



# Full wwPDB X-ray Structure Validation Report i

Feb 27, 2014 – 01:37 PM GMT

PDB ID : 1DR1  
Title : 2.2 ANGSTROMS CRYSTAL STRUCTURE OF CHICKEN LIVER DI-HYDROFOLATE REDUCTASE COMPLEXED WITH NADP+ AND BIOPTERIN  
Authors : Mctigue, M.A.; Davies /II, J.F.; Kaufman, B.T.; Xuong, N.-H.; Kraut, J.  
Deposited on : 1992-03-14  
Resolution : 2.20 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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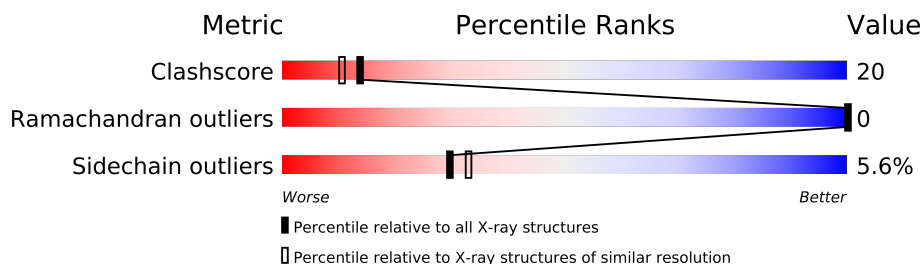
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.20 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	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	189	

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 1696 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

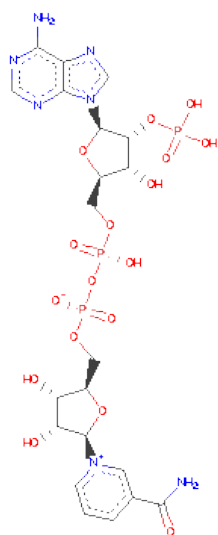
- Molecule 1 is a protein called DIHYDROFOLATE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	186	Total	C	N	O	S	0	1	0
			1497	967	248	276	6			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

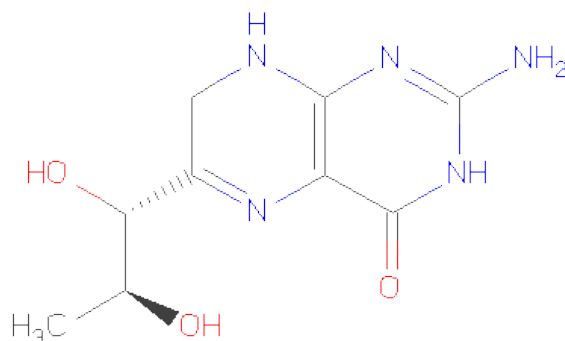
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDEPHOSPHATE (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
3	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 4 is 7,8-DIHYDROBIOPTERIN (three-letter code: HBI) (formula:  $C_9H_{13}N_5O_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	133	Total	O	0	0
			133	133		

i

Note EDS was not executed.

Chain A:



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.44Å 48.31Å 64.26Å 90.00° 125.10° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.20	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.20)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.140 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1696	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	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: CA, HBI, 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	1.06	0/1538	1.64	21/2081 (1.0%)

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	1

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	132	ARG	NE-CZ-NH2	-8.21	116.20	120.30
1	A	28	ARG	NE-CZ-NH2	-7.93	116.33	120.30
1	A	171	GLU	OE1-CD-OE2	7.48	132.27	123.30
1	A	36	ARG	NE-CZ-NH1	7.34	123.97	120.30
1	A	173	ASP	CB-CG-OD1	7.07	124.66	118.30
1	A	145	ASP	CB-CG-OD1	6.83	124.45	118.30
1	A	62	GLU	OE1-CD-OE2	6.53	131.14	123.30
1	A	178	LYS	CA-CB-CG	6.42	127.52	113.40
1	A	97	LEU	CB-CA-C	6.29	122.16	110.20
1	A	44	GLU	CA-CB-CG	6.22	127.09	113.40
1	A	126	GLU	CG-CD-OE2	-6.22	105.86	118.30
1	A	168	ASP	CB-CG-OD1	6.08	123.77	118.30
1	A	28	ARG	CD-NE-CZ	-6.01	115.18	123.60
1	A	78	GLU	OE1-CD-OE2	-5.86	116.27	123.30
1	A	65	ARG	NE-CZ-NH2	-5.72	117.44	120.30
1	A	172	GLU	CG-CD-OE2	-5.39	107.53	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	129	ILE	CA-CB-CG2	5.28	121.46	110.90
1	A	157	LYS	CB-CA-C	-5.23	99.93	110.40
1	A	94	ASP	CB-CG-OD2	-5.23	113.59	118.30
1	A	131	HIS	N-CA-CB	-5.20	101.24	110.60
1	A	151	ILE	CA-CB-CG2	5.12	121.14	110.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	65	ARG	Sidechain

