



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 17, 2021 – 06:49 PM EDT

PDB ID : 5RP3
Title : PanDDA analysis group deposition – Proteinase K crystal structure Apo14
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Deposited on : 2020-09-23
Resolution : 1.09 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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 : 2.20
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) : 2.20

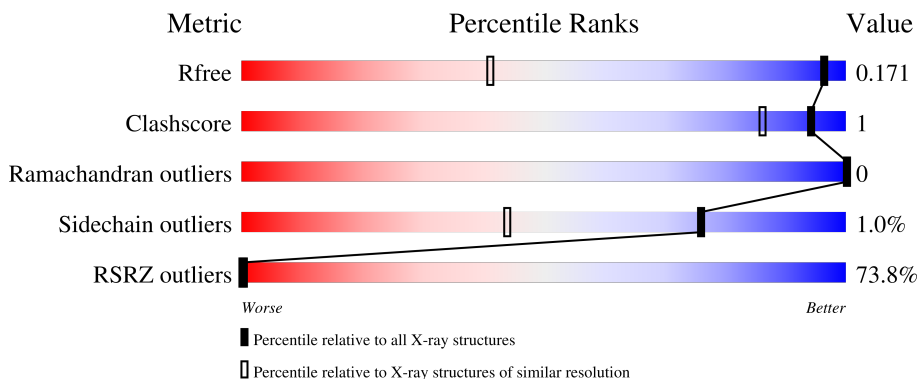
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

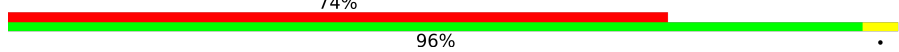
The reported resolution of this entry is 1.09 Å.

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	1619 (1.14-1.06)
Clashscore	141614	1671 (1.14-1.06)
Ramachandran outliers	138981	1615 (1.14-1.06)
Sidechain outliers	138945	1613 (1.14-1.06)
RSRZ outliers	127900	1588 (1.14-1.06)

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 ≥ 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	279	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2367 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 Proteinase K.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	279	2023	1244	355	414	10	0	17	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	207	ASP	SER	conflict	UNP P06873

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

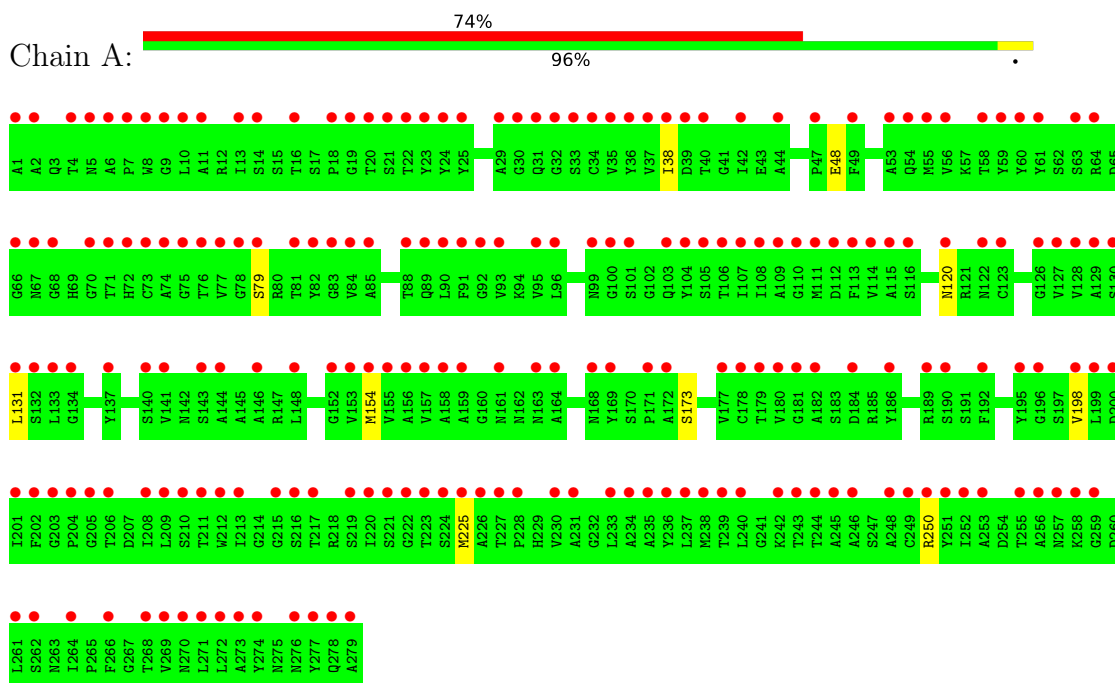
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	339	Total 339	O 339	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: Proteinase K



