



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:07 PM UTC

PDB ID : 1F8G / pdb_00001f8g
Title : THE X-RAY STRUCTURE OF NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE FROM RHODOSPIRILLUM RUBRUM COMPLEXED WITH NAD⁺
Authors : Buckley, P.A.; Baz Jackson, J.; Schneider, T.; White, S.A.; Rice, D.W.; Baker, P.J.
Deposited on : 2000-06-30
Resolution : 2.00 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)
Xtriage (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

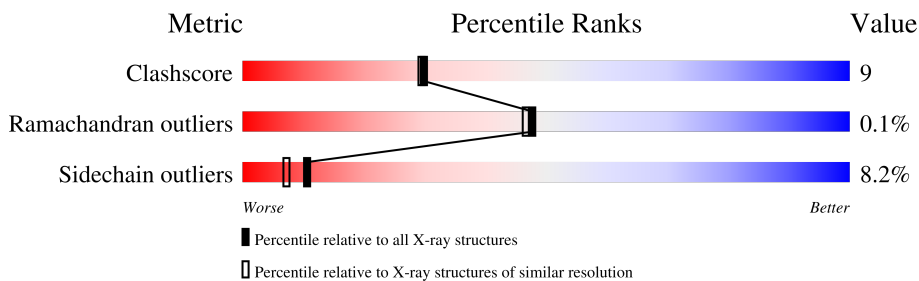
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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	384	 81% 16% ...
1	B	384	 80% 16% ..
1	C	384	 79% 16% ...
1	D	384	 70% 24% ...

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12733 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 NUCLEOTIDE TRANSHYDROGENASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	382	Total	C	N	O	S	Se	0	0	0
			2795	1763	480	535	3	14			
1	B	381	Total	C	N	O	S	Se	0	0	0
			2792	1761	482	531	3	15			
1	C	375	Total	C	N	O	S	Se	0	0	0
			2759	1742	476	523	3	15			
1	D	377	Total	C	N	O	S	Se	0	0	0
			2770	1749	477	526	3	15			

There are 60 discrepancies between the modelled and reference sequences:

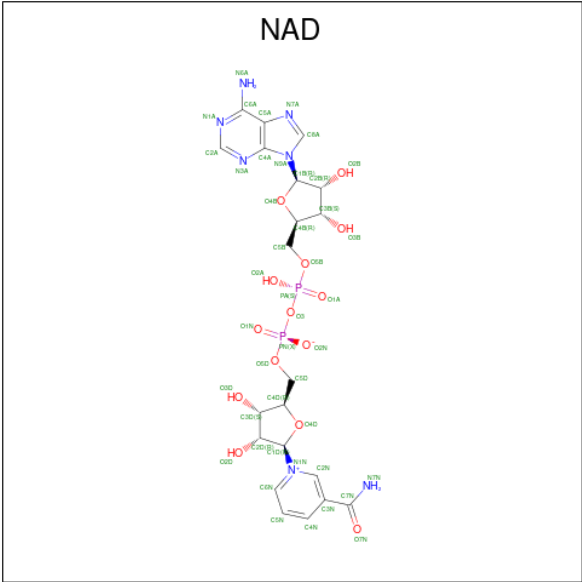
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP Q60164
A	78	MSE	MET	modified residue	UNP Q60164
A	97	MSE	MET	modified residue	UNP Q60164
A	122	MSE	MET	modified residue	UNP Q60164
A	125	MSE	MET	modified residue	UNP Q60164
A	134	MSE	MET	modified residue	UNP Q60164
A	162	MSE	MET	modified residue	UNP Q60164
A	163	MSE	MET	modified residue	UNP Q60164
A	164	MSE	MET	modified residue	UNP Q60164
A	199	MSE	MET	modified residue	UNP Q60164
A	226	MSE	MET	modified residue	UNP Q60164
A	239	MSE	MET	modified residue	UNP Q60164
A	280	MSE	MET	modified residue	UNP Q60164
A	284	MSE	MET	modified residue	UNP Q60164
A	356	MSE	MET	modified residue	UNP Q60164
B	1	MSE	MET	modified residue	UNP Q60164
B	78	MSE	MET	modified residue	UNP Q60164
B	97	MSE	MET	modified residue	UNP Q60164
B	122	MSE	MET	modified residue	UNP Q60164
B	125	MSE	MET	modified residue	UNP Q60164
B	134	MSE	MET	modified residue	UNP Q60164

