wwPDB X-ray Structure Validation Summary Report (i)

Nov 20, 2023 – 06:05 PM JST

PDB ID	:	7D3J
Title	:	Crystal structure of the Cas12i1 R-loop complex after target DNA cleavage
Authors	:	Zhang, B.; Luo, D.Y.; Li, Y.; OuYang, S.Y.
Deposited on	:	2020-09-19
Resolution	:	2.45 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

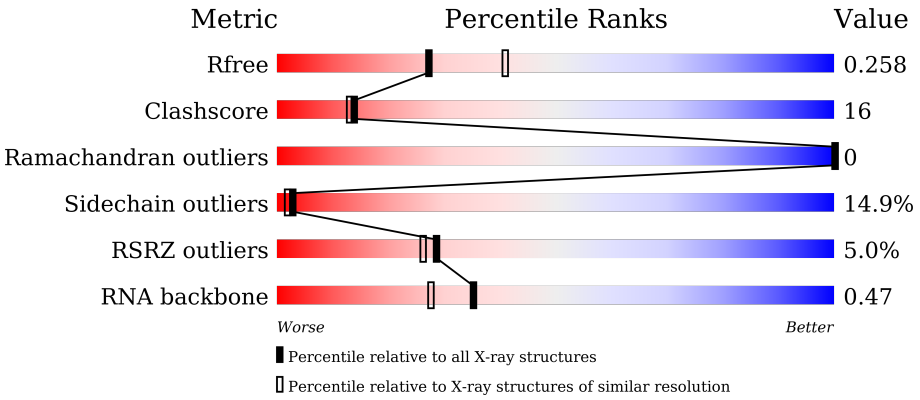
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)
RNA backbone	3102	1001 (2.80-2.12)

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 <=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	1101	5%, 64%, 27%, 7%
2	B	43	9%, 28%, 56%, 14%
3	C	40	42%, 28%, 30%
4	D	40	5%, 20%, 28%, 10%, 42%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 10727 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 12i1-WT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1077	Total	C	N	O	S	0	0	0
			8717	5545	1507	1625	40			

- Molecule 2 is a RNA chain called RNA (43-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	43	Total	C	N	O	P	0	0	0
			914	409	158	304	43			

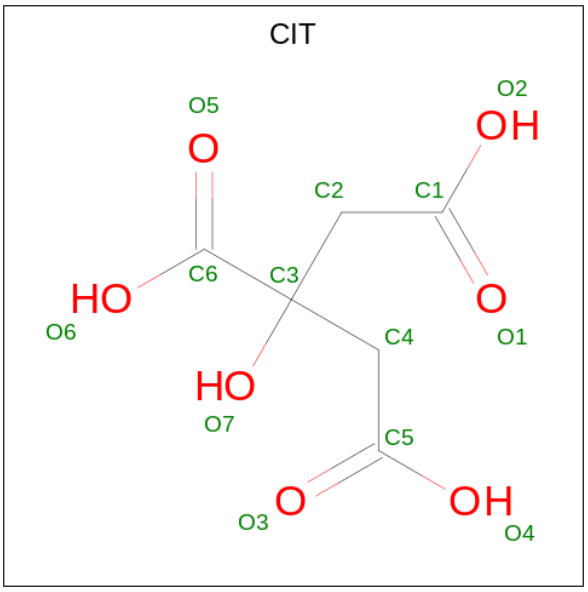
- Molecule 3 is a DNA chain called DNA (28-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	28	Total	C	N	O	P	0	0	0
			568	274	98	168	28			

- Molecule 4 is a DNA chain called DNA (23-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	23	Total	C	N	O	P	0	0	0
			475	227	88	137	23			

- Molecule 5 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 13 6 7	0	0

- Molecule 6 is water.

