



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 12, 2024 – 09:01 AM EDT

PDB ID : 1KR2
Title : CRYSTAL STRUCTURE OF HUMAN NMN/NAMN ADENYLYL TRANSFERASE COMPLEXED WITH TIAZOFURIN ADENINE DINUCLEOTIDE (TAD)
Authors : Zhou, T.; Kurnasov, O.; Tomchick, D.R.; Binns, D.D.; Grishin, N.V.; Marquez, V.E.; Osterman, A.L.; Zhang, H.
Deposited on : 2002-01-08
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

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

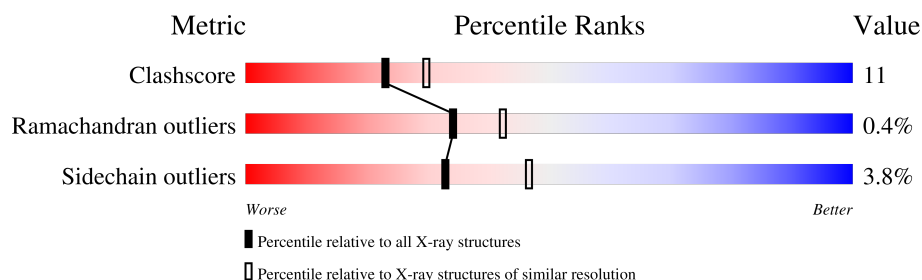
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (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 ≥ 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	279	
1	B	279	
1	C	279	
1	D	279	
1	E	279	
1	F	279	

2 Entry composition [i](#)

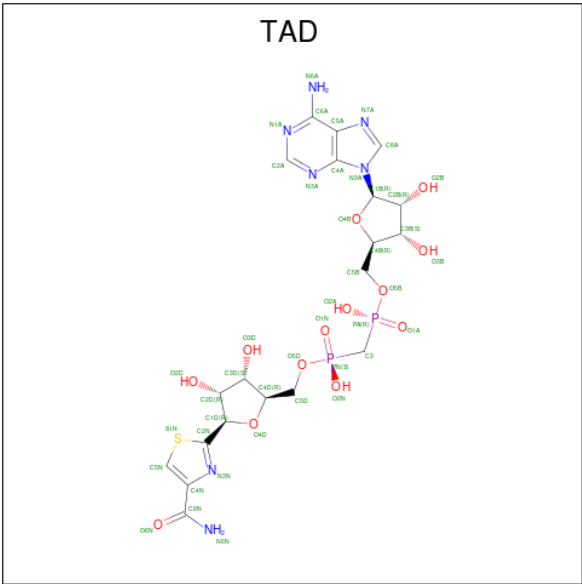
There are 3 unique types of molecules in this entry. The entry contains 12192 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 NICOTINAMIDE MONONUCLEOTIDE ADENYLYL TRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	233	Total	C	N	O	S	0	0	0
			1875	1195	331	343	6			
1	B	233	Total	C	N	O	S	0	0	0
			1875	1195	331	343	6			
1	C	233	Total	C	N	O	S	0	0	0
			1875	1195	331	343	6			
1	D	233	Total	C	N	O	S	0	0	0
			1875	1195	331	343	6			
1	E	232	Total	C	N	O	S	0	0	0
			1866	1190	330	340	6			
1	F	231	Total	C	N	O	S	0	0	0
			1861	1187	329	339	6			

- Molecule 2 is BETA-METHYLENE-THIAZOLE-4-CARBOXYAMIDE-ADENINE DINUCLEOTIDE (three-letter code: TAD) (formula: C₂₀H₂₇N₇O₁₃P₂S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 43	C 20	N 7	O 13	P 2	S 1	0	0
2	B	1	Total 43	C 20	N 7	O 13	P 2	S 1	0	0
2	C	1	Total 43	C 20	N 7	O 13	P 2	S 1	0	0
2	D	1	Total 43	C 20	N 7	O 13	P 2	S 1	0	0
2	E	1	Total 43	C 20	N 7	O 13	P 2	S 1	0	0
2	F	1	Total 43	C 20	N 7	O 13	P 2	S 1	0	0

- Molecule 3 is water.

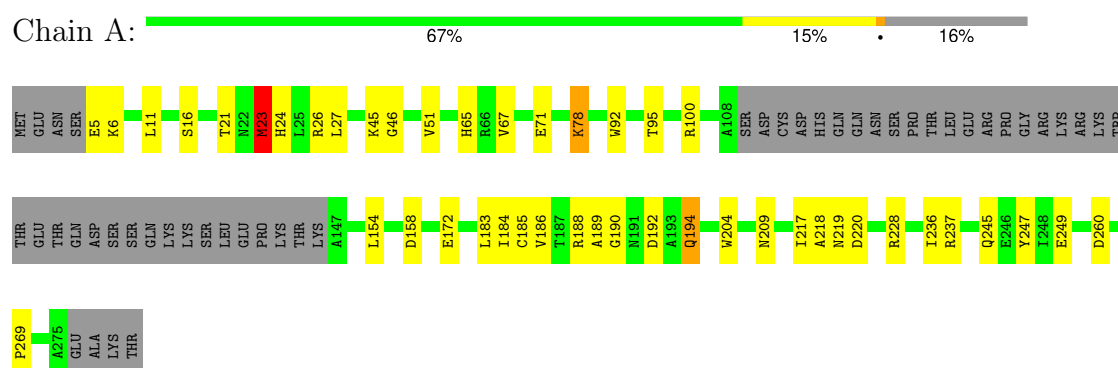
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	155	Total 155	O 155	0	0
3	B	128	Total 128	O 128	0	0
3	C	168	Total 168	O 168	0	0
3	D	103	Total 103	O 103	0	0
3	E	83	Total 83	O 83	0	0
3	F	70	Total 70	O 70	0	0

