



Full wwPDB NMR Structure Validation Report ⓘ

Mar 30, 2026 – 01:54 AM UTC

PDB ID : 1YKG / pdb_00001ykg
Title : Solution structure of the flavodoxin-like domain from the Escherichia coli sulfite reductase
Authors : Sibille, N.; Blackledge, M.; Brutscher, B.; Coves, J.; Bersch, B.
Deposited on : 2005-01-18

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A user guide is available at

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

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)
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

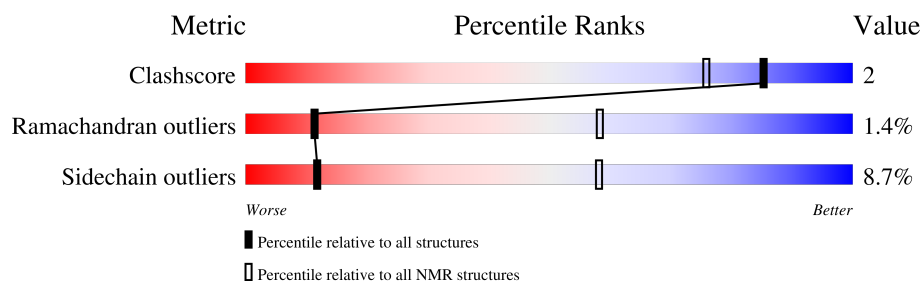
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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	167	

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

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
2	A	FMN	300	15	-

2 Ensemble composition and analysis ⓘ

This entry contains 15 models. Model 3 is the overall representative, medoid model (most similar to other models). The authors have identified model 2 as representative, based on the following criterion: *fewest violations*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:63-A:133, A:145-A:204 (131)	0.47	3

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 2 clusters. No single-model clusters were found.

Cluster number	Models
1	2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 13, 14, 15
2	1, 11

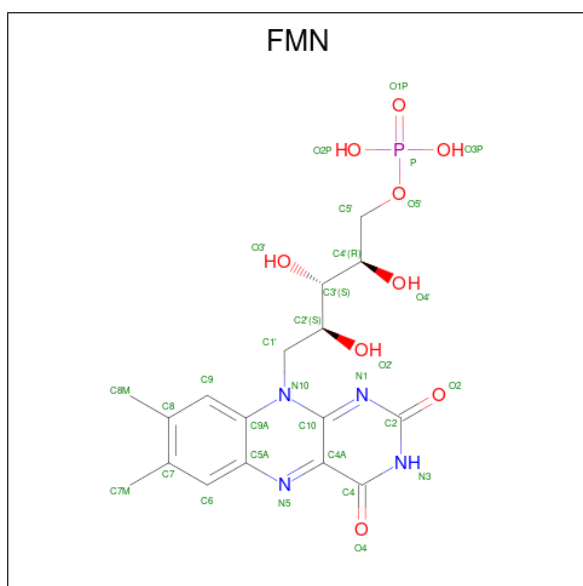
3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2311 atoms, of which 1154 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Sulfite reductase [NADPH] flavoprotein alpha-component.

Mol	Chain	Residues	Atoms						Trace
1	A	146	Total	C	H	N	O	S	0
			2261	712	1135	194	219	1	

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



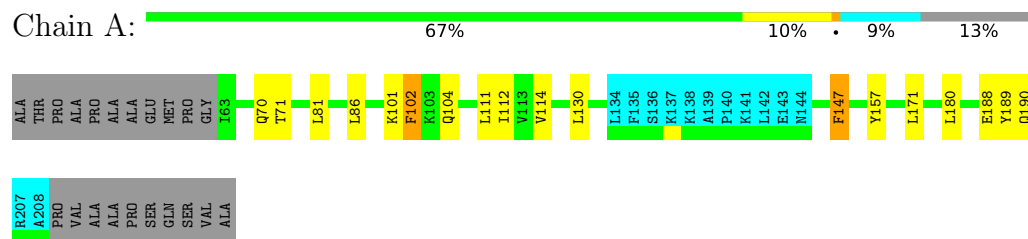
Mol	Chain	Residues	Atoms					
2	A	1	Total	C	H	N	O	P
			50	17	19	4	9	1

