



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 07:46 AM UTC

PDB ID : 1EFK / pdb_00001efk
Title : STRUCTURE OF HUMAN MALIC ENZYME IN COMPLEX WITH KE-TOMALONATE
Authors : Yang, Z.; Floyd, D.L.; Loeber, G.; Tong, L.
Deposited on : 2000-02-09
Resolution : 2.60 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

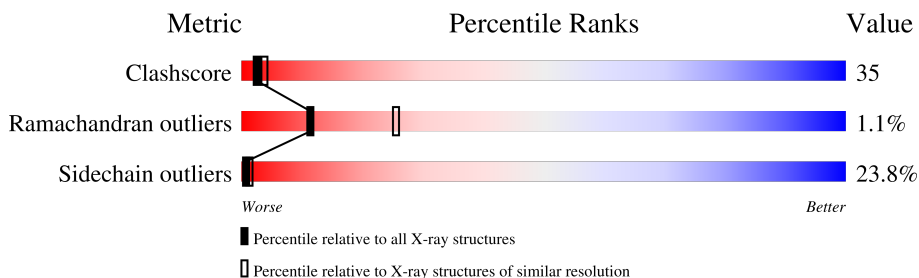
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)

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	584	
1	B	584	
1	C	584	
1	D	584	

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
4	MAK	A	603	-	X	-	-
4	MAK	C	2603	-	X	-	-
4	MAK	D	3603	-	X	-	-

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 17931 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 MALIC ENZYME.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	553	4367	2796	744	804	9	14	0	0	0
1	B	553	4367	2796	744	804	9	14	0	0	0
1	C	553	4367	2796	744	804	9	14	0	0	0
1	D	553	4367	2796	744	804	9	14	0	0	0

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	MSE	MET	modified residue	UNP P23368
A	38	MSE	MET	modified residue	UNP P23368
A	47	MSE	MET	modified residue	UNP P23368
A	75	MSE	MET	modified residue	UNP P23368
A	86	MSE	MET	modified residue	UNP P23368
A	108	MSE	MET	modified residue	UNP P23368
A	177	MSE	MET	modified residue	UNP P23368
A	219	MSE	MET	modified residue	UNP P23368
A	239	MSE	MET	modified residue	UNP P23368
A	325	MSE	MET	modified residue	UNP P23368
A	327	MSE	MET	modified residue	UNP P23368
A	343	MSE	MET	modified residue	UNP P23368
A	407	MSE	MET	modified residue	UNP P23368
A	539	MSE	MET	modified residue	UNP P23368
B	29	MSE	MET	modified residue	UNP P23368
B	38	MSE	MET	modified residue	UNP P23368
B	47	MSE	MET	modified residue	UNP P23368
B	75	MSE	MET	modified residue	UNP P23368
B	86	MSE	MET	modified residue	UNP P23368
B	108	MSE	MET	modified residue	UNP P23368
B	177	MSE	MET	modified residue	UNP P23368

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Chain	Residue	Modelled	Actual	Comment	Reference
B	219	MSE	MET	modified residue	UNP P23368
B	239	MSE	MET	modified residue	UNP P23368
B	325	MSE	MET	modified residue	UNP P23368
B	327	MSE	MET	modified residue	UNP P23368
B	343	MSE	MET	modified residue	UNP P23368
B	407	MSE	MET	modified residue	UNP P23368
B	539	MSE	MET	modified residue	UNP P23368
C	29	MSE	MET	modified residue	UNP P23368
C	38	MSE	MET	modified residue	UNP P23368
C	47	MSE	MET	modified residue	UNP P23368
C	75	MSE	MET	modified residue	UNP P23368
C	86	MSE	MET	modified residue	UNP P23368
C	108	MSE	MET	modified residue	UNP P23368
C	177	MSE	MET	modified residue	UNP P23368
C	219	MSE	MET	modified residue	UNP P23368
C	239	MSE	MET	modified residue	UNP P23368
C	325	MSE	MET	modified residue	UNP P23368
C	327	MSE	MET	modified residue	UNP P23368
C	343	MSE	MET	modified residue	UNP P23368
C	407	MSE	MET	modified residue	UNP P23368
C	539	MSE	MET	modified residue	UNP P23368
D	29	MSE	MET	modified residue	UNP P23368
D	38	MSE	MET	modified residue	UNP P23368
D	47	MSE	MET	modified residue	UNP P23368
D	75	MSE	MET	modified residue	UNP P23368
D	86	MSE	MET	modified residue	UNP P23368
D	108	MSE	MET	modified residue	UNP P23368
D	177	MSE	MET	modified residue	UNP P23368
D	219	MSE	MET	modified residue	UNP P23368
D	239	MSE	MET	modified residue	UNP P23368
D	325	MSE	MET	modified residue	UNP P23368
D	327	MSE	MET	modified residue	UNP P23368
D	343	MSE	MET	modified residue	UNP P23368
D	407	MSE	MET	modified residue	UNP P23368
D	539	MSE	MET	modified residue	UNP P23368

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

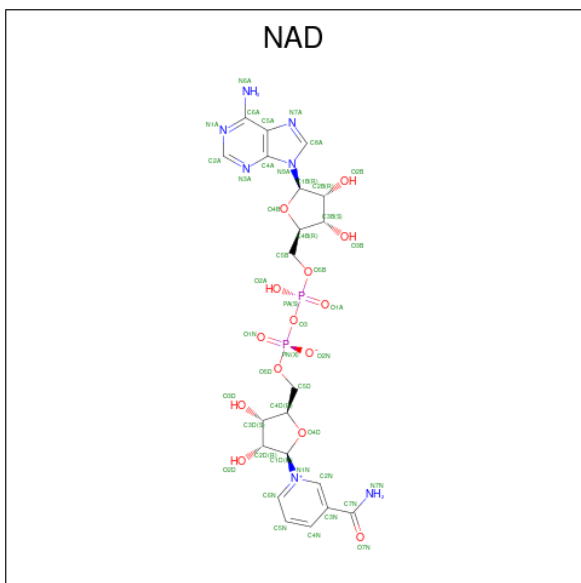
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0

