



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:00 PM GMT

PDB ID : 1N3I  
Title : Crystal Structure of Mycobacterium tuberculosis PNP with transition state analog DADMe-ImmH  
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Deposited on : 2002-10-28  
Resolution : 1.90 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

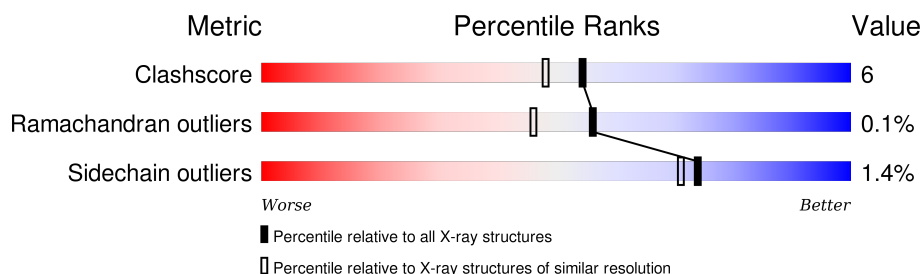
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)

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. 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	268	
1	B	268	
1	C	268	

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
3	DIH	A	401	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DIH	B	402	X	-	-	-
3	DIH	C	403	X	-	-	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6180 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 Purine Nucleoside Phosphorylase.

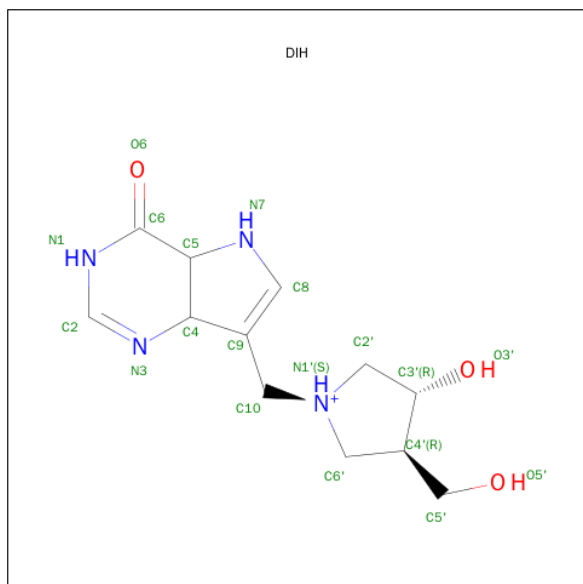
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	262	Total	C	N	O	S	0	0	0
			1892	1189	345	354	4			
1	B	262	Total	C	N	O	S	0	0	0
			1892	1189	345	354	4			
1	C	262	Total	C	N	O	S	0	0	0
			1892	1189	345	354	4			

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is 3-HYDROXY-4-HYDROXYMETHYL-1-(4-OXO-4,4A,5,7A-TETRAHYDRO-3H-PYRROLO[3,2-D]PYRIMIDIN-7-YLMETHYL)-PYRROLIDINIUM (three-letter code: DIH) (formula:  $C_{12}H_{19}N_4O_3$ ).




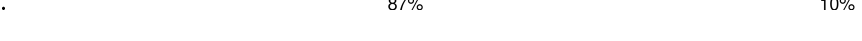
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			19	12	4	3		
3	B	1	Total	C	N	O	0	0
			19	12	4	3		
3	C	1	Total	C	N	O	0	0
			19	12	4	3		

- Molecule 4 is water.

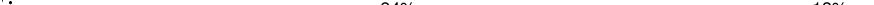
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	150	Total	O	0	0
			150	150		
4	B	132	Total	O	0	0
			132	132		
4	C	150	Total	O	0	0
			150	150		



Note EDS was not executed.

- Chain A: 
- 
- | Label | Color  |
|-------|--------|
| MET   | Grey   |
| ALA   | Grey   |
| ASP   | Grey   |
| PRO   | Grey   |
| ARG   | Grey   |
| PRO   | Grey   |
| D7    | Green  |
| P8    | Green  |
| D9    | Yellow |
| R13   | Yellow |
| I25   | Yellow |
| I39   | Yellow |
| S47   | Yellow |
| P48   | Yellow |
| I77   | Yellow |
| R81   | Yellow |
| V82   | Yellow |
| M119  | Orange |
| H139  | Orange |
| P147  | Yellow |
| G150  | Yellow |
| V154  | Yellow |
| A159  | Yellow |
| E166  | Yellow |
| I194  | Yellow |
| H195  | Green  |
| M196  | Green  |
| L200  | Yellow |
| H211  | Yellow |
| R217  | Yellow |
| A218  | Yellow |
| L228  | Yellow |
| L232  | Yellow |
| A233  | Yellow |
| T237  | Yellow |
| G250  | Yellow |
| M257  | Yellow |
| L260  | Yellow |
| V264  | Yellow |
| F268  | Green  |

