



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 26, 2026 – 04:24 AM EDT

PDB ID : 9CDW / pdb\_00009cdw  
Title : Crystal structure of HP1alpha chromoshadow domain in complex with KAP1 peptide  
Authors : Selvam, K.; Singh, R.K.; Gaurav, N.; Kutateladze, T.G.  
Deposited on : 2024-06-25  
Resolution : 2.40 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

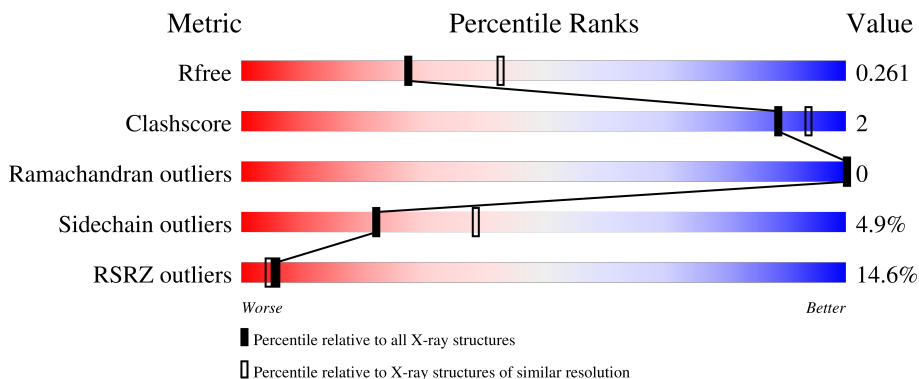
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
$R_{free}$	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 of 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	64	
1	B	64	
1	C	64	
1	D	64	
2	E	6	

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Mol	Chain	Length	Quality of chain
2	F	6	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a green segment on the left labeled '83%', a red segment in the middle labeled '17%', and a yellow segment on the right labeled '17%'. Above the bar, the text '100%' is centered, indicating the total length of the chain.</p>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2221 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 Chromobox protein homolog 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	64	Total	C	N	O	S	0	0	0
			512	326	83	99	4			
1	B	64	Total	C	N	O	S	0	0	0
			506	322	83	97	4			
1	C	64	Total	C	N	O	S	0	0	0
			512	326	83	99	4			
1	D	64	Total	C	N	O	S	0	0	0
			512	326	83	99	4			

- Molecule 2 is a protein called Transcription intermediary factor 1-beta peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	6	Total	C	N	O	0	0	0
			47	30	9	8			
2	F	6	Total	C	N	O	0	0	0
			47	30	9	8			

- Molecule 3 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 10 6 4	0	0
3	B	1	Total C O 10 6 4	0	0
3	D	1	Total C O 10 6 4	0	0

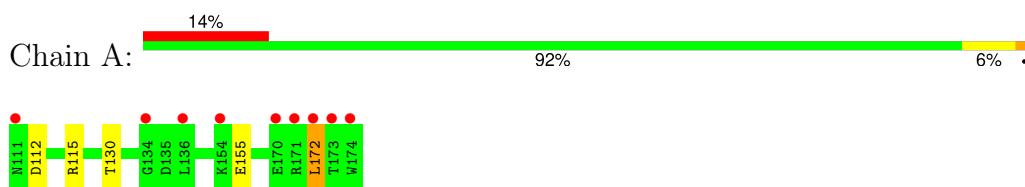
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	11	Total O 11 11	0	0
4	B	14	Total O 14 14	0	0
4	C	9	Total O 9 9	0	0
4	D	21	Total O 21 21	0	0

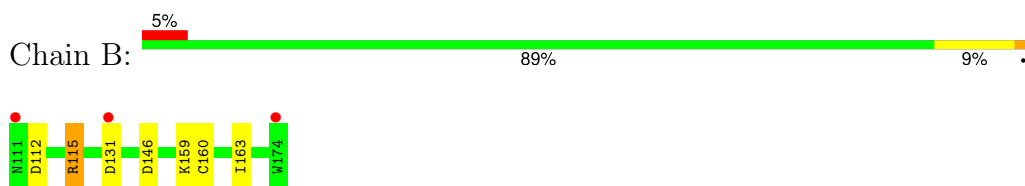
### 3 Residue-property plots [i](#)

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.