3 Residue-property plots [i](#)

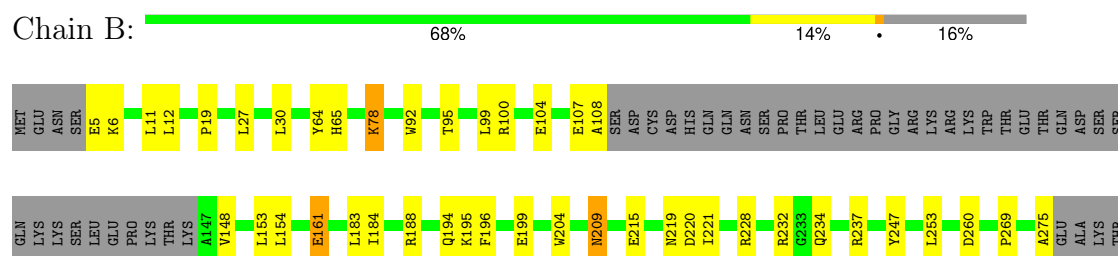
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

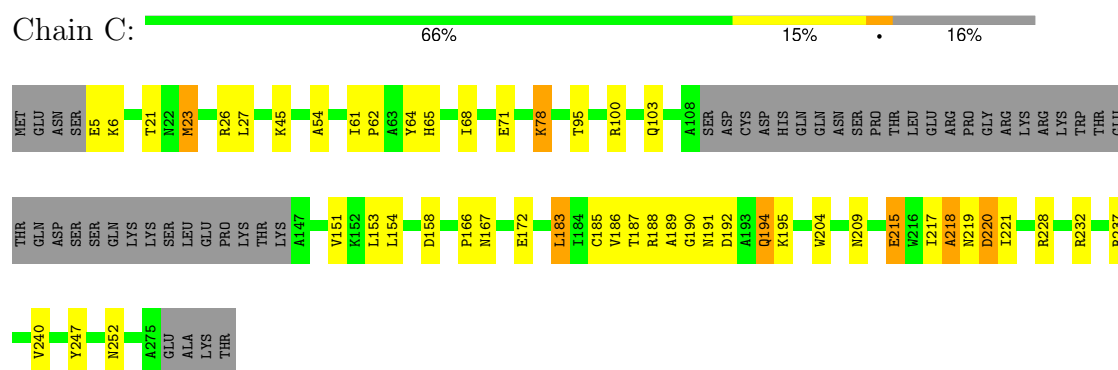
- Molecule 1: NICOTINAMIDE MONONUCLEOTIDE ADENYLYL TRANSFERASE



- Molecule 1: NICOTINAMIDE MONONUCLEOTIDE ADENYLYL TRANSFERASE

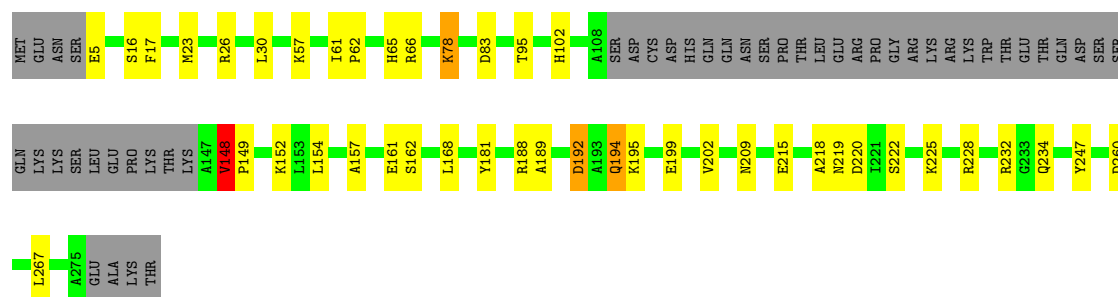


- Molecule 1: NICOTINAMIDE MONONUCLEOTIDE ADENYLYL TRANSFERASE



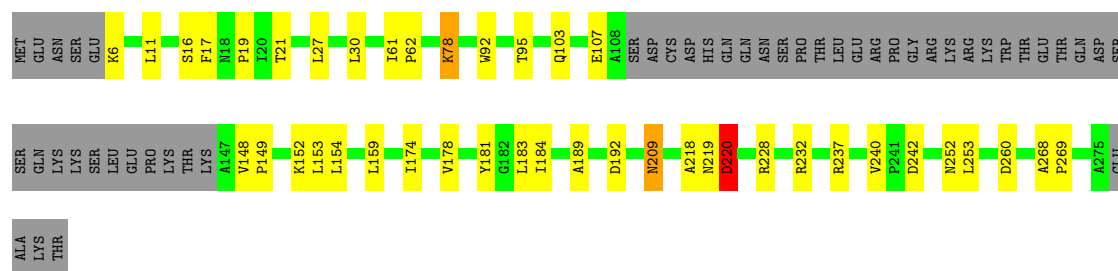
- Molecule 1: NICOTINAMIDE MONONUCLEOTIDE ADENYLYL TRANSFERASE

