



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 16, 2024 – 08:11 PM EDT

PDB ID : 5HEI  
Title : Structure of B. megaterium NfrA2  
Authors : Vigouroux, A.; Morera, S.  
Deposited on : 2016-01-06  
Resolution : 2.84 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

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<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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
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)	:	2.37.1

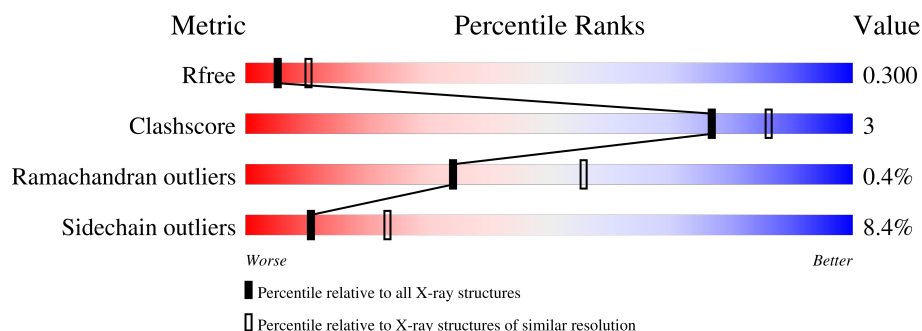
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.84 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	1031 (2.86-2.82)
Clashscore	141614	1078 (2.86-2.82)
Ramachandran outliers	138981	1050 (2.86-2.82)
Sidechain outliers	138945	1051 (2.86-2.82)

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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	253	82% 15% ..
1	B	253	82% 15% .
1	C	253	83% 14% .
1	D	253	83% 13% ..
1	E	253	85% 11% ..
1	F	253	83% 13% ..
1	G	253	85% 11% ..

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Mol	Chain	Length	Quality of chain
1	H	253	<div><div></div><div>80%</div><div>15%</div><div>• •</div></div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15833 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 NfrA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	246	Total	C	N	O	S	0	0	0
			1913	1202	332	374	5			
1	B	246	Total	C	N	O	S	0	0	0
			1913	1202	332	374	5			
1	C	245	Total	C	N	O	S	0	0	0
			1905	1197	331	373	4			
1	D	246	Total	C	N	O	S	0	0	0
			1913	1202	332	374	5			
1	E	246	Total	C	N	O	S	0	0	0
			1913	1202	332	374	5			
1	F	246	Total	C	N	O	S	0	0	0
			1913	1202	332	374	5			
1	G	246	Total	C	N	O	S	0	0	0
			1913	1202	332	374	5			
1	H	246	Total	C	N	O	S	0	0	0
			1913	1202	332	374	5			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	246	LYS	-	expression tag	UNP A0A0K0VJM8
A	247	GLY	-	expression tag	UNP A0A0K0VJM8
A	248	HIS	-	expression tag	UNP A0A0K0VJM8
A	249	HIS	-	expression tag	UNP A0A0K0VJM8
A	250	HIS	-	expression tag	UNP A0A0K0VJM8
A	251	HIS	-	expression tag	UNP A0A0K0VJM8
A	252	HIS	-	expression tag	UNP A0A0K0VJM8
A	253	HIS	-	expression tag	UNP A0A0K0VJM8
B	246	LYS	-	expression tag	UNP A0A0K0VJM8
B	247	GLY	-	expression tag	UNP A0A0K0VJM8
B	248	HIS	-	expression tag	UNP A0A0K0VJM8
B	249	HIS	-	expression tag	UNP A0A0K0VJM8
B	250	HIS	-	expression tag	UNP A0A0K0VJM8

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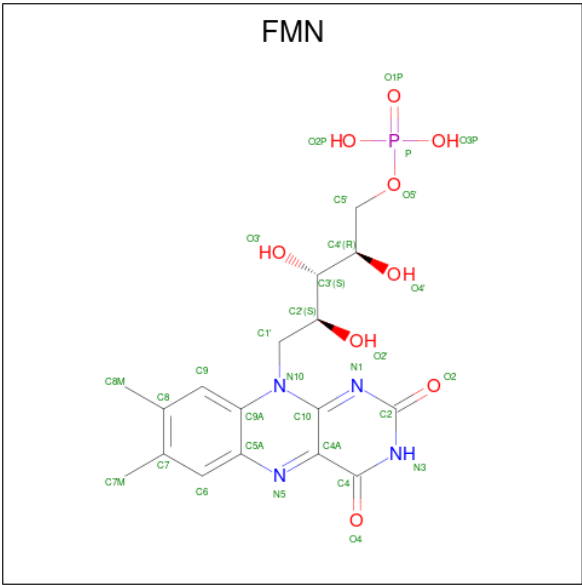
Chain	Residue	Modelled	Actual	Comment	Reference
B	251	HIS	-	expression tag	UNP A0A0K0VJM8
B	252	HIS	-	expression tag	UNP A0A0K0VJM8
B	253	HIS	-	expression tag	UNP A0A0K0VJM8
C	246	LYS	-	expression tag	UNP A0A0K0VJM8
C	247	GLY	-	expression tag	UNP A0A0K0VJM8
C	248	HIS	-	expression tag	UNP A0A0K0VJM8
C	249	HIS	-	expression tag	UNP A0A0K0VJM8
C	250	HIS	-	expression tag	UNP A0A0K0VJM8
C	251	HIS	-	expression tag	UNP A0A0K0VJM8
C	252	HIS	-	expression tag	UNP A0A0K0VJM8
C	253	HIS	-	expression tag	UNP A0A0K0VJM8
D	246	LYS	-	expression tag	UNP A0A0K0VJM8
D	247	GLY	-	expression tag	UNP A0A0K0VJM8
D	248	HIS	-	expression tag	UNP A0A0K0VJM8
D	249	HIS	-	expression tag	UNP A0A0K0VJM8
D	250	HIS	-	expression tag	UNP A0A0K0VJM8
D	251	HIS	-	expression tag	UNP A0A0K0VJM8
D	252	HIS	-	expression tag	UNP A0A0K0VJM8
D	253	HIS	-	expression tag	UNP A0A0K0VJM8
E	246	LYS	-	expression tag	UNP A0A0K0VJM8
E	247	GLY	-	expression tag	UNP A0A0K0VJM8
E	248	HIS	-	expression tag	UNP A0A0K0VJM8
E	249	HIS	-	expression tag	UNP A0A0K0VJM8
E	250	HIS	-	expression tag	UNP A0A0K0VJM8
E	251	HIS	-	expression tag	UNP A0A0K0VJM8
E	252	HIS	-	expression tag	UNP A0A0K0VJM8
E	253	HIS	-	expression tag	UNP A0A0K0VJM8
F	246	LYS	-	expression tag	UNP A0A0K0VJM8
F	247	GLY	-	expression tag	UNP A0A0K0VJM8
F	248	HIS	-	expression tag	UNP A0A0K0VJM8
F	249	HIS	-	expression tag	UNP A0A0K0VJM8
F	250	HIS	-	expression tag	UNP A0A0K0VJM8
F	251	HIS	-	expression tag	UNP A0A0K0VJM8
F	252	HIS	-	expression tag	UNP A0A0K0VJM8
F	253	HIS	-	expression tag	UNP A0A0K0VJM8
G	246	LYS	-	expression tag	UNP A0A0K0VJM8
G	247	GLY	-	expression tag	UNP A0A0K0VJM8
G	248	HIS	-	expression tag	UNP A0A0K0VJM8
G	249	HIS	-	expression tag	UNP A0A0K0VJM8
G	250	HIS	-	expression tag	UNP A0A0K0VJM8
G	251	HIS	-	expression tag	UNP A0A0K0VJM8
G	252	HIS	-	expression tag	UNP A0A0K0VJM8

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Chain	Residue	Modelled	Actual	Comment	Reference
G	253	HIS	-	expression tag	UNP A0A0K0VJM8
H	246	LYS	-	expression tag	UNP A0A0K0VJM8
H	247	GLY	-	expression tag	UNP A0A0K0VJM8
H	248	HIS	-	expression tag	UNP A0A0K0VJM8
H	249	HIS	-	expression tag	UNP A0A0K0VJM8
H	250	HIS	-	expression tag	UNP A0A0K0VJM8
H	251	HIS	-	expression tag	UNP A0A0K0VJM8
H	252	HIS	-	expression tag	UNP A0A0K0VJM8
H	253	HIS	-	expression tag	UNP A0A0K0VJM8

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C<sub>17</sub>H<sub>21</sub>N<sub>4</sub>O<sub>9</sub>P).