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1497	0	1491	60	0
2	A	1	0	0	0	0
3	A	48	0	25	3	0
4	A	17	0	13	2	0
5	A	133	0	0	6	0
All	All	1696	0	1529	62	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 20.

All (62) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:108:LYS:HB3	1:A:108:LYS:NZ	1.72	1.03
1:A:108:LYS:HB3	1:A:108:LYS:HZ2	1.40	0.87
1:A:108:LYS:CB	1:A:108:LYS:NZ	2.37	0.86
1:A:108:LYS:HB3	1:A:108:LYS:HZ3	1.43	0.80
1:A:35:GLN:NE2	1:A:70:ARG:HH12	1.81	0.79
1:A:151:ILE:CD1	1:A:156:PHE:HB2	2.14	0.78
1:A:102:SER:HB2	1:A:103:PRO:HD2	1.66	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:94:ASP:OD1	1:A:127:LYS:NZ	2.16	0.77
1:A:13:ASN:HD22	1:A:13:ASN:H	1.32	0.75
1:A:151:ILE:CD1	1:A:156:PHE:CB	2.66	0.73
1:A:35:GLN:HE21	1:A:70:ARG:HH12	1.35	0.71
1:A:139:LEU:C	1:A:140:HIS:CD2	2.67	0.68
1:A:40:THR:O	1:A:111:MET:CE	2.43	0.67
1:A:151:ILE:HD11	1:A:156:PHE:HB2	1.76	0.67
1:A:11:CYS:HB2	1:A:140:HIS:O	1.95	0.66
1:A:108:LYS:CB	1:A:108:LYS:HZ2	2.06	0.65
1:A:132:ARG:NH2	5:A:725:HOH:O	2.29	0.65
1:A:151:ILE:HD12	1:A:156:PHE:HB2	1.79	0.64
1:A:151:ILE:HD11	1:A:156:PHE:CB	2.29	0.63
1:A:105:LEU:CD2	1:A:108:LYS:HZ1	2.13	0.62
1:A:102:SER:CB	1:A:103:PRO:HD2	2.31	0.61
1:A:13:ASN:ND2	1:A:13:ASN:H	1.98	0.61
1:A:139:LEU:O	1:A:140:HIS:CD2	2.55	0.60
1:A:108:LYS:CB	1:A:108:LYS:HZ3	2.08	0.59
1:A:13:ASN:HD22	1:A:13:ASN:N	2.00	0.58
1:A:100:LEU:HD13	1:A:112:VAL:CG2	2.36	0.55
1:A:132:ARG:NH1	1:A:183:GLN:OE1	2.39	0.55
1:A:16:ILE:O	3:A:191:NAP:H2N	2.07	0.55
1:A:40:THR:O	1:A:111:MET:HE3	2.08	0.53
1:A:35:GLN:HE22	1:A:70:ARG:HH22	1.59	0.51
1:A:100:LEU:HD13	1:A:112:VAL:HG21	1.92	0.51
3:A:191:NAP:H4N	4:A:198:HBI:H71	1.92	0.51
1:A:101:ASP:HA	1:A:106:LYS:HD3	1.93	0.49
1:A:151:ILE:HD12	1:A:156:PHE:CB	2.39	0.49
1:A:127:LYS:HB3	1:A:129:ILE:HG23	1.94	0.49
1:A:91:LYS:HE3	5:A:279:HOH:O	2.12	0.49
1:A:111:MET:CE	5:A:240:HOH:O	2.61	0.48
1:A:111:MET:HE1	5:A:240:HOH:O	2.13	0.48
1:A:55:LYS:HE2	1:A:55:LYS:HB3	1.33	0.47
1:A:77:ARG:HD2	5:A:393:HOH:O	2.13	0.47
1:A:42:HIS:C	1:A:43:VAL:HG23	2.35	0.47
1:A:4:LEU:O	1:A:131:HIS:HA	2.15	0.47
1:A:13:ASN:ND2	1:A:141:GLU:HG2	2.30	0.46
1:A:71:ILE:CD1	1:A:109:VAL:HG22	2.45	0.46
1:A:1:VAL:O	1:A:129:ILE:HD12	2.16	0.46
1:A:148:PHE:HE2	1:A:151:ILE:HG22	1.81	0.45
3:A:191:NAP:C4N	4:A:198:HBI:H71	2.47	0.45
1:A:102:SER:O	1:A:106:LYS:HB2	2.17	0.44
1:A:105:LEU:HD23	1:A:108:LYS:NZ	2.33	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:100:LEU:HD13	1:A:112:VAL:HG22	2.00	0.43
1:A:151:ILE:HD12	1:A:156:PHE:CG	2.54	0.43
1:A:129:ILE:HG13	1:A:130:ASN:N	2.33	0.42
1:A:43:VAL:HG11	1:A:46:LYS:HD2	2.01	0.42
1:A:72:ASN:N	1:A:72:ASN:HD22	2.17	0.42
1:A:71:ILE:HD12	1:A:109:VAL:HG22	2.02	0.41
1:A:105:LEU:HD23	1:A:105:LEU:HA	1.66	0.41
1:A:42:HIS:O	1:A:43:VAL:HG23	2.21	0.41
1:A:63:LYS:HB2	5:A:655:HOH:O	2.21	0.41
1:A:28:ARG:HD3	1:A:28:ARG:HH11	1.52	0.41
1:A:42:HIS:O	1:A:43:VAL:CG2	2.69	0.41
1:A:66:PRO:HB3	1:A:85:GLY:O	2.21	0.41
1:A:175:ILE:HD12	1:A:175:ILE:HG23	1.91	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	185/189 (98%)	178 (96%)	7 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	163/168 (97%)	153 (94%)	10 (6%)	26	28

