121	THR	CA-CB	7.22	1.66	1.54
1	A	183	ALA	CA-CB	-7.20	1.42	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	106	ASN	N-CA	-7.12	1.37	1.46
1	A	38	THR	CA-CB	-7.04	1.43	1.53
1	A	29	ARG	CA-CB	-7.00	1.41	1.53
1	A	31	LYS	C-O	7.00	1.32	1.23
1	A	195	ASP	C-O	6.99	1.32	1.24
1	A	95	MET	N-CA	6.97	1.54	1.46
1	A	182	MET	CG-SD	-6.92	1.63	1.80
1	A	191	LYS	C-N	-6.84	1.25	1.33
1	A	158	THR	C-O	6.80	1.31	1.24
1	A	43	ALA	CA-CB	-6.76	1.42	1.53
1	A	23	TYR	C-O	6.73	1.32	1.24
1	A	39	VAL	CA-C	-6.72	1.44	1.52
1	A	9	SER	C-N	6.58	1.40	1.33
1	A	182	MET	C-N	-6.58	1.25	1.33
1	A	187	GLN	C-O	6.56	1.32	1.24
1	A	96	TYR	N-CA	6.54	1.54	1.46
1	A	175	GLY	C-O	6.45	1.32	1.23
1	A	23	TYR	CA-C	-6.45	1.44	1.52
1	A	27	GLN	C-O	6.39	1.31	1.24
1	A	84	LYS	CA-C	6.35	1.61	1.52
1	A	5	VAL	C-O	-6.33	1.17	1.24
1	A	98	PHE	N-CA	-6.25	1.37	1.46
1	A	26	GLU	C-N	-6.25	1.25	1.33
1	A	172	PHE	C-O	6.21	1.31	1.24
1	A	193	ALA	N-CA	-6.18	1.39	1.46
1	A	178	TYR	CA-C	6.17	1.63	1.52
1	A	1	SER	CA-CB	-6.16	1.41	1.53
1	A	22	ASP	C-O	6.06	1.31	1.24
1	A	31	LYS	N-CA	-6.06	1.38	1.45
1	A	87	ASP	CA-CB	6.05	1.63	1.53
1	A	188	SER	C-N	-6.02	1.25	1.33
1	A	26	GLU	N-CA	5.85	1.53	1.46
1	A	146	ASP	CA-C	-5.82	1.43	1.52
1	A	162	PHE	CG-CD1	-5.80	1.26	1.38
1	A	22	ASP	CA-C	-5.73	1.45	1.52
1	A	31	LYS	CD-CE	5.72	1.69	1.52
1	A	198	VAL	CA-C	5.69	1.60	1.52
1	A	101	SER	N-CA	-5.68	1.38	1.46
1	A	17	SER	C-O	5.68	1.30	1.24
1	A	180	PRO	C-N	-5.65	1.26	1.33
1	A	7	LYS	C-O	-5.62	1.17	1.23
1	A	198	VAL	C-N	-5.62	1.26	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	97	ASN	C-O	5.61	1.30	1.23
1	A	44	ALA	CA-C	-5.61	1.45	1.52
1	A	54	LEU	N-CA	5.61	1.53	1.46
1	A	33	SER	C-O	5.59	1.31	1.24
1	A	76	SER	CB-OG	-5.59	1.30	1.42
1	A	72	ALA	CA-C	-5.55	1.45	1.52
1	A	191	LYS	CE-NZ	5.55	1.66	1.49
1	A	133	LYS	CA-C	5.54	1.59	1.52
1	A	70	GLN	C-O	5.53	1.30	1.24
1	A	8	SER	CA-C	-5.53	1.45	1.52
1	A	1	SER	N-CA	5.50	1.56	1.46
1	A	171	VAL	C-O	-5.48	1.18	1.24
1	A	126	GLU	C-N	5.47	1.40	1.33
1	A	78	GLU	CA-C	-5.44	1.46	1.52
1	A	88	VAL	C-O	-5.43	1.18	1.24
1	A	30	GLU	CA-C	-5.39	1.45	1.52
1	A	25	VAL	C-N	-5.38	1.27	1.33
1	A	160	LEU	C-O	5.38	1.30	1.24
1	A	110	LEU	N-CA	5.35	1.53	1.46
1	A	53	GLU	CA-CB	-5.35	1.44	1.53
1	A	194	ILE	C-O	5.35	1.30	1.24
1	A	85	ALA	CA-CB	-5.34	1.44	1.53
1	A	46	PRO	CA-C	-5.34	1.45	1.52
1	A	68	ARG	C-O	5.33	1.30	1.24
1	A	3	VAL	C-N	5.28	1.40	1.33
1	A	166	THR	N-CA	-5.27	1.39	1.46
1	A	66	THR	CA-CB	5.26	1.61	1.53
1	A	157	SER	CA-CB	-5.24	1.45	1.53
1	A	197	ILE	C-O	5.23	1.30	1.24
1	A	26	GLU	CA-C	-5.22	1.46	1.52
1	A	83	LEU	CA-CB	5.21	1.61	1.53
1	A	141	GLY	C-O	5.20	1.30	1.23
1	A	98	PHE	CA-CB	5.17	1.61	1.53
1	A	39	VAL	N-CA	5.14	1.52	1.46
1	A	159	PHE	CA-C	5.11	1.59	1.52
1	A	137	ILE	CA-C	5.10	1.59	1.52
1	A	199	SER	CA-CB	-5.10	1.46	1.53
1	A	28	TRP	C-O	5.09	1.30	1.24
1	A	3	VAL	C-O	-5.07	1.18	1.24
1	A	124	GLY	N-CA	5.05	1.51	1.44
1	A	25	VAL	C-O	5.04	1.29	1.24
1	A	153	THR	C-O	5.04	1.29	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	183	ALA	N-CA	-5.04	1.40	1.46
1	A	36	GLU	C-N	-5.02	1.27	1.33
1	A	193	ALA	C-O	5.02	1.29	1.24

