



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 08:20 PM UTC

PDB ID : 6S6U / pdb_00006s6u
EMDB ID : EMD-10106
Title : Structure of Azospirillum brasilense Glutamate Synthase in a6b4 oligomeric state.
Authors : Chaves-Sanjuan, A.; Bolognesi, M.
Deposited on : 2019-07-03
Resolution : 3.50 Å(reported)

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A user guide is available at

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

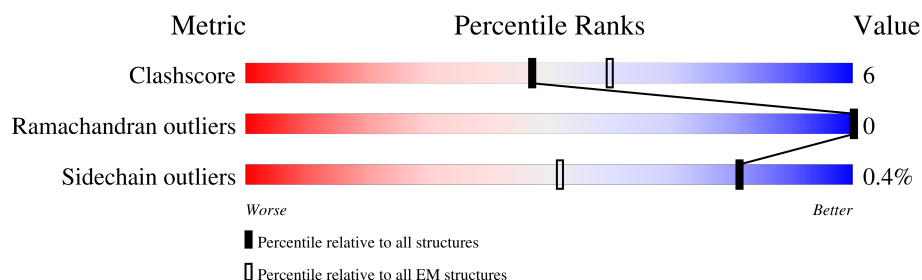
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	1515	83% 14% .
1	B	1515	83% 14% .
1	C	1515	82% 15% .
1	D	1515	83% 14% .
1	E	1515	82% 15% .
1	F	1515	83% 14% .
2	G	482	84% 13% .
2	H	482	80% 18% .
2	I	482	84% 14% .

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Mol	Chain	Length	Quality of chain
2	J	482	 A horizontal bar chart showing the quality of chain J. The bar is divided into two segments: a green segment representing 80% and a yellow segment representing 18%. A small grey segment is visible at the end of the bar.

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
6	FAD	H	503	X	-	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 82978 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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.

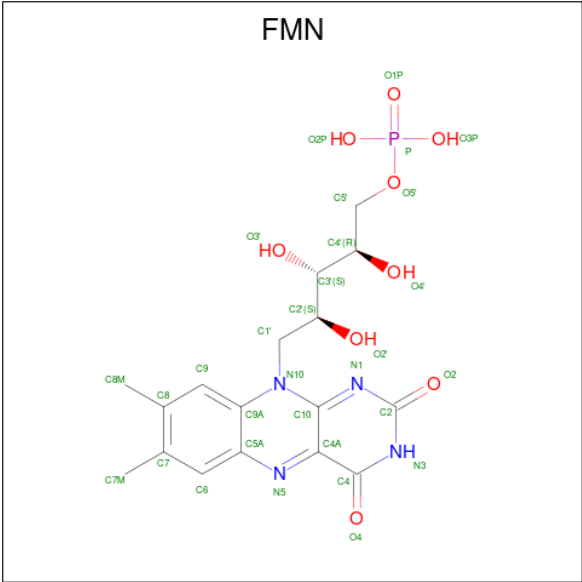
- Molecule 1 is a protein called Glutamate synthase [NADPH] large chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1472	Total 11337	C 7109	N 2036	O 2132	S 60	0	0
1	B	1472	Total 11337	C 7109	N 2036	O 2132	S 60	0	0
1	C	1472	Total 11337	C 7109	N 2036	O 2132	S 60	0	0
1	D	1472	Total 11337	C 7109	N 2036	O 2132	S 60	0	0
1	E	1472	Total 11337	C 7109	N 2036	O 2132	S 60	0	0
1	F	1472	Total 11337	C 7109	N 2036	O 2132	S 60	0	0

- Molecule 2 is a protein called Glutamate synthase [NADPH] small chain.

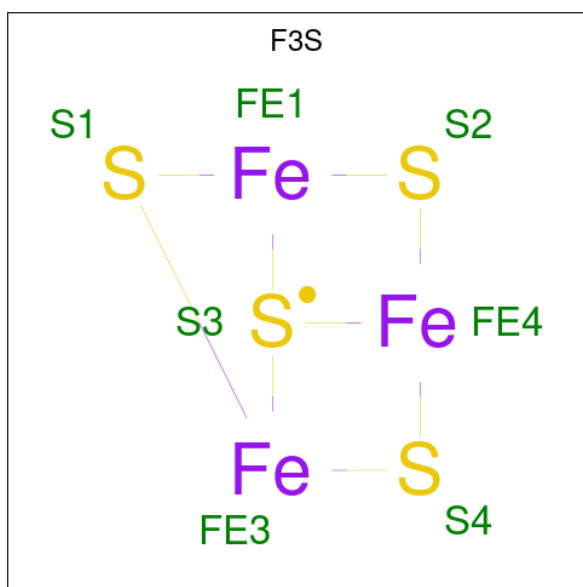
Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	472	Total 3613	C 2250	N 660	O 686	S 17	0	0
2	H	472	Total 3613	C 2250	N 660	O 686	S 17	0	0
2	I	472	Total 3613	C 2250	N 660	O 686	S 17	0	0
2	J	472	Total 3613	C 2250	N 660	O 686	S 17	0	0

- Molecule 3 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: C₁₇H₂₁N₄O₉P) (labeled as "Ligand of Interest" by depositor).



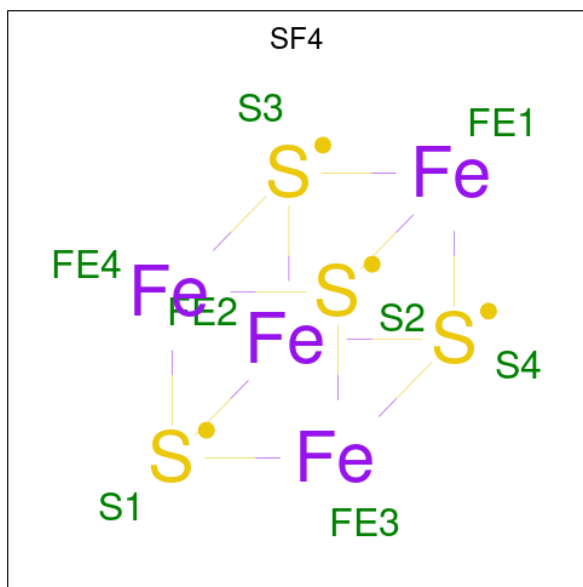
Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			31	17	4	9	1	
3	B	1	Total	C	N	O	P	0
			31	17	4	9	1	
3	C	1	Total	C	N	O	P	0
			31	17	4	9	1	
3	D	1	Total	C	N	O	P	0
			31	17	4	9	1	
3	E	1	Total	C	N	O	P	0
			31	17	4	9	1	
3	F	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 4 is FE3-S4 CLUSTER (CCD ID: F3S) (formula: Fe₃S₄).



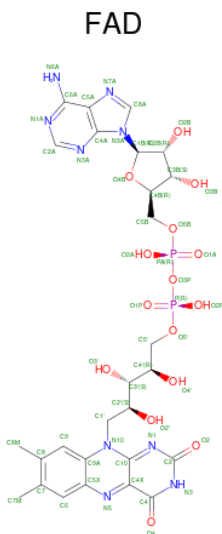
Mol	Chain	Residues	Atoms			AltConf
4	A	1	Total	Fe	S	0
			7	3	4	
4	B	1	Total	Fe	S	0
			7	3	4	
4	C	1	Total	Fe	S	0
			7	3	4	
4	D	1	Total	Fe	S	0
			7	3	4	
4	E	1	Total	Fe	S	0
			7	3	4	
4	F	1	Total	Fe	S	0
			7	3	4	

- Molecule 5 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			AltConf
5	G	1	Total	Fe	S	0
			8	4	4	
5	G	1	Total	Fe	S	0
			8	4	4	
5	H	1	Total	Fe	S	0
			8	4	4	
5	H	1	Total	Fe	S	0
			8	4	4	
5	I	1	Total	Fe	S	0
			8	4	4	
5	I	1	Total	Fe	S	0
			8	4	4	
5	J	1	Total	Fe	S	0
			8	4	4	
5	J	1	Total	Fe	S	0
			8	4	4	

- Molecule 6 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$) (labeled as "Ligand of Interest" by depositor).

