



# wwPDB X-ray Structure Validation Summary Report

Dec 16, 2023 – 07:41 PM EST

PDB ID : 2OHI  
Title : Crystal Structure of coenzyme F420H2 oxidase (FprA), a diiron flavoprotein, reduced state  
Authors : Seedorf, H.; Warkentin, E.; Ermler, U.  
Deposited on : 2007-01-10  
Resolution : 2.30 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)

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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

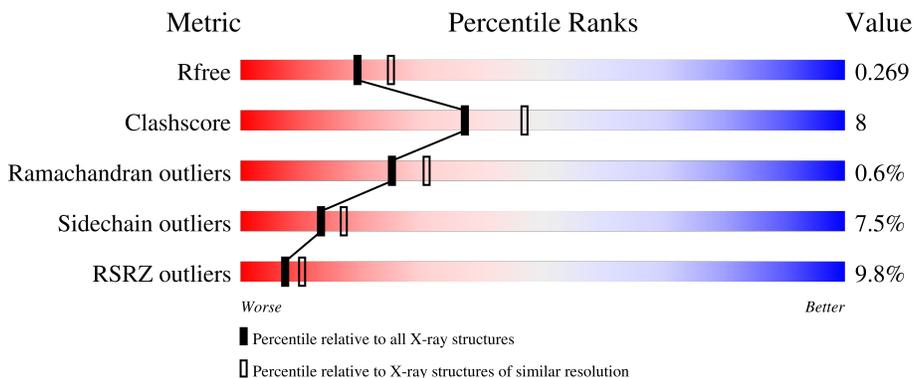
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	404	
1	B	404	
1	D	404	
1	E	404	
1	G	404	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
1	H	404	 9% 76% 20% •
1	I	404	 14% 77% 21% •
1	J	404	 8% 80% 18% •

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 25966 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 Type A flavoprotein fprA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	403	3166	2014	526	604	22	0	1	0
1	B	403	3162	2012	525	603	22	0	0	0
1	D	403	3178	2022	530	604	22	0	3	0
1	E	403	3168	2016	527	603	22	0	1	0
1	G	403	3166	2014	526	604	22	0	1	0
1	H	403	3162	2012	525	603	22	0	0	0
1	I	403	3162	2012	525	603	22	0	0	0
1	J	403	3169	2016	527	604	22	0	2	0

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

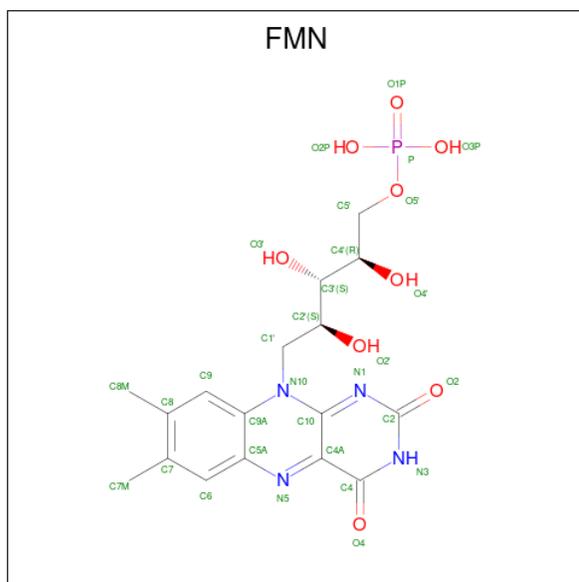
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Fe	0	0
			2	2		
2	B	2	Total	Fe	0	0
			2	2		
2	D	2	Total	Fe	0	0
			2	2		
2	E	2	Total	Fe	0	0
			2	2		
2	G	2	Total	Fe	0	0
			2	2		
2	H	2	Total	Fe	0	0
			2	2		

*Continued on next page...*

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	I	2	Total Fe 2 2	0	0
2	J	2	Total Fe 2 2	0	0

- Molecule 3 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
3	A	1	Total C N O P 31 17 4 9 1	0	0
3	B	1	Total C N O P 31 17 4 9 1	0	0
3	D	1	Total C N O P 31 17 4 9 1	0	0
3	E	1	Total C N O P 31 17 4 9 1	0	0
3	G	1	Total C N O P 31 17 4 9 1	0	0
3	H	1	Total C N O P 31 17 4 9 1	0	0
3	I	1	Total C N O P 31 17 4 9 1	0	0
3	J	1	Total C N O P 31 17 4 9 1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	1	Total Cl 1 1	0	0
4	H	1	Total Cl 1 1	0	0
4	J	2	Total Cl 2 2	0	0

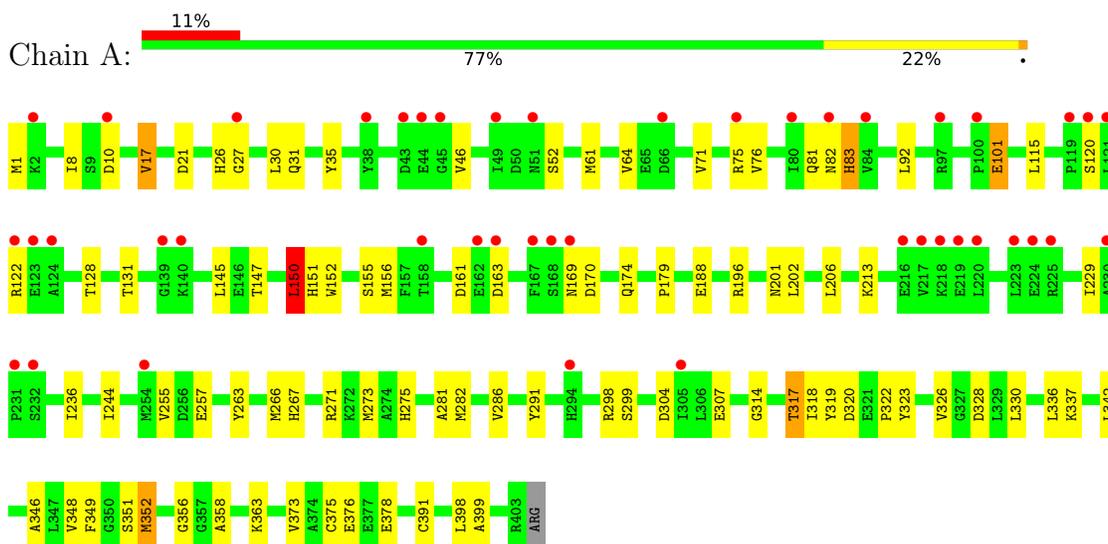
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	46	Total O 46 46	0	0
5	B	47	Total O 47 47	0	0
5	D	57	Total O 57 57	0	0
5	E	42	Total O 42 42	0	0
5	G	50	Total O 50 50	0	0
5	H	45	Total O 45 45	0	0
5	I	33	Total O 33 33	0	0
5	J	45	Total O 45 45	0	0

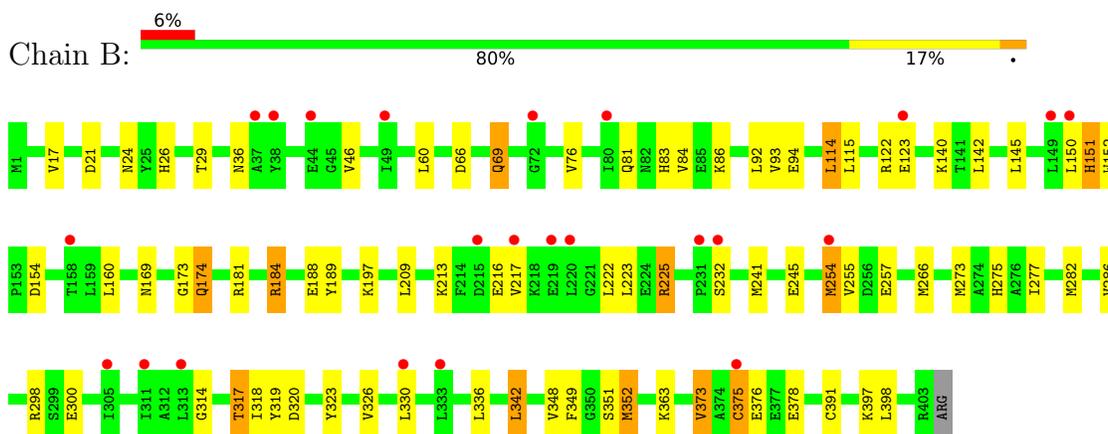
### 3 Residue-property plots [i](#)

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.

