



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 6, 2022 – 12:19 AM JST

PDB ID : 7F72  
Title : Rv3094c in complex with FAD and ETH.  
Authors : Wang, Z.X.; Ouyang, S.Y.  
Deposited on : 2021-06-27  
Resolution : 1.64 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](mailto: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>.

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

MolProbity : 4.02b-467  
Mogul : ?? (???), CSD ??CSD?? (????)  
Xtriage (Phenix) : 1.13  
EDS : 2.29  
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) : 2.29

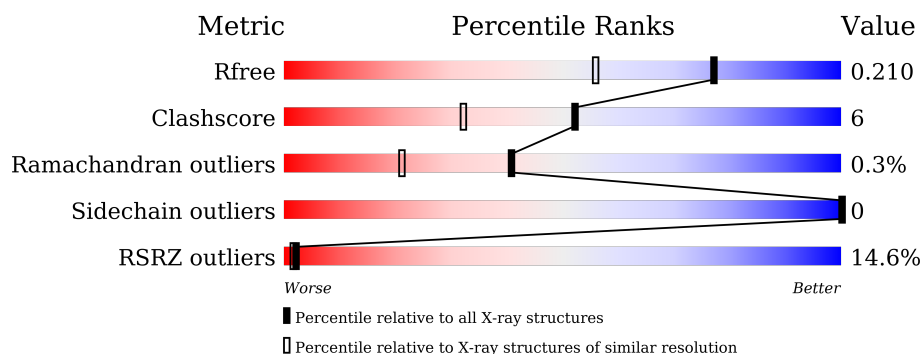
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.64 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))
$R_{free}$	130704	3122 (1.66-1.62)
Clashscore	141614	3268 (1.66-1.62)
Ramachandran outliers	138981	3215 (1.66-1.62)
Sidechain outliers	138945	3215 (1.66-1.62)
RSRZ outliers	127900	3079 (1.66-1.62)

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  $\geq 3$ , 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	376	

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
3	FMN	A	402	X	-	X	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5762 atoms, of which 2795 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.

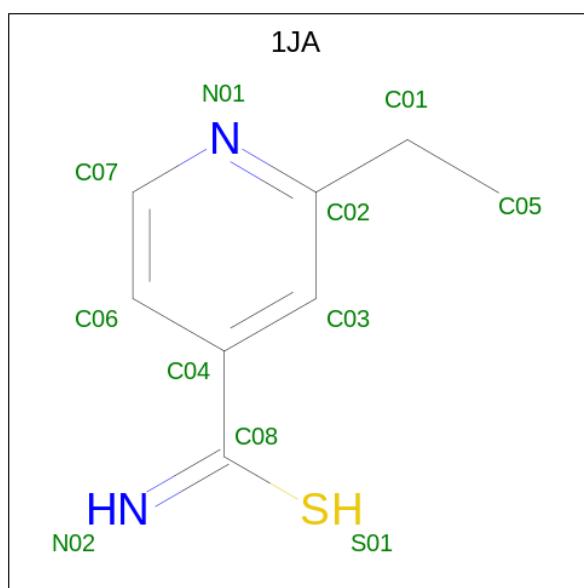
- Molecule 1 is a protein called Rv3094c.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	370	5551	1743	2766	516	515	11	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	VAL	-	expression tag	UNP O05773
A	252	THR	SER	engineered mutation	UNP O05773

