



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 2HQA  
Title : Crystal structure of the catalytic alpha subunit of E. Coli replicative DNA polymerase III  
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Deposited on : 2006-07-18  
Resolution : 2.60 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

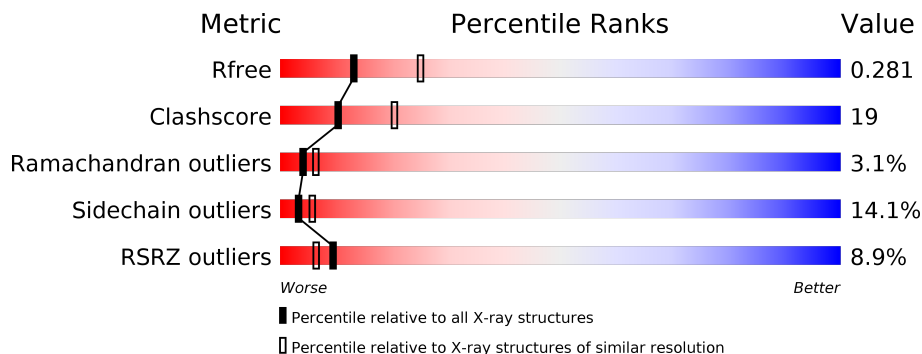
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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))
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 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  $\leq 5\%$ . 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	917	

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
2	PO4	A	920	-	-	X	-

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7267 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 III alpha subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	910	7148	4548	1219	1341	10	30	0	0	0

There are 30 discrepancies between the modelled and reference sequences:

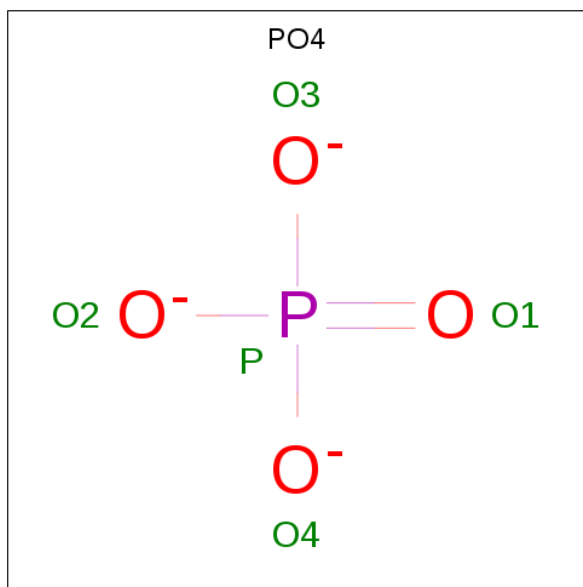
Chain	Residue	Modelled	Actual	Comment	Reference
A	17	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	36	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	136	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	240	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	246	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	286	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	335	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	345	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	399	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	408	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	421	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	436	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	469	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	497	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	571	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	599	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	616	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	631	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	647	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	691	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	707	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	712	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	720	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	742	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	783	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	787	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	791	MSE	MET	MODIFIED RESIDUE	UNP P10443

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Chain	Residue	Modelled	Actual	Comment	Reference
A	807	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	884	MSE	MET	MODIFIED RESIDUE	UNP P10443
A	899	MSE	MET	MODIFIED RESIDUE	UNP P10443

- 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 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0
2	A	1	Total O P 5 4 1	0	0

