



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 03:54 pm BST

PDB ID : 2ACS  
Title : AN ANION BINDING SITE IN HUMAN ALDOSE REDUCTASE: MECHANISTIC IMPLICATIONS FOR THE BINDING OF CITRATE, CACODYLATE, AND GLUCOSE-6-PHOSPHATE  
Authors : Harrison, D.H.; Bohren, K.M.; Gabbay, K.H.; Petsko, G.A.; Ringe, D.  
Deposited on : 1994-04-15  
Resolution : 1.76 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (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) : 2.11

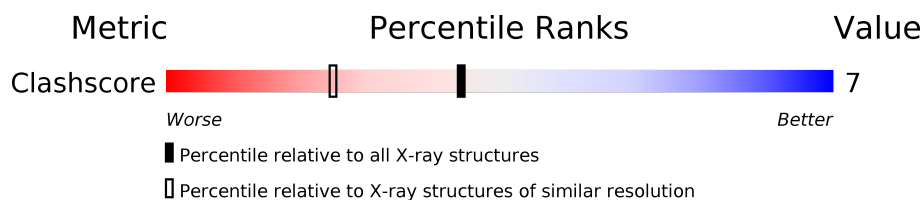
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.76 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	2466 (1.76-1.76)

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2768 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	314	Total	C	N	O	S	0	0	0
			2512	1614	424	462	12			

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



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

- Molecule 3 is CITRIC ACID (three-letter code: CIT) (formula: C<sub>6</sub>H<sub>8</sub>O<sub>7</sub>).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	195	Total	O	0	0
			195	195		

SEQUENCE-PLOTS INFOmissingINFO

### 3 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, $\alpha$ , $\beta$ , $\gamma$	50.11Å 67.20Å 92.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.76	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.76)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.169 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2768	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

## 4 Model quality

### 4.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAP, CIT

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	0.70	0/2574	0.67	0/3495

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	9

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	209	TYR	Sidechain
1	A	220	ALA	Peptide
1	A	221	LYS	Peptide
1	A	224	ASP	Peptide
1	A	232	ARG	Sidechain
1	A	268	ARG	Sidechain
1	A	293	ARG	Sidechain
1	A	296	ARG	Sidechain
1	A	3	ARG	Sidechain

## 4.2 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	2512	0	2525	34	0
2	A	48	0	25	3	0
3	A	13	0	5	2	0
4	A	195	0	0	3	0
All	All	2768	0	2555	34	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 7.