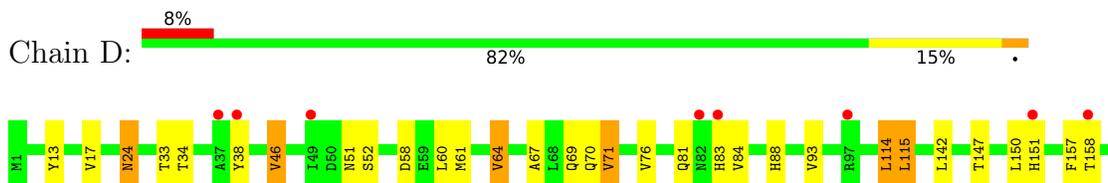
- Molecule 1: Type A flavoprotein fprA

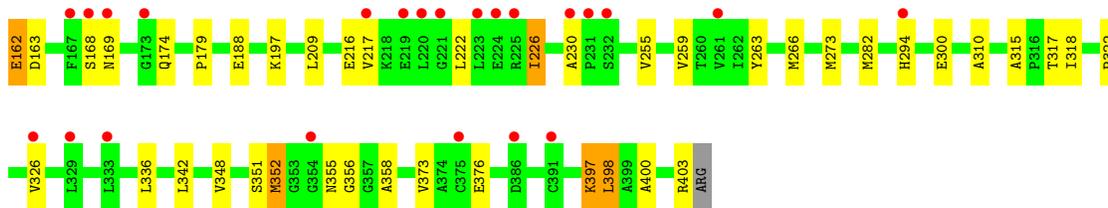


- Molecule 1: Type A flavoprotein fprA

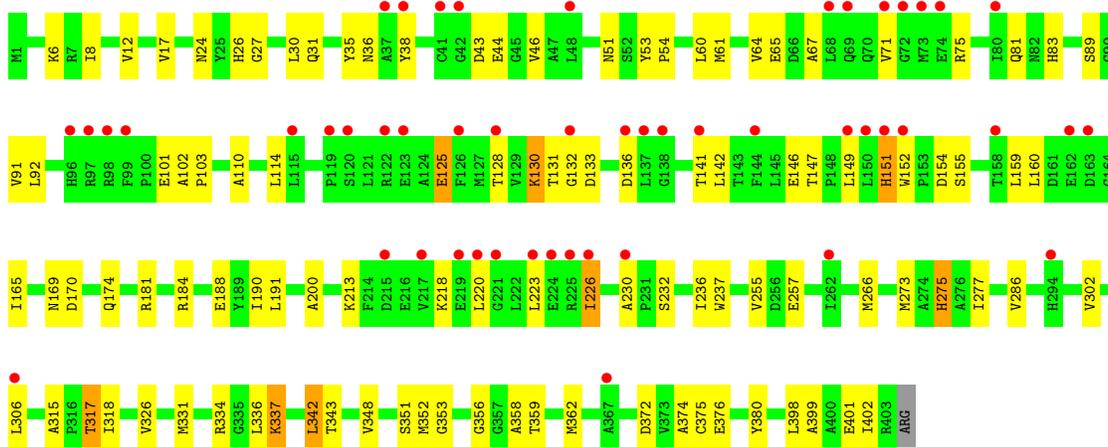


- Molecule 1: Type A flavoprotein fprA

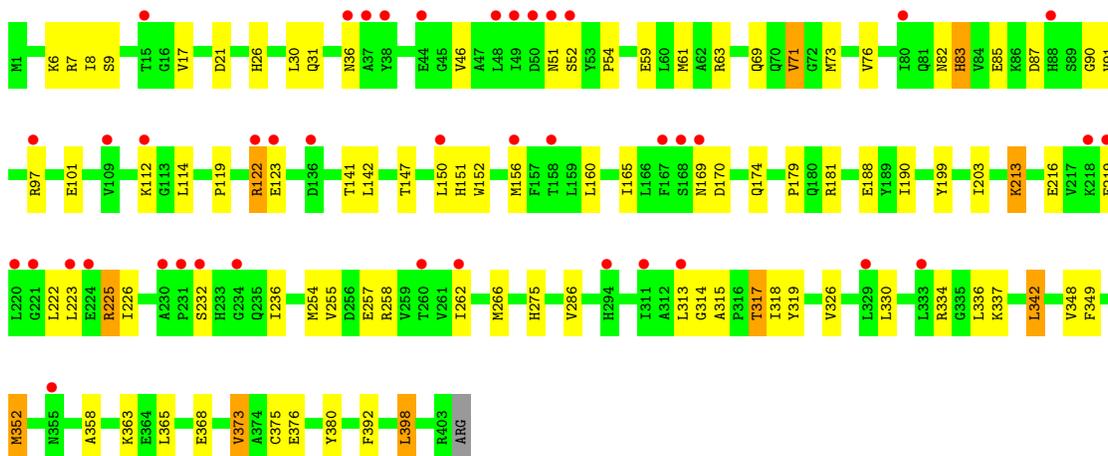
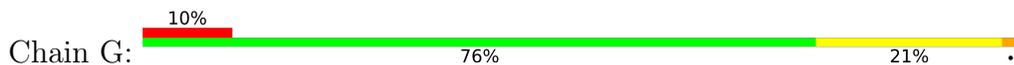




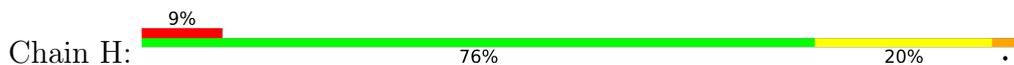
• Molecule 1: Type A flavoprotein fprA

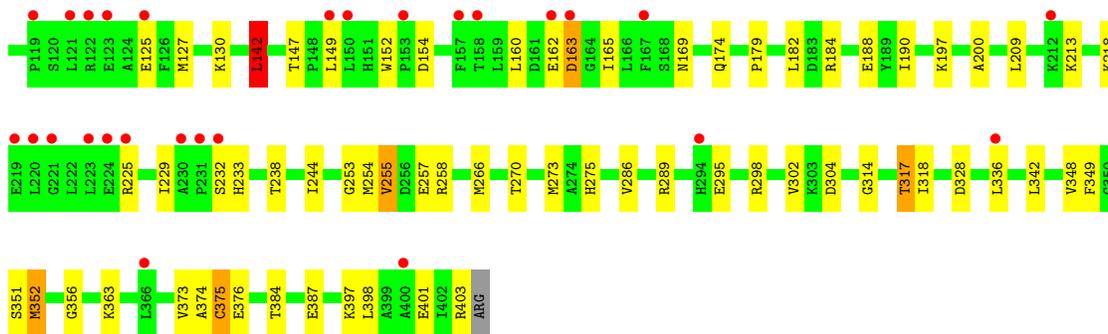


• Molecule 1: Type A flavoprotein fprA

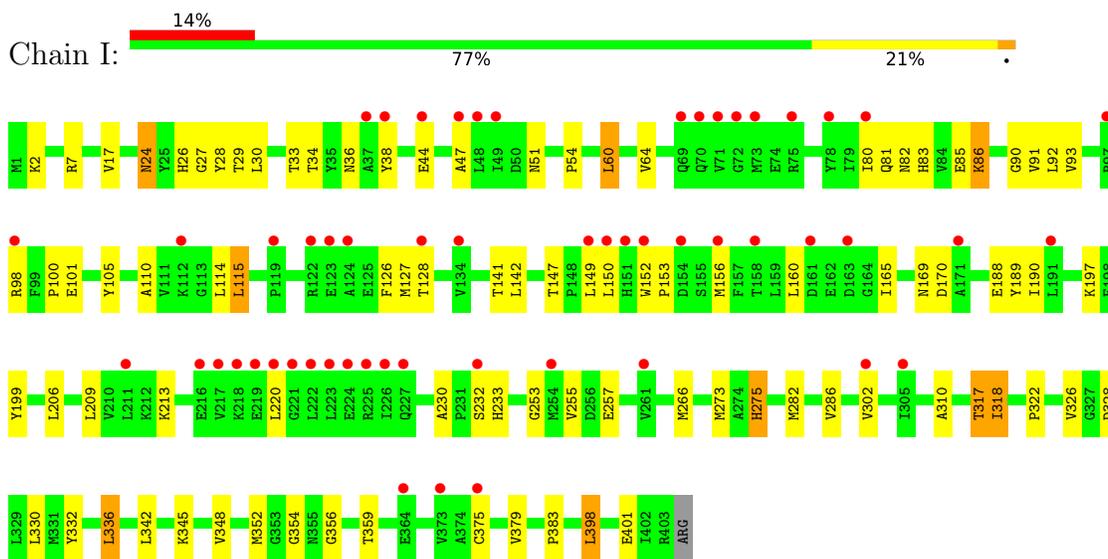


• Molecule 1: Type A flavoprotein fprA

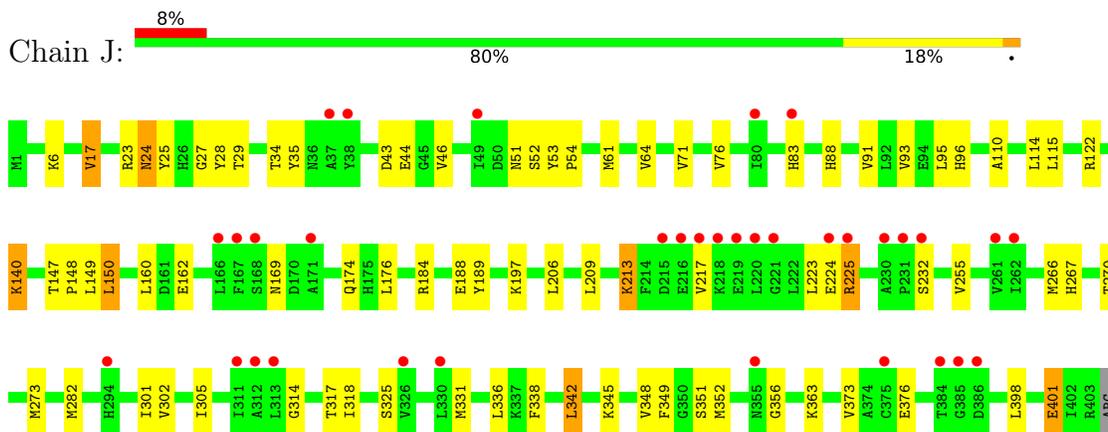




- Molecule 1: Type A flavoprotein fprA



- Molecule 1: Type A flavoprotein fprA



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	97.80Å 123.11Å 135.86Å 90.00° 103.40° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 29.58 – 2.28	Depositor EDS
% Data completeness (in resolution range)	78.9 (20.00-2.30) 77.6 (29.58-2.28)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	6.60	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.75 (at 2.29Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.203 , 0.269 0.203 , 0.269	Depositor DCC
$R_{free}$ test set	6932 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.3	Xtrriage
Anisotropy	0.370	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 59.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	25966	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.97 % 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 7.3444e-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: FMN, CL, FE

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	0.66	2/3237 (0.1%)	0.66	1/4386 (0.0%)
1	B	0.54	0/3229	0.69	2/4375 (0.0%)
1	D	0.52	0/3259	0.65	0/4416
1	E	0.92	9/3240 (0.3%)	0.73	8/4390 (0.2%)
1	G	0.52	0/3237	0.69	2/4386 (0.0%)
1	H	0.60	4/3229 (0.1%)	0.67	1/4375 (0.0%)
1	I	0.50	0/3229	0.63	0/4375
1	J	0.53	0/3246	0.68	1/4398 (0.0%)
All	All	0.61	15/25906 (0.1%)	0.67	15/35101 (0.0%)