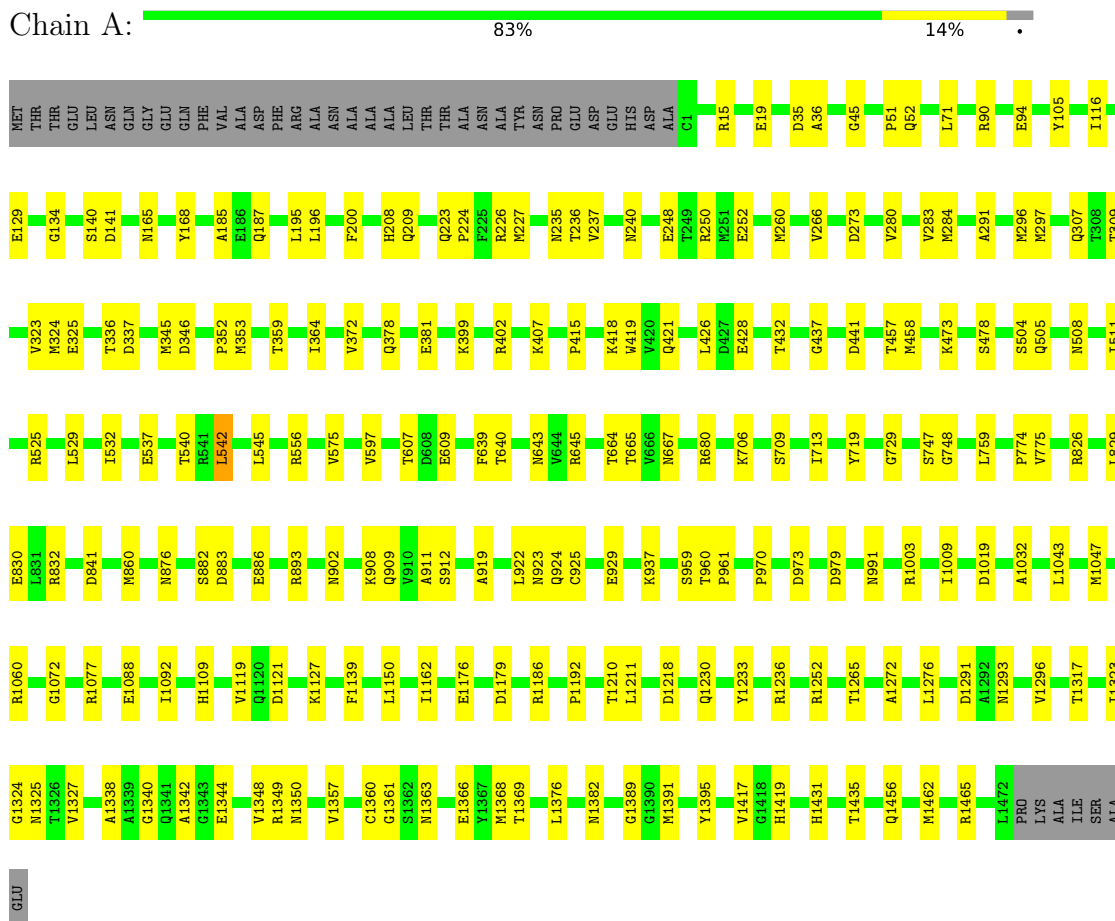


Mol	Chain	Residues	Atoms					AltConf
6	G	1	Total 53	C 27	N 9	O 15	P 2	0
6	H	1	Total 53	C 27	N 9	O 15	P 2	0
6	I	1	Total 53	C 27	N 9	O 15	P 2	0
6	J	1	Total 53	C 27	N 9	O 15	P 2	0

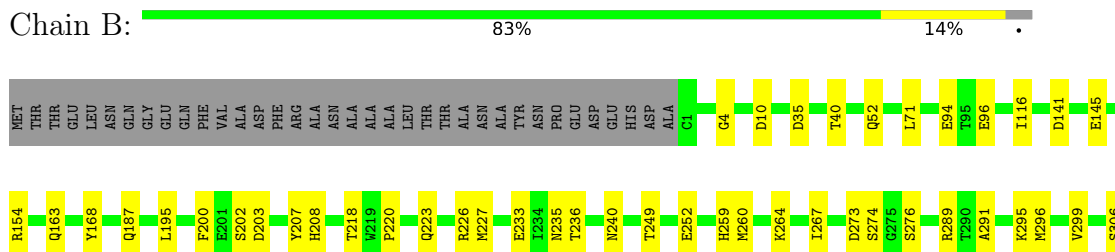
3 Residue-property plots

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.

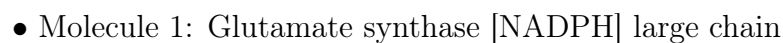
- Molecule 1: Glutamate synthase [NADPH] large chain



- Molecule 1: Glutamate synthase [NADPH] large chain

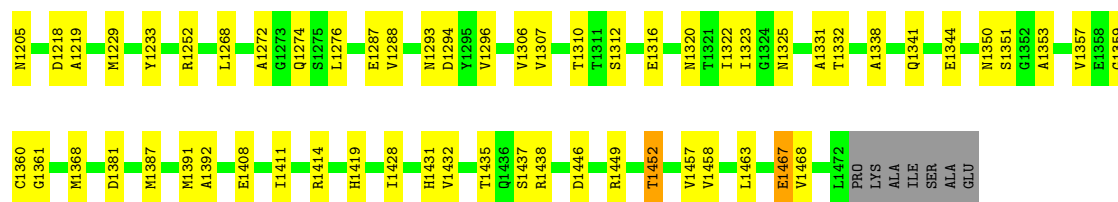


14%



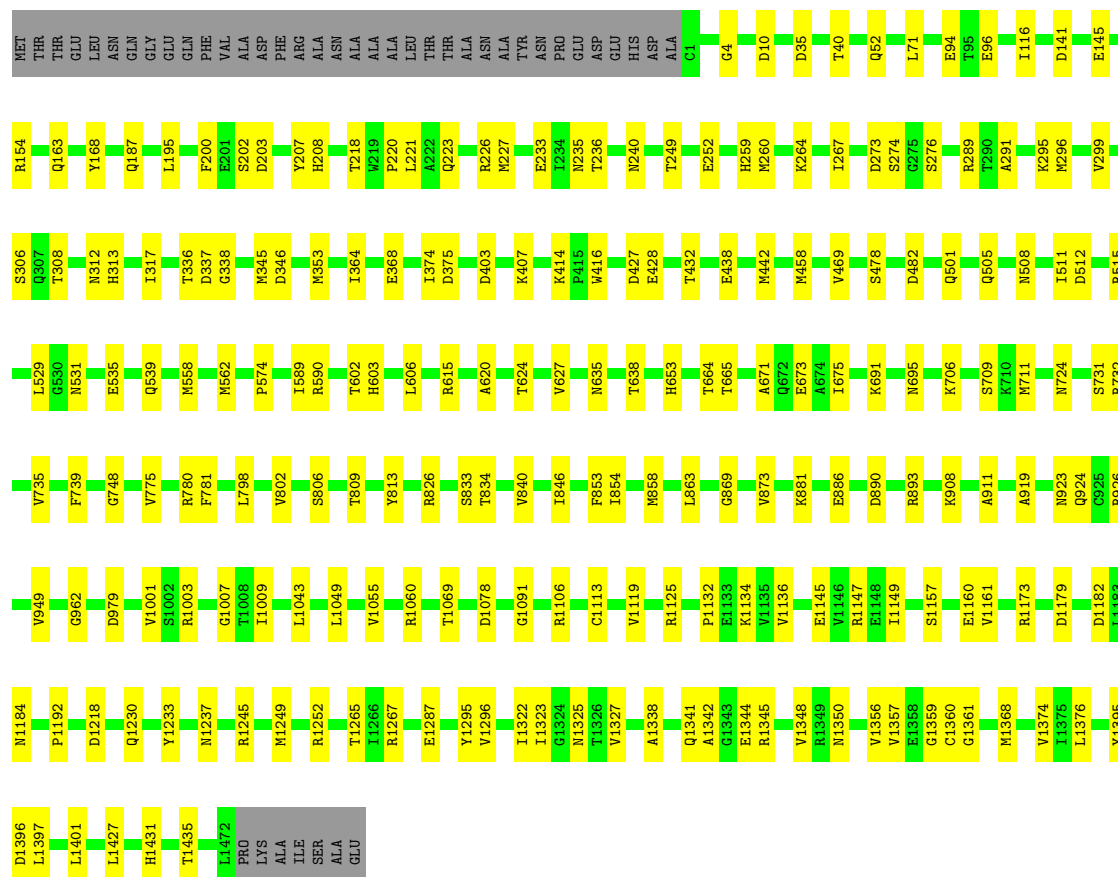
15%





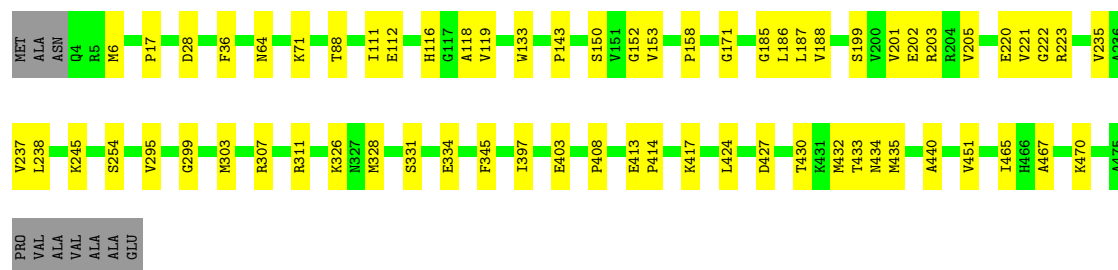
• Molecule 1: Glutamate synthase [NADPH] large chain

