



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:03 PM UTC

PDB ID : 1GOX / pdb_00001gox
Title : REFINED STRUCTURE OF SPINACH GLYCOLATE OXIDASE AT 2
ANGSTROMS RESOLUTION
Authors : Lindqvist, Y.
Deposited on : 1989-06-14
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	:	4-5-2 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

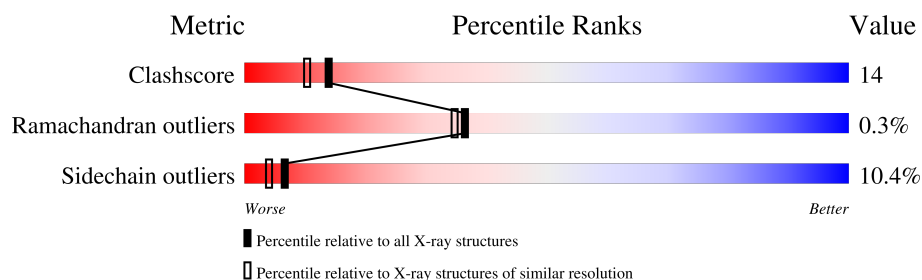
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	370	

2 Entry composition [i](#)

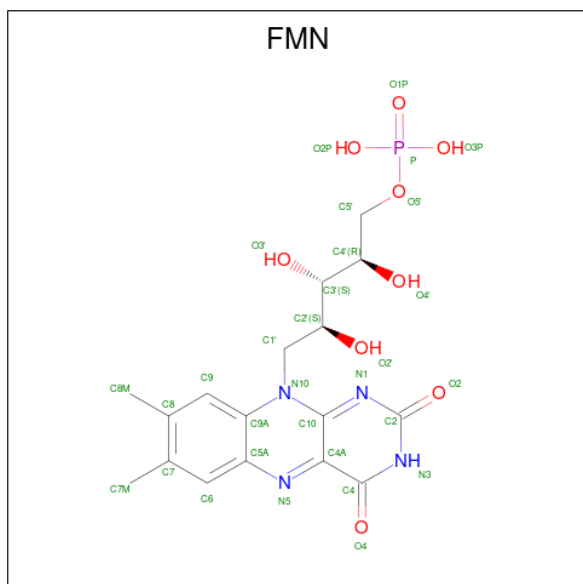
There are 3 unique types of molecules in this entry. The entry contains 3028 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 (S)-2-HYDROXY-ACID OXIDASE, PEROXISOMAL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	351	Total	C	N	O	S	0	0	0
			2699	1720	471	495	13			

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

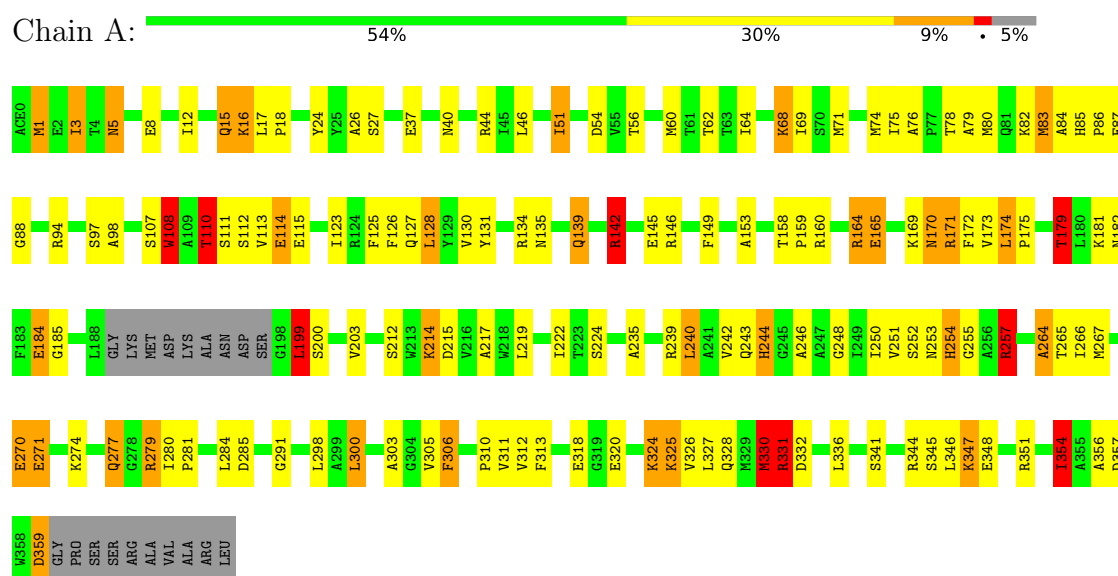


3 Residue-property plots

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: (S)-2-HYDROXY-ACID OXIDASE, PEROXISOMAL