All (98) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	23	TYR	O-C-N	-10.71	109.94	122.15
1	A	184	ALA	O-C-N	-10.46	111.30	122.07
1	A	32	HIS	CA-C-O	-9.95	112.41	121.67
1	A	33	SER	O-C-N	9.70	133.57	122.22
1	A	33	SER	N-CA-C	9.38	122.50	111.71
1	A	30	GLU	N-CA-C	-9.02	102.04	113.23
1	A	26	GLU	CA-C-N	8.61	132.14	120.44
1	A	26	GLU	C-N-CA	8.61	132.14	120.44
1	A	178	TYR	O-C-N	8.58	133.35	122.37
1	A	3	VAL	CA-C-O	8.38	129.19	120.39
1	A	184	ALA	CA-C-N	8.23	131.64	120.54
1	A	184	ALA	C-N-CA	8.23	131.64	120.54
1	A	19	GLN	N-CA-C	-8.22	102.40	111.36
1	A	23	TYR	CA-C-N	7.75	130.51	120.44
1	A	23	TYR	C-N-CA	7.75	130.51	120.44
1	A	87	ASP	N-CA-C	7.66	123.10	112.45
1	A	99	ASN	OD1-CG-ND2	-7.59	115.01	122.60
1	A	19	GLN	CA-C-O	-7.52	112.45	120.42
1	A	137	ILE	O-C-N	7.30	132.44	122.88
1	A	160	LEU	N-CA-C	-7.21	103.35	111.07
1	A	130	THR	CA-CB-CG2	-7.21	98.24	110.50
1	A	188	SER	O-C-N	-7.20	112.87	122.23
1	A	188	SER	N-CA-C	-7.08	102.98	111.69
1	A	140	ARG	CA-C-N	7.04	127.62	119.94
1	A	140	ARG	C-N-CA	7.04	127.62	119.94
1	A	9	SER	CA-C-O	7.04	129.24	121.56
1	A	32	HIS	CA-C-N	6.99	130.35	120.28
1	A	32	HIS	C-N-CA	6.99	130.35	120.28
1	A	193	ALA	CA-C-N	6.92	129.28	120.56
1	A	193	ALA	C-N-CA	6.92	129.28	120.56
1	A	118	PHE	O-C-N	6.91	130.82	123.42
1	A	137	ILE	CA-C-O	-6.88	112.61	120.66
1	A	4	LEU	O-C-N	6.88	131.05	123.27
1	A	163	ILE	N-CA-C	-6.87	104.90	112.80
1	A	15	SER	CA-C-N	6.83	129.99	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	15	SER	C-N-CA	6.83	129.99	120.29
1	A	86	HIS	O-C-N	-6.77	115.31	123.10
1	A	180	PRO	O-C-N	-6.70	113.59	122.64
1	A	175	GLY	CA-C-N	6.64	129.56	120.46
1	A	175	GLY	C-N-CA	6.64	129.56	120.46
1	A	184	ALA	CA-C-O	-6.62	113.87	120.82
1	A	186	ALA	CA-C-O	-6.50	114.00	120.70
1	A	36	GLU	O-C-N	6.48	130.59	123.27
1	A	84	LYS	CA-C-O	-6.39	111.76	119.49
1	A	3	VAL	O-C-N	-6.38	116.37	123.26
1	A	22	ASP	CA-C-N	6.33	129.28	120.29
1	A	22	ASP	C-N-CA	6.33	129.28	120.29
1	A	196	SER	O-C-N	-6.26	115.48	122.12