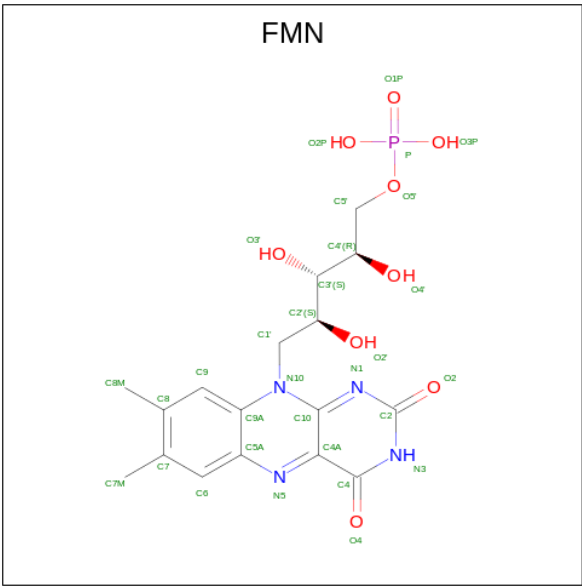
- Molecule 2 is 2-ethylpyridine-4-carboximidothioic acid (three-letter code: 1JA) (formula:  $C_8H_{10}N_2S$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	H	N	S			
2	A	1	21	8	10	2	1		0	0

- Molecule 3 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula:  $C_{17}H_{21}N_4O_9P$ )

(labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	P	0	0
			50	17	19	4	9	1		

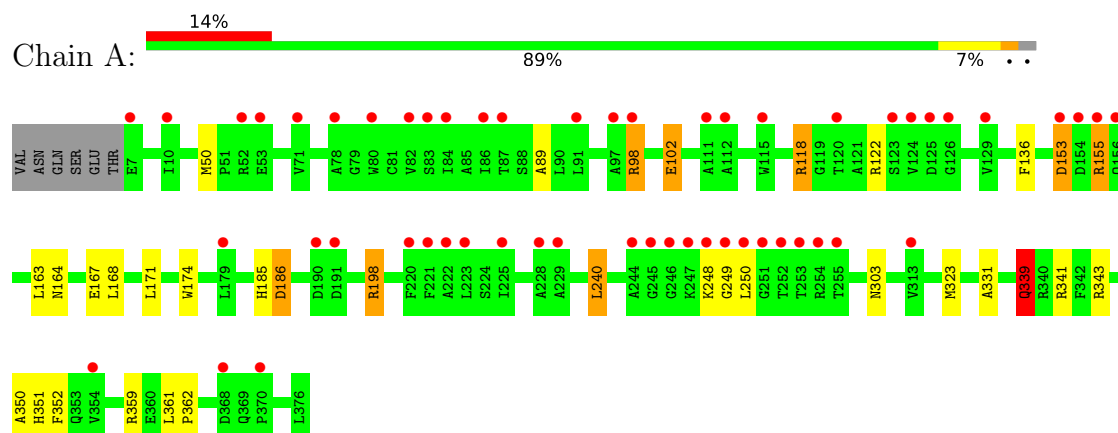
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	140	Total	O	0	0
			140	140		

### 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: Rv3094c



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	134.10Å 134.10Å 109.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.38 – 1.64 35.25 – 1.64	Depositor EDS
% Data completeness (in resolution range)	99.9 (27.38-1.64) 99.9 (35.25-1.64)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.20 (at 1.64Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, $R_{free}$	0.185 , 0.210 0.185 , 0.210	Depositor DCC
$R_{free}$ test set	2961 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.4	Xtriage
Anisotropy	0.156	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.44 , 44.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5762	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: 1JA, 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	0.65	4/2838 (0.1%)	1.12	22/3858 (0.6%)

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 (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	186	ASP	CB-CG	-9.97	1.30	1.51
1	A	118	ARG	CG-CD	8.03	1.72	1.51
1	A	102	GLU	CG-CD	-7.25	1.41	1.51
1	A	240	LEU	CG-CD2	-6.77	1.26	1.51