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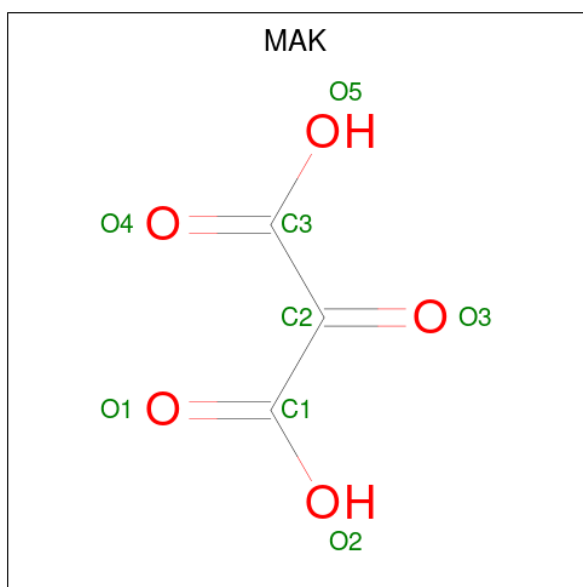
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O P 44 21 7 14 2	0	0
3	A	1	Total C N O P 44 21 7 14 2	9	0
3	B	1	Total C N O P 44 21 7 14 2	0	0
3	B	1	Total C N O P 44 21 7 14 2	9	0
3	C	1	Total C N O P 44 21 7 14 2	0	0
3	C	1	Total C N O P 44 21 7 14 2	9	0
3	D	1	Total C N O P 44 21 7 14 2	0	0
3	D	1	Total C N O P 44 21 7 14 2	9	0

- Molecule 4 is ALPHA-KETOMALONIC ACID (CCD ID: MAK) (formula: $C_3H_2O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 8 3 5	0	0
4	B	1	Total C O 8 3 5	0	0
4	C	1	Total C O 8 3 5	0	0
4	D	1	Total C O 8 3 5	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	25	Total O 25 25	0	0
5	B	18	Total O 18 18	0	0
5	C	16	Total O 16 16	0	0
5	D	16	Total O 16 16	0	0

4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	229.60Å 118.60Å 113.10Å 90.00° 109.60° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60	Depositor
% Data completeness (in resolution range)	94.0 (20.00-2.60)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.218 , 0.301	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	17931	wwPDB-VP
Average B, all atoms (Å ²)	28.0	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: NAD, MAK, MG

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	0.53	0/4447	1.00	17/5998 (0.3%)
1	B	0.54	0/4447	1.01	20/5998 (0.3%)
1	C	0.55	0/4447	1.01	19/5998 (0.3%)
1	D	0.54	0/4447	0.99	17/5998 (0.3%)
All	All	0.54	0/17788	1.00	73/23992 (0.3%)

There are no bond length outliers.

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	470	ILE	N-CA-C	9.26	118.94	111.62
1	D	470	ILE	N-CA-C	9.21	118.90	111.62
1	A	470	ILE	N-CA-C	8.71	118.50	111.62
1	D	556	ARG	N-CA-C	7.66	121.50	112.93
1	C	150	TRP	CA-C-N	7.61	126.88	118.97

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	4367	0	4407	369	0
1	B	4367	0	4407	324	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4367	0	4407	227	0
1	D	4367	0	4407	339	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	88	0	52	4	0
3	B	88	0	52	5	0
3	C	88	0	52	3	0
3	D	88	0	52	3	0
4	A	8	0	0	1	0
4	B	8	0	0	1	0
4	C	8	0	0	1	0
4	D	8	0	0	2	0
5	A	25	0	0	4	0
5	B	18	0	0	4	0
5	C	16	0	0	3	0
5	D	16	0	0	1	0
All	All	17931	0	17836	1234	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 35.

The worst 5 of 1234 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:210:ILE:H	1:C:210:ILE:HD13	1.00	1.10
1:D:140:ARG:HH22	1:D:233:ASP:HB3	1.15	1.09
1:D:177:MSE:HE1	1:D:181:VAL:HG23	1.34	1.06
1:A:327:MSE:HE3	1:A:337:ALA:HB1	1.38	1.06
1:B:354:ARG:HE	1:B:358:ILE:HD11	1.21	1.06

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	551/584 (94%)	512 (93%)	34 (6%)	5 (1%)	14	30
1	B	551/584 (94%)	512 (93%)	32 (6%)	7 (1%)	9	21
1	C	551/584 (94%)	513 (93%)	34 (6%)	4 (1%)	18	38
1	D	551/584 (94%)	499 (91%)	43 (8%)	9 (2%)	7	16
All	All	2204/2336 (94%)	2036 (92%)	143 (6%)	25 (1%)	11	25

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	332	LEU
1	B	332	LEU
1	C	332	LEU
1	D	270	ARG
1	D	332	LEU

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	469/483 (97%)	356 (76%)	113 (24%)	1	1
1	B	469/483 (97%)	359 (76%)	110 (24%)	1	1
1	C	469/483 (97%)	371 (79%)	98 (21%)	1	2
1	D	469/483 (97%)	344 (73%)	125 (27%)	0	1
All	All	1876/1932 (97%)	1430 (76%)	446 (24%)	1	1

5 of 446 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	72	LEU
1	D	559	ARG
1	C	404	ILE