1	A	26	GLU	O-C-N	-6.26	115.62	122.07
1	A	186	ALA	N-CA-C	-6.25	104.39	111.14
1	A	67	PRO	CB-CA-C	6.15	121.70	111.56
1	A	165	ILE	O-C-N	-6.14	116.80	121.96
1	A	40	ARG	NE-CZ-NH2	-6.14	113.67	119.20
1	A	30	GLU	O-C-N	-6.13	114.06	122.46
1	A	91	ILE	O-C-N	6.10	129.51	122.99
1	A	67	PRO	N-CA-CB	5.96	109.51	103.25
1	A	19	GLN	O-C-N	-5.96	115.36	122.15
1	A	157	SER	CA-C-O	5.78	127.08	120.90
1	A	176	ILE	CA-CB-CG2	5.78	120.33	110.50
1	A	161	GLY	O-C-N	-5.74	116.68	122.19
1	A	20	LEU	CA-C-N	5.68	128.17	120.44
1	A	20	LEU	C-N-CA	5.68	128.17	120.44
1	A	188	SER	CA-C-N	5.67	128.33	120.29
1	A	188	SER	C-N-CA	5.67	128.33	120.29
1	A	49	VAL	O-C-N	-5.59	116.52	122.61
1	A	85	ALA	O-C-N	-5.59	115.40	122.27
1	A	195	ASP	CA-C-O	-5.57	114.65	120.55
1	A	102	THR	CA-CB-OG1	-5.55	101.27	109.60
1	A	107	TYR	O-C-N	-5.53	116.28	122.03
1	A	26	GLU	N-CA-C	-5.51	105.17	111.07
1	A	78	GLU	O-C-N	-5.50	116.19	122.08
1	A	20	LEU	O-C-N	-5.48	115.53	122.27
1	A	51	ASP	CA-CB-CG	5.46	118.06	112.60
1	A	28	TRP	CA-C-O	-5.46	114.63	120.42
1	A	129	VAL	CA-C-O	5.43	128.21	121.64
1	A	17	SER	O-C-N	-5.40	115.21	122.23
1	A	183	ALA	N-CA-CB	5.39	118.05	110.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	140	ARG	O-C-N	-5.38	117.03	123.27
1	A	75	LEU	N-CA-C	-5.34	105.53	111.36
1	A	165	ILE	CA-C-N	5.33	131.04	121.66
1	A	165	ILE	C-N-CA	5.33	131.04	121.66
1	A	15	SER	CA-C-O	-5.31	114.70	120.81
1	A	130	THR	CB-CA-C	-5.26	100.24	109.71
1	A	31	LYS	CA-C-O	5.23	124.57	118.97
1	A	52	GLY	O-C-N	5.23	127.21	122.19
1	A	193	ALA	O-C-N	-5.22	116.69	122.07
1	A	37	ILE	CA-C-O	5.19	125.84	120.39
1	A	76	SER	CA-C-O	5.19	126.78	121.07
1	A	19	GLN	CA-C-N	5.19	128.19	120.31
1	A	19	GLN	C-N-CA	5.19	128.19	120.31
1	A	179	GLY	O-C-N	5.18	126.95	121.77
1	A	15	SER	N-CA-C	5.16	117.70	109.96
1	A	157	SER	O-C-N	-5.16	116.72	122.09
1	A	42	LEU	CA-C-O	-5.12	112.55	119.11
1	A	16	GLN	O-C-N	-5.11	116.33	122.15
1	A	142	GLY	O-C-N	-5.08	117.44	122.82
1	A	21	SER	N-CA-C	-5.03	105.71	111.14
1	A	123	ASN	CB-CA-C	5.02	119.31	110.37