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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 outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component

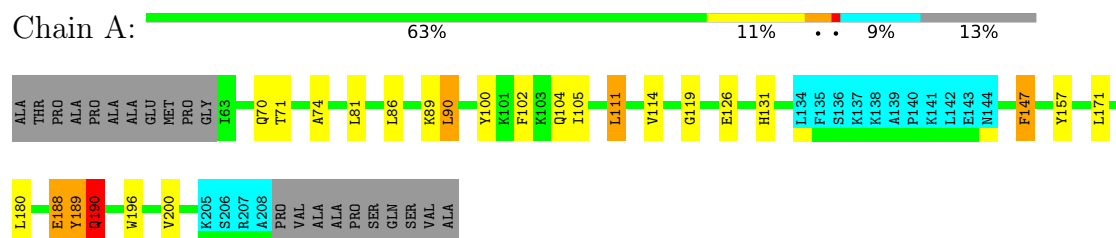


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

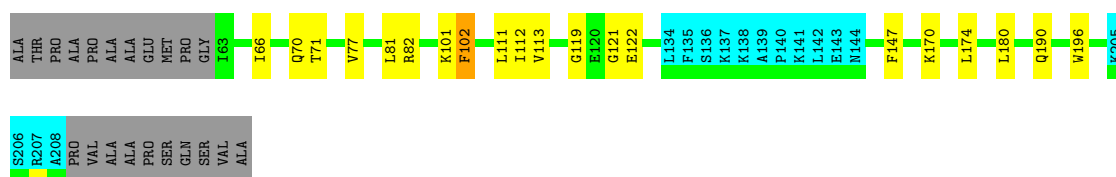
- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component