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	186	ASP	CB-CG-OD1	33.27	148.24	118.30
1	A	186	ASP	OD1-CG-OD2	-17.44	90.16	123.30
1	A	118	ARG	NE-CZ-NH2	-13.48	113.56	120.30
1	A	186	ASP	CB-CG-OD2	-11.82	107.67	118.30
1	A	359	ARG	NE-CZ-NH2	-11.24	114.68	120.30
1	A	98	ARG	NE-CZ-NH2	10.80	125.70	120.30
1	A	240	LEU	CB-CG-CD2	10.75	129.28	111.00
1	A	359	ARG	NE-CZ-NH1	9.59	125.10	120.30
1	A	118	ARG	CD-NE-CZ	8.65	135.71	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	98	ARG	CD-NE-CZ	-8.62	111.53	123.60
1	A	118	ARG	CG-CD-NE	-8.45	94.05	111.80
1	A	155	ARG	NE-CZ-NH1	-7.59	116.50	120.30
1	A	98	ARG	NE-CZ-NH1	-7.41	116.60	120.30
1	A	339	GLN	CG-CD-NE2	-7.31	99.15	116.70
1	A	341	ARG	NE-CZ-NH2	-7.20	116.70	120.30
1	A	118	ARG	NE-CZ-NH1	6.51	123.56	120.30
1	A	198	ARG	NE-CZ-NH1	6.13	123.36	120.30
1	A	155	ARG	NE-CZ-NH2	5.84	123.22	120.30
1	A	359	ARG	CG-CD-NE	5.51	123.37	111.80
1	A	186	ASP	N-CA-C	-5.42	96.37	111.00
1	A	341	ARG	CG-CD-NE	-5.40	100.47	111.80
1	A	155	ARG	CD-NE-CZ	5.11	130.75	123.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	118	ARG	Sidechain
1	A	155	ARG	Sidechain
1	A	186	ASP	Sidechain
1	A	339	GLN	Sidechain

## 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	2785	2766	2764	25	0
2	A	11	10	0	0	0
3	A	31	19	19	15	0
4	A	140	0	0	0	0
All	All	2967	2795	2783	31	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 6.

All (31) 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:102:GLU:OE2	1:A:198:ARG:NH2	1.73	1.20
3:A:402:FMN:H9	3:A:402:FMN:O3'	1.89	0.73
1:A:351:HIS:HA	3:A:402:FMN:H3'	1.71	0.72
1:A:339:GLN:HE21	1:A:343:ARG:HE	1.36	0.71
3:A:402:FMN:O1P	3:A:402:FMN:H4'	1.93	0.68
1:A:248:LYS:HD3	1:A:249:GLY:O	1.92	0.68
1:A:102:GLU:CD	1:A:198:ARG:HH21	1.98	0.67
1:A:136:PHE:CG	3:A:402:FMN:O2'	2.46	0.67
3:A:402:FMN:H9	3:A:402:FMN:C3'	2.33	0.58
1:A:352:PHE:CE1	3:A:402:FMN:H1'2	2.39	0.58
1:A:351:HIS:CD2	3:A:402:FMN:H1'1	2.41	0.56
1:A:174:TRP:CZ2	3:A:402:FMN:HM72	2.42	0.54
1:A:50:MET:HG3	1:A:89:ALA:HB1	1.89	0.53
1:A:136:PHE:CD1	3:A:402:FMN:O2'	2.62	0.53
3:A:402:FMN:O2'	3:A:402:FMN:C9	2.57	0.53
1:A:361:LEU:HB3	1:A:362:PRO:HD3	1.91	0.51
1:A:174:TRP:CH2	3:A:402:FMN:HM72	2.46	0.51
1:A:122:ARG:HA	1:A:153:ASP:OD1	2.11	0.50
1:A:350:ALA:O	3:A:402:FMN:H5'1	2.15	0.47
1:A:163:LEU:HD13	1:A:168:LEU:HD21	1.98	0.45
1:A:98:ARG:HH11	1:A:98:ARG:HD3	1.43	0.44
1:A:171:LEU:O	1:A:185:HIS:HB3	2.18	0.44
1:A:250:LEU:HD12	1:A:250:LEU:HA	1.88	0.44
1:A:303:ASN:OD1	1:A:362:PRO:HA	2.17	0.44
1:A:331:ALA:O	1:A:339:GLN:HB2	2.18	0.43
1:A:240:LEU:HD12	1:A:240:LEU:O	2.19	0.43
3:A:402:FMN:H9	3:A:402:FMN:C2'	2.48	0.43
1:A:164:ASN:HB2	1:A:167:GLU:OE1	2.19	0.43
1:A:352:PHE:CD1	3:A:402:FMN:H1'2	2.53	0.42
1:A:240:LEU:HD23	1:A:323:MET:SD	2.60	0.42
3:A:402:FMN:O2'	3:A:402:FMN:C9A	2.67	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	368/376 (98%)	359 (98%)	8 (2%)	1 (0%)	41	21