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Mol	Chain	Res	Type
1	D	551	LYS
1	D	376	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	69	HIS
1	D	321	ASN
1	C	305	HIS
1	D	305	HIS
1	D	485	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 4 are monoatomic - leaving 12 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	NAD	A	601	-	46,48,48	2.11	14 (30%)	64,73,73	1.83	9 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAD	D	3602	-	46,48,48	2.16	14 (30%)	64,73,73	1.84	11 (17%)
4	MAK	C	2603	2	7,7,7	2.08	5 (71%)	9,9,9	1.93	3 (33%)
4	MAK	A	603	2	7,7,7	1.85	3 (42%)	9,9,9	1.92	4 (44%)
4	MAK	B	1603	2	7,7,7	2.47	5 (71%)	9,9,9	1.92	3 (33%)
3	NAD	B	1602	-	46,48,48	2.23	14 (30%)	64,73,73	1.83	11 (17%)
3	NAD	D	3601	-	46,48,48	2.12	12 (26%)	64,73,73	1.89	9 (14%)
3	NAD	C	2601	-	46,48,48	2.02	11 (23%)	64,73,73	1.90	12 (18%)
3	NAD	B	1601	-	46,48,48	1.86	10 (21%)	64,73,73	1.86	11 (17%)
4	MAK	D	3603	2	7,7,7	2.23	5 (71%)	9,9,9	1.96	4 (44%)
3	NAD	C	2602	-	46,48,48	2.19	12 (26%)	64,73,73	1.83	11 (17%)
3	NAD	A	602	-	46,48,48	2.18	12 (26%)	64,73,73	1.85	11 (17%)

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	NAD	A	601	-	-	3/30/62/62	0/5/5/5
3	NAD	D	3602	-	-	5/30/62/62	0/5/5/5
4	MAK	C	2603	2	-	4/8/8/8	-
4	MAK	A	603	2	-	4/8/8/8	-
4	MAK	B	1603	2	-	1/8/8/8	-
3	NAD	B	1602	-	-	6/30/62/62	0/5/5/5
3	NAD	D	3601	-	-	2/30/62/62	0/5/5/5
3	NAD	C	2601	-	-	7/30/62/62	0/5/5/5
3	NAD	B	1601	-	-	5/30/62/62	0/5/5/5
4	MAK	D	3603	2	-	1/8/8/8	-
3	NAD	C	2602	-	-	5/30/62/62	0/5/5/5
3	NAD	A	602	-	-	6/30/62/62	0/5/5/5

The worst 5 of 117 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	3602	NAD	C2N-N1N	8.31	1.44	1.35
3	A	602	NAD	C2N-N1N	8.30	1.44	1.35
3	B	1602	NAD	C2N-N1N	8.30	1.44	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2602	NAD	C2N-N1N	7.91	1.43	1.35
3	C	2601	NAD	C2N-N1N	7.11	1.42	1.35

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2602	NAD	C5A-C4A-N3A	-6.22	118.16	126.72
3	A	602	NAD	C5A-C4A-N3A	-6.12	118.28	126.72
3	B	1602	NAD	C5A-C4A-N3A	-6.10	118.32	126.72
3	C	2601	NAD	C5A-C4A-N3A	-6.09	118.33	126.72
3	D	3602	NAD	C5A-C4A-N3A	-5.97	118.49	126.72

There are no chirality outliers.

5 of 49 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	NAD	O4D-C1D-N1N-C6N
3	A	602	NAD	C5B-O5B-PA-O2A
3	A	602	NAD	C5B-O5B-PA-O3
3	A	602	NAD	PA-O3-PN-O5D
3	B	1601	NAD	O4D-C1D-N1N-C2N

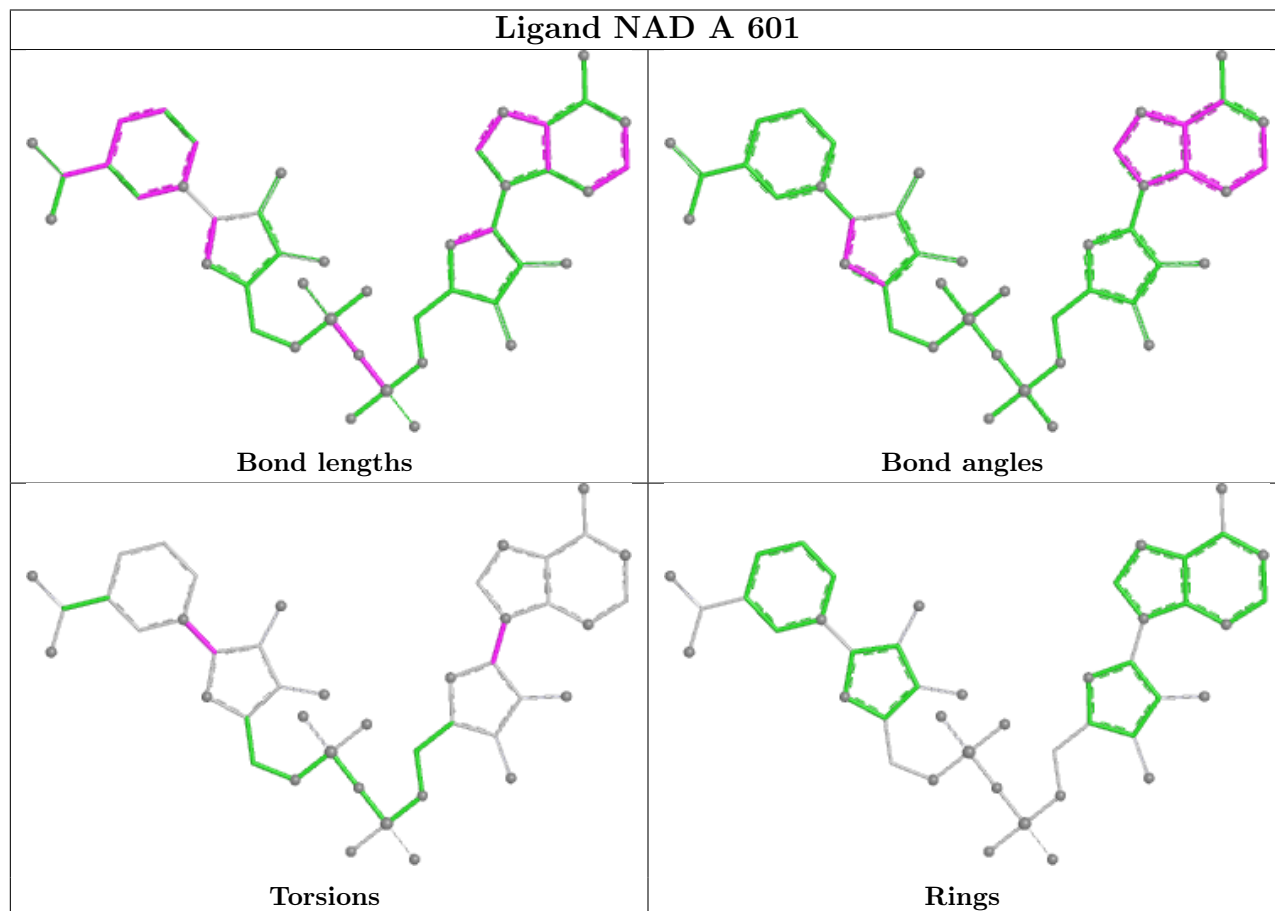
There are no ring outliers.