4.2.2 Score per residue for model 2

- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component

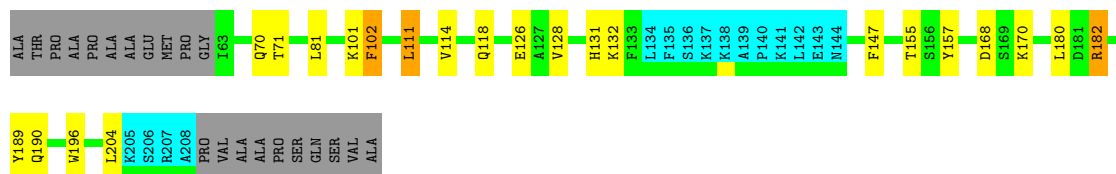




4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component

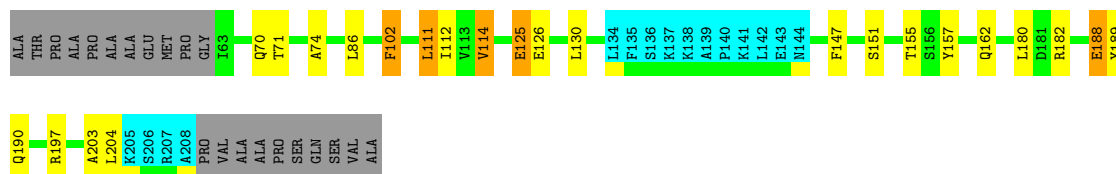
Chain A: 65% 12% 9% 13%



4.2.4 Score per residue for model 4

- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component

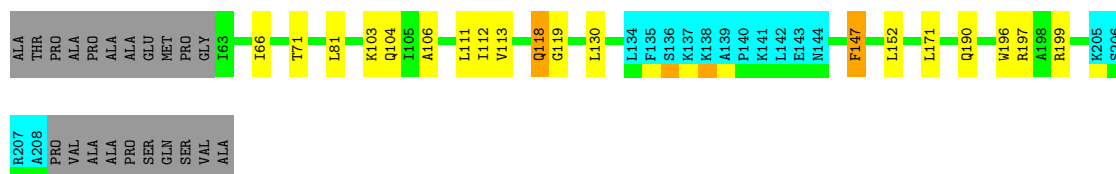
Chain A: 64% 11% 9% 13%



4.2.5 Score per residue for model 5

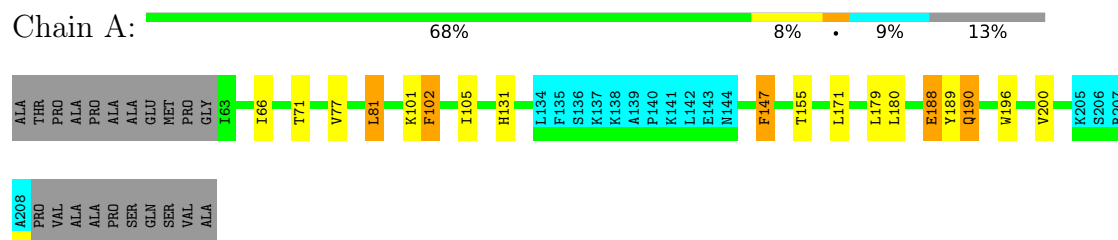
- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component