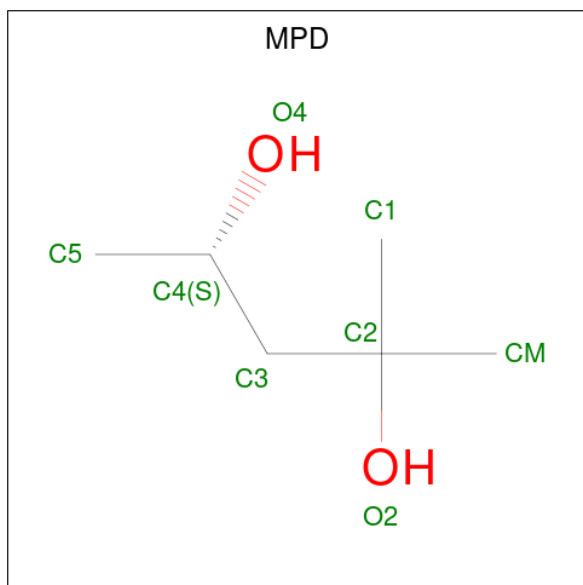
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	C	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	D	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	E	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	F	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	G	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

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

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula:  $C_6H_{14}O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			8	6	2		
3	H	1	Total	C	O	0	0
			8	6	2		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	G	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	23	Total	O	0	0
			23	23		
5	B	26	Total	O	0	0
			26	26		
5	C	41	Total	O	0	0
			41	41		
5	D	40	Total	O	0	0
			40	40		
5	E	19	Total	O	0	0
			19	19		
5	F	16	Total	O	0	0
			16	16		
5	G	36	Total	O	0	0
			36	36		

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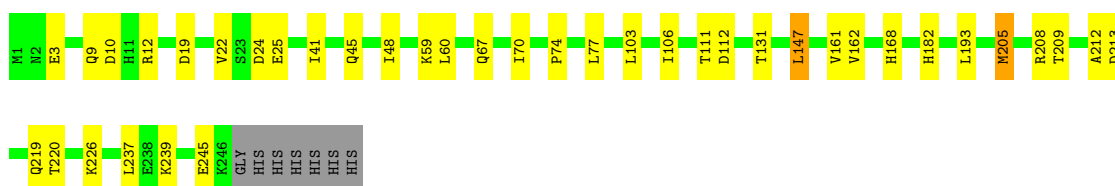
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	47	Total	O	0	0
			47	47		

### 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.

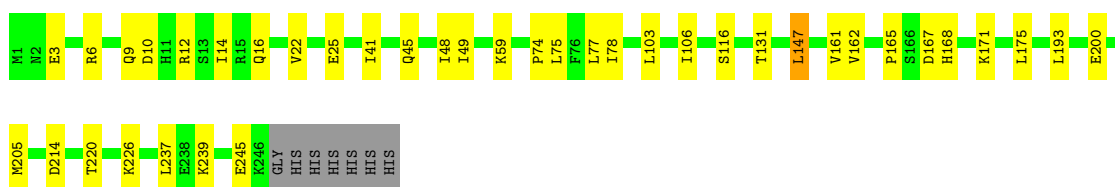
- Molecule 1: NfrA2

Chain A: 




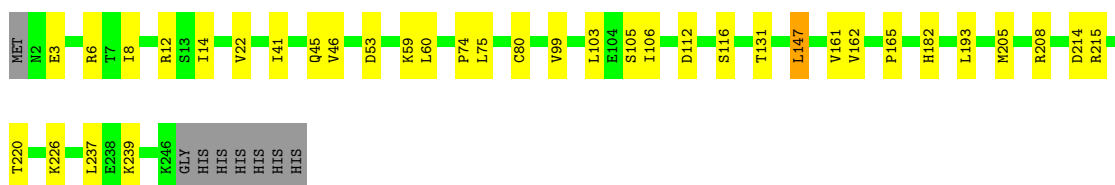
- Molecule 1: NfrA2

Chain B: 




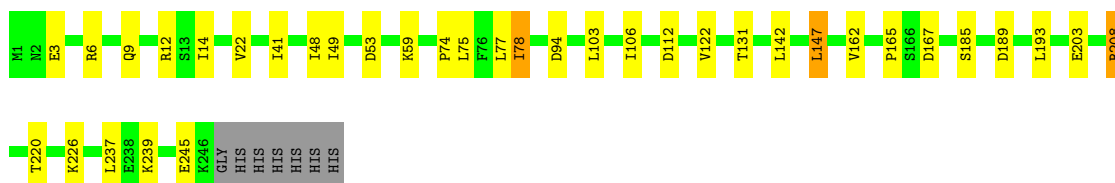
- Molecule 1: NfrA2

Chain C: 


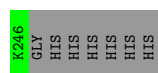
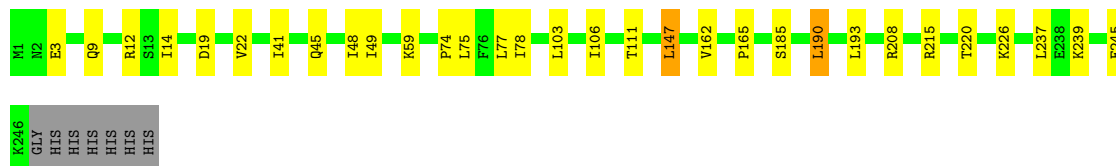


- Molecule 1: NfrA2


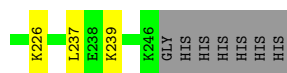
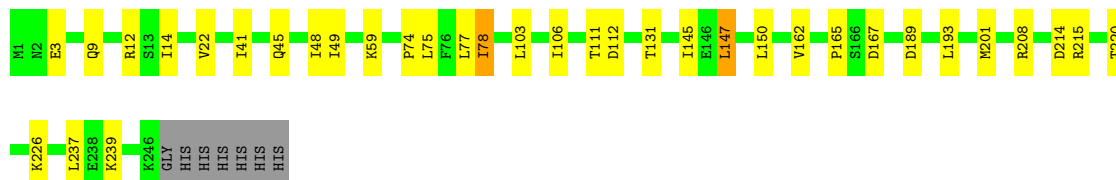
Chain D: 




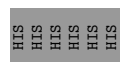
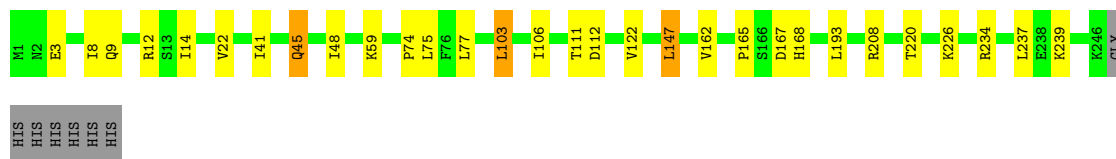
## ● Molecule 1: NfrA2

Chain E:  85% 11% ..


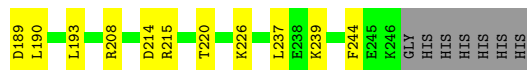
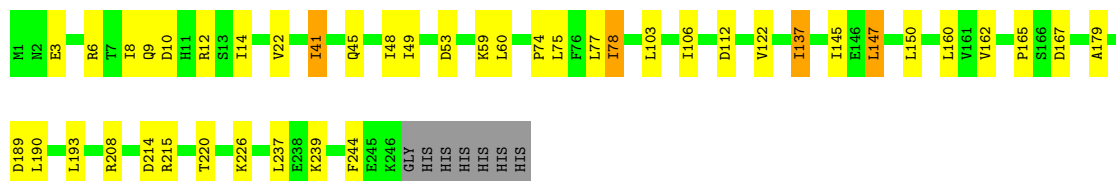
## ● Molecule 1: NfrA2

Chain F:  83% 13% ..

## ● Molecule 1: NfrA2

Chain G:  85% 11% ..

## ● Molecule 1: NfrA2

Chain H:  80% 15% ..

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.44Å 158.19Å 103.86Å 90.00° 102.21° 90.00°	Depositor
Resolution (Å)	28.63 – 2.84 48.33 – 2.84	Depositor EDS
% Data completeness (in resolution range)	97.2 (28.63-2.84) 97.3 (48.33-2.84)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.24	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.49 (at 2.86Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, $R_{free}$	0.203 , 0.247 0.251 , 0.300	Depositor DCC
$R_{free}$ test set	2222 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.8	Xtriage
Anisotropy	0.909	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 66.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	15833	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 35.91 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.4182e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MPD, FMN, SO4

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	0.41	0/1947	0.63	0/2636
1	B	0.41	0/1947	0.63	0/2636
1	C	0.42	0/1939	0.64	0/2626
1	D	0.41	0/1947	0.64	0/2636
1	E	0.41	0/1947	0.65	1/2636 (0.0%)
1	F	0.40	0/1947	0.62	0/2636
1	G	0.42	0/1947	0.63	0/2636
1	H	0.41	0/1947	0.63	0/2636
All	All	0.41	0/15568	0.63	1/21078 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	190	LEU	CA-CB-CG	6.03	129.17	115.30

There are no chirality outliers.

There are no planarity outliers.