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	1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	125	GLU	CD-OE2	27.93	1.56	1.25
1	E	132	GLY	C-O	18.60	1.53	1.23
1	A	101	GLU	CD-OE1	17.32	1.44	1.25
1	A	101	GLU	CD-OE2	17.25	1.44	1.25
1	E	43	ASP	CG-OD2	11.48	1.51	1.25

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	132	GLY	O-C-N	9.03	137.15	122.70
1	E	133	ASP	CB-CG-OD1	-8.86	110.33	118.30
1	E	43	ASP	CB-CG-OD2	-7.67	111.40	118.30
1	J	342	LEU	CA-CB-CG	6.39	129.99	115.30
1	G	398	LEU	CA-CB-CG	6.06	129.24	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	101	GLU	Sidechain

## 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	3166	0	3113	54	0
1	B	3162	0	3111	44	0
1	D	3178	0	3119	47	0
1	E	3168	0	3114	60	0
1	G	3166	0	3113	56	0
1	H	3162	0	3111	48	0
1	I	3162	0	3111	58	0
1	J	3169	0	3115	58	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
3	A	31	0	19	0	0
3	B	31	0	19	0	0
3	D	31	0	19	0	0
3	E	31	0	19	0	0
3	G	31	0	19	0	0
3	H	31	0	19	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	I	31	0	19	1	0
3	J	31	0	19	0	0
4	D	1	0	0	0	0
4	H	1	0	0	0	0
4	J	2	0	0	0	0
5	A	46	0	0	1	0
5	B	47	0	0	2	0
5	D	57	0	0	3	0
5	E	42	0	0	2	0
5	G	50	0	0	3	0
5	H	45	0	0	3	0
5	I	33	0	0	1	0
5	J	45	0	0	4	0
All	All	25966	0	25059	397	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 8.

The worst 5 of 397 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:130:LYS:CE	1:E:130:LYS:NZ	1.73	1.47
1:H:266:MET:SD	1:H:318:ILE:HD11	1.98	1.04
1:B:266:MET:SD	1:B:318:ILE:HD11	1.97	1.03
1:I:266:MET:SD	1:I:318:ILE:HD11	2.05	0.95
1:J:24:ASN:HD21	1:J:27:GLY:H	1.16	0.93

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	402/404 (100%)	384 (96%)	16 (4%)	2 (0%)	29	35
1	B	401/404 (99%)	382 (95%)	16 (4%)	3 (1%)	22	26
1	D	404/404 (100%)	388 (96%)	14 (4%)	2 (0%)	29	35
1	E	402/404 (100%)	377 (94%)	22 (6%)	3 (1%)	22	26
1	G	402/404 (100%)	386 (96%)	14 (4%)	2 (0%)	29	35
1	H	401/404 (99%)	381 (95%)	17 (4%)	3 (1%)	22	26
1	I	401/404 (99%)	374 (93%)	24 (6%)	3 (1%)	22	26
1	J	403/404 (100%)	388 (96%)	13 (3%)	2 (0%)	29	35
All	All	3216/3232 (100%)	3060 (95%)	136 (4%)	20 (1%)	25	31

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	255	VAL
1	B	375	CYS
1	D	255	VAL
1	J	150	LEU
1	B	255	VAL

### 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	336/336 (100%)	313 (93%)	23 (7%)	16	21
1	B	335/336 (100%)	306 (91%)	29 (9%)	10	12
1	D	338/336 (101%)	318 (94%)	20 (6%)	19	27
1	E	336/336 (100%)	308 (92%)	28 (8%)	11	14
1	G	336/336 (100%)	310 (92%)	26 (8%)	13	16
1	H	335/336 (100%)	303 (90%)	32 (10%)	8	10
1	I	335/336 (100%)	313 (93%)	22 (7%)	16	22
1	J	337/336 (100%)	316 (94%)	21 (6%)	18	25

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2688/2688 (100%)	2487 (92%)	201 (8%)	13 17

5 of 201 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	174	GLN
1	H	163	ASP
1	J	398	LEU
1	G	275	HIS
1	H	51	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	169	ASN
1	J	24	ASN
1	D	275	HIS
1	D	96	HIS
1	J	31	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 [i](#)

Of 28 ligands modelled in this entry, 20 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	FMN	B	1701	-	33,33,33	1.11	2 (6%)	48,50,50	1.54	11 (22%)
3	FMN	E	3701	-	33,33,33	1.14	2 (6%)	48,50,50	1.29	6 (12%)
3	FMN	D	2701	-	33,33,33	1.16	2 (6%)	48,50,50	1.40	9 (18%)
3	FMN	A	701	-	33,33,33	1.16	2 (6%)	48,50,50	1.35	6 (12%)
3	FMN	G	702	-	33,33,33	1.13	2 (6%)	48,50,50	1.45	10 (20%)
3	FMN	H	1702	-	33,33,33	1.16	2 (6%)	48,50,50	1.34	8 (16%)
3	FMN	I	2702	-	33,33,33	1.17	2 (6%)	48,50,50	1.26	7 (14%)
3	FMN	J	3702	-	33,33,33	1.21	2 (6%)	48,50,50	1.32	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
3	FMN	B	1701	-	-	3/18/18/18	0/3/3/3
3	FMN	E	3701	-	-	5/18/18/18	0/3/3/3
3	FMN	D	2701	-	-	3/18/18/18	0/3/3/3
3	FMN	A	701	-	-	2/18/18/18	0/3/3/3
3	FMN	G	702	-	-	0/18/18/18	0/3/3/3
3	FMN	H	1702	-	-	7/18/18/18	0/3/3/3
3	FMN	I	2702	-	-	0/18/18/18	0/3/3/3
3	FMN	J	3702	-	-	3/18/18/18	0/3/3/3

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	2701	FMN	C4A-N5	4.79	1.40	1.30
3	A	701	FMN	C4A-N5	4.74	1.40	1.30
3	G	702	FMN	C4A-N5	4.66	1.39	1.30
3	E	3701	FMN	C4A-N5	4.61	1.39	1.30
3	H	1702	FMN	C4A-N5	4.55	1.39	1.30

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	701	FMN	C4-C4A-N5	3.43	123.12	118.23
3	A	701	FMN	C4A-C10-N10	3.34	121.37	116.48
3	B	1701	FMN	C4-N3-C2	-3.33	119.49	125.64
3	B	1701	FMN	C4A-C10-N10	3.32	121.34	116.48
3	D	2701	FMN	C4-N3-C2	-3.28	119.59	125.64

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

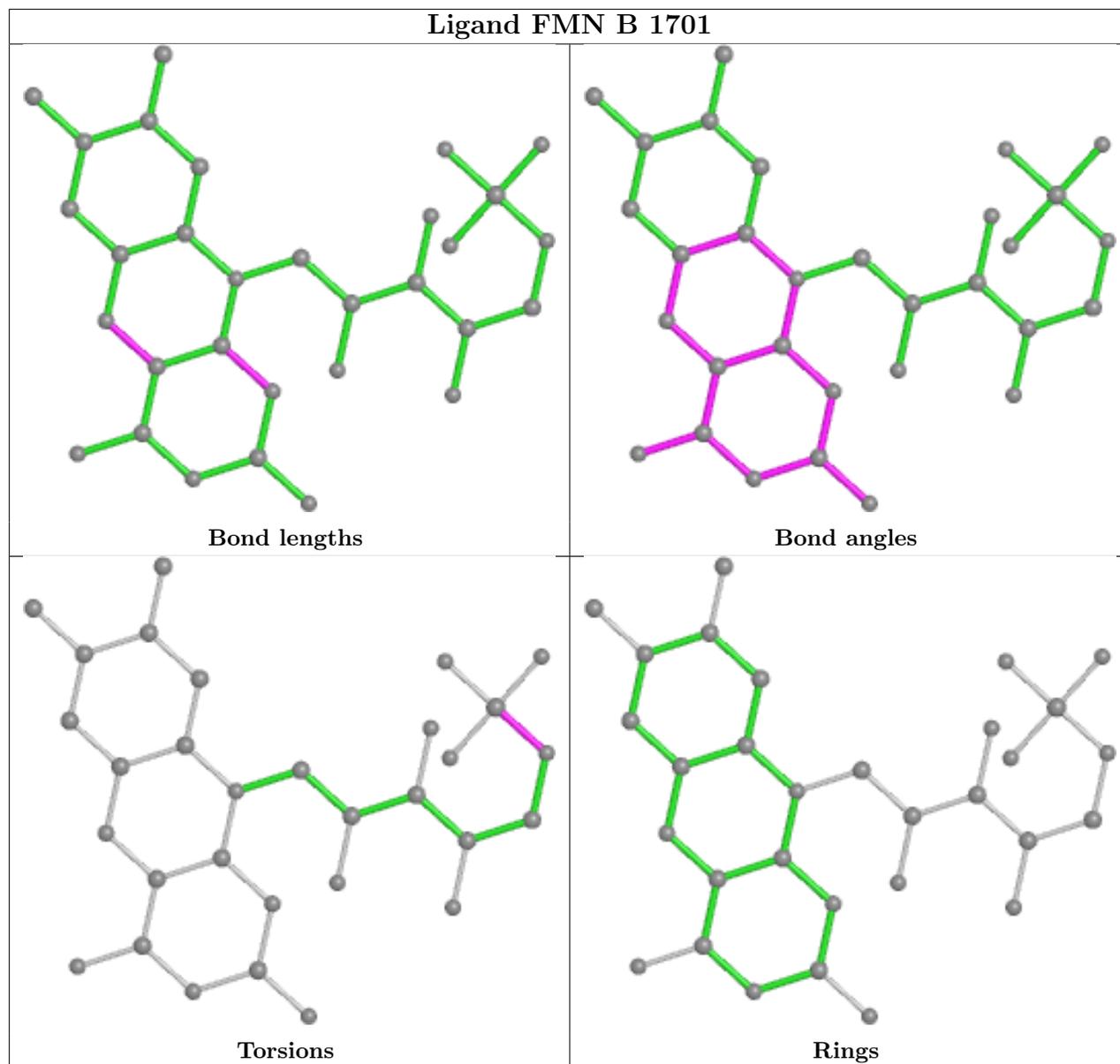
Mol	Chain	Res	Type	Atoms
3	A	701	FMN	C5'-O5'-P-O1P
3	B	1701	FMN	C5'-O5'-P-O1P
3	B	1701	FMN	C5'-O5'-P-O2P
3	H	1702	FMN	C5'-O5'-P-O2P
3	J	3702	FMN	C5'-O5'-P-O1P