Chain A: 67% 10% 9% 13%



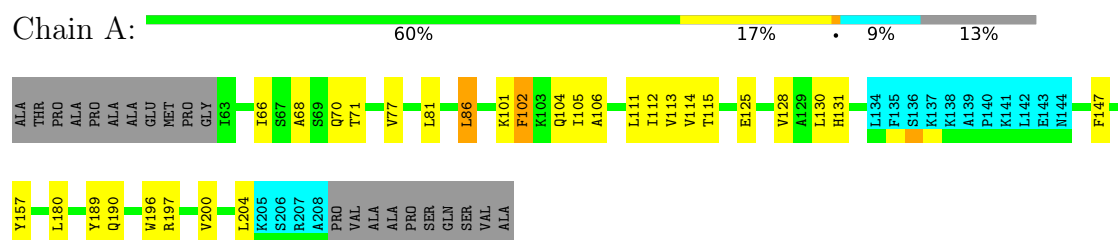
4.2.6 Score per residue for model 6

- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component



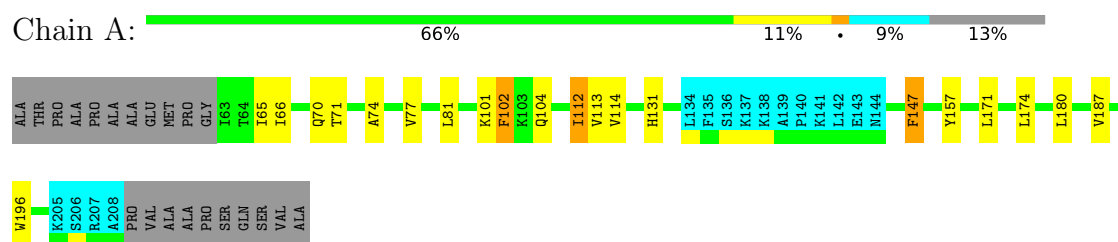
4.2.7 Score per residue for model 7

- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component



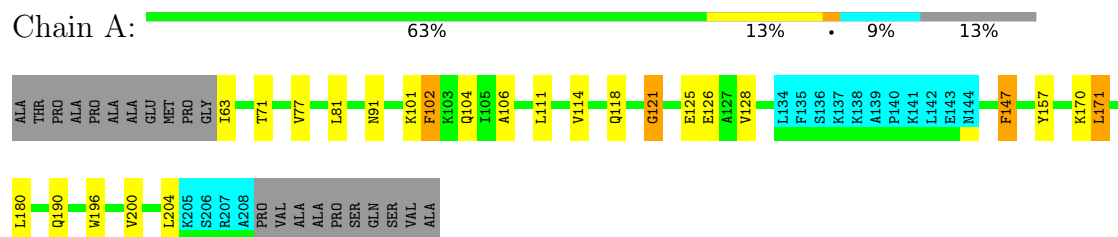
4.2.8 Score per residue for model 8

- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component



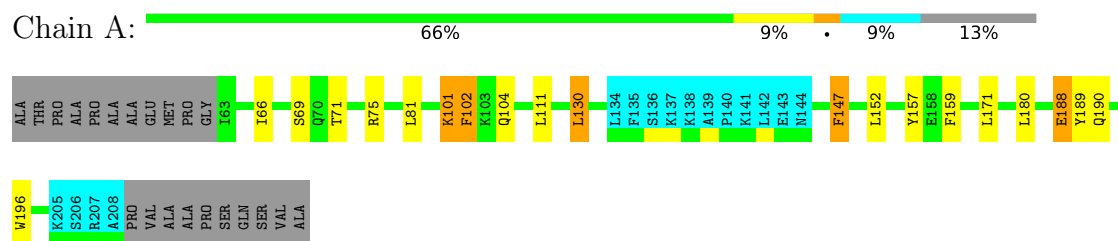
4.2.9 Score per residue for model 9

- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component

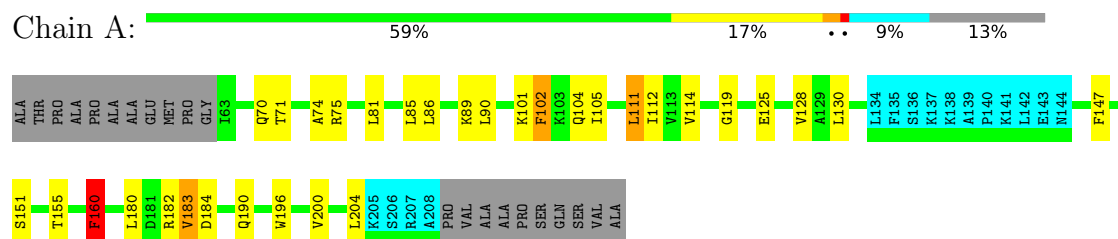


4.2.10 Score per residue for model 10

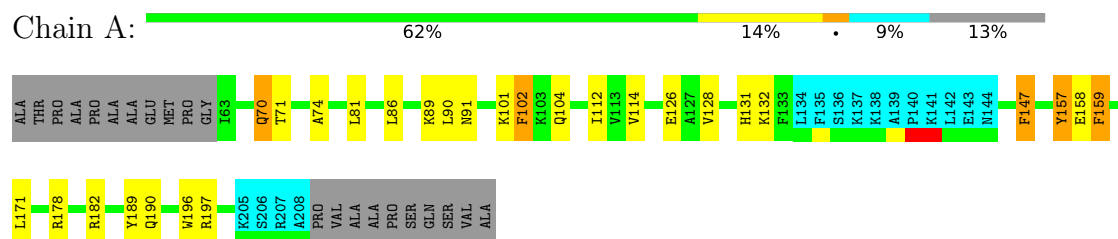
- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component



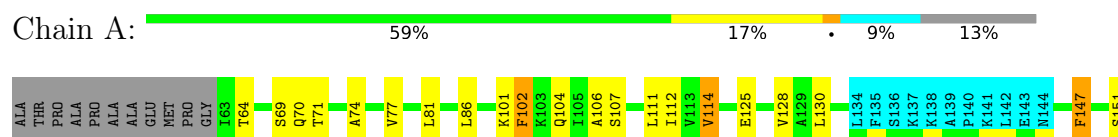
- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component



- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component



- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component

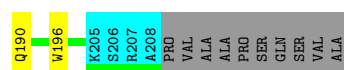




4.2.14 Score per residue for model 14

- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component

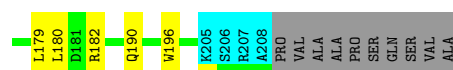
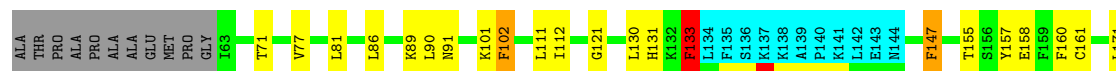
Chain A: 65% 10% 9% 13%



4.2.15 Score per residue for model 15

- Molecule 1: Sulfite reductase [NADPH] flavoprotein alpha-component

Chain A: 62% 14% 9% 13%



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 15 calculated structures, 15 were deposited, based on the following criterion: *initial selection based on experimental energy target function*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
Discover	structure solution	2.98
SCULPTOR	refinement	1

No chemical shift data was provided.

