



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:12 AM GMT

PDB ID : 2W9B  
Title : BINARY COMPLEX OF DPO4 BOUND TO N2,N2-DIMETHYL-DEOXYGUANOSINE MODIFIED DNA  
Authors : Eoff, R.L.; Zhang, H.; Kosekov, I.D.; Rizzo, C.J.; Egli, M.; Guengerich, F.P.  
Deposited on : 2009-01-22  
Resolution : 2.28 Å(reported)

This is a wwPDB X-ray Structure 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/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) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

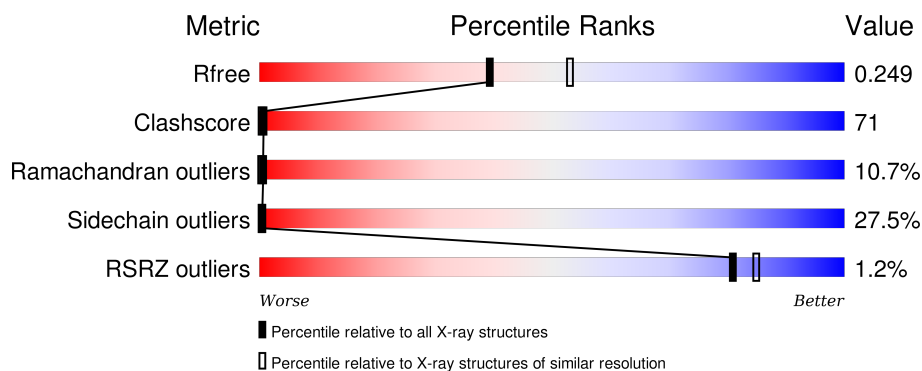
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.28 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))
$R_{free}$	91344	5193 (2.30-2.26)
Clashscore	102246	5929 (2.30-2.26)
Ramachandran outliers	100387	5851 (2.30-2.26)
Sidechain outliers	100360	5850 (2.30-2.26)
RSRZ outliers	91569	5204 (2.30-2.26)

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.

Mol	Chain	Length	Quality of chain
1	A	358	 14% 49% 27% 5% •
2	B	358	 19% 45% 26% 6% •
3	C	14	 21% 79%
3	D	14	 7% 21% 71%
4	E	18	 6% 50% 39% 11%

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Mol	Chain	Length	Quality of chain
4	F	18	

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	DOC	C	14[B]	-	-	X	-
4	O2G	F	5[F]	-	-	X	-
5	MG	A	1343	-	-	-	X
5	MG	B	1343	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6963 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 DNA POLYMERASE IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	342	Total	C	N	O	S	0	12	1
			2746	1760	475	504	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	223	ARG	LYS	CONFLICT	UNP Q97W02

- Molecule 2 is a protein called DNA POLYMERASE IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	343	Total	C	N	O	S	0	6	1
			2754	1766	476	505	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	14	Total	C	N	O	P	0	1	0
			309	147	63	85	14			
3	D	14	Total	C	N	O	P	0	1	0
			309	147	63	85	14			

- Molecule 4 is a DNA chain called 5'-D(\*TP\*CP\*AP\*TP\*M2GP\*GP\*AP\*AP\*TP\*CP\*CP\*TP\*TP\*CP\*CP\*CP\*CP\*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	16	Total	C	N	O	P	0	3	0
			319	155	54	95	15			
4	F	16	Total	C	N	O	P	0	3	0
			319	155	54	95	15			

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

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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	87	Total	O	0	0
			87	87		
6	B	56	Total	O	0	0
			56	56		
6	C	14	Total	O	0	0
			14	14		
6	D	20	Total	O	0	0
			20	20		
6	E	17	Total	O	0	0
			17	17		
6	F	9	Total	O	0	0
			9	9		





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.79Å 101.78Å 97.27Å 90.00° 91.95° 90.00°	Depositor
Resolution (Å)	28.75 – 2.28 28.75 – 2.25	Depositor EDS
% Data completeness (in resolution range)	96.4 (28.75-2.28) 86.5 (28.75-2.25)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.11 (at 2.24Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.239 , 0.251 0.237 , 0.249	Depositor DCC
$R_{free}$ test set	2231 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.7	Xtriage
Anisotropy	0.174	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 60.5	EDS
Estimated twinning fraction	0.085 for -h,-l,-k 0.085 for -h,l,k 0.308 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.33$ , $\langle L^2 \rangle = 0.16$	Xtriage
Outliers	0 of 45673 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6963	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.