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	153	ASP

### 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	275/282 (98%)	275 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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	339	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

2 ligands are modelled in this entry.

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	FMN	A	402	-	1/1/4/4	-	-

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	402	FMN	C3'

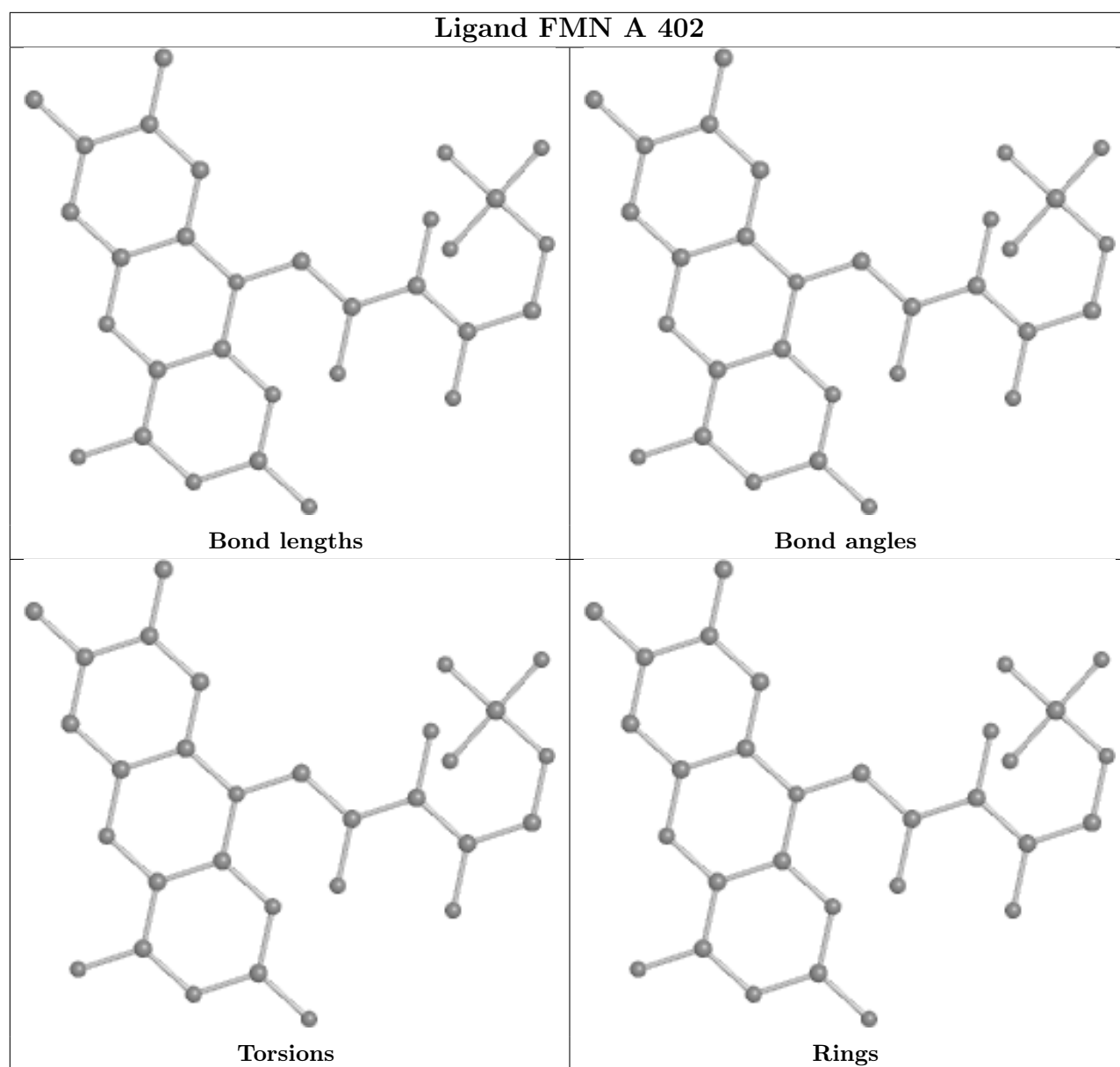
There are no torsion outliers.