- [illegible]

- Chain C:  84% 13% ..
- NET  
ALA  
ASP  
PRO  
ARG  
PRO  
I17  
L11  
A15  
I19  
I25  
G26  
E27  
E28  
V32  
W38  
I39  
P40  
A44  
I77  
R81  
W82  
L83  
H102  
P103  
G111  
V116  
M119  
H139  
P147  
R163  
E166  
I194  
R195  
M196  
L197  
Q198  
T199  
L200  
E211
- A233  
I236  
A254  
M257  
G258  
A259  
L260  
V264  
F268

## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.84Å 102.84Å 128.76Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 1.90	Depositor
% Data completeness (in resolution range)	94.8 (20.00-1.90)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.04	Depositor
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.183 , 0.213	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6180	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	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: PO4, DIH

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	0.28	0/1928	0.61	0/2637
1	B	0.27	0/1928	0.60	0/2637
1	C	0.27	0/1928	0.60	0/2637
All	All	0.27	0/5784	0.60	0/7911

There are no bond length outliers.

There are no bond angle outliers.

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	A	1892	0	1911	23	0
1	B	1892	0	1911	30	0
1	C	1892	0	1911	24	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
3	A	19	0	16	0	0
3	B	19	0	16	0	0
3	C	19	0	16	0	0
4	A	150	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	132	0	0	4	0
4	C	150	0	0	3	0
All	All	6180	0	5781	74	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 6.

