



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 03:05 AM EDT

PDB ID : 1G28
Title : STRUCTURE OF A FLAVIN-BINDING DOMAIN, LOV2, FROM THE CHIMERIC PHYTOCHROME/PHOTOTROPIN PHOTORECEPTOR PHY3
Authors : Crosson, S.; Moffat, K.
Deposited on : 2000-10-17
Resolution : 2.73 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

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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

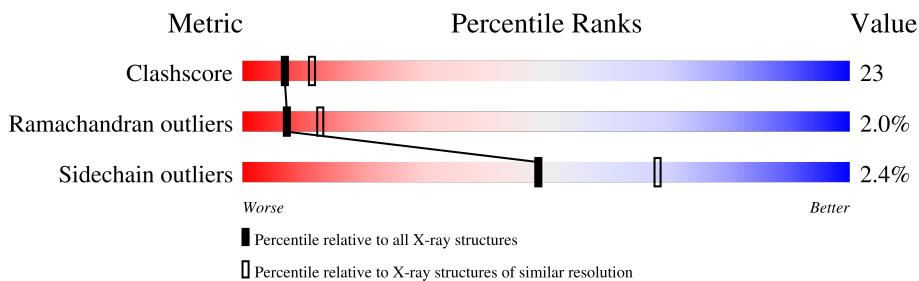
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.73 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	1322 (2.76-2.72)
Ramachandran outliers	138981	1297 (2.76-2.72)
Sidechain outliers	138945	1298 (2.76-2.72)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	104	 67% 29% .
1	B	104	 66% 30% .
1	C	104	 70% 26% .
1	D	104	 69% 27% .

2 Entry composition [i](#)

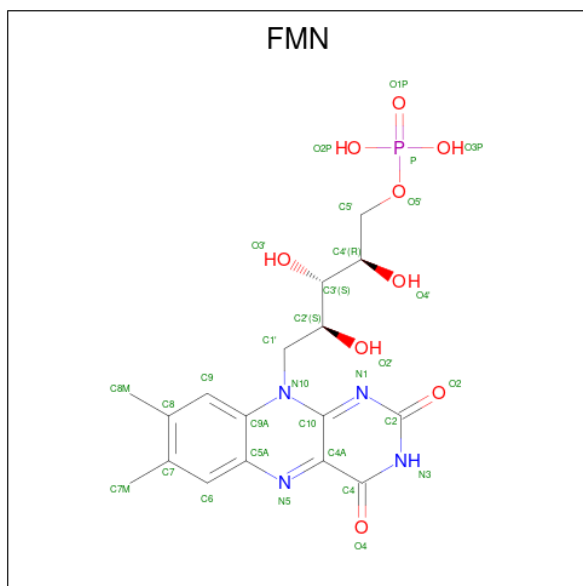
There are 3 unique types of molecules in this entry. The entry contains 3451 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PHY3 PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	104	Total	C	N	O	S	0	0	0
			819	519	142	155	3			
1	B	104	Total	C	N	O	S	0	0	0
			819	519	142	155	3			
1	C	104	Total	C	N	O	S	0	0	0
			819	519	142	155	3			
1	D	104	Total	C	N	O	S	0	0	0
			819	519	142	155	3			

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P).



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		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
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		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	16	Total	O	0	0
			16	16		
3	B	10	Total	O	0	0
			10	10		
3	C	14	Total	O	0	0
			14	14		
3	D	11	Total	O	0	0
			11	11		

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.

Note EDS was not executed.

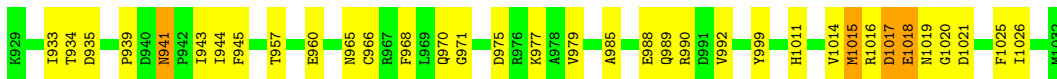
• Molecule 1: PHY3 PROTEIN

Chain A: 



• Molecule 1: PHY3 PROTEIN

Chain B: 



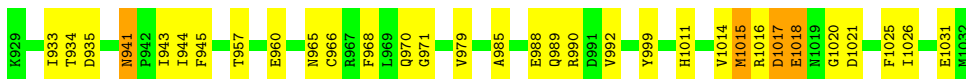
• Molecule 1: PHY3 PROTEIN

Chain C: 