Chain F: 83% 14%



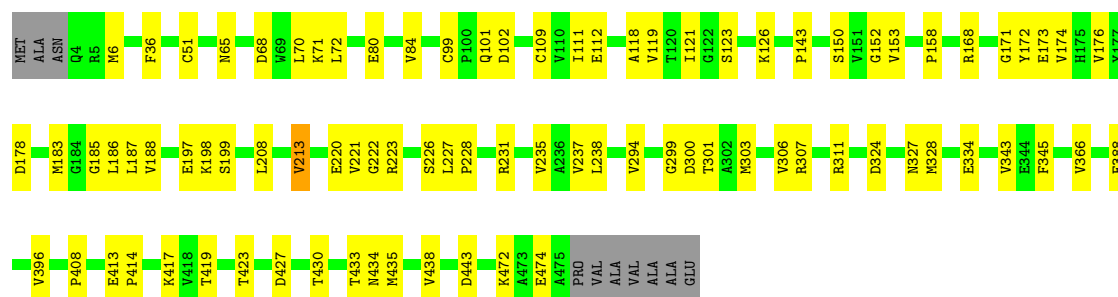
• Molecule 2: Glutamate synthase [NADPH] small chain

Chain G: 84% 13%



• Molecule 2: Glutamate synthase [NADPH] small chain

Chain H:  80% 18% .



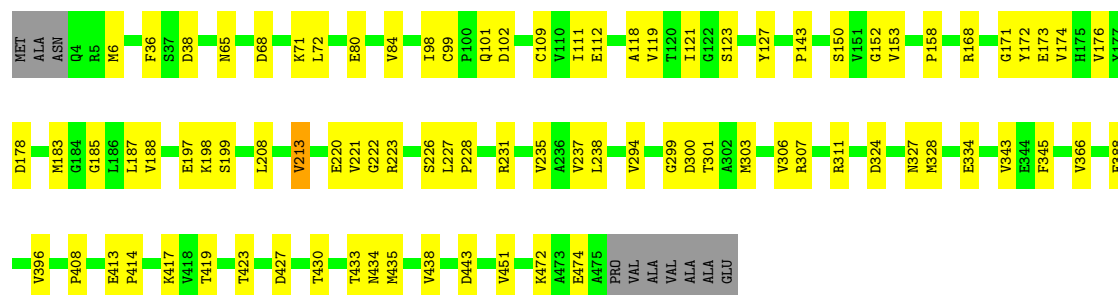
• Molecule 2: Glutamate synthase [NADPH] small chain

Chain I:  84% 14% .



• Molecule 2: Glutamate synthase [NADPH] small chain

Chain J:  80% 18% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	76146	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMN, F3S, FAD, SF4

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	0.16	0/11545	0.32	0/15613
1	B	0.15	0/11545	0.32	0/15613
1	C	0.16	0/11545	0.34	0/15613
1	D	0.16	0/11545	0.32	0/15613
1	E	0.16	0/11545	0.34	0/15613
1	F	0.15	0/11545	0.32	0/15613
2	G	0.16	0/3681	0.34	0/4988
2	H	0.15	0/3681	0.33	0/4988
2	I	0.16	0/3681	0.34	0/4988
2	J	0.15	0/3681	0.33	0/4988
All	All	0.16	0/83994	0.33	0/113630

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

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	11337	0	11355	128	0
1	B	11337	0	11355	128	0
1	C	11337	0	11355	138	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	11337	0	11355	129	0
1	E	11337	0	11355	140	0
1	F	11337	0	11355	127	0
2	G	3613	0	3553	40	0
2	H	3613	0	3553	59	0
2	I	3613	0	3553	41	0
2	J	3613	0	3553	60	0
3	A	31	0	19	0	0
3	B	31	0	19	1	0
3	C	31	0	19	1	0
3	D	31	0	19	0	0
3	E	31	0	19	0	0
3	F	31	0	19	1	0
4	A	7	0	0	0	0
4	B	7	0	0	1	0
4	C	7	0	0	0	0
4	D	7	0	0	0	0
4	E	7	0	0	0	0
4	F	7	0	0	1	0
5	G	16	0	0	0	0
5	H	16	0	0	0	0
5	I	16	0	0	0	0
5	J	16	0	0	0	0
6	G	53	0	31	7	0
6	H	53	0	31	9	0
6	I	53	0	31	8	0
6	J	53	0	31	13	0
All	All	82978	0	82580	997	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.

The worst 5 of 997 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)
6:H:503:FAD:H2'	6:H:503:FAD:H9	1.26	1.15
6:H:503:FAD:H9	6:H:503:FAD:C2'	2.01	0.91
1:A:235:ASN:OD1	1:A:508:ASN:ND2	2.06	0.88
1:D:235:ASN:OD1	1:D:508:ASN:ND2	2.06	0.88
6:I:503:FAD:H9	6:I:503:FAD:H2'	1.55	0.87

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1470/1515 (97%)	1421 (97%)	49 (3%)	0	100	100
1	B	1470/1515 (97%)	1429 (97%)	41 (3%)	0	100	100
1	C	1470/1515 (97%)	1427 (97%)	43 (3%)	0	100	100
1	D	1470/1515 (97%)	1421 (97%)	49 (3%)	0	100	100
1	E	1470/1515 (97%)	1429 (97%)	41 (3%)	0	100	100
1	F	1470/1515 (97%)	1429 (97%)	41 (3%)	0	100	100
2	G	470/482 (98%)	447 (95%)	23 (5%)	0	100	100
2	H	470/482 (98%)	444 (94%)	26 (6%)	0	100	100
2	I	470/482 (98%)	447 (95%)	23 (5%)	0	100	100
2	J	470/482 (98%)	445 (95%)	25 (5%)	0	100	100
All	All	10700/11018 (97%)	10339 (97%)	361 (3%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1201/1233 (97%)	1198 (100%)	3 (0%)	87	85
1	B	1201/1233 (97%)	1199 (100%)	2 (0%)	87	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	1201/1233 (97%)	1189 (99%)	12 (1%)	68	75
1	D	1201/1233 (97%)	1198 (100%)	3 (0%)	87	85
1	E	1201/1233 (97%)	1189 (99%)	12 (1%)	68	75
1	F	1201/1233 (97%)	1199 (100%)	2 (0%)	87	85
2	G	373/379 (98%)	373 (100%)	0	100	100
2	H	373/379 (98%)	371 (100%)	2 (0%)	81	80
2	I	373/379 (98%)	373 (100%)	0	100	100
2	J	373/379 (98%)	371 (100%)	2 (0%)	81	80
All	All	8698/8914 (98%)	8660 (100%)	38 (0%)	81	81

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	1332	THR
2	H	474	GLU
1	E	1381	ASP
1	F	438	GLU
2	J	474	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 167 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	1325	ASN
2	G	64	ASN
1	F	52	GLN
1	F	539	GLN
2	H	86	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