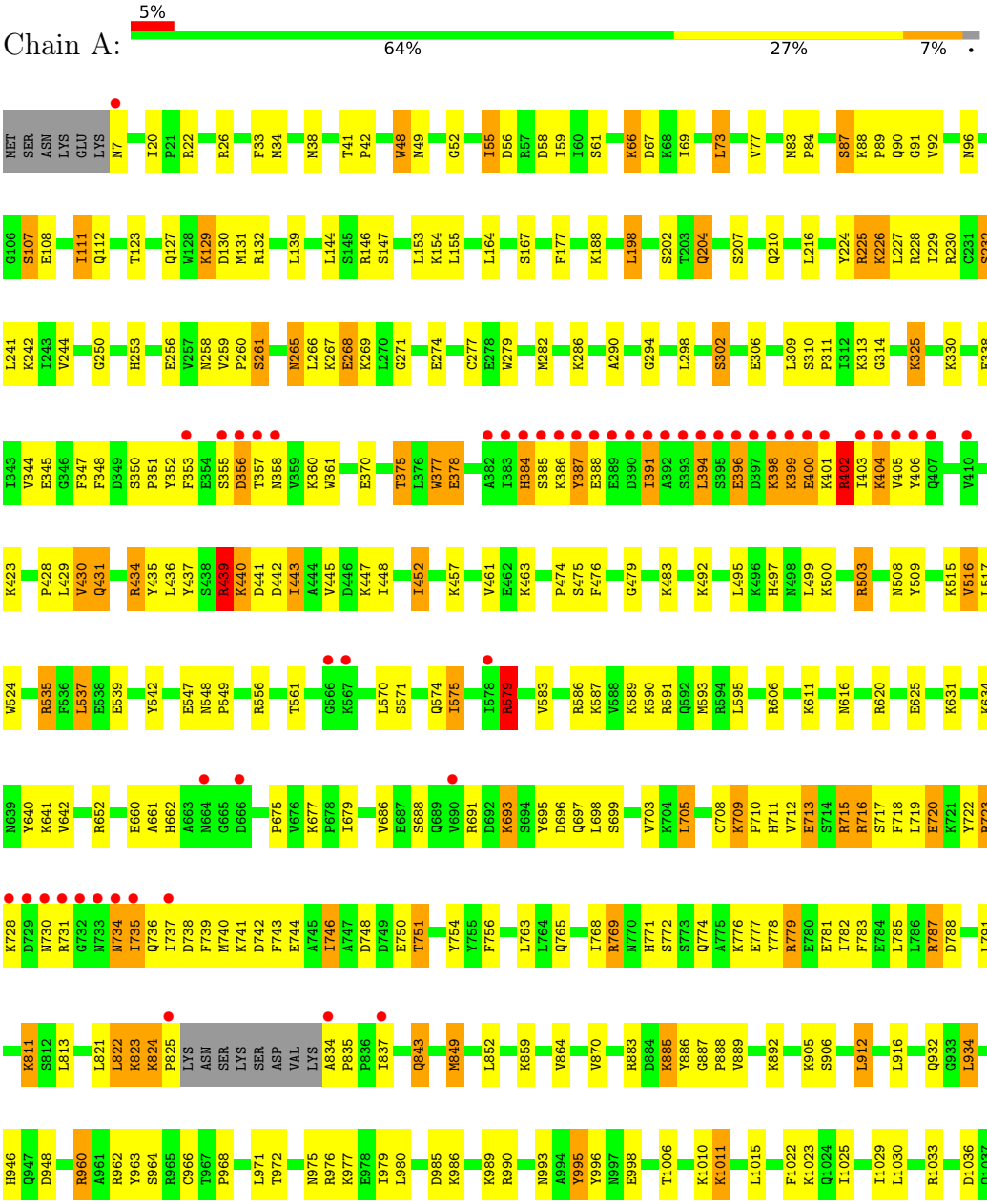
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	33	Total O 33 33	0	0
6	B	1	Total O 1 1	0	0
6	C	5	Total O 5 5	0	0
6	D	1	Total O 1 1	0	0

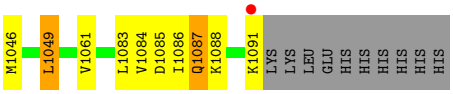
3 Residue-property plots (i)

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: 12i1-WT

Chain A:





• Molecule 2: RNA (43-MER)

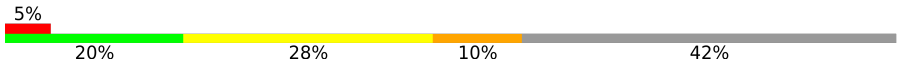
Chain B:

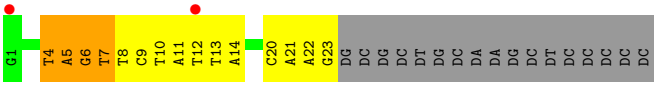
• Molecule 3: DNA (28-MER)

Chain C:

• Molecule 4: DNA (23-MER)

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	129.80Å 141.97Å 208.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.73 – 2.45 58.66 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.9 (58.73-2.45) 99.9 (58.66-2.45)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.32 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.220 , 0.257 0.220 , 0.258	Depositor DCC
R_{free} test set	3545 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	53.8	Xtriage
Anisotropy	0.008	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 33.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	10727	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.70% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: CIT

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	0.72	0/8895	0.74	0/11971
2	B	1.37	21/1021 (2.1%)	0.82	0/1588
3	C	0.71	1/635 (0.2%)	0.91	0/976
4	D	1.15	7/533 (1.3%)	0.79	0/821
All	All	0.83	29/11084 (0.3%)	0.76	0/15356

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	23

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	7	G	O3'-P	-8.24	1.51	1.61
2	B	29	A	O3'-P	-7.80	1.51	1.61
2	B	25	A	O3'-P	-7.47	1.52	1.61
2	B	26	U	O3'-P	-7.45	1.52	1.61
2	B	19	G	O3'-P	-7.42	1.52	1.61

There are no bond angle outliers.

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	132	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	22	ARG	Sidechain
1	A	225	ARG	Sidechain
1	A	228	ARG	Sidechain
1	A	233	ARG	Sidechain

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	8717	0	8774	301	0
2	B	914	0	459	13	0
3	C	568	0	319	11	0
4	D	475	0	261	20	0
5	A	13	0	5	2	0
6	A	33	0	0	0	0
6	B	1	0	0	0	0
6	C	5	0	0	0	0
6	D	1	0	0	0	0
All	All	10727	0	9818	324	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 16.

The worst 5 of 324 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:824:LYS:HE3	1:A:825:PRO:CD	1.59	1.31
1:A:575:ILE:HD11	1:A:579:ARG:NH2	1.48	1.27
1:A:824:LYS:CE	1:A:825:PRO:HD3	1.66	1.22
1:A:387:TYR:HB2	1:A:402:ARG:NH1	1.53	1.22
1:A:574:GLN:HG2	1:A:593:MET:CE	1.72	1.19

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	1073/1101 (98%)	1047 (98%)	26 (2%)	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	960/984 (98%)	817 (85%)	143 (15%)	3 2

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	811	LYS
1	A	843	GLN
1	A	989	LYS
1	A	386	LYS
1	A	385	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	942	ASN
1	A	993	ASN
1	A	1087	GLN

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Mol	Chain	Res	Type
1	A	997	ASN
1	A	381	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	42/43 (97%)	3 (7%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	2	U
2	B	17	U
2	B	24	U

There are no RNA pucker outliers to report.

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	$\#\|Z\| > 2$
5	CIT	A	1201	-	12,12,12	1.25	1 (8%)	17,17,17	1.73	2 (11%)

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
5	CIT	A	1201	-	-	5/16/16/16	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1201	CIT	C4-C3	2.14	1.56	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	1201	CIT	O6-C6-C3	4.58	121.00	113.05
5	A	1201	CIT	O4-C5-C4	2.51	122.41	114.35

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1201	CIT	C2-C3-C4-C5
5	A	1201	CIT	O7-C3-C4-C5
5	A	1201	CIT	C6-C3-C4-C5
5	A	1201	CIT	C3-C4-C5-O4
5	A	1201	CIT	C3-C4-C5-O3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1201	CIT	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

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^{th} 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	1077/1101 (97%)	0.37	53 (4%) 29 27	31, 56, 108, 162	0
2	B	43/43 (100%)	0.04	4 (9%) 8 5	37, 49, 92, 130	2 (4%)
3	C	28/40 (70%)	0.09	0 100 100	35, 47, 97, 128	0
4	D	23/40 (57%)	0.32	2 (8%) 10 7	40, 61, 130, 158	3 (13%)
All	All	1171/1224 (95%)	0.35	59 (5%) 28 26	31, 56, 110, 162	5 (0%)

The worst 5 of 59 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	392	ALA	7.7
1	A	403	ILE	7.0
1	A	393	SER	5.6
1	A	405	VAL	5.3
1	A	395	SER	5.1

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

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

6.3 Carbohydrates

There are no monosaccharides 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. The B-factors column lists the minimum, median, 95^{th} 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^2)	Q<0.9
5	CIT	A	1201	13/13	0.91	0.14	51,62,87,89	0

6.5 Other polymers (i)

There are no such residues in this entry.