• Molecule 1: PHY3 PROTEIN

Chain D: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	44.89Å 54.08Å 70.62Å 93.32° 94.01° 90.06°	Depositor
Resolution (Å)	35.16 – 2.73	Depositor
% Data completeness (in resolution range)	92.5 (35.16-2.73)	Depositor
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.247 , 0.272	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3451	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

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

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	0.44	0/834	0.64	0/1132
1	B	0.41	0/834	0.64	0/1132
1	C	0.43	0/834	0.64	0/1132
1	D	0.42	0/834	0.64	0/1132
All	All	0.43	0/3336	0.64	0/4528

There are no bond length outliers.

There are no bond angle outliers.

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	819	0	772	39	0
1	B	819	0	772	43	0
1	C	819	0	772	39	0
1	D	819	0	772	39	0
2	A	31	0	19	1	0
2	B	31	0	19	1	0
2	C	31	0	19	1	0
2	D	31	0	19	1	0
3	A	16	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	10	0	0	1	0
3	C	14	0	0	5	0
3	D	11	0	0	1	0
All	All	3451	0	3164	151	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 23.

The worst 5 of 151 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:D:957:THR:HG22	1:D:960:GLU:HG3	1.38	1.05
1:B:957:THR:HG22	1:B:960:GLU:HG3	1.40	1.03
1:A:957:THR:HG22	1:A:960:GLU:HG3	1.39	1.03
1:C:957:THR:HG22	1:C:960:GLU:HG3	1.39	1.01
1:C:934:THR:HG22	1:C:1025:PHE:HB2	1.48	0.96

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	102/104 (98%)	93 (91%)	7 (7%)	2 (2%)	7	13
1	B	102/104 (98%)	94 (92%)	6 (6%)	2 (2%)	7	13
1	C	102/104 (98%)	94 (92%)	6 (6%)	2 (2%)	7	13
1	D	102/104 (98%)	94 (92%)	6 (6%)	2 (2%)	7	13
All	All	408/416 (98%)	375 (92%)	25 (6%)	8 (2%)	7	13

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1018	GLU
1	B	1018	GLU
1	C	1018	GLU
1	D	1018	GLU
1	A	1017	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	85/93 (91%)	83 (98%)	2 (2%)	49	68
1	B	85/93 (91%)	83 (98%)	2 (2%)	49	68
1	C	85/93 (91%)	83 (98%)	2 (2%)	49	68
1	D	85/93 (91%)	83 (98%)	2 (2%)	49	68
All	All	340/372 (91%)	332 (98%)	8 (2%)	49	68

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	1015	MET
1	D	941	ASN
1	C	941	ASN
1	B	1015	MET
1	C	1015	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	970	GLN
1	D	1013	GLN
1	B	1013	GLN
1	C	941	ASN
1	C	970	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 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	D	4033	-	33,33,33	1.55	6 (18%)	48,50,50	1.10	3 (6%)
2	FMN	C	3033	-	33,33,33	1.58	7 (21%)	48,50,50	1.06	3 (6%)
2	FMN	A	1033	-	33,33,33	1.52	7 (21%)	48,50,50	1.10	3 (6%)
2	FMN	B	2033	-	33,33,33	1.50	6 (18%)	48,50,50	1.09	3 (6%)

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	D	4033	-	-	3/18/18/18	0/3/3/3
2	FMN	C	3033	-	-	3/18/18/18	0/3/3/3
2	FMN	A	1033	-	-	3/18/18/18	0/3/3/3
2	FMN	B	2033	-	-	3/18/18/18	0/3/3/3

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1033	FMN	C6-C5A	4.24	1.46	1.40
2	C	3033	FMN	C6-C5A	4.21	1.46	1.40
2	D	4033	FMN	C6-C5A	4.18	1.46	1.40
2	B	2033	FMN	C6-C5A	3.83	1.45	1.40
2	D	4033	FMN	C9A-C5A	3.31	1.46	1.41