24 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$
3	FMN	A	1501	-	33,33,33	1.09	2 (6%)	48,50,50	1.24	9 (18%)
3	FMN	B	1501	-	33,33,33	1.06	2 (6%)	48,50,50	1.25	8 (16%)
5	SF4	H	501	2	0,12,12	-	-	-	-	-
6	FAD	J	503	-	58,58,58	0.60	0	85,89,89	0.71	2 (2%)
5	SF4	I	502	2	0,12,12	-	-	-	-	-
4	F3S	C	1502	1	0,9,9	-	-	-	-	-
4	F3S	F	1502	1	0,9,9	-	-	-	-	-
3	FMN	F	1501	-	33,33,33	1.06	2 (6%)	48,50,50	1.24	7 (14%)
4	F3S	D	1502	1	0,9,9	-	-	-	-	-
5	SF4	I	501	2	0,12,12	-	-	-	-	-
5	SF4	G	502	2	0,12,12	-	-	-	-	-
6	FAD	I	503	-	58,58,58	0.61	0	85,89,89	0.65	1 (1%)
5	SF4	J	502	2	0,12,12	-	-	-	-	-
5	SF4	G	501	2	0,12,12	-	-	-	-	-
3	FMN	C	1501	-	33,33,33	1.07	2 (6%)	48,50,50	1.24	8 (16%)
6	FAD	G	503	-	58,58,58	0.62	0	85,89,89	0.70	1 (1%)
4	F3S	B	1502	1	0,9,9	-	-	-	-	-
6	FAD	H	503	-	58,58,58	0.60	0	85,89,89	0.73	1 (1%)
4	F3S	A	1502	1	0,9,9	-	-	-	-	-
3	FMN	D	1501	-	33,33,33	1.08	2 (6%)	48,50,50	1.24	9 (18%)
5	SF4	J	501	2	0,12,12	-	-	-	-	-
3	FMN	E	1501	-	33,33,33	1.08	2 (6%)	48,50,50	1.23	9 (18%)
5	SF4	H	502	2	0,12,12	-	-	-	-	-
4	F3S	E	1502	1	0,9,9	-	-	-	-	-

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	1501	-	-	0/18/18/18	0/3/3/3
3	FMN	B	1501	-	-	1/18/18/18	0/3/3/3
5	SF4	H	501	2	-	-	0/6/5/5
6	FAD	J	503	-	-	9/34/50/50	0/6/6/6
5	SF4	I	502	2	-	-	0/6/5/5
4	F3S	C	1502	1	-	-	0/3/3/3
4	F3S	F	1502	1	-	-	0/3/3/3
3	FMN	F	1501	-	-	1/18/18/18	0/3/3/3
4	F3S	D	1502	1	-	-	0/3/3/3
5	SF4	H	502	2	-	-	0/6/5/5
5	SF4	I	501	2	-	-	0/6/5/5
5	SF4	G	502	2	-	-	0/6/5/5
6	FAD	I	503	-	-	12/34/50/50	0/6/6/6
5	SF4	J	502	2	-	-	0/6/5/5
5	SF4	G	501	2	-	-	0/6/5/5
3	FMN	C	1501	-	-	1/18/18/18	0/3/3/3
6	FAD	G	503	-	-	7/34/50/50	0/6/6/6
4	F3S	B	1502	1	-	-	0/3/3/3
6	FAD	H	503	-	2/2/9/9	9/34/50/50	0/6/6/6
3	FMN	D	1501	-	-	0/18/18/18	0/3/3/3
5	SF4	J	501	2	-	-	0/6/5/5
3	FMN	E	1501	-	-	1/18/18/18	0/3/3/3
4	F3S	A	1502	1	-	-	0/3/3/3
4	F3S	E	1502	1	-	-	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	1501	FMN	C4A-N5	3.42	1.38	1.30
3	B	1501	FMN	C4A-N5	3.42	1.38	1.30
3	C	1501	FMN	C4A-N5	3.31	1.37	1.30
3	E	1501	FMN	C4A-N5	3.31	1.37	1.30
3	A	1501	FMN	C4A-N5	3.25	1.37	1.30

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1501	FMN	C4-N3-C2	-3.27	119.83	125.64

Continued on next page...

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1501	FMN	C4-N3-C2	-3.27	119.84	125.64
3	E	1501	FMN	C4-N3-C2	-3.27	119.84	125.64
3	A	1501	FMN	C4-N3-C2	-3.25	119.87	125.64
3	B	1501	FMN	C4-N3-C2	-3.24	119.88	125.64

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	H	503	FAD	C4'
6	H	503	FAD	C3'

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	G	503	FAD	C2'-C1'-N10-C10
6	G	503	FAD	N10-C1'-C2'-O2'
6	G	503	FAD	N10-C1'-C2'-C3'
6	H	503	FAD	C2'-C1'-N10-C9A
6	H	503	FAD	C2'-C1'-N10-C10

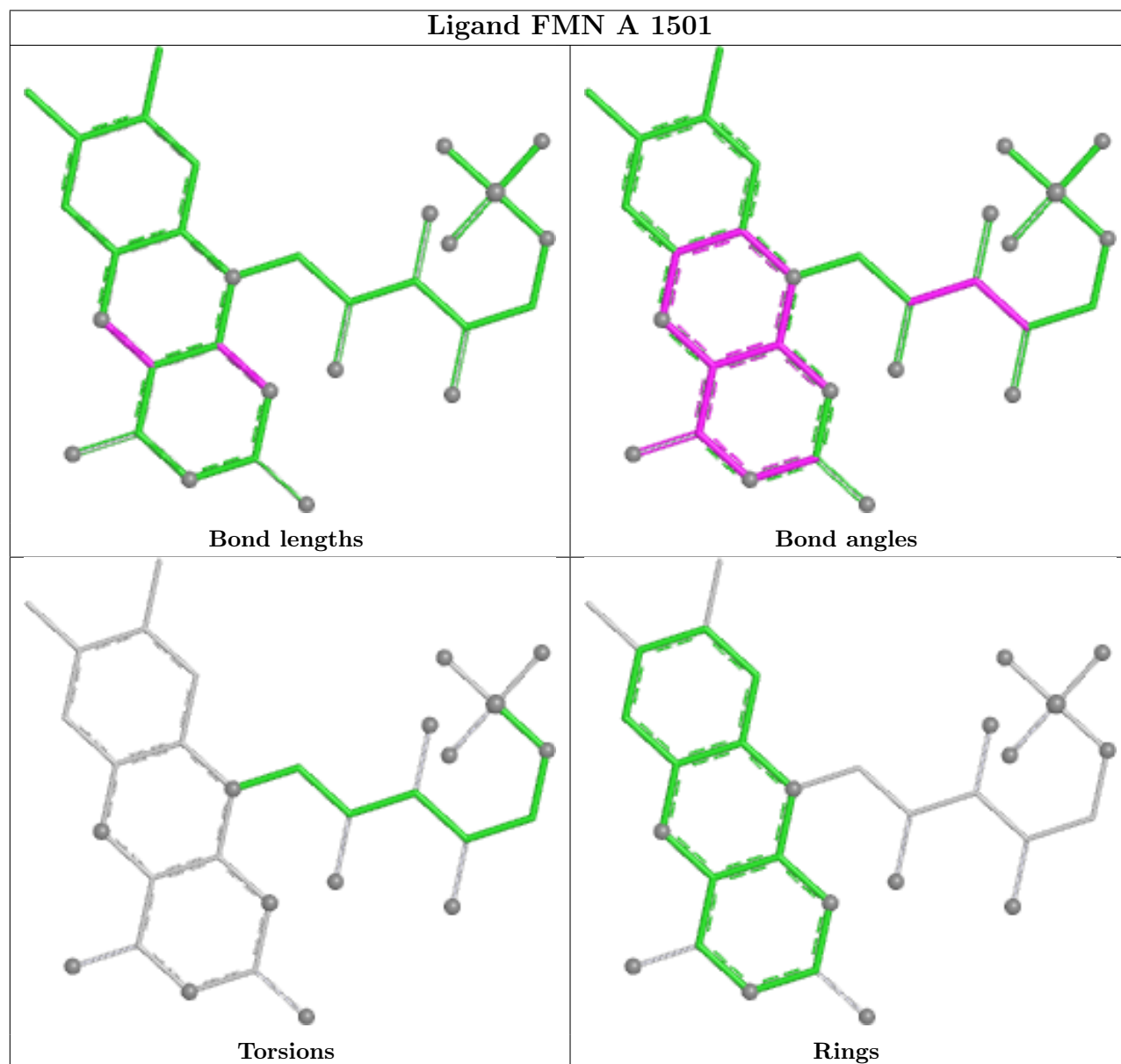
There are no ring outliers.