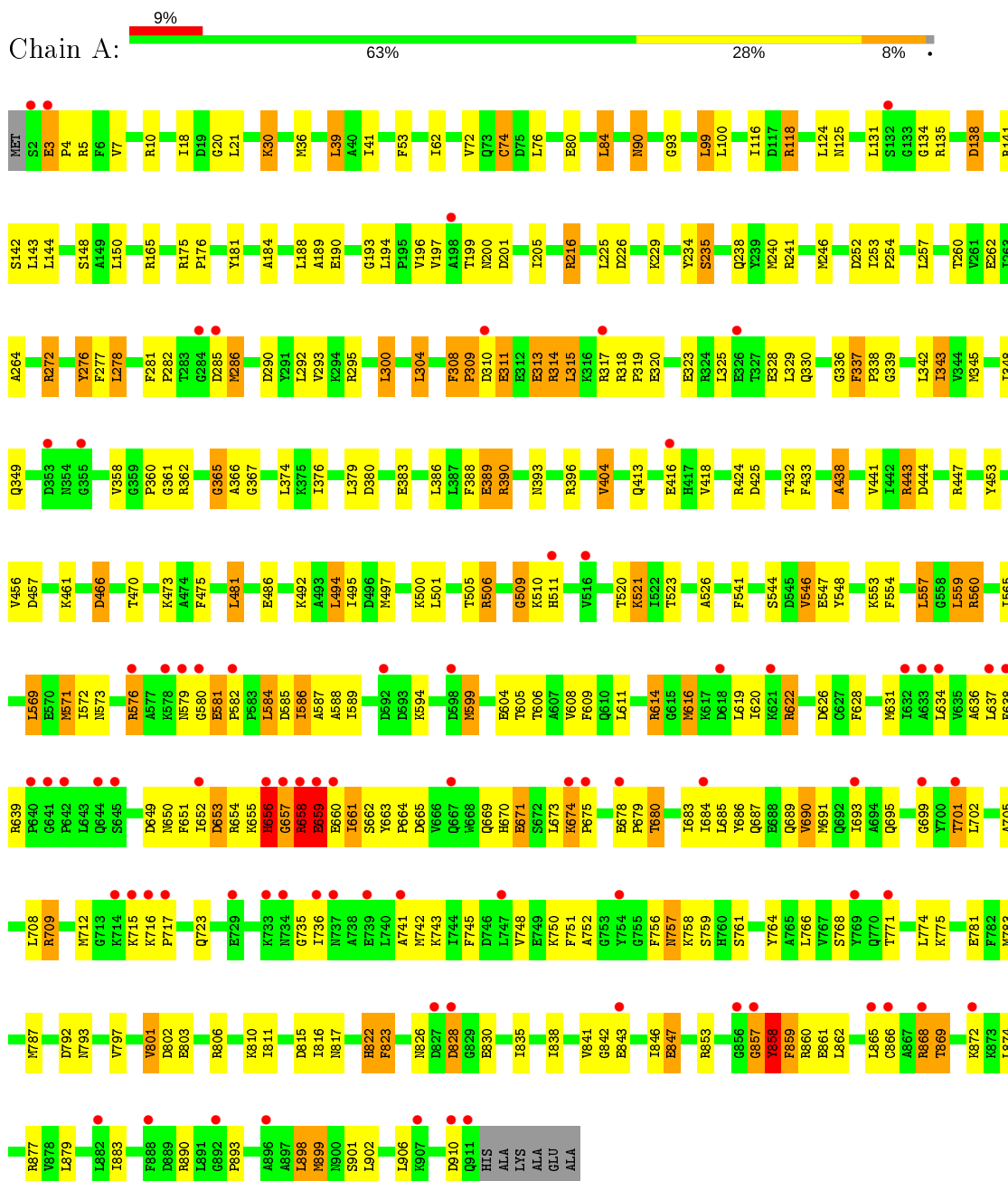
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	104	Total O 104 104	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 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 polymerase III alpha subunit



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.11Å 98.26Å 139.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60 19.91 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.7 (20.00-2.60) 96.7 (19.91-2.60)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.24 (at 2.59Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.219 , 0.287 0.215 , 0.281	Depositor DCC
$R_{free}$ test set	1736 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	68.2	Xtrriage
Anisotropy	0.062	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 69.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7267	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.79% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: PO4

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	0.57	0/7269	0.68	4/9778 (0.0%)

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	9

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	310	ASP	CB-CG-OD2	5.26	123.03	118.30
1	A	226	ASP	CB-CG-OD2	5.22	123.00	118.30
1	A	653	ASP	CB-CG-OD2	5.22	123.00	118.30
1	A	240	MSE	CG-SE-CE	-5.19	87.48	98.90

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	276	TYR	Peptide
1	A	308	PHE	Peptide
1	A	509	GLY	Peptide
1	A	656	HIS	Peptide
1	A	657	GLY	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	7148	0	7086	266	1
2	A	15	0	0	3	0
3	A	104	0	0	1	0
All	All	7267	0	7086	266	1

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 19.

The worst 5 of 266 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:656:HIS:HB2	1:A:657:GLY:HA2	1.17	1.13
1:A:659:GLU:HG2	1:A:660:GLU:H	1.08	1.10
1:A:7:VAL:H	1:A:260:THR:HG21	1.19	1.08
1:A:659:GLU:CG	1:A:660:GLU:H	1.68	1.04
1:A:822:HIS:O	1:A:823:PHE:HB2	1.56	1.02

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:GLU:OE2	1:A:877:ARG:NH2[4_565]	2.08	0.12

## 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	908/917 (99%)	798 (88%)	82 (9%)	28 (3%)	4 6

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	309	PRO
1	A	314	ARG
1	A	658	ARG
1	A	859	PHE
1	A	315	LEU

### 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	753/727 (104%)	647 (86%)	106 (14%)	3 6

5 of 106 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	425	ASP
1	A	559	LEU
1	A	865	LEU
1	A	466	ASP
1	A	500	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	601	GLN
1	A	669	GLN
1	A	793	ASN
1	A	349	GLN
1	A	757	ASN

### 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](#)

3 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	918	-	4,4,4	0.96	0	6,6,6	0.68	0
2	PO4	A	920	-	4,4,4	0.97	0	6,6,6	0.86	0
2	PO4	A	919	-	4,4,4	0.85	0	6,6,6	0.61	0

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.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	918	PO4	1	0
2	A	920	PO4	2	0

## 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	880/917 (95%)	0.49	78 (8%) <b>9</b> <b>6</b>	35, 65, 73, 86	0

The worst 5 of 78 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	310	ASP	7.0
1	A	579	ASN	5.0
1	A	580	GLY	4.7
1	A	872	LYS	4.7
1	A	634	LEU	4.7

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no monosaccharides 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. 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	PO4	A	920	5/5	0.92	0.53	78,81,82,83	0
2	PO4	A	918	5/5	0.93	0.21	88,88,89,89	0
2	PO4	A	919	5/5	0.96	0.29	82,82,83,84	0

## 6.5 Other polymers

There are no such residues in this entry.