



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 6, 2024 – 10:26 PM EST

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

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 : 1.8.5 (274361), CSD as541be (2020)
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) : 2.36

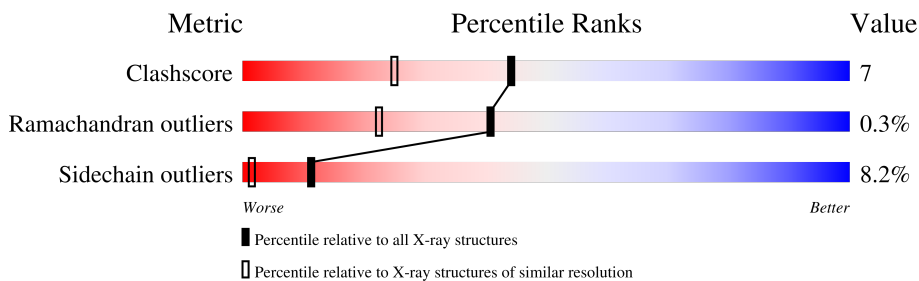
1 Overall quality at a glance

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)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)

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	83% 12% .

2 Entry composition [i](#)

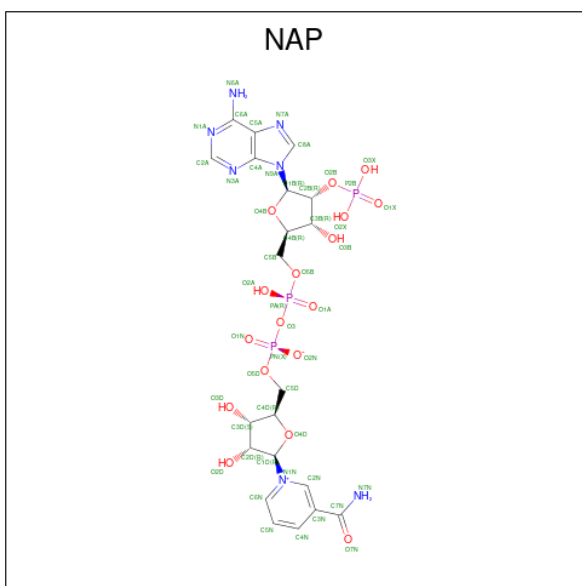
There are 4 unique types of molecules in this entry. The entry contains 2768 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
			Total	C	N	O	S			
1	A	314	2512	1614	424	462	12	0	0	0

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



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

- Molecule 3 is CITRIC ACID (three-letter code: CIT) (formula: C₆H₈O₇).



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

- Molecule 4 is water.


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

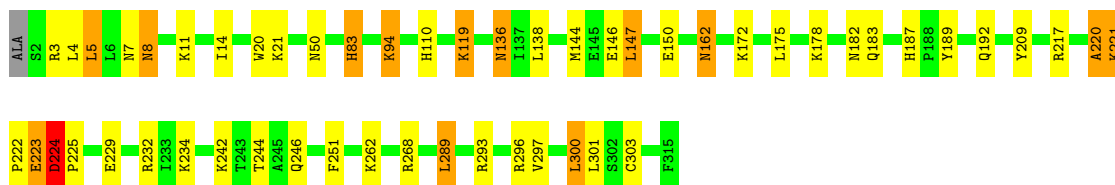
3 Residue-property plots [i](#)

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

Chain A:  83% 12%



4 Data and refinement statistics

Xtrriage (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	50.11Å 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.	Xtrriage
Total number of atoms	2768	wwPDB-VP
Average B, all atoms (Å ²)	13.0	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, 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	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

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	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:O	1:A:94:LYS:HD3	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:H	1:A:119:LYS:NZ	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.

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	312/315 (99%)	305 (98%)	6 (2%)	1 (0%)	41 22

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	ASP

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	280/280 (100%)	257 (92%)	23 (8%)	11 1

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	7	ASN
1	A	8	ASN
1	A	50	ASN
1	A	83	HIS
1	A	94	LYS
1	A	119	LYS
1	A	136	ASN
1	A	146	GLU
1	A	147	LEU
1	A	150	GLU
1	A	162	ASN
1	A	175	LEU
1	A	178	LYS
1	A	182	ASN
1	A	192	GLN
1	A	221	LYS
1	A	223	GLU
1	A	224	ASP
1	A	229	GLU
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 (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	50	ASN
1	A	83	HIS
1	A	110	HIS
1	A	136	ASN
1	A	160	ASN
1	A	162	ASN
1	A	182	ASN
1	A	183	GLN
1	A	187	HIS

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Mol	Chain	Res	Type
1	A	192	GLN
1	A	197	GLN
1	A	283	GLN
1	A	312	HIS

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](#)

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	NAP	A	316	-	45,52,52	1.25	5 (11%)	56,80,80	1.52	8 (14%)
3	CIT	A	317	-	12,12,12	3.63	4 (33%)	17,17,17	1.94	5 (29%)