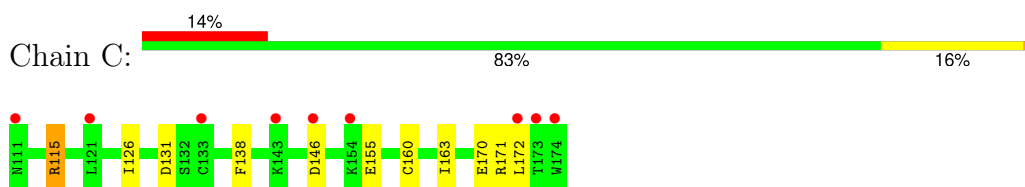
- Molecule 1: Chromobox protein homolog 5



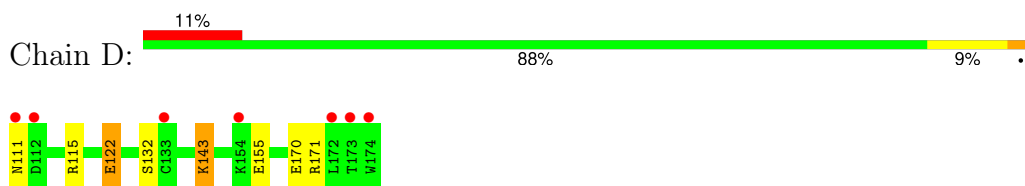
- Molecule 1: Chromobox protein homolog 5



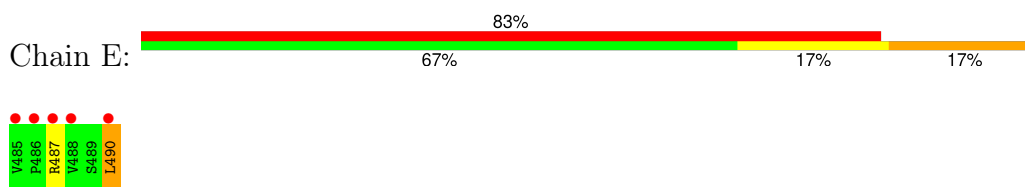
- Molecule 1: Chromobox protein homolog 5



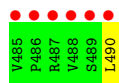
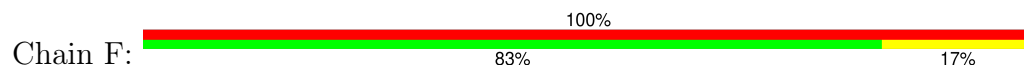
- Molecule 1: Chromobox protein homolog 5



- Molecule 2: Transcription intermediary factor 1-beta peptide



- Molecule 2: Transcription intermediary factor 1-beta peptide



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.81Å 107.81Å 64.61Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	37.87 – 2.40 37.87 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (37.87-2.40) 99.7 (37.87-2.40)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.28 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.8.0425	Depositor
R, $R_{free}$	0.235 , 0.252 0.243 , 0.261	Depositor DCC
$R_{free}$ test set	875 reflections (5.19%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.3	Xtrriage
Anisotropy	0.080	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 30.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.54$ , $\langle L^2 \rangle = 0.38$	Xtrriage
Estimated twinning fraction	0.033 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	2221	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.10 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.3882e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PGE

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	0.70	0/521	1.22	2/701 (0.3%)
1	B	0.75	0/515	1.30	5/693 (0.7%)
1	C	0.60	0/521	1.17	2/701 (0.3%)
1	D	0.70	0/521	1.29	4/701 (0.6%)
2	E	0.78	0/47	1.01	0/62
2	F	0.74	0/47	1.17	0/62
All	All	0.69	0/2172	1.24	13/2920 (0.4%)

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
1	B	0	1
1	C	0	2
1	D	0	2
2	E	0	1
All	All	0	7

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	122	GLU	CB-CA-C	6.32	119.65	109.41
1	A	112	ASP	CB-CA-C	6.17	123.19	110.31
1	B	115	ARG	NE-CZ-NH2	5.73	124.36	119.20
1	B	112	ASP	CA-CB-CG	5.68	118.28	112.60
1	D	155	GLU	N-CA-CB	-5.68	101.74	110.20