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ASN
1	A	31[A]	TYR
1	A	31[B]	TYR
1	A	72	ASN
1	A	81	GLU
1	A	84	LYS
1	A	107	SER
1	A	108	LYS
1	A	129	ILE
1	A	151	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	13	ASN
1	A	35	GLN
1	A	42	HIS
1	A	47	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	NAP	A	191	2	52,52,52	3.01	20 (38%)	80,80,80	2.26	27 (33%)
4	HBI	A	198	-	18,18,18	3.67	5 (27%)	23,26,26	4.83	14 (60%)

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	NAP	A	191	2	-	0/35/67/67	0/3/5/5
4	HBI	A	198	-	-	1/6/17/17	0/0/2/2

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	191	NAP	O4B-C4B	-11.30	1.18	1.45
3	A	191	NAP	C4N-C3N	8.40	1.53	1.39
4	A	198	HBI	C7-C6	-7.75	1.36	1.49
4	A	198	HBI	C7-N8	-7.51	1.30	1.45
4	A	198	HBI	C2-N1	7.42	1.42	1.33
4	A	198	HBI	C6-N5	6.83	1.37	1.28
3	A	191	NAP	C4A-N9A	-5.76	1.29	1.37
3	A	191	NAP	C2N-N1N	5.57	1.42	1.35
3	A	191	NAP	C5N-C4N	5.30	1.51	1.39
3	A	191	NAP	O4B-C1B	4.89	1.48	1.41
3	A	191	NAP	PN-O2N	-3.82	1.40	1.48
3	A	191	NAP	C2D-C1D	-3.64	1.48	1.53
3	A	191	NAP	C5A-C4A	-3.51	1.32	1.40
3	A	191	NAP	C2N-C3N	-3.38	1.34	1.38
3	A	191	NAP	C6N-C5N	-3.34	1.30	1.38
3	A	191	NAP	P2B-O3X	-3.19	1.43	1.54
3	A	191	NAP	C3B-C4B	2.99	1.61	1.53
3	A	191	NAP	O4D-C1D	2.92	1.45	1.41
3	A	191	NAP	PN-O1N	-2.60	1.42	1.48
4	A	198	HBI	O9-C9	-2.58	1.37	1.42
3	A	191	NAP	C6A-C5A	2.57	1.57	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	191	NAP	PN-O3	-2.25	1.55	1.60
3	A	191	NAP	C3N-C7N	-2.23	1.46	1.50
3	A	191	NAP	P2B-O2X	-2.10	1.47	1.54
3	A	191	NAP	O3D-C3D	2.07	1.48	1.43