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	68.08Å 68.08Å 102.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.72 – 1.09 56.72 – 1.09	Depositor EDS
% Data completeness (in resolution range)	93.8 (56.72-1.09) 93.8 (56.72-1.09)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 1.09Å)	Xtrriage
Refinement program	PHENIX 1.19.1	Depositor
R, R_{free}	0.163 , 0.173 0.162 , 0.171	Depositor DCC
R_{free} test set	4608 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	9.1	Xtrriage
Anisotropy	0.007	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 40.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	2367	wwPDB-VP
Average B, all atoms (Å ²)	11.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.17% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: SO4

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	0.31	0/2062	0.61	0/2804

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	2023	0	1900	5	0
2	A	5	0	0	0	0
3	A	339	0	0	2	6
All	All	2367	0	1900	5	6

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 1.

All (5) 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:173:SER:HA	1:A:198:VAL:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:ASN:ND2	3:A:1105:HOH:O	2.42	0.47
1:A:38:ILE:HD12	1:A:131[A]:LEU:HD11	2.02	0.41
1:A:48:GLU:HB3	1:A:79:SER:HB2	2.03	0.41
1:A:250[A]:ARG:NH1	3:A:1101:HOH:O	2.35	0.40

All (6) 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)
3:A:1123:HOH:O	3:A:1283:HOH:O[5_655]	1.70	0.50
3:A:1130:HOH:O	3:A:1252:HOH:O[8_665]	1.71	0.49
3:A:1341:HOH:O	3:A:1408:HOH:O[6_565]	1.88	0.32
3:A:1185:HOH:O	3:A:1347:HOH:O[6_465]	1.99	0.21
3:A:1363:HOH:O	3:A:1408:HOH:O[8_665]	2.04	0.16
3:A:1378:HOH:O	3:A:1378:HOH:O[8_665]	2.07	0.13

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	277/279 (99%)	269 (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	210/213 (99%)	208 (99%)	2 (1%)	76 44

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	154[A]	MET
1	A	225	MET

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

Mol	Chain	Res	Type
1	A	168	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](#)

1 ligand 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	SO4	A	1001	-	4,4,4	0.17	0	6,6,6	0.30	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.

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

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, 95th 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 ²)	Q<0.9
1	A	279/279 (100%)	2.64	206 (73%) 0 0	7, 9, 14, 23	17 (6%)

