



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 10:20 PM UTC

PDB ID : 1EMD / pdb_00001emd
Title : CRYSTAL STRUCTURE OF A TERNARY COMPLEX OF ESCHERICHIA COLI MALATE DEHYDROGENASE, CITRATE AND NAD AT 1.9 ANGSTROMS RESOLUTION
Authors : Hall, M.D.; Banaszak, L.J.
Deposited on : 1993-03-25
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

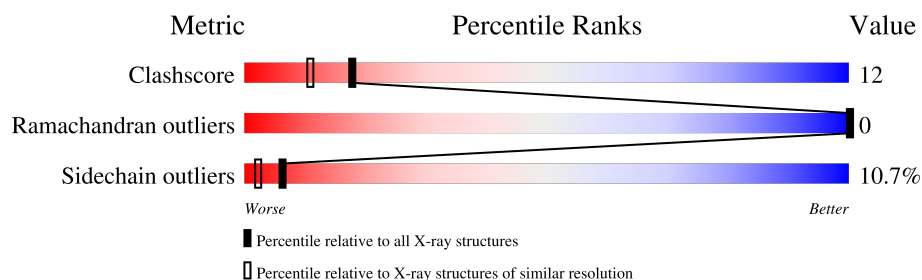
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)

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	312	 78% 17% . .

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2421 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 MALATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	312	Total	C	N	O	S	0	0	0
			2278	1441	390	440	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	80	ARG	ALA	conflict	UNP P61889
A	307	GLN	GLU	conflict	UNP P61889

- Molecule 2 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		

- 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 44	C 21	N 7	O 14	P 2	0	0

- Molecule 4 is water.

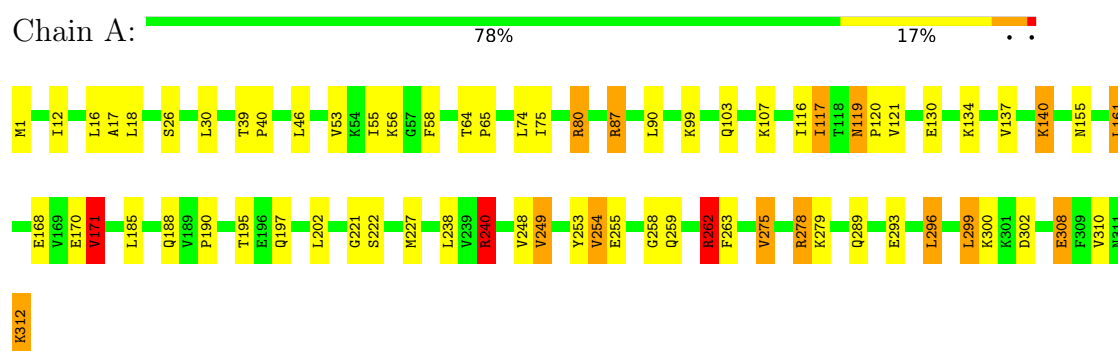
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	86	Total O 86 86	0	0

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.

Note EDS was not executed.

• Molecule 1: MALATE DEHYDROGENASE



4 Data and refinement statistics

Xtriage (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	116.80Å 43.05Å 83.74Å 90.00° 130.10° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.90	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.195 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2421	wwPDB-VP
Average B, all atoms (Å ²)	20.0	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: CIT, 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	0.78	5/2306 (0.2%)	1.08	10/3121 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	258	GLY	C-N	-9.38	1.21	1.34
1	A	259	GLN	CA-CB	6.80	1.64	1.53
1	A	171	VAL	CA-CB	6.78	1.59	1.54
1	A	275	VAL	CA-CB	5.26	1.60	1.54
1	A	53	VAL	CA-CB	5.01	1.60	1.54

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	259	GLN	CA-CB-CG	22.16	158.42	114.10
1	A	259	GLN	N-CA-CB	13.32	130.73	110.22
1	A	259	GLN	CB-CA-C	-7.34	97.05	110.63
1	A	117	ILE	N-CA-C	-5.88	107.08	112.96
1	A	170	GLU	CA-C-N	-5.82	118.27	123.33
1	A	170	GLU	C-N-CA	-5.82	118.27	123.33
1	A	249	VAL	N-CA-C	5.36	115.83	108.12
1	A	258	GLY	CA-C-N	5.35	127.98	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	258	GLY	C-N-CA	5.35	127.98	120.28
1	A	171	VAL	N-CA-C	5.04	113.61	107.61

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	240	ARG	Sidechain
1	A	253	TYR	Sidechain
1	A	262	ARG	Sidechain
1	A	278	ARG	Sidechain
1	A	80	ARG	Sidechain
1	A	87	ARG	Sidechain

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	2278	0	2367	57	0
2	A	13	0	6	2	0
3	A	44	0	26	20	0
4	A	86	0	0	1	0
All	All	2421	0	2399	58	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 12.

All (58) 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:A:227:MET:SD	3:A:314:NAD:H4N	1.99	1.02
1:A:227:MET:HG2	3:A:314:NAD:H5N	1.47	0.96
1:A:119:ASN:H	3:A:314:NAD:H1D	1.47	0.80
1:A:227:MET:SD	3:A:314:NAD:C4N	2.75	0.75
1:A:195:THR:OG1	1:A:197:GLN:HG2	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:MET:CG	3:A:314:NAD:H5N	2.22	0.69
1:A:262:ARG:HD2	1:A:263:PHE:CE2	2.29	0.68
1:A:12:ILE:CD1	3:A:314:NAD:H6N	2.24	0.67
1:A:80:ARG:HD2	1:A:222:SER:H	1.58	0.66
1:A:296:LEU:O	1:A:300:LYS:HG2	1.96	0.65
1:A:117:ILE:O	3:A:314:NAD:C2N	2.45	0.65
1:A:99:LYS:HE2	1:A:103:GLN:HE22	1.62	0.65
1:A:30:LEU:HD23	1:A:55:ILE:HD12	1.82	0.62
1:A:140:LYS:H	1:A:140:LYS:HD2	1.64	0.62
1:A:161:LEU:HD12	1:A:202:LEU:HD11	1.82	0.61
1:A:308:GLU:O	1:A:312:LYS:HG3	2.01	0.61
1:A:140:LYS:H	1:A:140:LYS:CD	2.14	0.61
1:A:12:ILE:HD12	3:A:314:NAD:H51N	1.84	0.60
1:A:117:ILE:HG23	3:A:314:NAD:C5N	2.33	0.59
1:A:119:ASN:N	3:A:314:NAD:H1D	2.15	0.59
1:A:155:ASN:HD21	1:A:171:VAL:H	1.52	0.57
2:A:313:CIT:O3	3:A:314:NAD:C2N	2.55	0.55
1:A:119:ASN:HB2	3:A:314:NAD:O2D	2.06	0.54
1:A:75:ILE:O	1:A:117:ILE:HB	2.08	0.54
1:A:289:GLN:O	1:A:293:GLU:HG3	2.08	0.53
1:A:240:ARG:HH12	1:A:248:VAL:HG22	1.74	0.53
1:A:80:ARG:CD	1:A:222:SER:H	2.21	0.52
1:A:188:GLN:O	1:A:190:PRO:HD3	2.10	0.52
1:A:155:ASN:HD22	1:A:171:VAL:HG13	1.75	0.52
1:A:119:ASN:OD1	1:A:120:PRO:HA	2.11	0.51
1:A:255:GLU:HB2	1:A:263:PHE:CE1	2.45	0.51
1:A:39:THR:HB	1:A:40:PRO:HD3	1.94	0.50
1:A:64:THR:HB	1:A:65:PRO:HD3	1.93	0.50
1:A:117:ILE:CG2	3:A:314:NAD:C5N	2.90	0.50
1:A:119:ASN:ND2	3:A:314:NAD:H2N	2.27	0.49
1:A:103:GLN:O	1:A:107:LYS:HG2	2.12	0.49
1:A:58:PHE:HB3	4:A:327:HOH:O	2.13	0.49
1:A:140:LYS:HD2	1:A:140:LYS:N	2.28	0.47
1:A:121:VAL:HG23	3:A:314:NAD:H71N	1.79	0.47
1:A:155:ASN:ND2	1:A:171:VAL:H	2.13	0.46
1:A:140:LYS:H	1:A:140:LYS:CE	2.29	0.46
1:A:75:ILE:HD12	1:A:116:ILE:HD13	1.97	0.45
1:A:80:ARG:NH1	1:A:221:GLY:HA3	2.31	0.45
1:A:130:GLU:HB3	1:A:310:VAL:HG11	1.98	0.45
1:A:121:VAL:CG2	3:A:314:NAD:N7N	2.80	0.44
1:A:254:VAL:HG13	1:A:278:ARG:HH11	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:ILE:HD13	3:A:314:NAD:H5N	2.00	0.42
1:A:140:LYS:CD	1:A:140:LYS:N	2.82	0.42
1:A:238:LEU:HA	1:A:238:LEU:HD23	1.82	0.41
1:A:17:ALA:HB1	1:A:46:LEU:HD11	2.03	0.41
1:A:119:ASN:ND2	2:A:313:CIT:O3	2.54	0.41
1:A:140:LYS:HB3	1:A:140:LYS:HE3	1.71	0.41
1:A:202:LEU:HD23	1:A:202:LEU:HA	1.95	0.41
1:A:117:ILE:HG22	3:A:314:NAD:C6N	2.51	0.41
1:A:121:VAL:HG21	3:A:314:NAD:N7N	2.35	0.40
1:A:299:LEU:O	1:A:302:ASP:HB2	2.21	0.40
1:A:30:LEU:O	1:A:55:ILE:HA	2.21	0.40
1:A:227:MET:SD	3:A:314:NAD:C5N	3.09	0.40

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	310/312 (99%)	306 (99%)	4 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	242/242 (100%)	216 (89%)	26 (11%)	6 2

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	16	LEU
1	A	18	LEU
1	A	26	SER
1	A	56	LYS
1	A	74	LEU
1	A	87	ARG
1	A	90	LEU
1	A	119	ASN
1	A	134	LYS
1	A	137	VAL
1	A	140	LYS
1	A	161	LEU
1	A	168	GLU
1	A	171	VAL
1	A	185	LEU
1	A	240	ARG
1	A	249	VAL
1	A	254	VAL
1	A	262	ARG
1	A	275	VAL
1	A	279	LYS
1	A	296	LEU
1	A	299	LEU
1	A	308	GLU
1	A	312	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	GLN
1	A	103	GLN
1	A	155	ASN
1	A	207	GLN
1	A	208	ASN
1	A	259	GLN
1	A	307	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 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	CIT	A	313	-	12,12,12	3.03	7 (58%)	17,17,17	2.59	10 (58%)
3	NAD	A	314	-	46,48,48	1.48	5 (10%)	64,73,73	2.04	22 (34%)

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	CIT	A	313	-	-	0/16/16/16	-
3	NAD	A	314	-	-	5/30/62/62	0/5/5/5

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	313	CIT	C3-C6	-6.38	1.46	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	314	NAD	C2N-N1N	6.31	1.41	1.35
2	A	313	CIT	C2-C3	5.54	1.60	1.54
3	A	314	NAD	O4D-C1D	3.80	1.45	1.40
2	A	313	CIT	C4-C3	3.35	1.58	1.54
2	A	313	CIT	O7-C3	2.96	1.48	1.43
3	A	314	NAD	C5A-N7A	-2.94	1.33	1.39
3	A	314	NAD	C4A-N9A	-2.83	1.31	1.37
2	A	313	CIT	O4-C5	2.33	1.38	1.30
2	A	313	CIT	C4-C5	-2.27	1.43	1.50
2	A	313	CIT	O2-C1	-2.09	1.23	1.30
3	A	314	NAD	C4N-C3N	-2.02	1.36	1.39

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	314	NAD	C6N-N1N-C2N	-5.42	117.26	121.88
2	A	313	CIT	O4-C5-C4	4.26	127.85	114.35
3	A	314	NAD	C5A-C4A-N3A	-4.24	120.88	126.72
2	A	313	CIT	C3-C4-C5	-4.14	102.59	113.92
3	A	314	NAD	C2N-N1N-C1D	3.92	127.79	119.13
2	A	313	CIT	O5-C6-C3	-3.84	114.66	122.09
3	A	314	NAD	N3A-C4A-N9A	3.72	133.49	127.17
2	A	313	CIT	O1-C1-C2	-3.70	112.47	122.95
3	A	314	NAD	O5D-C5D-C4D	3.52	120.98	108.99
3	A	314	NAD	C4A-N9A-C1B	-3.32	118.86	126.63
3	A	314	NAD	C3N-C7N-N7N	-3.31	113.66	117.74
3	A	314	NAD	O3-PA-O1A	-3.27	100.87	110.70
3	A	314	NAD	C4B-O4B-C1B	-3.25	102.29	109.47
3	A	314	NAD	C6A-C5A-N7A	-3.14	126.03	132.09
3	A	314	NAD	N3A-C2A-N1A	-3.11	123.87	128.58
3	A	314	NAD	C4A-N9A-C8A	2.85	108.73	105.74
3	A	314	NAD	C6A-C5A-C4A	2.83	121.04	117.18
2	A	313	CIT	O3-C5-C4	-2.78	115.06	122.95
2	A	313	CIT	O7-C3-C6	2.76	112.87	108.96
2	A	313	CIT	O4-C5-O3	-2.72	116.35	123.33
3	A	314	NAD	O4B-C1B-N9A	2.58	113.05	108.09
3	A	314	NAD	C6N-N1N-C1D	-2.52	114.78	119.73
2	A	313	CIT	O6-C6-O5	2.44	131.68	123.86
3	A	314	NAD	O2N-PN-O5D	2.38	118.34	107.57
3	A	314	NAD	C3B-C2B-C1B	-2.34	97.04	101.46
3	A	314	NAD	O2B-C2B-C1B	2.33	118.14	110.10
2	A	313	CIT	O7-C3-C4	-2.30	104.12	109.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	314	NAD	N9A-C8A-N7A	-2.26	110.73	113.94
2	A	313	CIT	C2-C3-C6	-2.22	105.12	110.03
3	A	314	NAD	C2N-C3N-C4N	2.19	120.80	118.26
3	A	314	NAD	O4D-C4D-C5D	-2.13	102.50	109.33
3	A	314	NAD	C2A-N1A-C6A	2.12	122.21	118.73

There are no chirality outliers.

All (5) torsion outliers are listed below:

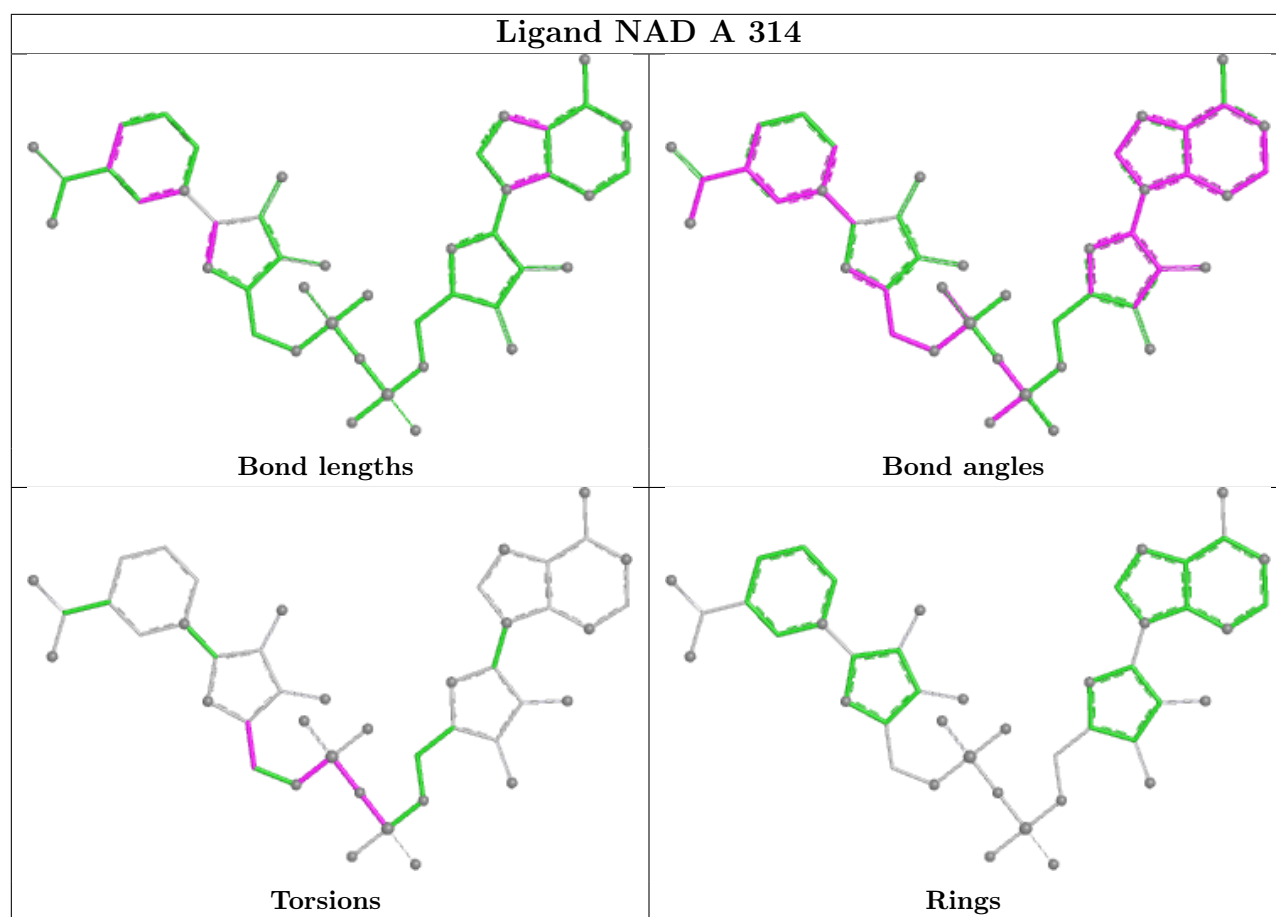
Mol	Chain	Res	Type	Atoms
3	A	314	NAD	PN-O3-PA-O5B
3	A	314	NAD	C5D-O5D-PN-O3
3	A	314	NAD	C5D-O5D-PN-O1N
3	A	314	NAD	PA-O3-PN-O2N
3	A	314	NAD	O4D-C4D-C5D-O5D

There are no ring outliers.

2 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	313	CIT	2	0
3	A	314	NAD	20	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.