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	316	-	-	3/31/67/67	0/5/5/5
3	CIT	A	317	-	-	4/16/16/16	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	317	CIT	C2-C3	11.14	1.67	1.53
2	A	316	NAP	C2N-N1N	3.98	1.39	1.35
3	A	317	CIT	C2-C1	3.02	1.60	1.50
3	A	317	CIT	O6-C6	-2.33	1.21	1.30
2	A	316	NAP	P2B-O3X	-2.32	1.45	1.54
2	A	316	NAP	C6N-N1N	2.31	1.41	1.35
3	A	317	CIT	O4-C5	-2.22	1.23	1.30
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 (13) 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	O6-C6-C3	4.33	120.57	113.05
2	A	316	NAP	PN-O3-PA	3.69	145.50	132.83
3	A	317	CIT	C3-C2-C1	3.53	122.35	113.81
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
3	A	317	CIT	O2-C1-O1	-2.99	115.84	123.30
3	A	317	CIT	O6-C6-O5	-2.51	115.83	123.82
3	A	317	CIT	C3-C4-C5	-2.29	108.27	113.81
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 (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	317	CIT	O7-C3-C6-O5
3	A	317	CIT	O7-C3-C6-O6
3	A	317	CIT	C4-C3-C6-O5
3	A	317	CIT	C4-C3-C6-O6
2	A	316	NAP	PA-O3-PN-O5D

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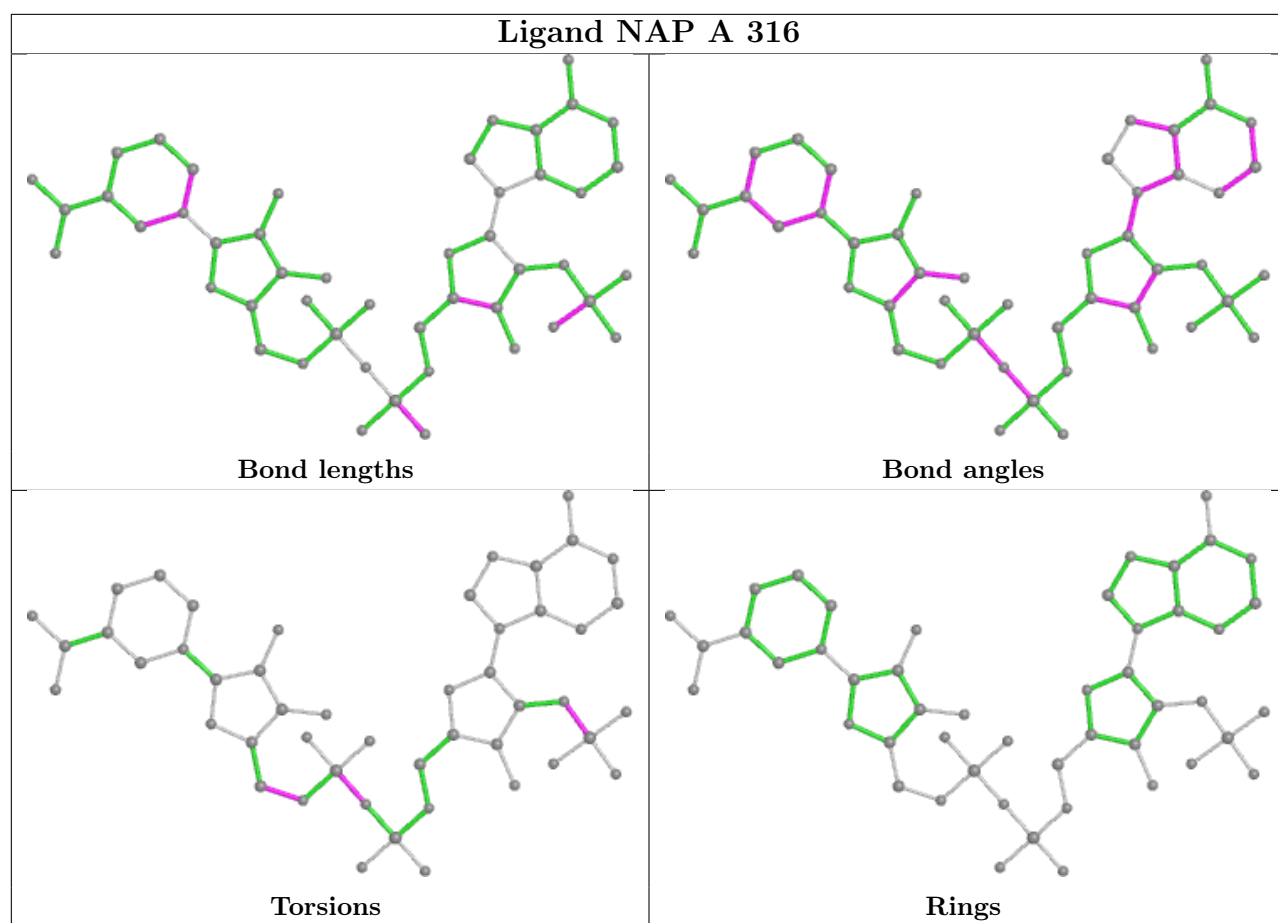
Mol	Chain	Res	Type	Atoms
2	A	316	NAP	C4D-C5D-O5D-PN
2	A	316	NAP	C2B-O2B-P2B-O2X

There are no ring outliers.

2 monomers are involved in 5 short contacts:

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