



# wwPDB X-ray Structure Validation Summary Report

Feb 26, 2014 – 06:14 PM GMT

PDB ID : 1BPY  
Title : HUMAN DNA POLYMERASE BETA COMPLEXED WITH GAPPED DNA  
AND DDCTP  
Authors : Sawaya, H. Pelletier M.R.; Prasad, R.; Wilson, S.H.; Kraut, J.  
Deposited on : 1997-04-15  
Resolution : 2.20 Å (reported)

This is a wwPDB validation summary 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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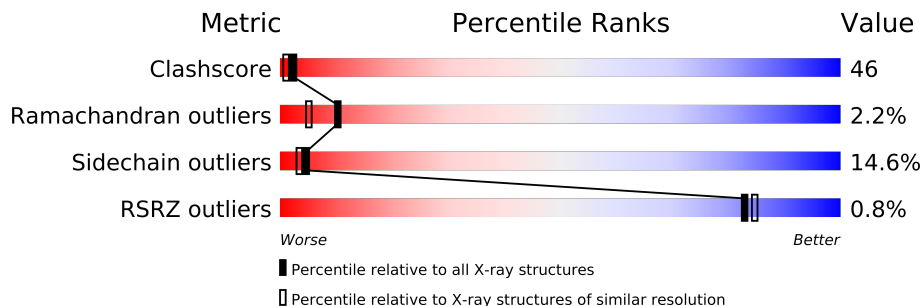
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
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)
RSRZ outliers	66119	2939 (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.

Mol	Chain	Length	Quality of chain
1	T	16	
2	P	10	
3	D	5	
4	A	335	

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 3597 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 DNA chain called DNA (5'-D(\*CP\*CP\*GP\*AP\*CP\*GP\*GP\*CP\*GP\*CP\*AP\*TP\*CP\*AP\*GP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	T	16	Total	C	N	O	P	0	0	0
			323	153	63	92	15			

- Molecule 2 is a DNA chain called DNA (5'-D(\*GP\*CP\*TP\*GP\*AP\*TP\*GP\*CP\*GP\*DO C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	10	Total	C	N	O	P	0	0	0
			202	97	38	58	9			

- Molecule 3 is a DNA chain called DNA (5'-D(\*GP\*TP\*CP\*GP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	5	Total	C	N	O	P	0	0	0
			106	49	20	32	5			

- Molecule 4 is a protein called PROTEIN (DNA POLYMERASE BETA).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	326	Total	C	N	O	S	0	0	0
			2614	1652	457	496	9			

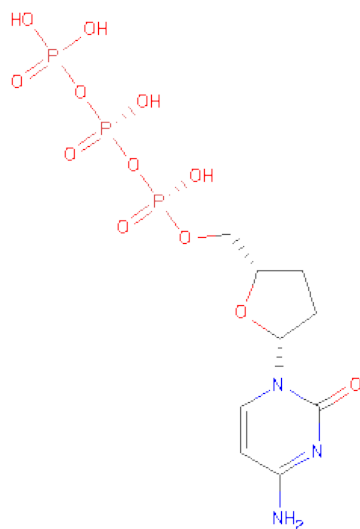
- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Mg	0	0
			2	2		

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Na	0	0
			2	2		

- Molecule 7 is 2',3'-DIDEOXYCYTIDINE5'-TRIPHOSPHATE (three-letter code: DCT) (formula:  $C_9H_{16}N_3O_{12}P_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	N	O	P	0	0
			27	9	3	12	3		

- Molecule 8 is water.

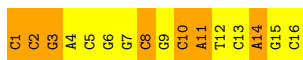
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	223	Total	O	0	0
			223	223		
8	D	27	Total	O	0	0
			27	27		
8	P	21	Total	O	0	0
			21	21		
8	T	50	Total	O	0	0
			50	50		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

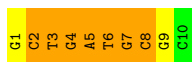
- Molecule 1: DNA (5'-D(\*CP\*CP\*GP\*AP\*CP\*GP\*GP\*CP\*GP\*CP\*AP\*TP\*CP\*AP\*GP\*C)-3')

Chain T: 