There are no chirality outliers.

There are no planarity outliers.

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	1476	0	1490	14	0
2	A	31	0	19	0	0
3	A	8	0	11	3	0
4	A	117	0	0	1	0
All	All	1632	0	1520	14	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 5.

All (14) 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:29:ARG:NH1	4:A:293:HOH:O	1.83	1.08
1:A:172:PHE:H	3:A:203:EDO:H11	1.23	1.02
1:A:172:PHE:H	3:A:203:EDO:C1	2.05	0.66
1:A:31:LYS:HD3	1:A:198:VAL:HG12	1.78	0.65
1:A:172:PHE:N	3:A:203:EDO:H11	2.06	0.63
1:A:80:ILE:HD11	1:A:113:ARG:HG3	1.89	0.53
1:A:57:ALA:HB2	1:A:69:GLN:HB3	1.91	0.52
1:A:29:ARG:HG2	1:A:37:ILE:HD12	1.95	0.49
1:A:31:LYS:HD3	1:A:198:VAL:CG1	2.46	0.46
1:A:31:LYS:HE3	1:A:199:SER:HB3	1.98	0.45
1:A:89:ILE:O	1:A:134:ALA:HA	2.17	0.45
1:A:57:ALA:HB2	1:A:69:GLN:CB	2.46	0.45
1:A:54:LEU:O	1:A:58:LEU:HG	2.19	0.42
1:A:66:THR:OG1	1:A:69:GLN:HG3	2.19	0.41

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	190/200 (95%)	185 (97%)	5 (3%)	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	157/162 (97%)	152 (97%)	5 (3%)	34 7

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	29	ARG
1	A	113	ARG
1	A	121	THR
1	A	188	SER

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	123	ASN

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](#)

3 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	$\# Z > 2$
3	EDO	A	203	-	3,3,3	1.44	0	2,2,2	1.61	0
3	EDO	A	202	-	3,3,3	1.16	0	2,2,2	0.19	0
2	FMN	A	201	-	33,33,33	3.00	22 (66%)	48,50,50	3.35	28 (58%)