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Chain	Residue	Modelled	Actual	Comment	Reference
B	162	MSE	MET	modified residue	UNP Q60164
B	163	MSE	MET	modified residue	UNP Q60164
B	164	MSE	MET	modified residue	UNP Q60164
B	199	MSE	MET	modified residue	UNP Q60164
B	226	MSE	MET	modified residue	UNP Q60164
B	239	MSE	MET	modified residue	UNP Q60164
B	280	MSE	MET	modified residue	UNP Q60164
B	284	MSE	MET	modified residue	UNP Q60164
B	356	MSE	MET	modified residue	UNP Q60164
C	1	MSE	MET	modified residue	UNP Q60164
C	78	MSE	MET	modified residue	UNP Q60164
C	97	MSE	MET	modified residue	UNP Q60164
C	122	MSE	MET	modified residue	UNP Q60164
C	125	MSE	MET	modified residue	UNP Q60164
C	134	MSE	MET	modified residue	UNP Q60164
C	162	MSE	MET	modified residue	UNP Q60164
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C	239	MSE	MET	modified residue	UNP Q60164
C	280	MSE	MET	modified residue	UNP Q60164
C	284	MSE	MET	modified residue	UNP Q60164
C	356	MSE	MET	modified residue	UNP Q60164
D	1	MSE	MET	modified residue	UNP Q60164
D	78	MSE	MET	modified residue	UNP Q60164
D	97	MSE	MET	modified residue	UNP Q60164
D	122	MSE	MET	modified residue	UNP Q60164
D	125	MSE	MET	modified residue	UNP Q60164
D	134	MSE	MET	modified residue	UNP Q60164
D	162	MSE	MET	modified residue	UNP Q60164
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D	164	MSE	MET	modified residue	UNP Q60164
D	199	MSE	MET	modified residue	UNP Q60164
D	226	MSE	MET	modified residue	UNP Q60164
D	239	MSE	MET	modified residue	UNP Q60164
D	280	MSE	MET	modified residue	UNP Q60164
D	284	MSE	MET	modified residue	UNP Q60164
D	356	MSE	MET	modified residue	UNP Q60164

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			35	15	5	13	2		
2	C	1	Total	C	N	O	P	0	0
			35	15	5	13	2		
2	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	406	Total	O	0	0
			406	406		
3	B	398	Total	O	0	0
			398	398		
3	C	389	Total	O	0	0
			389	389		
3	D	266	Total	O	0	0
			266	266		

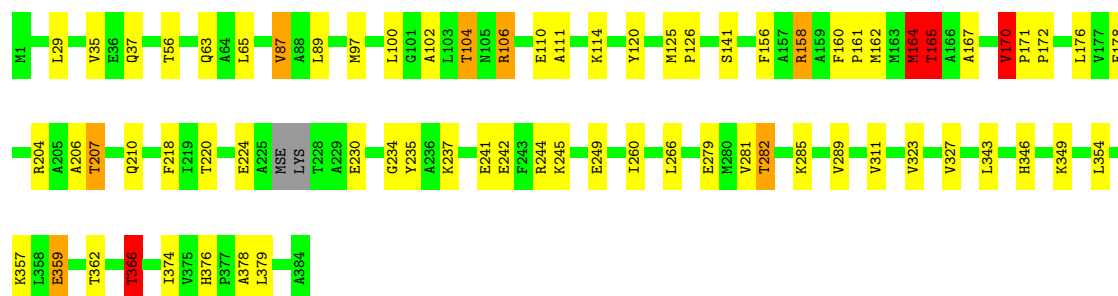
3 Residue-property plots

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.

Note EDS was not executed.

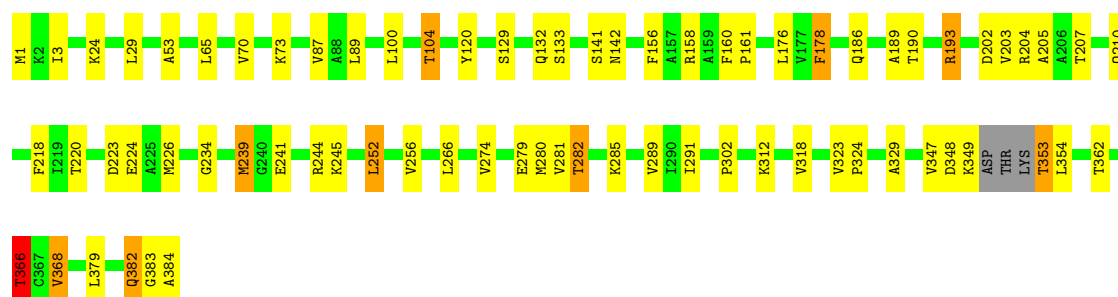
• Molecule 1: NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE

Chain A: 



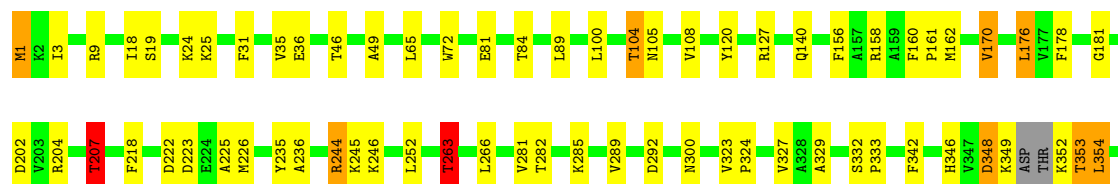
• Molecule 1: NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE

Chain B: 



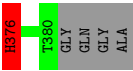
• Molecule 1: NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE

Chain C: 





● Molecule 1: NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE



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	65.90Å 116.60Å 102.00Å 90.00° 104.22° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.00)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.210 , 0.260	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12733	wwPDB-VP
Average B, all atoms (Å ²)	31.0	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

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	0.55	0/2818	1.39	23/3798 (0.6%)
1	B	0.55	0/2814	1.33	8/3789 (0.2%)
1	C	0.56	1/2781 (0.0%)	1.38	15/3743 (0.4%)
1	D	0.50	0/2792	1.33	15/3760 (0.4%)
All	All	0.54	1/11205 (0.0%)	1.36	61/15090 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	377	PRO	N-CD	5.41	1.55	1.47

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	237	LYS	CA-C-O	13.23	134.77	121.14
1	C	170	VAL	N-CA-CB	-12.69	98.92	112.37
1	C	170	VAL	CB-CA-C	11.78	121.55	110.13
1	A	237	LYS	N-CA-C	10.71	121.94	108.45
1	C	348	ASP	CA-CB-CG	10.42	123.02	112.60

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	2795	0	2911	38	0
1	B	2792	0	2916	48	0
1	C	2759	0	2887	39	0
1	D	2770	0	2897	75	0
2	A	44	0	26	0	0
2	B	35	0	19	3	0
2	C	35	0	19	1	0
2	D	44	0	26	0	0
3	A	406	0	0	4	0
3	B	398	0	0	3	0
3	C	389	0	0	5	0
3	D	266	0	0	5	0
All	All	12733	0	11701	196	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 9.

The worst 5 of 196 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:263:THR:HG23	1:D:300:ASN:HD22	1.26	0.99
1:C:202:ASP:HB3	1:C:207:THR:HG21	1.48	0.94
1:D:263:THR:HG22	1:D:292:ASP:HA	1.53	0.90
1:A:97:MSE:HE1	1:A:343:LEU:HD13	1.52	0.90
1:A:162:MSE:SE	1:A:164:MSE:HE3	2.23	0.88

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	378/384 (98%)	370 (98%)	8 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	377/384 (98%)	367 (97%)	10 (3%)	0	100	100
1	C	371/384 (97%)	357 (96%)	13 (4%)	1 (0%)	36	35
1	D	373/384 (97%)	360 (96%)	12 (3%)	1 (0%)	36	35
All	All	1499/1536 (98%)	1454 (97%)	43 (3%)	2 (0%)	48	46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	223	ASP
1	D	376	HIS

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	293/281 (104%)	268 (92%)	25 (8%)	10	7
1	B	293/281 (104%)	273 (93%)	20 (7%)	14	11
1	C	291/281 (104%)	266 (91%)	25 (9%)	10	6
1	D	292/281 (104%)	266 (91%)	26 (9%)	9	6
All	All	1169/1124 (104%)	1073 (92%)	96 (8%)	10	7

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	245	LYS
1	D	84	THR
1	C	263	THR
1	C	327	VAL
1	D	106	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	105	ASN
1	D	210	GLN
1	D	300	ASN
1	D	142	ASN
1	B	210	GLN

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](#)