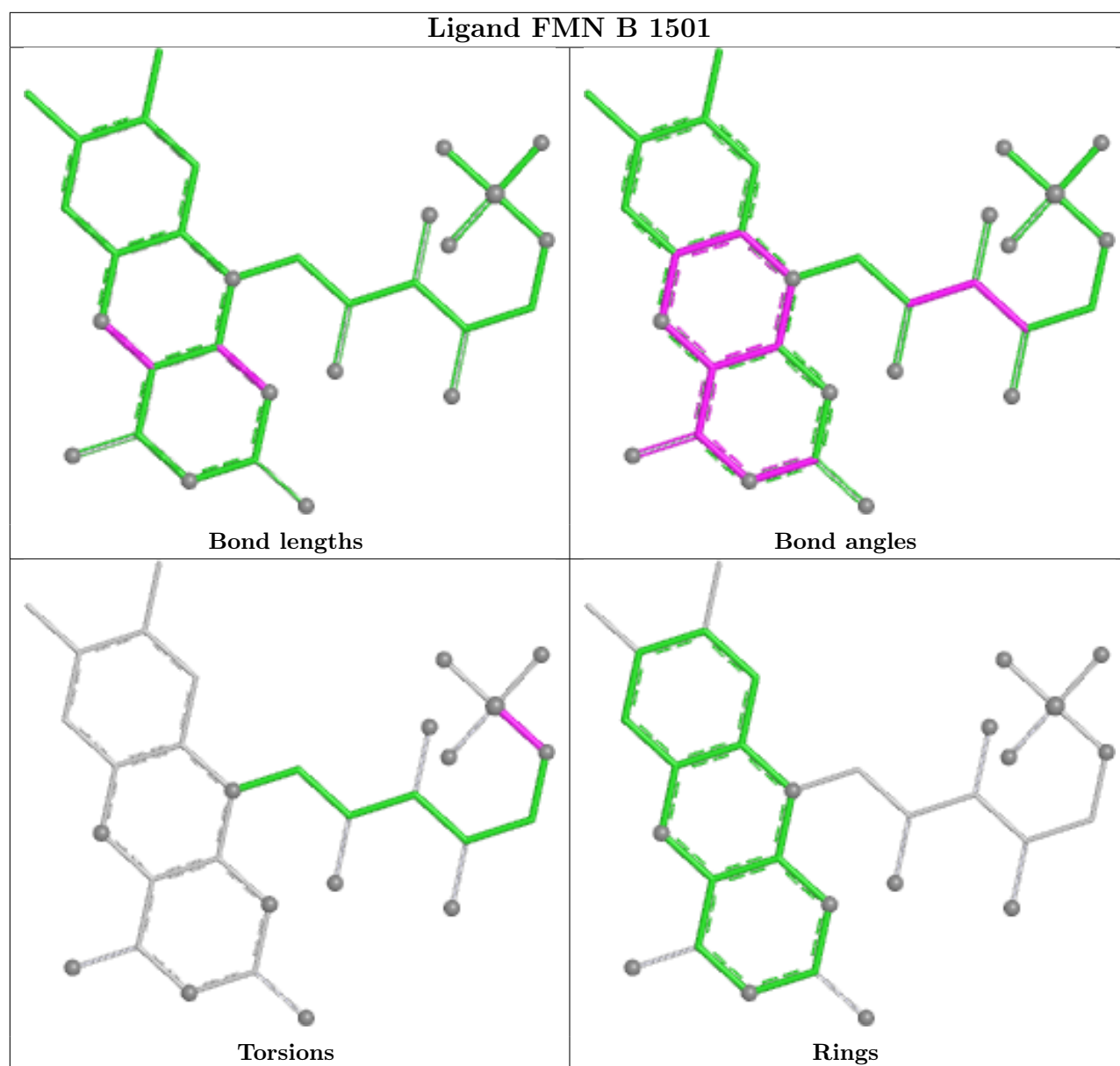
9 monomers are involved in 42 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1501	FMN	1	0
6	J	503	FAD	13	0
4	F	1502	F3S	1	0
3	F	1501	FMN	1	0
6	I	503	FAD	8	0
3	C	1501	FMN	1	0
6	G	503	FAD	7	0
4	B	1502	F3S	1	0
6	H	503	FAD	9	0

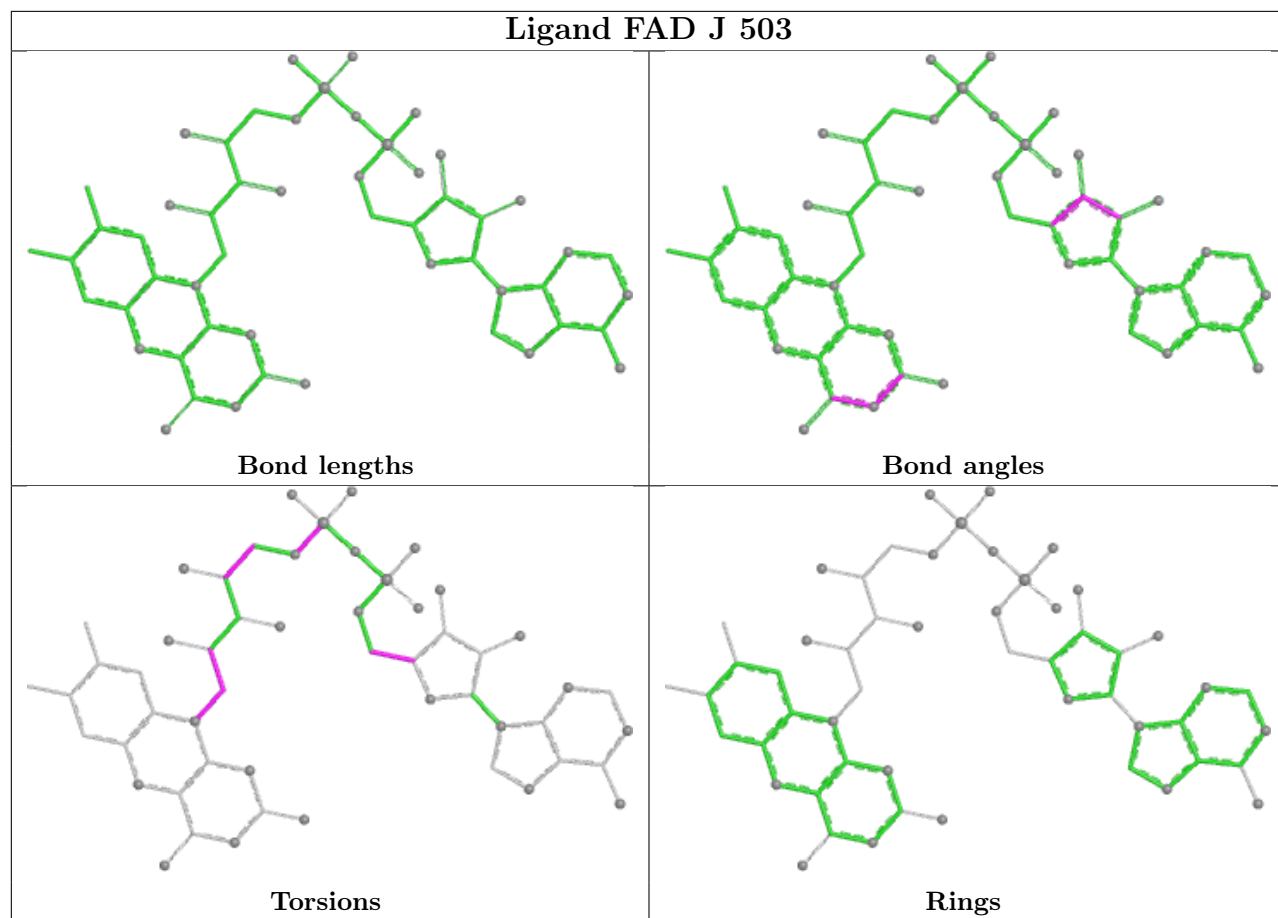
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

