



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:26 PM UTC

PDB ID : 1ADS / pdb_00001ads
Title : AN UNLIKELY SUGAR SUBSTRATE SITE IN THE 1.65 ANGSTROMS
STRUCTURE OF THE HUMAN ALDOSE REDUCTASE HOLOENZYME
IMPLICATED IN DIABETIC COMPLICATIONS
Authors : Wilson, D.K.; Quijcho, F.A.
Deposited on : 1992-07-08
Resolution : 1.65 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

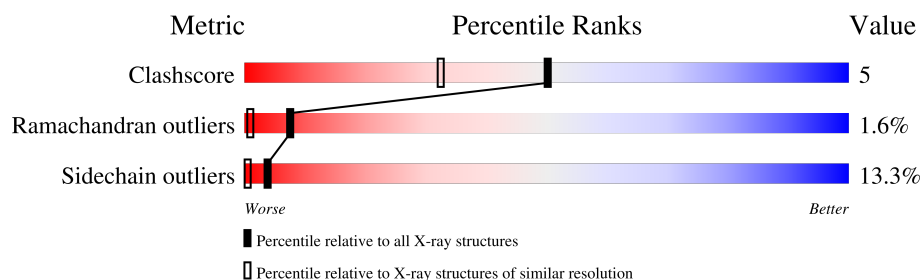
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)

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	315	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2665 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 ALDOSE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	315	Total	C	N	O	S	0	0	0
			2513	1615	424	462	12			

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is water.

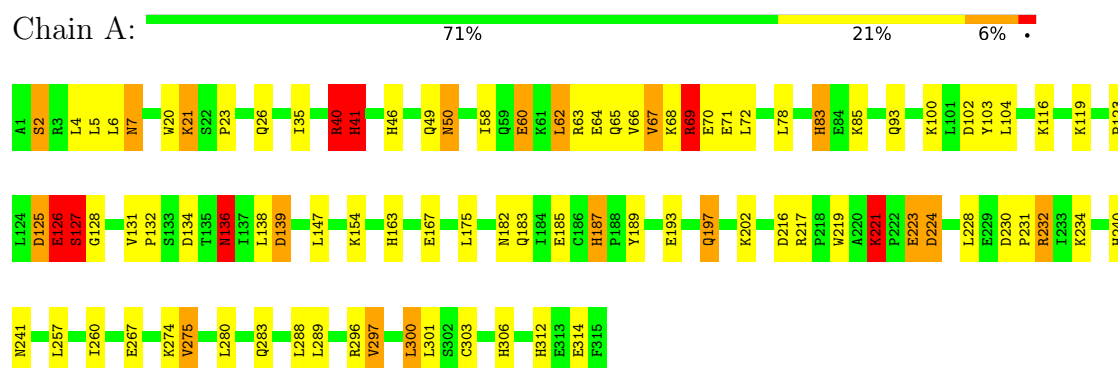
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	104	Total	O	0	0
			104	104		

3 Residue-property plots [i](#)

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: ALDOSE REDUCTASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.00Å 67.12Å 92.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.65	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-1.65)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.200 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2665	wwPDB-VP
Average B, all atoms (Å ²)	12.0	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: NAP

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	1.00	11/2575 (0.4%)	1.71	56/3496 (1.6%)

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	2

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	46	HIS	CG-ND1	-6.63	1.30	1.38
1	A	240	HIS	CD2-NE2	-6.50	1.30	1.37
1	A	46	HIS	CD2-NE2	-6.29	1.30	1.37
1	A	187	HIS	CD2-NE2	-6.27	1.30	1.37
1	A	306	HIS	CD2-NE2	-5.67	1.31	1.37
1	A	312	HIS	CD2-NE2	-5.59	1.31	1.37
1	A	41	HIS	CD2-NE2	-5.49	1.31	1.37
1	A	163	HIS	CD2-NE2	-5.29	1.32	1.37
1	A	83	HIS	CD2-NE2	-5.16	1.32	1.37
1	A	260	ILE	CA-CB	5.08	1.60	1.54
1	A	297	VAL	CA-CB	5.04	1.60	1.54

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	69	ARG	NE-CZ-NH2	-12.80	107.68	119.20
1	A	40	ARG	NE-CZ-NH2	-11.08	109.23	119.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	275	VAL	N-CA-CB	-9.86	97.58	112.67
1	A	69	ARG	NE-CZ-NH1	9.85	131.34	121.50
1	A	275	VAL	CB-CA-C	9.69	120.30	110.70
1	A	306	HIS	CB-CG-CD2	-7.94	120.88	131.20
1	A	49	GLN	OE1-CD-NE2	-7.90	114.70	122.60
1	A	139	ASP	CA-CB-CG	7.89	120.49	112.60
1	A	40	ARG	NE-CZ-NH1	7.67	129.18	121.50
1	A	41	HIS	CB-CG-CD2	-7.55	121.38	131.20
1	A	102	ASP	CA-CB-CG	7.45	120.05	112.60
1	A	283	GLN	OE1-CD-NE2	-7.42	115.18	122.60
1	A	7	ASN	OD1-CG-ND2	-7.30	115.30	122.60
1	A	182	ASN	OD1-CG-ND2	-7.30	115.30	122.60
1	A	223	GLU	O-C-N	7.18	132.44	123.32
1	A	7	ASN	CB-CG-ND2	6.93	126.80	116.40
1	A	306	HIS	CB-CG-ND1	6.84	132.95	122.70
1	A	7	ASN	CA-CB-CG	6.72	119.32	112.60
1	A	26	GLN	OE1-CD-NE2	-6.68	115.92	122.60
1	A	136	ASN	OD1-CG-ND2	-6.55	116.05	122.60
1	A	93	GLN	OE1-CD-NE2	-6.44	116.16	122.60
1	A	125	ASP	CA-CB-CG	6.39	118.99	112.60
1	A	314	GLU	CB-CG-CD	6.28	123.28	112.60
1	A	128	GLY	N-CA-C	6.14	127.74	113.18
1	A	67	VAL	N-CA-CB	-6.12	99.99	111.62
1	A	223	GLU	CA-CB-CG	-6.11	101.89	114.10
1	A	296	ARG	CA-C-N	6.09	129.07	120.42
1	A	296	ARG	C-N-CA	6.09	129.07	120.42
1	A	41	HIS	CB-CG-ND1	6.08	131.82	122.70
1	A	197	GLN	OE1-CD-NE2	-5.94	116.66	122.60
1	A	139	ASP	CB-CA-C	-5.94	101.56	110.88
1	A	240	HIS	CB-CG-CD2	-5.87	123.57	131.20
1	A	50	ASN	OD1-CG-ND2	-5.86	116.74	122.60
1	A	69	ARG	CD-NE-CZ	5.72	132.41	124.40
1	A	40	ARG	CD-NE-CZ	5.70	132.38	124.40
1	A	41	HIS	CA-CB-CG	5.60	119.40	113.80
1	A	296	ARG	N-CA-CB	-5.52	101.90	110.57
1	A	83	HIS	CB-CG-CD2	-5.47	124.08	131.20
1	A	126	GLU	N-CA-C	-5.36	99.39	110.80
1	A	131	VAL	CA-C-N	5.29	125.49	120.31
1	A	131	VAL	C-N-CA	5.29	125.49	120.31
1	A	49	GLN	CG-CD-NE2	5.29	124.33	116.40
1	A	267	GLU	CB-CG-CD	5.29	121.58	112.60
1	A	93	GLN	CG-CD-NE2	5.24	124.26	116.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	69	ARG	CB-CG-CD	5.24	123.34	111.30
1	A	221	LYS	N-CA-C	-5.22	98.26	109.81
1	A	23	PRO	CA-C-N	5.15	125.19	119.32
1	A	23	PRO	C-N-CA	5.15	125.19	119.32
1	A	134	ASP	CA-CB-CG	5.15	117.75	112.60
1	A	223	GLU	CA-C-O	5.11	129.10	122.45
1	A	69	ARG	CG-CD-NE	-5.09	100.80	112.00
1	A	219	TRP	CE2-CD2-CG	-5.08	101.10	107.20
1	A	216	ASP	CA-CB-CG	5.08	117.67	112.60
1	A	193	GLU	CA-CB-CG	-5.07	103.95	114.10
1	A	241	ASN	OD1-CG-ND2	-5.01	117.58	122.60
1	A	2	SER	CA-C-O	-5.01	113.35	120.51

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	221	LYS	Peptide
1	A	224	ASP	Peptide

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	2513	0	2528	26	0
2	A	48	0	25	2	0
3	A	104	0	0	6	0
All	All	2665	0	2553	27	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 5.

All (27) 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:103:TYR:CE2	1:A:154:LYS:HE3	2.27	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:TRP:CE3	1:A:21:LYS:HE3	2.32	0.64
1:A:83:HIS:HE1	3:A:402:HOH:O	1.83	0.61
1:A:230:ASP:OD1	1:A:232:ARG:HD3	2.00	0.61
1:A:83:HIS:HD2	3:A:422:HOH:O	1.83	0.60
1:A:136:ASN:ND2	1:A:139:ASP:H	2.08	0.51
1:A:187:HIS:HD2	1:A:189:TYR:H	1.57	0.50
1:A:183:GLN:OE1	2:A:350:NAP:H2N	2.12	0.50
1:A:185:GLU:OE2	1:A:187:HIS:HE1	1.95	0.49
1:A:67:VAL:HG22	1:A:71:GLU:HG3	1.95	0.48
1:A:68:LYS:HB2	1:A:68:LYS:NZ	2.29	0.48
1:A:68:LYS:O	1:A:71:GLU:HG2	2.15	0.47
1:A:116:LYS:HE3	1:A:123:PRO:HB2	1.96	0.47
1:A:300:LEU:HD13	1:A:303:CYS:HB2	1.96	0.46
1:A:69:ARG:HD3	3:A:464:HOH:O	2.15	0.46
1:A:64:GLU:HB3	1:A:66:VAL:HG23	1.98	0.46
1:A:41:HIS:HE1	3:A:449:HOH:O	1.98	0.45
1:A:125:ASP:O	1:A:127:SER:N	2.50	0.45
1:A:35:ILE:O	1:A:40:ARG:NH2	2.49	0.45
1:A:58:ILE:HG22	1:A:62:LEU:HD22	1.99	0.44
2:A:350:NAP:H6N	2:A:350:NAP:H3D	1.99	0.44
1:A:60:GLU:CD	1:A:63:ARG:HH22	2.25	0.43
1:A:167:GLU:OE1	1:A:202:LYS:NZ	2.52	0.42
1:A:116:LYS:NZ	3:A:494:HOH:O	2.50	0.41
1:A:217:ARG:HD3	1:A:297:VAL:HG13	2.03	0.41
1:A:100:LYS:HE3	3:A:492:HOH:O	2.20	0.41
1:A:231:PRO:HA	1:A:234:LYS:HD2	2.04	0.40

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	313/315 (99%)	301 (96%)	7 (2%)	5 (2%)	7 1

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	127	SER
1	A	224	ASP
1	A	126	GLU
1	A	2	SER
1	A	221	LYS

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	279/280 (100%)	242 (87%)	37 (13%)	4 0

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	5	LEU
1	A	6	LEU
1	A	7	ASN
1	A	21	LYS
1	A	40	ARG
1	A	41	HIS
1	A	50	ASN
1	A	60	GLU
1	A	62	LEU
1	A	65	GLN
1	A	69	ARG
1	A	70	GLU
1	A	72	LEU
1	A	78	LEU
1	A	85	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	104	LEU
1	A	119	LYS
1	A	126	GLU
1	A	127	SER
1	A	132	PRO
1	A	136	ASN
1	A	138	LEU
1	A	147	LEU
1	A	175	LEU
1	A	197	GLN
1	A	223	GLU
1	A	228	LEU
1	A	232	ARG
1	A	257	LEU
1	A	274	LYS
1	A	275	VAL
1	A	280	LEU
1	A	288	LEU
1	A	289	LEU
1	A	300	LEU
1	A	301	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	HIS
1	A	50	ASN
1	A	83	HIS
1	A	93	GLN
1	A	136	ASN
1	A	171	ASN
1	A	187	HIS
1	A	192	GLN
1	A	256	ASN

5.3.3 RNA ⓘ

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](#)

1 ligand is 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	NAP	A	350	-	50,52,52	1.32	9 (18%)	71,80,80	1.08	5 (7%)

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	NAP	A	350	-	-	3/35/67/67	0/5/5/5

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	350	NAP	C2N-N1N	3.77	1.39	1.35
2	A	350	NAP	C5N-C4N	-3.09	1.33	1.38
2	A	350	NAP	C3N-C7N	-3.00	1.46	1.50
2	A	350	NAP	PA-O3	2.52	1.62	1.59
2	A	350	NAP	PA-O2A	-2.24	1.44	1.55
2	A	350	NAP	C5A-C4A	-2.16	1.35	1.39
2	A	350	NAP	C2N-C3N	2.09	1.42	1.39
2	A	350	NAP	P2B-O3X	-2.07	1.47	1.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	350	NAP	P2B-O2X	-2.02	1.47	1.54

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	350	NAP	O7N-C7N-N7N	-3.68	117.30	122.62
2	A	350	NAP	C3N-C7N-N7N	2.33	120.61	117.74
2	A	350	NAP	C5N-C4N-C3N	2.16	122.48	120.36
2	A	350	NAP	O4D-C4D-C3D	-2.05	101.09	105.15
2	A	350	NAP	O7N-C7N-C3N	2.02	122.06	119.60

There are no chirality outliers.