6 Model quality

6.1 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 (average) 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	0.64±0.01	0±0/1021 (0.0± 0.0%)	1.32±0.03	7±2/1381 (0.5± 0.1%)
All	All	0.64	0/15315 (0.0%)	1.32	104/20715 (0.5%)

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	Planarity
1	A	0.0±0.0	3.7±1.1
All	All	0	55

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	125	GLU	CA-C-N	9.32	139.34	121.54	4	1
1	A	125	GLU	C-N-CA	9.32	139.34	121.54	4	1
1	A	101	LYS	N-CA-C	-8.59	101.50	111.03	15	12
1	A	158	GLU	CA-C-O	-7.83	109.32	120.51	14	1
1	A	147	PHE	N-CA-C	7.25	120.19	109.24	10	14
1	A	133	PHE	CA-CB-CG	6.95	120.75	113.80	15	1
1	A	90	LEU	N-CA-C	6.93	125.56	110.80	12	3
1	A	70	GLN	N-CA-C	-6.73	103.41	111.69	2	9
1	A	131	HIS	CA-CB-CG	-6.62	107.18	113.80	15	7
1	A	102	PHE	CA-CB-CG	6.26	120.06	113.80	9	12
1	A	190	GLN	CA-C-O	-6.20	113.94	120.63	14	12
1	A	154	ASP	CA-CB-CG	6.12	118.72	112.60	13	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	86	LEU	N-CA-C	-6.11	104.62	111.28	1	7
1	A	118	GLN	N-CA-C	5.87	118.79	109.81	5	2
1	A	152	LEU	CB-CA-C	5.64	120.03	109.71	10	1
1	A	111	LEU	N-CA-CB	-5.55	102.06	110.77	14	6
1	A	203	ALA	N-CA-C	5.47	117.04	111.14	4	1
1	A	159	PHE	N-CA-C	-5.39	100.82	109.39	12	1
1	A	160	PHE	CA-CB-CG	5.24	119.04	113.80	11	1
1	A	184	ASP	N-CA-C	-5.24	100.19	108.73	11	1
1	A	114	VAL	CB-CA-C	5.23	117.78	110.99	4	2
1	A	183	VAL	CA-CB-CG2	5.18	119.20	110.40	11	1
1	A	190	GLN	O-C-N	-5.09	116.39	122.20	1	3
1	A	105	ILE	CA-C-N	5.08	127.09	120.28	1	1
1	A	105	ILE	C-N-CA	5.08	127.09	120.28	1	1
1	A	131	HIS	N-CA-CB	5.06	117.56	110.12	1	1
1	A	89	LYS	O-C-N	5.03	129.28	122.59	1	1

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	71	THR	Mainchain	15
1	A	102	PHE	Sidechain	12
1	A	157	TYR	Sidechain	11
1	A	188	GLU	Mainchain	4
1	A	189	TYR	Sidechain	3
1	A	121	GLY	Mainchain	2
1	A	100	TYR	Sidechain	1
1	A	147	PHE	Sidechain	1
1	A	125	GLU	Mainchain	1
1	A	197	ARG	Sidechain	1
1	A	75	ARG	Sidechain	1
1	A	178	ARG	Sidechain	1
1	A	158	GLU	Mainchain	1
1	A	182	ARG	Sidechain	1

6.2 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 each 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

averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1006	1000	998	5±2
All	All	15555	15285	15255	69