All (34) 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:224:ASP:HB3	1:A:225:PRO:HD3	1.41	0.98
1:A:224:ASP:HB3	1:A:225:PRO:CD	2.12	0.78
1:A:220:ALA:HB1	1:A:222:PRO:HA	1.78	0.64
1:A:110:HIS:HE1	3:A:317:CIT:O5	1.84	0.60
1:A:223:GLU:H	1:A:223:GLU:CD	2.06	0.58
1:A:172:LYS:HE3	4:A:906:HOH:O	2.04	0.58
1:A:220:ALA:HB1	1:A:222:PRO:CA	2.34	0.58
1:A:251:PHE:HZ	1:A:289:LEU:HD13	1.69	0.58
1:A:183:GLN:NE2	2:A:316:NAP:H2N	2.19	0.57
1:A:8:ASN:HD22	1:A:8:ASN:H	1.52	0.57
1:A:136:ASN:HD22	1:A:138:LEU:H	1.54	0.56
1:A:300:LEU:HD13	1:A:303:CYS:HB2	1.86	0.55
1:A:20:TRP:CE3	1:A:21:LYS:HE3	2.42	0.55
1:A:162:ASN:C	1:A:162:ASN:HD22	2.10	0.54
1:A:83:HIS:HD2	4:A:767:HOH:O	1.92	0.52
1:A:83:HIS:HE1	4:A:782:HOH:O	1.93	0.51
1:A:234:LYS:HG2	1:A:244:THR:HG21	1.94	0.48
1:A:183:GLN:NE2	2:A:316:NAP:H71N	2.13	0.47
1:A:110:HIS:CE1	3:A:317:CIT:O5	2.68	0.47
1:A:217:ARG:HD2	1:A:297:VAL:HG13	1.98	0.46
1:A:187:HIS:HD2	1:A:189:TYR:H	1.62	0.46
1:A:220:ALA:C	1:A:222:PRO:HA	2.38	0.44
1:A:217:ARG:CD	1:A:297:VAL:HG13	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:LYS:HD3	1:A:94:LYS:O	2.19	0.43
1:A:251:PHE:CZ	1:A:289:LEU:HD13	2.52	0.43
1:A:220:ALA:HB1	1:A:222:PRO:CG	2.50	0.42
1:A:262:LYS:O	2:A:316:NAP:H8A	2.20	0.42
1:A:4:LEU:HG	1:A:14:ILE:HG12	2.01	0.42
1:A:119:LYS:NZ	1:A:119:LYS:H	2.18	0.41
1:A:136:ASN:HD22	1:A:138:LEU:N	2.16	0.41
1:A:144:MET:O	1:A:147:LEU:HB2	2.20	0.41
1:A:242:LYS:HE3	1:A:246:GLN:OE1	2.21	0.41
1:A:220:ALA:CB	1:A:222:PRO:HA	2.50	0.40
1:A:5:LEU:HD23	1:A:11:LYS:HG3	2.02	0.40

There are no symmetry-related clashes.

## 4.3 Torsion angles [i](#)

### 4.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

### 4.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 4.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 4.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.



## 4.6 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
3	CIT	A	317	-	3,12,12	5.43	2 (66%)	3,17,17	3.68	2 (66%)
2	NAP	A	316	-	45,52,52	1.25	5 (11%)	56,80,80	1.52	8 (14%)

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	CIT	A	317	-	-	0/6/16/16	-
2	NAP	A	316	-	-	3/31/67/67	0/5/5/5

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	317	CIT	C2-C3	9.06	1.67	1.54
2	A	316	NAP	C2N-N1N	3.98	1.39	1.35
3	A	317	CIT	O7-C3	2.32	1.46	1.43
2	A	316	NAP	P2B-O3X	-2.32	1.45	1.54
2	A	316	NAP	C6N-N1N	2.31	1.41	1.35
2	A	316	NAP	PA-O2A	-2.13	1.45	1.55
2	A	316	NAP	C3B-C4B	-2.05	1.47	1.53

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	316	NAP	N3A-C2A-N1A	-5.16	120.61	128.68
3	A	317	CIT	C3-C2-C1	4.60	122.35	114.98
3	A	317	CIT	C3-C4-C5	-4.19	108.27	114.98
2	A	316	NAP	PN-O3-PA	3.69	145.50	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	316	NAP	C4A-C5A-N7A	3.30	112.84	109.40
2	A	316	NAP	C6N-N1N-C2N	-3.11	119.14	121.97
2	A	316	NAP	C2N-C3N-C4N	2.15	120.70	118.26
2	A	316	NAP	O3D-C3D-C4D	2.13	117.20	111.05
2	A	316	NAP	C1B-N9A-C4A	-2.07	123.01	126.64
2	A	316	NAP	C2B-C3B-C4B	2.06	106.47	101.99

There are no chirality outliers.