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
3	EDO	A	203	-	-	1/1/1/1	-
3	EDO	A	202	-	-	1/1/1/1	-
2	FMN	A	201	-	-	0/18/18/18	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	201	FMN	C9A-C5A	6.91	1.52	1.41
2	A	201	FMN	O4-C4	5.39	1.33	1.23
2	A	201	FMN	C4A-C10	4.61	1.57	1.44
2	A	201	FMN	C9-C8	-4.52	1.33	1.39
2	A	201	FMN	C8M-C8	-3.83	1.43	1.51
2	A	201	FMN	C2-N1	-3.78	1.28	1.36
2	A	201	FMN	C8-C7	3.61	1.49	1.40
2	A	201	FMN	C9A-N10	-3.56	1.35	1.41
2	A	201	FMN	C5A-N5	-3.47	1.33	1.39
2	A	201	FMN	C5'-C4'	-3.46	1.47	1.51
2	A	201	FMN	C1'-C2'	3.31	1.57	1.52
2	A	201	FMN	O2-C2	-3.19	1.18	1.24
2	A	201	FMN	C9-C9A	-3.15	1.34	1.39
2	A	201	FMN	O4'-C4'	3.08	1.49	1.43
2	A	201	FMN	C2-N3	3.06	1.45	1.39
2	A	201	FMN	C4-N3	-2.91	1.33	1.38
2	A	201	FMN	P-O5'	-2.76	1.51	1.60
2	A	201	FMN	C1'-N10	2.69	1.54	1.47
2	A	201	FMN	P-O1P	2.64	1.58	1.50
2	A	201	FMN	C6-C5A	-2.15	1.36	1.40
2	A	201	FMN	O5'-C5'	2.08	1.52	1.44
2	A	201	FMN	C4A-C4	-2.06	1.37	1.44

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	201	FMN	C4-C4A-N5	7.35	128.36	118.21
2	A	201	FMN	C9A-N10-C10	6.60	130.81	120.75
2	A	201	FMN	C4'-C3'-C2'	-5.53	104.37	113.57
2	A	201	FMN	C6-C5A-N5	5.47	127.52	118.44
2	A	201	FMN	C9-C9A-N10	5.29	128.96	121.85
2	A	201	FMN	C5A-C9A-N10	-5.07	113.39	117.97
2	A	201	FMN	C5A-N5-C4A	5.04	126.23	118.09
2	A	201	FMN	C4A-C4-N3	5.00	125.97	113.25
2	A	201	FMN	C10-N1-C2	4.69	127.00	116.85
2	A	201	FMN	C7M-C7-C6	4.48	127.46	119.57
2	A	201	FMN	C5A-C6-C7	4.47	129.10	120.83
2	A	201	FMN	N10-C10-N1	4.39	131.44	118.51
2	A	201	FMN	C6-C5A-C9A	-4.34	113.09	119.05
2	A	201	FMN	C9A-C9-C8	4.27	127.80	119.22
2	A	201	FMN	C4A-C10-N10	-3.77	111.09	116.48
2	A	201	FMN	C9A-C5A-N5	-3.70	118.53	122.45
2	A	201	FMN	O4-C4-C4A	-3.56	117.14	126.53
2	A	201	FMN	O2-C2-N1	3.51	127.63	121.80
2	A	201	FMN	C4-N3-C2	-3.36	119.67	125.64
2	A	201	FMN	O2P-P-O5'	3.13	114.82	106.67
2	A	201	FMN	C1'-N10-C9A	-3.11	114.59	120.63
2	A	201	FMN	C4-C4A-C10	-3.11	111.60	116.93
2	A	201	FMN	C6-C7-C8	-3.05	115.22	119.69
2	A	201	FMN	C4A-C10-N1	-2.92	117.44	124.59
2	A	201	FMN	C10-C4A-N5	-2.67	119.35	124.81
2	A	201	FMN	C8M-C8-C9	2.15	123.36	119.57
2	A	201	FMN	O5'-P-O1P	-2.07	100.85	106.44
2	A	201	FMN	C9-C8-C7	-2.03	116.71	119.69

There are no chirality outliers.

All (2) torsion outliers are listed below:

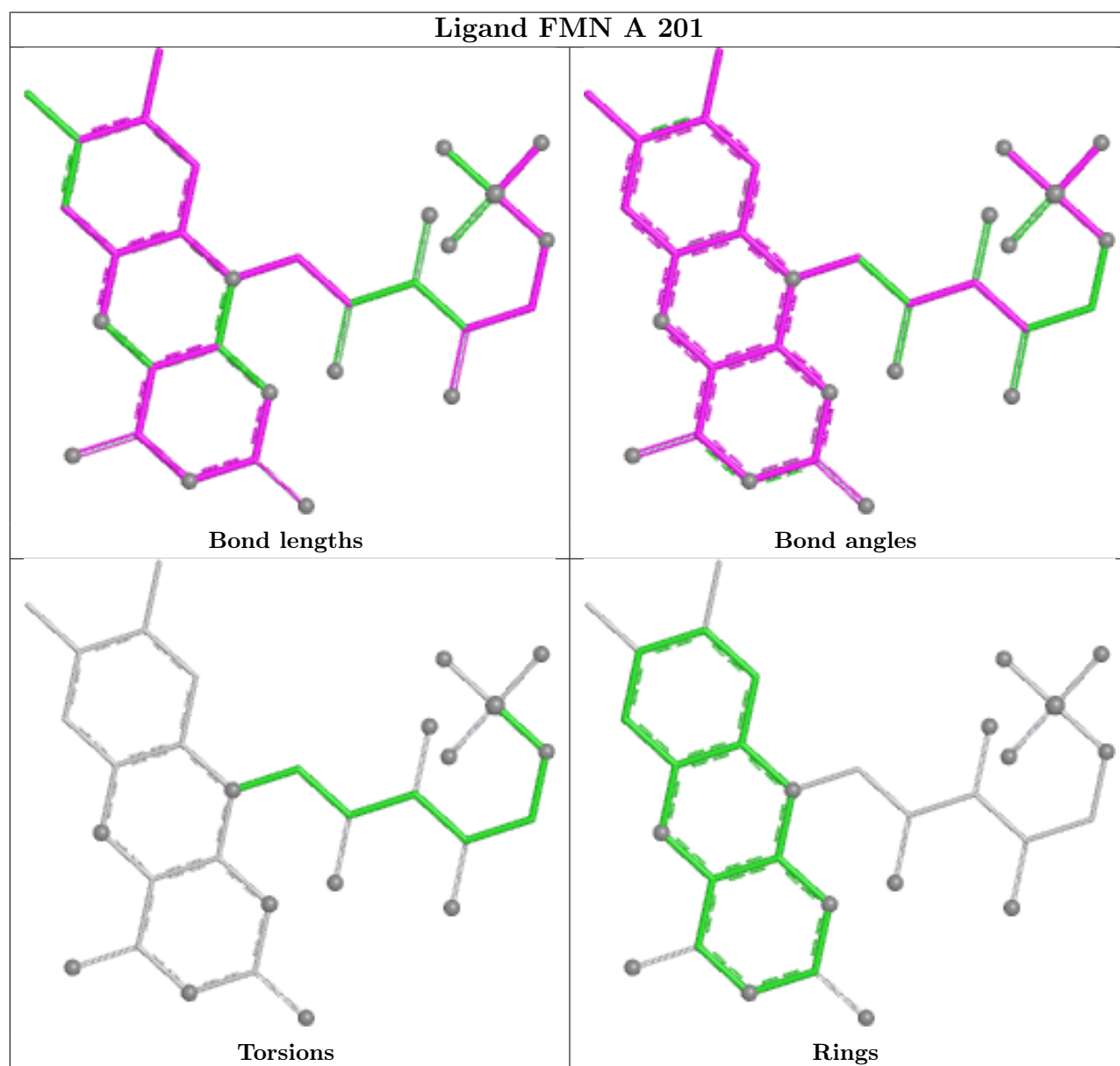
Mol	Chain	Res	Type	Atoms
3	A	202	EDO	O1-C1-C2-O2
3	A	203	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	203	EDO	3	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 [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	194/200 (97%)	0.28	13 (6%) 24 25	9, 15, 31, 43	2 (1%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	57	ALA	4.8
1	A	58	LEU	4.2
1	A	34	ALA	3.4
1	A	178	TYR	3.4
1	A	67	PRO	3.1
1	A	180	PRO	2.9
1	A	65	LEU	2.9
1	A	14	TYR	2.7
1	A	179	GLY	2.7
1	A	31	LYS	2.6
1	A	32	HIS	2.6
1	A	123	ASN	2.3
1	A	183	ALA	2.2

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](#)