### 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	1913	0	1906	16	0
1	B	1913	0	1906	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1905	0	1894	11	0
1	D	1913	0	1906	12	0
1	E	1913	0	1906	9	0
1	F	1913	0	1906	11	0
1	G	1913	0	1906	13	0
1	H	1913	0	1906	20	0
2	A	31	0	19	0	0
2	B	31	0	19	0	0
2	C	31	0	19	0	0
2	D	31	0	19	0	0
2	E	31	0	19	0	0
2	F	31	0	19	0	0
2	G	31	0	19	0	0
2	H	31	0	19	0	0
3	C	8	0	14	0	0
3	H	8	0	14	1	0
4	C	5	0	0	0	0
4	D	10	0	0	0	0
4	G	5	0	0	0	0
4	H	5	0	0	0	0
5	A	23	0	0	0	0
5	B	26	0	0	0	0
5	C	41	0	0	0	0
5	D	40	0	0	0	0
5	E	19	0	0	0	0
5	F	16	0	0	0	0
5	G	36	0	0	0	0
5	H	47	0	0	0	0
All	All	15833	0	15416	92	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 3.

The worst 5 of 92 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:E:3:GLU:HB3	1:F:3:GLU:HB3	1.63	0.80
1:G:103:LEU:HD11	1:H:244:PHE:CZ	2.19	0.77
1:D:48:ILE:HD11	1:D:77:LEU:HB3	1.66	0.76
1:H:48:ILE:HD11	1:H:77:LEU:HB3	1.67	0.76
1:C:14:ILE:HG21	1:C:165:PRO:HB3	1.68	0.76

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	244/253 (96%)	234 (96%)	9 (4%)	1 (0%)	34	56
1	B	244/253 (96%)	234 (96%)	9 (4%)	1 (0%)	34	56
1	C	243/253 (96%)	234 (96%)	8 (3%)	1 (0%)	34	56
1	D	244/253 (96%)	236 (97%)	7 (3%)	1 (0%)	34	56
1	E	244/253 (96%)	236 (97%)	7 (3%)	1 (0%)	34	56
1	F	244/253 (96%)	236 (97%)	7 (3%)	1 (0%)	34	56
1	G	244/253 (96%)	235 (96%)	8 (3%)	1 (0%)	34	56
1	H	244/253 (96%)	235 (96%)	8 (3%)	1 (0%)	34	56
All	All	1951/2024 (96%)	1880 (96%)	63 (3%)	8 (0%)	34	56

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	ILE
1	B	41	ILE
1	E	41	ILE
1	F	41	ILE
1	H	41	ILE

### 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	205/211 (97%)	184 (90%)	21 (10%)	7	15
1	B	205/211 (97%)	187 (91%)	18 (9%)	10	21
1	C	204/211 (97%)	187 (92%)	17 (8%)	11	24
1	D	205/211 (97%)	185 (90%)	20 (10%)	8	16
1	E	205/211 (97%)	191 (93%)	14 (7%)	16	31
1	F	205/211 (97%)	189 (92%)	16 (8%)	12	26
1	G	205/211 (97%)	191 (93%)	14 (7%)	16	31
1	H	205/211 (97%)	187 (91%)	18 (9%)	10	21
All	All	1639/1688 (97%)	1501 (92%)	138 (8%)	11	23

5 of 138 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	193	LEU
1	G	239	LYS
1	H	147	LEU
1	C	116	SER
1	C	112	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	210	ASN
1	E	9	GLN
1	H	9	GLN
1	F	210	ASN
1	G	9	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 [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

15 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
2	FMN	B	301	-	33,33,33	0.28	0	48,50,50	0.60	1 (2%)
4	SO4	H	303	-	4,4,4	0.16	0	6,6,6	0.15	0
2	FMN	D	301	-	33,33,33	0.32	0	48,50,50	0.59	1 (2%)
2	FMN	E	301	-	33,33,33	0.33	0	48,50,50	0.61	1 (2%)
3	MPD	C	302	-	7,7,7	1.04	1 (14%)	9,10,10	0.43	0
2	FMN	C	301	-	33,33,33	0.34	0	48,50,50	0.60	1 (2%)
4	SO4	G	302	-	4,4,4	0.12	0	6,6,6	0.10	0
2	FMN	A	301	-	33,33,33	0.34	0	48,50,50	0.62	1 (2%)
4	SO4	D	302	-	4,4,4	0.44	0	6,6,6	0.55	0
2	FMN	G	301	-	33,33,33	0.30	0	48,50,50	0.58	1 (2%)
4	SO4	C	303	-	4,4,4	0.16	0	6,6,6	0.09	0
4	SO4	D	303	-	4,4,4	0.20	0	6,6,6	0.17	0
2	FMN	F	301	-	33,33,33	0.33	0	48,50,50	0.61	1 (2%)
3	MPD	H	302	-	7,7,7	0.69	0	9,10,10	0.52	0
2	FMN	H	301	-	33,33,33	0.35	0	48,50,50	0.60	1 (2%)

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	B	301	-	-	3/18/18/18	0/3/3/3
2	FMN	D	301	-	-	3/18/18/18	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FMN	E	301	-	-	3/18/18/18	0/3/3/3
3	MPD	C	302	-	-	2/5/5/5	-
2	FMN	C	301	-	-	2/18/18/18	0/3/3/3
2	FMN	A	301	-	-	3/18/18/18	0/3/3/3
2	FMN	G	301	-	-	3/18/18/18	0/3/3/3
2	FMN	F	301	-	-	3/18/18/18	0/3/3/3
3	MPD	H	302	-	-	3/5/5/5	-
2	FMN	H	301	-	-	3/18/18/18	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	302	MPD	C3-C2	2.49	1.60	1.53

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	301	FMN	P-O5'-C5'	2.88	126.24	118.30
2	A	301	FMN	P-O5'-C5'	2.76	125.90	118.30
2	F	301	FMN	P-O5'-C5'	2.73	125.82	118.30
2	C	301	FMN	P-O5'-C5'	2.66	125.62	118.30
2	B	301	FMN	P-O5'-C5'	2.65	125.60	118.30

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

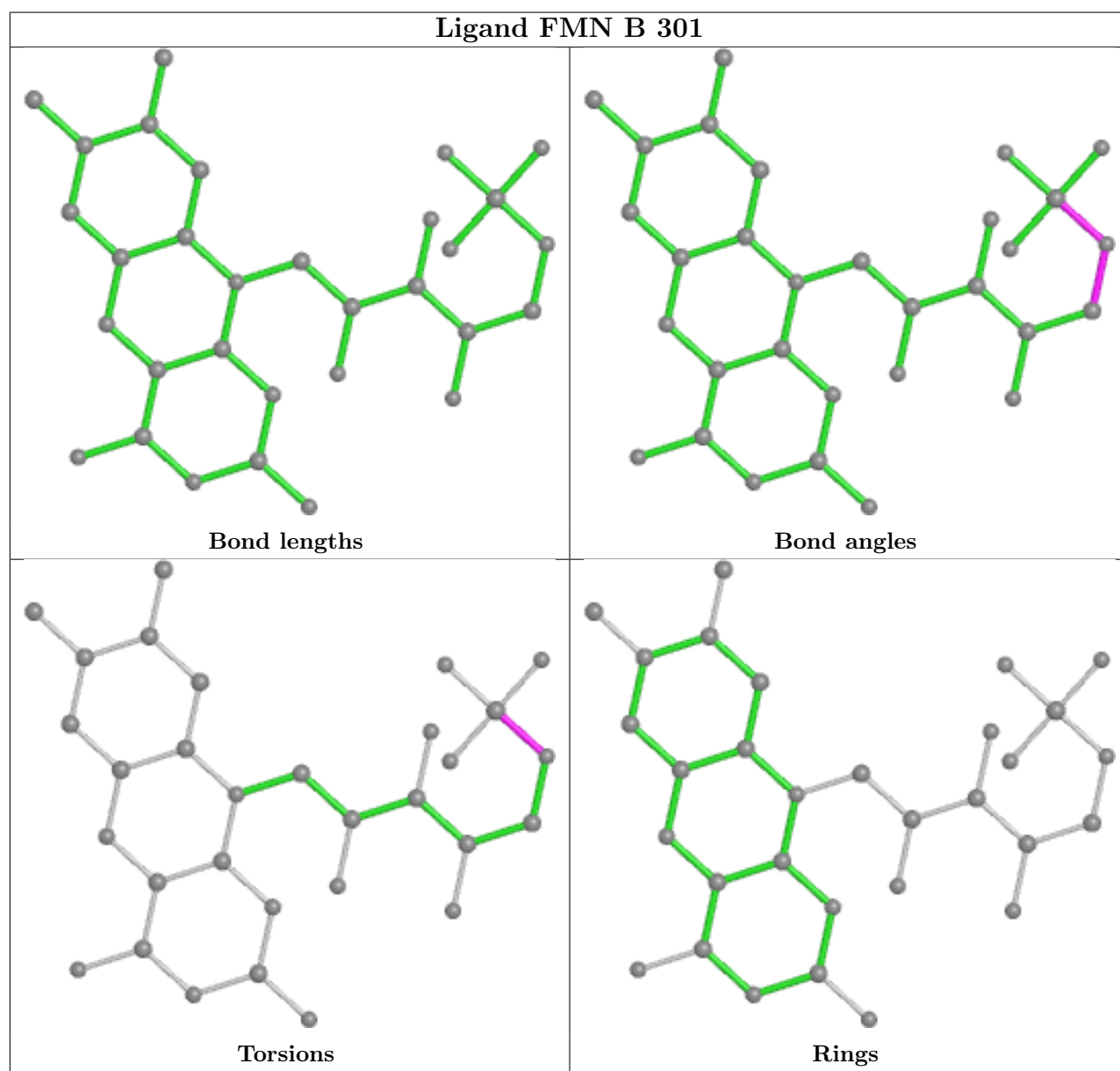
Mol	Chain	Res	Type	Atoms
2	A	301	FMN	C5'-O5'-P-O1P
2	A	301	FMN	C5'-O5'-P-O2P
2	B	301	FMN	C5'-O5'-P-O1P
2	B	301	FMN	C5'-O5'-P-O2P
2	C	301	FMN	C5'-O5'-P-O1P