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1033	FMN	C9-C9A-N10	2.60	125.35	121.85
2	C	3033	FMN	C9-C9A-N10	2.54	125.28	121.85
2	B	2033	FMN	C9-C9A-N10	2.54	125.27	121.85
2	D	4033	FMN	C9-C9A-N10	2.53	125.25	121.85
2	D	4033	FMN	C5A-C9A-N10	-2.50	115.71	117.97

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1033	FMN	C3'-C4'-C5'-O5'
2	B	2033	FMN	C3'-C4'-C5'-O5'
2	C	3033	FMN	C3'-C4'-C5'-O5'
2	D	4033	FMN	C3'-C4'-C5'-O5'
2	A	1033	FMN	O4'-C4'-C5'-O5'

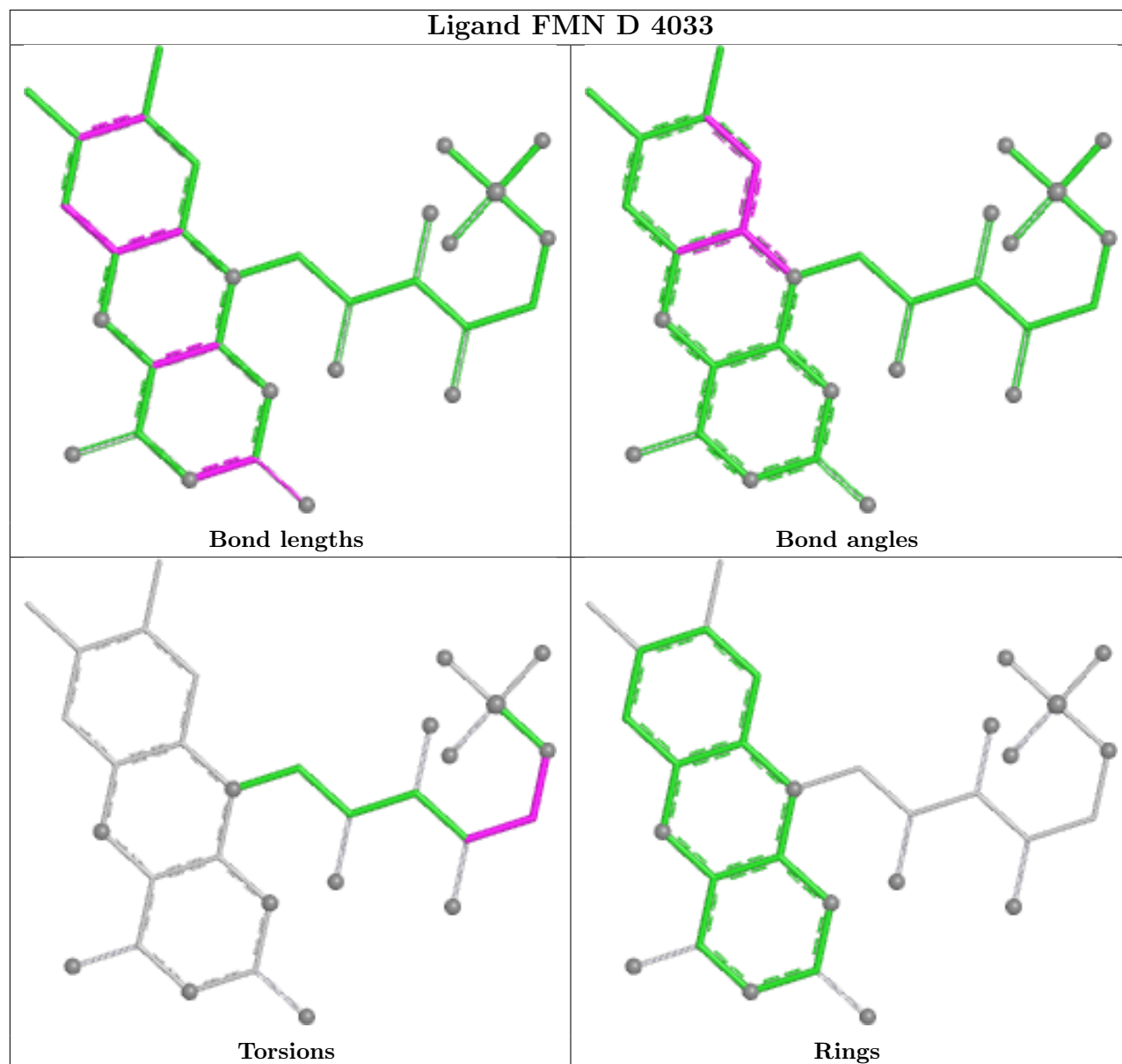
There are no ring outliers.