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 2.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:81:LEU:HD23	1:A:196:TRP:CZ3	0.79	2.11	6	2
1:A:81:LEU:HD22	1:A:196:TRP:CZ3	0.73	2.19	5	3
1:A:81:LEU:HD13	1:A:196:TRP:CZ3	0.71	2.20	7	6
1:A:81:LEU:HD22	1:A:196:TRP:CH2	0.67	2.24	10	6
1:A:125:GLU:O	1:A:128:VAL:HG12	0.66	1.90	7	3
1:A:157:TYR:O	1:A:159:PHE:N	0.63	2.31	12	1
1:A:147:PHE:CD2	1:A:171:LEU:HD23	0.59	2.33	14	2
1:A:147:PHE:CD2	1:A:171:LEU:HD13	0.58	2.33	12	7
1:A:81:LEU:HD11	1:A:200:VAL:CG2	0.57	2.29	13	3
1:A:160:PHE:O	1:A:161:CYS:HB3	0.54	2.02	15	1
1:A:167:PHE:O	1:A:171:LEU:HD22	0.53	2.04	14	1
1:A:128:VAL:O	1:A:132:LYS:HB2	0.53	2.04	3	1
1:A:119:GLY:O	1:A:122:GLU:OE1	0.52	2.28	2	1
1:A:68:ALA:HB3	1:A:115:THR:HA	0.51	1.82	7	1
1:A:81:LEU:HD21	1:A:200:VAL:CG2	0.48	2.38	6	1
1:A:74:ALA:HB1	1:A:114:VAL:HG23	0.48	1.85	12	5
1:A:81:LEU:HD21	1:A:200:VAL:HG21	0.48	1.86	6	1
1:A:147:PHE:CZ	1:A:171:LEU:HB3	0.48	2.43	14	1
1:A:81:LEU:HD12	1:A:197:ARG:HG3	0.48	1.86	7	1
1:A:188:GLU:O	1:A:190:GLN:N	0.46	2.45	6	3
1:A:160:PHE:O	1:A:161:CYS:CB	0.46	2.63	15	1
1:A:128:VAL:O	1:A:132:LYS:CB	0.45	2.64	12	1
1:A:111:LEU:O	1:A:111:LEU:HD23	0.45	2.11	11	2
1:A:111:LEU:HD23	1:A:111:LEU:C	0.45	2.36	11	1
1:A:68:ALA:N	1:A:114:VAL:O	0.43	2.50	7	1
1:A:63:ILE:N	1:A:91:ASN:O	0.43	2.51	9	1
1:A:125:GLU:O	1:A:128:VAL:HG22	0.43	2.14	13	1
1:A:74:ALA:HB1	1:A:114:VAL:CG1	0.43	2.44	1	1
1:A:168:ASP:OD2	1:A:182:ARG:NH1	0.42	2.53	3	1
1:A:65:ILE:HG23	1:A:112:ILE:HG22	0.41	1.91	8	1
1:A:85:LEU:O	1:A:89:LYS:N	0.41	2.53	11	1
1:A:104:GLN:C	1:A:106:ALA:N	0.41	2.78	13	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:SER:OG	1:A:74:ALA:HB3	0.41	2.16	13	1
1:A:74:ALA:HB1	1:A:114:VAL:CG2	0.40	2.46	11	1
1:A:104:GLN:O	1:A:107:SER:N	0.40	2.53	13	1
1:A:130:LEU:HD12	1:A:130:LEU:C	0.40	2.41	10	1
1:A:81:LEU:CD2	1:A:196:TRP:CZ3	0.40	3.04	12	1

6.3 Torsion angles

6.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. 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	130/167 (78%)	123±1 (95±1%)	5±1 (4±1%)	2±1 (1±1%)	11	58
All	All	1950/2505 (78%)	1852 (95%)	71 (4%)	27 (1%)	11	58

All 14 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	189	TYR	4
1	A	119	GLY	3
1	A	90	LEU	2
1	A	102	PHE	2
1	A	121	GLY	2
1	A	105	ILE	2
1	A	106	ALA	2
1	A	89	LYS	2
1	A	91	ASN	2
1	A	158	GLU	2
1	A	126	GLU	1
1	A	187	VAL	1
1	A	160	PHE	1
1	A	159	PHE	1