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	148.10Å 148.10Å 135.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.189 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3028	wwPDB-VP
Average B, all atoms (Å ²)	28.0	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, ACE

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	1.15	1/2745 (0.0%)	2.06	95/3717 (2.6%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	158	THR	CA-CB	5.32	1.59	1.53

All (95) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	125	PHE	CA-CB-CG	10.91	124.71	113.80
1	A	128	LEU	N-CA-CB	-9.74	96.17	111.56
1	A	142	ARG	CD-NE-CZ	-9.40	111.25	124.40
1	A	257	ARG	CD-NE-CZ	-8.69	112.24	124.40
1	A	254	HIS	CA-CB-CG	8.15	121.95	113.80
1	A	327	LEU	CA-C-O	-7.77	112.66	120.82
1	A	331	ARG	NE-CZ-NH2	-7.74	112.23	119.20
1	A	285	ASP	CA-CB-CG	7.74	120.34	112.60
1	A	239	ARG	NE-CZ-NH1	-7.73	113.77	121.50
1	A	255	GLY	CA-C-N	7.35	133.06	122.40
1	A	255	GLY	C-N-CA	7.35	133.06	122.40
1	A	170	ASN	CA-CB-CG	7.31	119.91	112.60
1	A	158	THR	N-CA-C	7.29	121.46	109.79
1	A	108	TRP	CB-CA-C	-7.24	98.33	110.56
1	A	128	LEU	CA-CB-CG	7.04	140.96	116.30
1	A	27	SER	N-CA-C	6.88	119.18	110.24
1	A	331	ARG	CD-NE-CZ	-6.83	114.83	124.40
1	A	108	TRP	CA-CB-CG	6.80	126.52	113.60
1	A	40	ASN	OD1-CG-ND2	-6.80	115.80	122.60
1	A	111	SER	CA-C-O	-6.79	112.45	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	165	GLU	N-CA-C	6.71	119.42	111.71
1	A	324	LYS	CA-C-N	6.70	129.25	120.28
1	A	324	LYS	C-N-CA	6.70	129.25	120.28
1	A	264	ALA	N-CA-C	-6.68	100.39	110.28
1	A	325	LYS	CA-C-N	6.67	129.09	120.56
1	A	325	LYS	C-N-CA	6.67	129.09	120.56
1	A	291	GLY	N-CA-C	-6.65	104.53	113.24
1	A	318	GLU	N-CA-C	6.63	121.02	112.41
1	A	313	PHE	CA-CB-CG	6.57	120.37	113.80
1	A	139	GLN	OE1-CD-NE2	6.53	129.13	122.60
1	A	357	ASP	CA-CB-CG	6.50	119.10	112.60
1	A	336	LEU	CA-C-N	6.45	129.44	120.29
1	A	336	LEU	C-N-CA	6.45	129.44	120.29
1	A	243	GLN	CG-CD-NE2	-6.43	106.76	116.40
1	A	98	ALA	CB-CA-C	6.42	120.96	110.88
1	A	115	GLU	N-CA-CB	6.41	119.64	110.16
1	A	354	ILE	N-CA-CB	-6.33	100.09	111.92
1	A	174	LEU	O-C-N	6.32	127.60	121.28
1	A	115	GLU	CA-C-O	-6.31	113.73	120.42
1	A	239	ARG	NH1-CZ-NH2	6.24	127.42	119.30
1	A	174	LEU	CA-C-O	-6.24	113.56	119.80
1	A	114	GLU	CA-C-O	-6.24	113.94	120.55
1	A	217	ALA	N-CA-C	-6.22	104.58	111.36