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	198	HBI	C4-C4A-C8A	12.43	123.06	114.55
4	A	198	HBI	C7-C6-N5	-9.82	117.32	122.52
3	A	191	NAP	C5N-C4N-C3N	-8.74	108.97	120.32
4	A	198	HBI	C7-N8-C8A	-6.57	113.89	121.36
3	A	191	NAP	O4B-C1B-C2B	-6.21	101.14	106.95
3	A	191	NAP	C2N-C3N-C4N	6.02	125.13	118.31
4	A	198	HBI	C6-C7-N8	5.99	127.84	114.52
4	A	198	HBI	C7-C6-C9	5.85	124.86	118.40
4	A	198	HBI	C11-C10-C9	-5.45	106.68	112.62
4	A	198	HBI	C4-N3-C2	5.34	128.84	119.51
3	A	191	NAP	C4B-O4B-C1B	5.30	115.51	109.75
4	A	198	HBI	C8A-C4A-N5	-4.94	118.12	123.15
4	A	198	HBI	N2-C2-N3	4.60	122.92	117.86
4	A	198	HBI	C4A-C8A-N8	4.55	124.47	119.17
3	A	191	NAP	O4D-C1D-N1N	3.98	112.03	107.95
4	A	198	HBI	C10-C9-C6	3.87	118.74	111.84
3	A	191	NAP	N3A-C2A-N1A	3.66	131.76	128.71
3	A	191	NAP	O3X-P2B-O2X	3.51	121.26	107.61
3	A	191	NAP	O3-PN-O1N	3.34	116.80	108.83
3	A	191	NAP	O3B-C3B-C4B	-3.33	101.28	111.08
3	A	191	NAP	C5B-C4B-C3B	-3.27	102.10	115.21
3	A	191	NAP	C3N-C7N-N7N	3.22	121.43	117.77
3	A	191	NAP	O7N-C7N-C3N	-3.15	116.02	119.58
3	A	191	NAP	C2B-C3B-C4B	-2.94	94.97	101.94
3	A	191	NAP	C8A-N9A-C4A	2.78	109.02	106.90
4	A	198	HBI	O10-C10-C9	-2.72	103.31	109.01
3	A	191	NAP	O2N-PN-O1N	-2.68	110.64	118.72
3	A	191	NAP	C5N-C6N-N1N	2.65	124.89	120.43
3	A	191	NAP	O4B-C1B-N9A	-2.58	106.04	108.44
4	A	198	HBI	N8-C8A-N1	-2.58	112.04	115.82
3	A	191	NAP	PN-O3-PA	2.56	143.95	132.95
3	A	191	NAP	C6N-N1N-C2N	-2.56	119.15	122.04
3	A	191	NAP	O5D-C5D-C4D	-2.47	99.87	108.94
3	A	191	NAP	C8A-N9A-C1B	-2.41	121.64	126.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	191	NAP	PN-O5D-C5D	2.40	128.56	120.24
4	A	198	HBI	N3-C2-N1	-2.37	118.46	121.78
3	A	191	NAP	C3B-C2B-C1B	-2.20	98.45	102.73
3	A	191	NAP	O3D-C3D-C4D	-2.14	104.78	111.08
3	A	191	NAP	O2B-P2B-O1X	-2.10	100.92	106.79
3	A	191	NAP	C6N-C5N-C4N	2.10	122.77	119.44
3	A	191	NAP	O2X-P2B-O2B	-2.09	101.06	107.09

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	198	HBI	O9-C9-C6-N5

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.