6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	104/130 (80%)	95±2 (91±2%)	9±2 (9±2%)	12	58
All	All	1560/1950 (80%)	1425 (91%)	135 (9%)	12	58

All 43 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	180	LEU	13
1	A	112	ILE	10
1	A	111	LEU	8
1	A	104	GLN	7
1	A	77	VAL	7
1	A	130	LEU	7
1	A	66	ILE	6
1	A	155	THR	6
1	A	204	LEU	6
1	A	182	ARG	5
1	A	126	GLU	4
1	A	113	VAL	4
1	A	170	LYS	4
1	A	151	SER	4
1	A	171	LEU	3
1	A	114	VAL	3
1	A	118	GLN	3
1	A	179	LEU	3
1	A	174	LEU	2
1	A	197	ARG	2
1	A	81	LEU	2
1	A	86	LEU	2
1	A	200	VAL	2
1	A	101	LYS	2
1	A	183	VAL	2
1	A	189	TYR	1
1	A	190	GLN	1
1	A	82	ARG	1
1	A	102	PHE	1

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Mol	Chain	Res	Type	Models (Total)
1	A	162	GLN	1
1	A	188	GLU	1
1	A	103	LYS	1
1	A	152	LEU	1
1	A	199	ARG	1
1	A	105	ILE	1
1	A	69	SER	1
1	A	75	ARG	1
1	A	159	PHE	1
1	A	160	PHE	1
1	A	70	GLN	1
1	A	64	THR	1
1	A	133	PHE	1
1	A	158	GLU	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	FMN	A	300	-	33,33,33	1.45±0.03	3±0 (9±1%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	FMN	A	300	-	48,50,50	1.39±0.10	8±2 (16±3%)

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	300	-	3±0,3,4,4	0±0,18,18,18	0±0,3,3,3

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	A	300	FMN	C4A-N5	4.68	1.40	1.30	2	15
2	A	300	FMN	C10-N1	3.62	1.40	1.33	12	15
2	A	300	FMN	C10-N10	2.93	1.43	1.37	15	15
2	A	300	FMN	C5'-C4'	2.38	1.55	1.51	3	3
2	A	300	FMN	C5A-N5	2.06	1.35	1.39	11	1

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	A	300	FMN	C5A-C9A-N10	4.32	121.88	117.97	14	14
2	A	300	FMN	C4'-C3'-C2'	4.30	120.72	113.57	9	6
2	A	300	FMN	O3'-C3'-C4'	3.62	100.71	108.93	6	2
2	A	300	FMN	C4-C4A-N5	3.33	122.80	118.21	2	14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	A	300	FMN	C5'-C4'-C3'	3.20	118.25	112.22	6	4
2	A	300	FMN	C10-C4A-N5	3.18	118.31	124.81	2	15
2	A	300	FMN	O3'-C3'-C2'	3.11	101.87	108.93	15	4
2	A	300	FMN	C4A-C10-N10	2.92	120.67	116.48	6	15
2	A	300	FMN	C8M-C8-C9	2.82	114.61	119.57	8	5
2	A	300	FMN	C4A-C10-N1	2.77	117.80	124.59	11	15
2	A	300	FMN	C9A-N10-C10	2.66	116.69	120.75	14	8
2	A	300	FMN	C6-C5A-N5	2.39	114.48	118.44	11	2
2	A	300	FMN	C1'-N10-C9A	2.34	125.18	120.63	6	3
2	A	300	FMN	O3P-P-O5'	2.32	100.62	106.67	2	1
2	A	300	FMN	O2'-C2'-C3'	2.25	114.51	109.25	13	2
2	A	300	FMN	O3P-P-O2P	2.23	116.15	107.80	15	6
2	A	300	FMN	C1'-C2'-C3'	2.17	115.55	109.66	9	1
2	A	300	FMN	O5'-C5'-C4'	2.16	115.14	109.36	15	1
2	A	300	FMN	C10-N1-C2	2.06	121.30	116.85	11	2