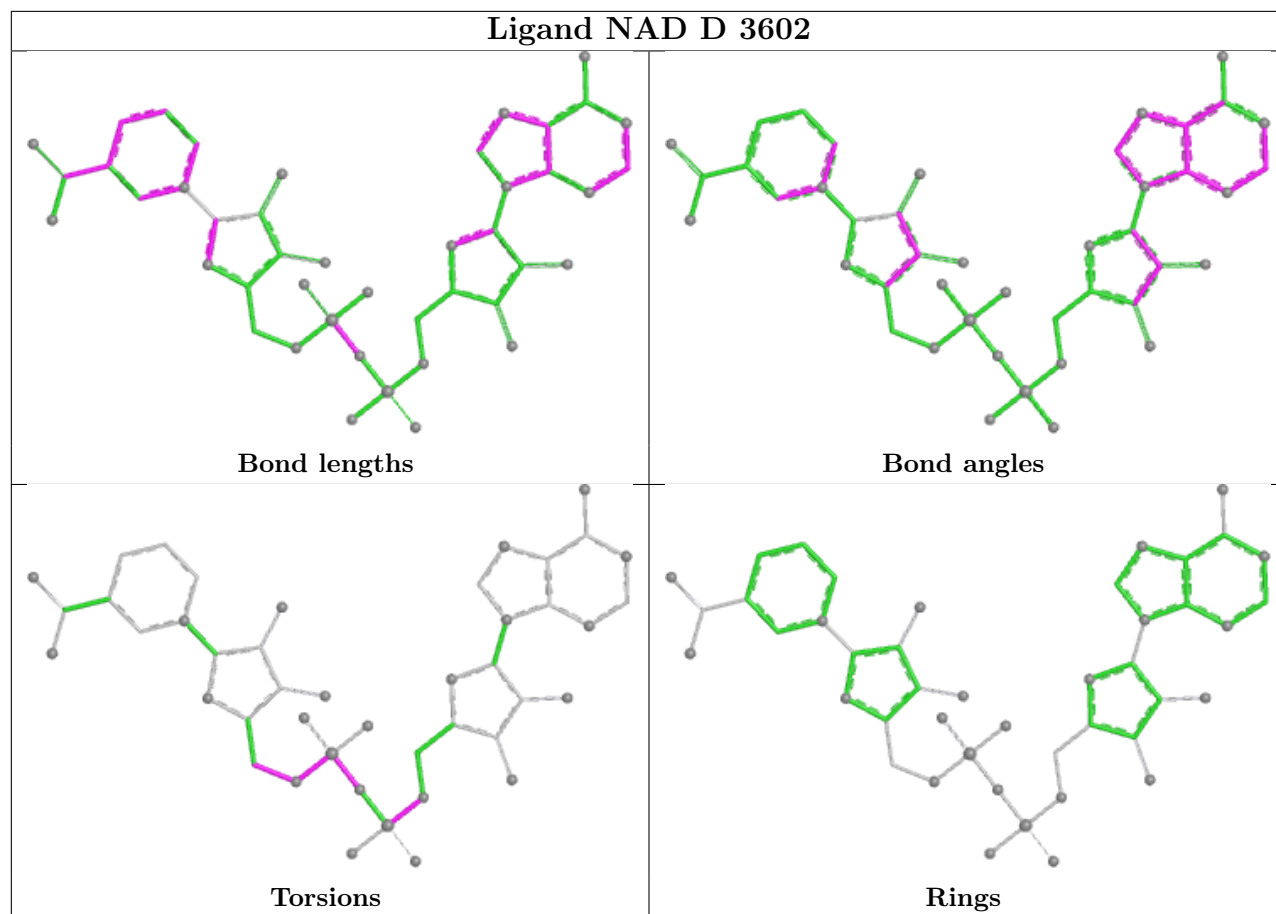
10 monomers are involved in 20 short contacts:

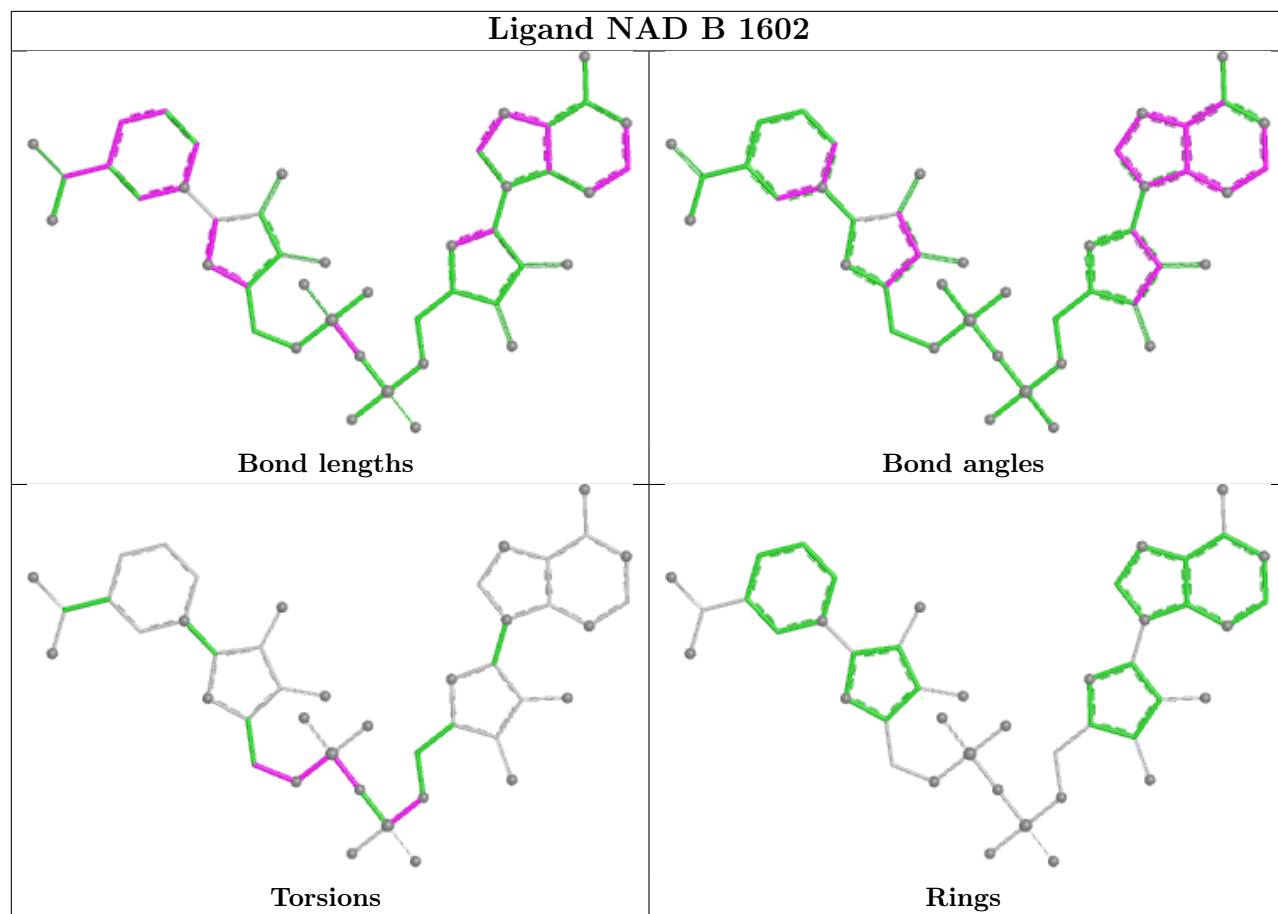
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	NAD	3	0
4	C	2603	MAK	1	0
4	A	603	MAK	1	0
4	B	1603	MAK	1	0
3	B	1602	NAD	1	0
3	D	3601	NAD	3	0
3	C	2601	NAD	3	0
3	B	1601	NAD	4	0
4	D	3603	MAK	2	0
3	A	602	NAD	1	0