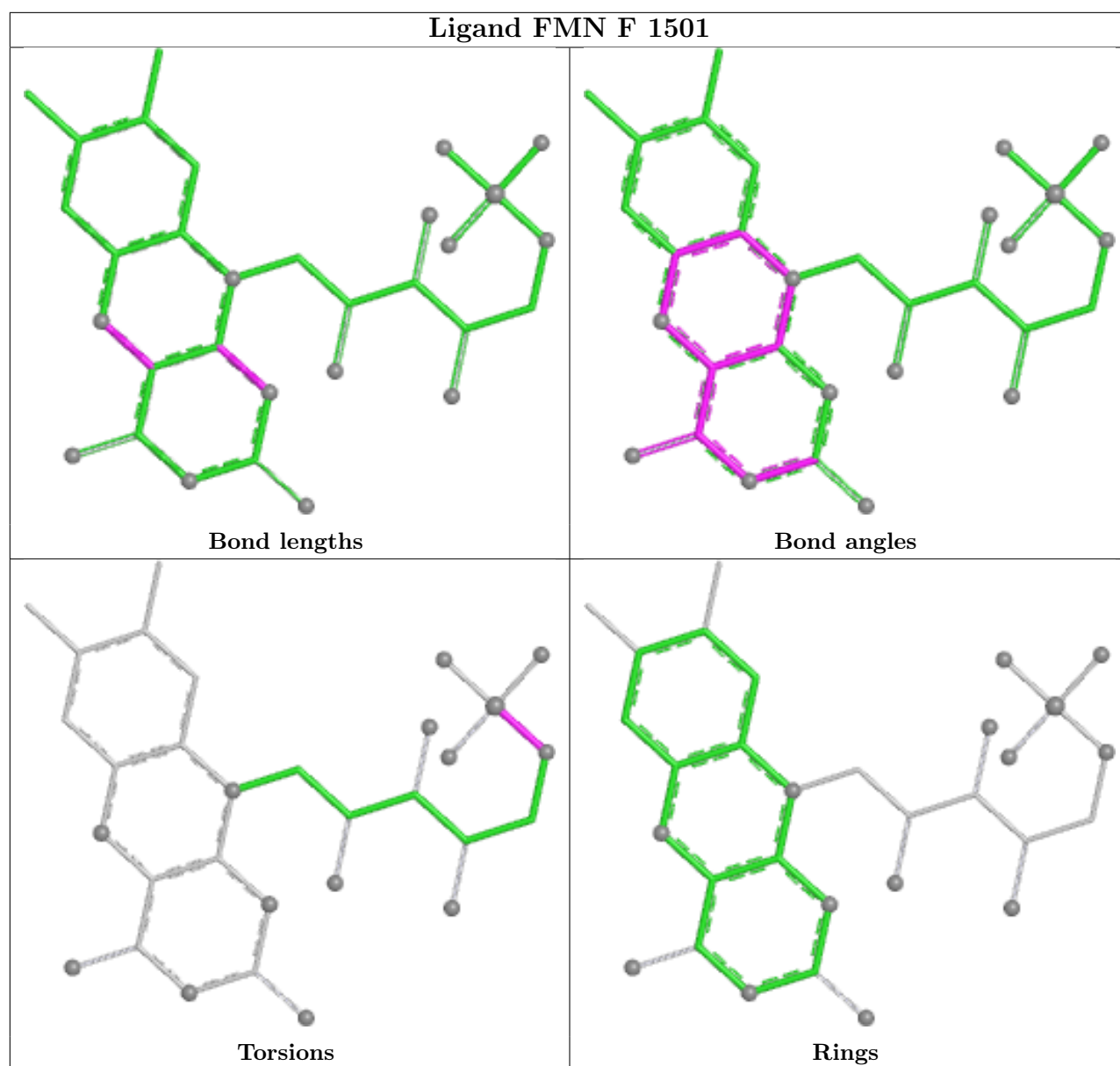
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents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