## 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: O2G, MG, 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	A	1.58	32/2785 (1.1%)	1.57	30/3741 (0.8%)
2	B	1.58	28/2794 (1.0%)	1.59	30/3753 (0.8%)
3	C	2.69	25/308 (8.1%)	2.81	33/476 (6.9%)
3	D	2.45	18/308 (5.8%)	2.43	26/476 (5.5%)
4	E	2.21	16/327 (4.9%)	2.44	23/498 (4.6%)
4	F	2.14	11/327 (3.4%)	2.85	38/498 (7.6%)
All	All	1.76	130/6849 (1.9%)	1.85	180/9442 (1.9%)

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
2	B	0	1

The worst 5 of 130 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	12	TYR	CD2-CE2	-9.92	1.24	1.39
2	B	122	TYR	CD2-CE2	-9.40	1.25	1.39
4	E	11	DC	C2-O2	-9.15	1.16	1.24
3	C	11	DT	C1'-N1	9.07	1.61	1.49
4	E	4[E]	DT	P-OP2	8.89	1.64	1.49

The worst 5 of 180 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	5	DG	O4'-C1'-N9	15.90	119.13	108.00
4	F	13	DT	O4'-C1'-N1	-15.62	97.06	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	10	DC	O5'-P-OP1	-13.78	93.30	105.70
4	F	12	DT	O4'-C1'-N1	13.55	117.48	108.00
2	B	336	ARG	NE-CZ-NH1	-11.01	114.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	238	ARG	Peptide

## 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	2746	0	2872	446	0
2	B	2754	0	2880	407	0
3	C	309	0	167	28	0
3	D	309	0	170	25	0
4	E	319	0	181	33	0
4	F	319	0	181	37	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	87	0	0	21	0
6	B	56	0	0	14	0
6	C	14	0	0	2	0
6	D	20	0	0	5	0
6	E	17	0	0	0	0
6	F	9	0	0	4	0
All	All	6963	0	6451	928	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 71.

The worst 5 of 928 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)
6:B:2010:HOH:O	3:D:14[A]:DOC:H3'2	1.28	1.27
1:A:144:ILE:HA	6:A:2001:HOH:O	1.28	1.25
1:A:115[A]:VAL:HG11	1:A:120:GLU:O	1.33	1.25
1:A:109:LEU:HA	6:A:2038:HOH:O	1.37	1.24
1:A:298:ARG:HH11	1:A:298:ARG:CG	1.49	1.23

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	340/358 (95%)	237 (70%)	65 (19%)	38 (11%)	0	0
2	B	341/358 (95%)	238 (70%)	68 (20%)	35 (10%)	1	0
All	All	681/716 (95%)	475 (70%)	133 (20%)	73 (11%)	0	0

5 of 73 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	PHE
1	A	36	ARG
1	A	117[A]	ASP
1	A	146	LYS
1	A	173	ARG

### 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	300/315 (95%)	219 (73%)	81 (27%)	0	0
2	B	301/315 (96%)	217 (72%)	84 (28%)	0	0
All	All	601/630 (95%)	436 (72%)	165 (28%)	0	0

5 of 165 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	326	ASP
2	B	63	GLU
2	B	293	LEU
1	A	328	ARG
2	B	19	LEU