4 monomers are involved in 4 short contacts:

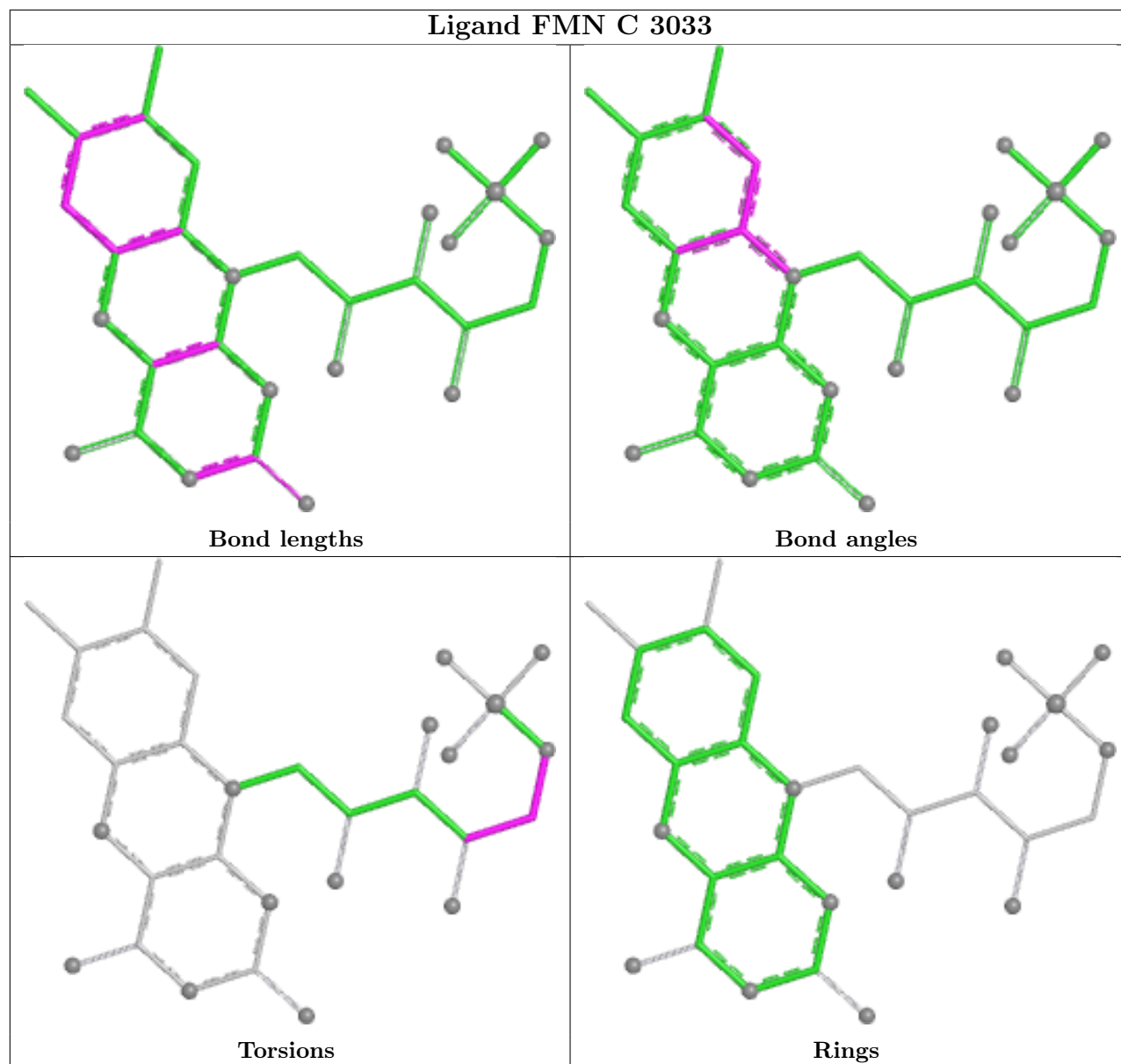
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	4033	FMN	1	0
2	C	3033	FMN	1	0
2	A	1033	FMN	1	0
2	B	2033	FMN	1	0

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

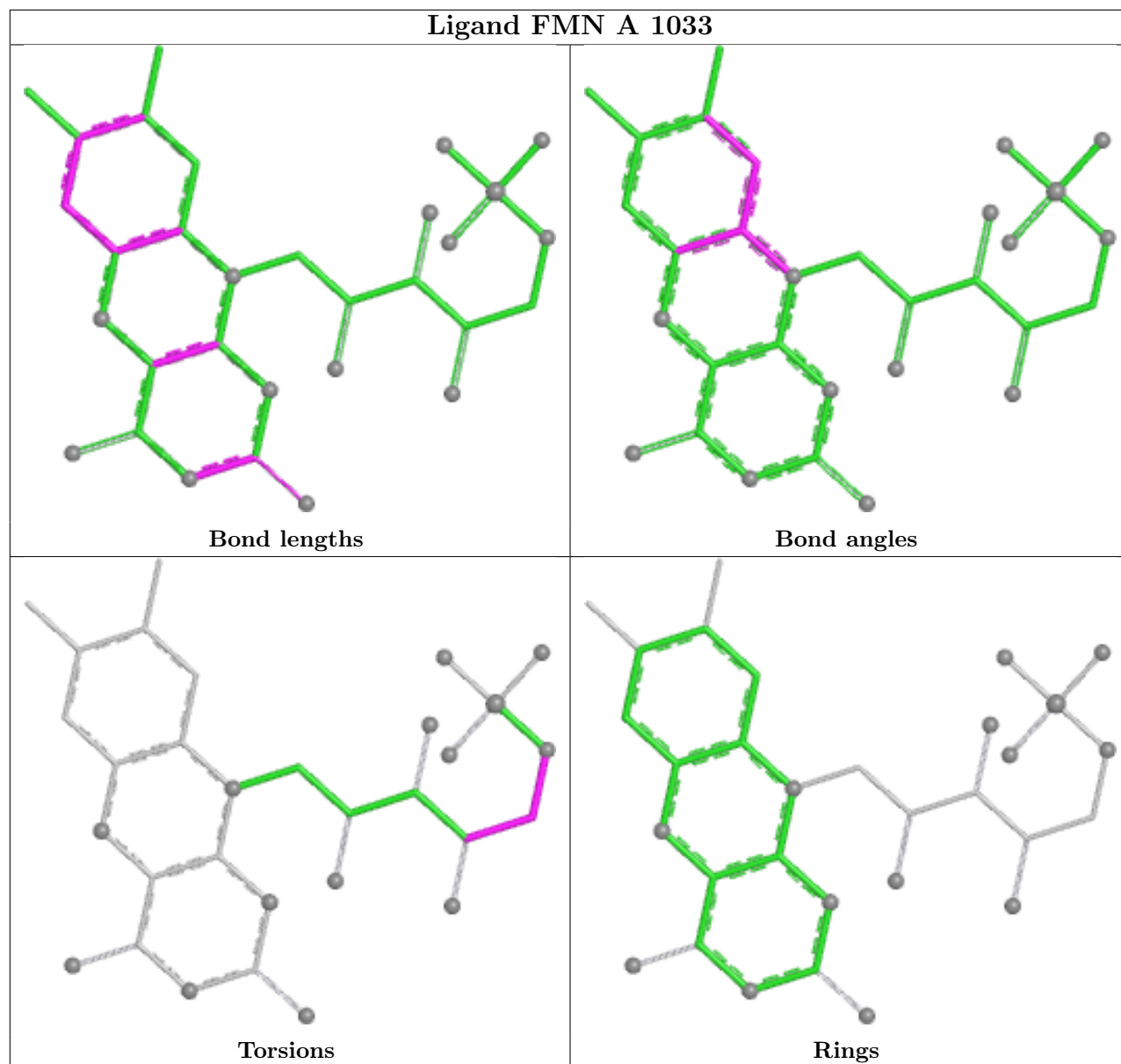
in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