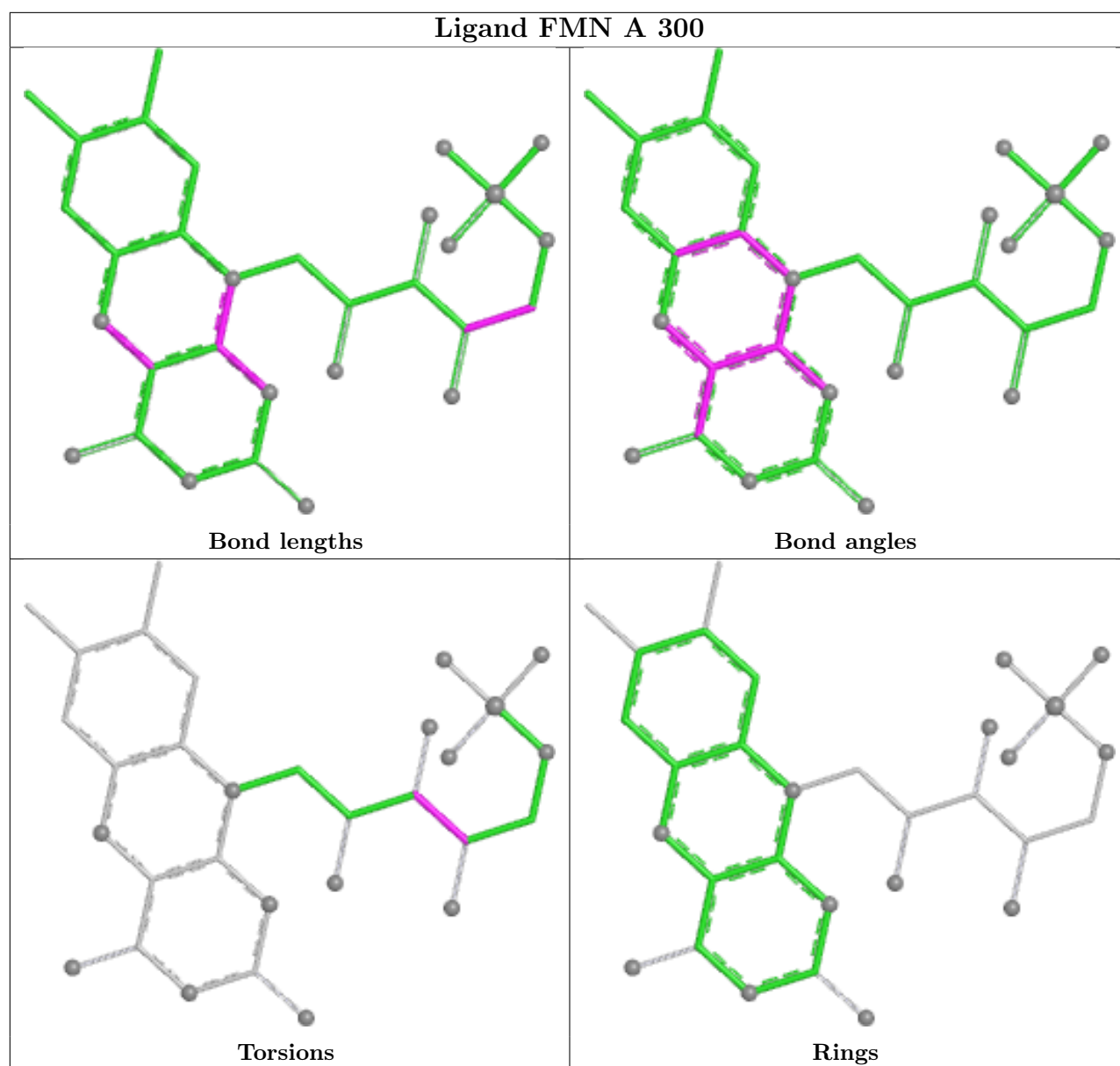
All unique chiral outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Models (Total)
2	A	300	FMN	C2'	15
2	A	300	FMN	C3'	15
2	A	300	FMN	C4'	15

There are no torsion outliers.

There are no ring outliers.

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.



6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided