



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 17, 2024 – 10:41 AM EDT

PDB ID : 3GPD
Title : TWINNING IN CRYSTALS OF HUMAN SKELETAL MUSCLE D-GLYCE
RALDEHYDE-3-PHOSPHATE DEHYDROGENASE
Authors : Watson, H.C.; Campbell, J.C.
Deposited on : 1983-06-20
Resolution : 3.50 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)
Xtrriage (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) : 2.37.1

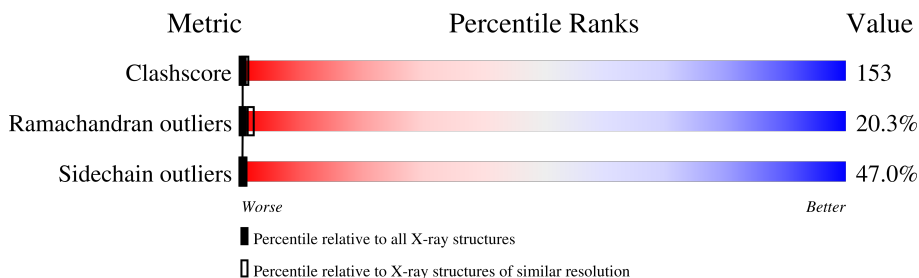
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)

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	G	334	
1	R	334	

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
2	SO4	G	338	-	-	X	-
2	SO4	G	340	-	-	X	-
2	SO4	R	338	-	-	X	-
3	NAD	G	336	X	-	-	-

2 Entry composition [i](#)

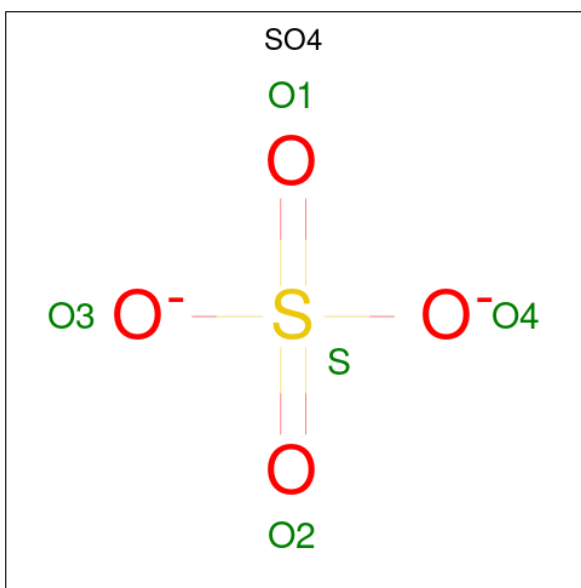
There are 3 unique types of molecules in this entry. The entry contains 5154 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 D-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.

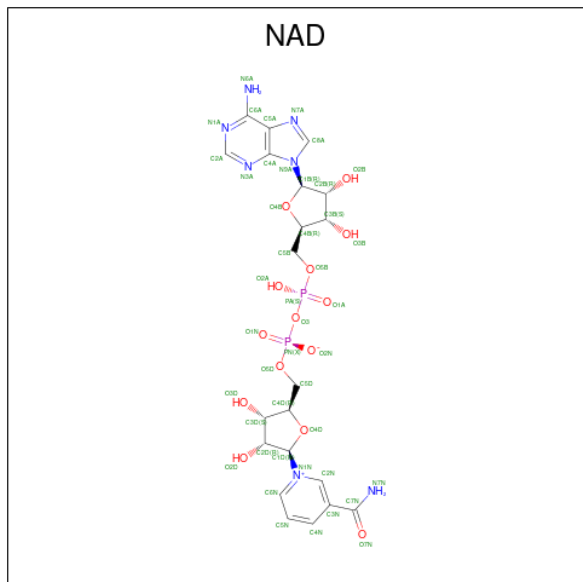
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	R	334	2523	1601	431	479	12	0	0	0
1	G	334	2523	1601	431	479	12	0	0	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	R	1	5	4	1	0	0
2	R	1	5	4	1	0	0
2	G	1	5	4	1	0	0
2	G	1	5	4	1	0	0

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	R	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	G	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

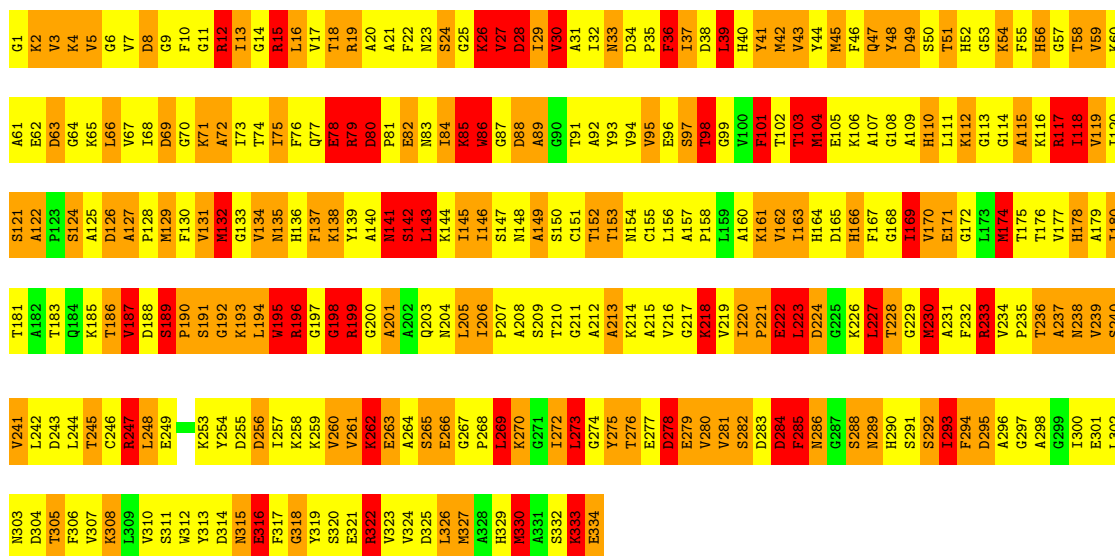
3 Residue-property plots

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.

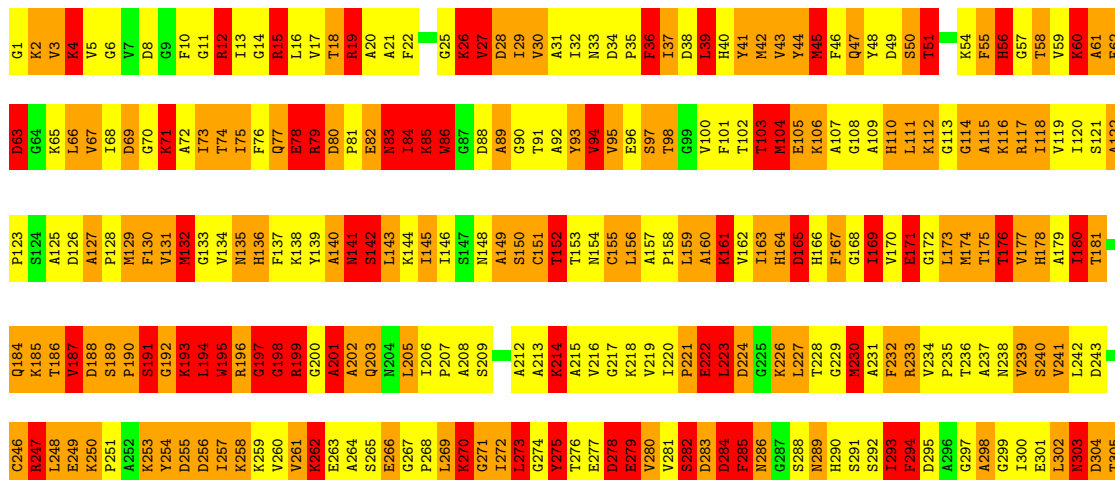
• Molecule 1: D-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

Chain R: 



• Molecule 1: D-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

Chain G: 



F306	V307	K308	L309	V310	S311	M312	Y313	D314	M315	E316	F317	G318	Y319	S320	E321	R322	V323	V324	D325	L326	M327	A328	H329	M330	A331	S332	K333	E334
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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	132.40Å 97.90Å 81.60Å 90.00° 114.30° 90.00°	Depositor
Resolution (Å)	(Not available) – 3.50	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-3.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	unknown	Depositor
R, R_{free}	0.330 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	5154	wwPDB-VP
Average B, all atoms (Å ²)	0.0	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, SO4

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	G	1.40	11/2573 (0.4%)	2.06	121/3479 (3.5%)
1	R	1.12	3/2573 (0.1%)	1.67	54/3479 (1.6%)
All	All	1.27	14/5146 (0.3%)	1.87	175/6958 (2.5%)

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	198	GLY	N-CA	8.67	1.59	1.46
1	G	195	TRP	CB-CG	7.61	1.64	1.50
1	G	329	HIS	CB-CG	6.51	1.61	1.50
1	G	70	GLY	N-CA	6.48	1.55	1.46
1	G	279	GLU	N-CA	6.37	1.59	1.46

The worst 5 of 175 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	G	279	GLU	O-C-N	10.67	139.77	122.70
1	G	278	ASP	O-C-N	-10.53	105.85	122.70
1	G	196	ARG	O-C-N	10.25	140.63	123.20
1	G	196	ARG	CB-CA-C	9.98	130.36	110.40
1	R	27	VAL	O-C-N	9.88	138.50	122.70

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	G	2523	0	2515	794	25
1	R	2523	0	2518	780	20
2	G	10	0	0	6	0
2	R	10	0	0	3	0
3	G	44	0	24	14	0
3	R	44	0	26	8	0
All	All	5154	0	5083	1561	25

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 153.

The worst 5 of 1561 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:R:1:GLY:CA	1:R:28:ASP:HA	1.14	1.57
1:G:3:VAL:H	1:G:27:VAL:CG1	1.19	1.55
1:R:3:VAL:CB	1:R:27:VAL:HG13	1.32	1.55
1:R:1:GLY:C	1:R:28:ASP:HA	1.30	1.49
1:R:3:VAL:HG23	1:R:27:VAL:CG2	1.41	1.48

The worst 5 of 25 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:267:GLY:CA	1:G:166:HIS:ND1[3_545]	1.06	1.14
1:R:263:GLU:OE1	1:G:260:VAL:CA[3_545]	1.27	0.93
1:R:308:LYS:CG	1:G:173:LEU:CD1[2_555]	1.33	0.87
1:R:260:VAL:CA	1:G:263:GLU:OE1[3_545]	1.45	0.75
1:R:263:GLU:OE2	1:G:259:LYS:O[3_545]	1.52	0.68

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	G	332/334 (99%)	198 (60%)	68 (20%)	66 (20%)	0	1
1	R	332/334 (99%)	205 (62%)	58 (18%)	69 (21%)	0	1
All	All	664/668 (99%)	403 (61%)	126 (19%)	135 (20%)	0	1

5 of 135 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	R	2	LYS
1	R	4	LYS
1	R	12	ARG
1	R	26	LYS
1	R	30	VAL

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	G	267/267 (100%)	140 (52%)	127 (48%)	0	0
1	R	267/267 (100%)	143 (54%)	124 (46%)	0	0
All	All	534/534 (100%)	283 (53%)	251 (47%)	0	0

5 of 251 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	307	VAL
1	G	261	VAL
1	G	63	ASP
1	G	257	ILE
1	G	301	GLU

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	G	141	ASN
1	G	289	ASN
1	G	315	ASN
1	G	166	HIS
1	R	303	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
3	NAD	G	336	-	42,48,48	3.34	13 (30%)	50,73,73	2.85	14 (28%)
3	NAD	R	336	-	42,48,48	2.25	7 (16%)	50,73,73	2.50	15 (30%)
2	SO4	R	340	1	4,4,4	0.24	0	6,6,6	0.11	0
2	SO4	G	340	1	4,4,4	0.24	0	6,6,6	0.11	0
2	SO4	G	338	-	4,4,4	0.25	0	6,6,6	0.11	0
2	SO4	R	338	-	4,4,4	0.24	0	6,6,6	0.11	0

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	R	336	-	-	9/26/62/62	0/5/5/5
3	NAD	G	336	-	1/1/11/11	10/26/62/62	0/5/5/5

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	336	NAD	C2N-N1N	9.43	1.45	1.35
3	R	336	NAD	PN-O3	8.63	1.68	1.59
3	G	336	NAD	PN-O3	8.10	1.68	1.59
3	G	336	NAD	C2B-C3B	-7.76	1.32	1.53
3	G	336	NAD	C3N-C7N	7.11	1.61	1.50

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	R	336	NAD	O4B-C1B-N9A	8.15	119.55	108.75
3	G	336	NAD	C1B-N9A-C4A	-8.08	112.44	126.64
3	G	336	NAD	C5N-C4N-C3N	-8.06	112.44	120.36
3	R	336	NAD	C5N-C4N-C3N	-7.63	112.86	120.36
3	G	336	NAD	C6N-N1N-C2N	-6.98	115.94	121.88

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	G	336	NAD	C2B

5 of 19 torsion outliers are listed below:

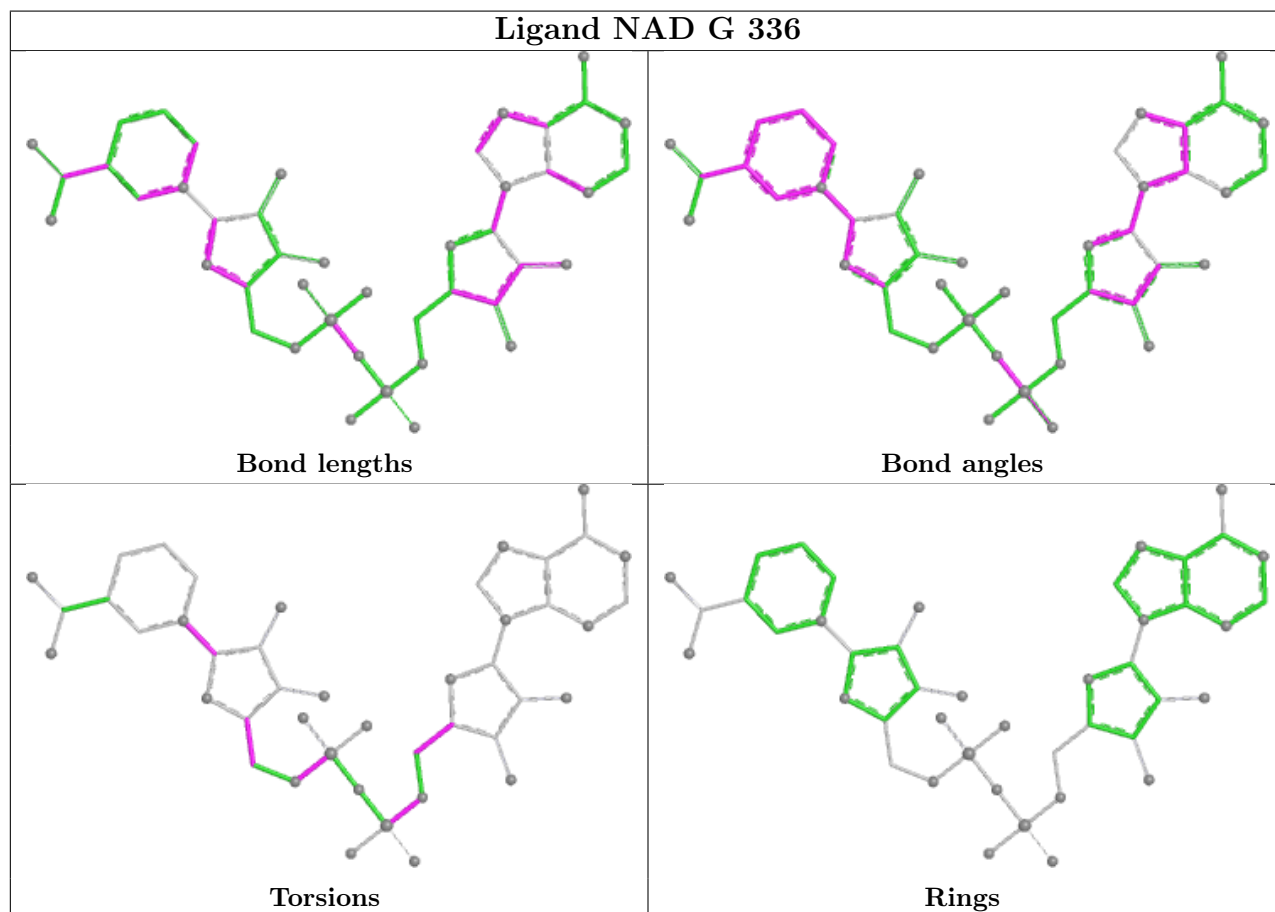
Mol	Chain	Res	Type	Atoms
3	G	336	NAD	C5D-O5D-PN-O3
3	G	336	NAD	C5D-O5D-PN-O1N
3	G	336	NAD	C5D-O5D-PN-O2N
3	G	336	NAD	O4D-C1D-N1N-C2N
3	G	336	NAD	O4D-C1D-N1N-C6N