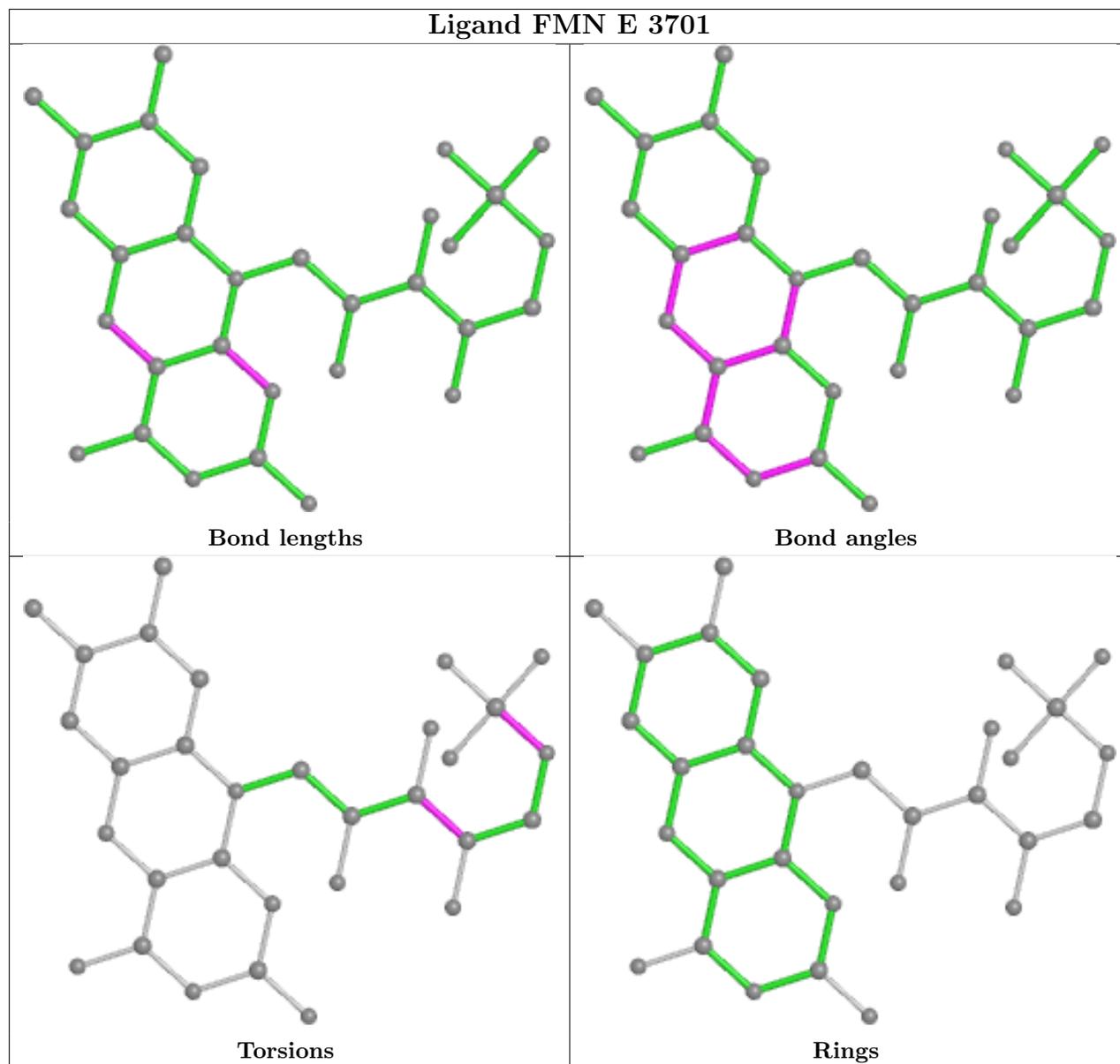
There are no ring outliers.

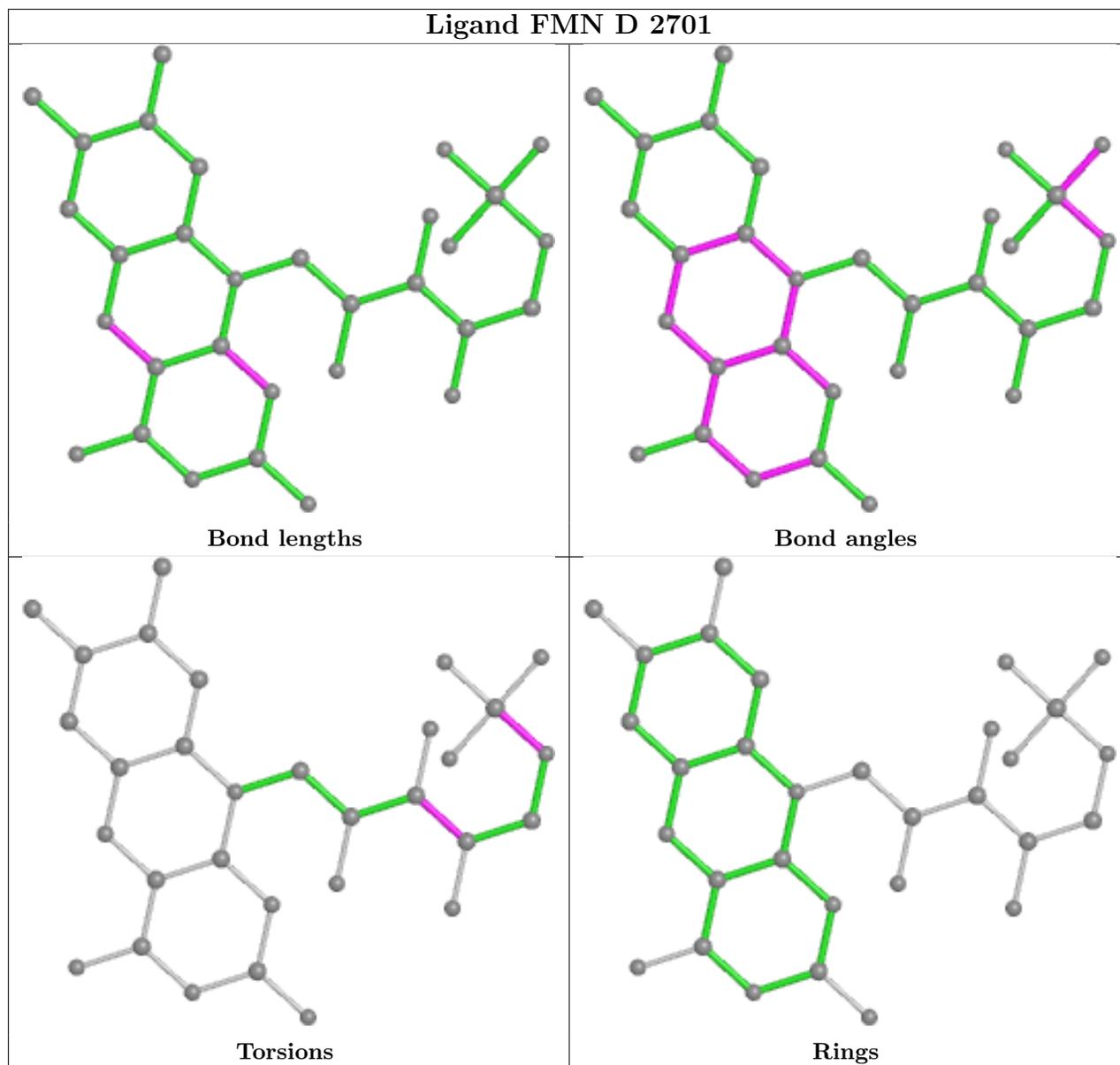
1 monomer is involved in 1 short contact:

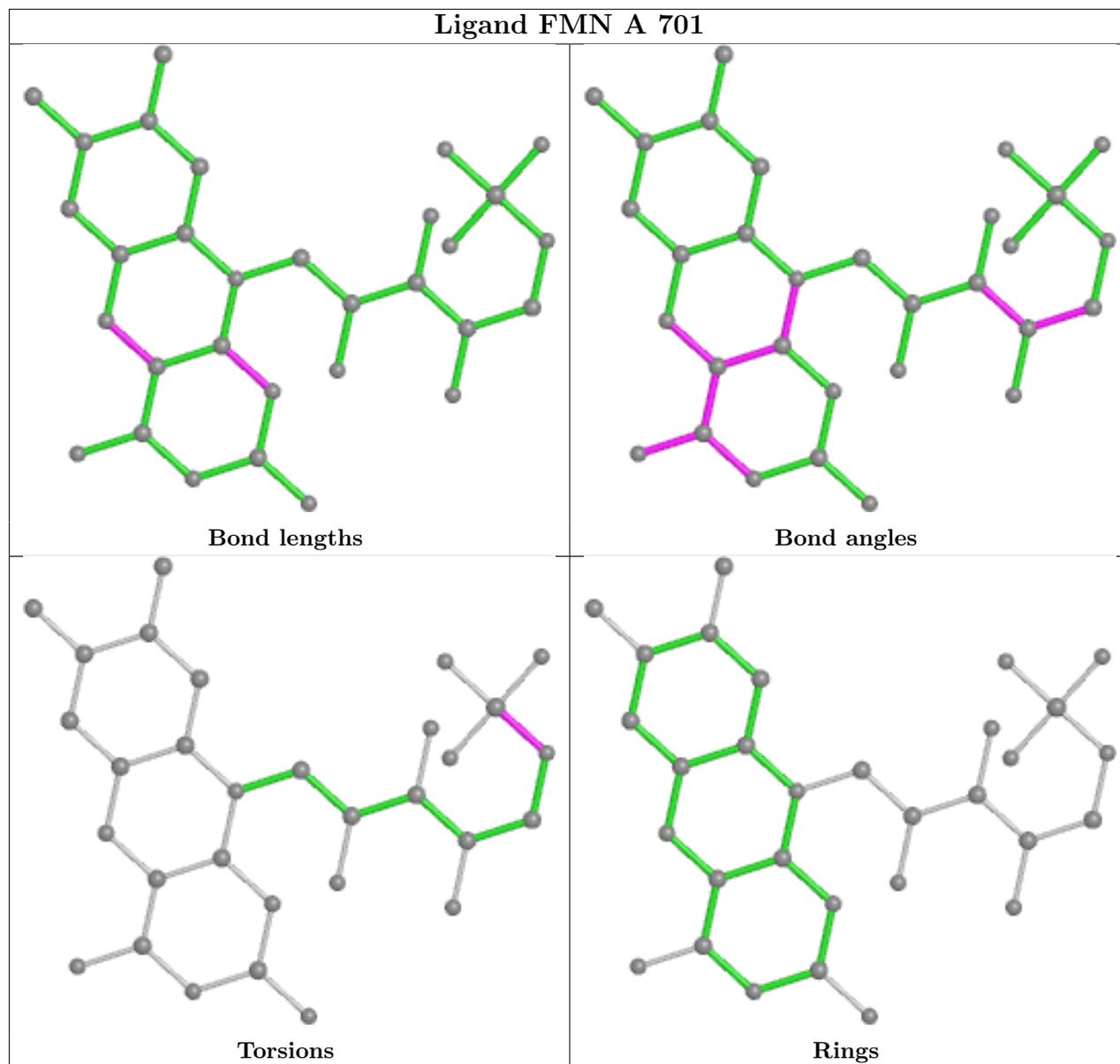
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	2702	FMN	1	0

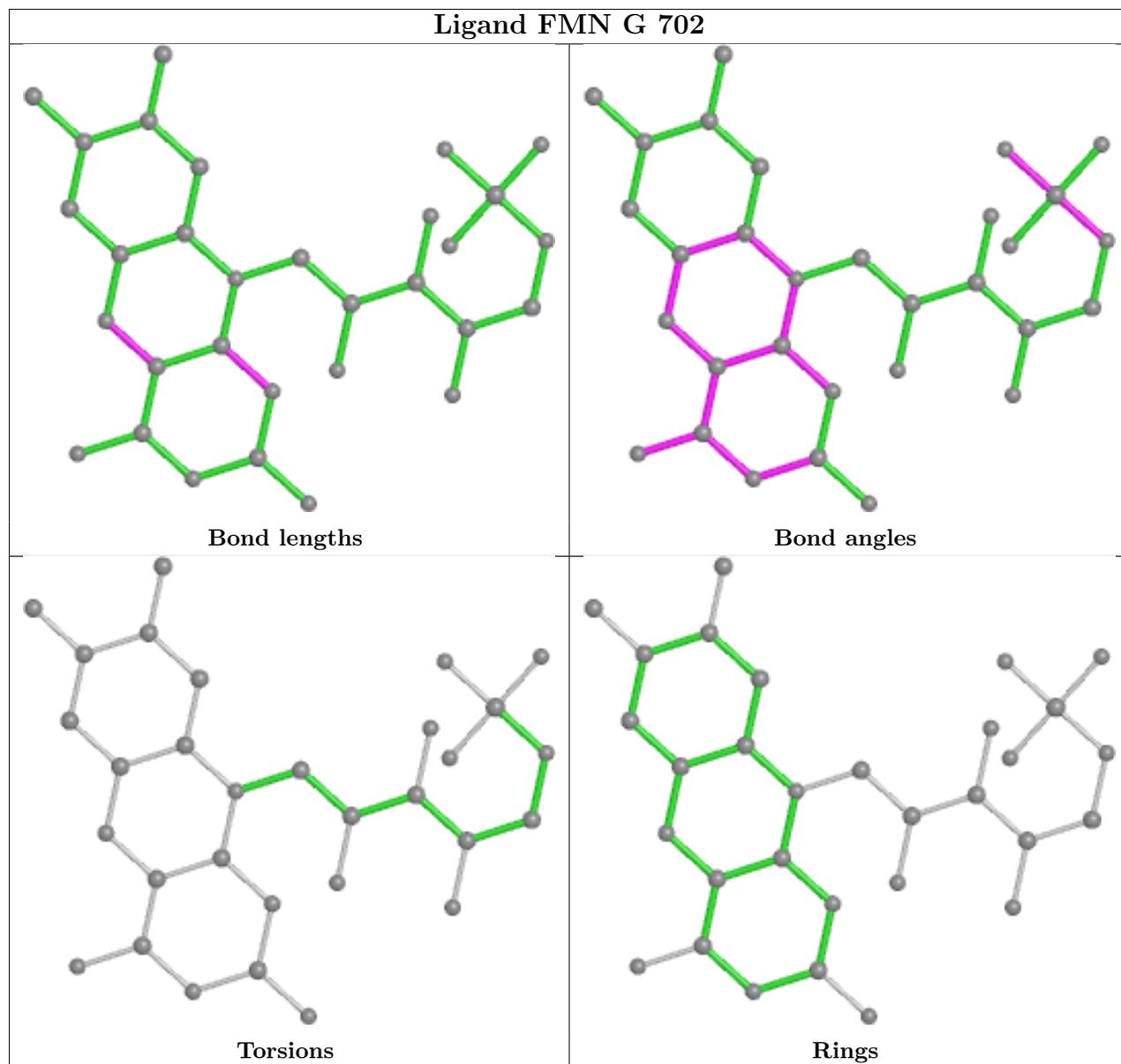
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