1	A	179	THR	CA-CB-OG1	-6.21	100.28	109.60
1	A	250	ILE	N-CA-CB	6.20	119.48	111.67
1	A	243	GLN	OE1-CD-NE2	6.12	128.72	122.60
1	A	354	ILE	CA-CB-CG2	6.06	120.80	110.50
1	A	5	ASN	CA-C-N	6.05	128.18	120.56
1	A	5	ASN	C-N-CA	6.05	128.18	120.56
1	A	199	LEU	O-C-N	5.93	129.56	122.27
1	A	146	ARG	CB-CA-C	-5.92	101.58	110.88
1	A	248	GLY	O-C-N	5.85	130.30	122.70
1	A	185	GLY	CA-C-O	5.85	124.27	118.77
1	A	160	ARG	NE-CZ-NH2	-5.79	113.99	119.20
1	A	15	GLN	CB-CG-CD	5.70	122.29	112.60
1	A	303	ALA	N-CA-C	-5.68	106.35	113.28
1	A	142	ARG	NE-CZ-NH2	5.67	124.30	119.20
1	A	164	ARG	NE-CZ-NH1	5.64	127.14	121.50
1	A	171	ARG	N-CA-C	-5.63	103.98	111.02
1	A	159	PRO	N-CA-C	-5.59	106.10	113.65
1	A	113	VAL	CA-CB-CG2	5.59	119.90	110.40
1	A	107	SER	CA-C-N	5.58	131.58	122.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	107	SER	C-N-CA	5.58	131.58	122.65
1	A	26	ALA	N-CA-C	5.51	117.37	111.36
1	A	306	PHE	CA-CB-CG	5.49	119.29	113.80
1	A	251	VAL	N-CA-CB	5.47	117.31	111.46
1	A	94	ARG	CD-NE-CZ	-5.46	116.76	124.40
1	A	253	ASN	N-CA-C	-5.46	104.88	112.30
1	A	240	LEU	N-CA-C	-5.44	105.43	111.36
1	A	114	GLU	CG-CD-OE1	5.43	130.89	118.40
1	A	250	ILE	O-C-N	5.43	129.99	122.88
1	A	310	PRO	CA-C-N	5.38	127.43	120.70
1	A	310	PRO	C-N-CA	5.38	127.43	120.70
1	A	56	THR	O-C-N	5.38	127.90	122.09
1	A	114	GLU	N-CA-CB	5.33	117.95	110.12
1	A	110	THR	N-CA-C	-5.30	106.68	112.72
1	A	24	TYR	CA-CB-CG	-5.28	104.40	113.90
1	A	244	HIS	CA-C-N	5.25	131.71	121.41
1	A	244	HIS	C-N-CA	5.25	131.71	121.41
1	A	114	GLU	O-C-N	5.25	127.69	122.12
1	A	114	GLU	CB-CG-CD	5.24	121.51	112.60
1	A	359	ASP	CB-CG-OD2	-5.22	106.38	118.40
1	A	246	ALA	CA-C-O	-5.22	115.47	121.47
1	A	130	VAL	CB-CA-C	5.18	119.78	111.29
1	A	84	ALA	CA-C-O	-5.16	113.70	120.00
1	A	312	VAL	CA-CB-CG2	5.16	119.17	110.40
1	A	98	ALA	N-CA-C	-5.15	105.56	111.07
1	A	97	SER	O-C-N	5.12	127.99	122.15
1	A	18	PRO	N-CA-C	-5.09	103.29	111.38
1	A	271	GLU	CG-CD-OE1	5.09	130.11	118.40
1	A	330	MET	CA-C-O	-5.04	115.08	120.42
1	A	24	TYR	CA-C-N	5.03	127.28	120.44
1	A	24	TYR	C-N-CA	5.03	127.28	120.44
1	A	270	GLU	N-CA-C	5.03	117.41	111.33
1	A	83	MET	N-CA-C	-5.00	105.92	112.23

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	2699	0	2756	78	0
2	A	31	0	19	1	0
3	A	298	0	0	8	2
All	All	3028	0	2775	79	2

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 14.