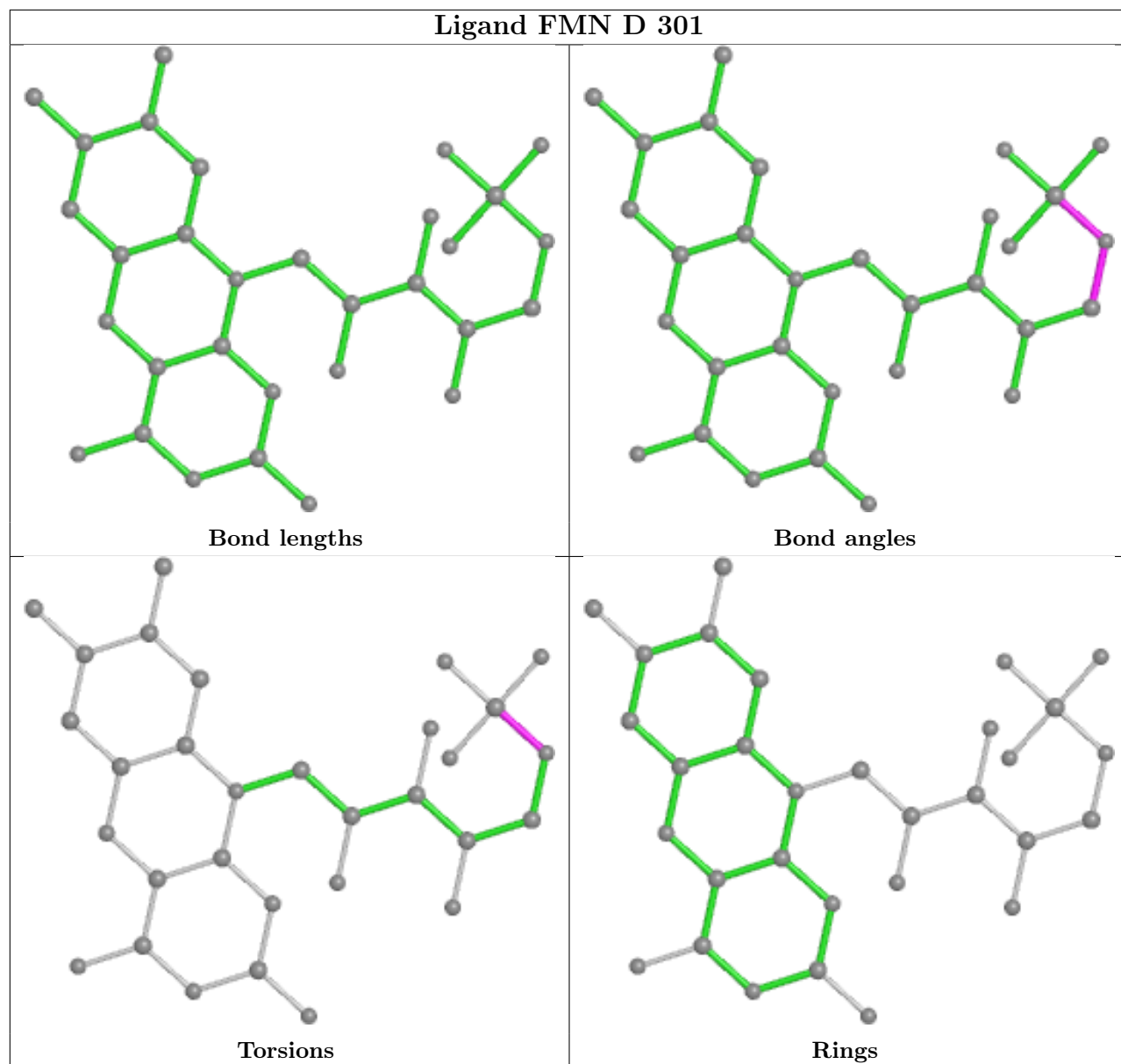
There are no ring outliers.

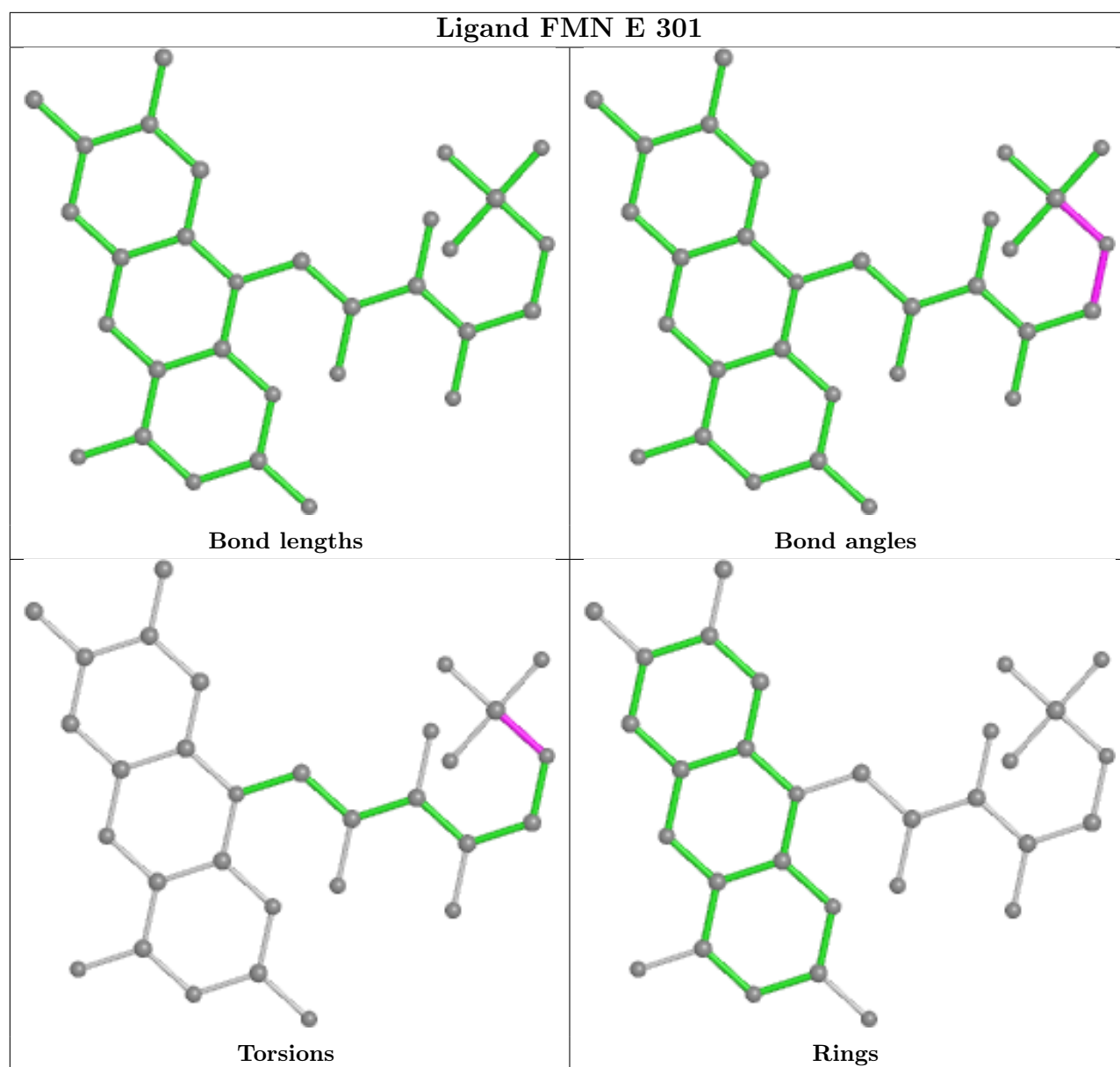
1 monomer is involved in 1 short contact:

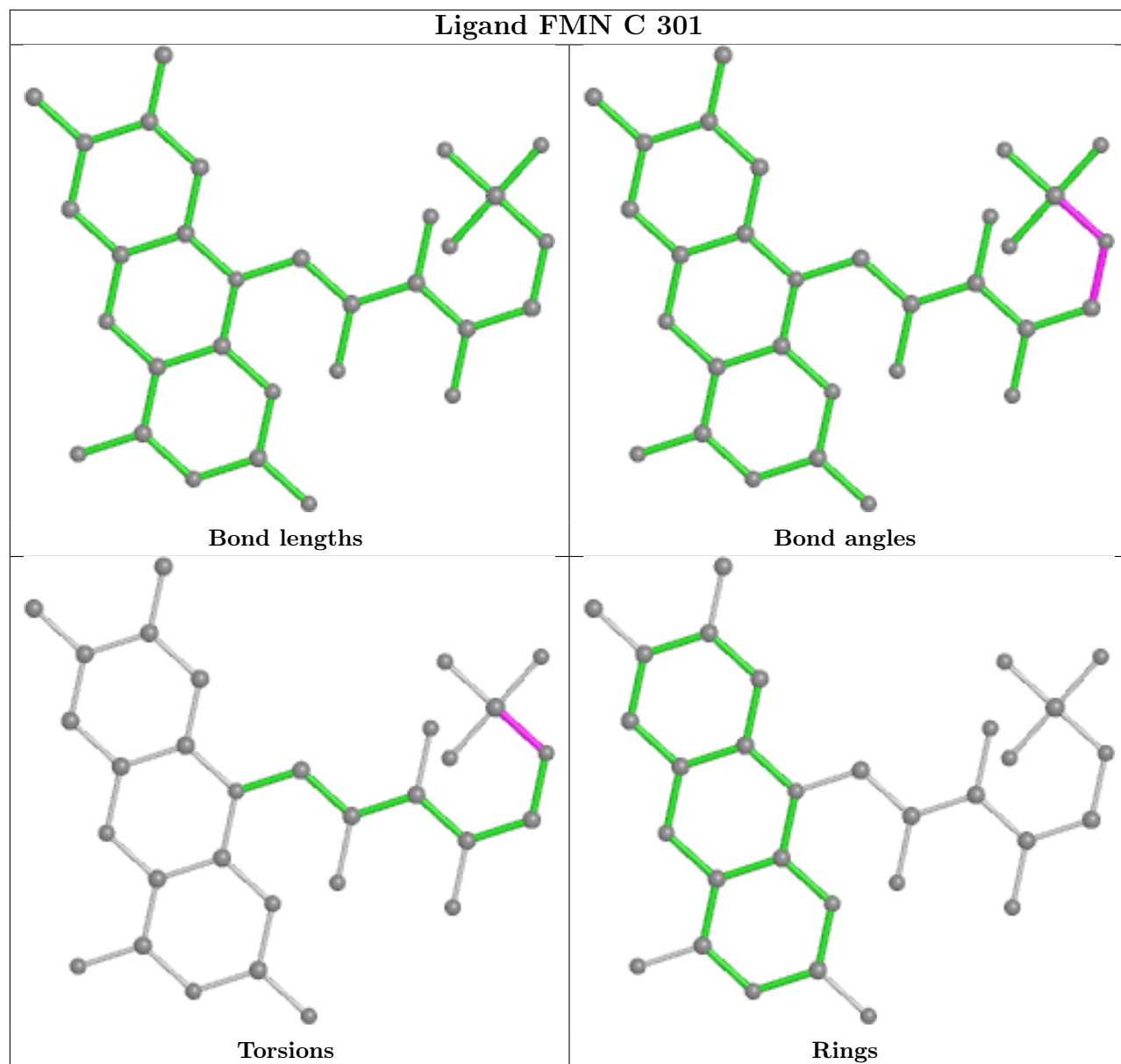
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	302	MPD	1	0

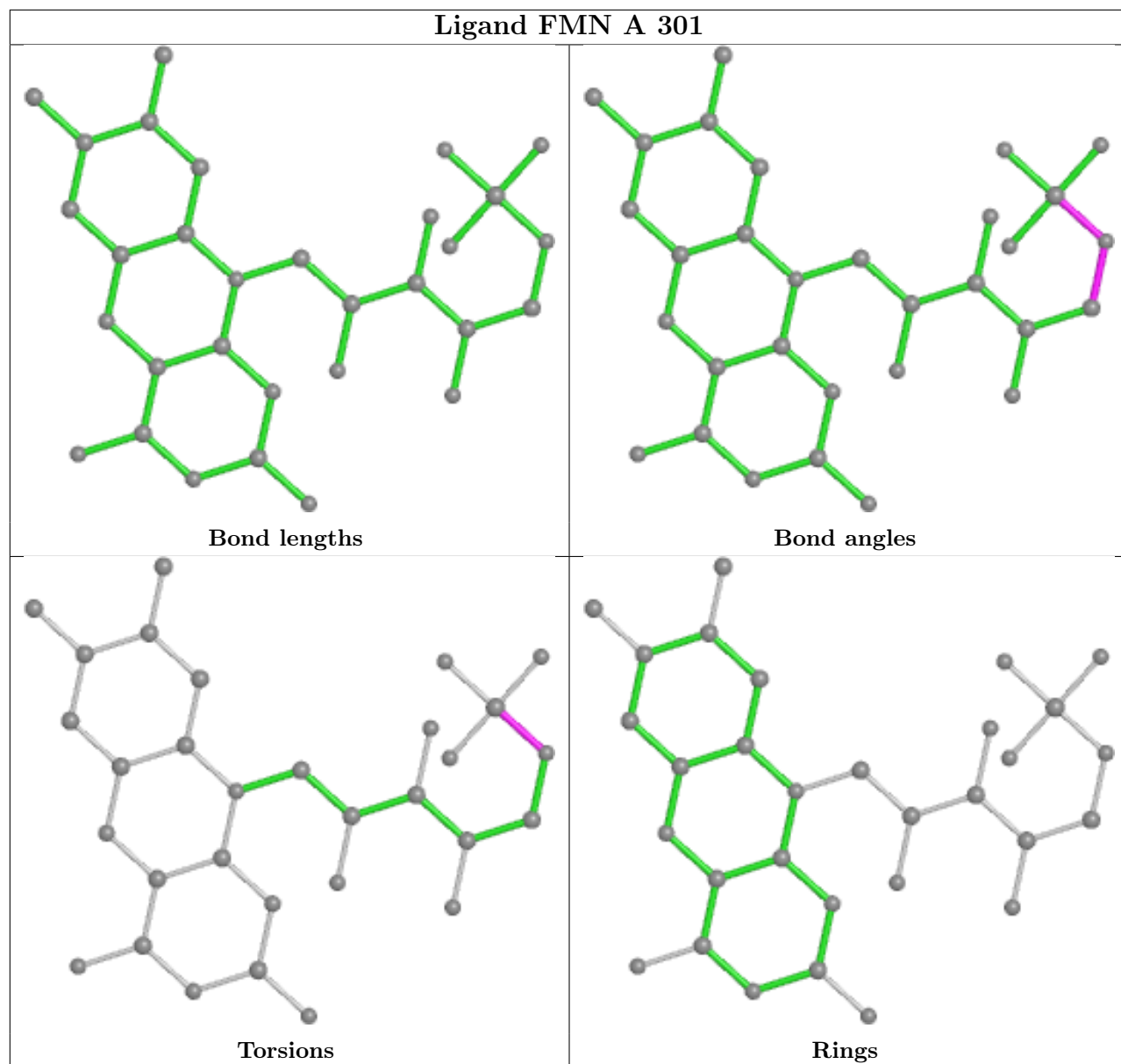
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