Chain D:  68% 14% 16%



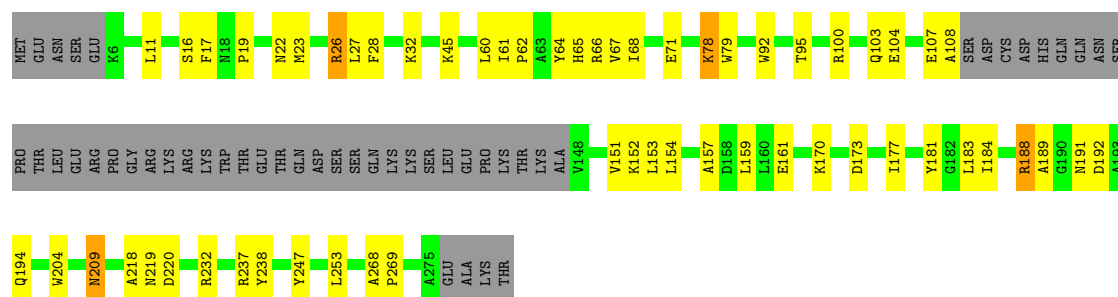
• Molecule 1: NICOTINAMIDE MONONUCLEOTIDE ADENYLYL TRANSFERASE

Chain E:  68% 14% 17%



• Molecule 1: NICOTINAMIDE MONONUCLEOTIDE ADENYLYL TRANSFERASE

Chain F:  62% 20% 17%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	131.48Å 89.39Å 137.75Å 90.00° 117.42° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.30)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.203 , 0.231	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12192	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: TAD

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	0.68	1/1912 (0.1%)	0.76	0/2588
1	B	0.70	0/1912	0.78	1/2588 (0.0%)
1	C	0.70	0/1912	0.81	1/2588 (0.0%)
1	D	0.66	0/1912	0.77	1/2588 (0.0%)
1	E	0.57	0/1903	0.73	2/2576 (0.1%)
1	F	0.57	0/1898	0.74	1/2569 (0.0%)
All	All	0.65	1/11449 (0.0%)	0.76	6/15497 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	23	MET	CG-SD	5.10	1.94	1.81

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	183	LEU	CA-CB-CG	6.54	130.35	115.30
1	B	253	LEU	N-CA-C	6.07	127.38	111.00
1	D	148	VAL	N-CA-C	5.89	126.90	111.00
1	F	26	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	E	220	ASP	N-CA-C	5.47	125.78	111.00

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	1875	0	1903	55	0
1	B	1875	0	1903	42	0
1	C	1875	0	1903	61	0
1	D	1875	0	1903	39	0
1	E	1866	0	1897	33	0
1	F	1861	0	1892	43	0
2	A	43	0	25	1	0
2	B	43	0	25	1	0
2	C	43	0	25	1	0
2	D	43	0	25	5	0
2	E	43	0	25	2	0
2	F	43	0	25	2	0
3	A	155	0	0	13	0
3	B	128	0	0	11	0
3	C	168	0	0	18	0
3	D	103	0	0	6	0
3	E	83	0	0	4	0
3	F	70	0	0	4	0
All	All	12192	0	11551	263	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 11.

The worst 5 of 263 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:C:23:MET:HB3	3:C:941:HOH:O	1.29	1.27
1:D:78:LYS:H	1:D:78:LYS:HD2	1.11	1.10
1:B:78:LYS:H	1:B:78:LYS:HD2	0.98	1.09
1:B:78:LYS:H	1:B:78:LYS:CD	1.69	1.03
1:E:219:ASN:HA	1:F:219:ASN:OD1	1.60	1.00

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 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	229/279 (82%)	223 (97%)	6 (3%)	0	100	100
1	B	229/279 (82%)	221 (96%)	8 (4%)	0	100	100
1	C	229/279 (82%)	219 (96%)	8 (4%)	2 (1%)	17	20
1	D	229/279 (82%)	218 (95%)	10 (4%)	1 (0%)	34	42
1	E	228/279 (82%)	221 (97%)	6 (3%)	1 (0%)	34	42
1	F	227/279 (81%)	220 (97%)	6 (3%)	1 (0%)	34	42
All	All	1371/1674 (82%)	1322 (96%)	44 (3%)	5 (0%)	34	42

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	220	ASP
1	D	148	VAL
1	E	220	ASP
1	F	218	ALA
1	C	218	ALA

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	204/248 (82%)	197 (97%)	7 (3%)	37	51
1	B	204/248 (82%)	196 (96%)	8 (4%)	32	46
1	C	204/248 (82%)	195 (96%)	9 (4%)	28	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	204/248 (82%)	197 (97%)	7 (3%)	37	51
1	E	203/248 (82%)	197 (97%)	6 (3%)	41	57
1	F	203/248 (82%)	194 (96%)	9 (4%)	28	39
All	All	1222/1488 (82%)	1176 (96%)	46 (4%)	33	47