All (3) torsion outliers are listed below:

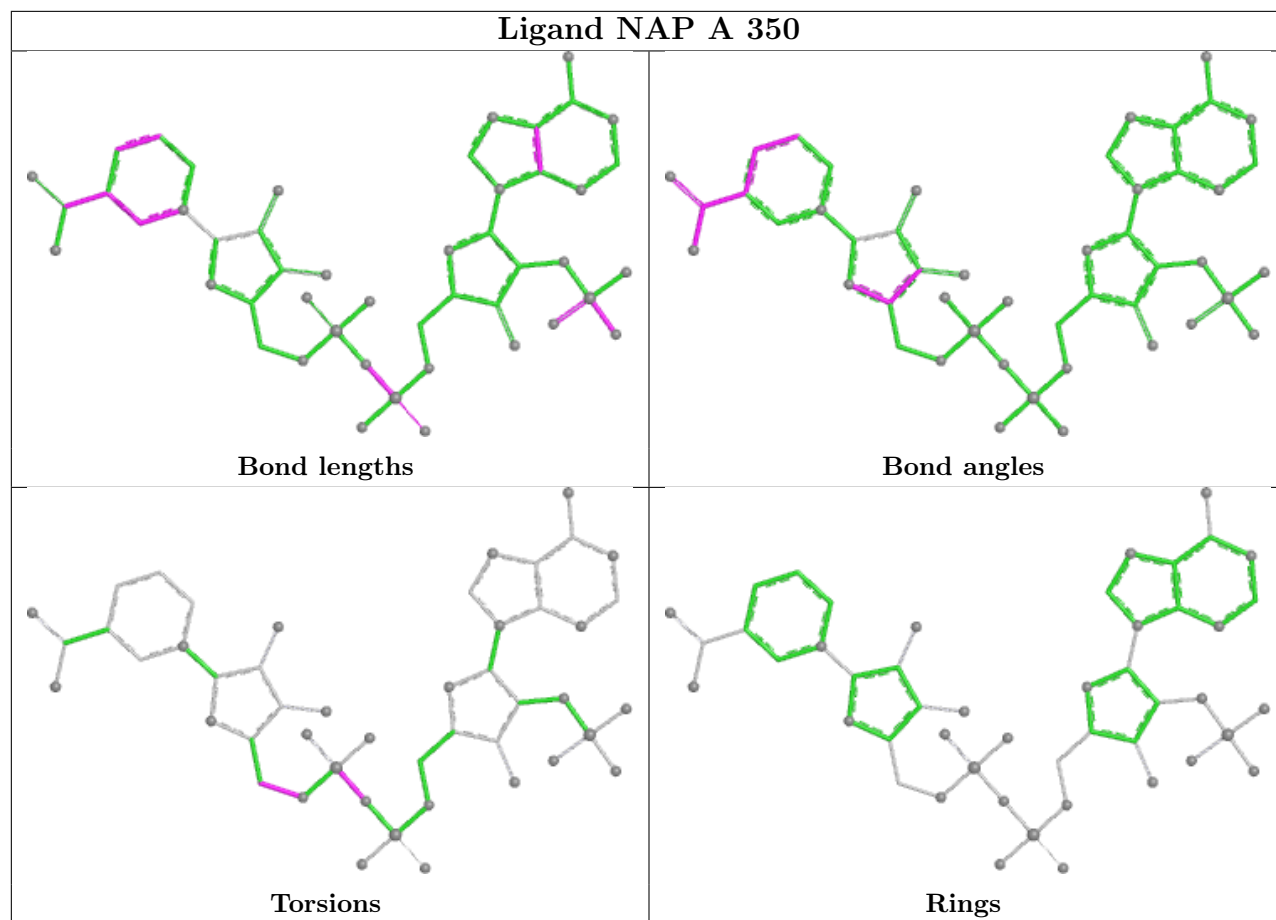
Mol	Chain	Res	Type	Atoms
2	A	350	NAP	PA-O3-PN-O5D
2	A	350	NAP	C4D-C5D-O5D-PN
2	A	350	NAP	PA-O3-PN-O2N

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	350	NAP	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.