All (3) torsion outliers are listed below:

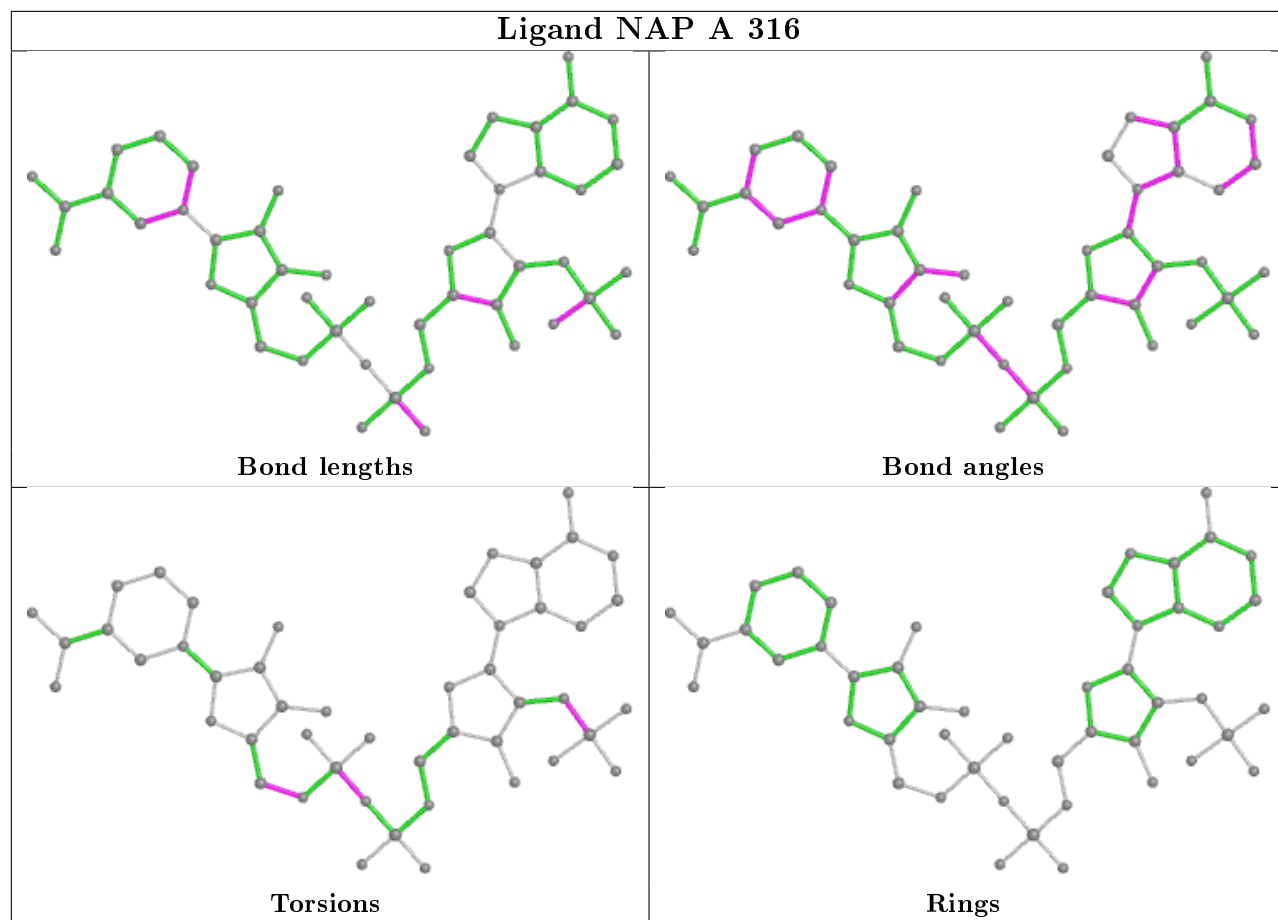
Mol	Chain	Res	Type	Atoms
2	A	316	NAP	PA-O3-PN-O5D
2	A	316	NAP	C4D-C5D-O5D-PN
2	A	316	NAP	C2B-O2B-P2B-O2X

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	317	CIT	2	0
2	A	316	NAP	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.



#### 4.7 Other polymers [i](#)

There are no such residues in this entry.

#### 4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 5 Fit of model and data ⓘ

### 5.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

### 5.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

### 5.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

### 5.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

### 5.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.