All (74) 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:B:125:ARG:HD2	1:B:127:ASP:OD2	1.93	0.68
1:C:25:ILE:HD12	1:C:81:ARG:NH1	2.12	0.63
1:B:119:ASN:HD22	1:B:119:ASN:C	2.03	0.62
1:A:119:ASN:HD22	1:A:119:ASN:C	2.05	0.58
1:C:119:ASN:C	1:C:119:ASN:HD22	2.06	0.58
1:B:124:LEU:HD23	1:B:198:GLN:HG3	1.85	0.58
1:A:260:LEU:O	1:A:264:VAL:HG23	2.04	0.58
1:B:25:ILE:HD12	1:B:81:ARG:NH1	2.18	0.58
1:A:228:LEU:HD22	1:A:257:MET:CE	2.34	0.57
1:B:133:PRO:HB3	1:B:257:MET:SD	2.46	0.56
1:B:217:ARG:HD3	4:B:566:HOH:O	2.06	0.56
1:C:44:ALA:HB3	1:C:258:GLY:HA3	1.87	0.56
1:B:260:LEU:O	1:B:264:VAL:HG23	2.07	0.55
1:A:9:ASP:O	1:A:13:ARG:HG3	2.07	0.55
1:A:77:ILE:HD12	1:A:82:VAL:HG21	1.91	0.53
1:B:154:VAL:HG21	1:B:218:ALA:HB2	1.91	0.51
1:A:25:ILE:HD13	1:A:81:ARG:HD2	1.93	0.51
1:C:211:HIS:HE1	4:C:512:HOH:O	1.93	0.50
1:A:147:PRO:HD3	1:A:211:HIS:CD2	2.47	0.50
1:B:39:LEU:C	1:B:39:LEU:HD23	2.32	0.50
1:A:196:MET:HG3	1:B:200:LEU:HD22	1.95	0.48
1:B:232:LEU:HD12	1:B:237:THR:CG2	2.43	0.48
1:A:200:LEU:HD22	1:C:196:MET:HG3	1.95	0.48
1:C:38:TRP:CZ3	1:C:257:MET:HB3	2.49	0.48
1:B:257:MET:HG2	4:B:921:HOH:O	2.14	0.47
1:A:232:LEU:HD12	1:A:237:THR:CG2	2.44	0.47
1:B:196:MET:HG3	1:C:200:LEU:HD22	1.96	0.47
1:A:228:LEU:HD22	1:A:257:MET:SD	2.55	0.47
1:A:211:HIS:HE1	4:A:508:HOH:O	1.96	0.47
1:B:211:HIS:HE1	4:B:501:HOH:O	1.98	0.47
1:A:228:LEU:CD2	1:A:250:GLY:HA2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:147:PRO:HD3	1:C:211:HIS:CD2	2.51	0.46
1:B:257:MET:CG	4:B:921:HOH:O	2.63	0.46
1:C:11:LEU:HD23	4:C:929:HOH:O	2.16	0.45
1:A:154:VAL:HG21	1:A:218:ALA:HB2	1.98	0.45
1:A:228:LEU:HD21	1:A:250:GLY:HA2	1.99	0.45
1:A:217:ARG:HD3	4:A:648:HOH:O	2.16	0.45
1:A:159:ALA:HA	1:A:217:ARG:HD2	1.99	0.44
1:C:32:VAL:HG22	1:C:116:VAL:HB	1.98	0.44
1:C:39:LEU:C	1:C:39:LEU:HD23	2.37	0.44
1:C:28:HIS:CG	1:C:83:LEU:HG	2.51	0.44
1:C:139:HIS:C	1:C:139:HIS:CD2	2.91	0.43
1:B:139:HIS:CD2	1:B:139:HIS:C	2.92	0.43
1:C:40:PRO:HG2	1:C:254:ALA:CB	2.48	0.43
1:A:39:LEU:HD23	1:A:39:LEU:C	2.38	0.43
1:C:77:ILE:HD12	1:C:82:VAL:HG21	2.01	0.43
1:A:139:HIS:CD2	1:A:139:HIS:C	2.91	0.43
1:B:172:ASP:HB3	1:B:175:LEU:HG	2.01	0.42
1:B:11:LEU:HG	1:B:102:HIS:CE1	2.54	0.42
1:B:62:PRO:HA	1:B:63:PRO:HD3	1.93	0.42
1:A:119:ASN:ND2	1:A:119:ASN:C	2.72	0.42
1:B:159:ALA:HA	1:B:217:ARG:HD2	2.02	0.42
1:C:102:HIS:HB3	1:C:103:PRO:HD3	2.01	0.42
1:C:194:ILE:O	1:C:198:GLN:HG3	2.19	0.42
1:C:195:ARG:HA	1:C:198:GLN:HE21	1.85	0.41
1:B:38:TRP:CZ3	1:B:257:MET:HB3	2.54	0.41
1:B:81:ARG:HG3	1:B:81:ARG:HH11	1.85	0.41
1:C:15:ALA:O	1:C:19:ILE:HG13	2.20	0.41
1:B:32:VAL:HG22	1:B:116:VAL:HB	2.03	0.41
1:B:81:ARG:HD3	1:B:81:ARG:HA	1.86	0.41
1:A:228:LEU:HD22	1:A:257:MET:HE3	2.01	0.41
1:B:194:ILE:HD12	1:B:233:ALA:HB1	2.01	0.41
1:C:27:GLU:HG3	1:C:111:GLY:HA3	2.03	0.41
1:B:196:MET:O	1:B:200:LEU:HG	2.21	0.41
1:C:233:ALA:O	1:C:236:ILE:HG12	2.20	0.41
1:B:228:LEU:HD21	1:B:250:GLY:HA2	2.01	0.41
1:B:119:ASN:ND2	1:B:119:ASN:C	2.71	0.41
1:B:102:HIS:HB3	1:B:103:PRO:HD3	2.03	0.41
1:B:28:HIS:CG	1:B:83:LEU:HG	2.56	0.40
1:C:163:ARG:HB2	4:C:763:HOH:O	2.19	0.40
1:C:11:LEU:HA	1:C:11:LEU:HD12	1.83	0.40
1:A:194:ILE:HD12	1:A:233:ALA:HB1	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:47:SER:HA	1:A:48:PRO:HD3	1.86	0.40
1:C:260:LEU:O	1:C:264:VAL:HG23	2.21	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	260/268 (97%)	254 (98%)	5 (2%)	1 (0%)	39	27
1	B	260/268 (97%)	255 (98%)	5 (2%)	0	100	100
1	C	260/268 (97%)	255 (98%)	5 (2%)	0	100	100
All	All	780/804 (97%)	764 (98%)	15 (2%)	1 (0%)	56	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	GLY

### 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	187/193 (97%)	184 (98%)	3 (2%)	70	66
1	B	187/193 (97%)	185 (99%)	2 (1%)	80	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	187/193 (97%)	184 (98%)	3 (2%)	70	66
All	All	561/579 (97%)	553 (99%)	8 (1%)	74	71

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	119	ASN
1	A	139	HIS
1	A	166	GLU
1	B	119	ASN
1	B	139	HIS
1	C	119	ASN
1	C	139	HIS
1	C	166	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	ASN
1	A	174	GLN
1	A	198	GLN
1	A	211	HIS
1	B	95	HIS
1	B	113	GLN
1	B	119	ASN
1	B	198	GLN
1	B	211	HIS
1	C	113	GLN
1	C	119	ASN
1	C	198	GLN
1	C	211	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules 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 [i](#)