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	194	GLN
1	E	252	ASN
1	D	209	ASN
1	E	78	LYS
1	F	19	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	76	ASN
1	F	209	ASN
1	D	209	ASN
1	F	102	HIS
1	D	194	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

6 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	TAD	D	812	-	36,47,47	1.53	6 (16%)	39,72,72	2.09	13 (33%)
2	TAD	A	809	-	36,47,47	1.35	3 (8%)	39,72,72	1.88	9 (23%)
2	TAD	C	811	-	36,47,47	1.28	5 (13%)	39,72,72	1.78	8 (20%)
2	TAD	F	814	-	36,47,47	1.53	6 (16%)	39,72,72	1.98	9 (23%)
2	TAD	E	813	-	36,47,47	1.49	5 (13%)	39,72,72	2.18	10 (25%)
2	TAD	B	810	-	36,47,47	1.45	5 (13%)	39,72,72	2.18	11 (28%)

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	TAD	D	812	-	-	6/18/62/62	0/5/5/5
2	TAD	A	809	-	-	8/18/62/62	0/5/5/5
2	TAD	C	811	-	-	7/18/62/62	0/5/5/5
2	TAD	F	814	-	-	7/18/62/62	0/5/5/5
2	TAD	E	813	-	-	7/18/62/62	0/5/5/5
2	TAD	B	810	-	-	7/18/62/62	0/5/5/5

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	814	TAD	O4B-C1B	5.73	1.48	1.40
2	E	813	TAD	O4B-C1B	4.78	1.47	1.40
2	B	810	TAD	O4B-C1B	4.36	1.46	1.40
2	A	809	TAD	O4B-C1B	4.21	1.46	1.40
2	D	812	TAD	O4B-C1B	4.11	1.46	1.40

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	813	TAD	O6N-C6N-C4N	6.62	125.20	119.65
2	A	809	TAD	N3A-C2A-N1A	-6.32	120.09	128.67
2	F	814	TAD	N3A-C2A-N1A	-6.28	120.14	128.67
2	C	811	TAD	N3A-C2A-N1A	-6.26	120.17	128.67
2	E	813	TAD	N3A-C2A-N1A	-6.23	120.22	128.67

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

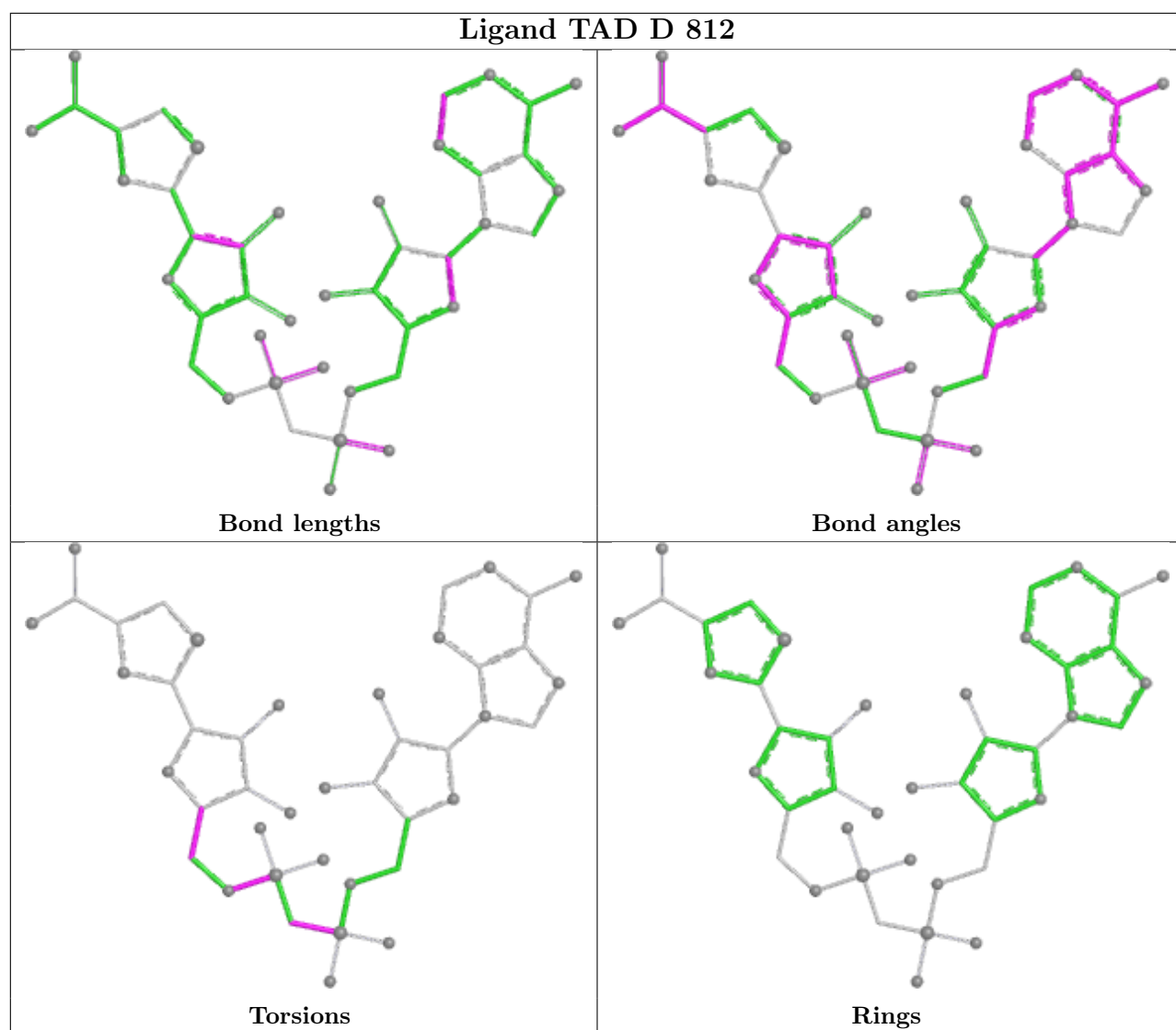
Mol	Chain	Res	Type	Atoms
2	A	809	TAD	C5D-O5D-PN-O1N
2	B	810	TAD	PN-C3-PA-O5B
2	B	810	TAD	PA-C3-PN-O1N
2	B	810	TAD	PA-C3-PN-O2N
2	B	810	TAD	C5D-O5D-PN-O1N

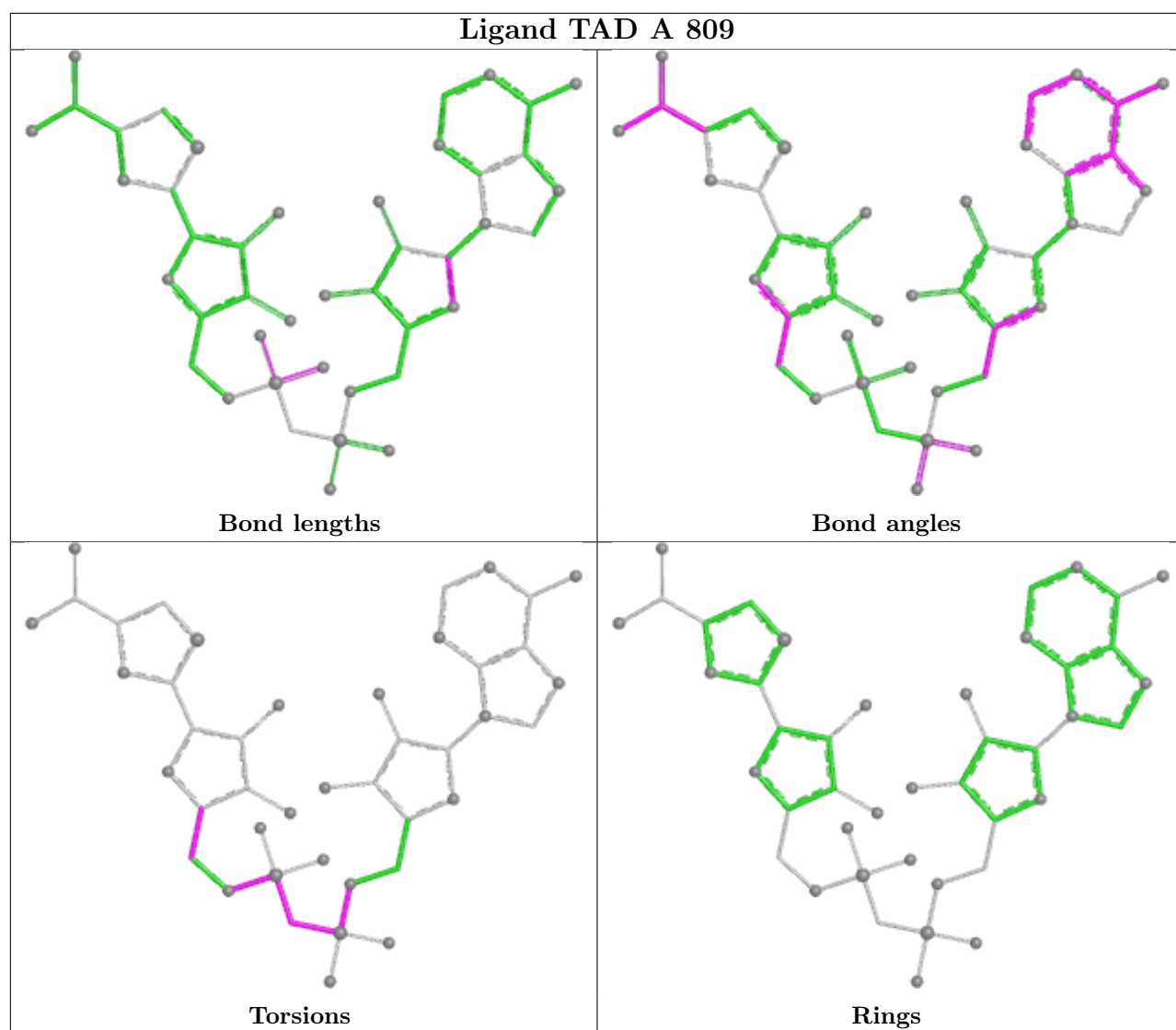
There are no ring outliers.

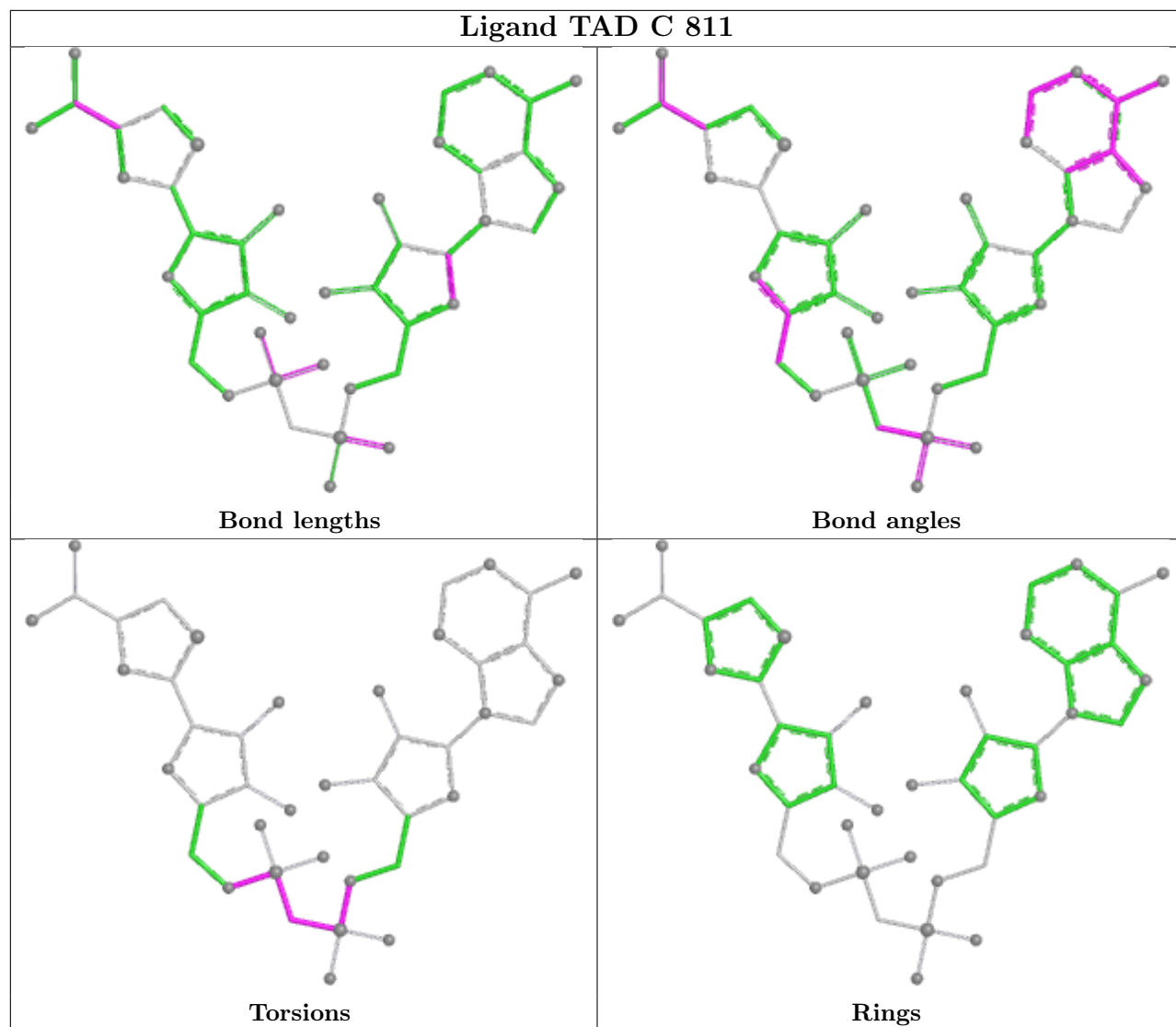
6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	812	TAD	5	0
2	A	809	TAD	1	0
2	C	811	TAD	1	0
2	F	814	TAD	2	0
2	E	813	TAD	2	0
2	B	810	TAD	1	0

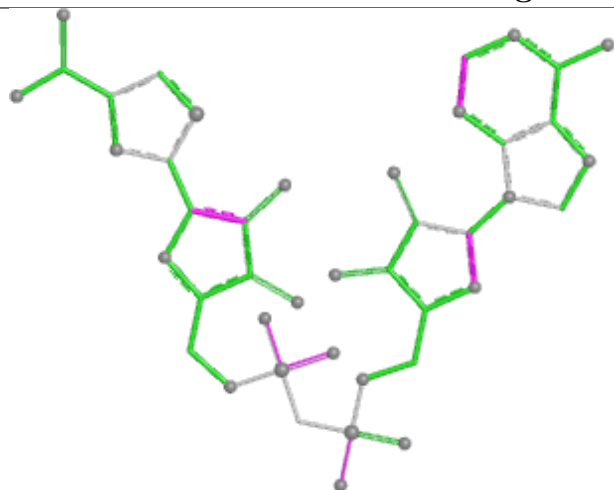
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