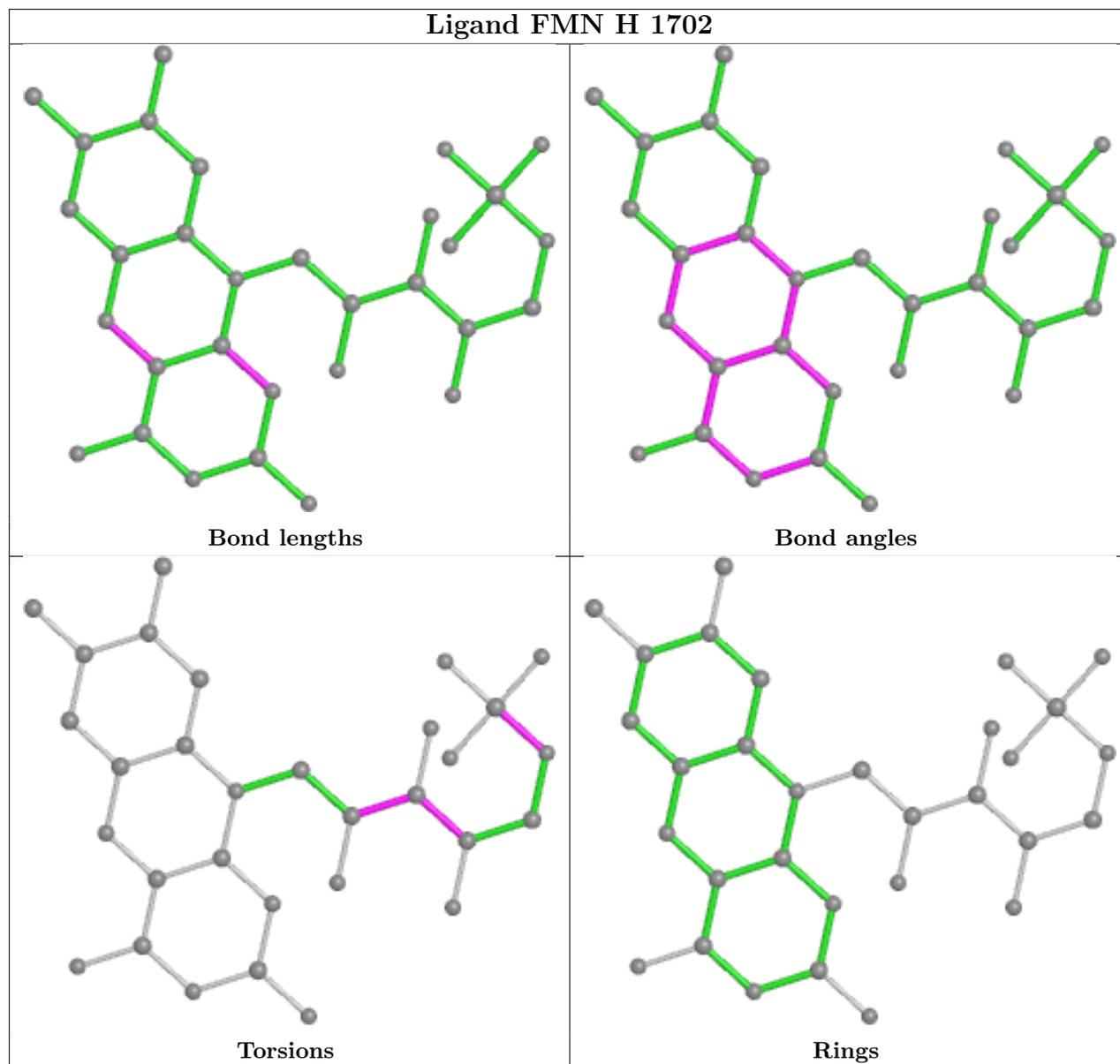


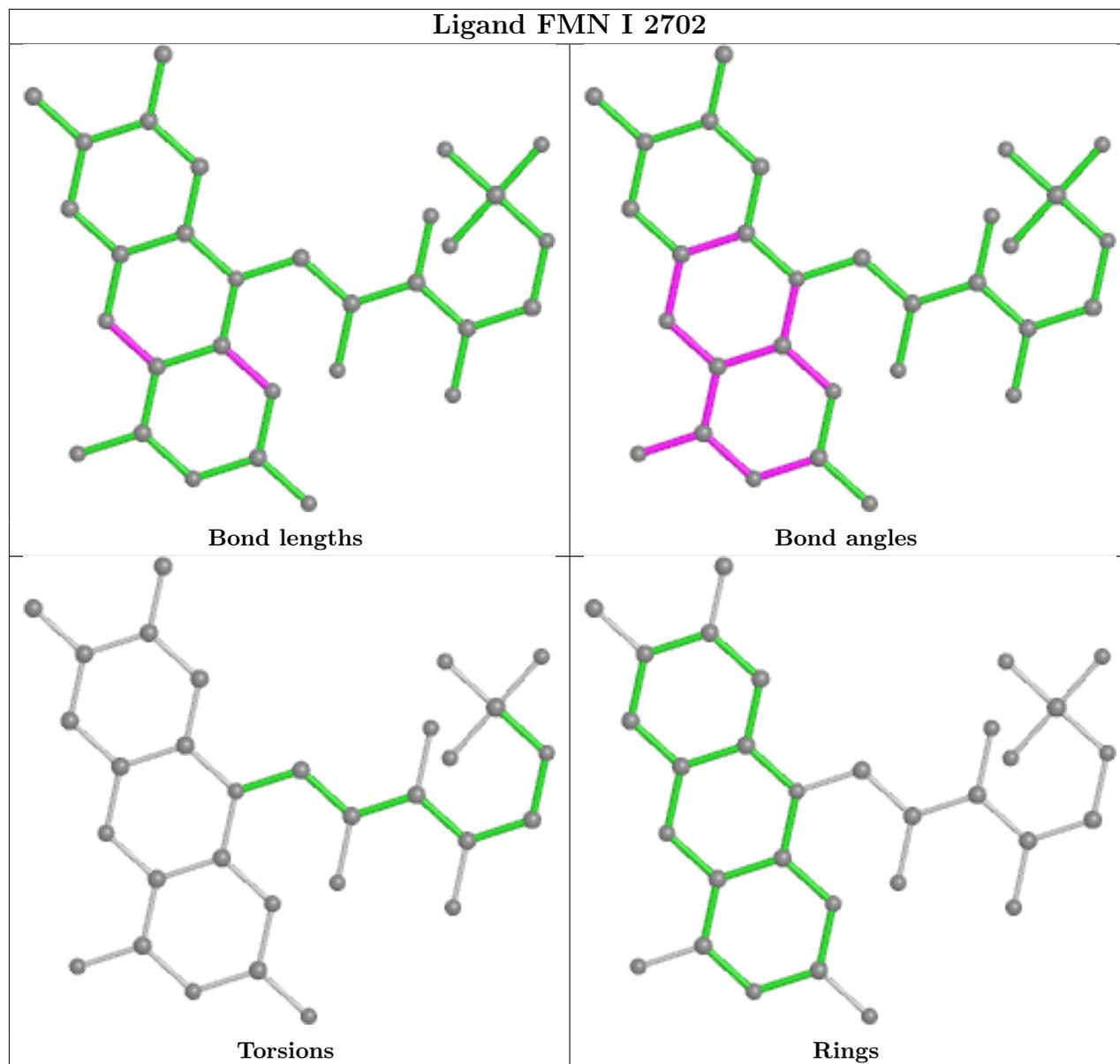


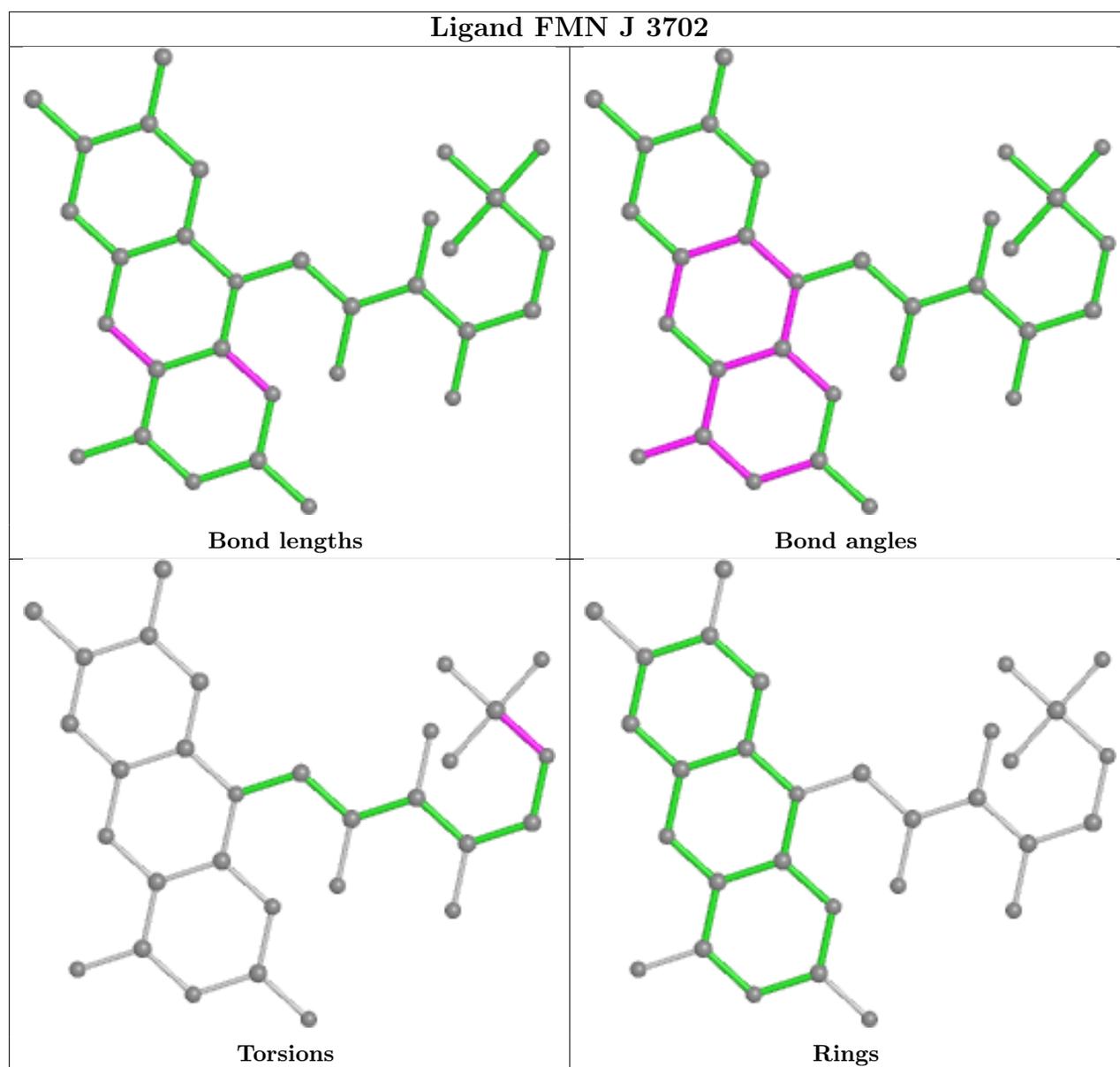












## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	403/404 (99%)	0.79	44 (10%) 5 8	35, 43, 56, 64	0
1	B	403/404 (99%)	0.57	23 (5%) 23 30	35, 43, 56, 65	0
1	D	403/404 (99%)	0.60	31 (7%) 13 17	34, 42, 55, 64	0
1	E	403/404 (99%)	0.89	50 (12%) 4 5	35, 43, 55, 64	0
1	G	403/404 (99%)	0.67	42 (10%) 6 9	34, 42, 55, 65	0
1	H	403/404 (99%)	0.70	38 (9%) 8 11	35, 43, 55, 65	0
1	I	403/404 (99%)	0.85	55 (13%) 3 4	35, 43, 55, 63	0
1	J	403/404 (99%)	0.56	34 (8%) 11 15	34, 43, 56, 65	0
All	All	3224/3232 (99%)	0.70	317 (9%) 7 10	34, 43, 56, 65	0

The worst 5 of 317 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	223	LEU	7.5
1	E	151[A]	HIS	7.4
1	E	223	LEU	7.3
1	I	223	LEU	7.0
1	I	217	VAL	7.0