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	115	ARG	Sidechain
1	B	115	ARG	Sidechain
1	C	115	ARG	Sidechain
1	C	171	ARG	Sidechain
1	D	115	ARG	Sidechain

## 5.2 Too-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 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	512	0	503	2	0
1	B	506	0	492	2	0
1	C	512	0	503	2	0
1	D	512	0	503	3	0
2	E	47	0	53	1	0
2	F	47	0	53	0	0
3	A	10	0	14	1	0
3	B	10	0	14	0	0
3	D	10	0	14	1	0
4	A	11	0	0	0	0
4	B	14	0	0	0	0
4	C	9	0	0	0	0
4	D	21	0	0	1	0
All	All	2221	0	2149	8	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 2.

The worst 5 of 8 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:D:111:ASN:O	3:D:201:PGE:H5	1.56	1.05
1:D:122:GLU:HG3	4:D:303:HOH:O	1.90	0.71
1:A:130:THR:HB	3:A:201:PGE:H62	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:146:ASP:O	1:D:111:ASN:ND2	2.34	0.59
1:C:160:CYS:HB2	1:C:163:ILE:HD12	1.91	0.52

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	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
1	B	62/64 (97%)	61 (98%)	1 (2%)	0	100	100
1	C	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
1	D	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
2	E	4/6 (67%)	4 (100%)	0	0	100	100
2	F	4/6 (67%)	4 (100%)	0	0	100	100
All	All	256/268 (96%)	248 (97%)	8 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	54/54 (100%)	53 (98%)	1 (2%)	50	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	52/54 (96%)	51 (98%)	1 (2%)	50	71
1	C	54/54 (100%)	50 (93%)	4 (7%)	13	22
1	D	54/54 (100%)	51 (94%)	3 (6%)	19	33
2	E	6/6 (100%)	5 (83%)	1 (17%)	2	3
2	F	6/6 (100%)	5 (83%)	1 (17%)	2	3
All	All	226/228 (99%)	215 (95%)	11 (5%)	22	39

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	143	LYS
1	D	170	GLU
2	F	490	LEU
2	E	490	LEU
1	C	170	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	111	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 oligosaccharides 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	$\# Z  > 2$
3	PGE	D	201	-	9,9,9	0.40	0	8,8,8	0.41	0
3	PGE	A	201	-	9,9,9	0.44	0	8,8,8	0.40	0
3	PGE	B	201	-	9,9,9	0.36	0	8,8,8	0.27	0

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	PGE	D	201	-	-	3/7/7/7	-
3	PGE	A	201	-	-	7/7/7/7	-
3	PGE	B	201	-	-	4/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	201	PGE	C3-C4-O3-C5
3	A	201	PGE	O2-C3-C4-O3
3	A	201	PGE	O3-C5-C6-O4
3	A	201	PGE	O1-C1-C2-O2
3	A	201	PGE	C6-C5-O3-C4

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	201	PGE	1	0
3	A	201	PGE	1	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	64/64 (100%)	0.54	9 (14%) 6 5	24, 40, 80, 85	0
1	B	64/64 (100%)	0.43	3 (4%) 36 32	26, 39, 69, 83	0
1	C	64/64 (100%)	0.93	9 (14%) 6 5	35, 52, 81, 97	0
1	D	64/64 (100%)	0.55	7 (10%) 10 8	26, 39, 71, 83	0
2	E	6/6 (100%)	3.39	5 (83%) 0 0	84, 98, 110, 122	0
2	F	6/6 (100%)	4.14	6 (100%) 0 0	87, 94, 116, 130	0
All	All	268/268 (100%)	0.75	39 (14%) 6 4	24, 43, 86, 130	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	486	PRO	6.6
2	F	485	VAL	6.4
1	D	111	ASN	6.0
2	E	485	VAL	5.9
2	E	486	PRO	4.8

### 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 oligosaccharides 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
3	PGE	D	201	10/10	0.68	0.26	59,74,83,85	0
3	PGE	B	201	10/10	0.84	0.20	56,75,78,82	0
3	PGE	A	201	10/10	0.84	0.16	63,69,72,72	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.