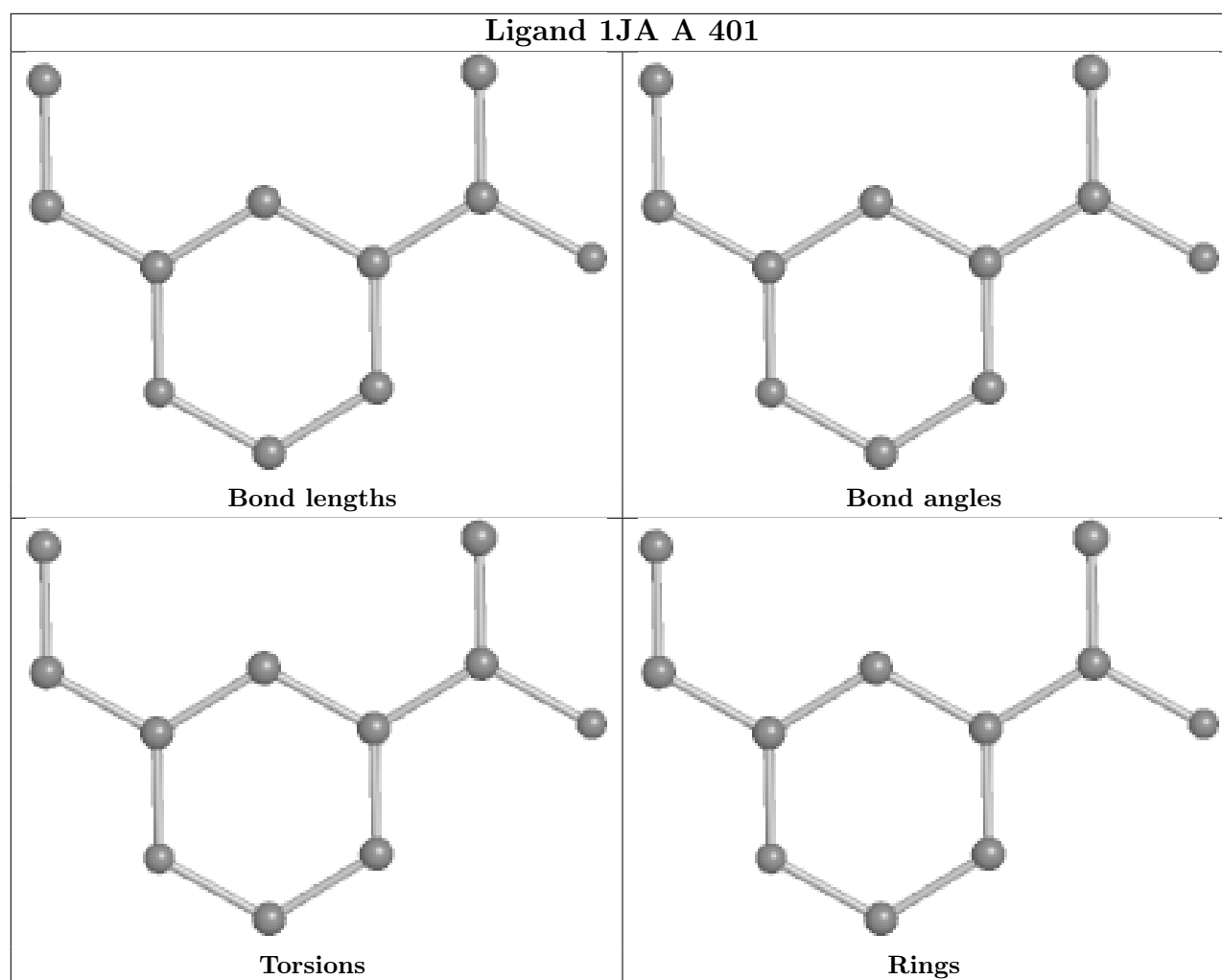
There are no ring outliers.