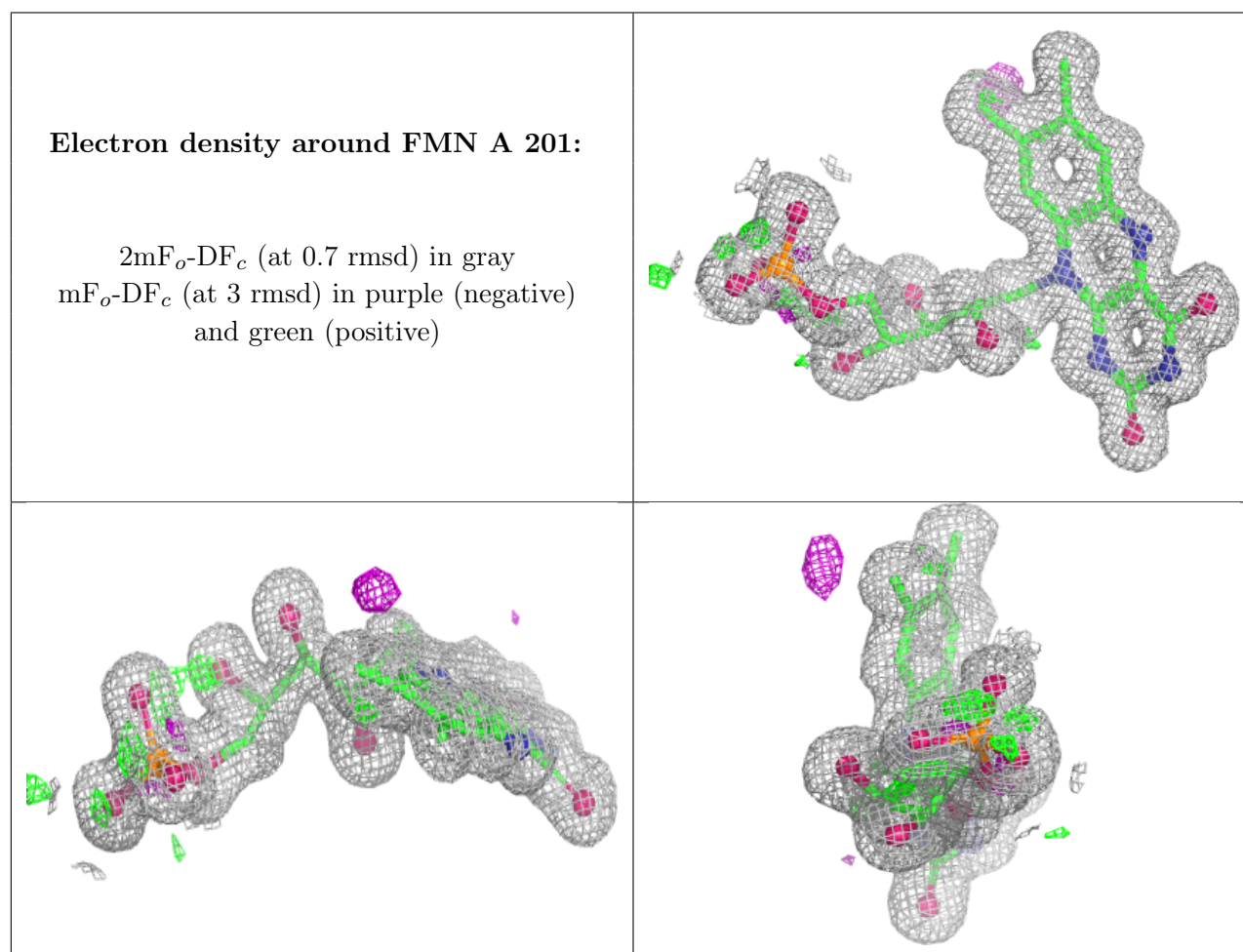
There are no oligosaccharides in this entry.

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
3	EDO	A	203	4/4	0.81	0.15	16,22,35,38	0
3	EDO	A	202	4/4	0.95	0.08	9,11,12,18	4
2	FMN	A	201	31/31	0.98	0.05	6,10,13,13	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.