



# wwPDB X-ray Structure Validation Summary Report

Oct 3, 2023 – 04:58 AM EDT

PDB ID : 6O4K  
Title : Structure of ALDH7A1 mutant E399Q complexed with NAD  
Authors : Tanner, J.J.; Korasick, D.A.; Laciak, A.R.  
Deposited on : 2019-02-28  
Resolution : 2.06 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

<https://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 : **FAILED**  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : **FAILED**  
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) : 2.35.1

## 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 2.06 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 32399 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 Alpha-aminoadipic semialdehyde dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	509	3858	2450	670	721	17	0	0	0
1	B	509	3867	2459	673	718	17	0	1	0
1	C	509	3868	2459	675	717	17	0	2	0
1	D	509	3822	2430	666	709	17	0	0	0
1	E	509	3864	2453	670	724	17	0	1	0
1	F	509	3863	2451	671	724	17	0	0	0
1	G	507	3820	2426	666	711	17	0	0	0
1	H	509	3839	2436	670	716	17	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

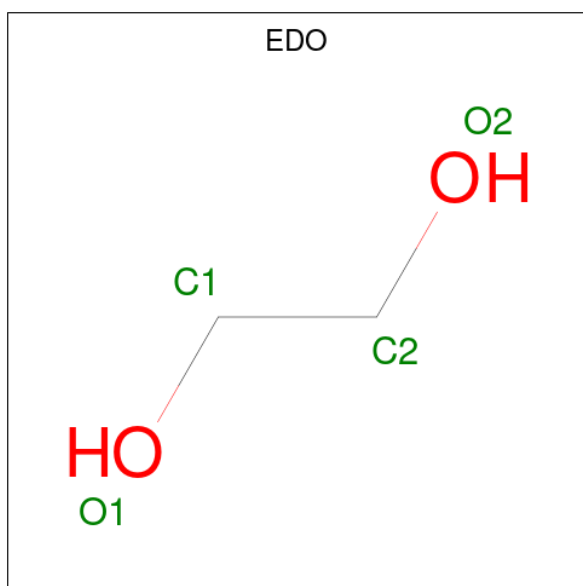
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P49419
A	0	HIS	-	expression tag	UNP P49419
A	399	GLN	GLU	engineered mutation	UNP P49419
B	-1	GLY	-	expression tag	UNP P49419
B	0	HIS	-	expression tag	UNP P49419
B	399	GLN	GLU	engineered mutation	UNP P49419
C	-1	GLY	-	expression tag	UNP P49419
C	0	HIS	-	expression tag	UNP P49419
C	399	GLN	GLU	engineered mutation	UNP P49419
D	-1	GLY	-	expression tag	UNP P49419
D	0	HIS	-	expression tag	UNP P49419
D	399	GLN	GLU	engineered mutation	UNP P49419
E	-1	GLY	-	expression tag	UNP P49419

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Chain	Residue	Modelled	Actual	Comment	Reference
E	0	HIS	-	expression tag	UNP P49419
E	399	GLN	GLU	engineered mutation	UNP P49419
F	-1	GLY	-	expression tag	UNP P49419
F	0	HIS	-	expression tag	UNP P49419
F	399	GLN	GLU	engineered mutation	UNP P49419
G	-1	GLY	-	expression tag	UNP P49419
G	0	HIS	-	expression tag	UNP P49419
G	399	GLN	GLU	engineered mutation	UNP P49419
H	-1	GLY	-	expression tag	UNP P49419
H	0	HIS	-	expression tag	UNP P49419
H	399	GLN	GLU	engineered mutation	UNP P49419

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	F	1	Total C O 4 2 2	0	0
2	F	1	Total C O 4 2 2	0	0

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C<sub>21</sub>H<sub>27</sub>N<sub>7</sub>O<sub>14</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	B	1	Total	C	N	O	P	0	1
			54	20	10	20	4		
3	C	1	Total	C	N	O	P	0	1
			54	20	10	20	4		
3	D	1	Total	C	N	O	P	0	1
			54	20	10	20	4		
3	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	F	1	Total	C	N	O	P	0	1
			54	20	10	20	4		
3	G	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	H	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Cl 1	0	0
4	B	1	Total Cl 1	0	0
4	C	1	Total Cl 1	0	0
4	D	1	Total Cl 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	2	Total Cl 2 2	0	0
4	G	1	Total Cl 1 1	0	0
4	H	1	Total Cl 1 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	200	Total O 200 200	0	0
5	B	136	Total O 136 136	0	0
5	C	153	Total O 153 153	0	0
5	D	125	Total O 125 125	0	0
5	E	173	Total O 173 173	0	0
5	F	162	Total O 162 162	0	0
5	G	140	Total O 140 140	0	0
5	H	161	Total O 161 161	0	0

MolProbity and EDS failed to run properly - this section is therefore empty.

### 3 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	155.36Å 159.11Å 157.72Å 90.00° 95.22° 90.00°	Depositor
Resolution (Å)	49.06 – 2.06	Depositor
% Data completeness (in resolution range)	93.6 (49.06-2.06)	Depositor
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.59 (at 2.07Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.191 , 0.246	Depositor
Wilson B-factor (Å <sup>2</sup> )	32.2	Xtrriage
Anisotropy	0.339	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	32399	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	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 22.58 % 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 5.5420e-03. 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.

## 4 Model quality [i](#)

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

MolProbity failed to run properly - this section is therefore empty.

### 4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

### 4.3 Torsion angles [i](#)

#### 4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

#### 4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

### 4.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 4.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 8 are monoatomic - leaving 16 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
2	EDO	B	601	-	3,3,3	0.48	0	2,2,2	0.31	0
3	NAD	D	601[A]	-	24,29,48	4.93	8 (33%)	29,45,73	1.48	2 (6%)
3	NAD	B	602[A]	-	24,29,48	4.85	9 (37%)	29,45,73	1.52	3 (10%)
3	NAD	G	601	-	24,29,48	4.81	8 (33%)	29,45,73	1.39	3 (10%)
3	NAD	F	603[B]	-	24,29,48	4.86	8 (33%)	29,45,73	1.46	3 (10%)
3	NAD	H	601	-	24,29,48	4.82	8 (33%)	29,45,73	1.41	3 (10%)
3	NAD	C	601[B]	-	24,29,48	4.95	9 (37%)	29,45,73	1.48	3 (10%)
2	EDO	F	601	-	3,3,3	0.50	0	2,2,2	0.28	0
3	NAD	D	601[B]	-	24,29,48	4.93	8 (33%)	29,45,73	1.50	3 (10%)
3	NAD	B	602[B]	-	24,29,48	4.82	8 (33%)	29,45,73	1.57	5 (17%)
2	EDO	F	602	-	3,3,3	0.46	0	2,2,2	0.42	0
3	NAD	F	603[A]	-	24,29,48	4.82	8 (33%)	29,45,73	1.43	2 (6%)
3	NAD	E	601	-	24,29,48	4.89	7 (29%)	29,45,73	1.59	6 (20%)
3	NAD	C	601[A]	-	24,29,48	4.92	9 (37%)	29,45,73	1.46	3 (10%)
2	EDO	A	601	-	3,3,3	0.43	0	2,2,2	0.63	0
3	NAD	A	602	-	24,29,48	4.76	9 (37%)	29,45,73	1.33	3 (10%)

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	EDO	B	601	-	-	1/1/1/1	-
3	NAD	D	601[A]	-	-	1/12/32/62	0/3/3/5
3	NAD	B	602[A]	-	-	7/12/32/62	0/3/3/5
3	NAD	G	601	-	-	4/12/32/62	0/3/3/5
3	NAD	F	603[B]	-	-	2/12/32/62	0/3/3/5
3	NAD	H	601	-	-	3/12/32/62	0/3/3/5
3	NAD	C	601[B]	-	-	2/12/32/62	0/3/3/5
2	EDO	F	601	-	-	0/1/1/1	-
3	NAD	D	601[B]	-	-	3/12/32/62	0/3/3/5
3	NAD	B	602[B]	-	-	4/12/32/62	0/3/3/5
2	EDO	F	602	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAD	F	603[A]	-	-	3/12/32/62	0/3/3/5
3	NAD	E	601	-	-	1/12/32/62	0/3/3/5
3	NAD	C	601[A]	-	-	5/12/32/62	0/3/3/5
2	EDO	A	601	-	-	1/1/1/1	-
3	NAD	A	602	-	-	3/12/32/62	0/3/3/5

The worst 5 of 99 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	601	NAD	C2B-C1B	-16.32	1.29	1.53
3	D	601[B]	NAD	C2B-C1B	-16.13	1.29	1.53
3	C	601[B]	NAD	C2B-C1B	-16.11	1.29	1.53
3	D	601[A]	NAD	C2B-C1B	-16.10	1.29	1.53
3	G	601	NAD	C2B-C1B	-16.08	1.29	1.53

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	601[B]	NAD	N3A-C2A-N1A	-5.44	120.17	128.68
3	B	602[A]	NAD	N3A-C2A-N1A	-5.43	120.19	128.68
3	D	601[B]	NAD	N3A-C2A-N1A	-5.42	120.20	128.68
3	D	601[A]	NAD	N3A-C2A-N1A	-5.41	120.22	128.68
3	C	601[A]	NAD	N3A-C2A-N1A	-5.39	120.25	128.68

There are no chirality outliers.

5 of 40 torsion outliers are listed below:

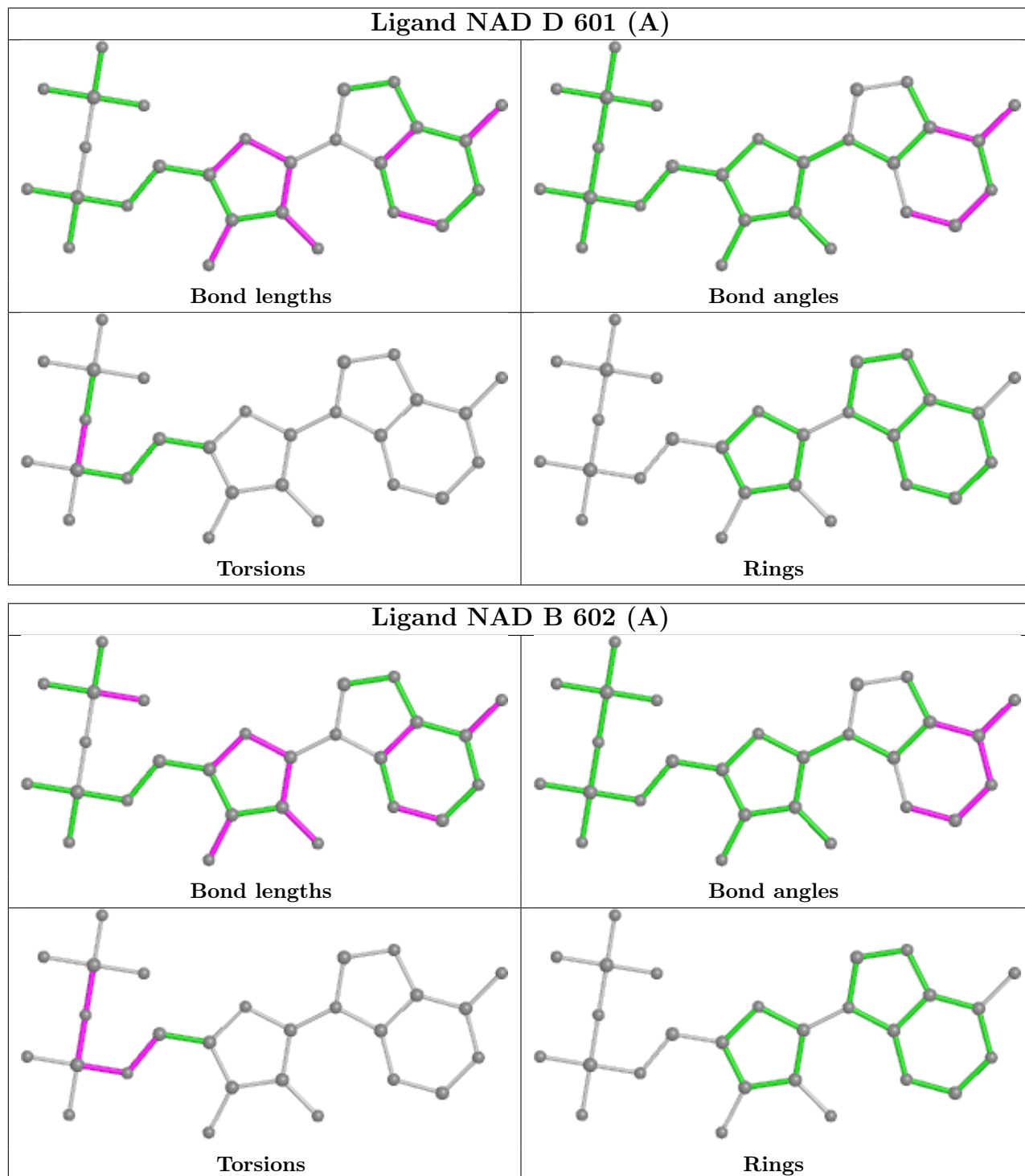
Mol	Chain	Res	Type	Atoms
3	A	602	NAD	C5B-O5B-PA-O1A
3	B	602[A]	NAD	C5B-O5B-PA-O1A
3	B	602[A]	NAD	C5B-O5B-PA-O2A
3	B	602[A]	NAD	PN-O3-PA-O5B
3	B	602[B]	NAD	PA-O3-PN-O2N

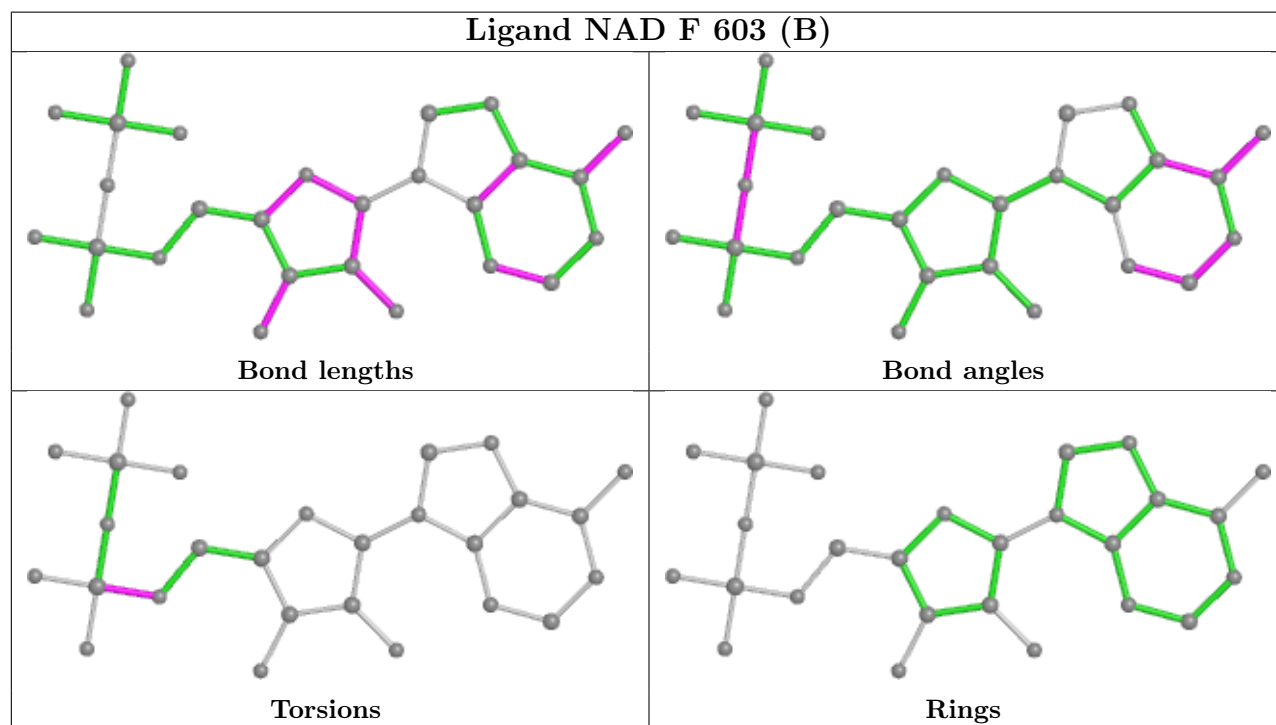
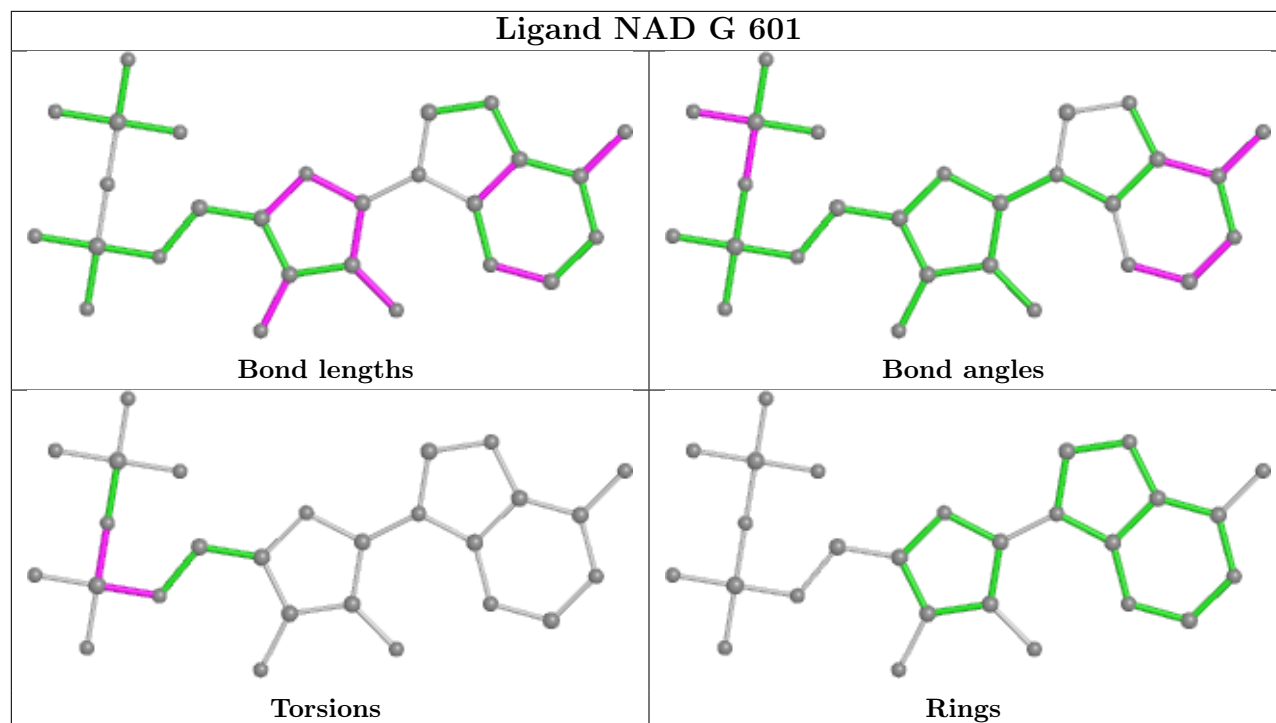
There are no ring outliers.

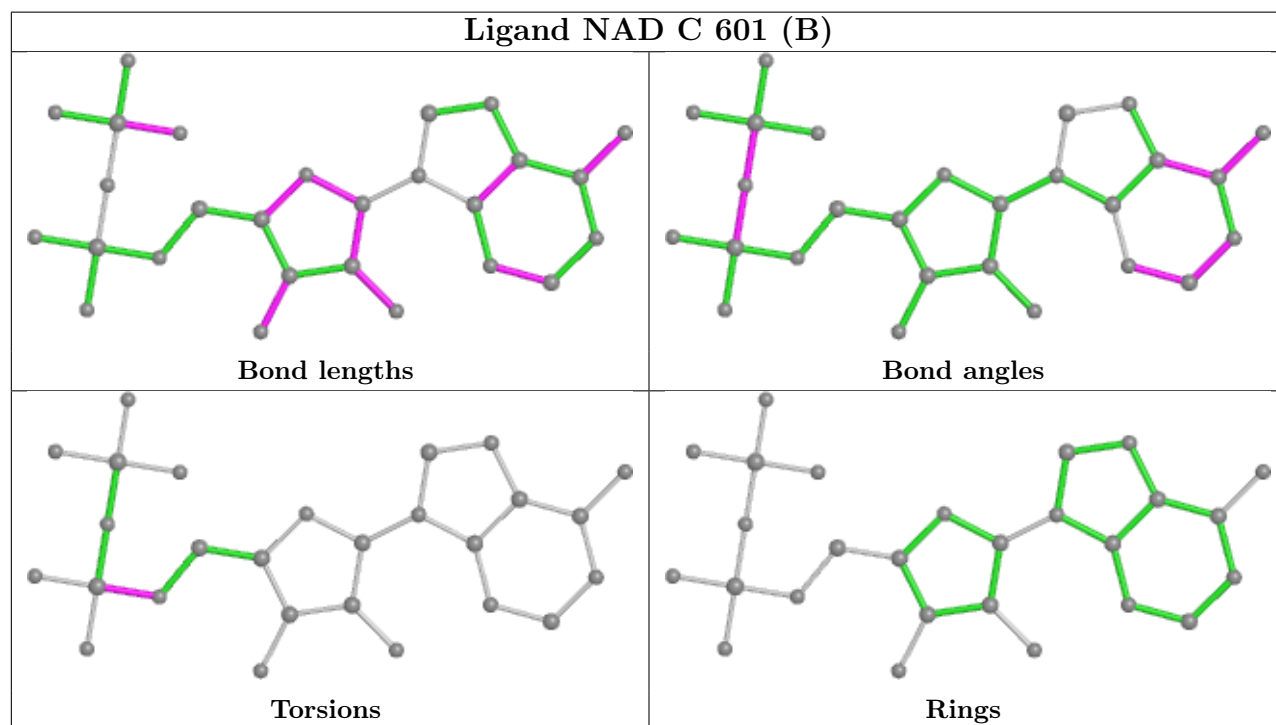
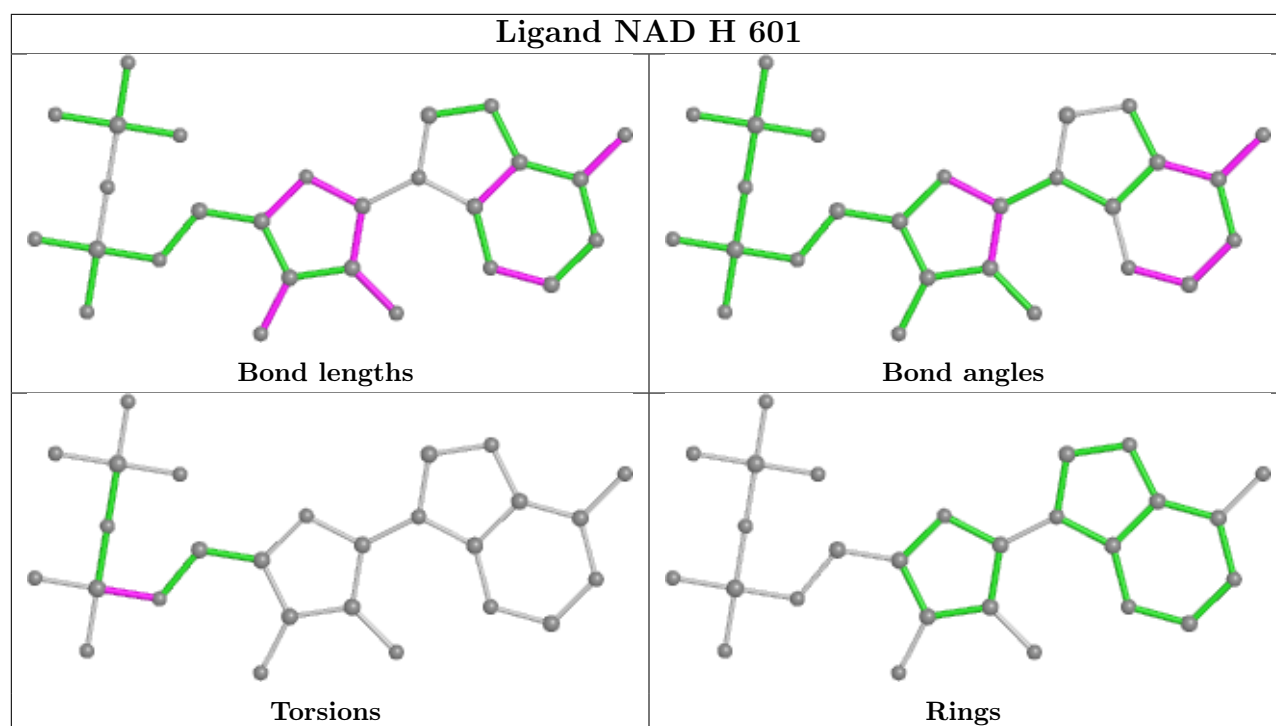
No monomer is involved in short contacts.

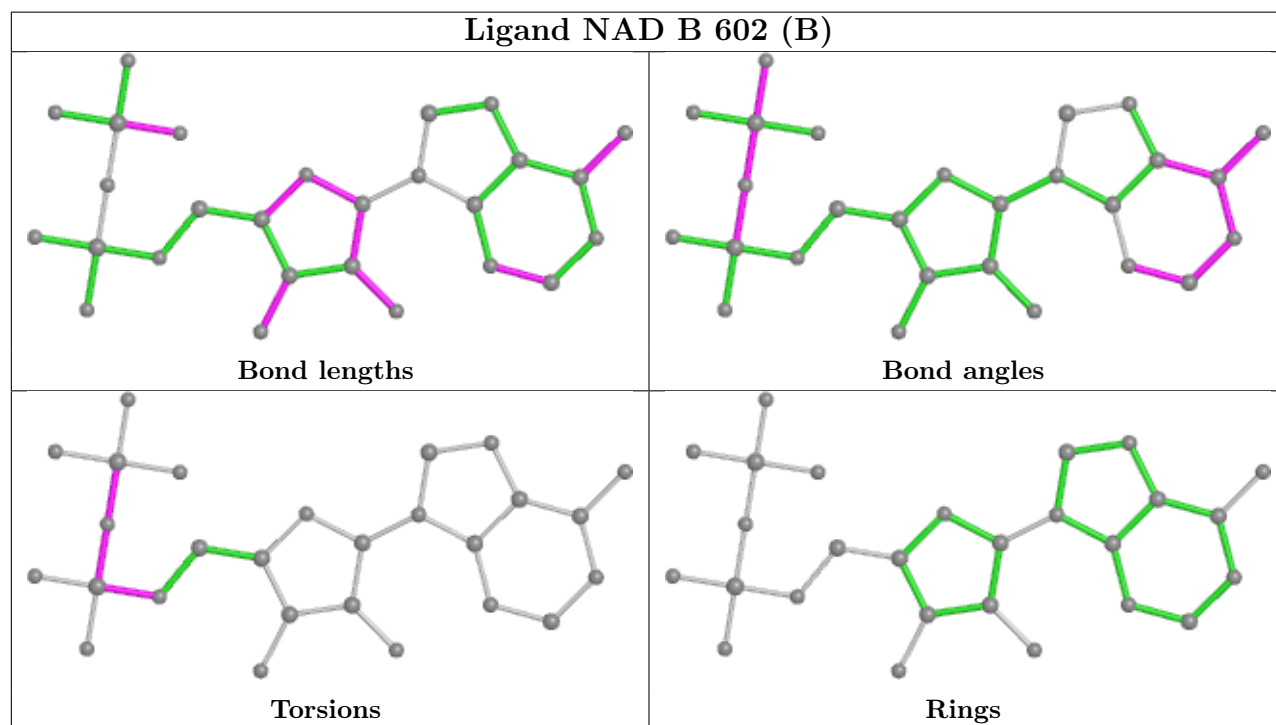
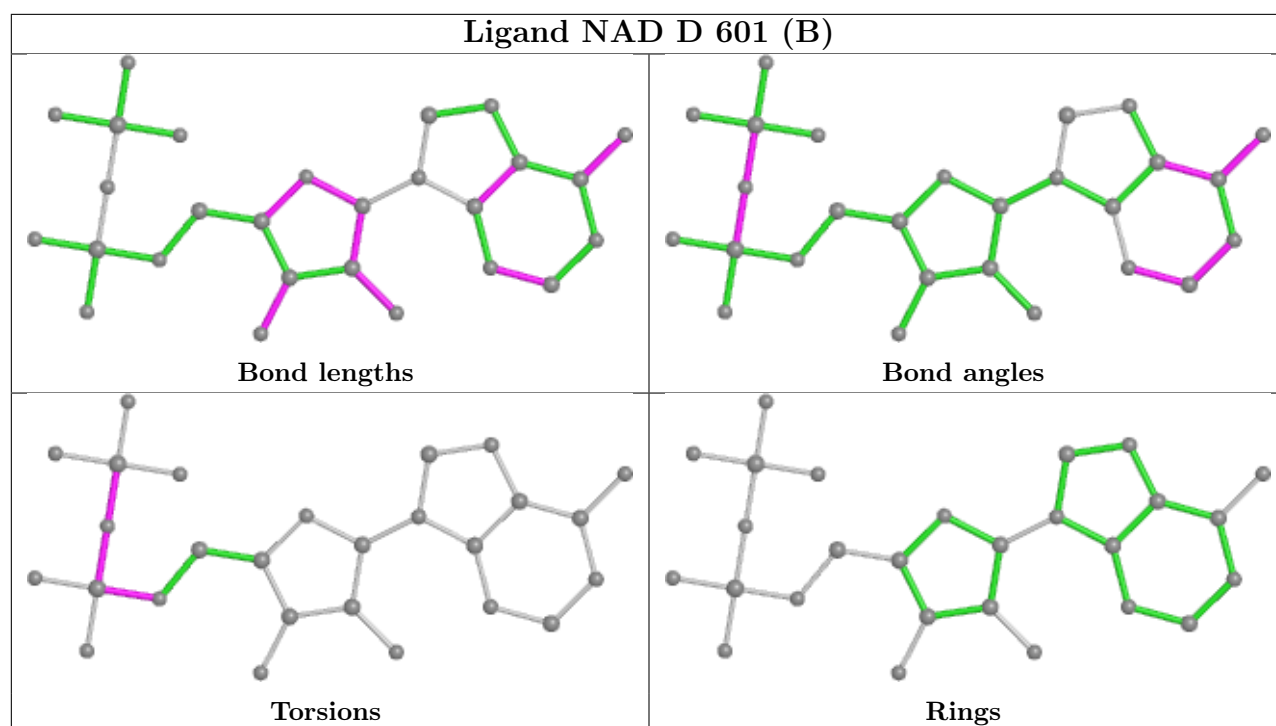
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

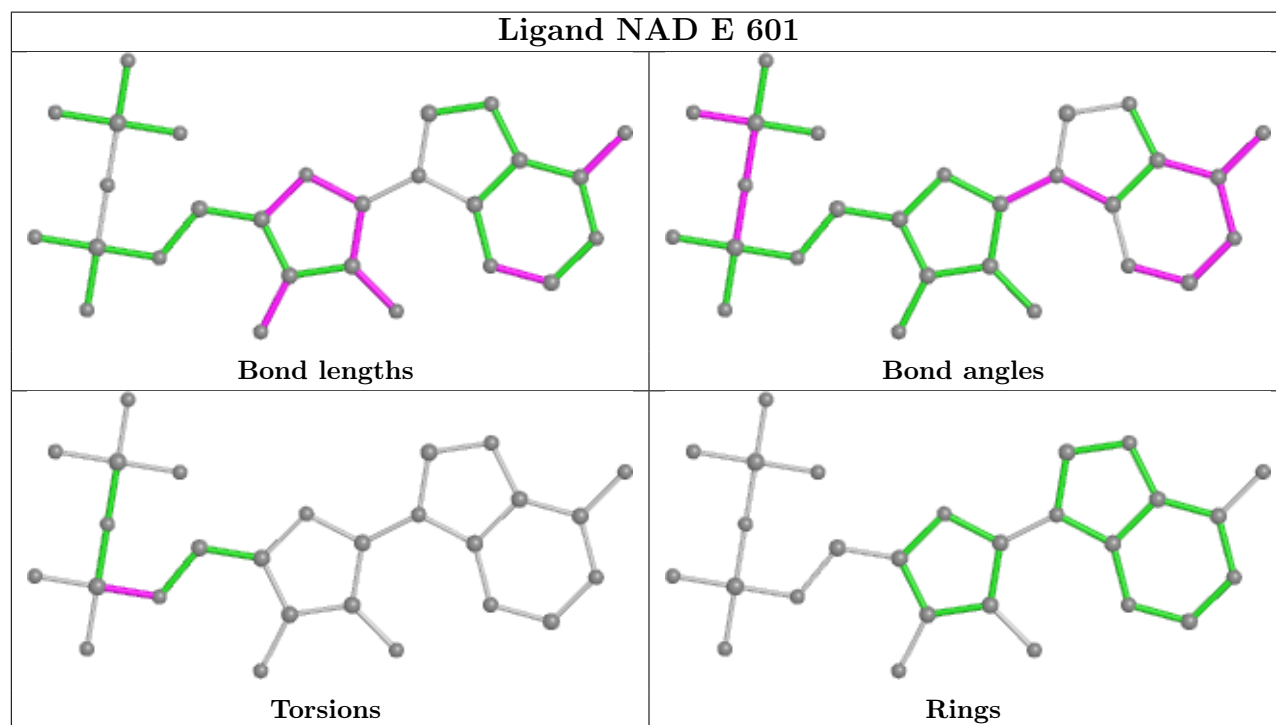
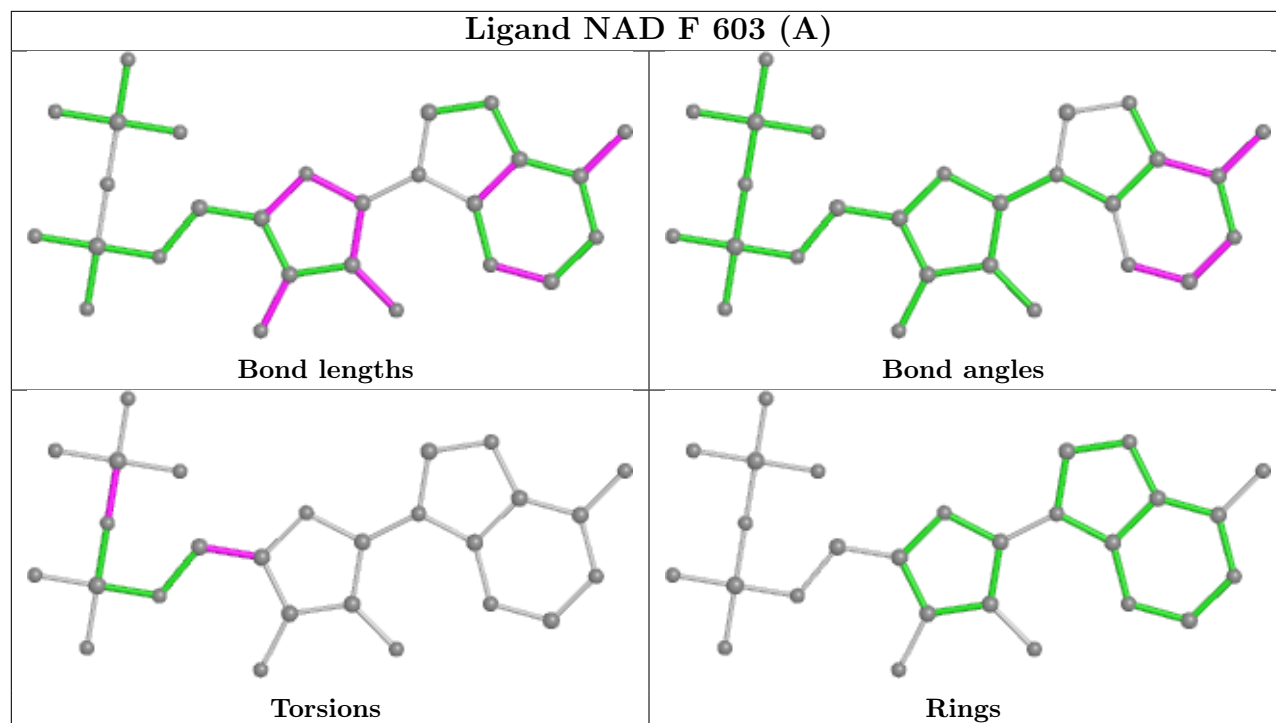
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question 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.

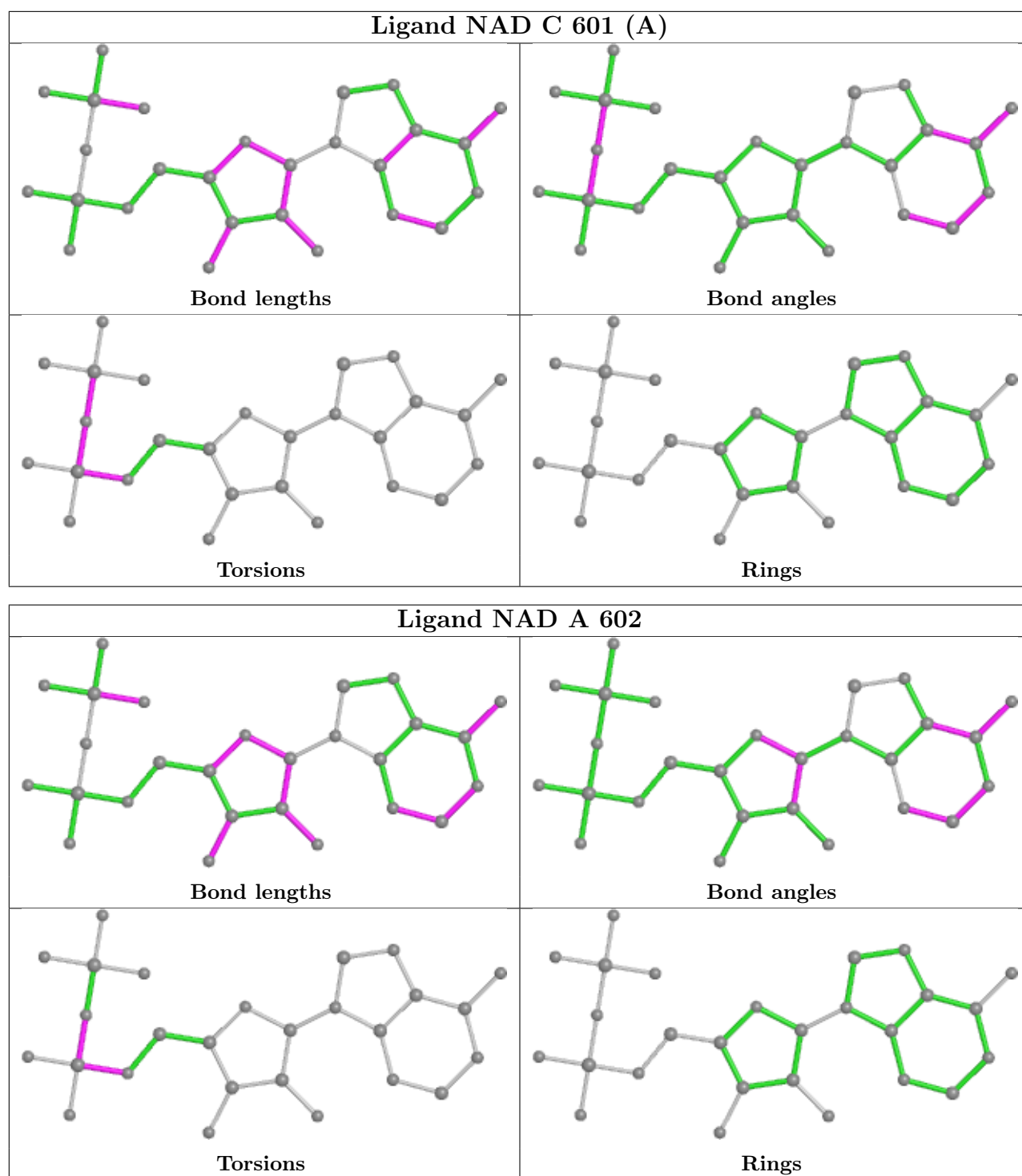












#### 4.7 Other polymers [\(i\)](#)

There are no such residues in this entry.



## 4.8 Polymer linkage issues

There are no chain breaks in this entry.

## 5 Fit of model and data

### 5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

### 5.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

### 5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

### 5.4 Ligands

EDS failed to run properly - this section is therefore empty.

### 5.5 Other polymers

EDS failed to run properly - this section is therefore empty.