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	NAD	D	2503	-	46,48,48	1.08	3 (6%)	64,73,73	1.79	7 (10%)
2	NAD	A	2500	-	46,48,48	1.09	3 (6%)	64,73,73	1.79	7 (10%)
2	NAD	C	2502	-	38,38,48	0.79	1 (2%)	53,58,73	0.90	2 (3%)
2	NAD	B	2501	-	38,38,48	0.80	0	53,58,73	0.77	2 (3%)

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	NAD	D	2503	-	-	1/30/62/62	0/5/5/5
2	NAD	A	2500	-	-	2/30/62/62	0/5/5/5
2	NAD	C	2502	-	-	3/22/51/62	0/4/4/5
2	NAD	B	2501	-	-	4/22/51/62	0/4/4/5

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2500	NAD	C3N-C7N	3.89	1.56	1.50
2	D	2503	NAD	C3N-C7N	3.89	1.56	1.50
2	A	2500	NAD	C6N-N1N	2.95	1.42	1.35
2	D	2503	NAD	C6N-N1N	2.92	1.42	1.35
2	D	2503	NAD	PA-O3	2.38	1.62	1.59

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2500	NAD	C5N-C4N-C3N	-7.50	112.99	120.36
2	D	2503	NAD	C5N-C4N-C3N	-7.19	113.29	120.36
2	A	2500	NAD	C6N-C5N-C4N	5.94	128.01	119.45
2	D	2503	NAD	C6N-C5N-C4N	5.81	127.82	119.45
2	D	2503	NAD	C5N-C6N-N1N	-5.13	113.38	120.38

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2501	NAD	C5D-O5D-PN-O3
2	B	2501	NAD	C5D-O5D-PN-O1N
2	B	2501	NAD	O4D-C4D-C5D-O5D
2	B	2501	NAD	C3D-C4D-C5D-O5D
2	C	2502	NAD	O4D-C4D-C5D-O5D

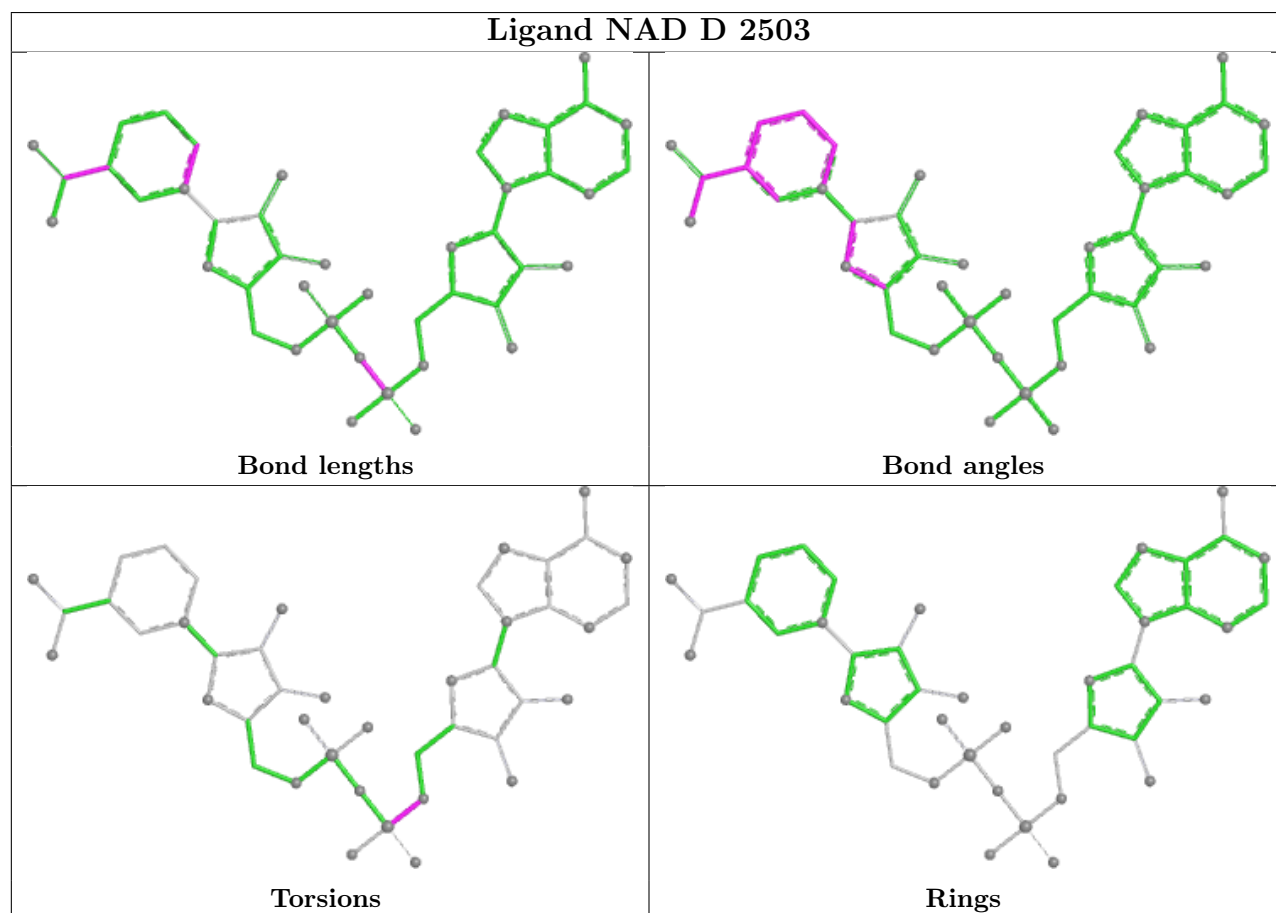
There are no ring outliers.