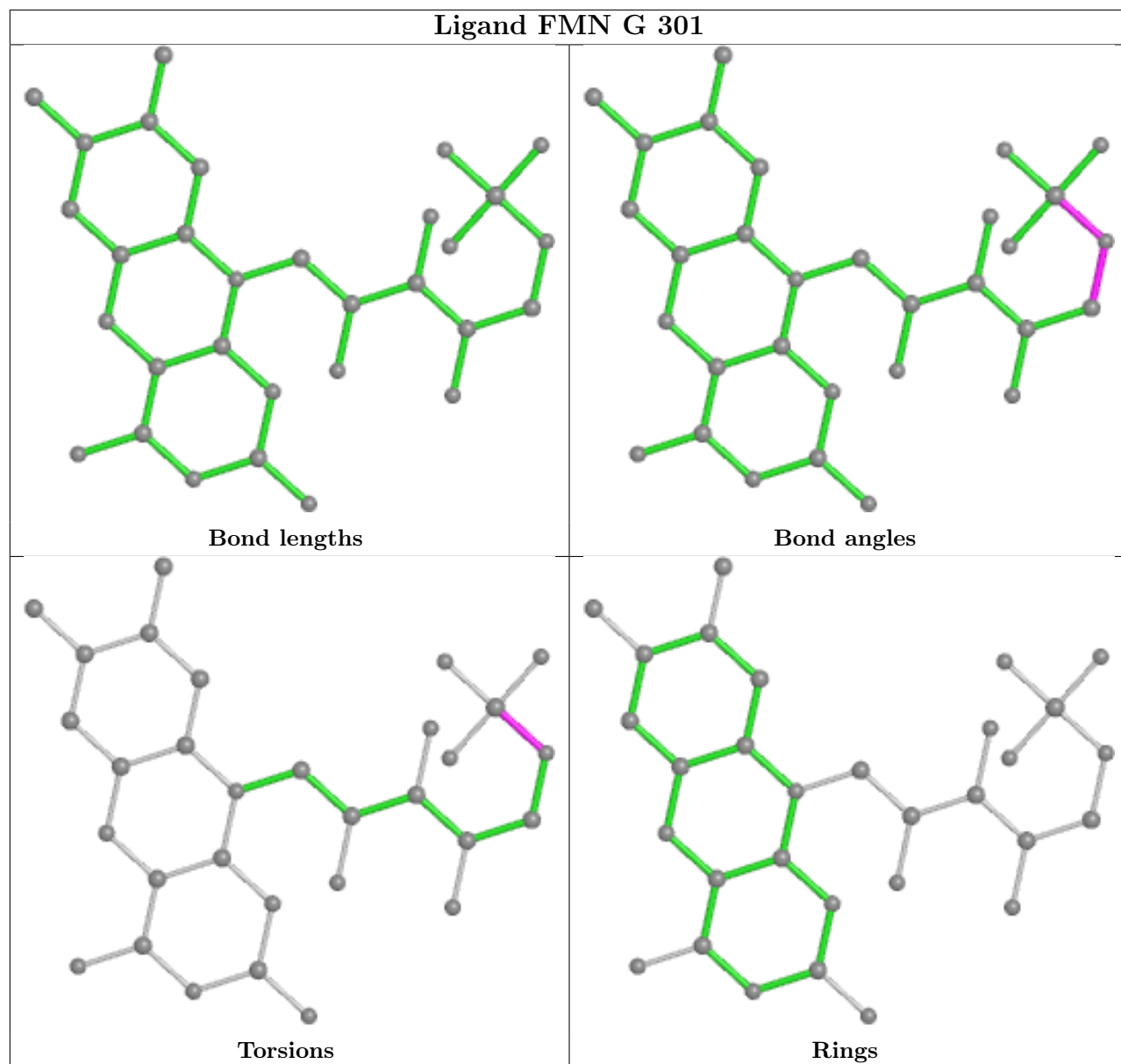




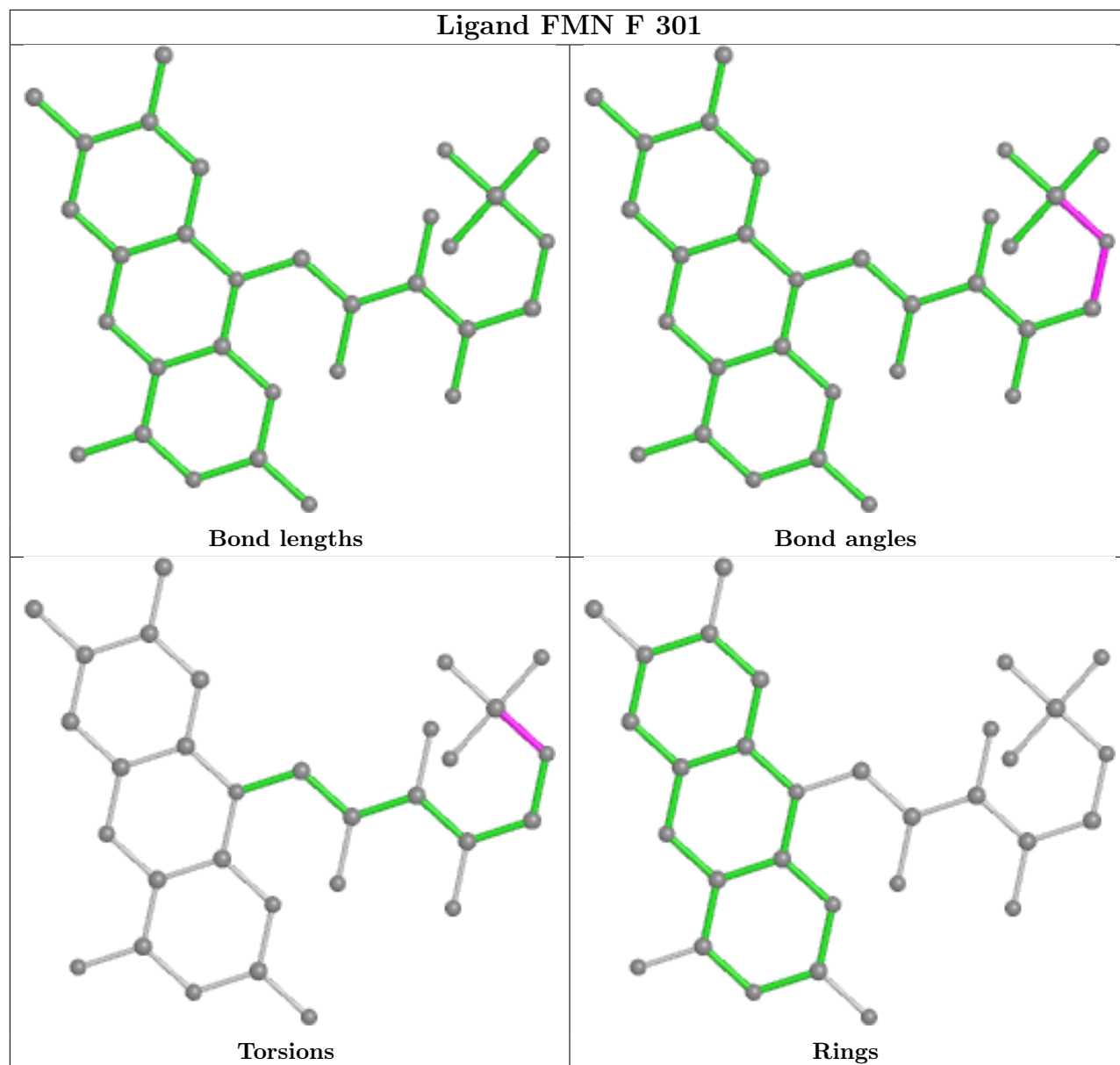


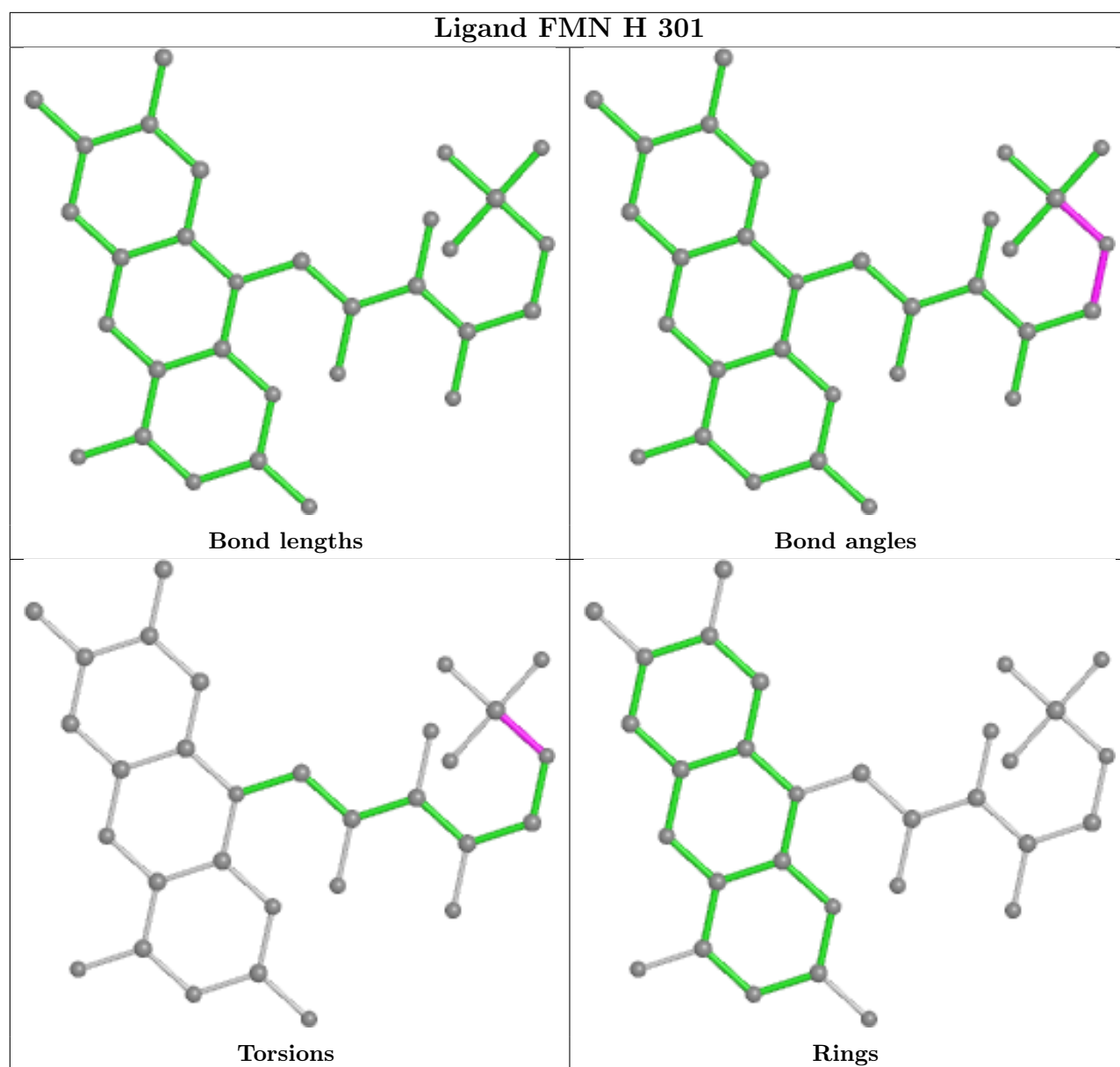












## 5.7 Other polymers [i](#)

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

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.