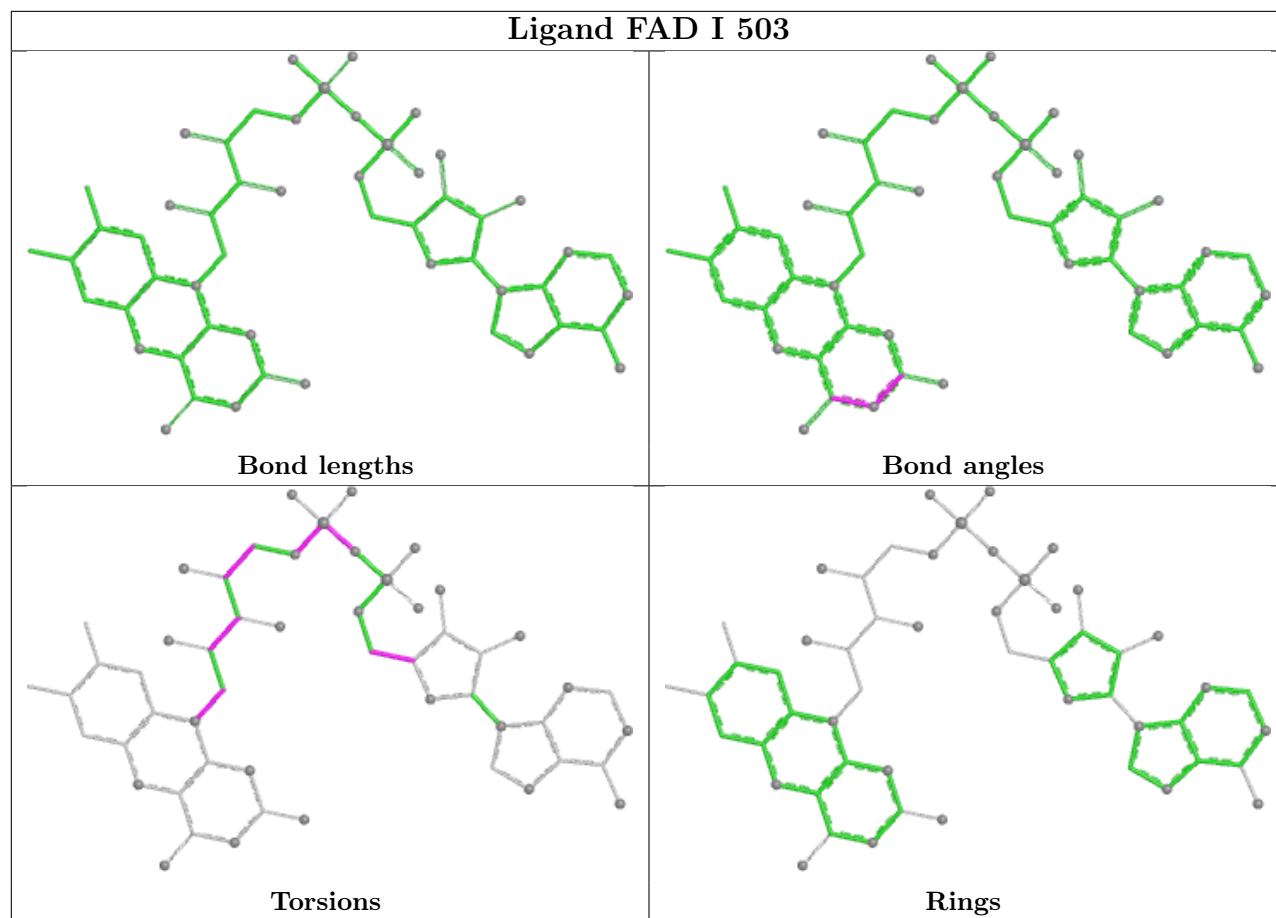


Ligand FAD J 503

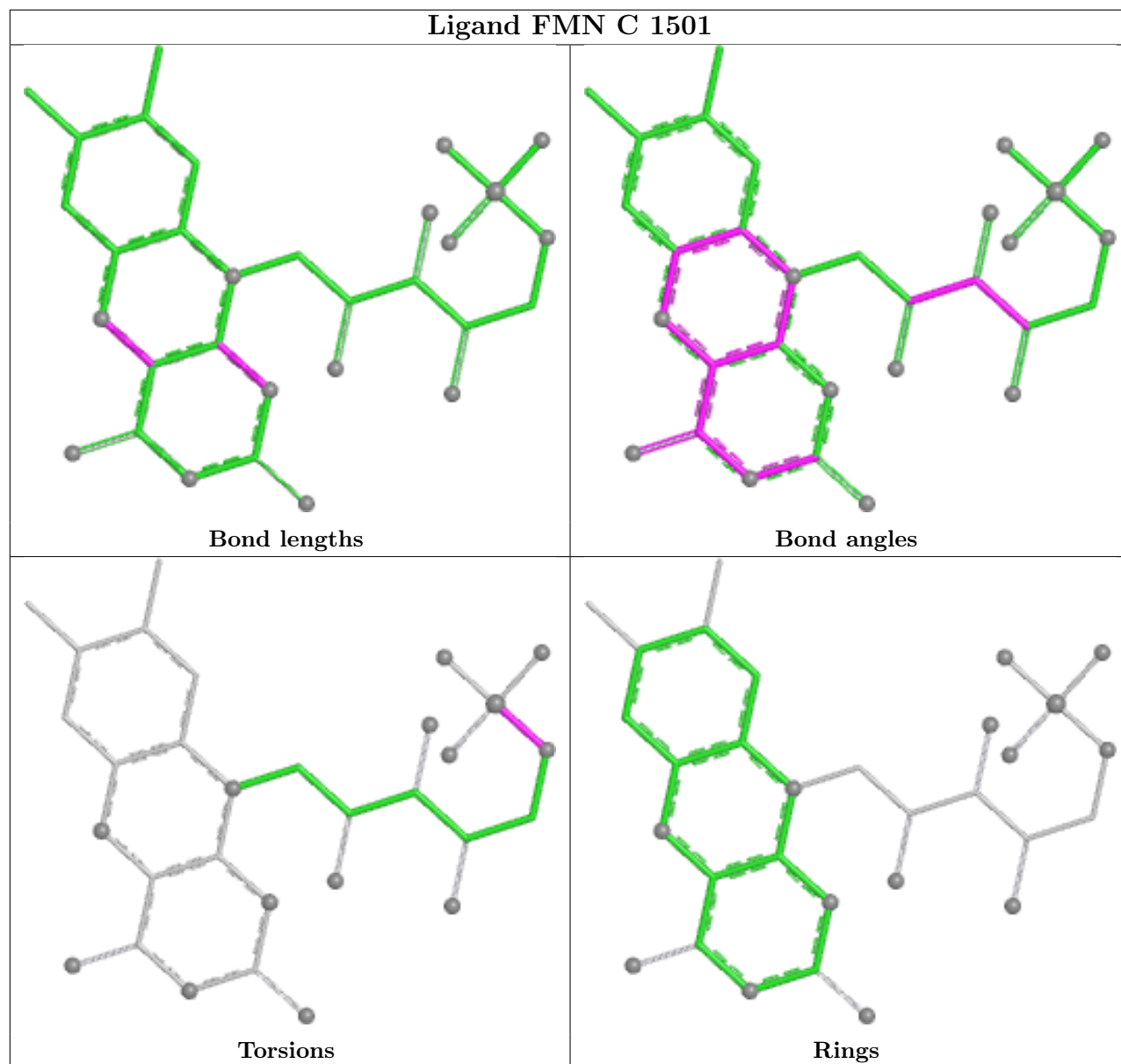


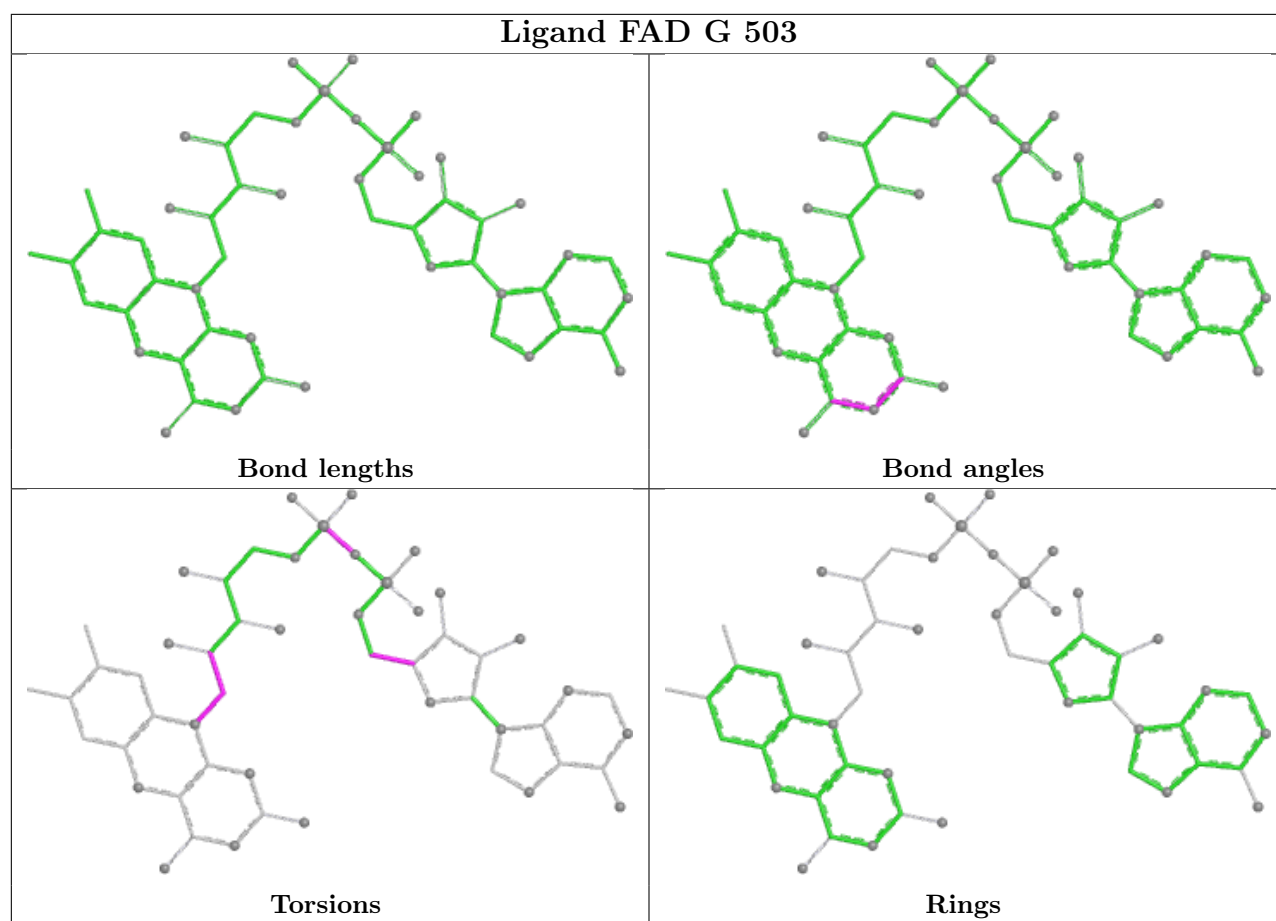


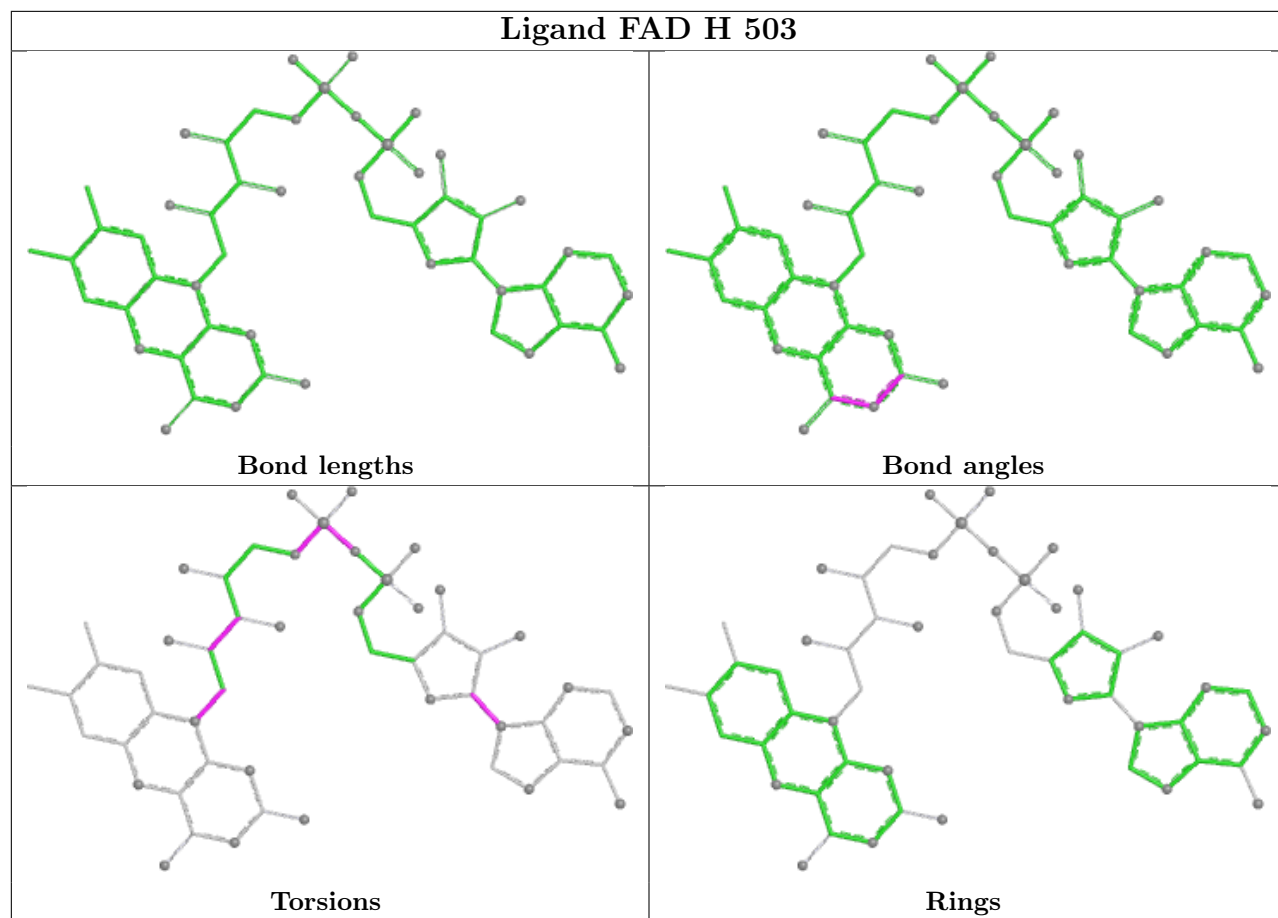
Ligand FAD I 503



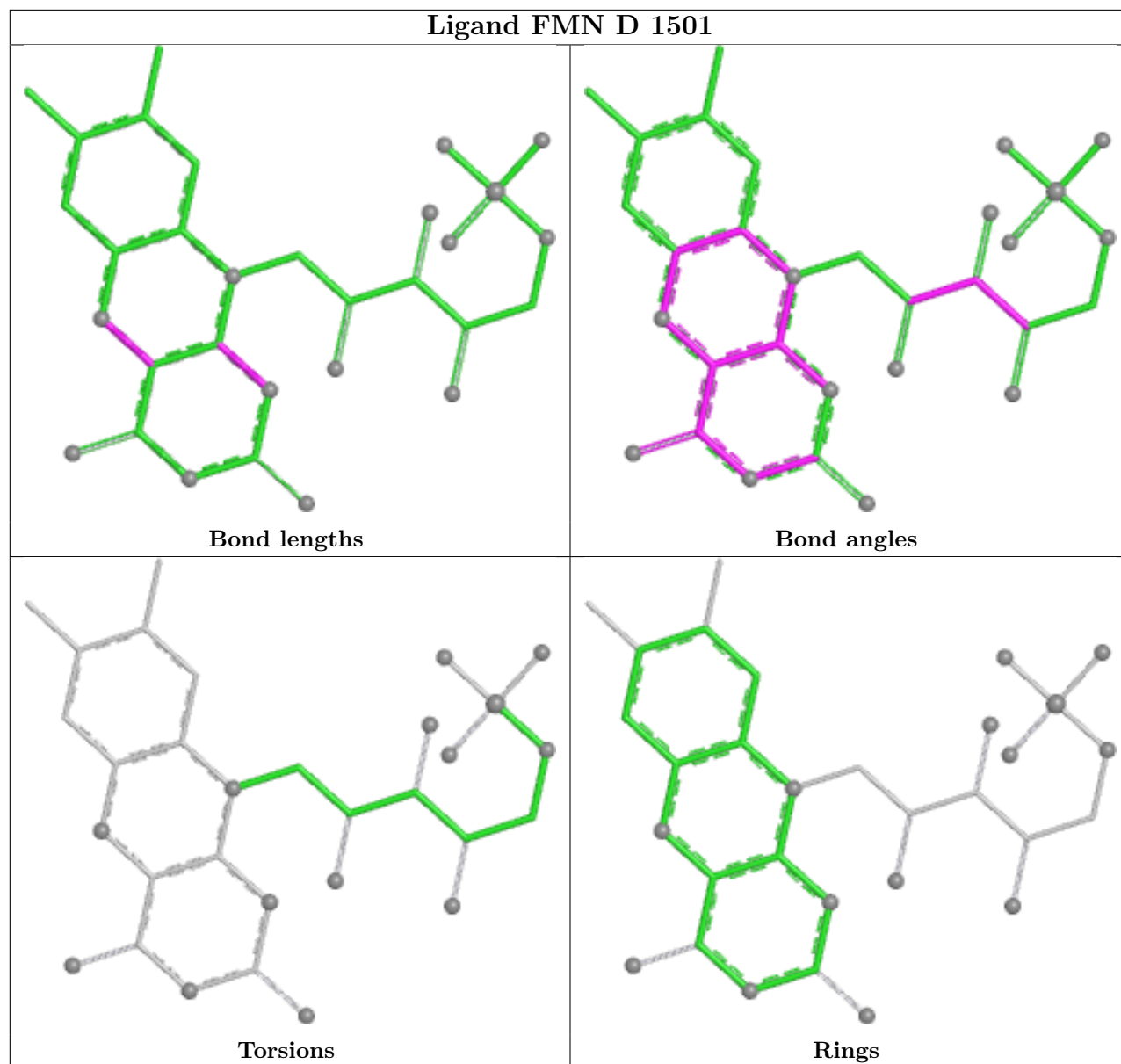
Ligand FMN C 1501