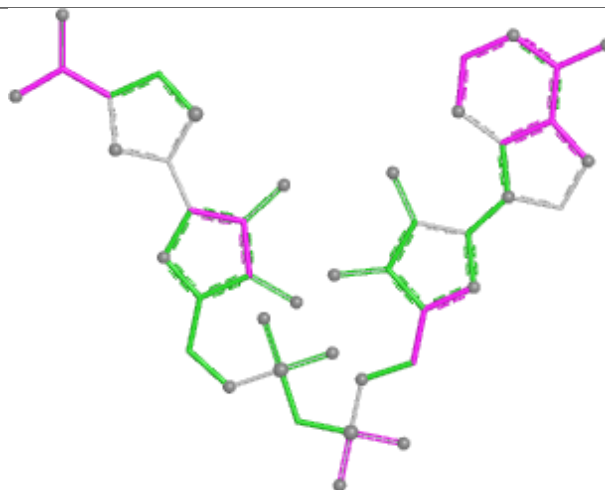




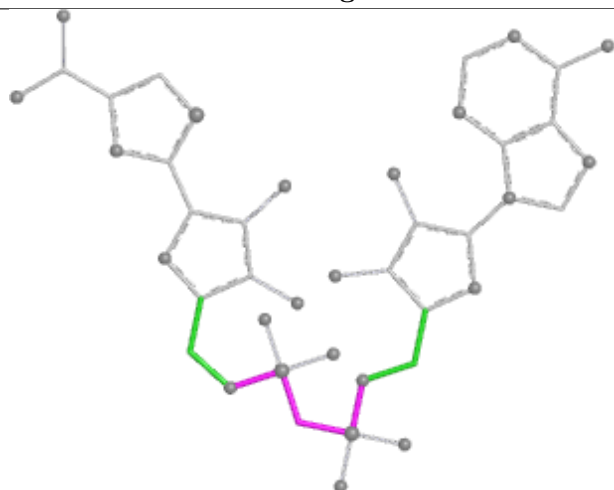
Ligand TAD F 814



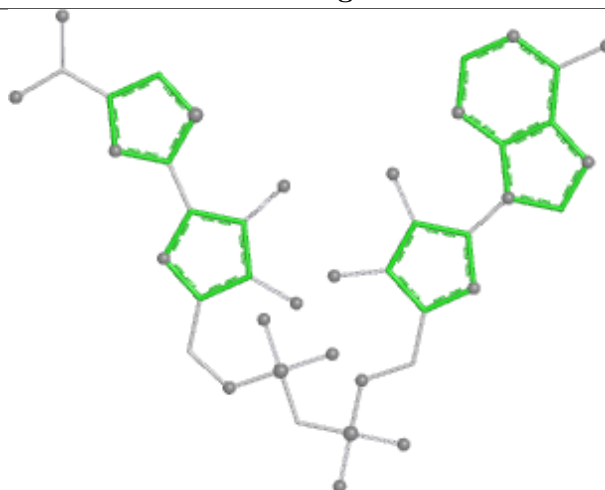
Bond lengths



Bond angles

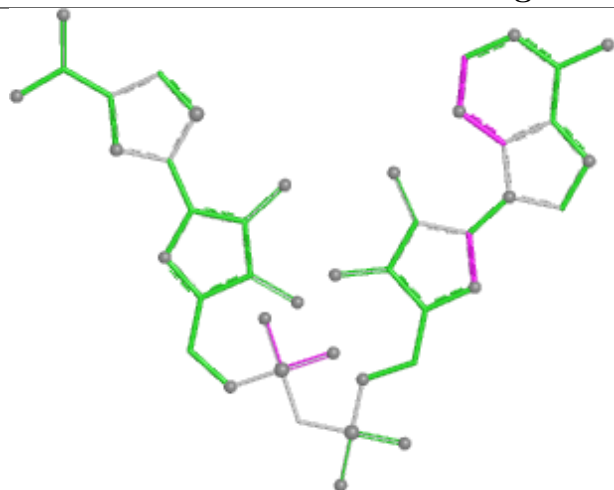


Torsions

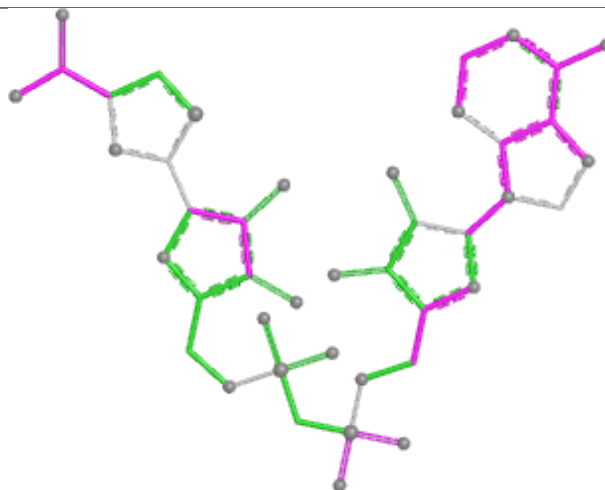


Rings

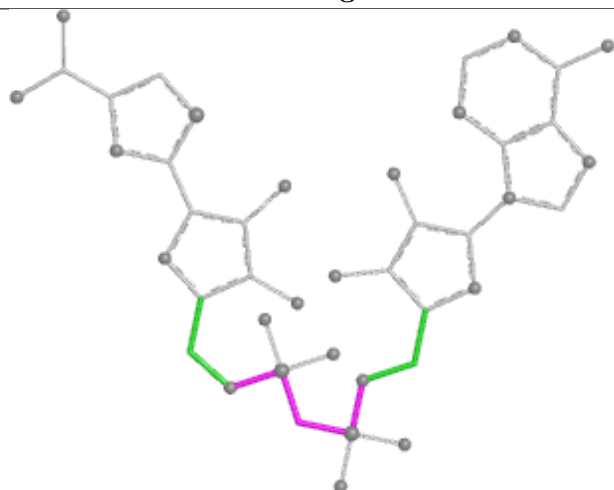
Ligand TAD E 813



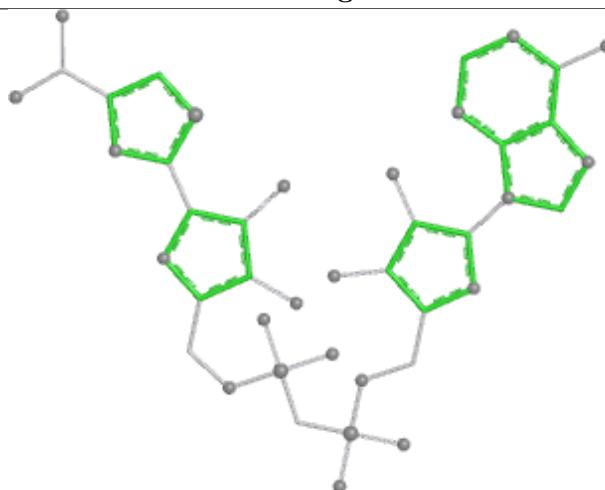
Bond lengths



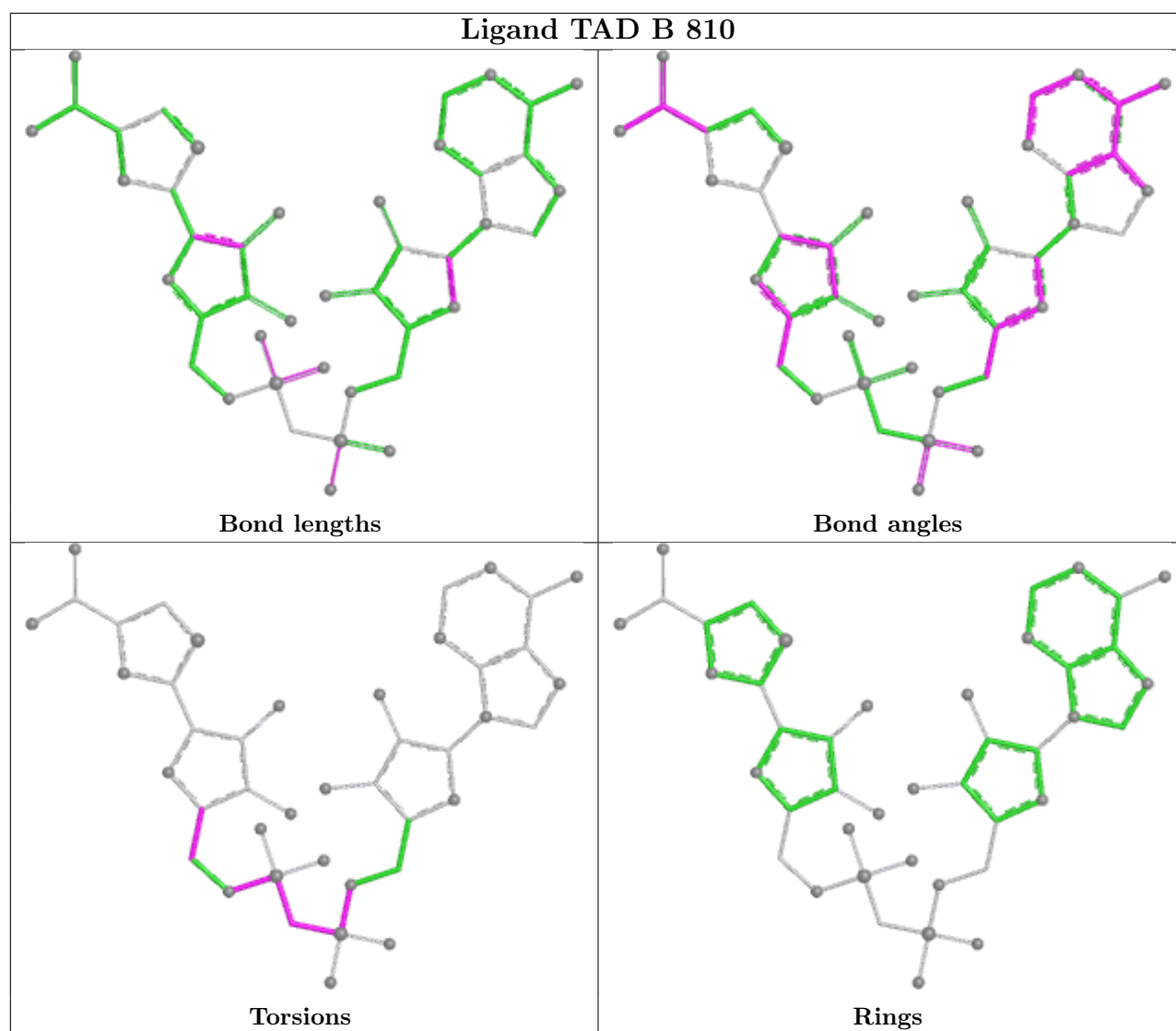
Bond angles



Torsions



Rings



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](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.