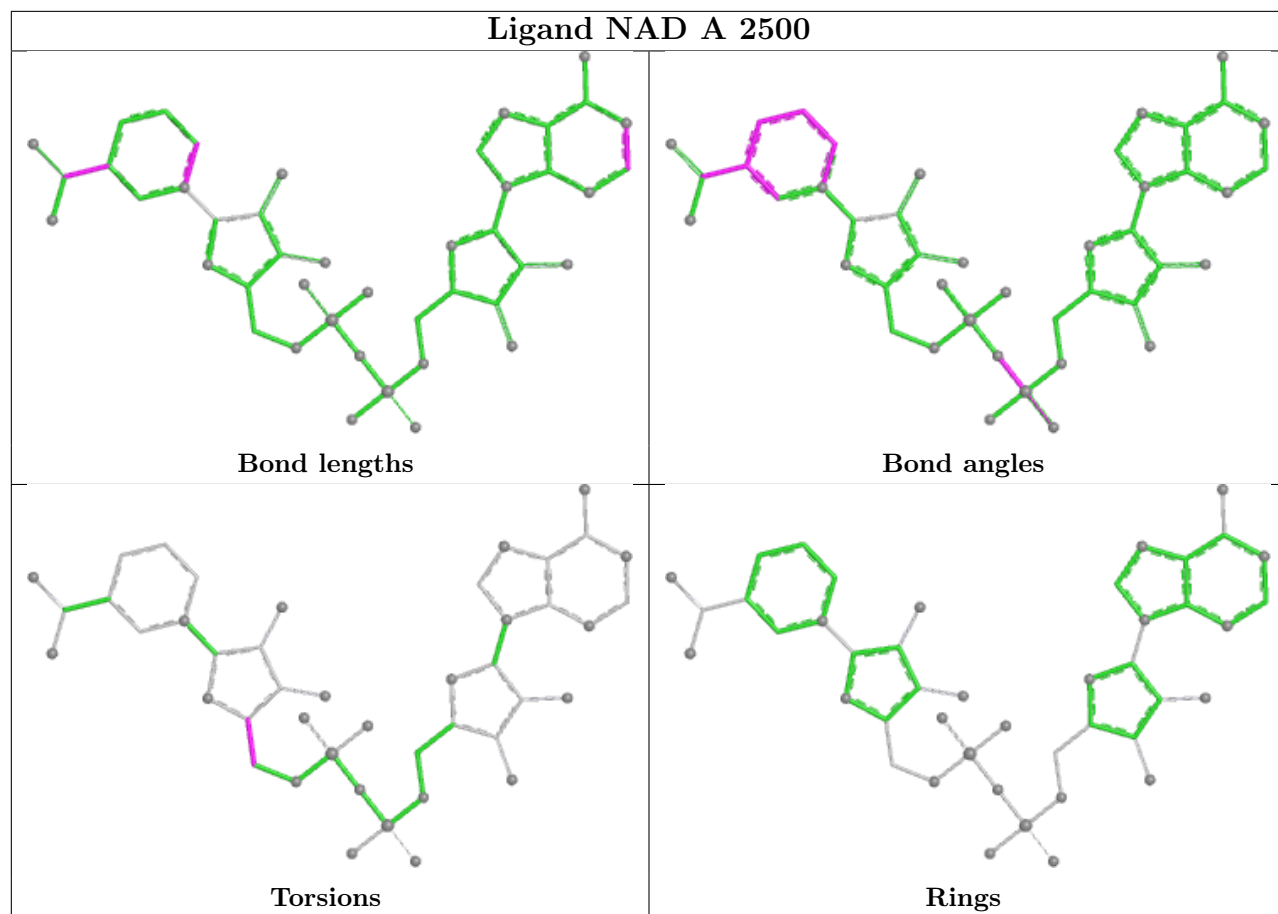
2 monomers are involved in 4 short contacts:

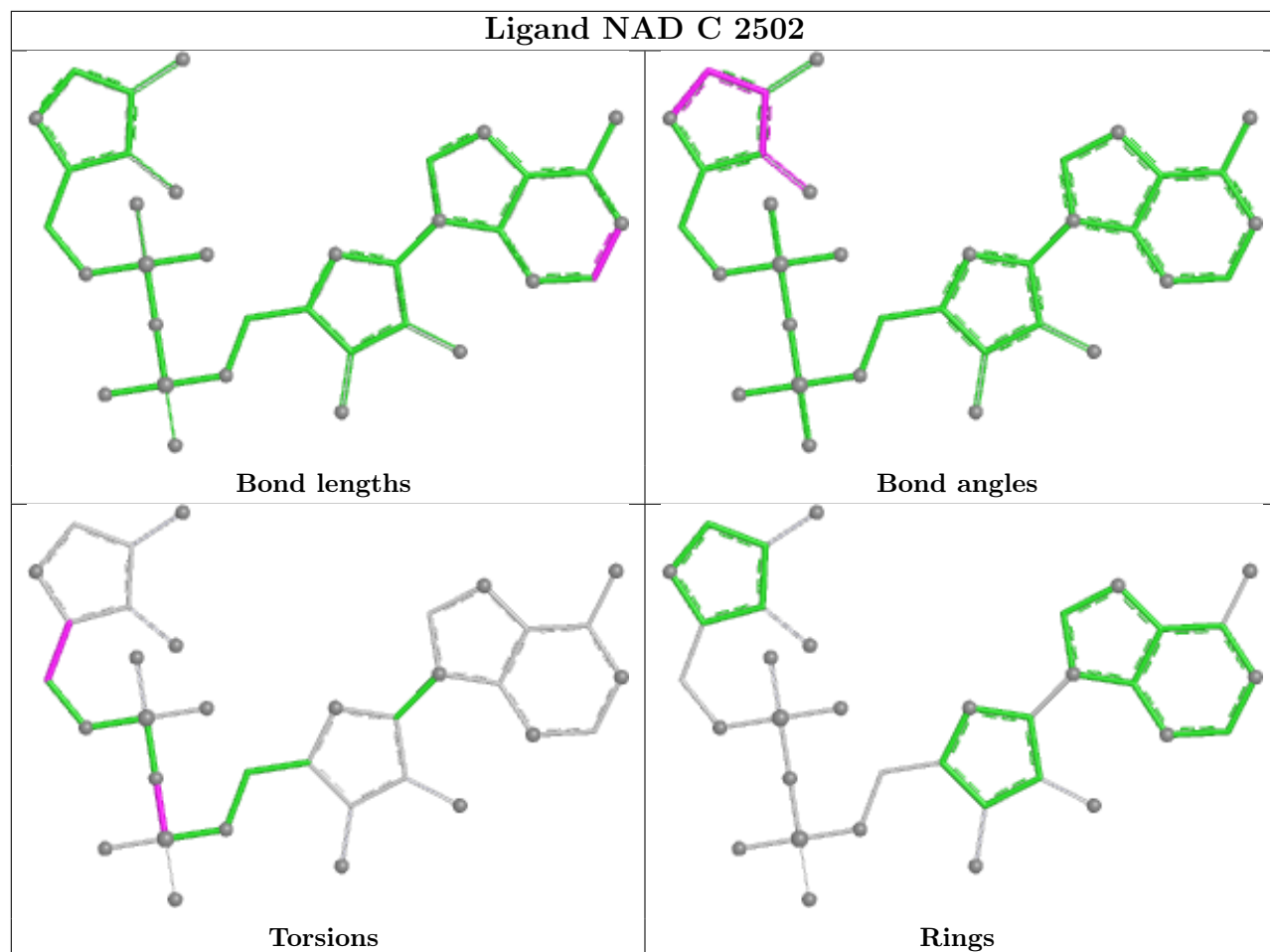
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2502	NAD	1	0
2	B	2501	NAD	3	0