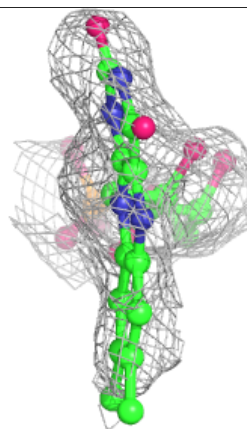
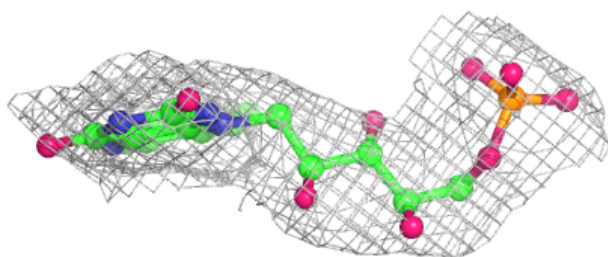
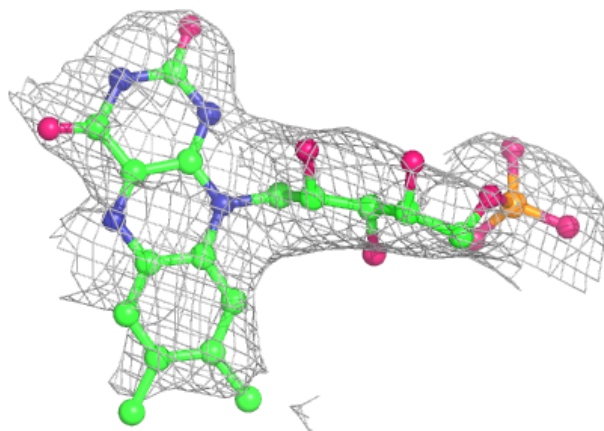
### 6.4 Ligands

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.

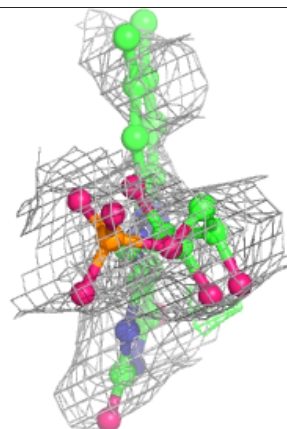
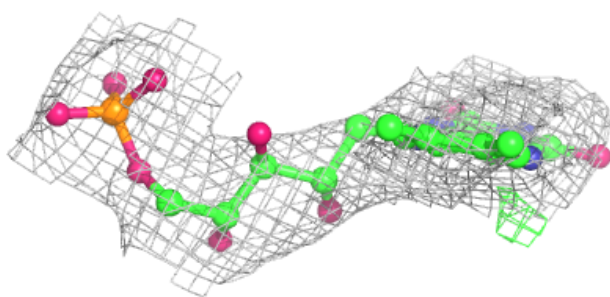
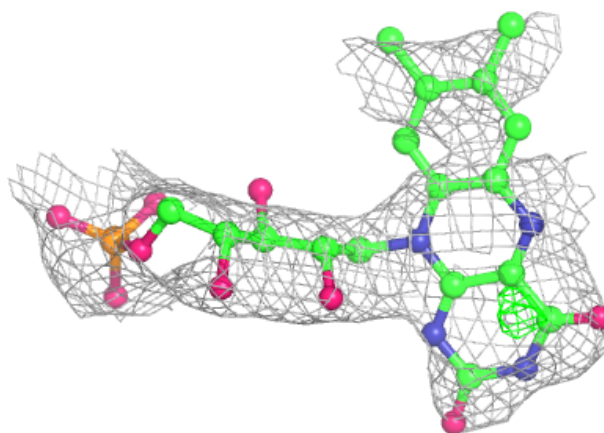
**Electron density around FMN A 301:**

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



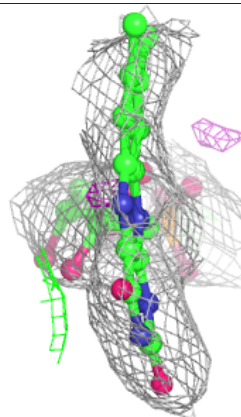
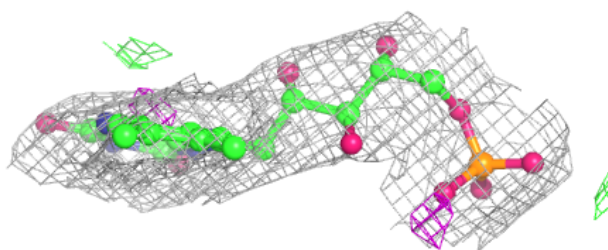
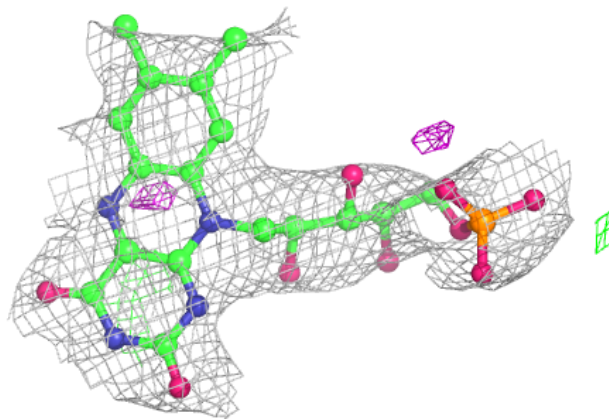
**Electron density around FMN B 301:**

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



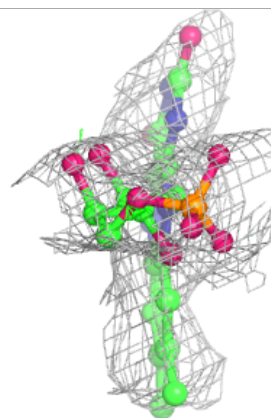
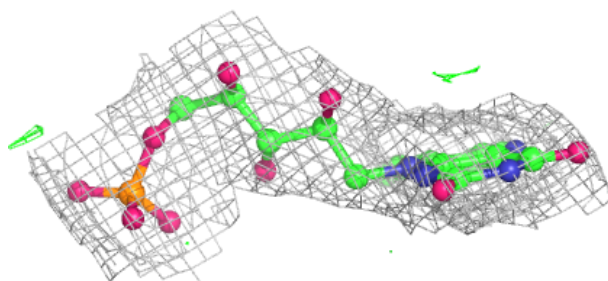
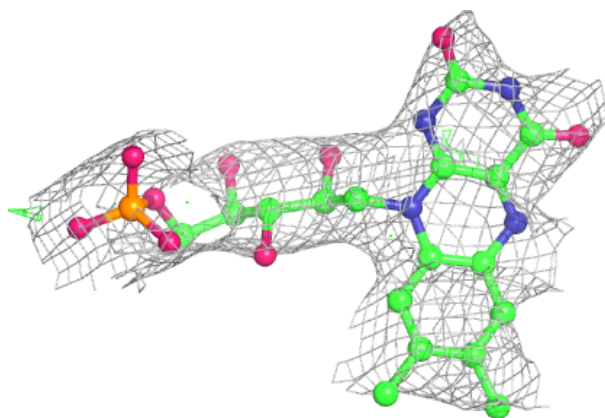
**Electron density around FMN C 301:**