There are no carbohydrates 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$
2	PO4	A	301	-	4,4,4	0.86	0	6,6,6	0.38	0
3	DIH	A	401	-	18,21,21	2.71	8 (44%)	15,30,30	3.40	7 (46%)
2	PO4	B	302	-	4,4,4	0.90	0	6,6,6	0.39	0
3	DIH	B	402	-	18,21,21	2.75	8 (44%)	15,30,30	3.28	7 (46%)
2	PO4	C	303	-	4,4,4	0.82	0	6,6,6	0.38	0
3	DIH	C	403	-	18,21,21	2.75	8 (44%)	15,30,30	3.32	7 (46%)

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	PO4	A	301	-	-	0/0/0/0	0/0/0/0
3	DIH	A	401	-	2/2/7/11	0/6/41/41	0/3/3/3
2	PO4	B	302	-	-	0/0/0/0	0/0/0/0
3	DIH	B	402	-	2/2/7/11	0/6/41/41	0/3/3/3
2	PO4	C	303	-	-	0/0/0/0	0/0/0/0
3	DIH	C	403	-	2/2/7/11	0/6/41/41	0/3/3/3

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	DIH	C5-N7	-5.88	1.39	1.46
3	C	403	DIH	C5-N7	-5.83	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	402	DIH	C5-N7	-5.64	1.39	1.46
3	C	403	DIH	C6'-C4'	-3.82	1.47	1.53
3	B	402	DIH	C6'-C4'	-3.70	1.47	1.53
3	A	401	DIH	C6'-C4'	-3.69	1.47	1.53
3	C	403	DIH	C5-C6	-3.50	1.46	1.53
3	B	402	DIH	C5-C6	-3.46	1.46	1.53
3	A	401	DIH	C5-C6	-3.30	1.47	1.53
3	C	403	DIH	C2'-N1'	-2.44	1.43	1.47
3	B	402	DIH	C2'-N1'	-2.26	1.43	1.47
3	A	401	DIH	C2'-C3'	-2.17	1.48	1.52
3	A	401	DIH	C2'-N1'	-2.16	1.44	1.47
3	C	403	DIH	C2'-C3'	-2.11	1.48	1.52
3	B	402	DIH	C2'-C3'	-2.08	1.48	1.52
3	A	401	DIH	C6-N1	3.97	1.44	1.37
3	C	403	DIH	C2-N1	4.03	1.43	1.35
3	B	402	DIH	C6-N1	4.04	1.44	1.37
3	C	403	DIH	C6-N1	4.17	1.44	1.37
3	B	402	DIH	C2-N1	4.27	1.43	1.35
3	A	401	DIH	C2-N1	4.30	1.43	1.35
3	C	403	DIH	C2-N3	4.71	1.39	1.29
3	A	401	DIH	C2-N3	4.78	1.39	1.29
3	B	402	DIH	C2-N3	4.95	1.40	1.29

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	DIH	C4-C9-C8	-6.20	104.18	110.53
3	C	403	DIH	C4-C9-C8	-6.05	104.34	110.53
3	B	402	DIH	C4-C9-C8	-5.92	104.47	110.53
3	A	401	DIH	C2'-N1'-C6'	-4.25	98.68	104.19
3	C	403	DIH	C2'-N1'-C6'	-4.17	98.78	104.19
3	B	402	DIH	C2'-N1'-C6'	-4.00	99.00	104.19
3	C	403	DIH	C10-C9-C4	2.10	125.64	122.83
3	B	402	DIH	C10-C9-C4	2.12	125.67	122.83
3	C	403	DIH	C6'-C4'-C3'	2.27	107.39	103.82
3	A	401	DIH	C6'-C4'-C3'	2.31	107.46	103.82
3	A	401	DIH	C10-C9-C4	2.33	125.94	122.83
3	B	402	DIH	C6'-C4'-C3'	2.36	107.53	103.82
3	A	401	DIH	O3'-C3'-C2'	3.68	119.89	110.78
3	B	402	DIH	O3'-C3'-C2'	3.77	120.11	110.78
3	C	403	DIH	O3'-C3'-C2'	3.81	120.21	110.78
3	B	402	DIH	O6-C6-C5	4.41	126.59	119.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	DIH	O6-C6-C5	4.47	126.70	119.47
3	C	403	DIH	O6-C6-C5	4.49	126.73	119.47
3	C	403	DIH	O5'-C5'-C4'	6.86	126.58	111.45
3	B	402	DIH	O5'-C5'-C4'	6.91	126.68	111.45
3	A	401	DIH	O5'-C5'-C4'	7.28	127.49	111.45

All (6) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	402	DIH	C4
3	B	402	DIH	C5
3	C	403	DIH	C4
3	C	403	DIH	C5
3	A	401	DIH	C4
3	A	401	DIH	C5

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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 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.