All (79) 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:174:LEU:HD12	1:A:175:PRO:HD2	1.49	0.93
1:A:108:TRP:HZ3	1:A:131:TYR:HH	0.96	0.93
1:A:80:MET:HE3	1:A:174:LEU:HD13	1.57	0.85
1:A:279:ARG:HG2	1:A:279:ARG:HH11	1.42	0.85
1:A:164:ARG:HD3	1:A:257:ARG:HB3	1.63	0.81
1:A:37:GLU:OE1	1:A:44:ARG:NH2	2.14	0.80
1:A:264:ALA:HB3	1:A:267:MET:HG2	1.67	0.76
1:A:5:ASN:OD1	1:A:8:GLU:HG3	1.84	0.76
1:A:68:LYS:HB2	1:A:68:LYS:NZ	2.03	0.74
1:A:320:GLU:OE1	1:A:324:LYS:NZ	2.21	0.72
1:A:60:MET:HE1	1:A:331:ARG:HB2	1.71	0.72
1:A:108:TRP:HZ3	1:A:131:TYR:OH	1.73	0.70
1:A:80:MET:HE2	1:A:83:MET:HE2	1.75	0.69
1:A:68:LYS:HB2	1:A:68:LYS:HZ3	1.58	0.68
1:A:64:ILE:HD12	1:A:69:ILE:HD11	1.78	0.65
1:A:199:LEU:O	1:A:203:VAL:HG13	1.96	0.65
1:A:123:ILE:HD11	3:A:541:HOH:O	1.98	0.64
1:A:80:MET:HE2	1:A:83:MET:CE	2.31	0.61
1:A:212:SER:OG	1:A:214:LYS:HD2	2.01	0.61
1:A:179:THR:HG21	1:A:184:GLU:OE2	2.00	0.60
1:A:277:GLN:HG3	3:A:646:HOH:O	2.04	0.58
1:A:78:THR:O	1:A:79:ALA:HB2	2.04	0.57
1:A:3:ILE:HD11	1:A:12:ILE:CD1	2.35	0.56
1:A:279:ARG:HG2	1:A:279:ARG:NH1	2.13	0.53
1:A:331:ARG:NH1	3:A:389:HOH:O	2.32	0.53
1:A:126:PHE:HB2	1:A:149:PHE:CD1	2.45	0.52
1:A:51:ILE:HG22	3:A:412:HOH:O	2.10	0.52
1:A:326:VAL:O	1:A:330:MET:HG3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:ILE:HD11	1:A:300:LEU:HD23	1.92	0.51
1:A:60:MET:HE3	1:A:71:MET:HB3	1.93	0.51
1:A:199:LEU:HB2	3:A:594:HOH:O	2.10	0.50
1:A:75:ILE:HG23	1:A:311:VAL:HG21	1.93	0.50
1:A:85:HIS:CD2	1:A:87:GLU:H	2.30	0.49
1:A:85:HIS:HD2	1:A:87:GLU:H	1.61	0.49
1:A:3:ILE:HD11	1:A:12:ILE:HD13	1.94	0.49
1:A:242:VAL:HG11	1:A:279:ARG:HD3	1.94	0.49
1:A:356:ALA:HB3	1:A:359:ASP:OD1	2.13	0.49
2:A:370:FMN:C4	3:A:404:HOH:O	2.61	0.49
1:A:64:ILE:HD13	1:A:74:MET:SD	2.53	0.48
1:A:254:HIS:O	1:A:257:ARG:HG3	2.14	0.48
1:A:345:SER:OG	1:A:348:GLU:HG3	2.15	0.47
1:A:235:ALA:HB2	1:A:271:GLU:HG2	1.97	0.47
1:A:240:LEU:O	1:A:244:HIS:HD2	1.98	0.47
1:A:80:MET:HE1	1:A:172:PHE:HZ	1.80	0.46
1:A:252:SER:HA	1:A:265:THR:HG21	1.97	0.46
1:A:274:LYS:HB3	1:A:274:LYS:HE2	1.71	0.46
1:A:54:ASP:O	1:A:344:ARG:HD2	2.16	0.46
1:A:12:ILE:O	1:A:16:LYS:HG2	2.17	0.45
1:A:142:ARG:NH2	1:A:145:GLU:OE2	2.48	0.45
1:A:270:GLU:O	1:A:274:LYS:HG3	2.17	0.45
1:A:46:LEU:O	1:A:354:ILE:HA	2.17	0.44
1:A:330:MET:HE2	1:A:330:MET:HB3	1.65	0.44
1:A:16:LYS:HG3	1:A:17:LEU:N	2.33	0.44
1:A:127:GLN:HA	1:A:153:ALA:O	2.17	0.44
1:A:347:LYS:HB3	1:A:347:LYS:NZ	2.33	0.44
1:A:267:MET:HE3	1:A:267:MET:HB3	1.54	0.44
1:A:224:SER:HB2	3:A:507:HOH:O	2.17	0.44
1:A:142:ARG:HH21	1:A:145:GLU:CD	2.27	0.43
1:A:179:THR:HG22	1:A:181:LYS:HD2	2.00	0.43
1:A:214:LYS:HD3	1:A:215:ASP:N	2.33	0.43
1:A:325:LYS:HE3	1:A:325:LYS:HB2	1.82	0.43
1:A:51:ILE:H	1:A:51:ILE:HG13	1.60	0.42
1:A:80:MET:HA	1:A:110:THR:HG23	2.01	0.42
1:A:165:GLU:O	1:A:169:LYS:HG3	2.19	0.42
1:A:37:GLU:HG3	1:A:264:ALA:HB2	2.01	0.42
1:A:170:ASN:O	1:A:171:ARG:C	2.62	0.42
1:A:76:ALA:HB2	1:A:306:PHE:HB3	2.00	0.42
1:A:82:LYS:HG2	1:A:86:PRO:O	2.19	0.42
1:A:62:THR:HB	1:A:346:LEU:HD12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:THR:HB	1:A:346:LEU:CD1	2.50	0.42
1:A:112:SER:HA	1:A:182:ASN:OD1	2.20	0.42
1:A:257:ARG:HH11	1:A:257:ARG:HD2	1.60	0.41
1:A:280:ILE:HB	1:A:281:PRO:HD2	2.01	0.41
1:A:131:TYR:O	1:A:134:ARG:NH1	2.53	0.41
1:A:135:ASN:O	1:A:139:GLN:HG3	2.21	0.40
1:A:284:LEU:O	1:A:305:VAL:HA	2.22	0.40
1:A:341:SER:HB3	3:A:414:HOH:O	2.21	0.40
1:A:1:MET:H	1:A:1:MET:HG2	1.52	0.40
1:A:328:GLN:NE2	1:A:332:ASP:OD2	2.55	0.40