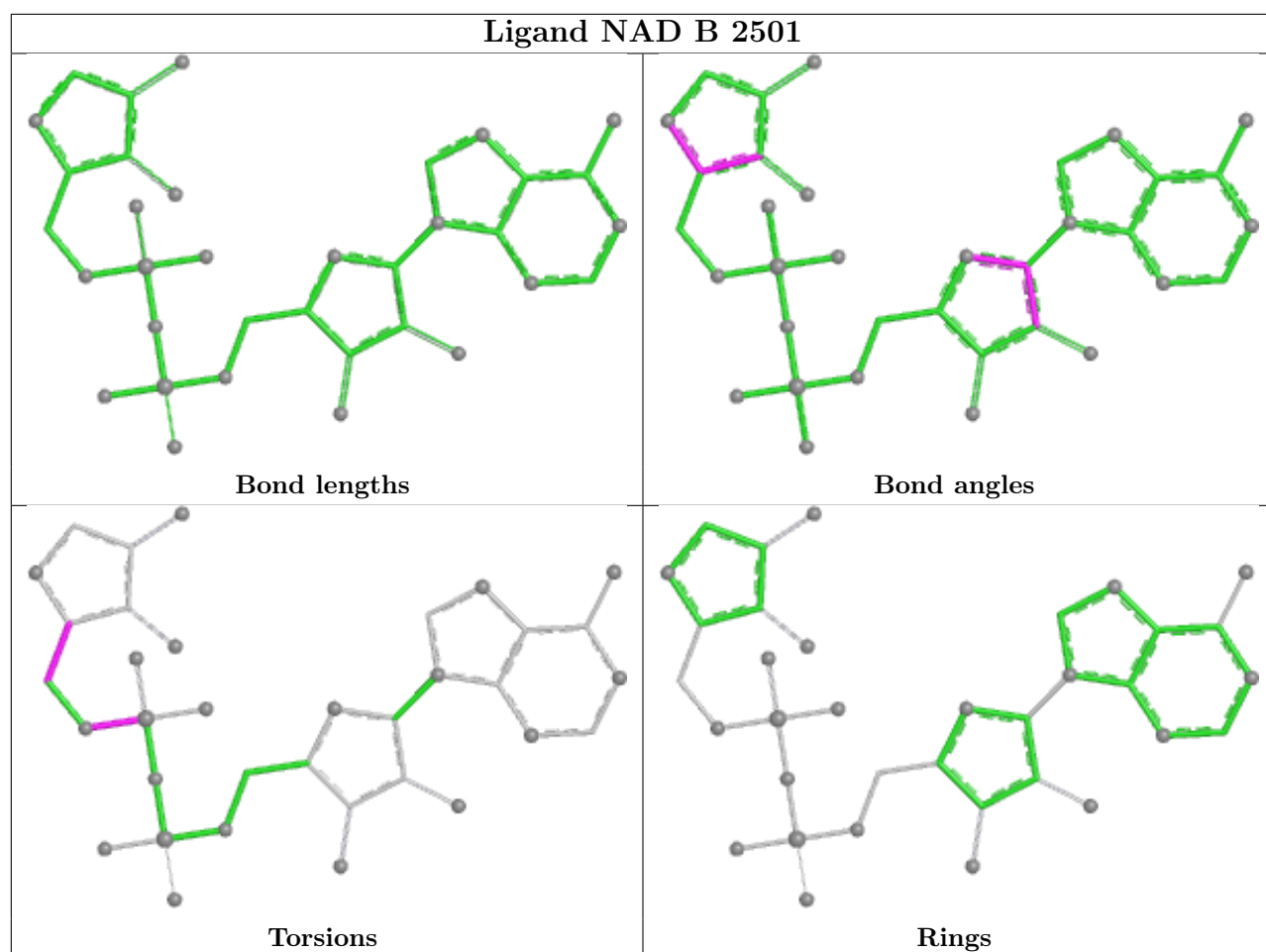
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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.