### 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

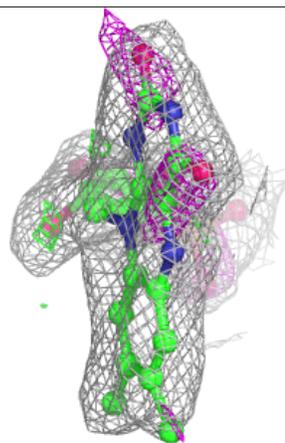
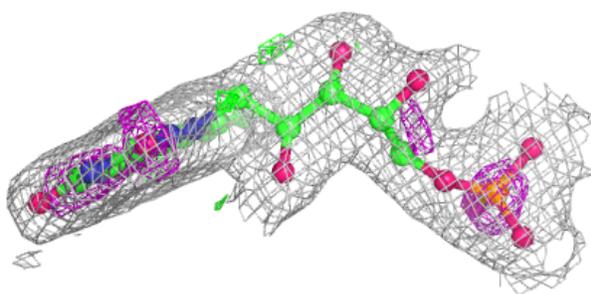
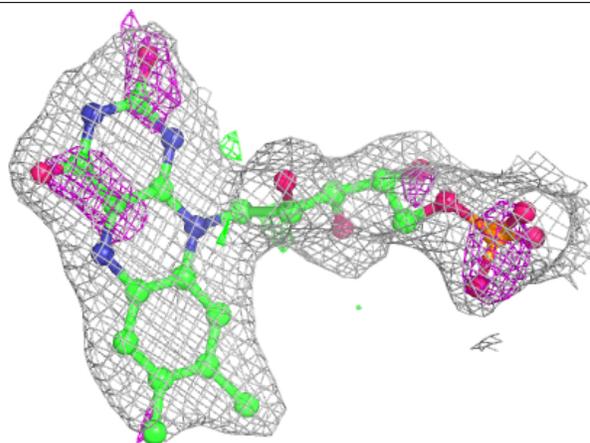
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	CL	J	3505	1/1	0.86	0.21	37,37,37,37	1
2	FE	I	2503	1/1	0.91	0.25	63,63,63,63	1
2	FE	J	3503	1/1	0.93	0.19	48,48,48,48	1
3	FMN	D	2701	31/31	0.93	0.13	37,40,43,44	0
2	FE	B	1503	1/1	0.93	0.08	45,45,45,45	1
2	FE	H	1503	1/1	0.95	0.08	44,44,44,44	1
2	FE	E	3503	1/1	0.96	0.26	58,58,58,58	1
3	FMN	G	702	31/31	0.96	0.11	29,32,34,35	0
3	FMN	I	2702	31/31	0.96	0.11	29,33,34,35	0
3	FMN	J	3702	31/31	0.96	0.11	38,41,42,42	0
4	CL	D	2504	1/1	0.96	0.05	41,41,41,41	1
4	CL	H	1504	1/1	0.96	0.12	47,47,47,47	1
4	CL	J	3504	1/1	0.96	0.06	36,36,36,36	1
3	FMN	B	1701	31/31	0.96	0.10	33,35,39,40	0
2	FE	D	2503	1/1	0.97	0.08	36,36,36,36	1
3	FMN	E	3701	31/31	0.97	0.10	29,32,33,34	0
3	FMN	A	701	31/31	0.97	0.10	24,33,34,35	0
3	FMN	H	1702	31/31	0.97	0.11	28,35,36,36	0
2	FE	A	503	1/1	0.97	0.07	47,47,47,47	1
2	FE	I	2501	1/1	0.98	0.05	48,48,48,48	0
2	FE	H	1501	1/1	0.98	0.05	47,47,47,47	0
2	FE	E	3501	1/1	0.98	0.05	44,44,44,44	0
2	FE	B	1501	1/1	0.99	0.04	36,36,36,36	0
2	FE	A	501	1/1	0.99	0.02	45,45,45,45	0
2	FE	D	2501	1/1	0.99	0.06	39,39,39,39	0
2	FE	G	501	1/1	0.99	0.05	37,37,37,37	0
2	FE	J	3501	1/1	0.99	0.04	37,37,37,37	0
2	FE	G	503	1/1	0.99	0.07	32,32,32,32	1

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.

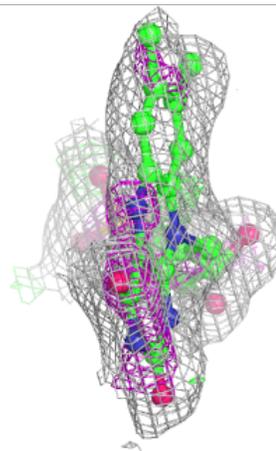
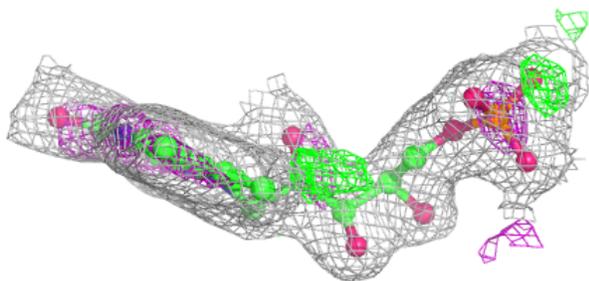
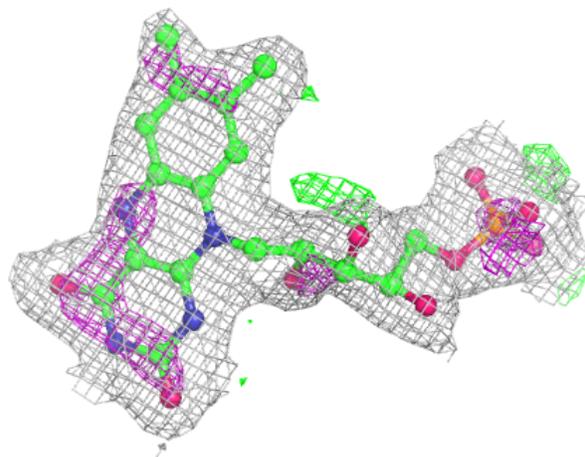
**Electron density around FMN D 2701:**

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



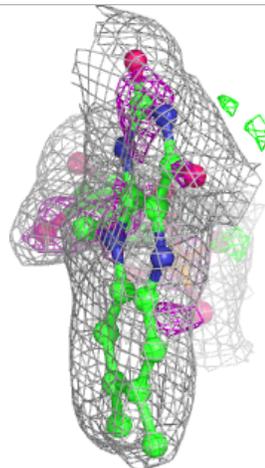
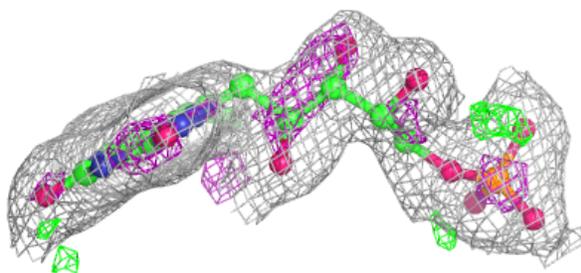
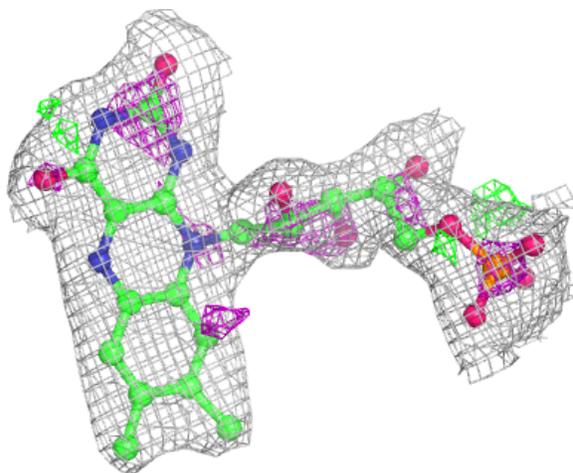
**Electron density around FMN G 702:**

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



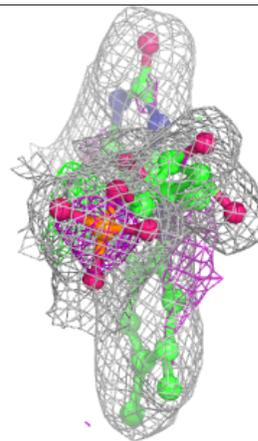
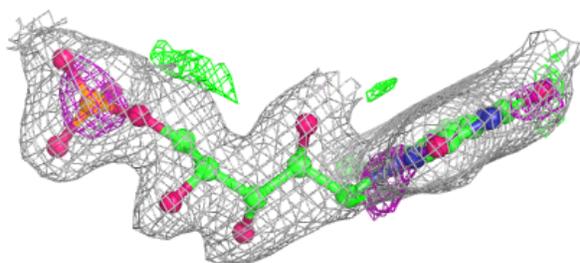
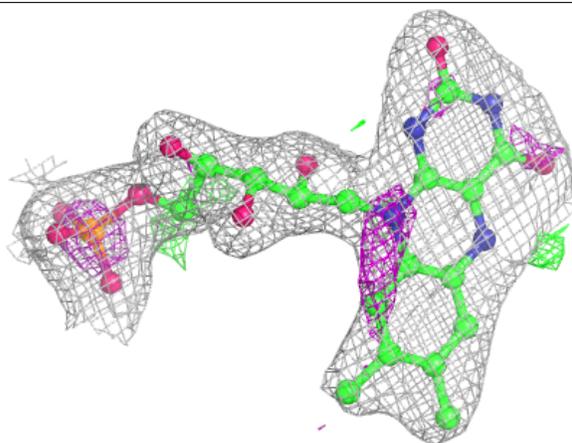
**Electron density around FMN I 2702:**

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



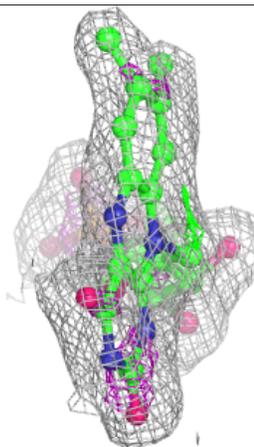
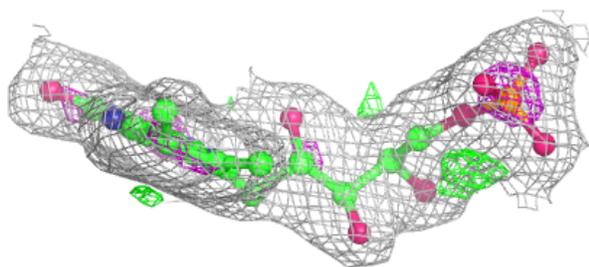
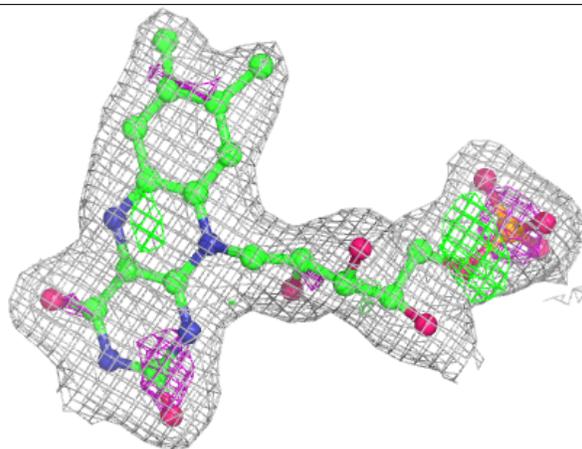
**Electron density around FMN J 3702:**