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



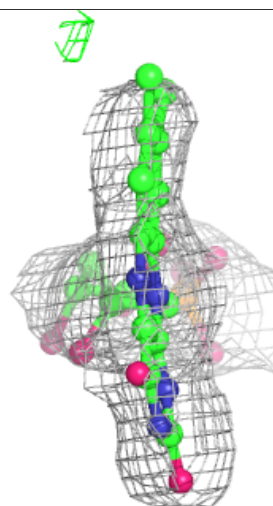
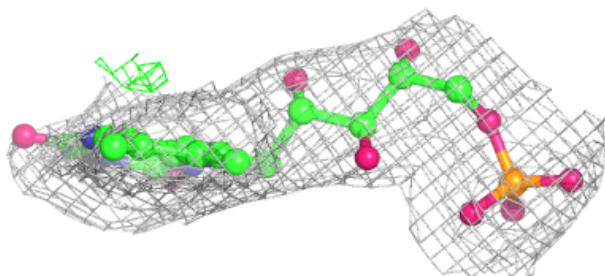
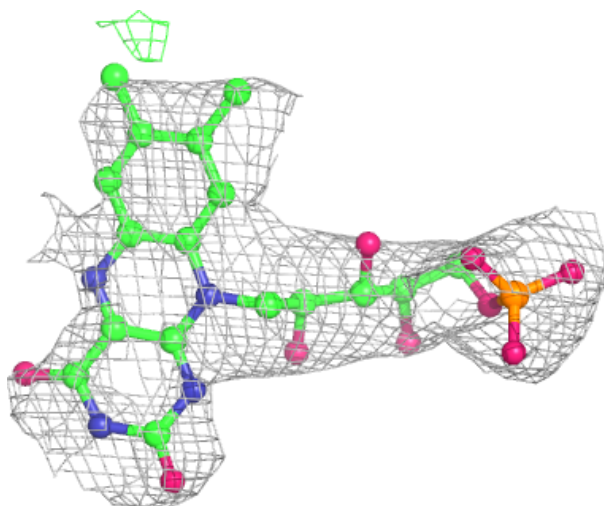
**Electron density around FMN D 301:**

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



**Electron density around FMN E 301:**

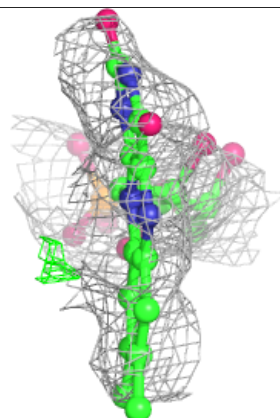
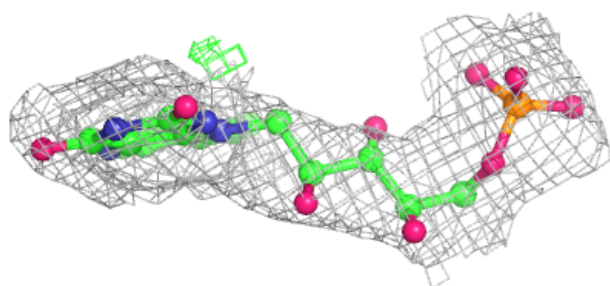
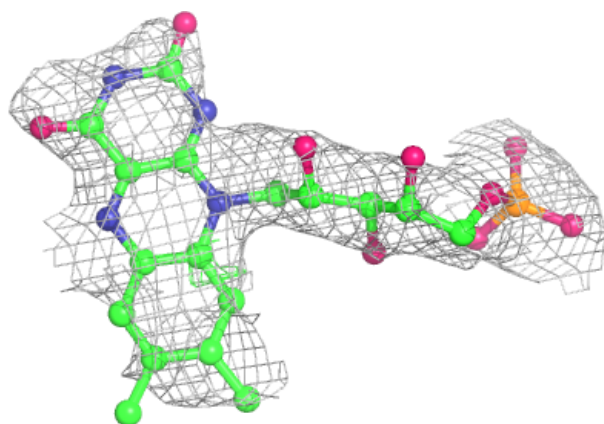
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





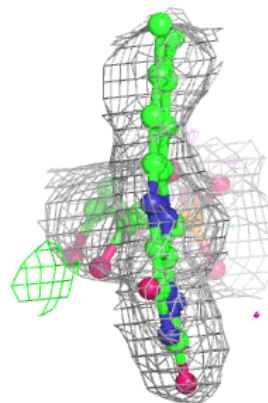
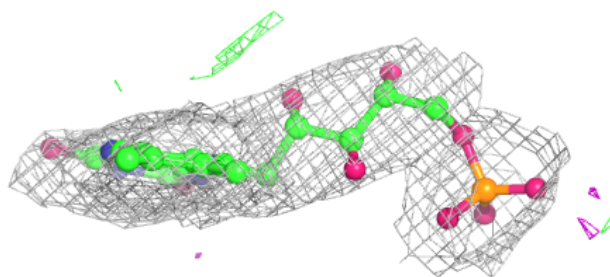
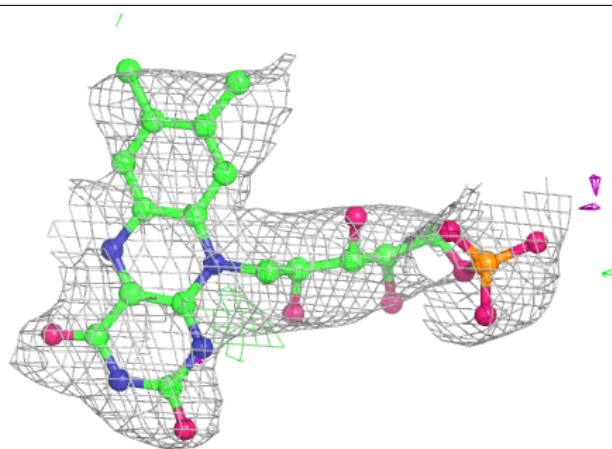
**Electron density around FMN F 301:**

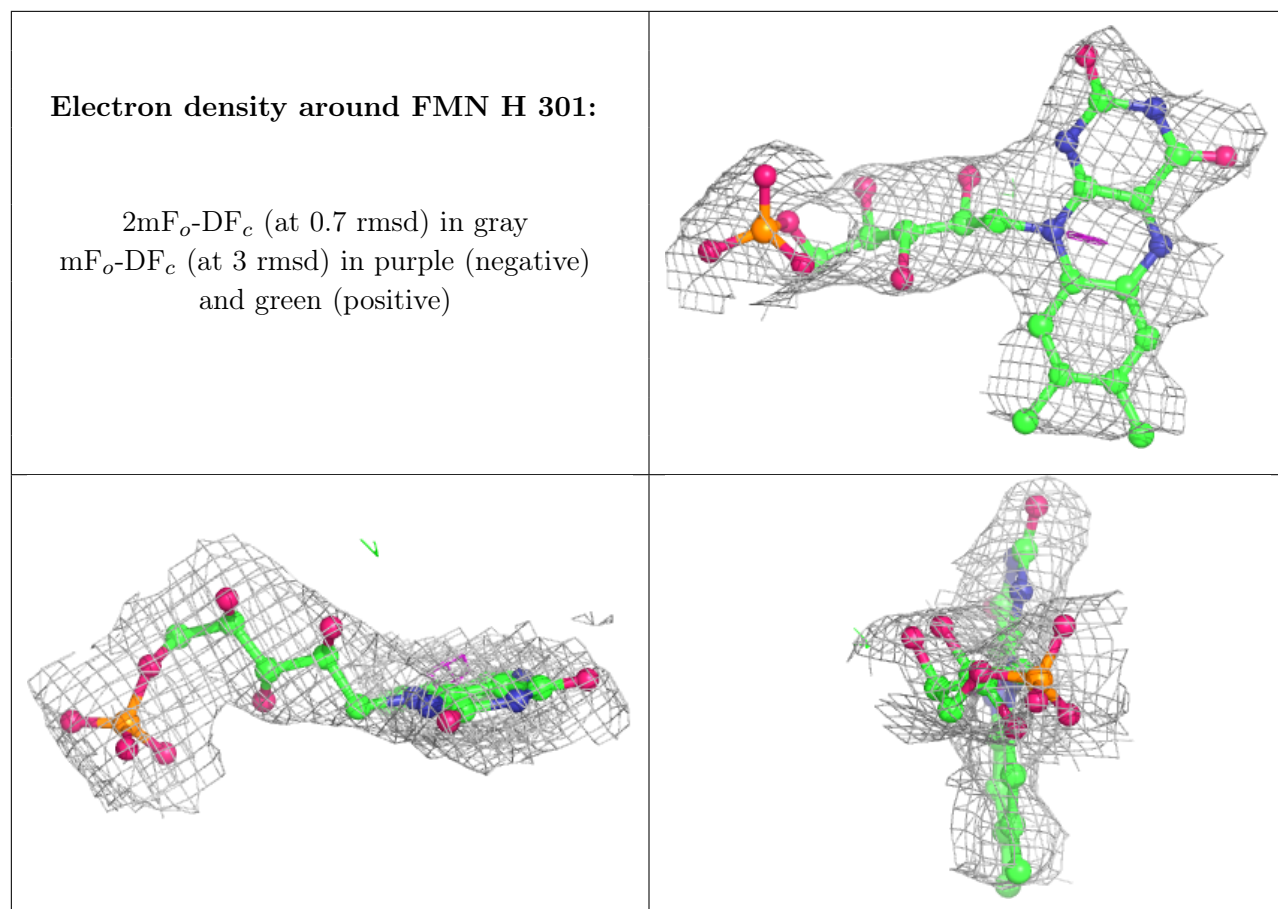
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around FMN G 301:**

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





## 6.5 Other polymers [i](#)

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