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	47	ASN
1	A	254	ASN
1	A	285	HIS
2	B	0	HIS
2	B	161	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues 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	DOC	C	14[A]	3	11,19,20	1.10	1 (9%)	14,26,29	2.28	5 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	DOC	C	14[B]	3	11,19,20	0.85	0	14,26,29	1.54	2 (14%)
3	DOC	D	14[A]	3	11,19,20	1.16	1 (9%)	14,26,29	2.21	4 (28%)
3	DOC	D	14[B]	3	11,19,20	1.33	1 (9%)	14,26,29	2.16	3 (21%)
4	O2G	E	5[E]	4	17,26,27	2.35	5 (29%)	23,38,41	2.40	7 (30%)
4	O2G	F	5[F]	4	17,26,27	1.35	2 (11%)	23,38,41	2.05	7 (30%)

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	DOC	C	14[A]	3	-	0/3/18/19	0/2/2/2
3	DOC	C	14[B]	3	-	0/3/18/19	0/2/2/2
3	DOC	D	14[A]	3	-	0/3/18/19	0/2/2/2
3	DOC	D	14[B]	3	-	0/3/18/19	0/2/2/2
4	O2G	E	5[E]	4	-	0/7/25/26	0/3/3/3
4	O2G	F	5[F]	4	-	0/7/25/26	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	5[E]	O2G	C6-C5	-5.78	1.29	1.41
4	E	5[E]	O2G	C4-N3	-3.91	1.29	1.35
3	C	14[A]	DOC	O4'-C4'	-2.61	1.38	1.44
3	D	14[A]	DOC	C6-C5	-2.18	1.33	1.38
4	E	5[E]	O2G	O6-C6	2.64	1.31	1.24

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	5[E]	O2G	C4-C5-N7	-5.57	104.36	109.48
3	D	14[B]	DOC	O4'-C4'-C5'	-5.49	101.44	109.54
4	E	5[E]	O2G	N3-C2-N1	-4.42	118.92	126.35
3	C	14[B]	DOC	O4'-C4'-C5'	-4.17	103.39	109.54
3	D	14[B]	DOC	O4'-C4'-C3'	-3.91	98.14	104.69

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 38 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	14[A]	DOC	2	0
3	C	14[B]	DOC	8	0
3	D	14[A]	DOC	5	0
3	D	14[B]	DOC	3	0
4	E	5[E]	O2G	3	0
4	F	5[F]	O2G	17	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	A	342/358 (95%)	0.04	5 (1%) 76 81	21, 31, 52, 63	11 (3%)
2	B	343/358 (95%)	-0.03	2 (0%) 90 93	21, 32, 52, 67	5 (1%)
3	C	13/14 (92%)	-0.56	0 100 100	24, 33, 45, 47	0
3	D	13/14 (92%)	-0.53	0 100 100	23, 35, 54, 57	0
4	E	15/18 (83%)	-0.07	1 (6%) 21 27	34, 45, 68, 89	1 (6%)
4	F	15/18 (83%)	0.53	1 (6%) 21 27	33, 52, 69, 91	2 (13%)
All	All	741/780 (95%)	-0.00	9 (1%) 81 85	21, 33, 54, 91	19 (2%)

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	3[F]	DA	12.1
4	E	3[E]	DA	4.7
2	B	250	THR	3.3
1	A	166	ILE	3.3
1	A	112[A]	SER	2.5

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

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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	DOC	C	14[B]	18/19	0.81	0.28	-	29,31,36,36	17
4	O2G	F	5[F]	24/25	0.85	0.28	-	66,76,77,77	13

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	DOC	C	14[A]	18/19	0.81	0.28	-	37,42,44,45	18
3	DOC	D	14[B]	18/19	0.88	0.25	-	42,42,42,42	18
3	DOC	D	14[A]	18/19	0.88	0.25	-	32,38,39,39	17
4	O2G	E	5[E]	24/25	0.83	0.20	-	68,71,78,79	13

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

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	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	MG	B	1343	1/1	0.98	0.26	4.92	42,42,42,42	0
5	MG	A	1343	1/1	0.91	0.20	4.72	53,53,53,53	0
5	MG	B	1342	1/1	0.94	0.16	0.86	47,47,47,47	0
5	MG	A	1342	1/1	0.97	0.09	-1.49	42,42,42,42	0

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

There are no such residues in this entry.