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



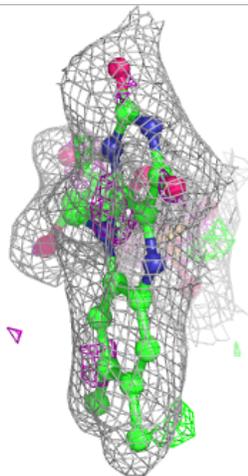
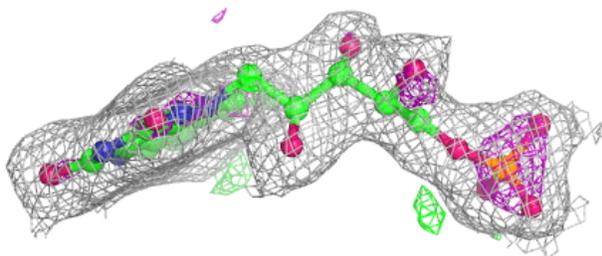
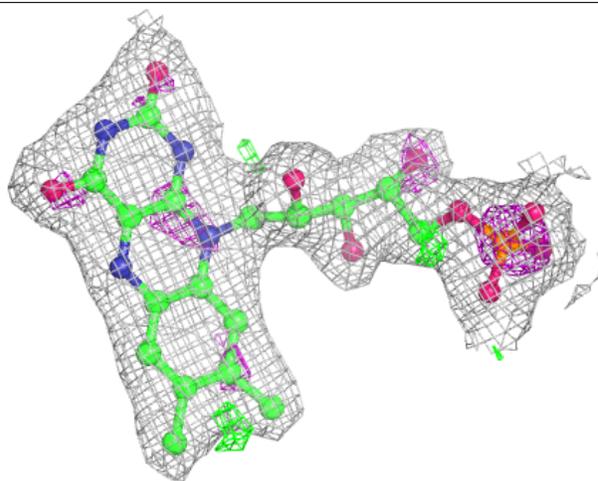
**Electron density around FMN B 1701:**

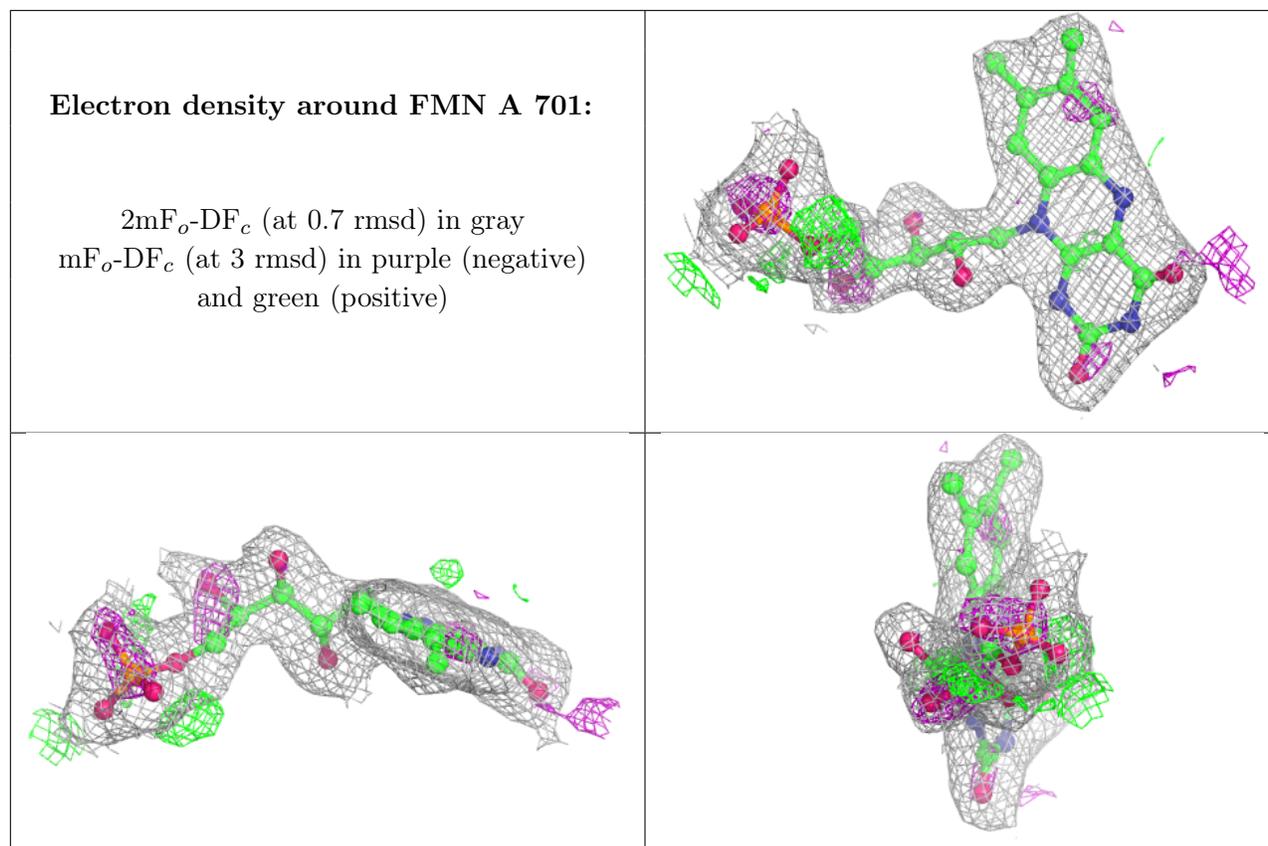
$2mF_o-DF_c$  (at 0.7 rnsd) in gray  
 $mF_o-DF_c$  (at 3 rnsd) in purple (negative)  
and green (positive)

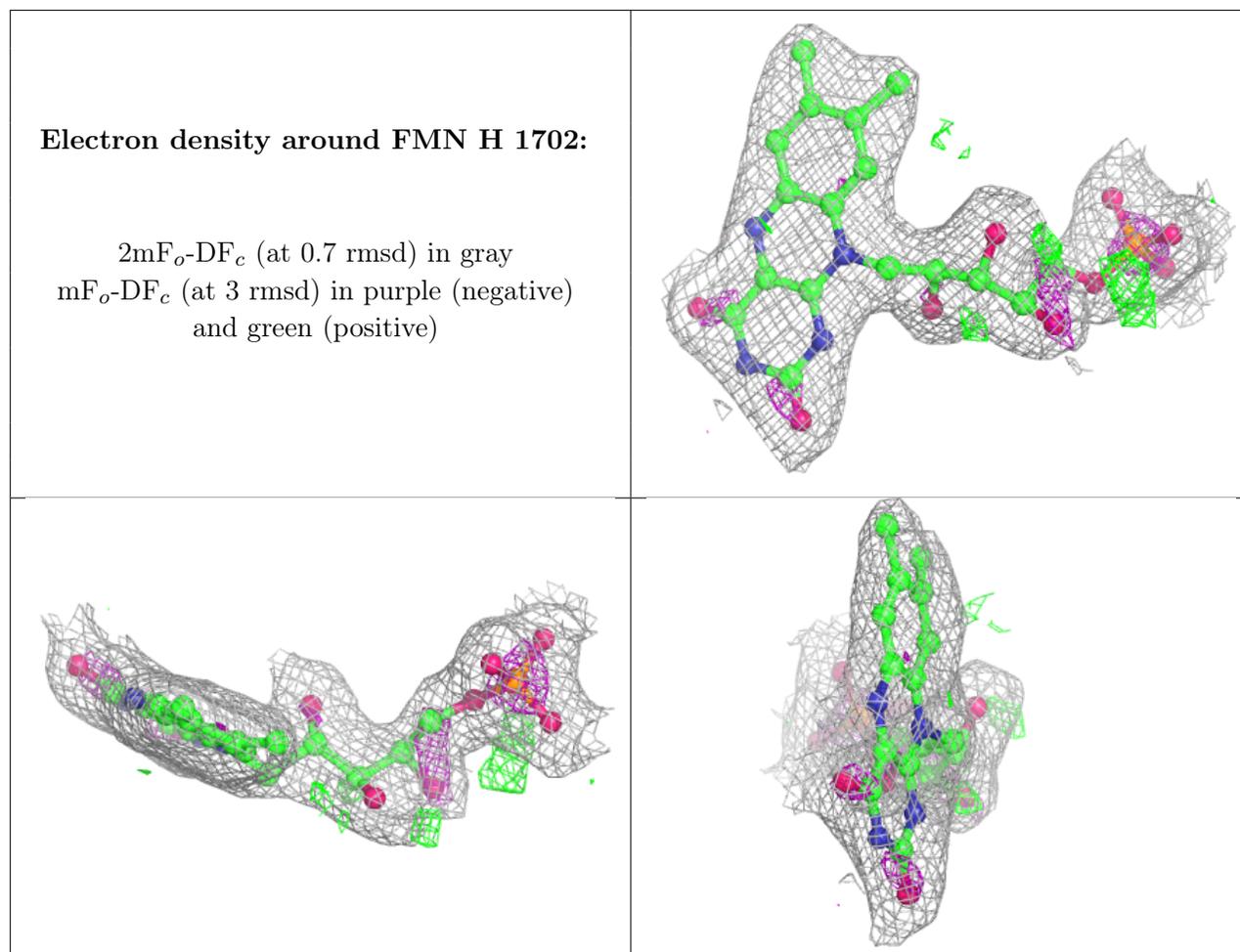


**Electron density around FMN E 3701:**

$2mF_o-DF_c$  (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.