- Molecule 2: DNA (5'-D(\*GP\*CP\*TP\*GP\*AP\*TP\*GP\*CP\*GP\*DOC)-3')

Chain P: 



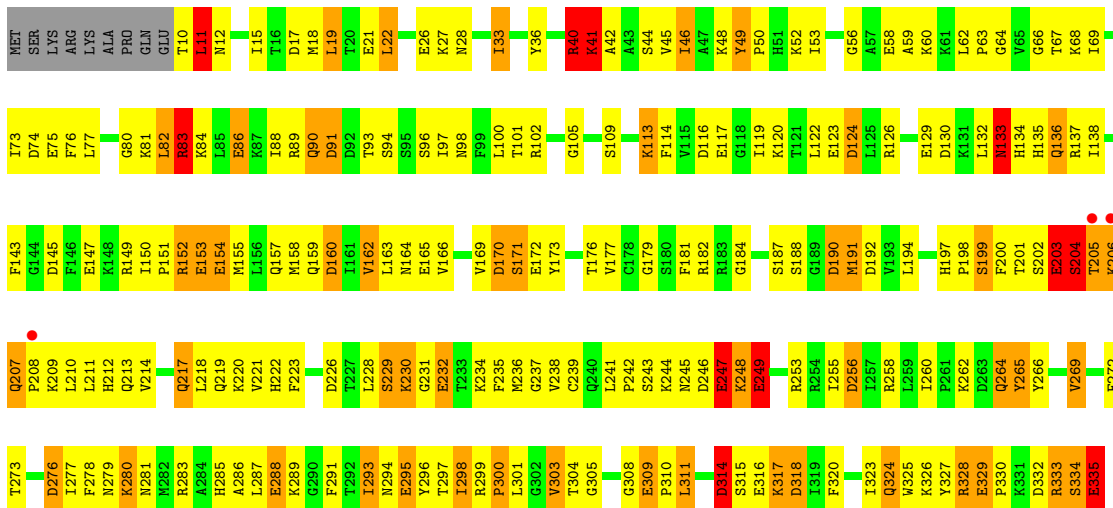
- Molecule 3: DNA (5'-D(\*GP\*TP\*CP\*GP\*G)-3')

Chain D: 



- Molecule 4: PROTEIN (DNA POLYMERASE BETA)

Chain A: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.54Å 79.82Å 54.94Å 90.00° 107.11° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 19.84 – 2.20	Depositor EDS
% Data completeness (in resolution range)	95.4 (20.00-2.20) 91.8 (19.84-2.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.12 (at 2.19Å)	Xtriage
Refinement program	TNT V. 5-D	Depositor
R, $R_{free}$	0.232 , 0.330 0.210 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	20.9	Xtriage
Anisotropy	0.849	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 102.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 21104 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3597	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.05% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, MG, DCT, DOC

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	T	2.01	11/362 (3.0%)	2.28	21/556 (3.8%)
2	P	2.09	6/206 (2.9%)	2.47	14/317 (4.4%)
3	D	2.14	3/118 (2.5%)	2.36	6/179 (3.4%)
4	A	1.22	21/2663 (0.8%)	1.75	63/3578 (1.8%)
All	All	1.43	41/3349 (1.2%)	1.90	104/4630 (2.2%)

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	5	DA	N9-C4	-10.09	1.31	1.37
3	D	1	DG	OP3-P	-8.54	1.50	1.61
4	A	232	GLU	CD-OE2	7.89	1.34	1.25
4	A	26	GLU	CD-OE1	7.70	1.34	1.25
4	A	117	GLU	CD-OE2	7.58	1.33	1.25

The worst 5 of 104 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	333	ARG	NE-CZ-NH1	11.27	125.94	120.30
2	P	5	DA	C8-N9-C4	11.02	110.21	105.80
4	A	137	ARG	NE-CZ-NH1	10.54	125.57	120.30
1	T	3	DG	O4'-C1'-N9	-10.51	100.64	108.00
4	A	204	SER	N-CA-C	9.91	137.75	111.00

There are no chirality outliers.

There are no planarity outliers.