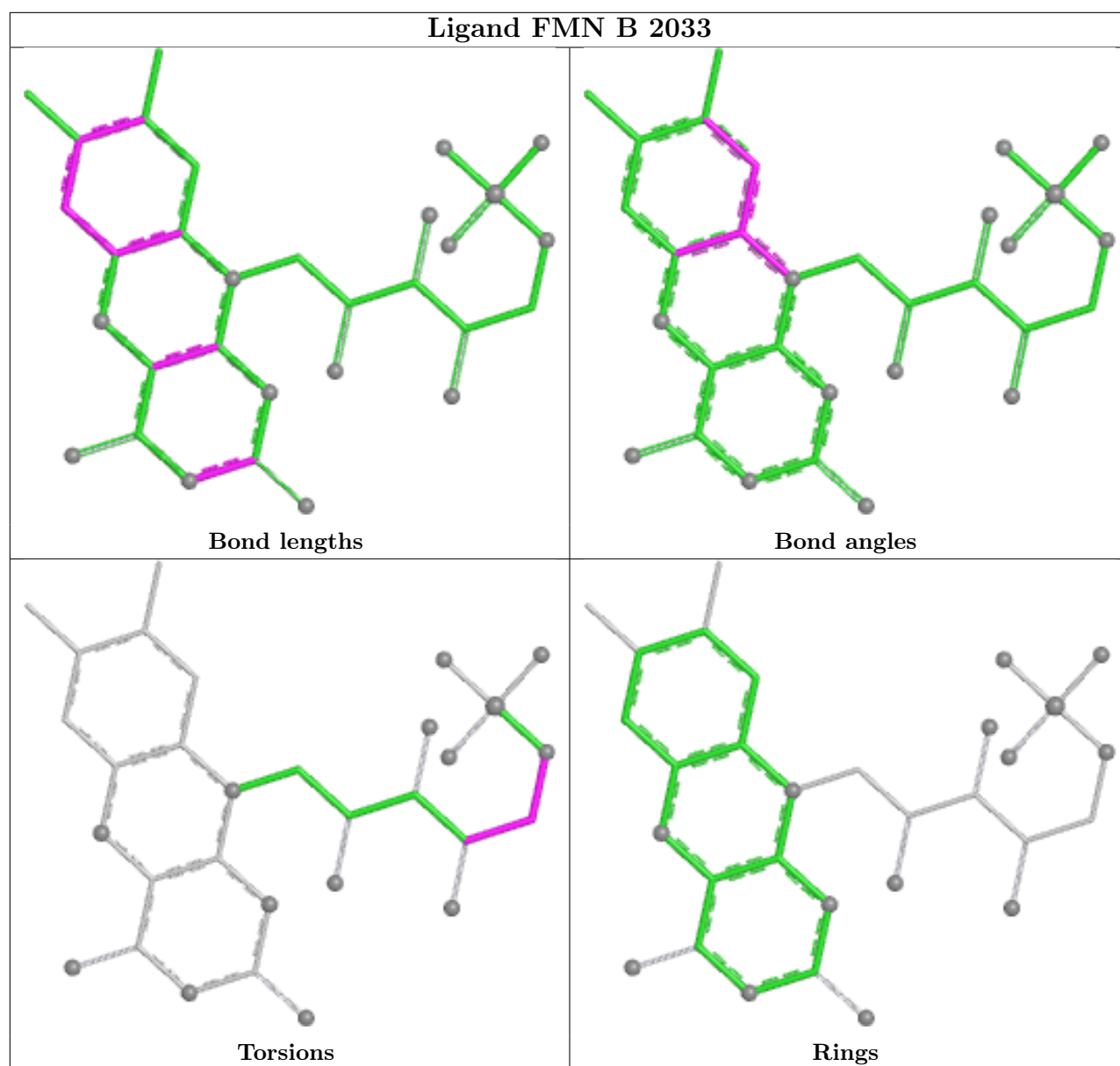


Ligand FMN C 3033



Ligand FMN A 1033





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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.