1 monomer is involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	FMN	15	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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	370/376 (98%)	0.93	54 (14%) 2 2	23, 35, 66, 126	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	252	THR	16.3
1	A	251	GLY	14.6
1	A	245	GLY	9.7
1	A	253	THR	9.6
1	A	254	ARG	9.0
1	A	248	LYS	8.3
1	A	250	LEU	7.9
1	A	125	ASP	7.1
1	A	246	GLY	6.8
1	A	154	ASP	6.1
1	A	124	VAL	5.9
1	A	98	ARG	5.4
1	A	255	THR	5.3
1	A	80	TRP	5.0
1	A	84	ILE	4.9
1	A	249	GLY	4.4
1	A	225	ILE	4.3
1	A	368	ASP	4.2
1	A	370	PRO	4.2
1	A	126	GLY	4.1
1	A	52	ARG	3.7
1	A	223	LEU	3.2
1	A	156	GLN	3.1
1	A	129	VAL	3.1
1	A	82	VAL	3.0
1	A	221	PHE	3.0
1	A	123	SER	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	220	PHE	2.9
1	A	112	ALA	2.9
1	A	10	ILE	2.8
1	A	115	TRP	2.8
1	A	313	VAL	2.8
1	A	87	THR	2.7
1	A	228	ALA	2.7
1	A	354	VAL	2.6
1	A	244	ALA	2.6
1	A	111	ALA	2.5
1	A	191	ASP	2.5
1	A	155	ARG	2.5
1	A	153	ASP	2.5
1	A	120	THR	2.4
1	A	83	SER	2.3
1	A	91	LEU	2.3
1	A	222	ALA	2.3
1	A	86	ILE	2.3
1	A	97	ALA	2.2
1	A	53	GLU	2.2
1	A	71	VAL	2.2
1	A	247	LYS	2.1
1	A	7	GLU	2.1
1	A	179	LEU	2.1
1	A	229	ALA	2.1
1	A	78	ALA	2.1
1	A	190	ASP	2.0

## 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 monosaccharides 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,