## 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	T	323	0	179	13	0
2	P	202	0	114	5	0
3	D	106	0	57	9	0
4	A	2614	0	2635	269	0
5	A	2	0	0	0	0
6	A	2	0	0	0	0
7	A	27	0	12	0	0
8	A	223	0	0	20	0
8	D	27	0	0	2	0
8	P	21	0	0	2	0
8	T	50	0	0	3	0
All	All	3597	0	2997	286	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 46.

The worst 5 of 286 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:150:ILE:HD12	4:A:155:MET:HE1	1.28	1.12
4:A:285:HIS:HD2	4:A:323:ILE:HD12	1.17	1.07
4:A:230:LYS:HG3	4:A:235:PHE:HD1	1.13	1.06
4:A:316:GLU:H	4:A:317:LYS:NZ	1.53	1.06
4:A:207:GLN:HB3	4:A:209:LYS:HG2	1.41	1.03

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
4	A	324/335 (97%)	285 (88%)	32 (10%)	7 (2%)	10 5

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	11	LEU
4	A	179	GLY
4	A	202	SER
4	A	220	LYS
4	A	143	PHE

### 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
4	A	287/295 (97%)	245 (85%)	42 (15%)	5 3

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	A	152	ARG
4	A	191	MET
4	A	317	LYS
4	A	162	VAL
4	A	171	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
4	A	157	GLN
4	A	217	GLN
4	A	279	ASN
4	A	136	GLN
4	A	264	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

1 non-standard protein/DNA/RNA residue 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	DOC	P	10	1,2	17,19,20	1.27	1 (5%)	20,26,29	1.81	5 (25%)

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	DOC	P	10	1,2	-	0/5/18/19	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	10	DOC	C2-N1	4.02	1.42	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	10	DOC	C2'-C1'-N1	4.02	120.69	112.66
2	P	10	DOC	O4'-C1'-C2'	3.93	111.07	106.37
2	P	10	DOC	C2-N3-C4	3.55	120.71	115.57
2	P	10	DOC	C2'-C3'-C4'	2.34	107.21	102.74
2	P	10	DOC	P-O5'-C5'	-2.22	114.54	123.19

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	$\# Z  > 2$
7	DCT	A	338	5	28,28,28	1.66	5 (17%)	40,43,43	1.45	6 (15%)

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
7	DCT	A	338	5	-	0/19/31/31	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	338	DCT	C2-N1	-4.00	1.33	1.38
7	A	338	DCT	C1'-N1	-3.37	1.38	1.48
7	A	338	DCT	PB-O3B	-3.01	1.54	1.59
7	A	338	DCT	O4'-C1'	-2.95	1.35	1.42
7	A	338	DCT	PA-O2A	-2.74	1.42	1.55

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	338	DCT	C4'-O4'-C1'	5.64	112.40	110.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	338	DCT	C2-N3-C4	2.77	119.59	115.57
7	A	338	DCT	O4'-C1'-N1	2.57	112.50	107.68
7	A	338	DCT	C6-C5-C4	-2.29	116.52	117.47
7	A	338	DCT	O2G-PG-O1G	2.21	117.65	110.44

There are no chirality outliers.

There are no torsion outliers.

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 ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
1	T	16/16 (100%)	-0.51	0	100 100	41, 49, 68, 69	0
2	P	10/10 (100%)	-0.49	0	100 100	47, 53, 64, 66	0
3	D	5/5 (100%)	-0.71	0	100 100	38, 41, 44, 47	0
4	A	326/335 (97%)	-0.28	3 (0%)	81 82	32, 48, 70, 97	0
All	All	357/366 (97%)	-0.30	3 (0%)	83 85	32, 49, 70, 97	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	A	205	THR	3.5
4	A	208	PRO	3.3
4	A	206	LYS	2.7

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	DOC	P	10	18/19	0.08	-1.55	32,47,56,56	0

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
7	DCT	A	338	27/27	0.09	-1.09	27,41,48,57	0
5	MG	A	340	1/1	0.09	-1.36	49,49,49,49	0
6	NA	A	341	1/1	0.07	-1.53	29,29,29,29	0
5	MG	A	339	1/1	0.06	-2.85	45,45,45,45	0
6	NA	A	342	1/1	0.04	-4.03	38,38,38,38	0

## 6.5 Other polymers

There are no such residues in this entry.