All (2) 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)
3:A:656:HOH:O	3:A:656:HOH:O[16_555]	2.09	0.11
3:A:405:HOH:O	3:A:428:HOH:O[4_565]	2.19	0.01

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	347/370 (94%)	331 (95%)	15 (4%)	1 (0%)	36 35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	88	GLY

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	280/294 (95%)	251 (90%)	29 (10%)	7 4

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	3	ILE
1	A	15	GLN
1	A	16	LYS
1	A	51	ILE
1	A	68	LYS
1	A	108	TRP
1	A	110	THR
1	A	114	GLU
1	A	128	LEU
1	A	142	ARG
1	A	173	VAL
1	A	179	THR
1	A	184	GLU
1	A	199	LEU
1	A	200	SER
1	A	214	LYS
1	A	219	LEU
1	A	222	ILE
1	A	257	ARG
1	A	277	GLN
1	A	279	ARG
1	A	298	LEU
1	A	300	LEU
1	A	330	MET
1	A	331	ARG
1	A	347	LYS
1	A	351	ARG
1	A	354	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	15	GLN
1	A	57	ASN
1	A	85	HIS
1	A	244	HIS
1	A	328	GLN

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 ⓘ

There are no oligosaccharides 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	370	-	33,33,33	1.60	6 (18%)	48,50,50	1.62	7 (14%)

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	370	-	-	5/18/18/18	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	370	FMN	C5'-C4'	5.27	1.59	1.51
2	A	370	FMN	C6-C5A	2.79	1.44	1.40
2	A	370	FMN	C5A-N5	-2.54	1.34	1.39
2	A	370	FMN	P-O1P	2.52	1.58	1.50
2	A	370	FMN	C1'-N10	2.14	1.53	1.47
2	A	370	FMN	C10-N1	2.02	1.37	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	370	FMN	C4A-C10-N10	4.74	123.26	116.48
2	A	370	FMN	C9A-N10-C10	-4.01	114.63	120.75
2	A	370	FMN	C5'-C4'-C3'	-3.75	105.15	112.22
2	A	370	FMN	O3P-P-O5'	3.13	114.82	106.67
2	A	370	FMN	C10-N1-C2	2.93	123.18	116.85
2	A	370	FMN	C4A-C10-N1	-2.62	118.16	124.59
2	A	370	FMN	O3P-P-O1P	-2.26	102.01	110.83

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	370	FMN	O3'-C3'-C4'-C5'
2	A	370	FMN	C2'-C3'-C4'-C5'
2	A	370	FMN	O3'-C3'-C4'-O4'
2	A	370	FMN	C2'-C3'-C4'-O4'
2	A	370	FMN	C4'-C5'-O5'-P

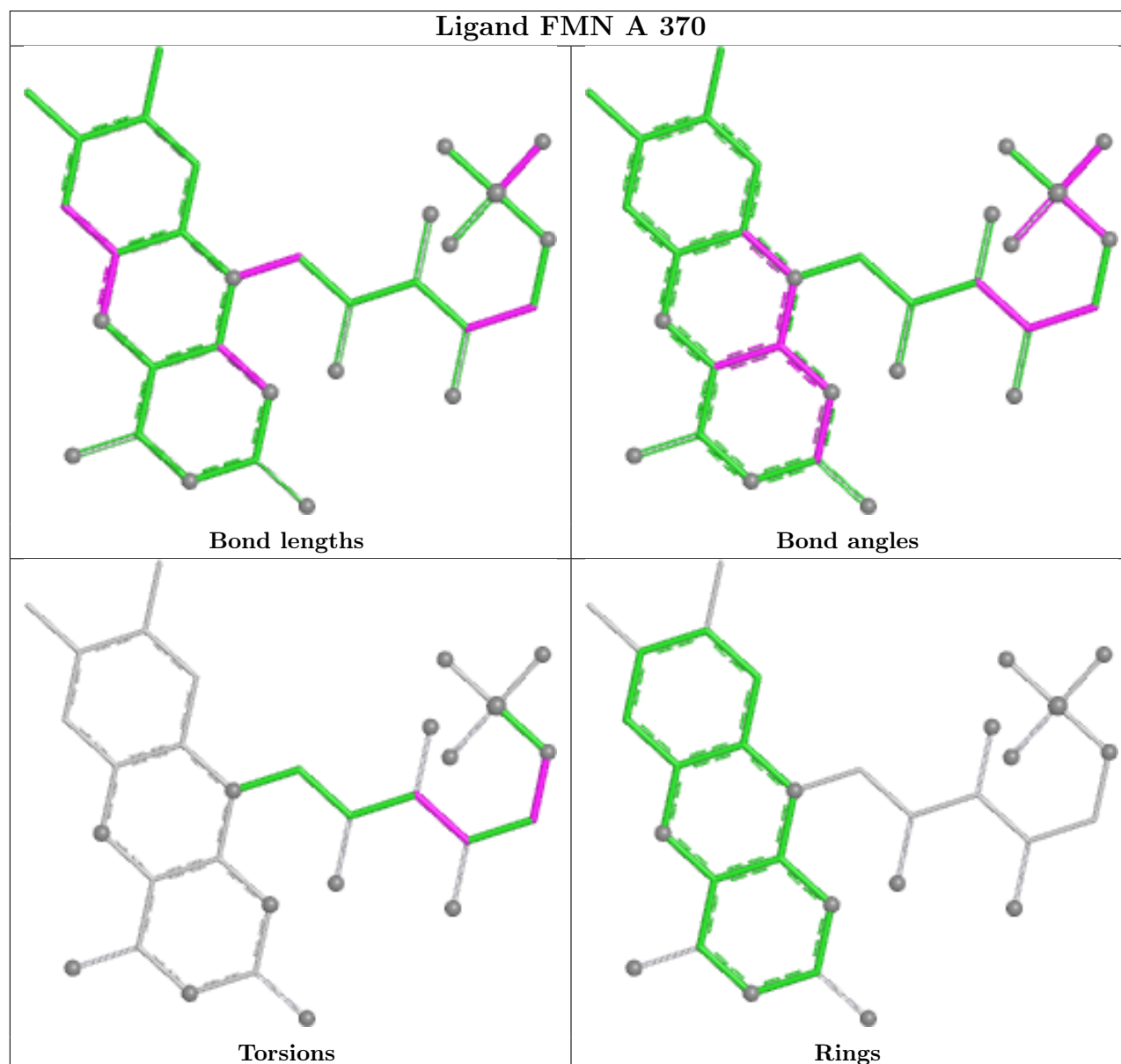
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	370	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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.