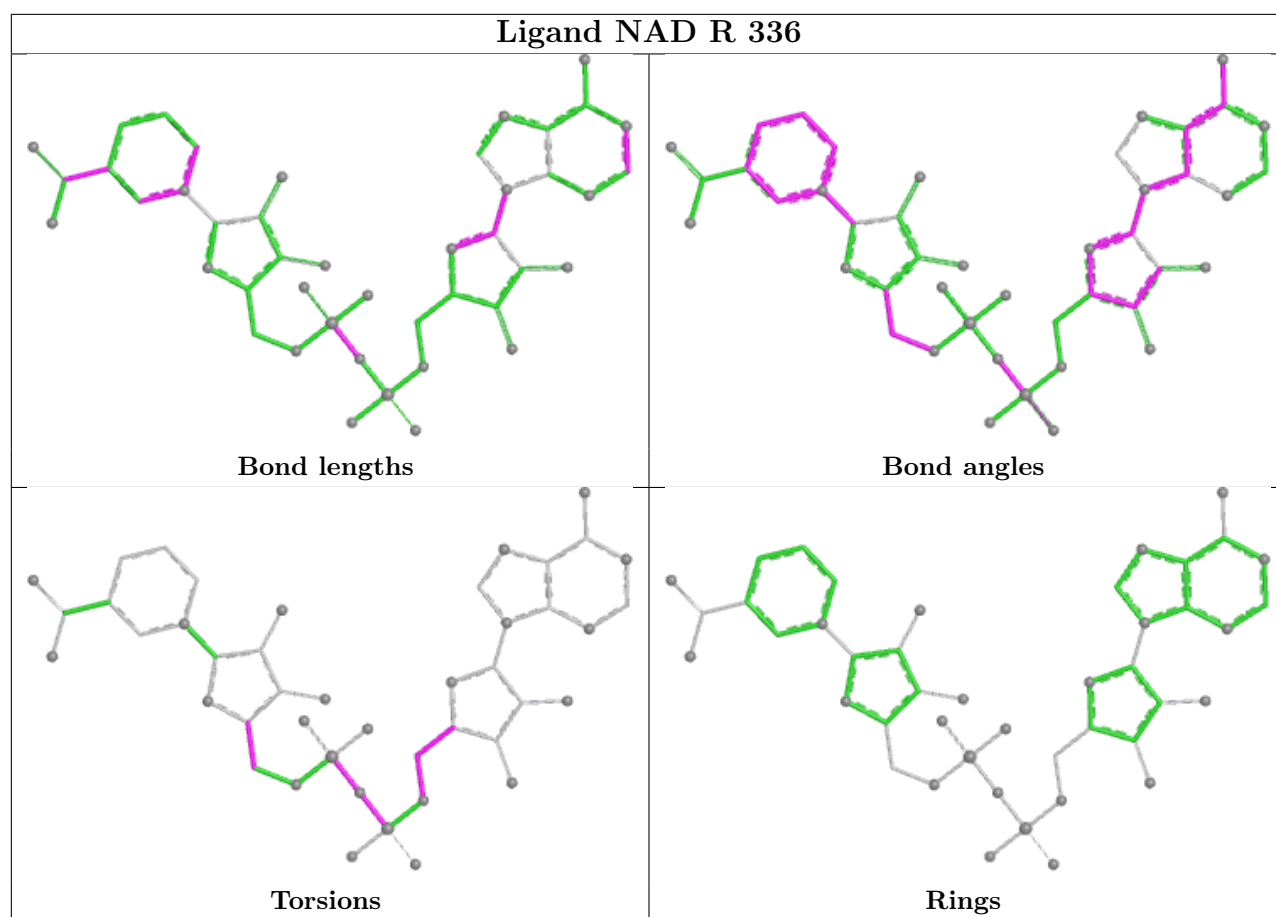
There are no ring outliers.

6 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	336	NAD	14	0
3	R	336	NAD	8	0
2	R	340	SO4	1	0
2	G	340	SO4	2	0
2	G	338	SO4	4	0
2	R	338	SO4	2	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.