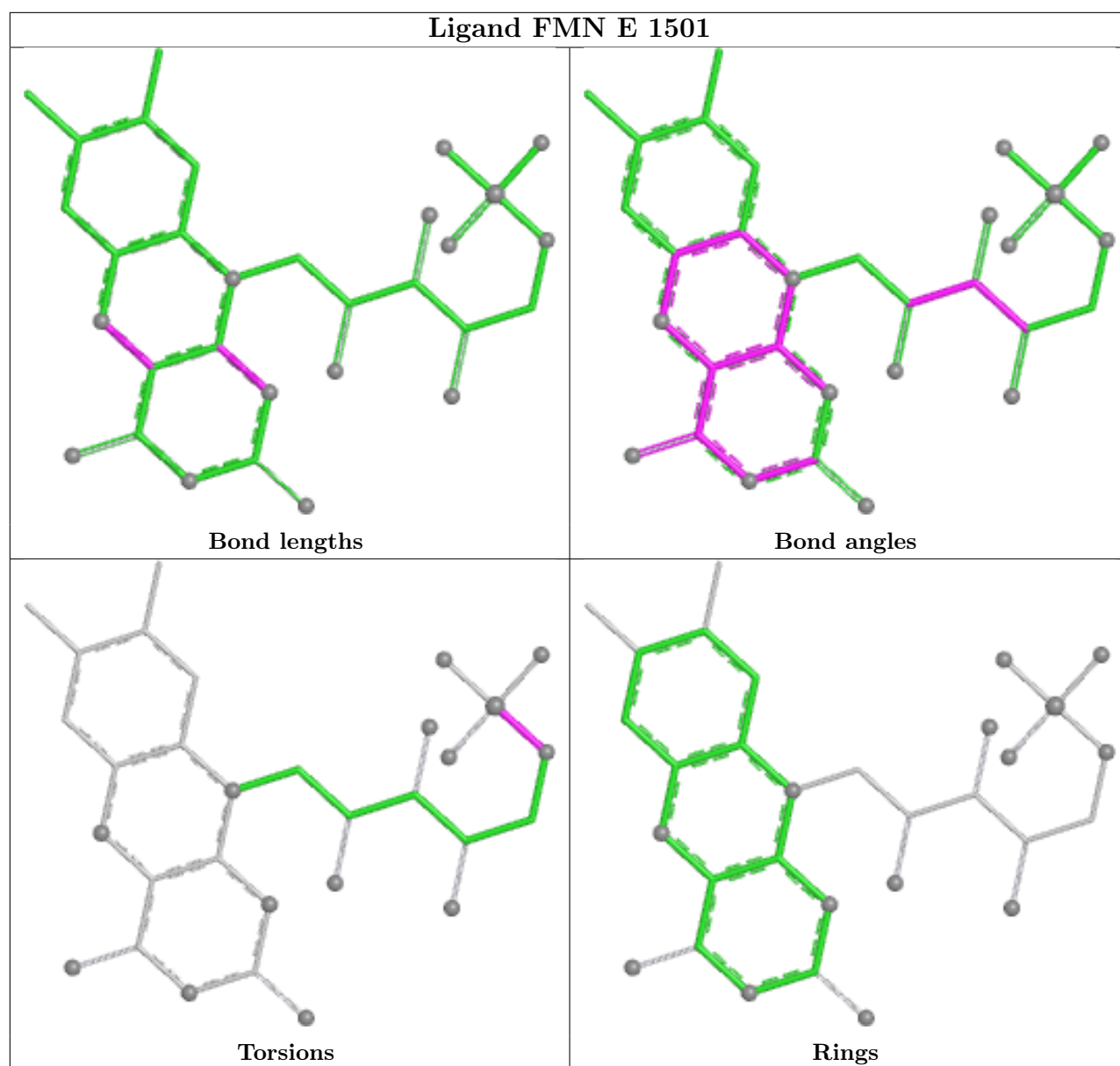






Ligand FMN D 1501





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 Map visualisation

This section contains visualisations of the EMDB entry EMD-10106. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.