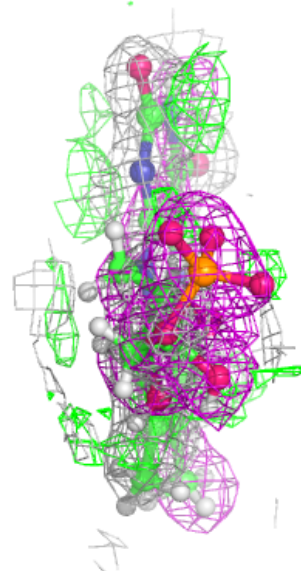
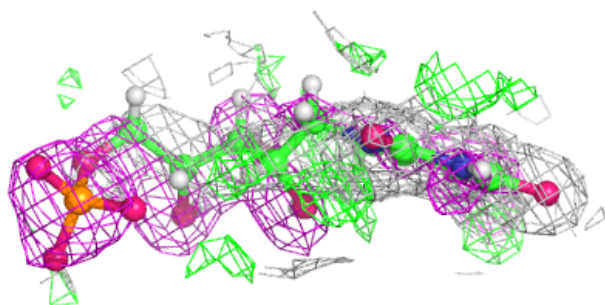
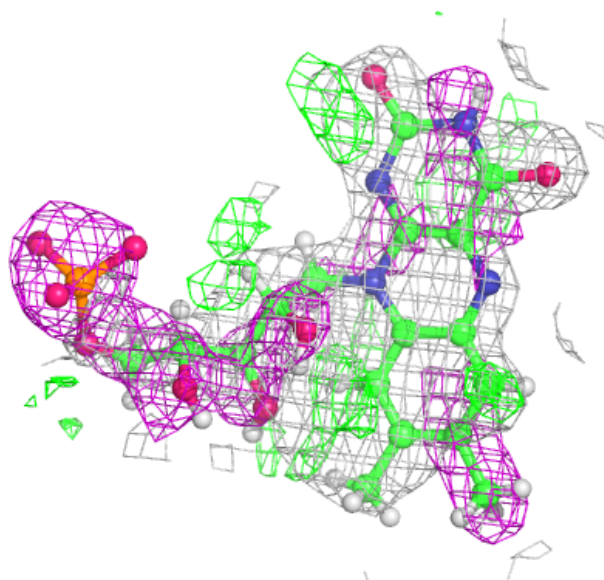
median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	FMN	A	402	31/31	0.48	0.33	40,53,68,91	0
2	1JA	A	401	11/11	0.78	0.30	42,63,85,102	21

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

**Electron density around FMN A 402:**

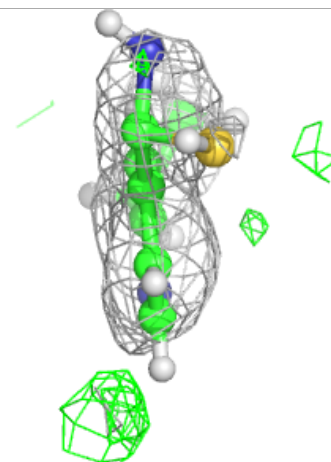
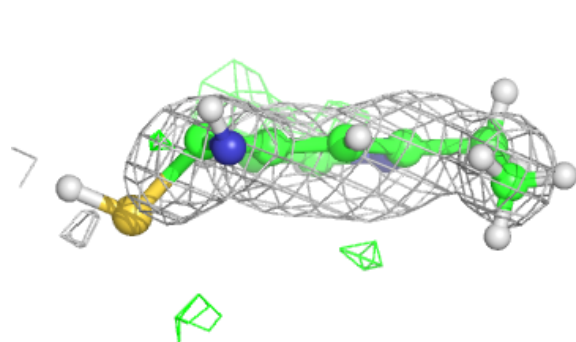
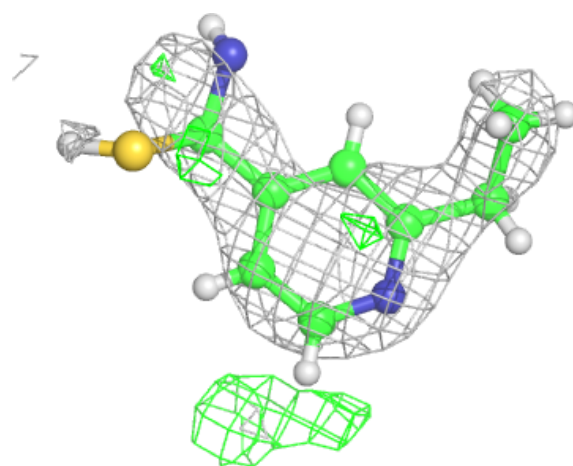
2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around 1JA A 401:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.