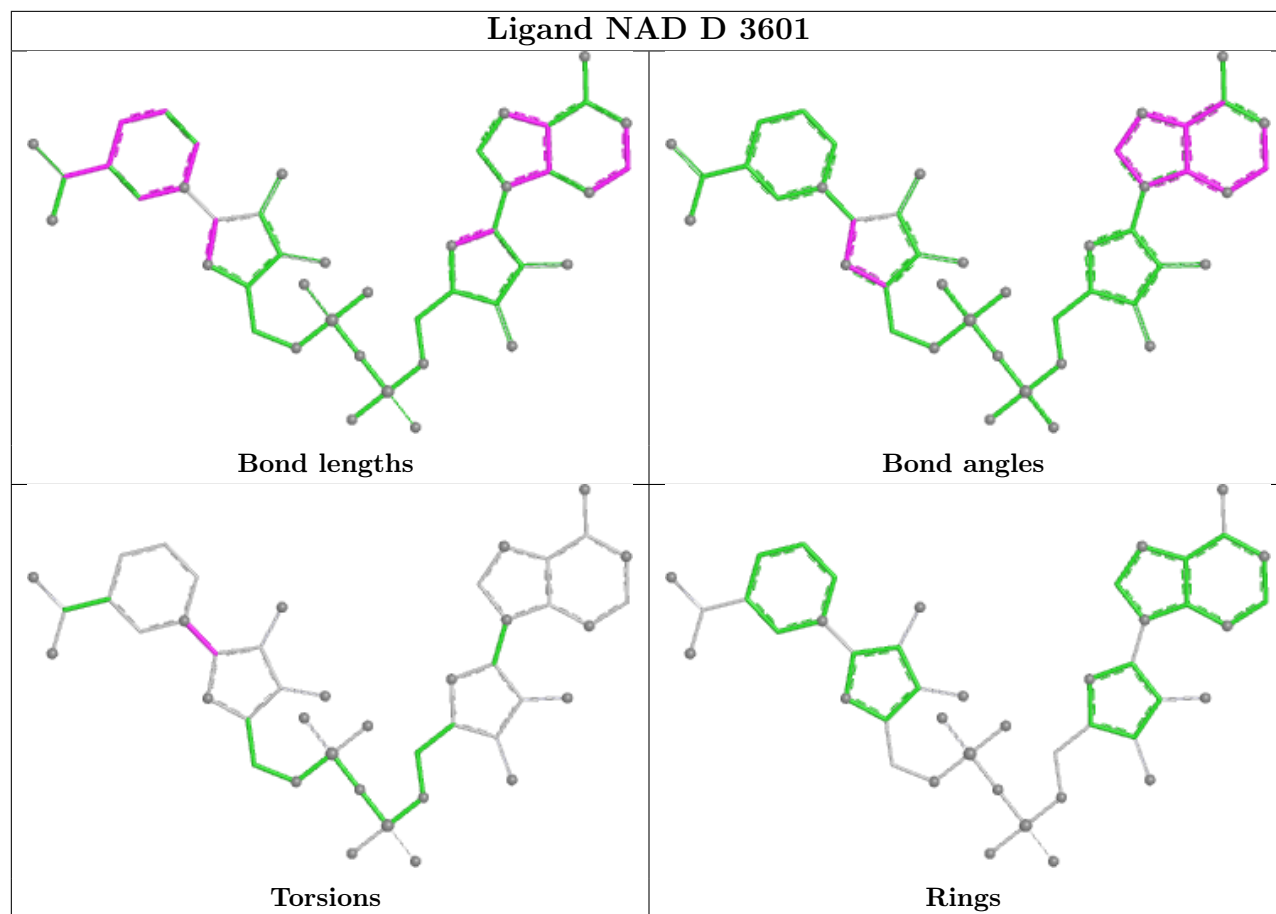
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

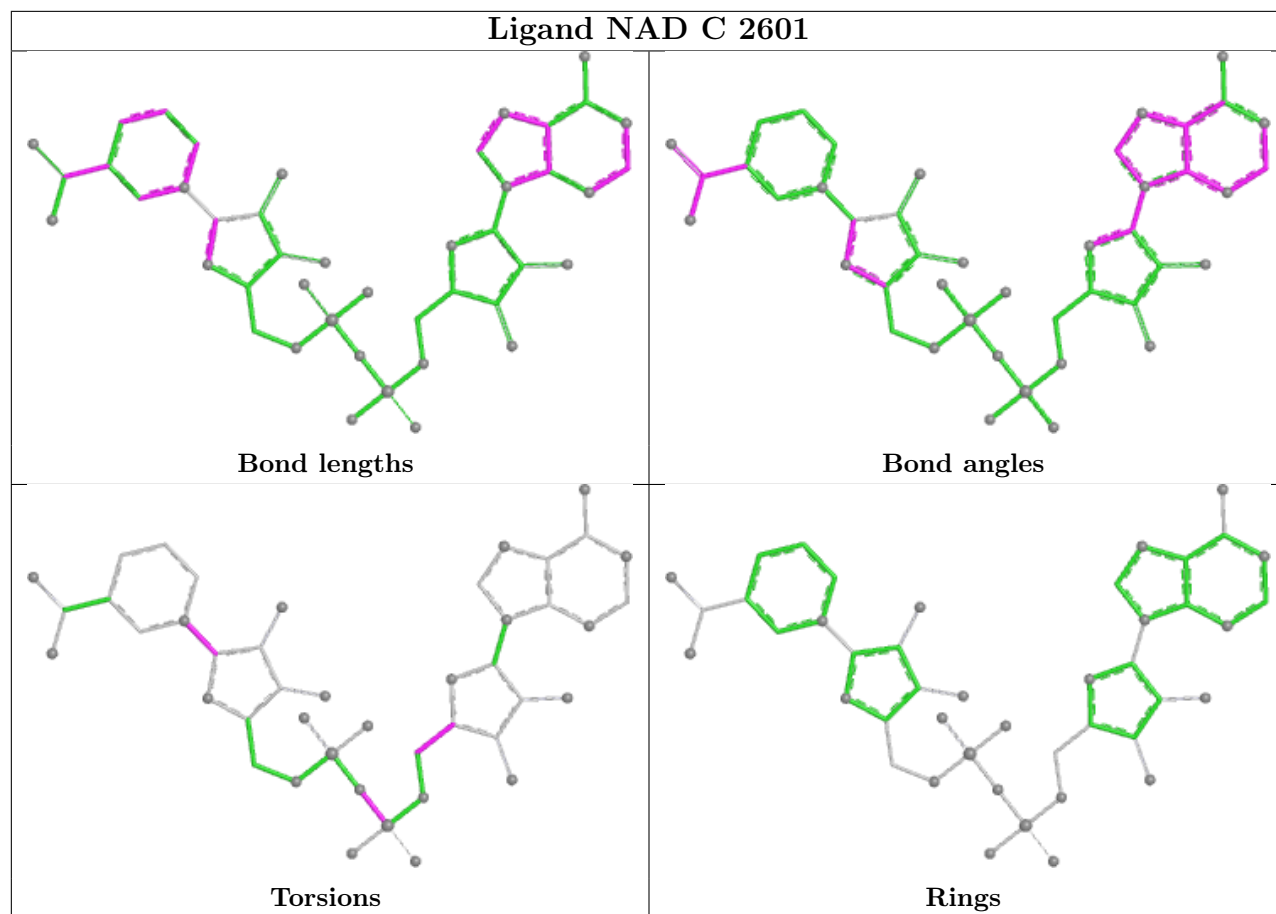
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question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