All (206) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	279	ALA	9.5
1	A	13[A]	ILE	5.4
1	A	198	VAL	5.0
1	A	64	ARG	4.7
1	A	201	ILE	4.6
1	A	93	VAL	4.5
1	A	34[A]	CYS	4.5
1	A	252	ILE	4.4
1	A	237	LEU	4.2
1	A	84	VAL	4.2
1	A	107	ILE	4.1
1	A	127	VAL	4.1
1	A	73	CYS	4.1
1	A	278	GLN	4.1
1	A	77	VAL	4.0
1	A	213	ILE	4.0
1	A	59	TYR	4.0
1	A	90	LEU	4.0
1	A	42	ILE	4.0
1	A	61	TYR	4.0
1	A	180	VAL	4.0
1	A	8	TRP	4.0
1	A	38	ILE	3.9
1	A	131[A]	LEU	3.9
1	A	104	TYR	3.9
1	A	106	THR	3.9
1	A	155	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	99	ASN	3.9
1	A	114	VAL	3.8
1	A	266	PHE	3.8
1	A	89	GLN	3.8
1	A	36	TYR	3.8
1	A	251	TYR	3.7
1	A	249	CYS	3.7
1	A	82	TYR	3.7
1	A	128	VAL	3.7
1	A	233	LEU	3.7
1	A	271	LEU	3.7
1	A	212	TRP	3.7
1	A	24	TYR	3.7
1	A	272	LEU	3.7
1	A	35	VAL	3.6
1	A	123	CYS	3.6
1	A	245	ALA	3.6
1	A	178	CYS	3.6
1	A	240	LEU	3.6
1	A	182	ALA	3.5
1	A	95	VAL	3.5
1	A	133	LEU	3.5
1	A	202	PHE	3.5
1	A	169	TYR	3.4
1	A	148	LEU	3.4
1	A	91[A]	PHE	3.4
1	A	208	ILE	3.3
1	A	49	PHE	3.3
1	A	10	LEU	3.3
1	A	31[A]	GLN	3.3
1	A	113	PHE	3.3
1	A	192	PHE	3.3
1	A	269	VAL	3.3
1	A	261	LEU	3.3
1	A	5	ASN	3.3
1	A	6	ALA	3.3
1	A	37	VAL	3.3
1	A	81	THR	3.3
1	A	177	VAL	3.2
1	A	164	ALA	3.2
1	A	60	TYR	3.1
1	A	11	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	112	ASP	3.1
1	A	195	TYR	3.1
1	A	204	PRO	3.1
1	A	21	SER	3.1
1	A	71	THR	3.1
1	A	236	TYR	3.1
1	A	179	THR	3.1
1	A	141	VAL	3.1
1	A	220	ILE	3.0
1	A	2	ALA	3.0
1	A	25	TYR	3.0
1	A	153	VAL	3.0
1	A	230	VAL	3.0
1	A	211	THR	3.0
1	A	56	VAL	3.0
1	A	1	ALA	3.0
1	A	231	ALA	3.0
1	A	76	THR	3.0
1	A	54[A]	GLN	2.9
1	A	16	THR	2.9
1	A	18	PRO	2.9
1	A	88	THR	2.9
1	A	158	ALA	2.9
1	A	96	LEU	2.9
1	A	143[A]	SER	2.9
1	A	186	TYR	2.9
1	A	115	ALA	2.9
1	A	152	GLY	2.9
1	A	238[A]	MET	2.9
1	A	74	ALA	2.9
1	A	273	ALA	2.9
1	A	75	GLY	2.8
1	A	85	ALA	2.8
1	A	259	GLY	2.8
1	A	206	THR	2.8
1	A	227	THR	2.8
1	A	129	ALA	2.8
1	A	66	GLY	2.8
1	A	234	ALA	2.8
1	A	235	ALA	2.8
1	A	256	ALA	2.8
1	A	30	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	226	ALA	2.7
1	A	78	GLY	2.7
1	A	23	TYR	2.7
1	A	68	GLY	2.7
1	A	137	TYR	2.7
1	A	196	GLY	2.7
1	A	159	ALA	2.7
1	A	134	GLY	2.7
1	A	157	VAL	2.6
1	A	171	PRO	2.6
1	A	161[A]	ASN	2.6
1	A	32	GLY	2.6
1	A	58	THR	2.6
1	A	276	ASN	2.6
1	A	29	ALA	2.6
1	A	146	ALA	2.6
1	A	126	GLY	2.6
1	A	242[A]	LYS	2.6
1	A	22	THR	2.5
1	A	244	THR	2.5
1	A	108	ILE	2.5
1	A	100	GLY	2.5
1	A	222	GLY	2.5
1	A	156	ALA	2.5
1	A	163	ASN	2.5
1	A	101	SER	2.5
1	A	130	SER	2.5
1	A	181	GLY	2.5
1	A	246	ALA	2.5
1	A	154[A]	MET	2.5
1	A	103	GLN	2.5
1	A	224	SER	2.5
1	A	239	THR	2.4
1	A	105	SER	2.4
1	A	219[A]	SER	2.4
1	A	221	SER	2.4
1	A	277	TYR	2.4
1	A	144	ALA	2.4
1	A	253	ALA	2.4
1	A	19	GLY	2.4
1	A	110	GLY	2.4
1	A	40	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	223	THR	2.4
1	A	203	GLY	2.4
1	A	210	SER	2.4
1	A	199	LEU	2.4
1	A	209	LEU	2.4
1	A	109	ALA	2.4
1	A	274	TYR	2.4
1	A	255	THR	2.3
1	A	120	ASN	2.3
1	A	225	MET	2.3
1	A	216[A]	SER	2.3
1	A	258	LYS	2.3
1	A	168	ASN	2.3
1	A	262	SER	2.3
1	A	47	PRO	2.3
1	A	172	ALA	2.3
1	A	140[A]	SER	2.3
1	A	217	THR	2.3
1	A	268	THR	2.3
1	A	39	ASP	2.3
1	A	257	ASN	2.3
1	A	53	ALA	2.3
1	A	63	SER	2.3
1	A	189	ARG	2.3
1	A	70	GLY	2.3
1	A	20	THR	2.2
1	A	72	HIS	2.2
1	A	228	PRO	2.2
1	A	205	GLY	2.2
1	A	243	THR	2.2
1	A	14	SER	2.2
1	A	250[A]	ARG	2.2
1	A	79	SER	2.2
1	A	92	GLY	2.2
1	A	67	ASN	2.2
1	A	122	ASN	2.2
1	A	264	ILE	2.2
1	A	215	GLY	2.1
1	A	33	SER	2.1
1	A	132	SER	2.1
1	A	200	ASP	2.1
1	A	248	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	83	GLY	2.1
1	A	44	ALA	2.1
1	A	9	GLY	2.1
1	A	4	THR	2.1
1	A	7	PRO	2.1
1	A	184	ASP	2.0
1	A	190	SER	2.0
1	A	111	MET	2.0
1	A	116	SER	2.0
1	A	55	MET	2.0
1	A	270	ASN	2.0

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, 95th 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(\AA^2)	Q<0.9
2	SO4	A	1001	5/5	0.90	0.15	10,10,14,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.