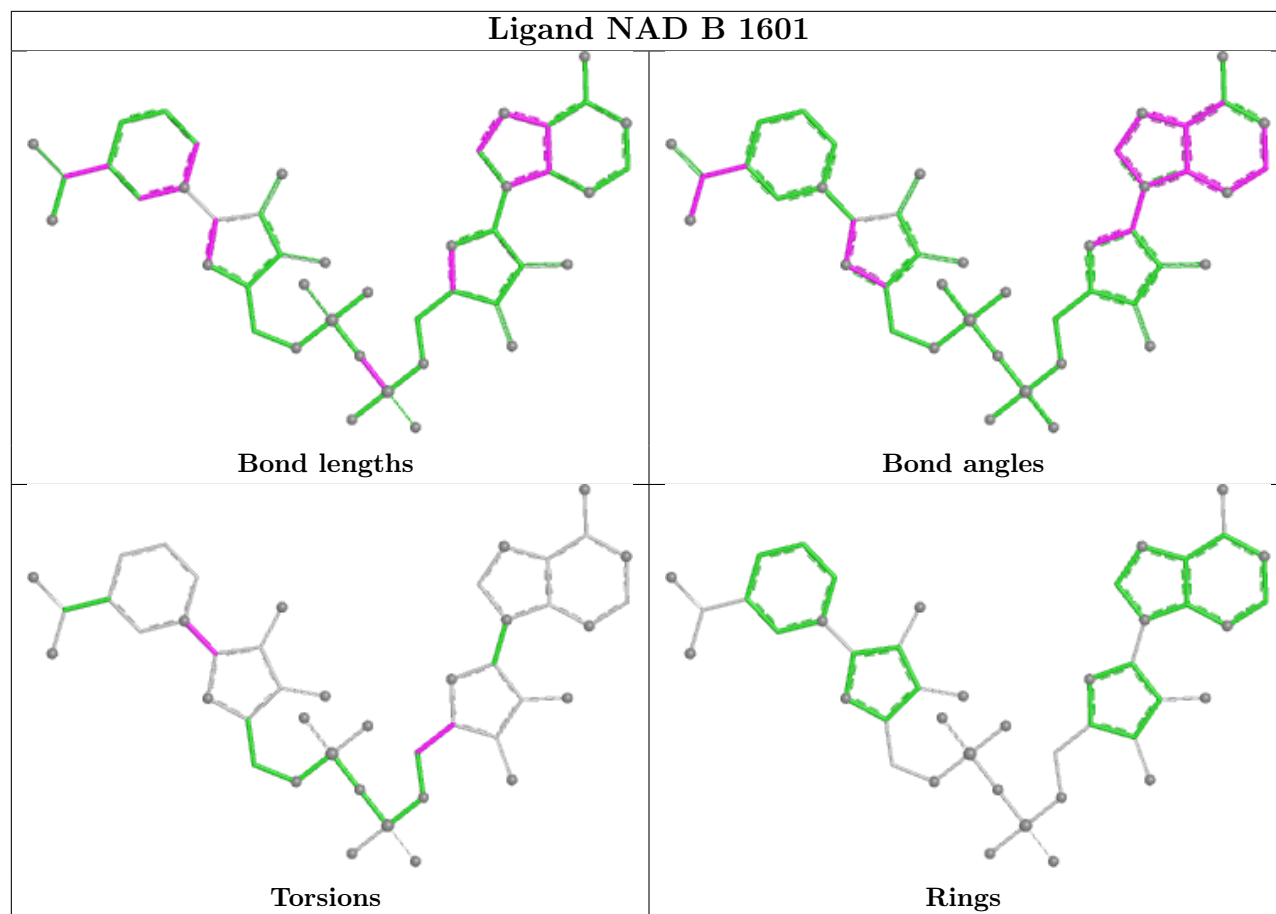


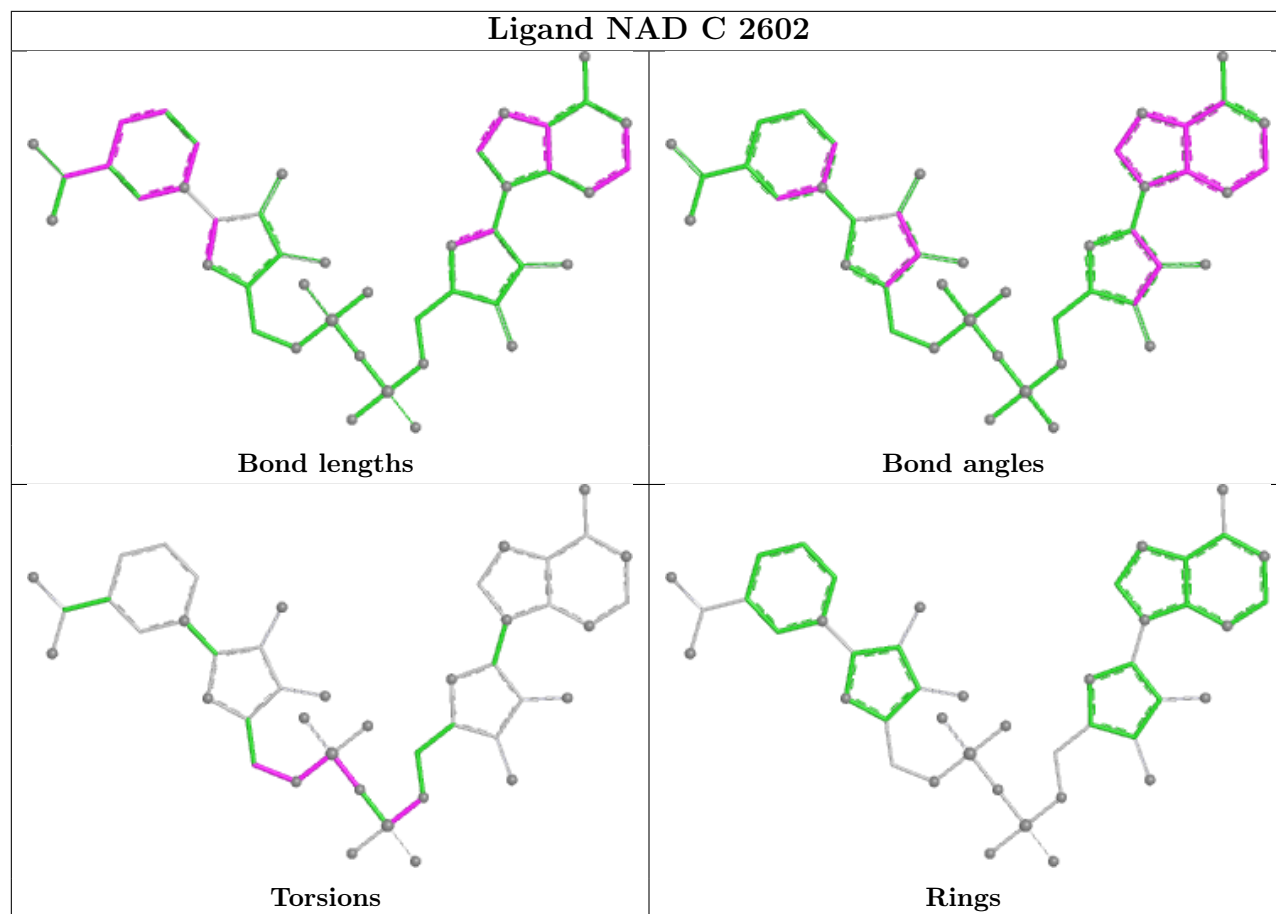


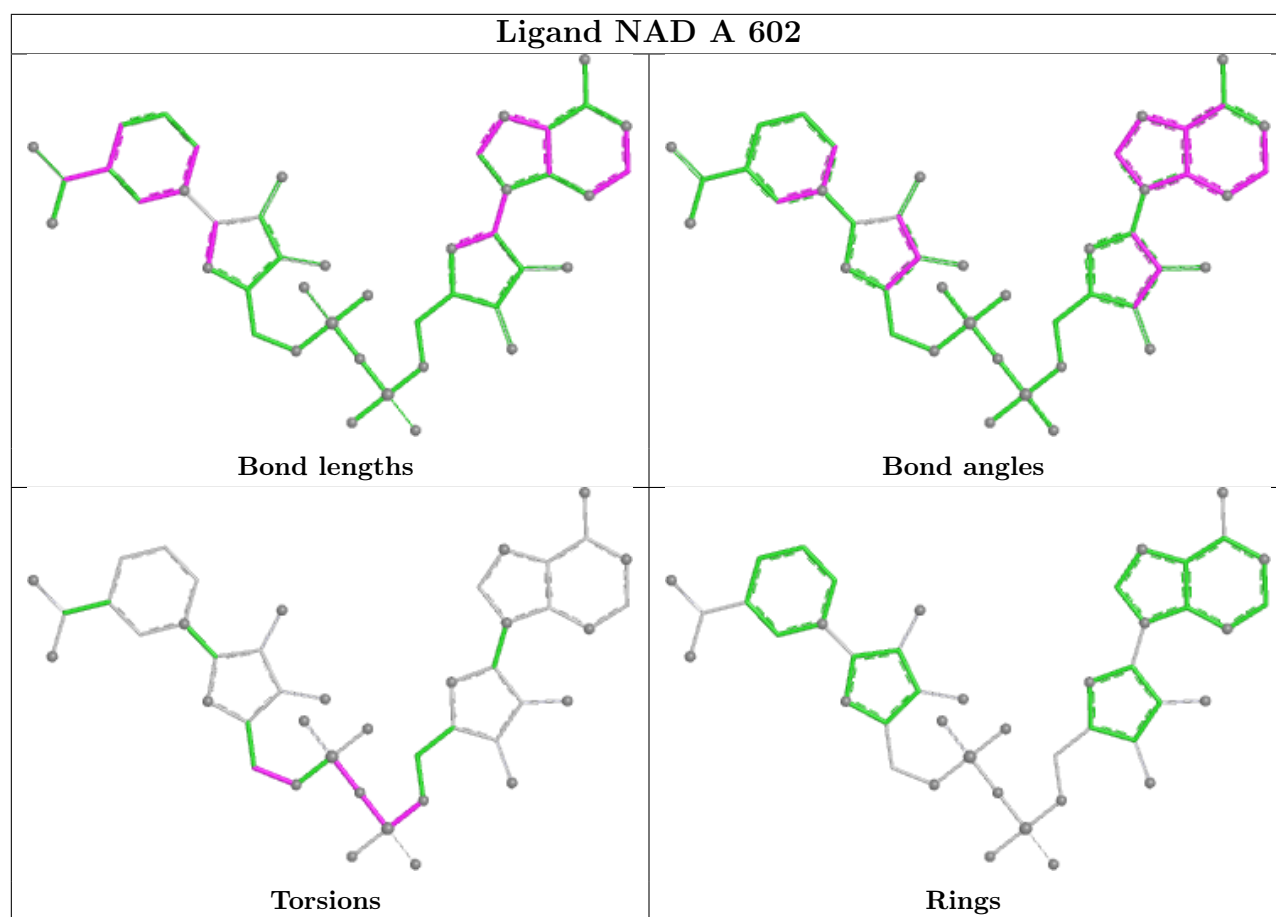












5.7 Other polymers [i](#)

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](#)

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.